Androgen Receptor and Glucocorticoid Receptor Interaction Study

Marko Laakso Biswajyoti Sahu Kristian Ovaska Olli A. Jänne Sampsa Hautaniemi

June 11, 2012

Abstract

This document is generated by Anduril [11] (Engine 1.2.11) and it provides a human readable summary for the network outputs.

Contents

1 Expression analysis for DHTDEX 6

2 Illumina quality control (raw) 7
- 2.1 Density plot . . . 7
- 2.2 Box plot . . . 9
- 2.3 Scatter plot . . . 10
- 2.4 MAXY-plot . . . 13
- 2.5 Sample relations (hierarchical clustering) . . . 17

3 Illumina quality control (normalized) 18
- 3.1 Density plot . . . 18
- 3.2 Box plot . . . 19
- 3.3 Scatter plot . . . 20
- 3.4 MAXY-plot . . . 23
- 3.5 Sample relations (hierarchical clustering) . . . 27

4 Summary of DEGs in DHTDEX 28

5 List of differentially expressed genes 28
- 5.1 Gene set: fcD_fcOver . . . 28
- 5.2 Gene set: fcD_fcUnder . . . 29
- 5.3 Gene set: fcDX_fcOver . . . 29
- 5.4 Gene set: fcDX_fcUnder . . . 30
- 5.5 Gene set: fcComb_fcOver . . . 30
- 5.6 Gene set: fcComb_fcUnder . . . 31
- 5.7 Gene set: fcD4_fcOver . . . 33
- 5.8 Gene set: fcD4_fcUnder . . . 33
- 5.9 Gene set: fcDX4_fcOver . . . 33
- 5.10 Gene set: fcDX4_fcUnder . . . 33
- 5.11 Gene set: fcCPA_fcOver . . . 33
- 5.12 Gene set: fcCPA_fcUnder . . . 34
- 5.13 Gene set: fcRU_fcOver . . . 34
- 5.14 Gene set: fcRU_fcUnder . . . 34
- 5.15 Gene set: fcCDX_fcOver . . . 34
- 5.16 Gene set: fcCDX_fcUnder . . . 35

6 Expression analysis for VCaP 36

7 Illumina quality control (raw) 37
- 7.1 Density plot . . . 37
- 7.2 Box plot . . . 38
- 7.3 Scatter plot . . . 39
- 7.4 MAXY-plot . . . 41
- 7.5 Sample relations (hierarchical clustering) . . . 43

8 Illumina quality control (normalized) 44
8.1 Density plot . . . 44
8.2 Box plot . . . 45
8.3 Scatter plot . . . 46
8.4 MAXY-plot . . . 48
8.5 Sample relations (hierarchical clustering) . . . 50

9 Summary of DEGs in VCaP 51

10 List of differentially expressed genes 51
10.1 Gene set: fcDv_fcOver . . . 51
10.2 Gene set: fcDv_fcUnder . . . 51
10.3 Gene set: fcDXv_fcOver . . . 52
10.4 Gene set: fcDXv_fcUnder . . . 52

11 Candidate report for DEG DHT CPA RU486 53
11.1 Moksiskaan candidate pathway . . . 53
11.1.1 GO enrichment of the candidate pathway . . . 67
11.2 Candidate genes . . . 83

12 Candidate report for DHT and DEX 85
12.1 Moksiskaan candidate pathway . . . 85
12.2 Candidate genes . . . 86
12.2.1 GO enrichment of all candidates . . . 95

13 Candidate report for DHT no DEX 99
13.1 Moksiskaan candidate pathway . . . 99
13.1.1 GO enrichment of the candidate pathway . . . 101
13.2 Candidate genes . . . 102

14 Candidate report for DEX no DHT 113
14.1 Moksiskaan candidate pathway . . . 113
14.1.1 GO enrichment of the candidate pathway . . . 115
14.2 Candidate genes . . . 119
14.2.1 GO enrichment of all candidates . . . 139

15 ChIP-seq peaks 144
15.1 AR DHT overlaps . . . 145
15.2 AR DHT overlaps (up) . . . 147
15.3 AR DHT overlaps (down) . . . 149
15.4 AR DHT overlaps (stable) . . . 151
15.5 AR CPA overlaps . . . 153
15.6 AR CPA overlaps (up) . . . 155
15.7 AR CPA overlaps (down) . . . 157

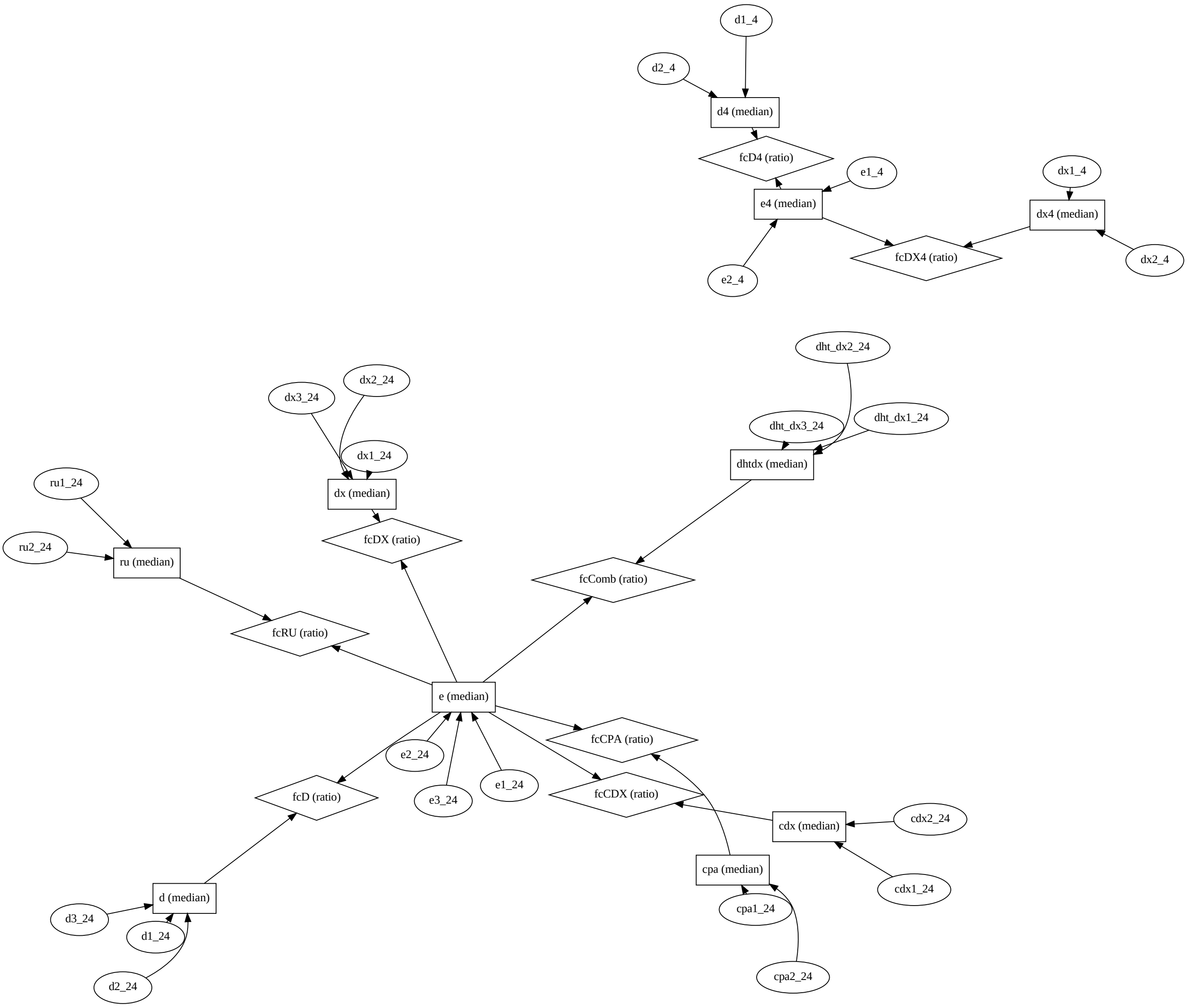
15.8 AR CPA overlaps (stable) . . . 159
15.9 AR RU486 overlaps . . . 161
15.10 AR RU486 overlaps (up) . . . 163
15.11 AR RU486 overlaps (down) . . . 165
15.12 AR RU486 overlaps (stable) . . . 167
15.13 AR DHT vs AR CPA overlaps . . . 169
15.14 AR DHT vs AR CPA overlaps (up) . . . 171
15.15 AR DHT vs AR CPA overlaps (down) . . . 173
15.16 AR DHT vs AR CPA overlaps (stable) . . . 175
15.17 AR DHT vs AR CPA unique for ARDHTrrO . . . 177
15.18 AR DHT vs AR CPA unique for ARDHTrrO (up) . . . 179
15.19 AR DHT vs AR CPA unique for ARDHTrrO (down) . . . 181
15.20 AR DHT vs AR CPA unique for ARDHTrrO (stable) . . . 183
15.21 AR DHT vs AR CPA unique for ARCPArrO . . . 185
15.22 AR DHT vs AR CPA unique for ARCPArrO (up) . . . 187
15.23 AR DHT vs AR CPA unique for ARCPArrO (down) . . . 189
15.24 AR DHT vs AR CPA unique for ARCPArrO (stable) . . . 191
15.25 AR DHT vs AR RU486 overlaps . . . 193
15.26 AR DHT vs AR RU486 overlaps (up) . . . 195
15.27 AR DHT vs AR RU486 overlaps (down) . . . 197
15.28 AR DHT vs AR RU486 overlaps (stable) . . . 199
15.29 AR DHT vs AR RU486 unique for ARDHTrrO . . . 201
15.30 AR DHT vs AR RU486 unique for ARDHTrrO (up) . . . 203
15.31 AR DHT vs AR RU486 unique for ARDHTrrO (down) . . . 205
15.32 AR DHT vs AR RU486 unique for ARDHTrrO (stable) . . . 207
15.33 AR DHT vs AR RU486 unique for ARRU486rrO . . . 209
15.34 AR DHT vs AR RU486 unique for ARRU486rrO (up) . . . 211
15.35 AR DHT vs AR RU486 unique for ARRU486rrO (down) . . . 213
15.36 AR DHT vs AR RU486 unique for ARRU486rrO (stable) . . . 215
15.37 AR CPA vs AR RU486 overlaps . . . 217
15.38 AR CPA vs AR RU486 overlaps (up) . . . 219
15.39 AR CPA vs AR RU486 overlaps (down) . . . 221
15.40 AR CPA vs AR RU486 overlaps (stable) . . . 223
15.41 AR CPA vs AR RU486 unique for ARCPArrO . . . 225
15.42 AR CPA vs AR RU486 unique for ARCPArrO (up) . . . 227
15.43 AR CPA vs AR RU486 unique for ARCPArrO (down) . . . 229
15.44 AR CPA vs AR RU486 unique for ARCPArrO (stable) . . . 231
15.45 AR CPA vs AR RU486 unique for ARRU486rrO . . . 233
15.46 AR CPA vs AR RU486 unique for ARRU486rrO (up) . . . 235
15.47 AR CPA vs AR RU486 unique for ARRU486rrO (down) . . . 237
15.48 AR CPA vs AR RU486 unique for ARRU486rrO (stable) . . . 239

15.49GR DEX overlaps . . . 241
15.50GR DEX overlaps (up) . . . 243
15.51GR DEX overlaps (down) . . . 245
15.52GR DEX overlaps (stable) . . . 247
15.53AR DHT vs GR DEX overlaps . . . 249
15.54AR DHT vs GR DEX overlaps (up) . . . 251
15.55AR DHT vs GR DEX overlaps (down) . . . 253
15.56AR DHT vs GR DEX overlaps (stable) . . . 255
15.57AR DHT vs GR DEX unique for ARDHTrrO . . . 257
15.58AR DHT vs GR DEX unique for ARDHTrrO (up) . . . 259
15.59AR DHT vs GR DEX unique for ARDHTrrO (down) . . . 261
15.60AR DHT vs GR DEX unique for ARDHTrrO (stable) . . . 263
15.61AR DHT vs GR DEX unique for GRDEXrrO . . . 265
15.62AR DHT vs GR DEX unique for GRDEXrrO (up) . . . 267
15.63AR DHT vs GR DEX unique for GRDEXrrO (down) . . . 269
15.64AR DHT vs GR DEX unique for GRDEXrrO (stable) . . . 271
15.65AR LNCaP vs VCaP DHT overlaps . . . 273
15.66AR LNCaP vs VCaP DHT overlaps (up) . . . 275
15.67AR LNCaP vs VCaP DHT overlaps (down) . . . 277
15.68AR LNCaP vs VCaP DHT overlaps (stable) . . . 279
15.69AR LNCaP vs VCaP DHT unique for ARDHTrrO . . . 281
15.70AR LNCaP vs VCaP DHT unique for ARDHTrrO (up) . . . 283
15.71AR LNCaP vs VCaP DHT unique for ARDHTrrO (down) . . . 285
15.72AR LNCaP vs VCaP DHT unique for ARDHTrrO (stable) . . . 287
15.73AR LNCaP vs VCaP DHT unique for ARvcap . . . 289
15.74AR LNCaP vs VCaP DHT unique for ARvcap (up) . . . 291
15.75AR LNCaP vs VCaP DHT unique for ARvcap (down) . . . 293
15.76AR LNCaP vs VCaP DHT unique for ARvcap (stable) . . . 295
15.77GR LNCaP vs VCaP DEX overlaps . . . 297
15.78GR LNCaP vs VCaP DEX overlaps (up) . . . 299
15.79GR LNCaP vs VCaP DEX overlaps (down) . . . 301
15.80GR LNCaP vs VCaP DEX overlaps (stable) . . . 303
15.81GR LNCaP vs VCaP DEX unique for GRDEXrrO . . . 305
15.82GR LNCaP vs VCaP DEX unique for GRDEXrrO (up) . . . 307
15.83GR LNCaP vs VCaP DEX unique for GRDEXrrO (down) . . . 309
15.84GR LNCaP vs VCaP DEX unique for GRDEXrrO (stable) . . . 311
15.85GR LNCaP vs VCaP DEX unique for GRvcap . . . 313
15.86GR LNCaP vs VCaP DEX unique for GRvcap (up) . . . 316
15.87GR LNCaP vs VCaP DEX unique for GRvcap (down) . . . 318
15.88GR LNCaP vs VCaP DEX unique for GRvcap (stable) . . . 320
15.89R configuration . . . 335
15.90System configurations . . . 335

1 Expression analysis for DHTDEX

Group	Definition	Description
fcD	ratio(d/e)	DHT 24h samples divided by their controls
fcDX	ratio(dx/e)	Dex 24h samples divided by their controls
fcComb	ratio(dhtdx/e)	combined 24h samples divided by their controls
fcD4	ratio(d4/e4)	DHT 4h samples divided by their controls
fcDX4	ratio(dx4/e4)	Dex 4h samples divided by their controls
fcCPA	ratio(cpa/e)	Cyproterone asetate 24h samples divided by their controls
fcRU	ratio(ru/e)	RU486 24h samples divided by their controls
fcCDX	ratio(cdx/e)	Casodex 24h samples divided by their controls
e	median(e1_24, e2_24, e3_24)	controls 24h
d	median(d1_24, d2_24, d3_24)	DHT cases 24h
dx	median(dx1_24, dx2_24, dx3_24)	dexamethasone cases 24h
dhtdx	median(dht_dx1_24, dht_dx2_24, dht_dx3_24)	combined cases 24h
e4	median(e1_4, e2_4)	controls 4h
d4	median(d1_4, d2_4)	DHT cases 4h
dx4	median(dx1_4, dx2_4)	dexamethasone cases 4h
cpa	median(cpa1_24, cpa2_24)	Cyproterone acetate (AR agonist) 24h
ru	median(ru1_24, ru2_24)	RU486 (partial agonist/antagonist) cases 24h
cdx	median(cdx1_24, cdx2_24)	Casodex (antagonist) cases 24h

Table 1: Sample groups



2 Illumina quality control (raw)

2.1 Density plot

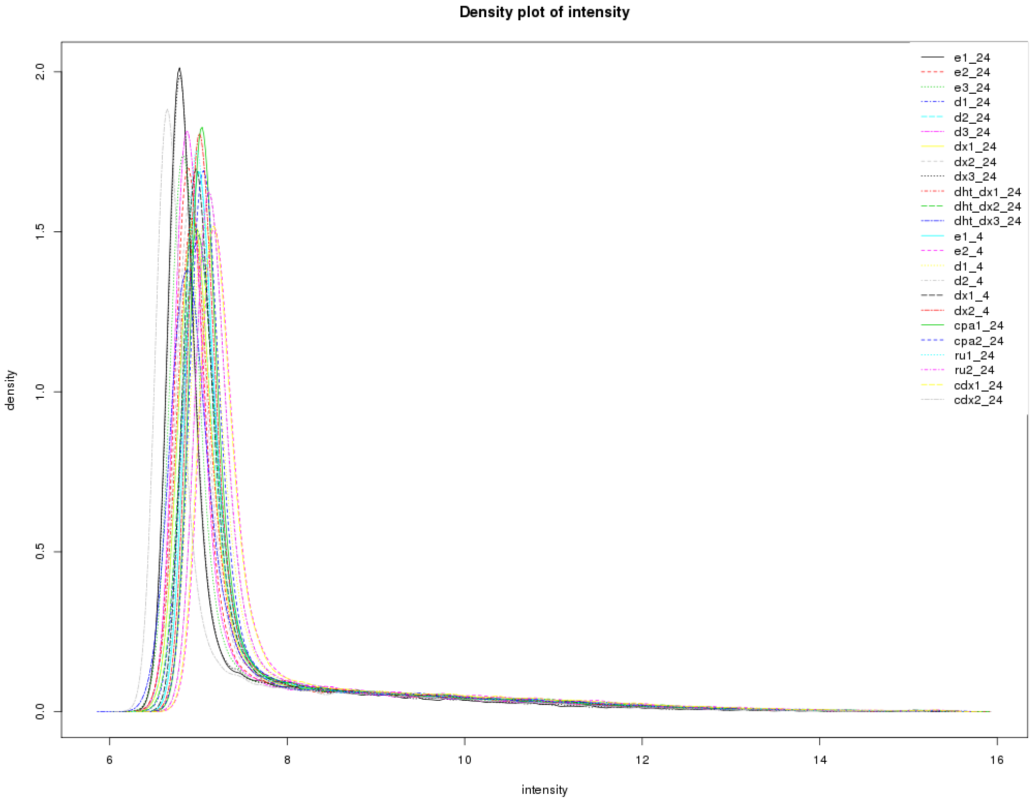


Figure 1: Density plot indicates the distribution of variables.

2.2 Box plot

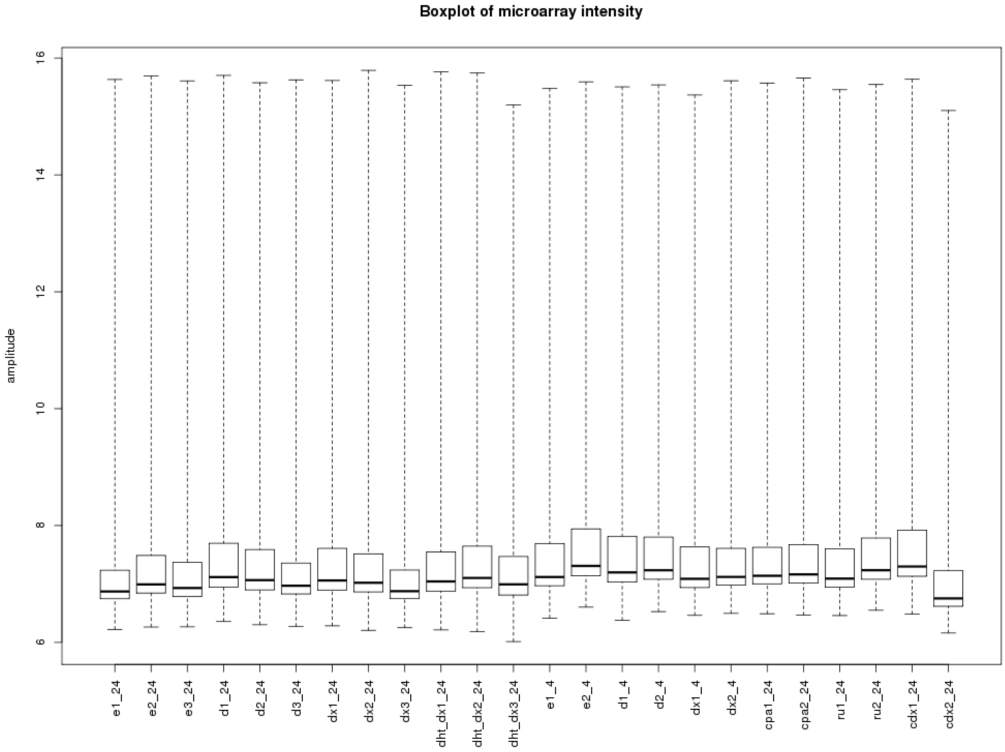


Figure 2: The bold line shows the location of median. The filled rectangle contains values between 25'th and 75'th percentile. The extremes show locations of minimum and maximum.

2.3 Scatter plot

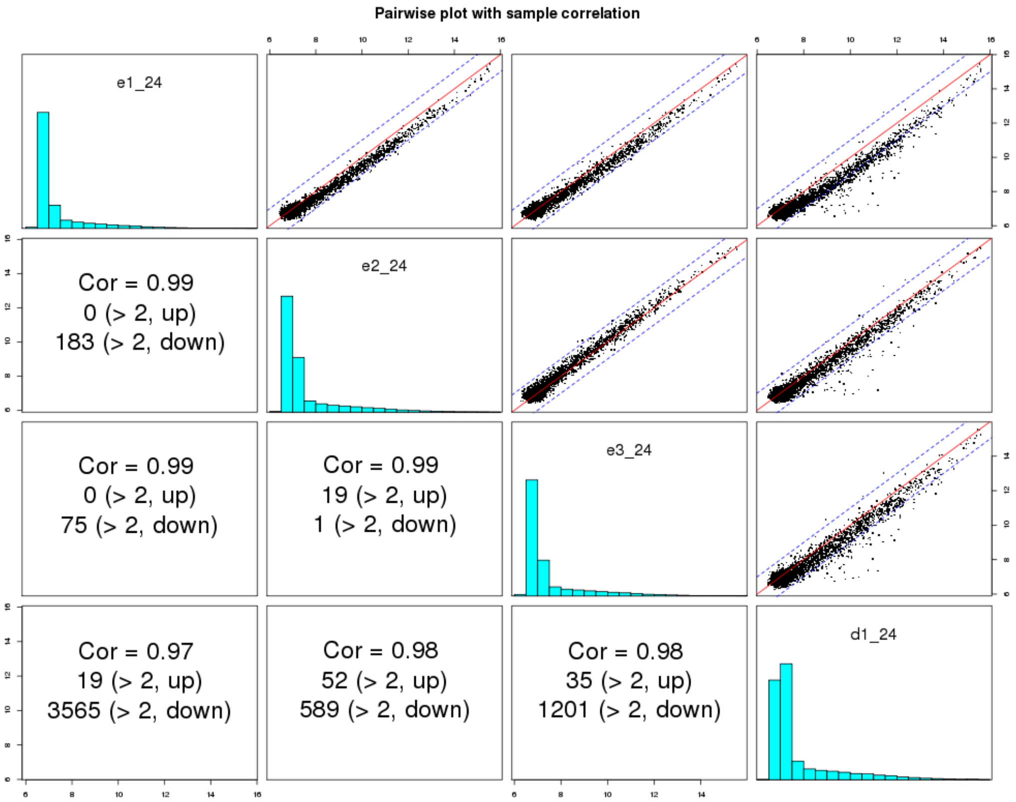


Figure 3: Scatter plot illustrates the degree of sample correlation.

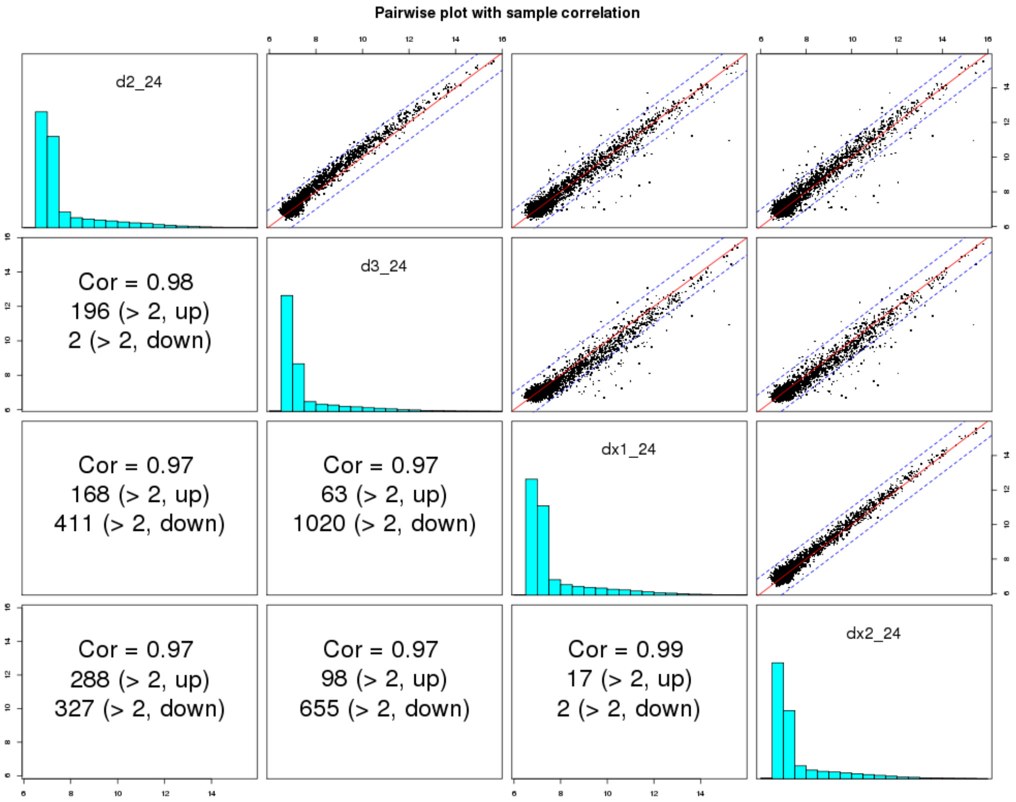


Figure 4: Scatter plot illustrates the degree of sample correlation.

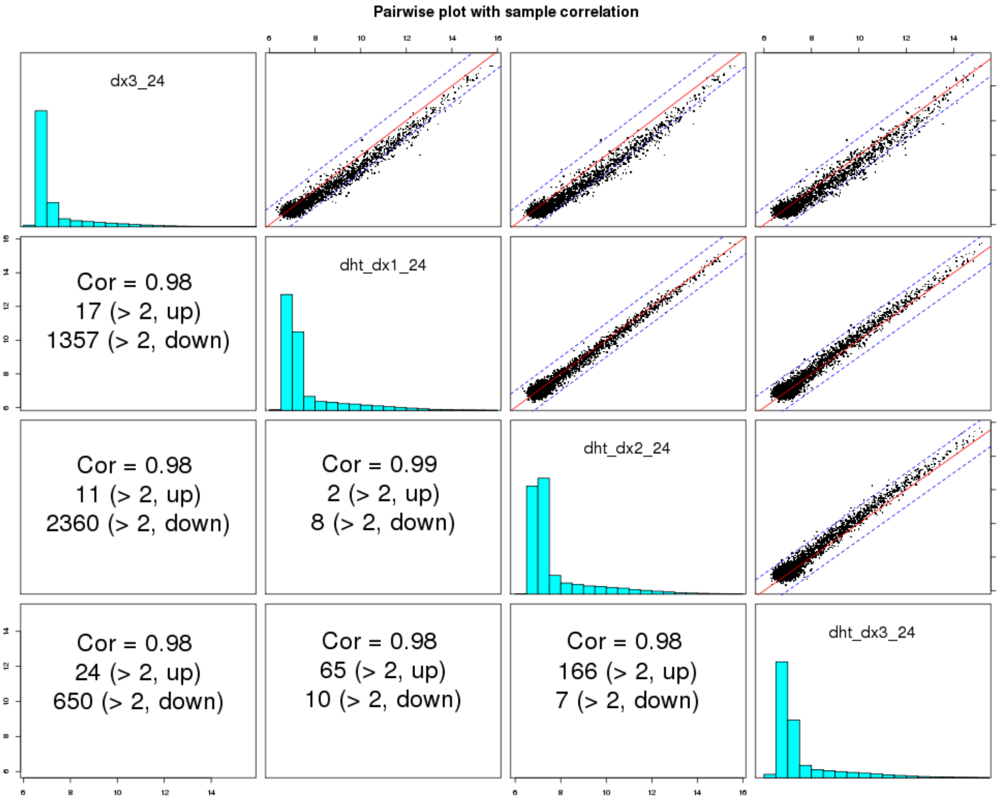


Figure 5: Scatter plot illustrates the degree of sample correlation.

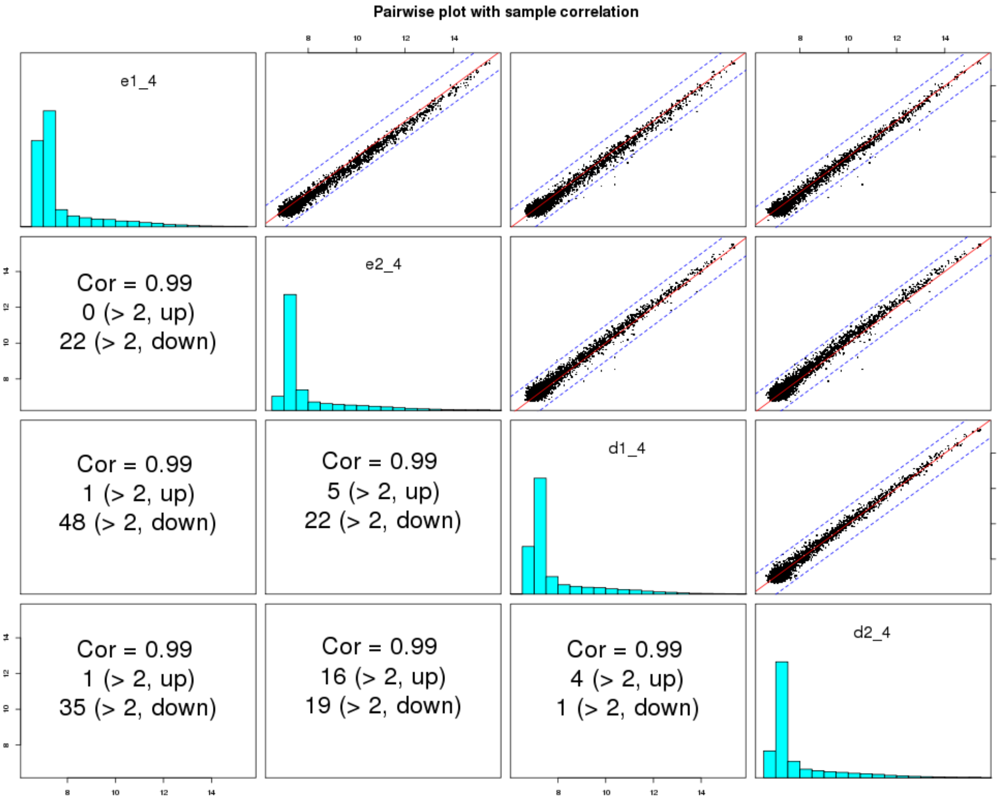


Figure 6: Scatter plot illustrates the degree of sample correlation.

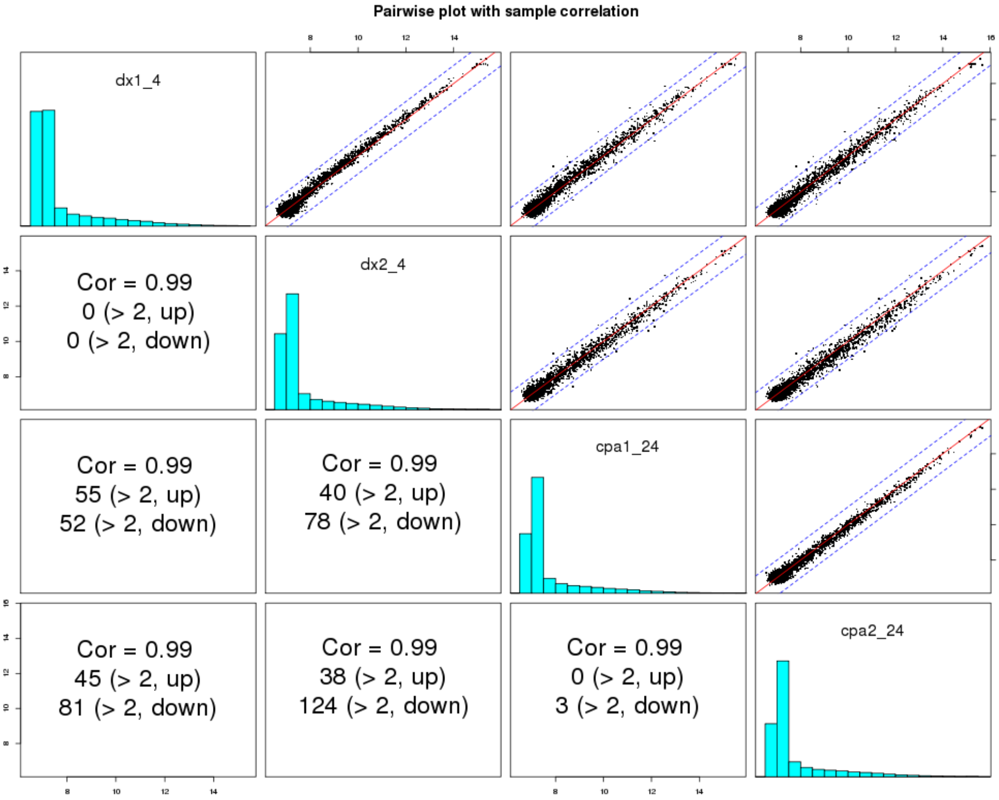


Figure 7: Scatter plot illustrates the degree of sample correlation.

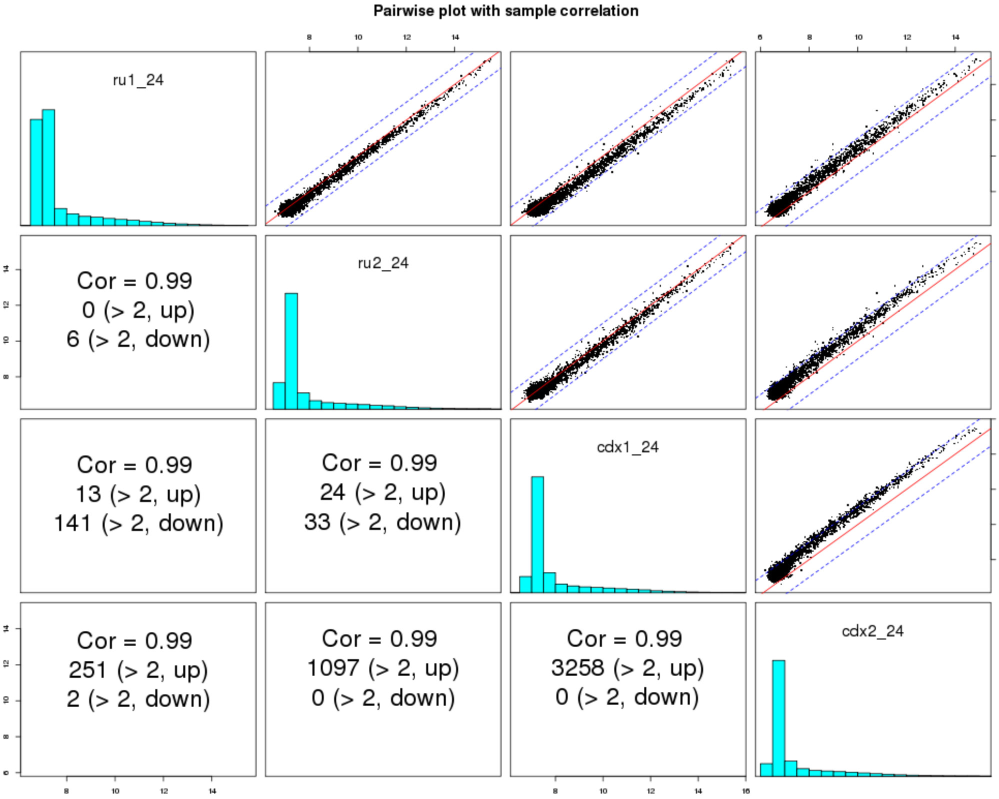


Figure 8: Scatter plot illustrates the degree of sample correlation.

2.4 MAXY-plot

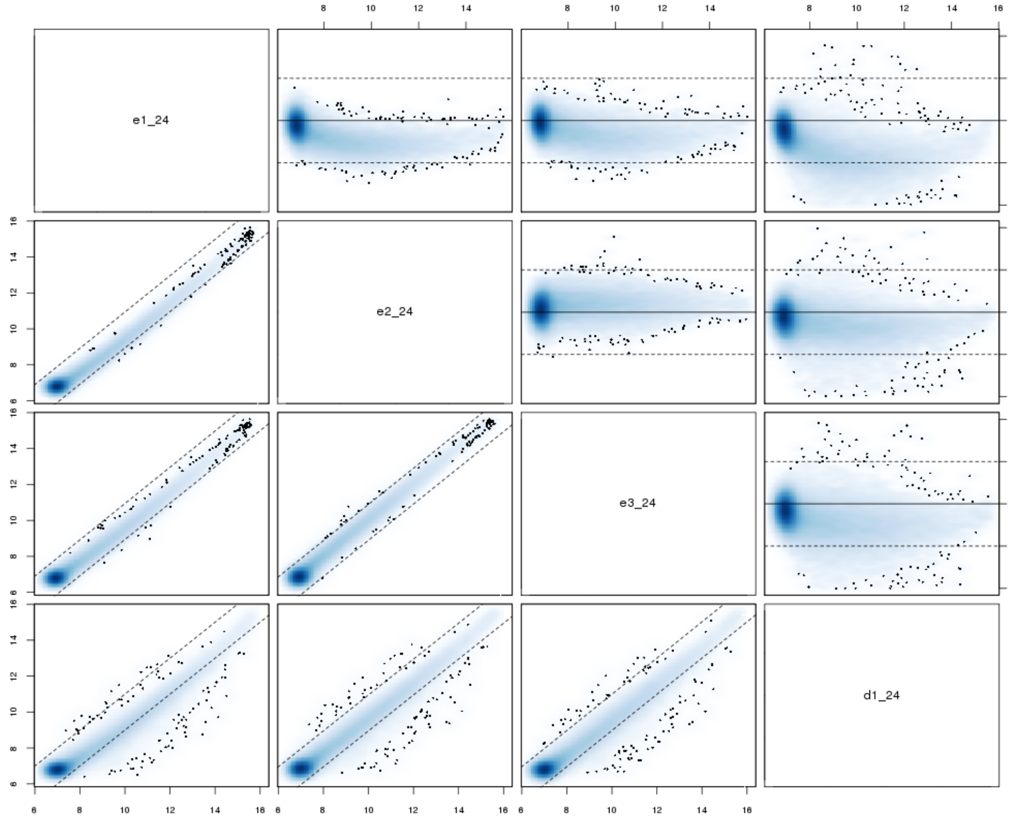


Figure 9: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

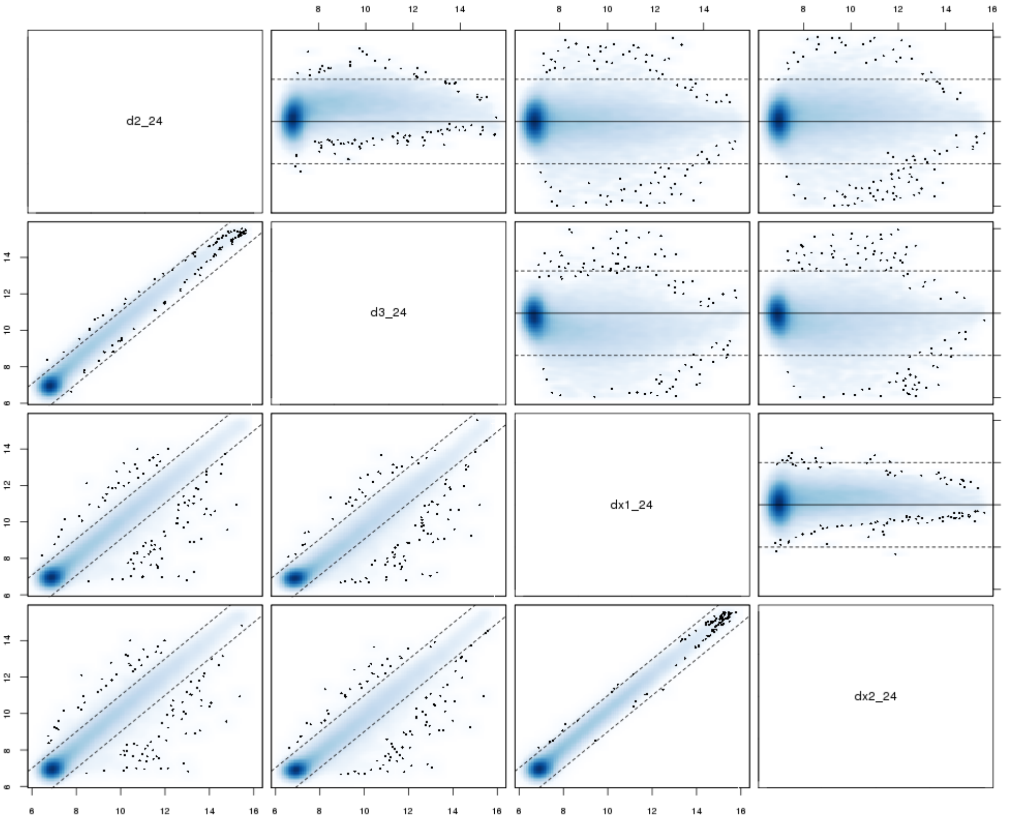


Figure 10: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

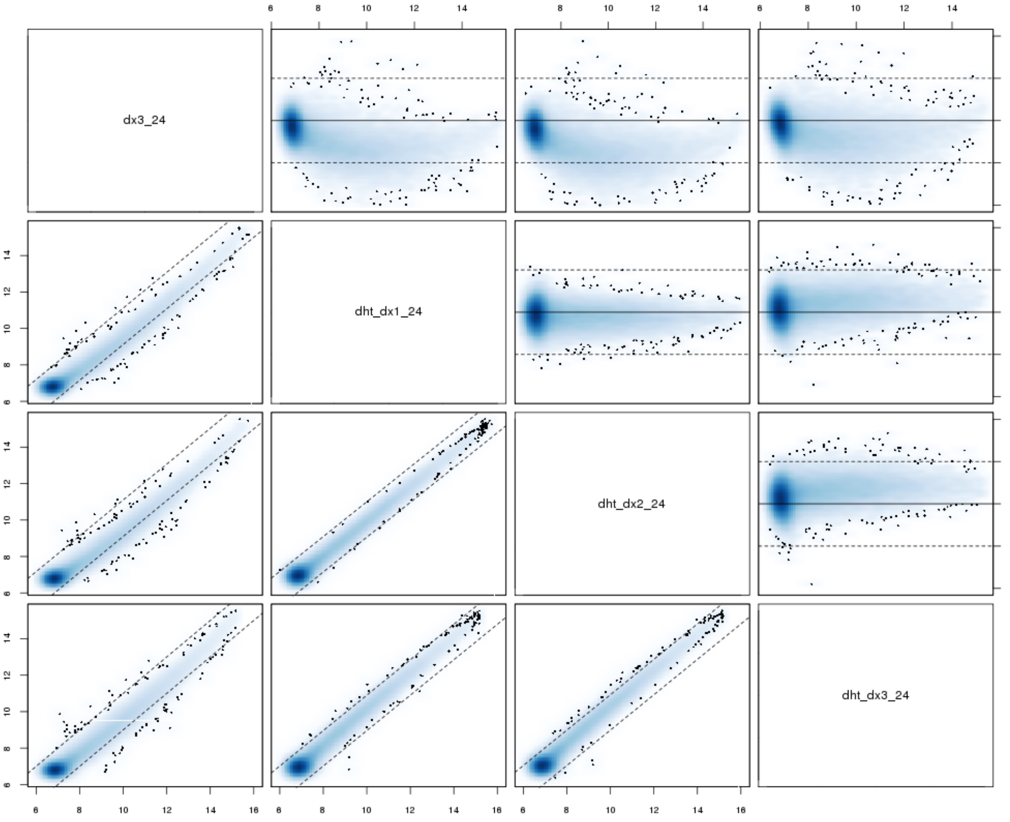


Figure 11: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

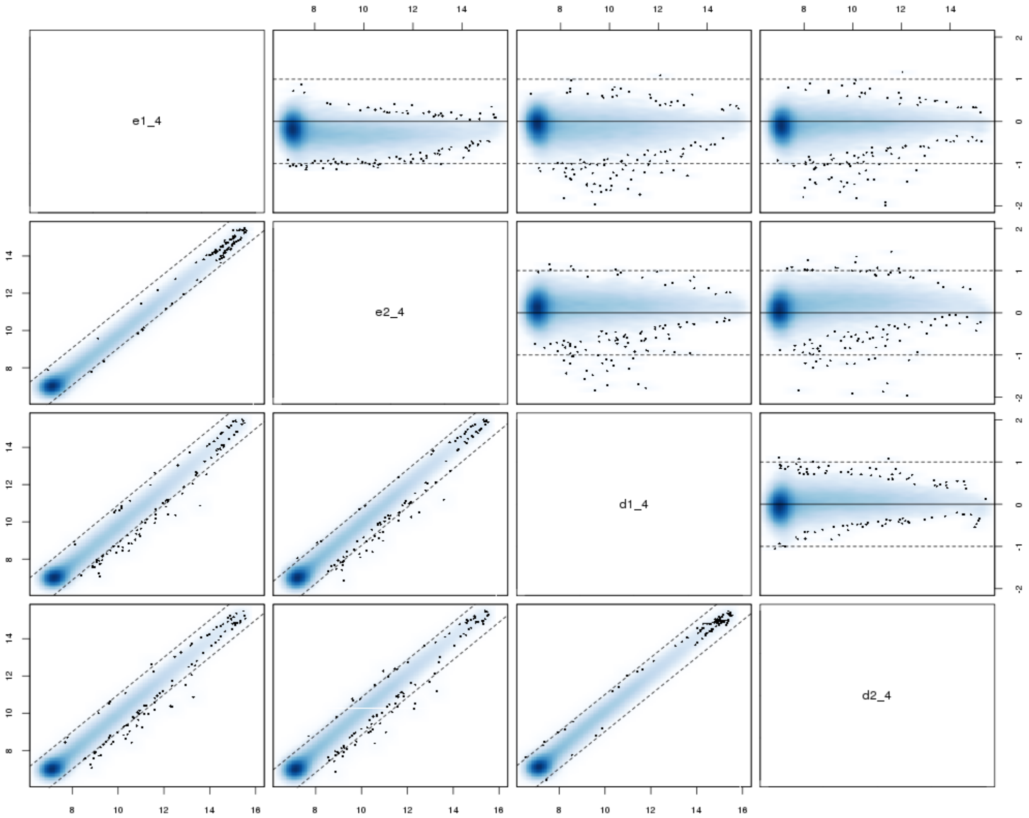


Figure 12: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

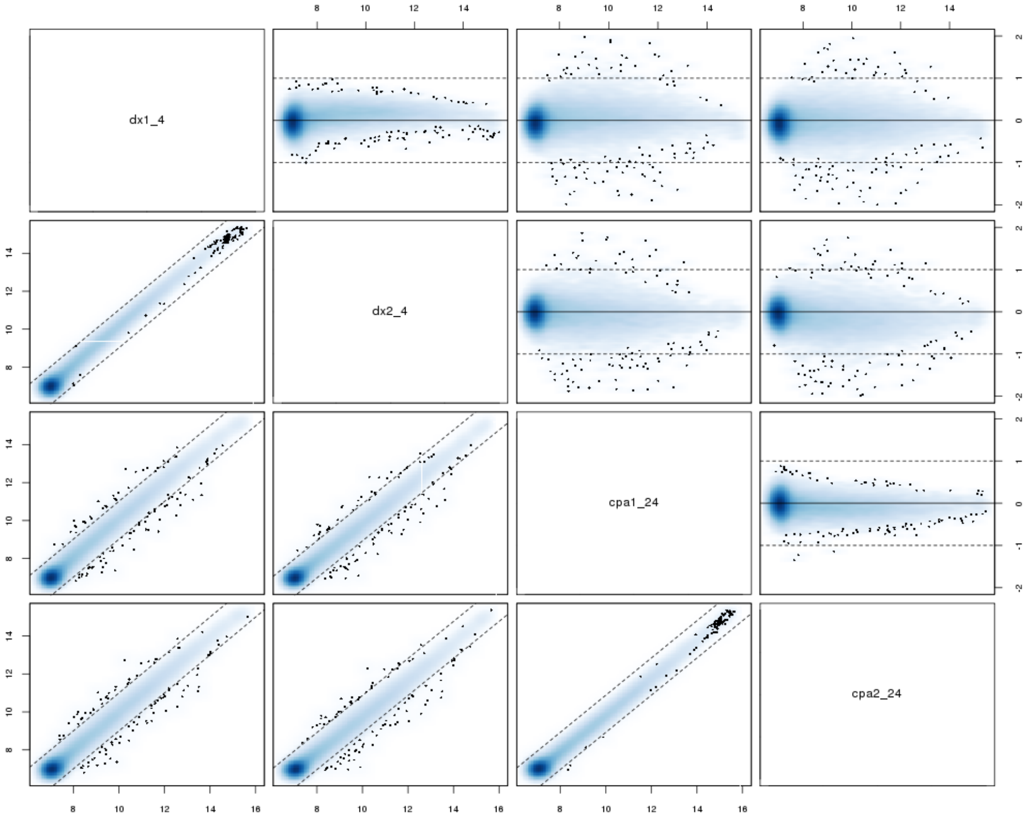


Figure 13: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

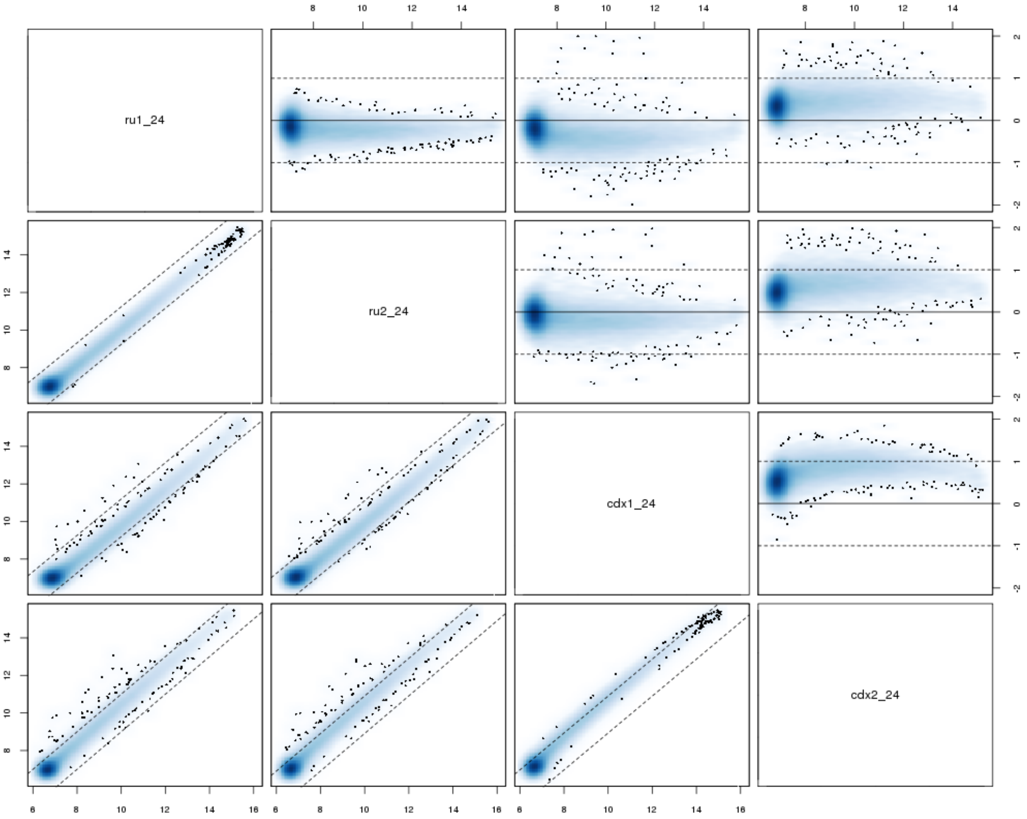


Figure 14: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

2.5 Sample relations (hierarchical clustering)

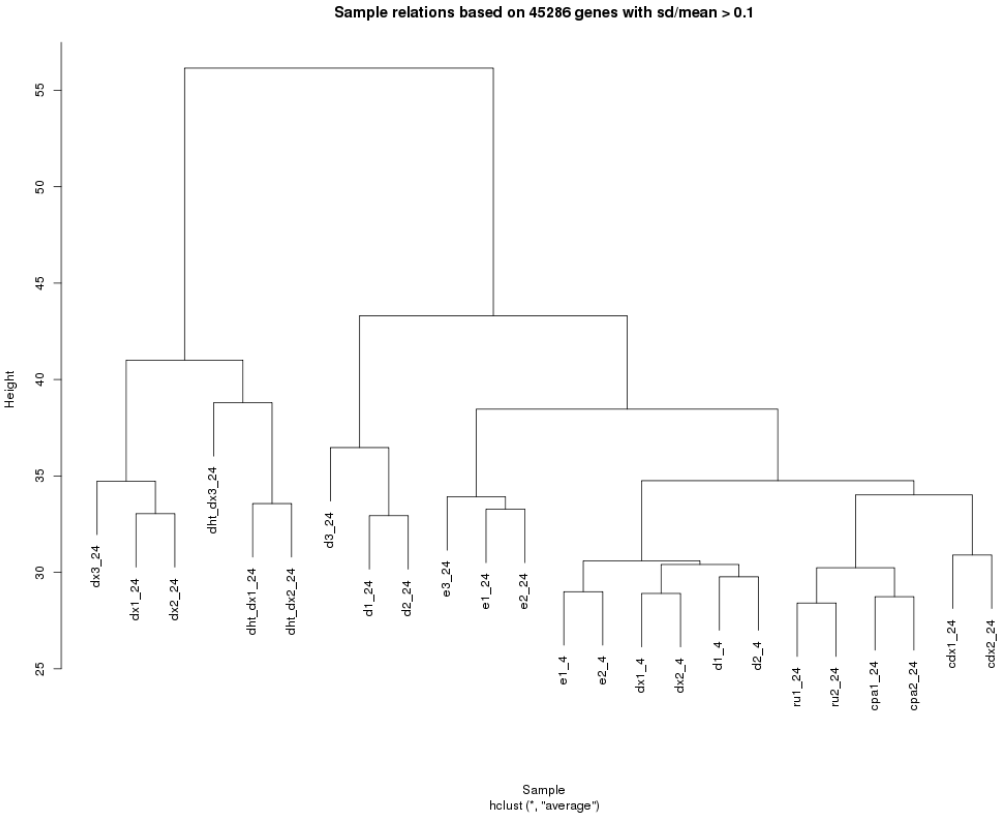


Figure 15: Hierarchical clustering is the assignment of a set of observations into subsets (clusters) so that observations in the same cluster are similar in some sense.

3 Illumina quality control (normalized)

3.1 Density plot

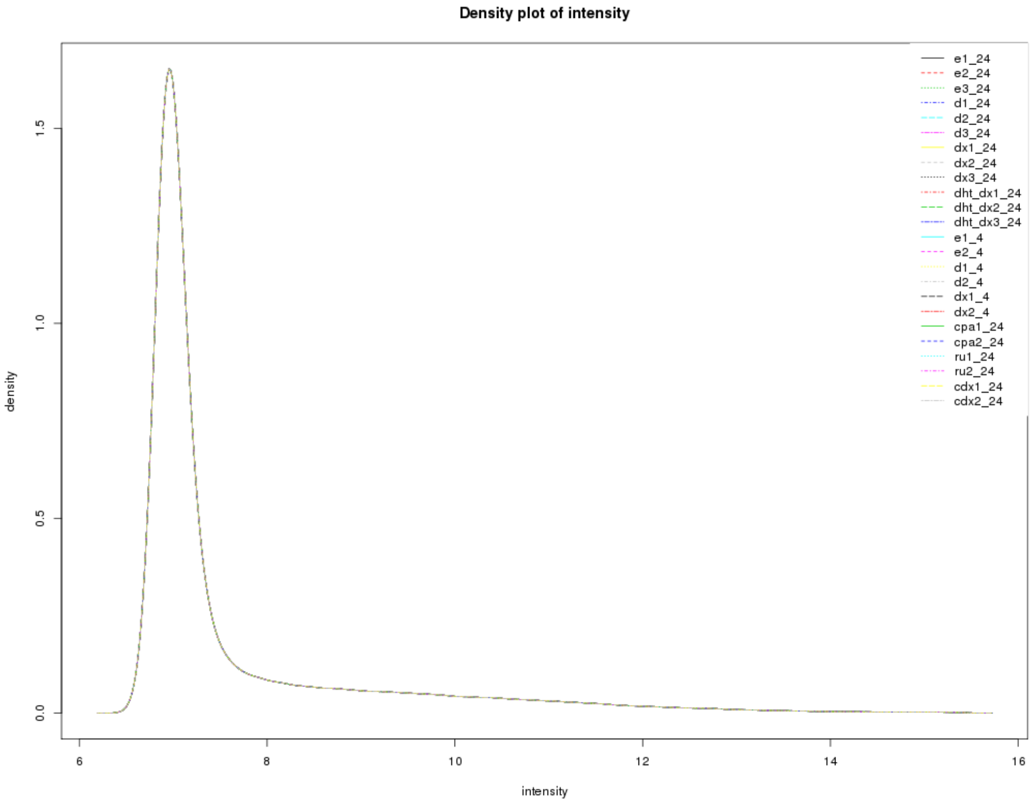


Figure 16: Density plot indicates the distribution of variables.

3.2 Box plot

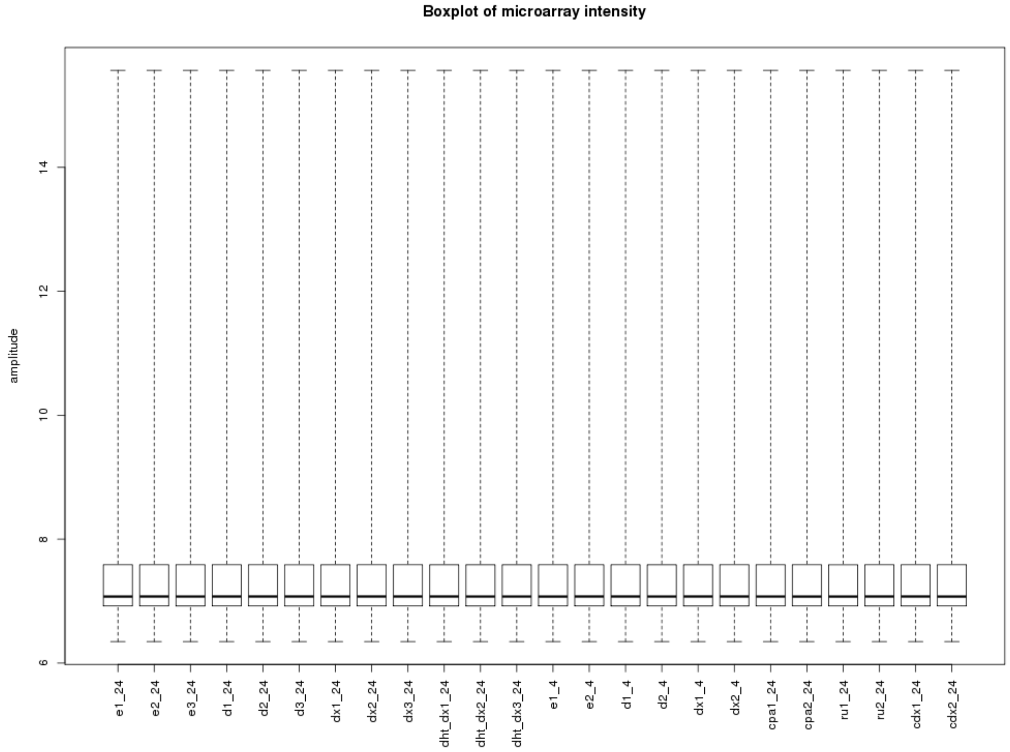


Figure 17: The bold line shows the location of median. The filled rectangle contains values between 25'th and 75'th percentile. The extremes show locations of minimum and maximum.

3.3 Scatter plot

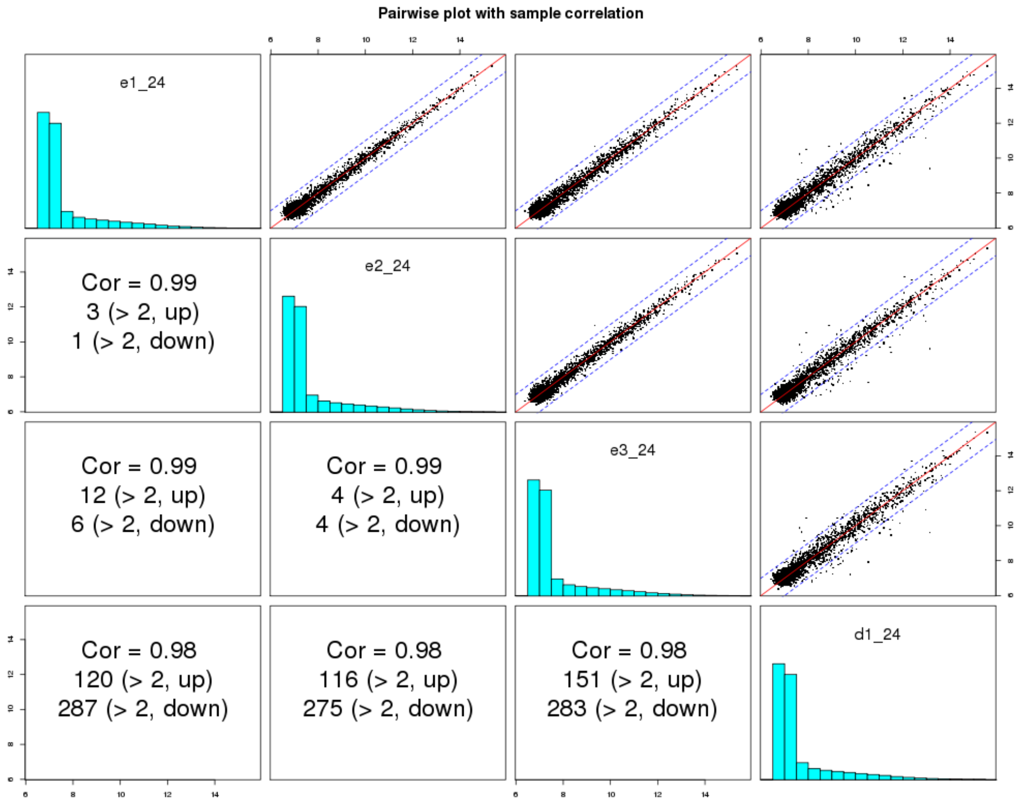


Figure 18: Scatter plot illustrates the degree of sample correlation.

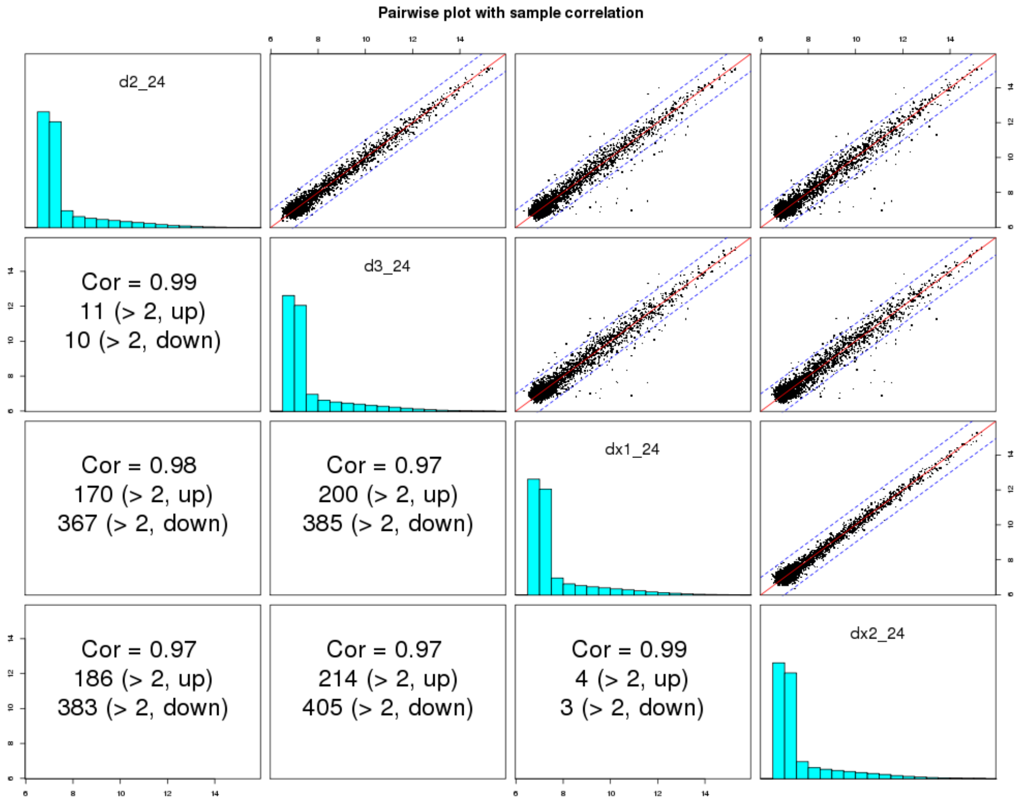


Figure 19: Scatter plot illustrates the degree of sample correlation.

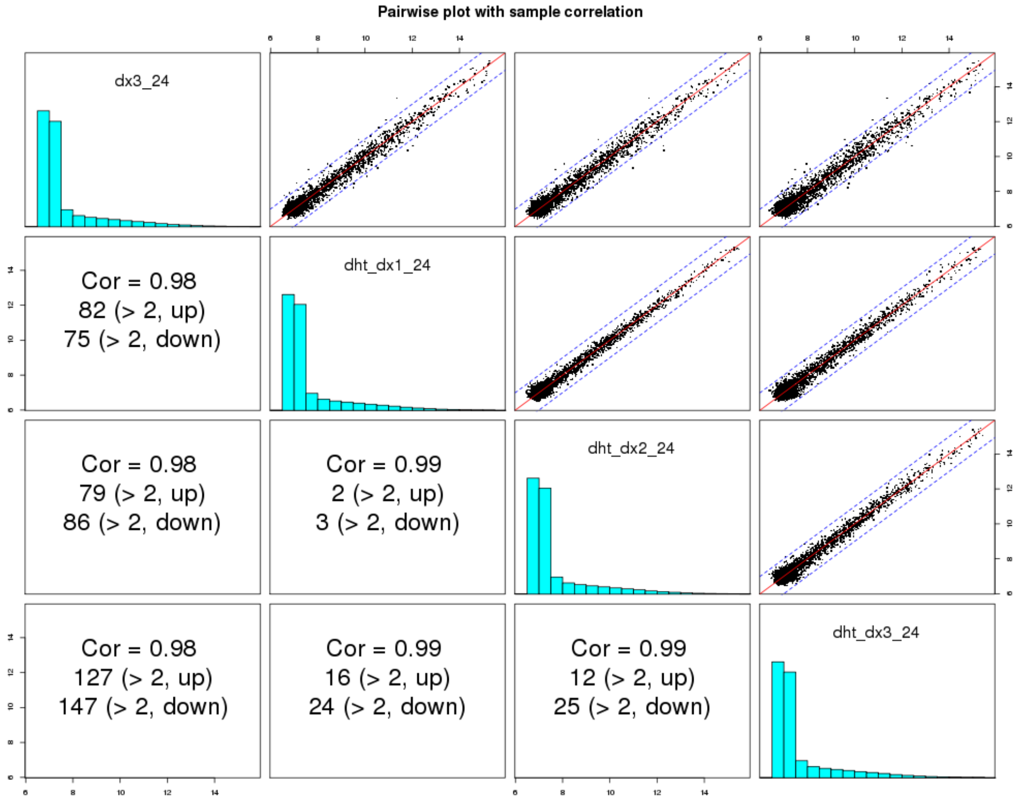


Figure 20: Scatter plot illustrates the degree of sample correlation.

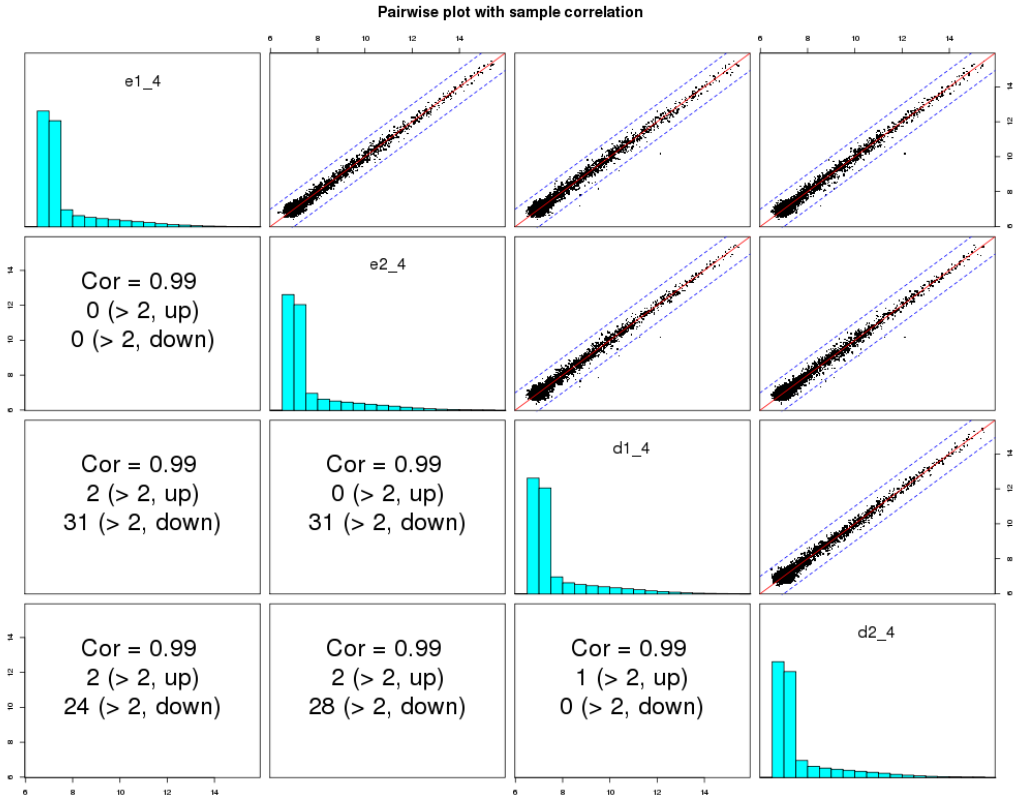


Figure 21: Scatter plot illustrates the degree of sample correlation.

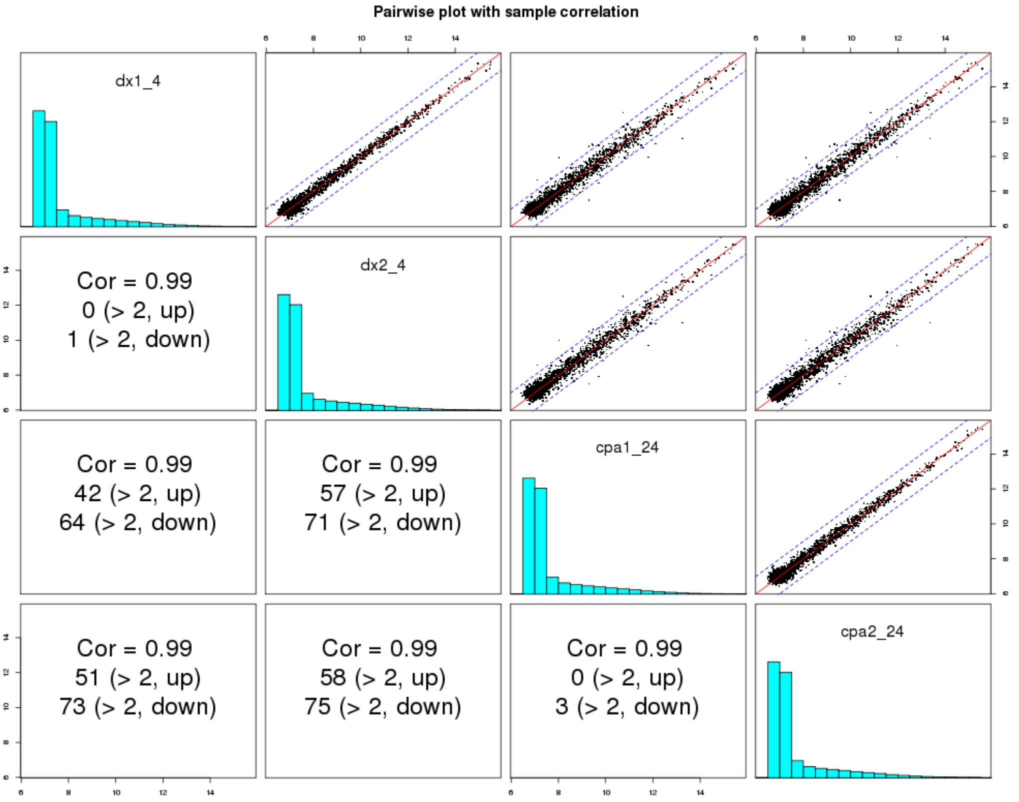


Figure 22: Scatter plot illustrates the degree of sample correlation.

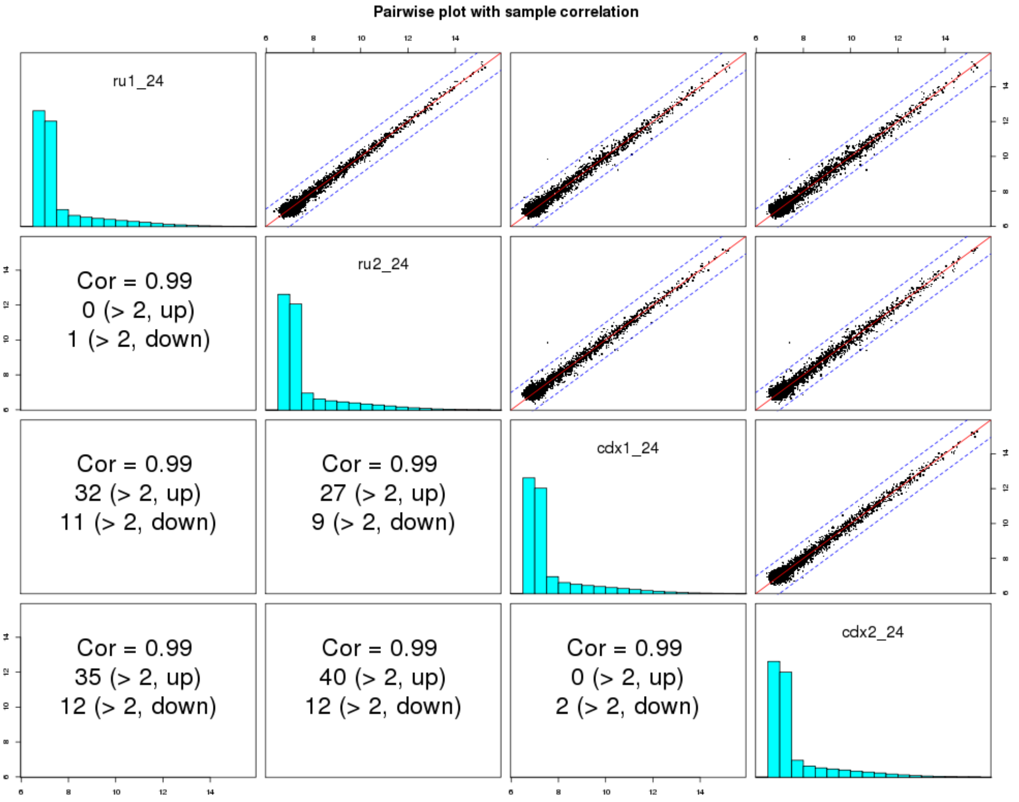


Figure 23: Scatter plot illustrates the degree of sample correlation.

3.4 MAXY-plot

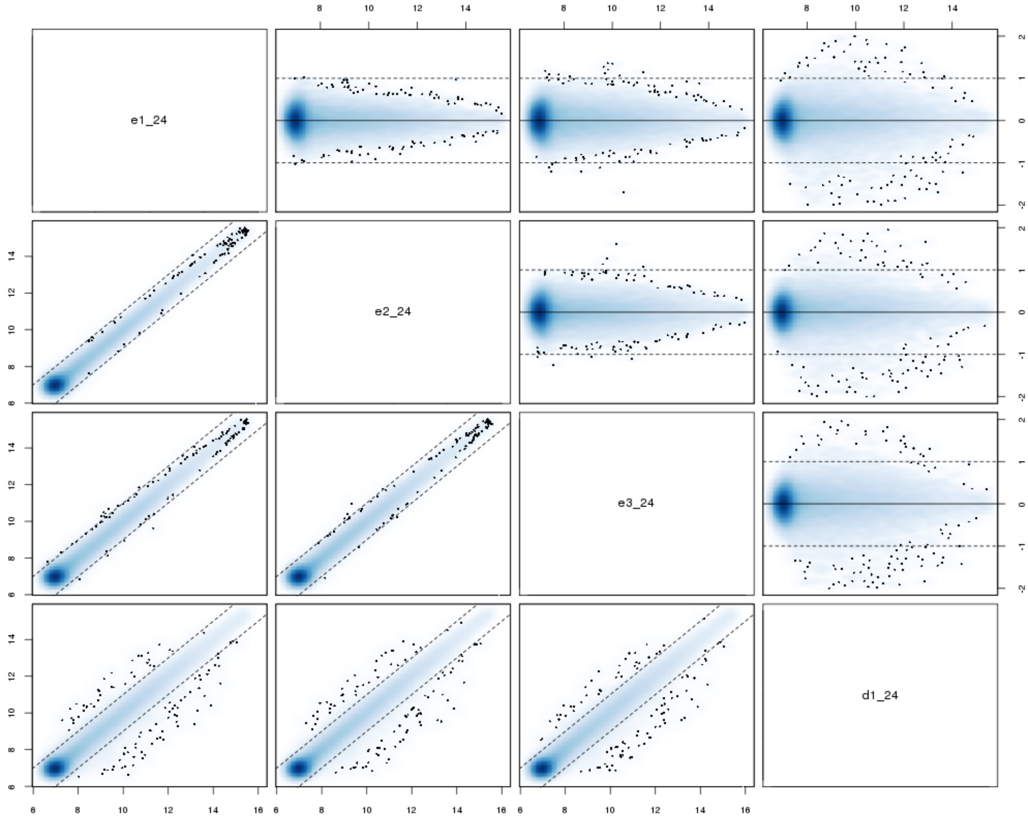


Figure 24: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

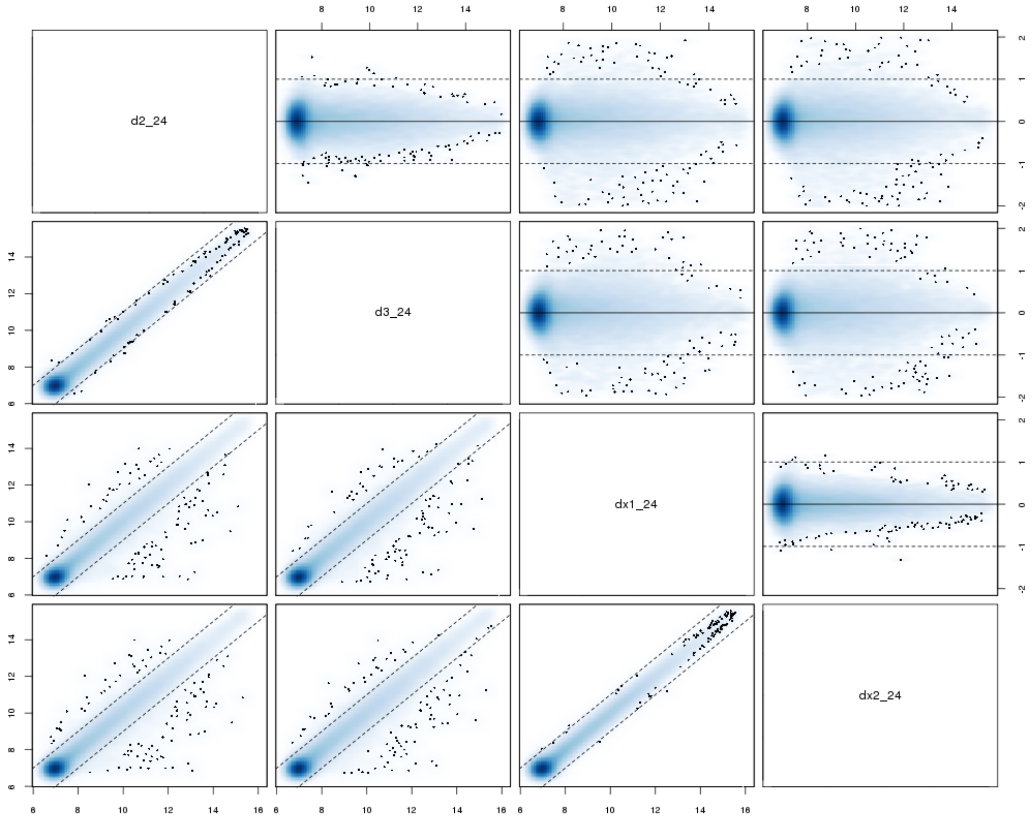


Figure 25: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

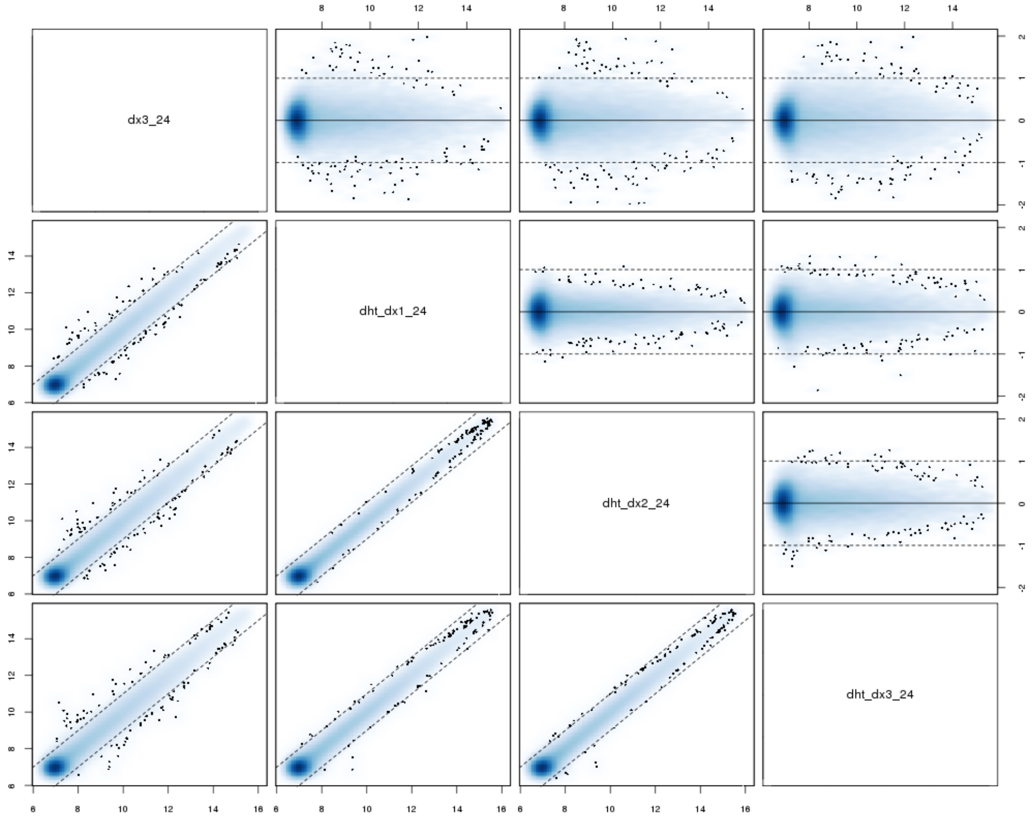


Figure 26: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

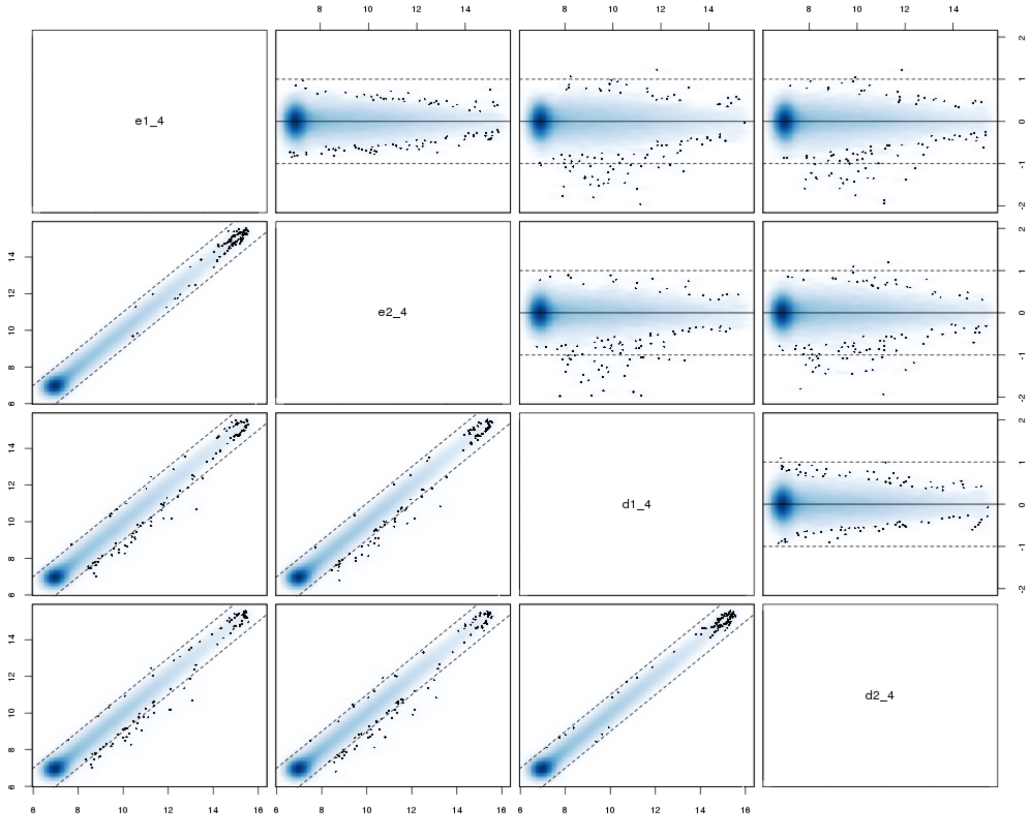


Figure 27: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

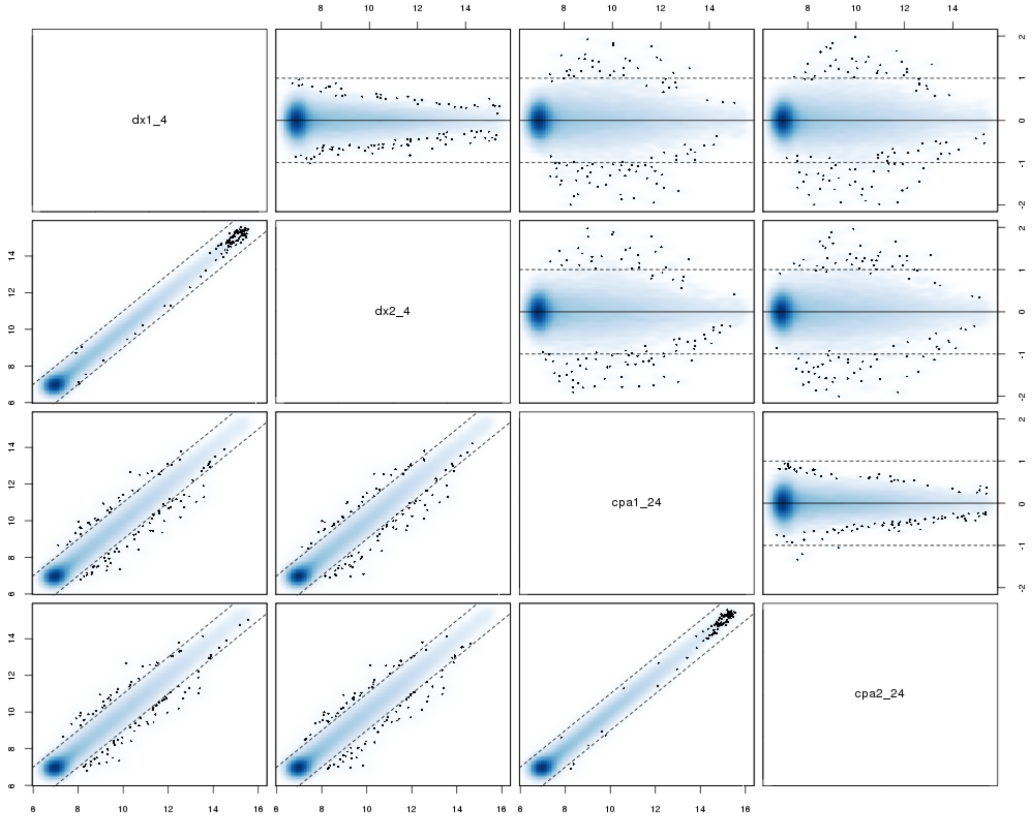


Figure 28: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

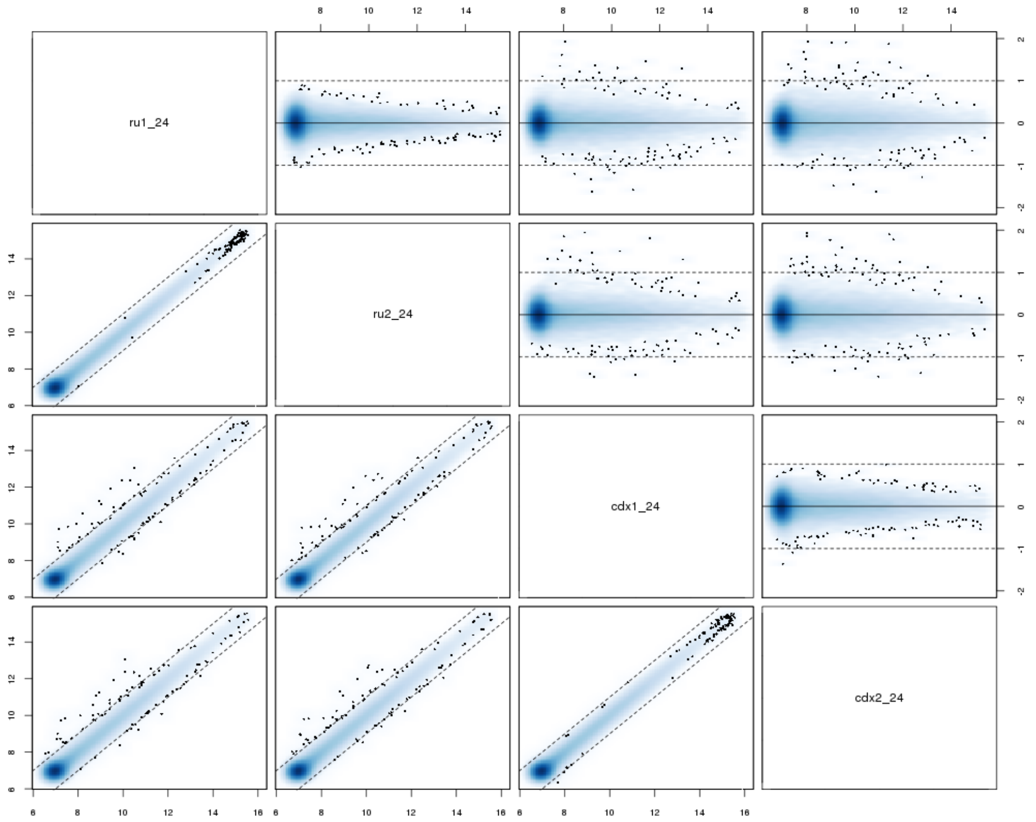


Figure 29: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

3.5 Sample relations (hierarchical clustering)

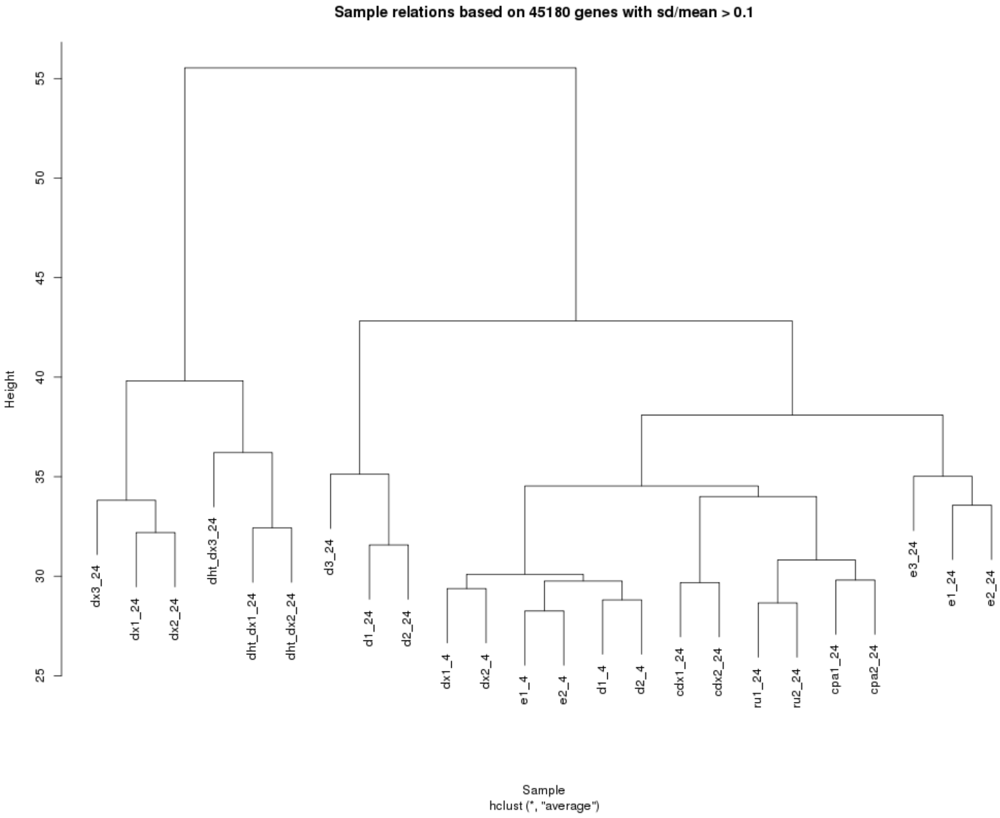


Figure 30: Hierarchical clustering is the assignment of a set of observations into subsets (clusters) so that observations in the same cluster are similar in some sense.

4 Summary of DEGs in DHTDEX

Gene set	Size
fcD_fcOver	246
fcD_fcUnder	146
fcDX_fcOver	417
fcDX_fcUnder	120
fcComb_fcOver	719
fcComb_fcUnder	643
fcD4_fcOver	29
fcD4_fcUnder	2
fcDX4_fcOver	26
fcDX4_fcUnder	0
fcCPA_fcOver	172
fcCPA_fcUnder	85
fcRU_fcOver	127
fcRU_fcUnder	28
fcCDX_fcOver	124
fcCDX_fcUnder	9

5 List of differentially expressed genes

Overexpressed genes are sorted with the most overexpressed first and underexpressed genes with the most underexpressed first. Genes go by the column first and then by row.

5.1 Gene set: fcD_fcOver

Number of genes: 246

FKBP5
SLC45A3
PGC
TMEFF2
NDRG1
SAT1
ST6GALNAC1
EAF2
UGT2B28
ELL2P1
ELL2
SOCS2
TMPRSS2
TUBA3D
SNAI2
MICAL1
PCDH20
INPP4B
HPGD
ERRFI1
TM4SF1
S100P
PMEPA1
LRIG1
STK39
NBL1
HERC5
ABCC4
ZNF385B
NCAPD3
SORD
TSKU
ELOVL5
UGT2B11
SLC41A1
ELOVL2
LPAR3
TMEM79
SPDEF
PPAP2A
PTGER4
PHGR1
C3orf58
ZBTB16
PRAGMIN
AC061975.9
HOMER2
TUBA3E
ALDH1A3
GLRX
MBOAT2
ACSL3
CYP11A1
C1orf116
AL162497.1
IRS2
RAB3B
RGS2
ECI2
KLK3
ANKRD37
RP11-18F14.2
HES1
GNMT
TIPARP
JAG1
HERC3
EXTL2
LCP1
ODC1
TBC1D4
SLC35F2
PAK1IP1
MYBPC1
SLC2A12
RP11-312J18.5
KRT8
CREB3L4
MUM1L1
SMS
CENPN
PPFIBP2
DBI
LRRFIP2
ZBTB24
ADAMTS1
CLDN8
KCNN2
SLC16A6
ATAD2
KLK4
NFKBIA
FZD5
CROT
MAPK6
UAP1
CTD-2653M23.1
C9orf152
SASH1
BCAP29
SGK1
CEBPD
PACS1
PAQR4
BRP44
CYP2U1
ORM2
APOD
SNORD88C
CRISPLD2
WIPI1
SHROOM3
CBLL1
ORM1
RP11-529H2.2
VPS26B
ITGAV
ZNF18
SLC26A3
CAP2
KLK2
IQGAP2
MTOR
LONRF1
ADH1C
ACAD8
LIMCH1
WWC1
ATMIN
GUCY1A3
YIPF1
TBC1D8
PYGB
CTD-2008A1.2
MLPH
WDYHV1
HIST2H2BE
MYCBP2
C1orf21
ZMIZ1
PRKCH
HIPK2
MERTK
ACAA1
HEBP2
ADH1A
CORO1B
SPOCK1
PPAPDC2
CMC2
ENDOD1
ENDOD1
DNM1L
HES6
C6orf52
REP15
C2orf76
HMGCS1
HMGXB3
B2M
PDIA5
DHCR24
KCNMA1
SLC16A3
SAP30
MAP7D1
MAK
DNAJB9
C4orf34
RASSF3
PEA15
KRT8P33
TNFRSF19
CTSO
TUBA3C
TSC22D1
SMPD2
ST3GAL4
C19orf48
SNORD88B
MYOF
TM4SF18
CAPZB
C1QTNF9B-AS1
NUDT9
TP53TG1
SOX4
TEX2
TEX2
ATP1A1
F2RL1
KIF5C
PNLIP
KLF15
KRT19
RHOBTB3
CHRNA2
INSIG1
MCEE
SPON2
BBS4
HERC6
SLC4A4
SLC43A1
MPZL1
ODZ1
TRPM4
FAM105A
NEDD4L
IGF1R
MCPH1
CREB3L2
SLC30A7
C17orf48
MPHOSPH9
SDCBP
KLHL29
THBS1
CALU
NRIP1
AC020915.4
SEMA4A
CNTNAP2
MGAT2
FZD8
CLCN2
APIP
ADRB2
SEC24B
CNDP2
ZBTB10
CDYL2
EFNB2
TNS3
SPRY2
LYPLAL1
GOLGB1
CRIP2
RP11-1267H10.4
RAB4A
SPHAR
USP10
GLRX2
PTPRCAP
FDFT1
MOB4

5.2 Gene set: fcD_fcUnder

Number of genes: 146

ACPP
CXCR7
DDC
LRRN1
CBLN2
CAMK2N1
LRRC31
LMO4
MT1A
FAM198B
RP11-343H19.2
MT1X
RP11-181C21.4
COLEC12
RILPL2
C11orf92
NCOA7
BCHE
UGT2B17
SLITRK3
ATP1B1
EXOG
TRIB1
ID2
GCG
NUP93
IFIH1
CALD1
RP11-279F6.1
FAM113B
REEP1
FAM217B
HOXC13
RP11-510N19.5
GALNTL4
TXNIP
PITX1
SERPINI1
ARHGAP10
TMEM144
RP11-124L9.6
PRKD1
EPHX1
GRB10
ADD3
SLC30A3
RP11-124L9.2
RP11-124L9.1
RP11-1264N5.1
IGFBP3
RNF144B
MT1F
HTRA1
RP11-497H16.5
GUSBP9
TSHZ3
RP11-1198D22.1
AC078802.1
PELI2
FFAR2
TULP4
NIPSNAP3A
GATA2
BARD1
SDC4
RP11-1415C14.4
RP11-589F5.4
KIAA1467
GOLIM4
GC
RASL11B
CPNE3
EDN2
MAPKAPK3
ZIC2
DEPTOR
SUSD4
GLDC
C5orf30
GUSBP3
ZNF467
C1orf53
NUCB2
TMEM140
SELENBP1
SI
TGM3
GPER
RP11-195E2.1
RASL11A
GUSBP2
MECOM
ADCY1
EFHD1
NAP1L3
GALK1
RP11-823P9.1
RP11-98J23.2
RP11-1415C14.3
RAI14
TRNP1
CCDC28B
POLA2
ST3GAL1
FAM134B
PPP1R14C
PDGFRL
ST6GALNAC4
NETO1
ZNF503
NUPR1
HOXC9
SQRDL
CDR2L
SLC7A5
ITPK1
ATP12A
AIDA
TMEM158
AC010170.1
CHST15
SRPX
LGI2
C9orf64
FBXO2
PNMA6C
PNMA6A
IL27RA
AC073869.2
FIGNL1
MYT1
CTSH
FAM46C
METRN
IFI35
FZD2
ABCB9
C7orf49
SLC44A1
INSIG2
BAMBI
PLCH1
CHST13
ARHGEF3
HSPA12A
HBQ1

5.3 Gene set: fcDX_fcOver

Number of genes: 417

S100P
PGC
TUBA3D
CTGF
TUBA3E
TIPARP
PNLIP
ACTA2
SNAI2
TUBA3C
FKBP5
DUSP1
TMEM56
CDKN1C
RGS2
ERRFI1
CST1
SGK1
LEPREL1
CRISPLD2
ATOH8
LONRF1
PHLDA1
CEBPD
RP5-955M13.3
PTGER4
SPSB1
ELL2P1
ELL2
GNMT
SRD5A1
ETNK2
GBP2
SCNN1G
OLAH
MSX1
KRT6A
SLC39A14
PHGR1
SLC25A18
CHST3
COL6A1
CYR61
COL6A2
KRT8
AL162497.1
IRS2
MFSD6
ARG1
NSDHL
GLRX
MUM1L1
CDC42EP4
SOCS2
CITED1
S100A10
SLC39A11
BIRC3
TBC1D8
AC061975.9
ZBTB16
LRIG1
PRKAB2
SLC10A1
KRT8P33
ZFP36
FAM129B
WIPI1
GHR
CSRNP1
ABCC8
SLC30A1
PALLD
KLF15
ATP1A1
MBOAT2
PHLDA2
ELOVL5
JAG1
CH17-12M21.1
SPINK13
FADS1
PYGB
CLEC16A
ZDHHC8P1
TTC21A
CA12
SLPI
ATAD2
F2RL1
TSKU
SLC4A7
SPOCK1
PPAP2A
GATSL3
RP1-130H16.18
IRX3
HPGD
JAK2
FBXO31
FAM105A
NPC1
STX12
CREB3L2
RGCC
PHACTR2
PEBP4
APOD
SNX33
TNFRSF12A
LCP1
TDRD9
NUDT16
STAT3
AL163636.6
ALPP
NET1
STK35
PTPLA
CAP2
GADD45B
MSANTD4
FERMT2
PACS1
ANG
RNASE4
MYL12A
CD68
PROS1
WDR60
C9orf152
SLC31A2
RP11-529H2.2
TMEM61
MAFB
ABCD3
C5orf4
ODC1
OSBPL5
B3GALT4
SAT1
SHROOM3
ACSL3
EDEM1
GMNN
DAPK3
DOCK5
CAPN13
LRRFIP2
SLCO4A1
FAM65B
RP11-18F14.2
KRT72
CRYAB
KLF6
PRKCE
BBX
LRRC8A
KIAA0232
MYBPC1
ZNF185
BIRC2
SHC1
SIPA1L2
LIN7B
ANO6
ASIP
SLC27A3
SLC2A5
HIPK2
ZNF189
GORASP1
RNASE4
ELF1
CTD-2653M23.1
ELOVL1
TBC1D22A
ACAA1
TNFAIP3
PPP1R14C
AGT
FAM214B
ADRB2
ZNF18
PAK1IP1
GBAP1
ZYX
TSC22D1
CNTN3
TRIM48
MAP1LC3B
PACSIN2
LGALSL
PRPS2
GIPC1
SLC44A3
CKB
SPRYD5
KIAA0513
HSD11B2
SCNN1A
FXYD3
PLXNA1
C1orf198
HIBCH
C1orf172
RGS19
S1PR3
FBRSL1
MED23
DNAJB9
ASB9
CEBPB
BCL7C
IP6K3
TMEM43
TMEM37
BTD
SSR1
AP001468.1
INSIG1
CAPN2
WDFY2
MSMO1
RP11-397D21.1
MEAF6
C5orf46
SLC5A6
RNF115
HARS
NFIL3
SPRY2
BRP44
SOCS1
SEPT11
RRAS
PRDX6
TMED5
FAM58A
UBE2Q2P2
TSC22D3
SERPINA3
C14orf132
F5
BEST2
C8orf42
USP38
KIAA0040
EGFLAM
DBI
OCEL1
PPL
KRT16
FTH1P3
MRFAP1
MICAL2
NFIB
MICAL1
MERTK
MBNL1
CCDC6
RNASE12
RNASE12
SLC38A2
LNX2
RP11-802E16.3
KCNK1
AP3S1
ARPC5
CD99
USP10
PITX1
ACTG2
TBC1D16
ZFHX3
SSX2IP
MAOA
TRIM29
NBL1
TPM2
TSC2
PPTC7
LRRC16A
TSPYL2
HADH
SAR1B
TP53INP2
ABHD3
HSD17B4
AP000442.4
MIR22HG
DDX19A
TXNDC11
HES1
PIAS1
FOXO3
TOR1AIP2
RALY
ITGAV
PDLIM5
ZBTB25
DLG5
FMO4
PLCXD1
PGF
CLGN
SCAP
DDIT4
DERA
CHSY1
ZCCHC11
WDYHV1
HSD17B11
KIAA1522
ZNF622
KIAA1324L
DCUN1D3
RAB3B
NANS
RETSAT
AC093162.5
DNAJC3
ANKRD37
DHCR24
C18orf8
PPA1
DPH3
ARCN1
FAIM3

FOXO1
FOS
ST3GAL4
OGFRL1
PDLIM1
C17orf80
STK39
KRT73
TUBB2A
PHACTR3
SLC22A23
RASD1
RHOB
GPER
AZGP1
C8orf84
SLC16A3
NFKBIA
KCNMA1
TP53I3
PQLC1
RP11-125K10.4
RCL1
PLXNB2
GBE1
FAM107A
AC093323.3
VCL
RP11-259O2.2
ATG16L1
ACSL1
KIF5C
OFD1
C17orf48
KCNG1
TPM1
CST3
NDRG1
FLVCR2
C1orf122
PDIA5
CTDSPL
GBA
GBAP1
GBA
GBF1
HOMER2
FAM177A1
CNN2
KLF9
LIFR
PDHA1
TPD52L1
EAF2
GBP1
PEA15
TNFRSF1A
KLHL36
ENPP3
PSCA
AASS
TNKS1BP1
RBBP7
JUN
DNER
TRNP1
CHN2
ASB13
GPR153
CNST
EFNA1
CPEB4
VILL
NFE2L1
AZI2
ZBTB24
ARSA
GOLPH3
HSPB8
CRY2
C6orf89
KIF13B
RIT1
GOLGA5
RP11-796E2.3
BTG1
ISG20
ACPL2

5.4 Gene set: fcDX_fcUnder

Number of genes: 120

ACPP
RP11-181C21.4
RILPL2
CAMK2N1
CARM1
FAM198B
MAPKAPK3
SLITRK3
CXCR7
TRIB1
LRRC31
SLC7A5
IFIH1
LRRN1
COLEC12
UGT2B17
MYO6
BAMBI
DDC
CXCL16
SNORD97
SEPT3
GULP1
BCHE
HTRA1
IRF2BPL
FAM65A
TRIM25
IGSF9
PIGK
DEPTOR
MESP1
RP11-195E2.1
TJP3
CBLN2
NKD2
GEMIN4
SAPCD2
AIDA
SEMA6A
AC010296.1
RP11-510N19.5
MMD
RP11-279F6.1
C20orf27
CGN
ASNS
P2RY11
MAST4
PPAN-P2RY11
PPAN
STC2
GLDC
FAM108C1
C9orf64
ARG2
CDT1
RANGAP1
RP11-350O14.18
FJX1
RHPN2
PIGQ
MCM2
RPUSD1
RP11-167H9.6
NPM3
FANCG
TCEA3
MLF1IP
SLC2A6
NCS1
RAP1GAP
ID2
PAQR4
KIF20A
RP1-256G22.1
AC078802.1
CLDND2
FAM134B
ZIC2
FAM216A
HSPA4L
C12orf52
CDCA7L
TLE2
MMP11
VASN
C16orf59
RP11-124L9.2
RP11-124L9.1
RP11-1264N5.1
RNF220
TROAP
HS3ST1
ARHGAP10
HIST3H2A
XXyac-YRM2039.2
TMEM144
HNRNPA1
SUSD4
PRKD1
FIGNL1
WDR6
RP11-124L9.6
ARHGEF2
FRAT2
ZNF664
E2F2
KAZALD1
ENHO
PRAC
CCDC92
LYSMD2
KBTBD11
MYB
HOXC13
PNMA3
LIN7A
RAB17
CAPN5

5.5 Gene set: fcComb_fcOver

Number of genes: 719

PGC
TUBA3D
TIPARP
TUBA3E
S100P
CTGF
ACTA2
PNLIP
TUBA3C
PTGER4
ERRFI1
FKBP5
TMEM56
SNAI2
CDKN1C
LEPREL1
DUSP1
ATOH8
GNMT
RGS2
SCNN1G
LONRF1
SGK1
CST1
FOS
ELL2P1
ELL2
PHLDA1
CEBPD
RP5-955M13.3
CRISPLD2
SRD5A1
AL162497.1
IRS2
FADS1
GLRX
KLF15
RP11-125K10.4
RCL1
CA12
LCP1
TUBB2A
NBL1
FBXO31
CDC42EP4
PLXNB2
AC093323.3
SPOCK1
VCL
ST6GALNAC1
SPRY2
JAK2
SLCO4A1
SORD
PYGB
TRIM48
PALLD
C9orf152
PHACTR2
MERTK
KLF6
SLC45A3
TTC21A
PHLDA2
LIFR
AL163636.6
SNX33
ANG
RP1-130H16.18
KCNG1
ODC1
HIPK2
DOCK5
MED23
WDYHV1
PEBP4
ACTG2
CHMP1B
S100A10
WDR60
MAP1LC3B
TDRD9
TNFRSF10A
PRPS2
CPEB4
PIAS1
SLPI
C8orf42
PROS1
FERMT2
KLHL36
GORASP1
KIF5C
TACC2
KIAA0040
STAT3
C5orf4
ABCC4
TNFRSF12A
CD68
SAR1B
IP6K3
GBA
DDX19A
RNF115
GOLPH3
KIAA0513
PPTC7
ATG16L1
GMNN
EEF2K
EFNA1
FLVCR2
DHCR24
TSC22D3
ELOVL2
SSR3
NFIB
MEAF6
RAB20
CTDSPL
KLF9
GBF1
DOLK
PPA1
HIST2H2BE
C6orf52
CKB
TMEM79
CAPZB
DNM1L
AP3S1
C4orf34
ASB9
RP11-61N20.3
INSIG1
EGFLAM
WDR55
RAB32
ITGA1
CCDC107
TMED5
C2orf76
OFD1
FAIM3
ZNF622
STEAP4
ZC3H12A
COPB1
HADH
TSC2
OCEL1
C6orf89
SLC33A1
ASB13
BRP44
WDFY2
WDR41
PITX1
MRPS23
ECI2
CCBL1
MLPH
PNPLA8
C18orf8
RALY
ABHD2
KCNK1
OSGIN2
GBP1
CREBRF
SPRY1
CLPTM1L
PAEP
TRIP12
TPM2
PDE8B
ARCN1
RP11-796E2.3
BTG1
TAF5L
GFPT1
ERICH1
FLNA
DMTF1
MICAL2
SCOC
KIF13B
KCTD10
FTH1P8
MGAT1
DLG5
DVL2
SUN2
SLC16A6
TPCN2
MAFB
RSPRY1
ORM2
MEF2D
SAP30
PPL
TPD52L1
CRY1
AC063976.6
MTM1
ACTN1
MTF1
MINPP1
ZNF518B
AP1G2
RP11-802E16.3
TRAPPC2P1
DECR1
YIPF1
COPG1
USP3
CHD1L
TMEM37
RP11-463J7.2
UBE2H
KLK3
KCNN2
IL6R
DHX36
KLF4
CETN2
FTH1
AL354822.1
NEDD4L
FDFT1
SERPINF2
PNMA1
TRPM4
HAPLN3
MYH9
GABRB3
DGCR2

MUM1L1
ETNK2
OLAH
MSX1
OGFRL1
FOXO1
COL6A1
KRT8
SPSB1
SLC25A18
SOCS2
ST3GAL4
COL6A2
PHACTR3
PHGR1
STK39
AC061975.9
MFSD6
SLC39A14
C17orf80
ARG1
CHST3
CYR61
SLC22A23
GBP2
RASD1
HPGD
BIRC3
LRIG1
KRT8P33
PDLIM1
SAT1
NSDHL
CH17-12M21.1
PRKAB2
CSRNP1
H19
WIPI1
KRT6A
NDRG1
TSKU
SLC30A1
RHOB
EAF2
CLEC16A
GBE1
SLC39A11
FAM105A
F2RL1
SIPA1L2
JAG1
ELOVL5
ZBTB16
ATAD2
ZFP36
NFKBIA
GHR
KRT73
TEDDM1
ATP1A1
RGCC
SPINK13
FAM129B
MBOAT2
TBC1D8
ABCC8
PPAP2A
ZDHHC8P1
PACS1
RNASE4
CAP2
LRRFIP2
TSC22D1
APOD
HOMER2
SLC4A7
TMEM61
ACSL3
PAK1IP1
DNAJB9
GADD45B
C17orf48
GPER
KIAA0232
SLC31A2
DNER
SLC10A1
CREB3L2
NPC1
B3GALT4
ABCD3
FAM65B
STX12
SLC16A3
AZGP1
SHROOM3
TNFAIP3
MYBPC1
DAPK3
RNASE4
MICAL1
LRRC8A
DBI
MYL12A
CTD-2653M23.1
PQLC1
ACSL1
ZNF18
PRKCE
S1PR3
RP11-529H2.2
TPM1
SPRYD5
TP53I3
RAB3B
STK35
KIAA1324L
KCNMA1
NET1
CST3
ISG20
RHOBTB3
ARSA
RNASE12
RNASE12
C3orf58
OSBPL5
MSX2
NUDT16
LGALSL
SLC38A2
ASIP
FAM214B
NFIL3
MSANTD4
EDEM1
PACSIN2
GATSL3
MSMO1
RP11-397D21.1
SLC26A3
ACAA1
AP001468.1
TSPYL2
RRAS
RP11-18F14.2
KRT72
ELF1
FAM177A1
CYP11A1
HIBCH
SLC27A3
PDLIM5
AZI2
USP10
HMGCS1
HERC5
CITED1
PSCA
RP11-259O2.2
CNN2
ITGAV
GBAP1
FXYD3
BBS10
PLXNA1
ENPP3
PEA15
ANKRD37
ABHD3
C1orf122
TBC1D16
AASS
CNST
FAM107A
SLC44A3
ZNF189
INPP4B
F5
PPAPDC2
BIRC2
FTH1P3
USP38
CCDC6
RETSAT
AC093162.5
PDIA5
B2M
ZFHX3
LPAR3
CRYAB
ANO6
ZYX
PDHA1
TOR1AIP2
BEST2
VPS37B
MBNL1
NCAPD3
CHN2
IDI1
CAPN13
TBC1D4
UGT2B28
LIN7B
GBA
GBAP1
UBE2HP1
ITGB1
PMEPA1
C1orf198
CEP120
PARP12
SHC1
ZNF385B
GLUD1
SCAP
TXNDC11
GNAL
MRFAP1
SSR1
NANS
C8orf84
RGS19
BCL7C
CTD-2008A1.2
FOXO3
ADRB2
C3orf70
ANKRA2
GIPC1
KRT18
TRIM24
SEC23B
RIT1
MAP7D1
UBE2Q2P2
HSD17B11
PTPN12
GOLGA5
C10orf26
IRF6
TP53INP2
COMMD1
ELOVL1
PLCXD1
SMAP1
RBM24
ZBTB24
PDZD2
PTPLA
CNTN3
RP4-697K14.7
HS1BP3
NT5DC3
VMP1
ZBTB25
NRD1
ALPP
ARPC5
FTH1P12
CEBPB
LRRC16A
BBX
CBLL1
TBC1D22A
FBRSL1
TBX15
BZW1P2
SCNN1A
DDIT4
SEC22C
SLC41A1
MIR22HG
NREP
TASP1
GABARAPL1
EDN2
SSX2IP
SERPINA3
ANXA5
CAMSAP2
RBM45
DNAJC3
WDR1
ARL8B
MORF4L2
HERC3
TNKS1BP1
ZCCHC11
FAM103A2P
FAM103A1
TEX2
TEX2
SOCS1
FMO4
FBXO8
NFE2L1
PAWR
CAPN2
C15orf23
LIMCH1
ZNF185
CLDN12
ZFAND5
ARMC12
DERA
THOC5
FADS2
LOX
ERLEC1
GPR89A
WDR26
TMEM150A
CLGN
PHLPP2
CCDC53
C1orf172
H1F0
MAOA
PTN
KIAA1191
SNIP1
AC018755.13
SIGLEC14
CD99
KCTD3
DPH3
HSPB8
C5orf51
ELMOD2
BTD
DNM2
EIF2AK3
TNFRSF1A
HBP1
FTH1P11
STXBP3
DYNLL1
ZC3HAV1
FAM58A
AC138649.1
ATMIN
TMPRSS2
LNX2
ATF6
C14orf166
RP3-412A9.11
SELS
KLHDC2
GALNT1
GRAMD3
TMEM43
PLEKHB2
TMED10
HSD17B4
C5orf46
CYP2R1
DSTN
CRY2
HIF1A
BCL2L1
SEC61B
DYNC1I2
CD9
C14orf132
ORM1
SEC24D
DCXR
P4HA1
AP005814.1
TRIM49L1
VILL
MCEE
FGD4
ALG11
AHNAK
RNASE11
COPS8
ESYT2
USMG5
MIR1307
FAM114A1
USP33
FICD
KCTD9
GPR153
YPEL5
VPS26B
ZCCHC6
EVL
RANBP10
MGAT2
KIAA1217
GOLGA4
PELO
MAP2K4
PDK4
TGM2
ALDH1A3
PNPLA2
PTPRN2
STX5
ZXDB
CES4A
TMED7
NFE2L2
LZTR1
VIPR1
STRBP
TCEAL3
SDF2
TSPAN31
P4HA2
COBLL1
TM2D2
ACOT9
CALD1
IL20RA
CALCOCO2
PHF1
MPZL1
C12orf44
STX19
PPP1R13L
UBE2Q2P3
SLC25A4
CRIP2
BSDC1
MRPL50
MIR600HG
C3orf25
YPEL3
PGM3
NAPG
ZFAND2A
PSMD8
AC010335.1
ELL
IMPA2
FTH1P2
PICK1
SQLE
RHOBTB2
OSBPL11
SERINC1
THBS1
BCAP29
KIAA1522
ZBTB8OSP2
CD99L2
VEZF1
TMEFF2
KIF5C
PJA2
ACPL2
NRP1
DAAM1
FIG4
RAB5A
SEC31A
KIAA0355
KIAA0355
ZBTB8OS
ITPKA
CHMP2B
MYL7
PRDX6
SPTB
HARS
KIAA0391
TMEM2
GPR89C
RAB8B
PEX13
BAIAP2
ODZ1
SPDEF
CD300LG
CDKN1A
TRNP1

5.6 Gene set: fcComb_fcUnder

Number of genes: 643

ACPP
CBLN2
CXCR7
F12
PSPH
AIF1L
NOTCH1
SLC25A19
TRIM45
PIK3IP1
C16orf88
RFC3
TP53INP1
GC
NME3
RP11-1023L17.1
LSM4
HOXC9
NPEPL1
RSL1D1
RALGPS1

DDC
LRRN1
RP11-279F6.1
UGT2B17
BCHE
RP11-181C21.4
MT1A
RP11-343H19.2
MT1X
SLITRK3
ZIC2
TRIB1
RILPL2
FAM198B
LRRC31
NUP93
PRKD1
COLEC12
LMO4
CAMK2N1
IFIH1
RP11-510N19.5
SLC7A5
RAI14
GATA2
GLDC
VASN
RP11-350O14.18
C11orf92
MAPKAPK3
RP11-124L9.6
MT1F
RP11-497H16.5
GUSBP9
HTRA1
MCM2
KBTBD11
HBQ1
RP11-124L9.2
RP11-124L9.1
RP11-1264N5.1
LRRC26
RP11-1198D22.1
RP11-1415C14.4
RP11-589F5.4
C5orf30
HMGCS2
STC2
JAG2
MYC
CXCL16
TMEM158
AC010170.1
NKD2
CGN
FIGNL1
GEMIN4
SLC27A2
LYSMD2
FERMT1
DEPTOR
BTG2
EXOG
LMNB1
SEPT3
BAMBI
CDCA5
TMEM144
KIF20A
MESP1
GCG
PIGK
CMBL
CSPG5
ADORA2B
GUSBP2
RSL24D1
IGSF9
BARD1
RP11-823P9.1
RP11-98J23.2
RP11-1415C14.3
METRN
AURKB
MYO6
MCM3
CHTF18
REEP1
SLC18B1
CAMK2B
RP11-195E2.1
WDR54
RASL11B
POLA2
TOP2A
RAB17
SEMA6A
AC010296.1
FAM111A
TUBA4A
KLHL35
ARHGEF2
KIF1A
FAM65A
SLC30A3
HJURP
LGI2
CAPN5
ZMYND15
GINS2
TARBP1
IRF2BPL
RP11-167H9.6
FJX1
FAM83D
MECOM
ATP1B1
MAP2K6
SLC29A1
MMD
B4GALNT4
SNAPC4
FAM81A
NOLC1
NCAM2
C8orf55
C8orf55
IL27RA
C16orf59
NPM3
ARG2
GUSBP3
TRIM25
CDT1
MCF2L-AS1
FAM216A
HOXC13
GAS6
AIDA
CCDC59
TSPAN9
RAP1GAP
CYFIP2
MIR25
MIR93
ADD3
CHST15
ASF1B
BCL2L12
GP1BB
CTSH
PLEKHH1
RNF144B
AURKA
ADCY1
RAB26
TJP3
TROAP
CCDC28B
OGDHL
TRIP13
TUBB4A
TYMS
SUSD4
ZNF462
AC010336.1
RALYL
OAF
PARD6A
C2CD2
ITGB1BP1
NT5DC2
CDC45
MTHFD2
FRAT2
CLDND2
C12orf52
PUS7
CCNB2
NFIX
RP4-751H13.6
SKA3
PAFAH1B3
ATIC
FBXO2
HCP5
PSAT1
RPUSD1
C1orf115
PBK
PLK4
TTF2
LRRC20
C20orf27
POC1A
AMACR
P2RY11
CDCA8
MYLIP
SREBF1
KIFC1
KIFC1
KIFC1
RP5-894A10.2
H2AFX
ARHGEF3
NCS1
GULP1
CENPM
KIF2C
RGS10
FBL
RCC2
SEPT9
SEPT9
PABPC4
GNG4
CECR5
RP11-789A7.1
PPAN-P2RY11
PPAN
RP11-318E3.4
FAM108C1
TULP4
PKMYT1
LRP11
RAN
ZNF503
RP1-256G22.1
FAM84B
ALKBH2
B3GALT6
GPR56
SALL2
TSHZ3
MAST4
HAGHL
CENPV
CDCA4
C20orf72
PTTG3P
CTD-2643K12.1
TK1
MCM5
HS3ST1
CTCF
PKNOX2
TSEN2
GUSBP4
RP11-497H16.8
SPTBN5
GALK1
CABLES1
CTB-78F1.2
ZNF239
ABHD14A
ANXA9
CD83
PNMA3
TESC
ATP12A
PFAS
PRR7
CKAP2L
PELI2
PPP1R14B
DPP7
SI
KAT2A
NUAK2
DKC1
SNORA74A
HOXA5
RAB6B
MRPL12
GRB10
CACNB3
SH2D4A
ATP2C2
C18orf56
ADA
SETMAR
FAM46C
LLGL1
ZNF467
NXT1
HSD3B7
FAM86C1
RP11-192N10.2
CKS1B
PLDN
PLEKHG4
ST6GALNAC4
UGT2B15
SNRNP40
E2F7
XRCC3
C1orf135
STAMBPL1
TP53
MIF4GD
PROM2
TLE2
FAM184A
LHX2
PIK3C2B
PSMB10
SNORD52
POLR3K
SLC2A6
SRSF6
MMP11
DNMT1
AC078802.1
FOLH1
AFG3L2
NME1
MYNN
RNFT2
GOLIM4
NT5M
ST7
SAC3D1
RHPN2
EFNB3
POLE3
RPL18AP16
ARL2
ATF5
C15orf39
KHSRP
MRPL35
FAM60A
FAM195A
LSM2
NUDT3
OIP5
ATP6V1E2
IMPDH2
C1orf53
EIF2B5
POLD2
POLD2P1
ADAP2
DFNA5
HAUS4
RP11-298I3.5
CPNE3
DDX55
ZNF581
LYAR
PRPF4
GPT2
MLST8
TGM3
CCNF
NOP14
SMARCD3
OVGP1
H2AFY2
AP3M2
NCAPG
CHCHD4
RNF220
SEPHS1
POLQ
ADCY9
TMEM97
KCTD15
RPA2
CHST14
EPB41L4A-AS1
HILPDA
DNASE2
SSBP3
NUDT1
CARHSP1
CDC7
FGD1
GSTO2
ADCY3
LSM7
HIST3H2A
MRP63
PIGQ
PRIM1
RPL28
SOHLH2
MANEA
RP11-509E16.1
SDCCAG3
C20orf20
MCM7
SORL1
NIP7
PGAM5
TFDP1
PDRG1
MELK
RMI2
PRR14
RPL31
ZNF787
ADAP1
CDK2
SAMM50
ANKRD16
CDK4
EZH2
PHLDB1
PLCH1
CDCA3
TGIF2
LRPPRC
NOTCH3
ZFP82
XPO5
GLRB
GS1-358P8.4
HIBADH
ZCCHC24
NUPR1
NR2C2AP
ASNS
NUP85
NETO1
CMTM8
RP11-31K13.1
TPX2
ABCA1
RNPS1P1
KIF20B
AC008738.1
UROS
DDX18
C9orf64
TMEM98
RNASEH2A
HSPA4L
HADHA
ACACB
MORC2-AS1
BYSL
LAMA5
POLR2I
CCDC92
UHRF1
RP11-424C20.2
MACROD1
RPL12
AC011737.2
RPL12P4
RP11-434O22.1
RP11-106M3.1
RPL12L3
RPL12P8
SPR
PAICS
TUBB
C1orf112
CTXN1
SNORA64
SPC25
PCBD1
TANC1
NRM
FAM136A
REEP6
CCNE1
POLR2H
ZNF219
THOC6
SFXN4
UBL4A
ZCWPW1
CDCA7
CLDN3
QRICH2
TOX2
FAM171A1
FAM173A
SAE1
ANAPC7
DBNDD1
CCDC85B
WDR6
NIPSNAP3A
NSMCE1
FOXRED1
GRIN2C
RCC1
RASEF
NELF
E2F5
MCTP2
RRS1
DBP
ZNF695
SLC46A1
HES6
CPLX1
MB
MATR3
ZNF296
SIX5
EVPL
TFAM
LGALS3BP
GSG2
POLE
C2orf55
ELL3
RP11-296A16.1
LARS2
RWDD2A
C2orf15
CCNA2
GLIPR2
EPHX1
SESN3
SAP18
SLC2A4RG
CENPF
DOPEY2
USP13
INTS9
MAGEF1
SCCPDH
AL592284.2
SETD8
PAQR4
TRAP1
CYCS
LRP5
TESK2
PIM2
TSPAN15
FUS
SF3A3
AMHR2
RECQL4
SIGIRR
SPIRE2
TOB1
NOP56
SH3GLB2
C17orf70
EME1
EFHD1
CHAF1B
FAM207A
TIMELESS
PTTG1

MCM6
CCDC169-SOHLH2
SAPCD2
SERPINI1
PRAC
CARM1
E2F2
FAM134B
CDCA7L
CXXC5
TCEA3
FFAR2
MCM4
CGNL1
FANCG
RP13-1032I1.10
SLC25A10
NCOA7
FAM113B
CENPA
ELF3
EXOSC5
RASL11A
C12orf26
KAZALD1
CENPB
ARHGAP10
BHLHE40
DCTPP1
ASAP2
MYT1
TMEM51
HNRNPA1
NUDT6
RANBP1
FEN1
PPFIA2
EXOSC2
C9orf123
SF3B3
KIF4A
HMBS
RP11-579D7.4
SAYSD1
FOXA1
FAN1
RFWD3
ATXN7L2
LAMC3
SMARCA4
KIAA0101
UBE2T
AIMP2
KNTC1
CYC1
PBX3
CFD
TLCD1
DLGAP5
MST4
CDCA2
SH3RF1
MCM10
LAS1L
GLTSCR2
SNORD23
ZFP36L2
B3GNT1
C7orf23

5.7 Gene set: fcD4_fcOver

Number of genes: 29

TMPRSS2
SLC45A3
TMEFF2
ELL2P1
ELL2
CEBPD
TIPARP
ZBTB16
PMEPA1
C1orf116
SNAI2
PRAGMIN
GLRX
NFKBIA
FKBP5
AL162497.1
IRS2
HES1
RP11-796E2.3
BTG1
ERRFI1
CLDN8
PRR15L
ADRB2
TUBA3D
EAF2
PPAPDC2
SGK3
ABCC4

5.8 Gene set: fcD4_fcUnder

Number of genes: 2

BAMBI
HOXC13

5.9 Gene set: fcDX4_fcOver

Number of genes: 26

SGK1
CEBPD
TUBA3D
PGC
ERRFI1
SNAI2
ELL2P1
ELL2
S100P
SPSB1
PRR15L
RGS2
TUBA3E
ZBTB16
KLF9
TMPRSS2
NFKBIA
TIPARP
PTGER4
FKBP5
SLC45A3
TUBA3C
PMEPA1
FAM43A
ZMIZ1
DDIT4

5.10 Gene set: fcDX4_fcUnder

Number of genes: 0

5.11 Gene set: fcCPA_fcOver

Number of genes: 172

TUBA3D
FKBP5
SLC45A3
TMEFF2
ELL2P1
ELL2
TMPRSS2
TUBA3E
EAF2
ELOVL5
PGC
RGS2
ABCC4
TM4SF1
PMEPA1
STK39
LRIG1
HPGD
MBOAT2
PRAGMIN
SGK1
FAM188B
TSKU
ADAMTS1
ECI2
INPP4B
ELOVL2
GMNN
PTMAP2
PTMA
ZBTB16
HOMER2
HERC5
ST6GALNAC1
PHGR1
PTGER4
PCDH20
ALDH1A3
TUBA3C
C1orf116
KLK4
MYBPC1
LINC00161
ADRB2
SLC41A1
FAM162A
KRT19
CENPN
DBI
PRR15L
BRP44
SOCS2
SLC39A10
AC061975.9
RPS4XP16
F2RL1
KCNMA1
HES1
STX19
AC069292.6
SAT1
SLC16A3
ERRFI1
THBS1
SPOCK1
CYP11A1
FZD6
RPL9
UAP1
LRRFIP2
CTC-479C5.11
NACAP1
METTL7A
SACS
CLGN
ODZ1
NOL5BP
MTDH
RP11-351I24.3
RP11-123C21.1
SAP30
PERP
SLC35F2
RPL23AP64
SHROOM3
ANK3
TUBA4A
ATMIN
RP11-796E2.3
BTG1
GUCY1A3
FAM43A
RP11-543B16.1
LPAR3
KLK2
TM4SF18
C19orf48
SNORD88B
HMGXB3
AC016712.2
EPHX2
RP11-473P24.2
WSB2
HMGB2
PTGES3
KIF11
SACM1L
RPL7A
SNORD36B
SNORD36A
USP49
CMC2
MALT1
TBC1D8
HERC3
C14orf166
TP53TG1
GOLGB1
RPS26P35
GGCT
ACSL3
CCP110
PPAP2A
RG9MTD1
C3orf58
ATAD2
RP11-118B13.1
PLA1A
RP11-61N20.3
RP11-463J7.2
KLF15
UGDH
S100P
NAE1
CMPK1
AL356585.3
TPI1P1
GLRX2
KLK3
RPS7P3
APOD
FAM116A
ACTR3
NDC80
FRG1
MCTS1
RP11-314P12.3

CROT
SNAI2
GLRX
INMT-FAM188B
ZMIZ1
AC005017.2
CEBPD
NDRG1
B2M
SORD
CDK1
MYO1B
RP11-110I1.11
AC073465.3
VPS13A
PRRT2
FAM98A
RP11-681N23.1
NFKBIA
RP11-18F14.2
ZNF385B
EXTL2
DCAF6
SSR3
MRPL19

5.12 Gene set: fcCPA_fcUnder

Number of genes: 85

LRRN1
DDC
ACPP
CBLN2
CAMK2N1
LRRC31
LMO4
CXCR7
HMGCS2
RILPL2
ST3GAL1
MT1A
RP11-343H19.2
MT1X
GALNTL4
HOXC13
NCOA7
SLITRK3
TULP4
FAM217B
FAM198B
UGT2B17
RP11-181C21.4
MYO6
ATP1B1
RP11-124L9.2
RP11-124L9.1
RP11-1264N5.1
ADD3
COLEC12
RP11-124L9.6
KIF5B
PITX1
BAMBI
SOX9
RP11-195E2.1
RP11-1415C14.4
RP11-589F5.4
GRB10
ID2
GOLIM4
ZNF467
GUSBP2
FAM113B
AC078802.1
RP11-1198D22.1
C5orf30
RP11-497H16.5
GUSBP9
ARHGEF3
SNORD97
CALD1
GULP1
RALB
EXOG
SUSD4
NUP93
PRKAR1B
RP11-318E3.4
SERPINI1
ZNF664
TRIB1
C2orf15
SLC44A1
RP11-823P9.1
RP11-98J23.2
RP11-1415C14.3
PKNOX2
REEP1
RAP1GAP
RP11-279F6.1
NUPR1
NIPSNAP3A
DEPTOR
C1orf53
PNMA6C
PNMA6A
C1orf115
SLC30A3
ST13P15
TSHZ3
ERGIC1
GATA2
GUSBP3
PCK2

5.13 Gene set: fcRU_fcOver

Number of genes: 127

TMEFF2
SLC45A3
TUBA3D
TMPRSS2
ABCC4
AC005017.2
FKBP5
FAM162A
ELOVL5
SGK1
PMEPA1
RPL9
EAF2
RPS26P35
RP11-118B13.1
RPL23AP64
RP11-110I1.11
FZD6
TM4SF1
USP49
RPS7P3
PTGES3
NOL5BP
RP11-485H8.2
RP13-923O23.5
AC007272.2
RP11-139F4.1
RP11-632K5.5
CTD-3064M3.6
ADAMTS1
TUBA4A
TUBA3E
STK39
PGC
PTMAP2
PTMA
MBOAT2
INMT-FAM188B
FAM188B
NACAP1
LRIG1
C14orf166
MCTS1
RPL23
RP11-543B16.1
CCP110
AC061975.9
GMNN
AL356585.3
CTC-479C5.11
WSB2
PRR15L
S100P
RP11-681N23.1
AZIN1
RP11-473P24.2
RP5-890O15.3
FTH1P3
TXNL1
KLK4
SACS
ECI2
FTH1P12
RP11-359H18.1
RP3-423B22.5
RP11-25I15.1
RG9MTD1
CENPN
FAM105A
KIF11
HNRNPA1P12
AC016712.2
ELL2P1
ELL2
SACM1L
MAK16
ACTR3
CUL4A
AC069292.6
ADRB2
PTTG3P
HMGB2
SLC25A22
SLC39A10
FTH1P8
RP11-351I24.3
RP11-123C21.1
RPS4XP16
FANCI
EIF3A
RP11-442A13.1
TRA2B
LINC00161
VPS13A
TPI1P1
FTH1P2
ECT2
RP11-16F15.2
TIMM8B
SNX10
FTH1P11
GTF2H2
CMPK1
THUMPD1
HMGB1P1
MRPL19
PRKAR1A
RBBP7
C19orf48
SNORD88B
MTDH
NAP1L1
ZIC3
NAE1
TM9SF3
AC073465.3
MNAT1
FAM8A1
MYBPC1
PFAS
IER3IP1
CDK1
RPL23AP4
AP006222.2
AP006222.1
TSKU
BRP44

5.14 Gene set: fcRU_fcUnder

Number of genes: 28

ACPP
LRRN1
DDC
GALNTL4
CAMK2N1
ST3GAL1
ST13P15
CBLN2
HOXC13
RILPL2
TULP4
PITX1
ZNF664
LRRC31
RP11-343H19.2
MT1X
PKNOX2
COLEC12
GRB10
KIF5B
RP11-318E3.4
LMO4
INO80E
TTYH3
UGT2B17
ATP1B1
GCG
SNORD97

5.15 Gene set: fcCDX_fcOver

Number of genes: 124

AC005017.2
CTC-479C5.11
FZD6
RPS4XP16
RP11-473P24.2
RP11-118B13.1
RPS7P3
FAM162A
RPL23AP64
RP11-110I1.11
RPL9
CTD-2329C7.1
WSB2
RP11-543B16.1
RPS26P35
AC069292.6
HNRNPA1P10
PRKAR1A
AC073465.3
RP11-442A13.1
RP11-16F15.2
RP5-890O15.3
PDIA3P
FTH1P3
NOL5BP
MCTS1
NACAP1
SLC25A22
PTGES3
NPTN
AP006222.2
AP006222.1
CMPK1
NAE1
AC016712.2
TIMM8B
AZIN1
COPS2
RPL23
ACTR3
ECT2
FTH1P8
FTH1P2
DR1
ANK3
MTDH
RP11-681N23.1
RP11-321C3.1
UBLCP1
FAM98A
NELF
EAF1
TPI1P2
KLHL7
SACM1L
PRKCI
HIF1A
TRA2B
MTMR6
PTBP2
UNG
RP11-781P14.3
AL356585.3
AC016292.3
RP11-83J16.1
CCP110
DBR1
RP11-148K1.12
SH3YL1
SLC38A2

RP11-485H8.2
RP13-923O23.5
AC007272.2
RP11-139F4.1
RP11-632K5.5
CTD-3064M3.6
PTMAP2
PTMA
TUBA4A
RP11-359H18.1
RP3-423B22.5
RP11-25I15.1
KIAA1244
TXNL1
C14orf166
USP49
HMGB1P1
AC061975.9
FTH1P12
MRPL19
FTH1P11
RPL14
HNRNPA1P12
RPL23AP4
YES1
AC016739.2
IL18
IER3IP1
NNT
PERP
CUL4A
METTL7A
HDHD2
RBBP7
IBTK
SYAP1
RG9MTD1
RP11-885N19.5
CENPW
GOLGB1
SREK1
ATF4
AC073621.1
EIF3A
MAK16
KIF11
NAA50
SNX10
YAP1
RNASEH2B
SUB1
SAP30L
RP11-118B22.3
RP11-267J23.4

5.16 Gene set: fcCDX_fcUnder

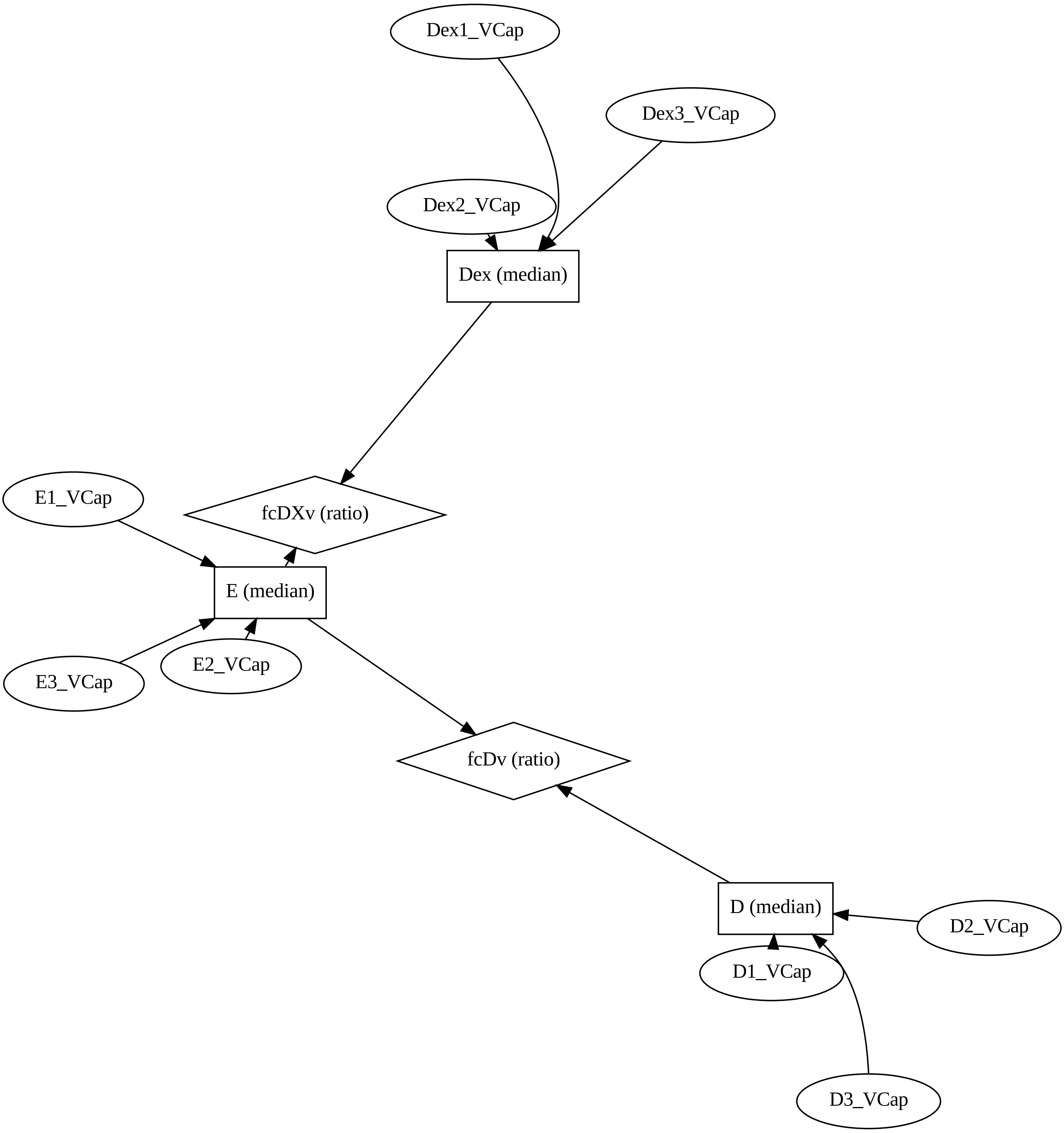
Number of genes: 9

ST13P15
PPDPF
TTYH3
LTBR
INO80E
YWHAE
TRUB1
ZNF664
AKT2

6 Expression analysis for VCaP

Group	Definition	Description
E	median(E1_VCap, E3_VCap, E2_VCap)	controls VCaP
D	median(D1_VCap, D3_VCap, D2_VCap)	DHT cases VCaP
Dex	median(Dex1_VCap, Dex3_VCap, Dex2_VCap)	dexamethasone cases VCaP
fcDv	ratio(D/E)	DHT VCaP samples divided by their controls
fcDXv	ratio(Dex/E)	Dex VCaP samples divided by their controls

Table 18: Sample groups



7 Illumina quality control (raw)

7.1 Density plot

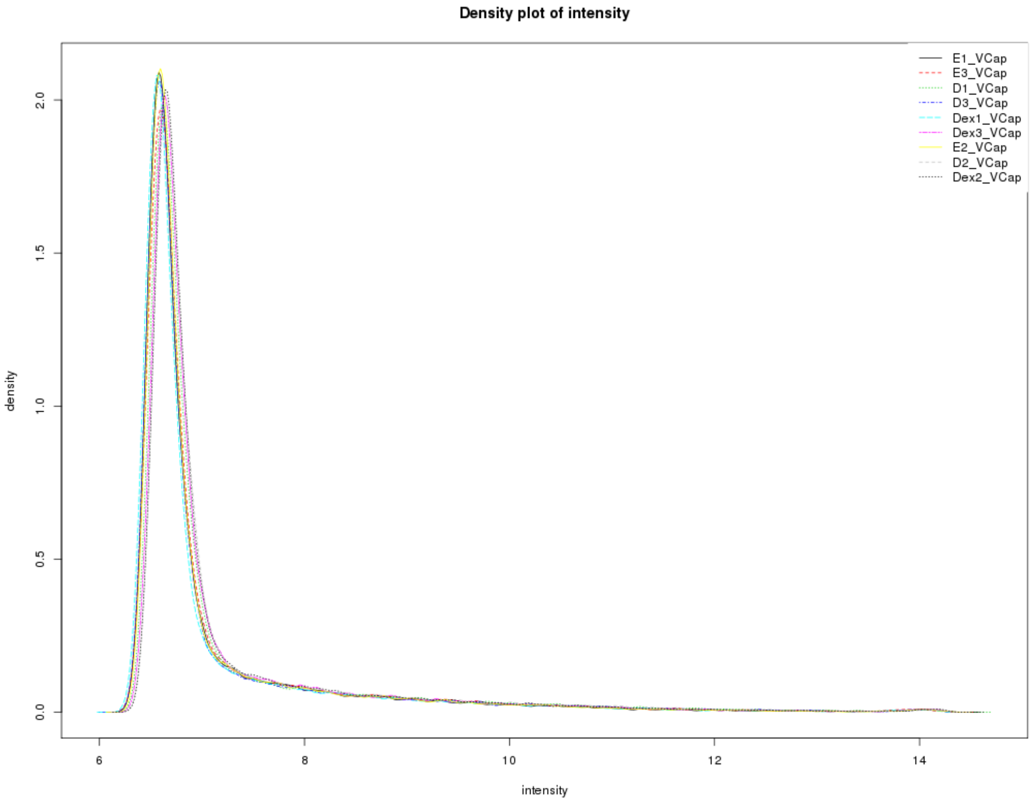


Figure 31: Density plot indicates the distribution of variables.

7.2 Box plot

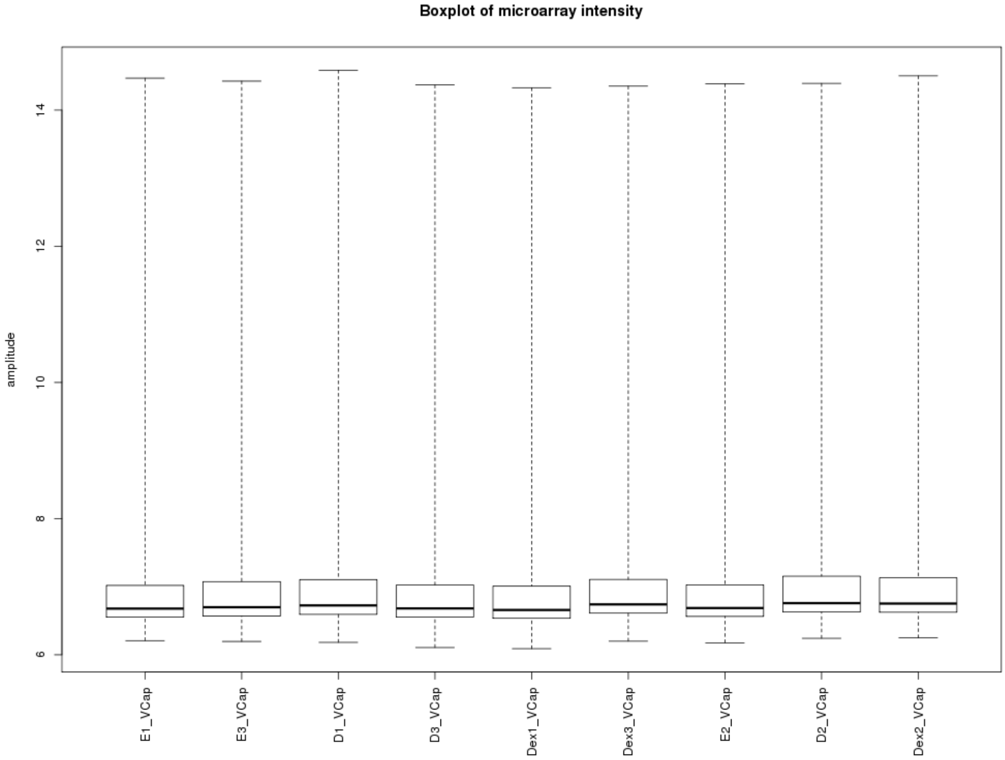


Figure 32: The bold line shows the location of median. The filled rectangle contains values between 25'th and 75'th percentile. The extremes show locations of minimum and maximum.

7.3 Scatter plot

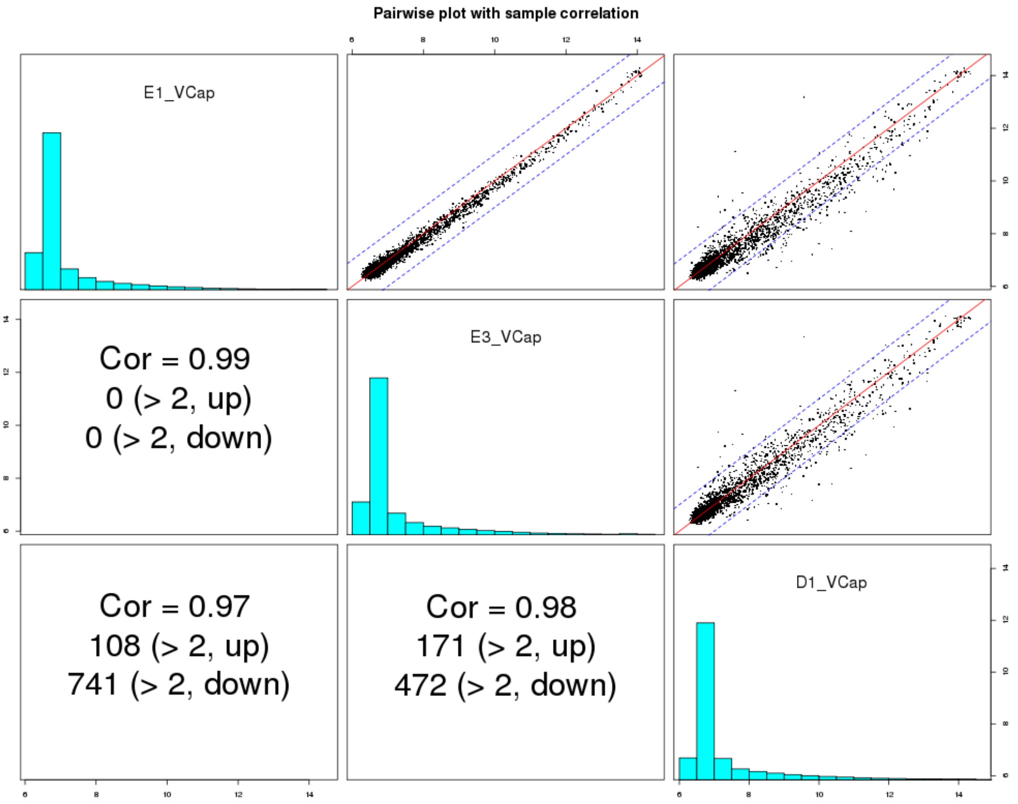


Figure 33: Scatter plot illustrates the degree of sample correlation.

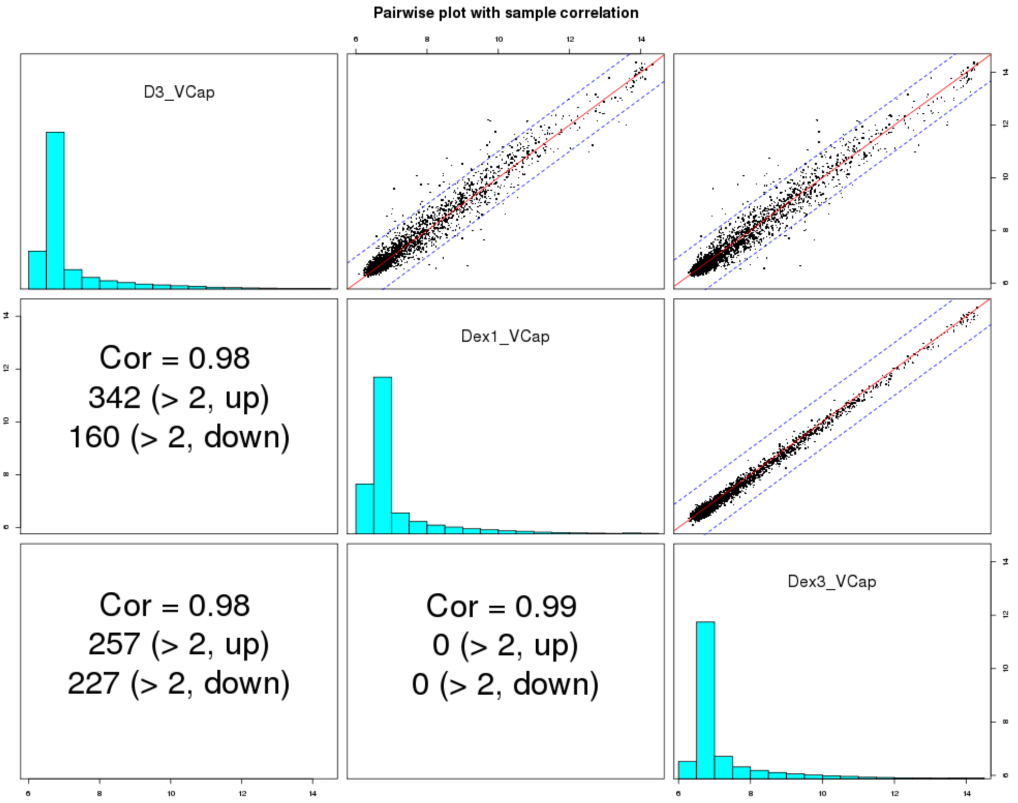


Figure 34: Scatter plot illustrates the degree of sample correlation.

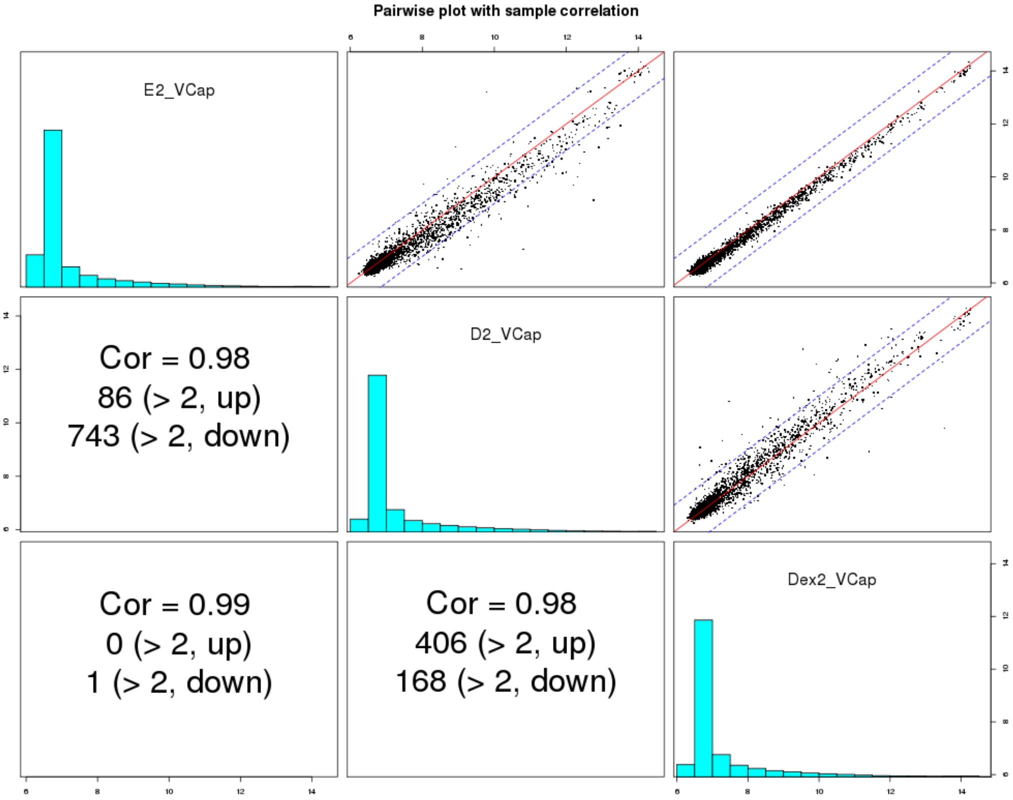


Figure 35: Scatter plot illustrates the degree of sample correlation.

7.4 MAXY-plot

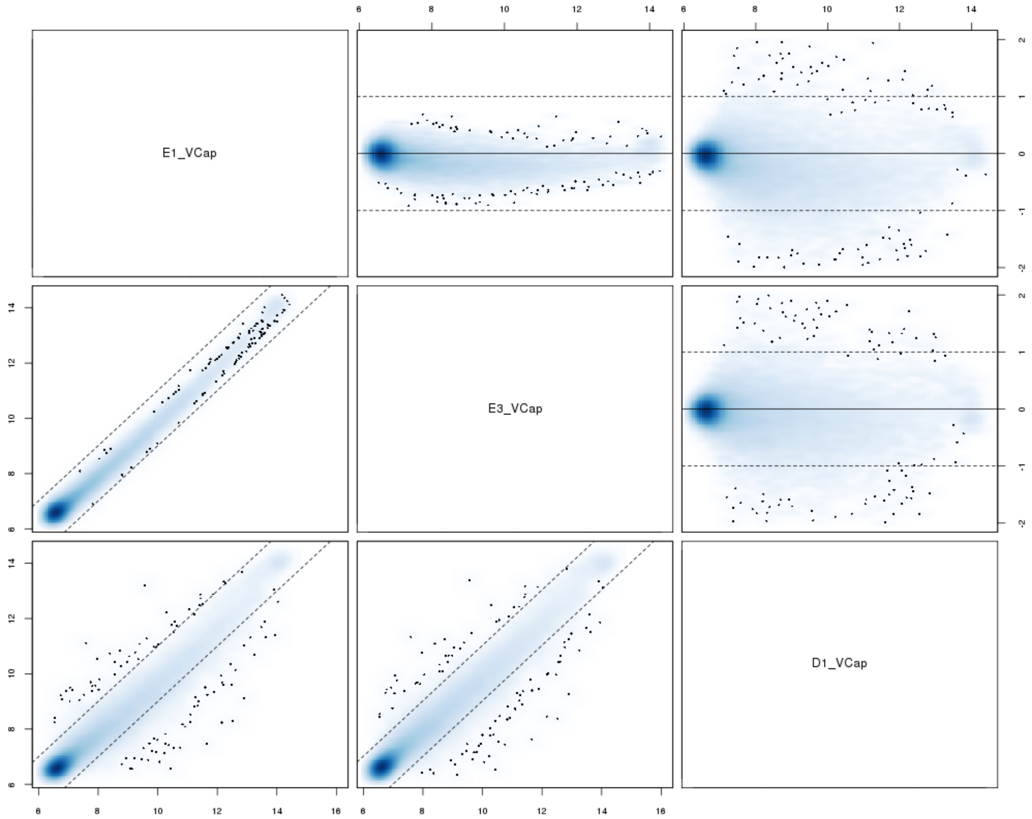


Figure 36: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

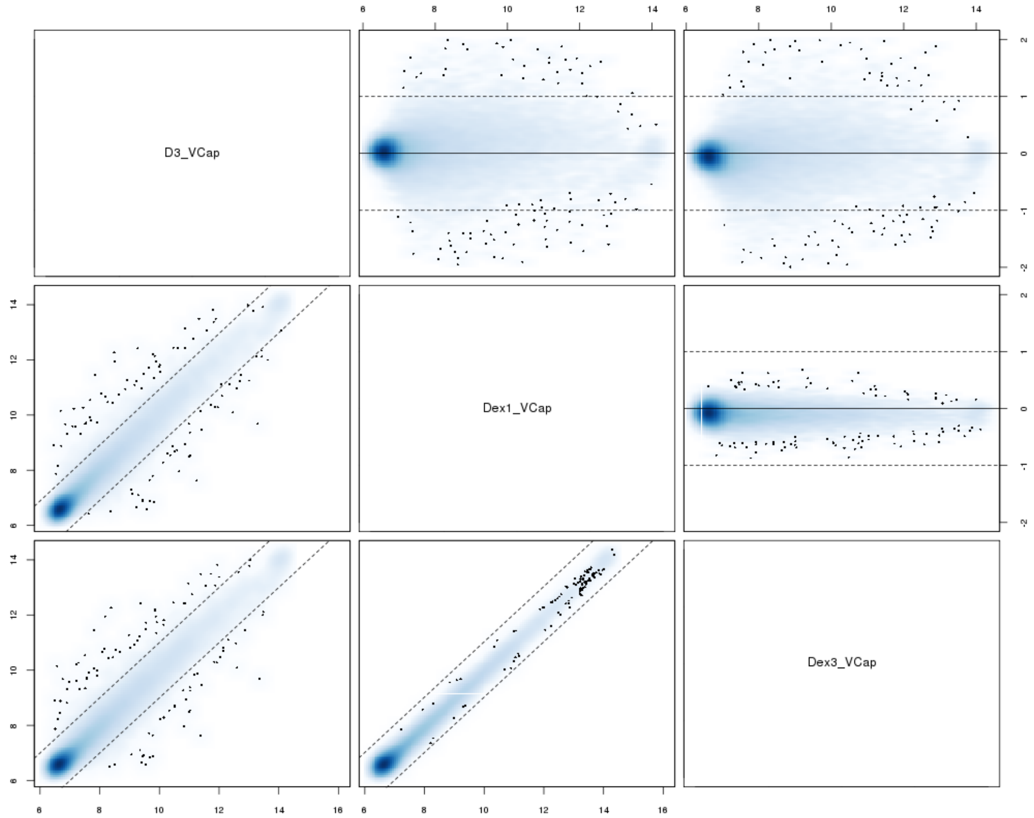


Figure 37: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

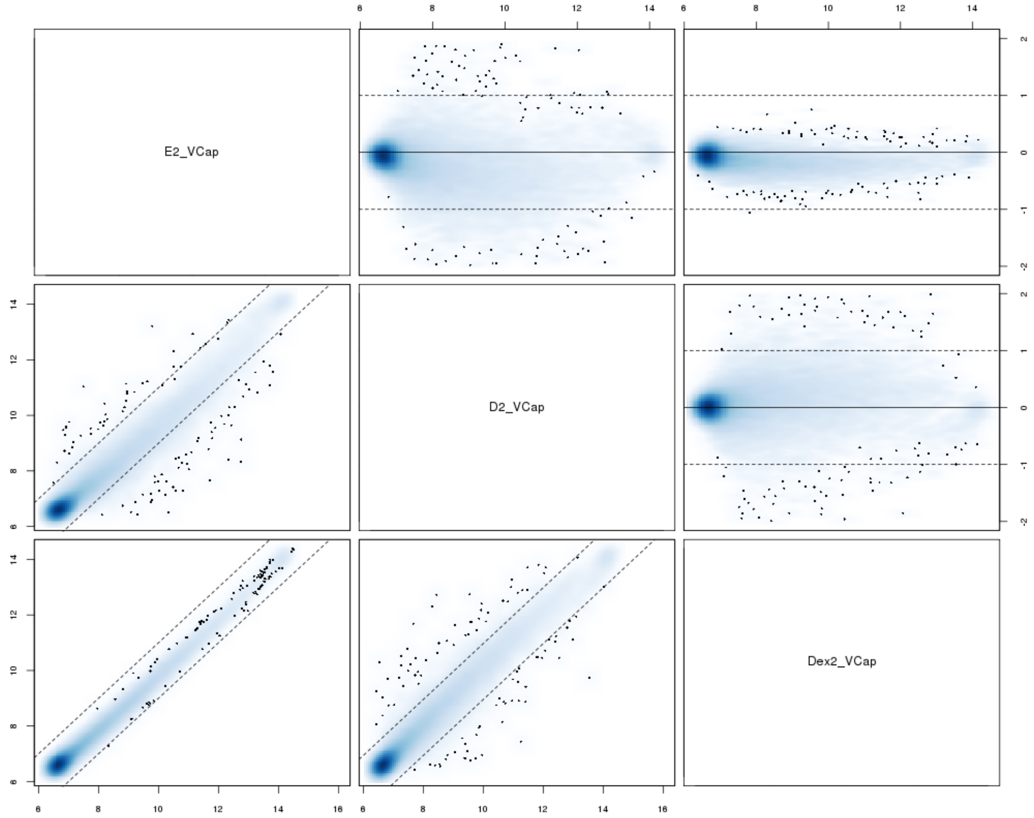


Figure 38: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

7.5 Sample relations (hierarchical clustering)

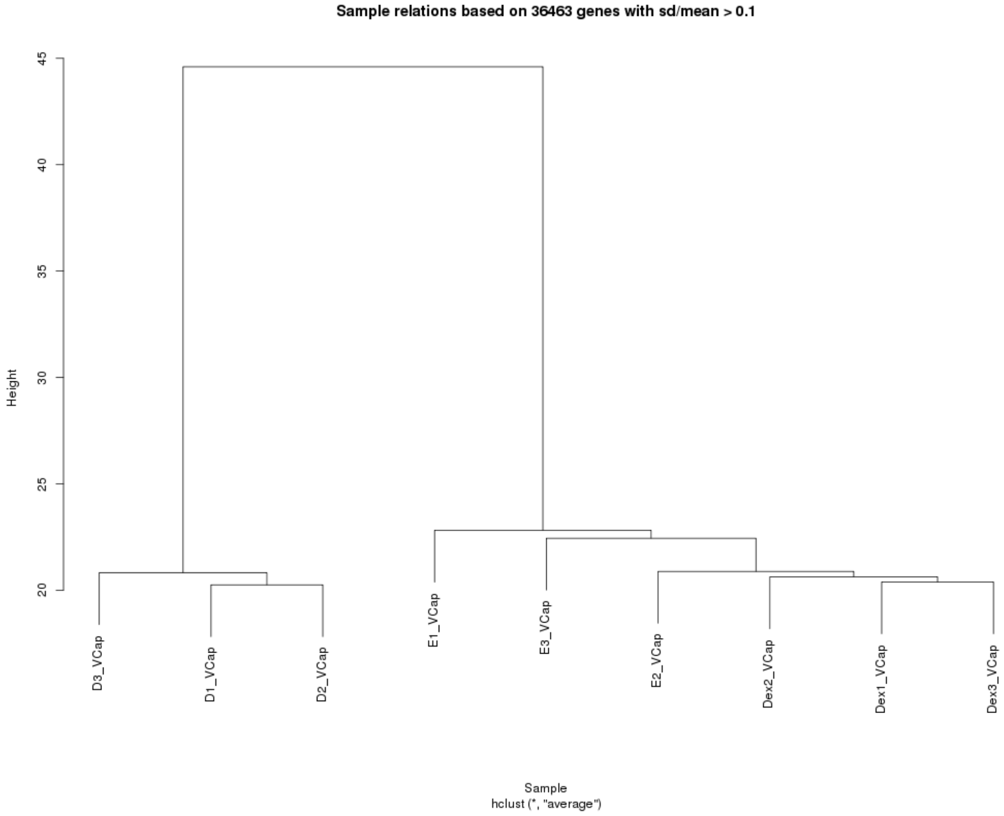


Figure 39: Hierarchical clustering is the assignment of a set of observations into subsets (clusters) so that observations in the same cluster are similar in some sense.

8 Illumina quality control (normalized)

8.1 Density plot

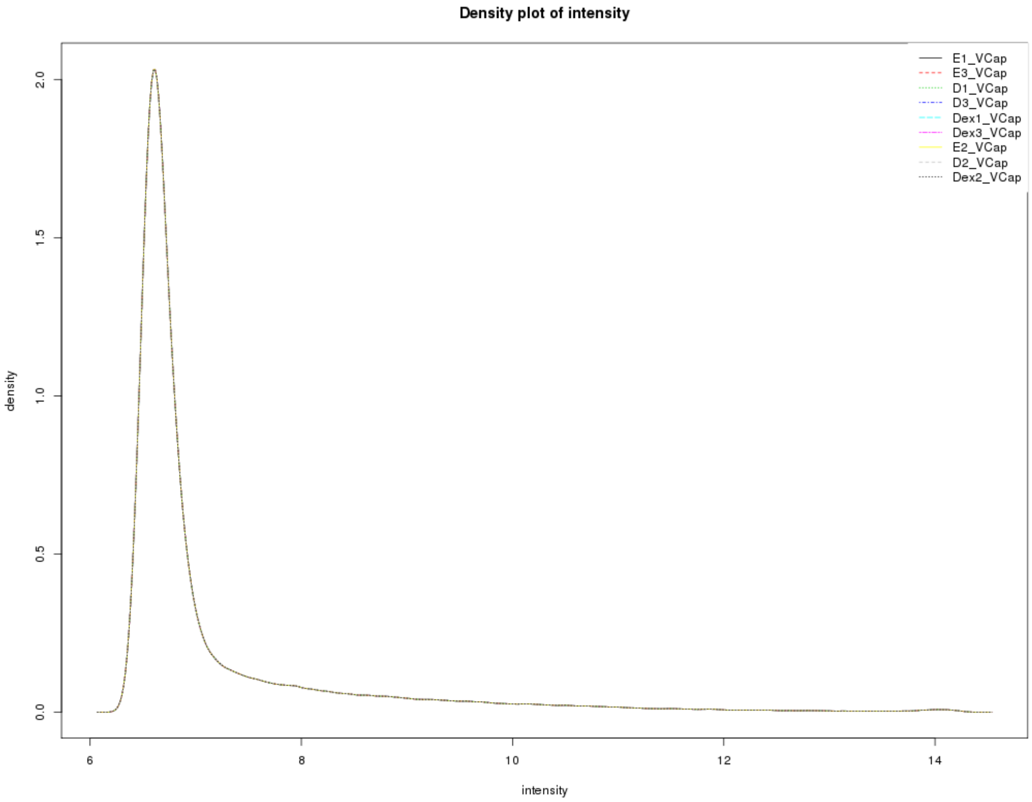


Figure 40: Density plot indicates the distribution of variables.

8.2 Box plot

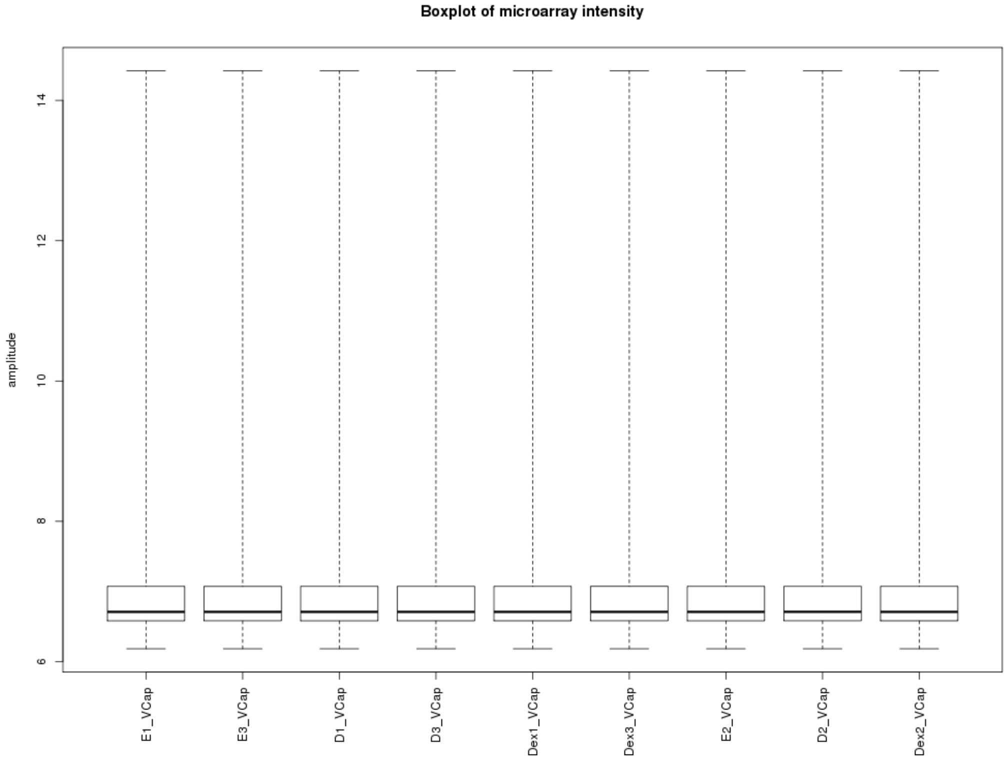


Figure 41: The bold line shows the location of median. The filled rectangle contains values between 25'th and 75'th percentile. The extremes show locations of minimum and maximum.

8.3 Scatter plot

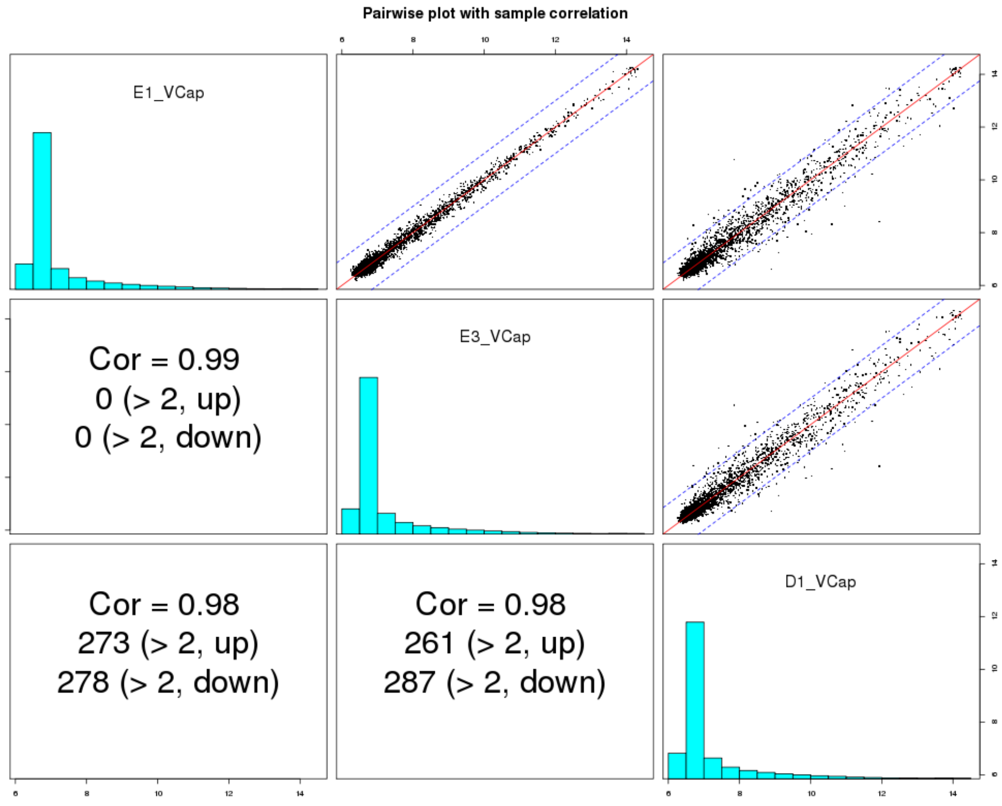


Figure 42: Scatter plot illustrates the degree of sample correlation.

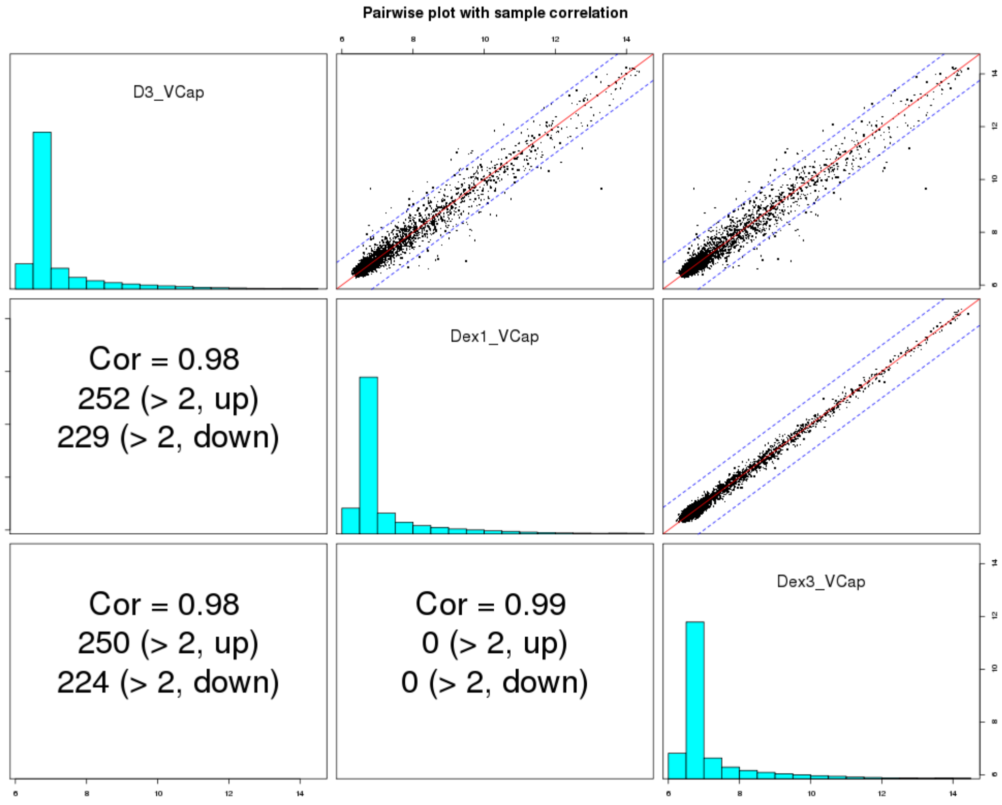


Figure 43: Scatter plot illustrates the degree of sample correlation.

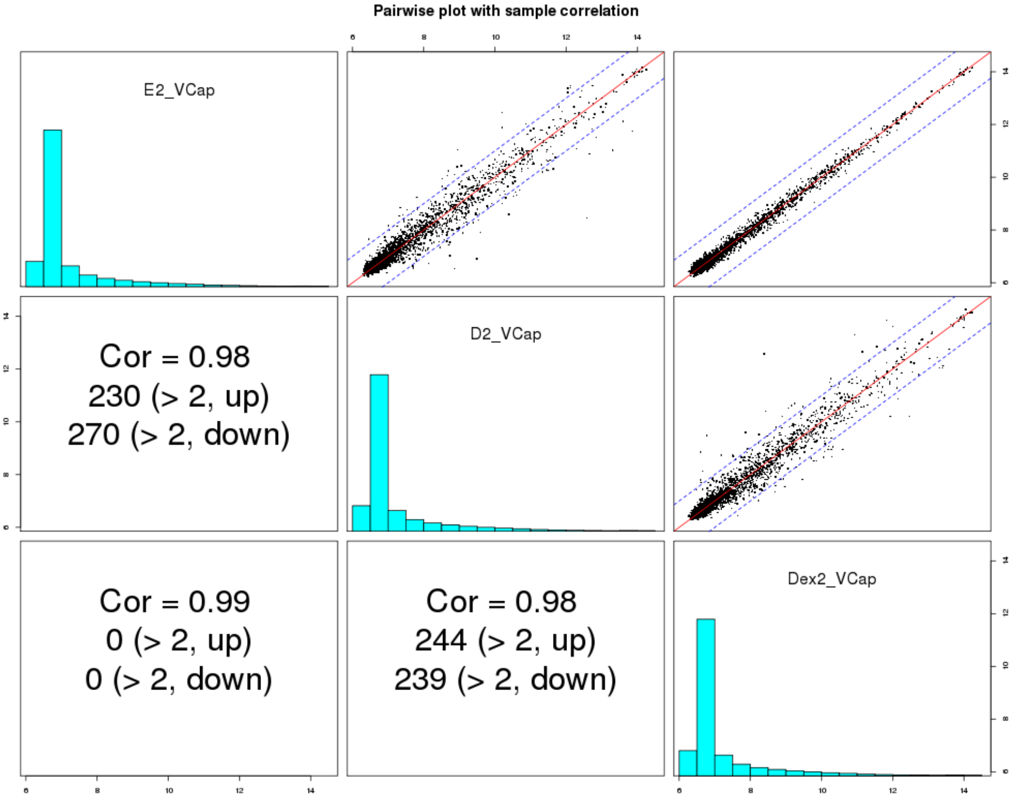


Figure 44: Scatter plot illustrates the degree of sample correlation.

8.4 MAXY-plot

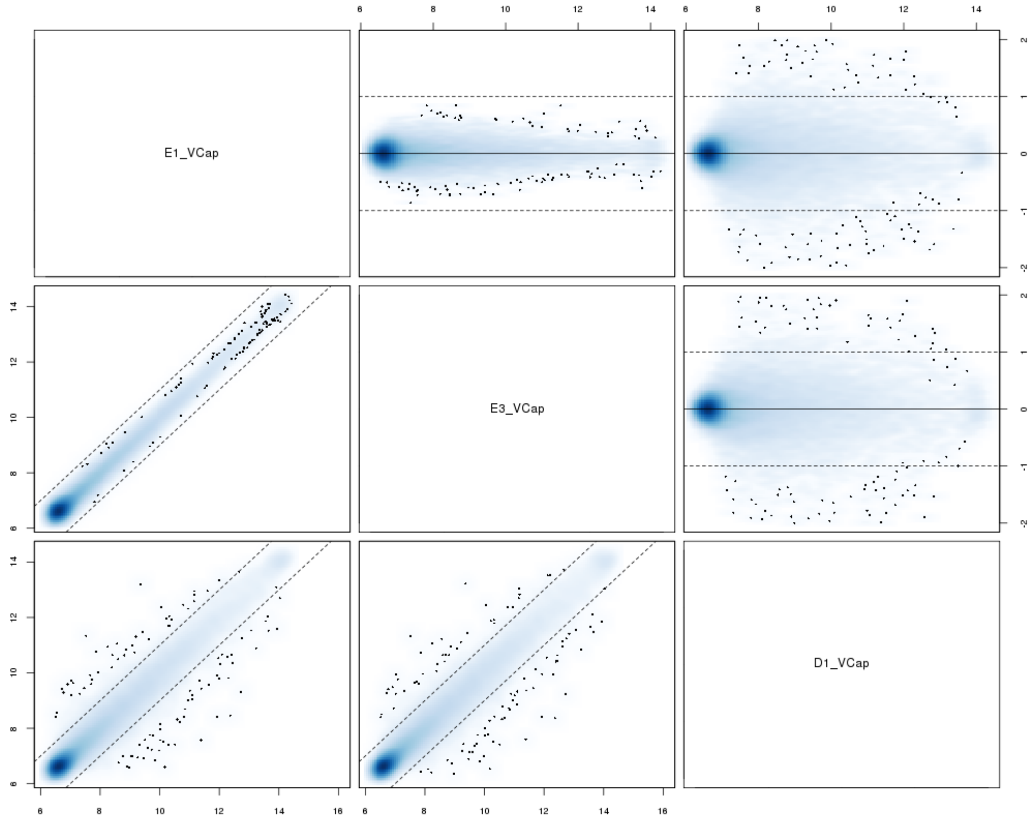


Figure 45: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

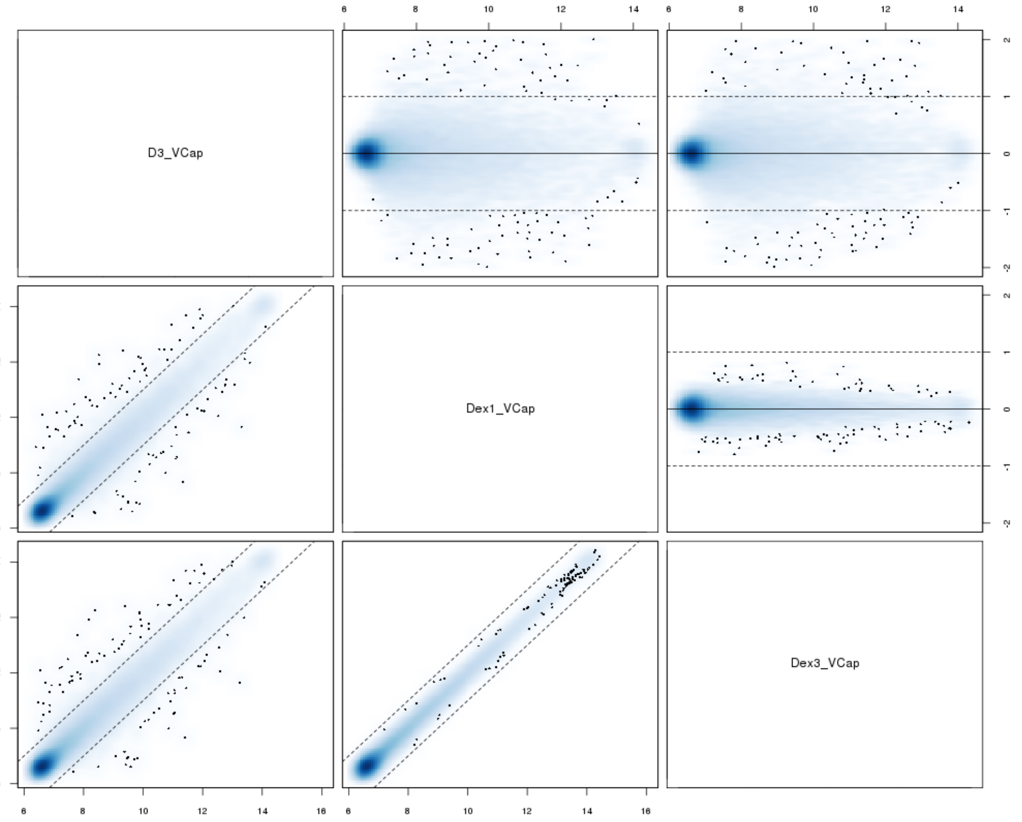


Figure 46: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

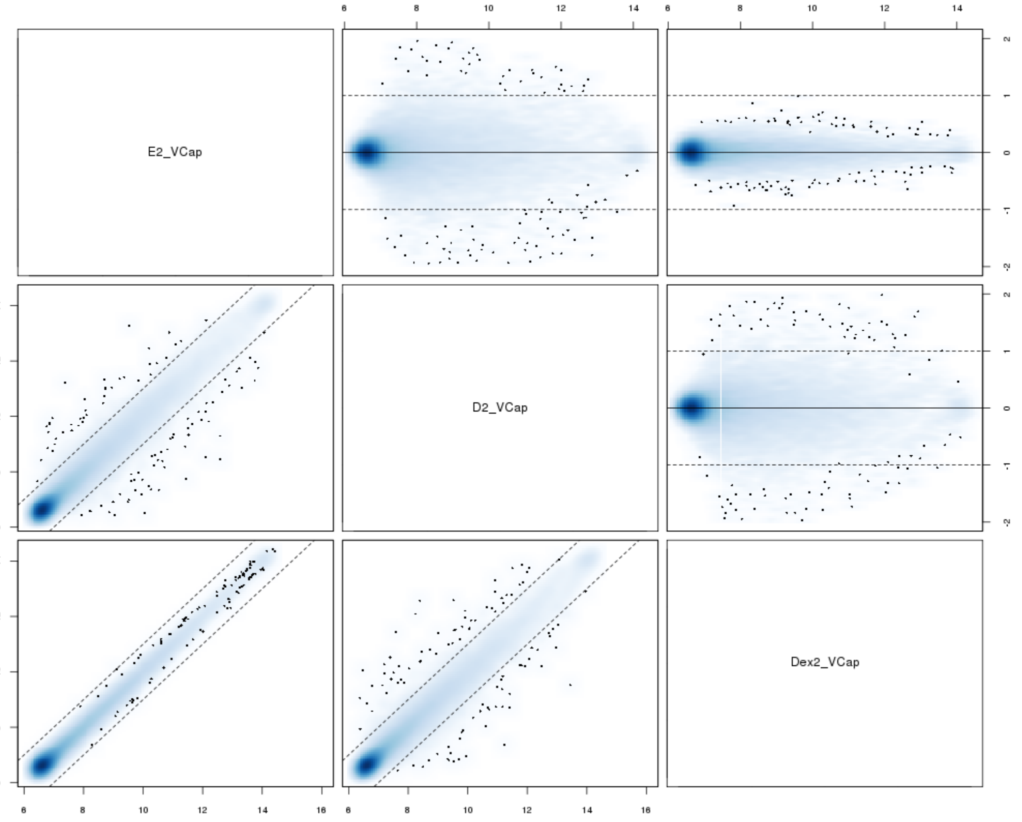


Figure 47: Scatter plots (in the lower left) illustrates the degree of sample correlation. MA-plots (in the upper right) visualizes intensity-dependent ratio of microarray data.

8.5 Sample relations (hierarchical clustering)

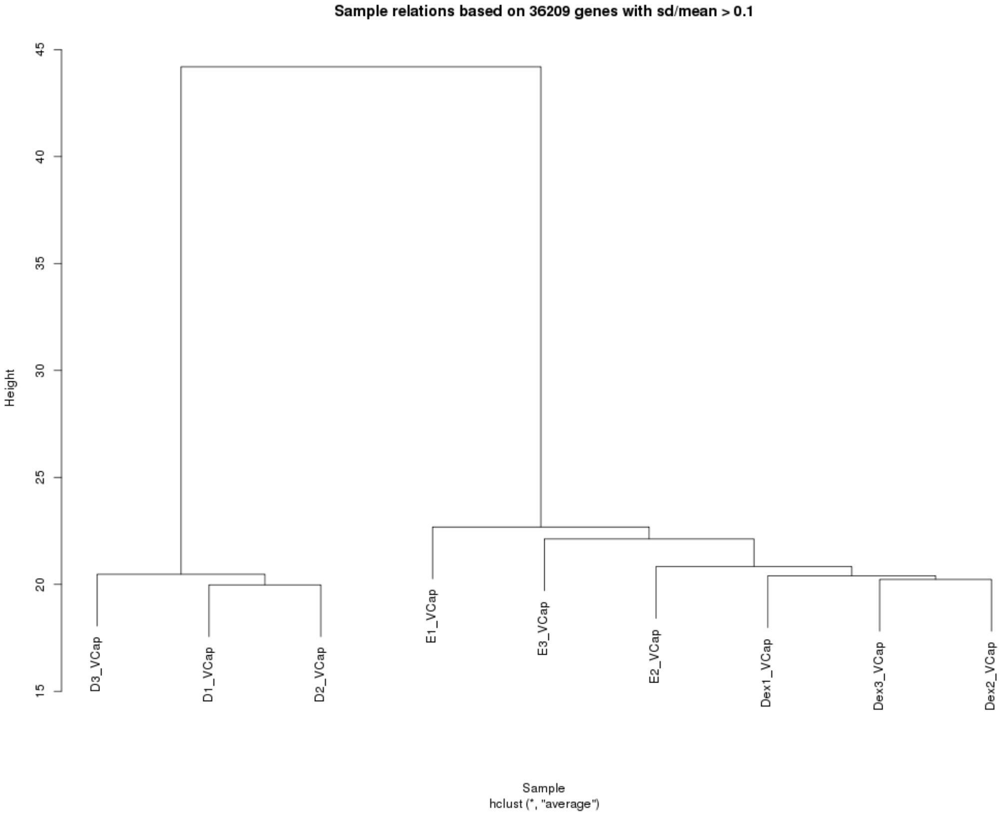


Figure 48: Hierarchical clustering is the assignment of a set of observations into subsets (clusters) so that observations in the same cluster are similar in some sense.

9 Summary of DEGs in VCaP

Gene set	Size
fcDv_fcOver	308
fcDv_fcUnder	282
fcDXv_fcOver	0
fcDXv_fcUnder	0

10 List of differentially expressed genes

Overexpressed genes are sorted with the most overexpressed first and underexpressed genes with the most underexpressed first. Genes go by the column first and then by row.

10.1 Gene set: fcDv_fcOver

Number of genes: 308

NCAPD3
ORM2
TMPRSS2
FKBP5
TUBA3D
AMACR
TUBA3E
SLC45A3
STEAP4
SPOCK1
NEFH
ALDH1A3
ACSL3
ERRFI1
RFPL3
DBI
SAT1
MBOAT2
CORO1B
HOMER2
PTPRCAP
SOCS2
AGR2
ATP1A1
CKLF
CTD-2224J9.2
TPM3P6
ODC1
ACAD8
NSDHL
TESC
DHCR24
ANKRD37
ELL2P1
ELL2
ZNF761
THOC5
HLA-DMB
SDF2L1
CKB
IL20RA
CDC42EP2
ATP2B4
DCXR
HMGCS1
B2M
ABCC4
AL391319.1
SMOC2
NDFIP2
EAF2
STK39
LIPG
MUM1L1
COQ10B
NDRG1
C22orf42
HIPK2
CRELD2
YIPF1
CYB5A
SPDEF
PPM1E
SMS
IDH1
CTD-2126E3.1
MAPK6
MRPL41
PRR15L
ADAMTS1
CMC2
TMEM79
LDLR
UGT2B11
HPGD
CEBPD
RP11-312J18.5
CECR6
CENPN
THYN1
TRIB2
C1QTNF3
NFKBIA
NBL1
EFR3A
LRIG1
ATP6V0A2
INSIG1
KLK4
PDCD4
RP11-397D21.1
VPS26B
DYNLL2
GLB1L2
GLIPR2
CYP1B1
LYN
ISG15
PHGR1
TUBA3C
MIR601
MAP7D1
G3BP2
VMP1
GNMT
C17orf62
SCD
CXADR
OSTF1
MANF
PMEPA1
C18orf8
TMEM8A
RP11-18F14.2
SNAP91
DNAJB11
TIPARP
CYTH1
EPDR1
HES4
IGF1R
HIST2H2BE
RAP1GAP
PPAPDC2
TBX15
NUDT22
ATP6V0D1
FAM189A2
ABHD3
ZNF217
WWC1
RP11-29G8.3
UCHL3
ZBTB16
C11orf48
C19orf10
AC061975.9
ARPC1B
MESP1
ARPC5L
C1orf87
SPPL2A
IDH3A
IDI1
COX17
COX17P1
ANXA1
FDFT1
TRIM68
TUBB4B
SERINC2
TMC6
BRP44
CNN3
FASN
HMGXB3
WIPI1
STEAP2
SASH1
MSMO1
UGT2B7
ZCCHC6
CLDN8
CTD-2653M23.1
HMG20B
UAP1
KRT8
FZD9
PSMD1
KIF22
COPE
EML1
HIGD1A
HIGD1AP1
SORD
SEC11C
AC012652.1
TAX1BP1
MERTK
CHPT1
P4HB
SLC35B1
INSM1
OCEL1
TOR2A
AMIGO3
BMPR1B
GTF2E2
PEA15
LRRFIP2
DHCR7
MFSD5
FKBP11
AC073610.5
FADS1
SOX9
ENDOD1
ENDOD1
FAM43A
CDK2AP2
KLK2
CYCSP55
CORO2A
CNDP2
STRA13
ACTR2
ZNF350
RNF103
CIB1
UCK2
ZFP36
ISOC2
LUZP1
NAAA
PRKCH
C1orf122
FICD
ATP6V0B
UGT2B28
ST6GALNAC1
TPM3
CCDC86
BCAR3
SEC61B
RRAS
CCND3
SLC15A2
HERC3
CREB3L2
PIAS1
MAP3K6
FAM18B1
DNAJB9
ELOVL6
TMED9
PRAGMIN
MAN2B2
DNASE2B
SELS
PTPLB
CD9
TUBG1
TMEM141
SQLE
GTF3C6
LAT2
GORASP1
IP6K1
TM9SF2
CHFR
TACC1
SLC4A7
ASCC1
CTC-554D6.1
SRP19
BOLA2
BOLA2B
RRP36
TRPM8
ENG
SHROOM3
MYOF
RPN1
MOB4
SURF4
PVRL2
HMGCS2
RP11-350O14.18
LRRC26
SLC35F2
SEC14L1
ARF4
APIP
ENO1
AP2S1
FAM107A
ALG8
ELOVL5
ARPC3
EHD4
KCNMA1
RAB11A
MYBPC1
MPZL1
ATP1B1
RALY
SMPD2
FZD5
ATAD2
C9orf91
TXNDC17
RP5-977B1.10
C20orf24
DNLZ
CYP2U1
FZD8
AEN
PPPDE2
DEGS1
CLINT1
NGLY1
CSRNP1
CTD-2008A1.2
ZNF35
GPCPD1
RABEP1
ARIH1
RHBDD2

10.2 Gene set: fcDv_fcUnder

Number of genes: 282

TRIB1
IGFBP3
DDC
PPFIA2
IGFBP2
MYC
MYL5
JUN
MPP1
TFF3
ATG7
PRSS23
HSD17B8
HSD17B8
HSD17B8
HSD17B8
SNHG5
CXCL16
RPL14
DOCK10
FAM110B
EPHA4
SLC25A23
ST13P15
IMPDH2
NAT14
SLC4A4
CYP4V2

ST7
ALB
NSG1
EPB41L4A-AS1
TTR
CCDC83
7SK
7SK
RN7SK
AC015849.1
RP11-161M6.4
AC009041.1
CMBL
CAMK2N1
C11orf92
C7orf41
MGP
ZNF385B
CTSF
TSPAN8
LTA4H
INSM2
CHGA
RNASET2
RP11-375B1.3
WNT2
SCGB1D2
HSD17B6
GNG4
MAFB
TSPAN7
FLNB
MACROD1
KIAA1199
FAM134B
ZNF581
CBR4
PRKD1
VSTM2L
CTNNBL1
RP11-781P14.3
C14orf135
JAM3
AKR1C3
RPL32P29
PRSS3
AP001816.1
PRAC
GLTSCR2
SNORD23
KHDRBS3
CCDC28A
MT3
AC073346.2
VPS37D
RP11-371B4.2
RP11-84A1.1
PRIM1
MUCL1
PAK1
COLEC12
SLC18B1
ITM2A
CADM1
BAMBI
C14orf132
MYT1
ZNF503
PLA2G7
KIAA1467
MST1P2
AC099668.5
MST1P9
MST1
SALL2
RAB17
EXOSC5
STC2
MMP10
NOV
MAP7D2
PNCK
POLR1E
SCGB2A1
KLHL35
TRAPPC6A
BCL11A
RP11-359H18.1
RP3-423B22.5
RP11-25I15.1
ABCC8
SEZ6
SPINK1
UBAP2L
C1orf115
MAPKAPK3
RP11-3L10.3
SH3RF1
LYPD6B
LANCL1
AR
EFNB2
RP11-4M23.7
SERPINI1
TOX2
CTC-435M10.3
BCKDHA
TMEM158
AC010170.1
NPEPL1
HSD17B8
HSD17B8
KLHL3
GRIA2
PTGER2
ENDOV
EIF4B
YPEL2
EPHB6
CCNG2
SCGN
SCNN1D
KIAA1875
CYB5D2
PRRT3
RAMP1
REEP1
TXNIP
SLC16A10
ARL6IP1
ZNF395
SCIN
HEBP1
CHGB
ARHGEF2
AC013404.1
PHB2
ABCC5
NTM
FAM171A1
LASP1
MID1
FERMT1
S100A10
RPL13AP6
TMEM145
HAUS4
RP11-298I3.5
GOLIM4
CAPRIN2
ERP27
ACSS1
WDR59
NRSN1
VTN
PELI2
MYH10
TMEM238
PHGDH
EIF3D
DHRS7
ISCU
AC016712.2
EIF3H
CTD-2329C7.1
NKX2-2
RP11-118H4.1
SNORD73A
PTGER4
DPYSL2
ZIC2
DGCR6L
AKR7A2
C20orf27
NCALD
RP11-832N8.1
ARHGEF3
WDR54
TMEM74B
CRIPAK
RP11-87M1.1
TOP1MT
RPS15A
RP11-824M15.1
SLC17A4
RPL23
YPEL1
FAM117B
EIF3L
FBLN2
PHKA2
LUM
CLYBL
PGAP3
BRD8
C17orf70
KBTBD11
SSH2
RP11-31K13.1
SUCLG2
RP11-162K6.1
SORL1
MAP3K5
RP11-16F15.2
SOX13
HNRNPA1P12
RPL12
AC011737.2
RPL12P4
RP11-434O22.1
RP11-106M3.1
RPL12L3
RPL12P8
RAB6B
GRAMD1A
PKIA
CAPN5
RP1-256G22.1
C11orf2
SGSM2
EIF2D
SNORD52
GSTA4
ZC2HC1A
RPS23
SH3GL3
RPL14P1
ABHD1
RP5-866L20.3
HNRNPA1P2
GATA2
DPYSL3
RNF144A
AC093107.7
RPLP0
OAF
OGDHL
FAM113A
GUCY1A3
DDIT4L
BTF3
C20orf72
GPSM1
TRNP1
NENF
CTSH
ZSCAN18
QARS
AL592188.3
AL592188.11
AL592188.4
AL592188.14
AL928646.1
PPOX

10.3 Gene set: fcDXv_fcOver

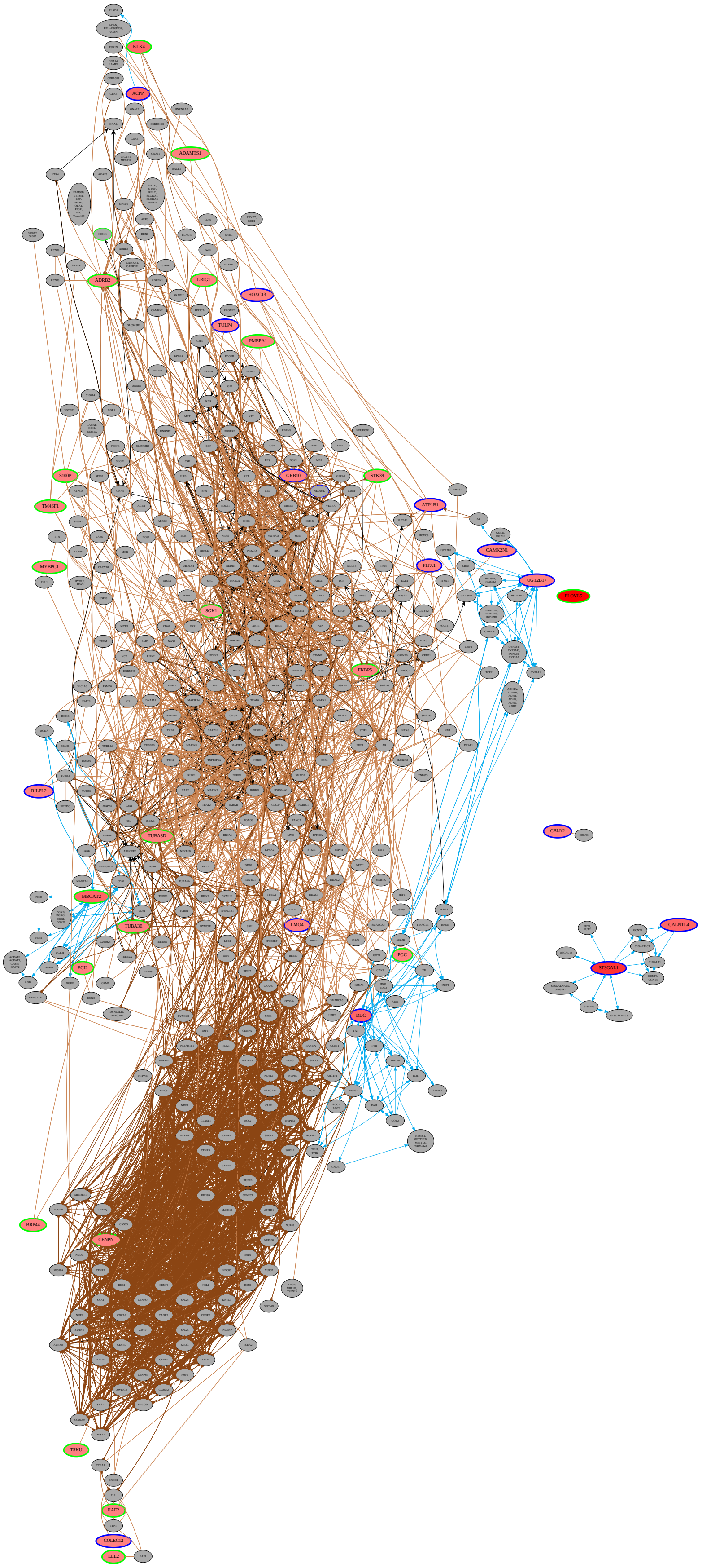
Number of genes: 0

10.4 Gene set: fcDXv_fcUnder

Number of genes: 0

11 Candidate report for DEG DHT CPA RU486

11.1 Moksiskaan candidate pathway



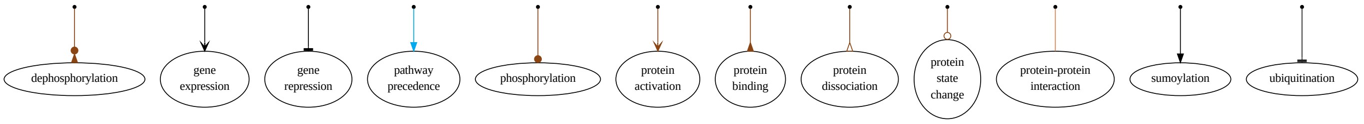


Figure 49: Known relationships between the candidate genes. Candidate genes are shown in red if they have only output connections. The ratio of input and output connections determines how light they are. Completely white genes have only input connections. The network of candidate genes is expanded by fetching genes 1 step(s) down stream. The down stream genes are shown on gray. Green and blue borders are referring to up and down regulated genes, respectively. Light grey is used to emphasize stably expressed genes. Known regulations are shown with bold borders whereas the predictions are kept thin.

Table 23: Descriptions of the intermediated genes between the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. This table has 465 rows.

name	description	studies
A2M	alpha-2-macroglobulin [Source:HGNC Symbol;Acc:7] locus=12:9220260-9268825	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE
AATK	apoptosis-associated tyrosine kinase [Source:HGNC Symbol;Acc:21] locus=17:79091095-79139877	tcgaColonMethyl, tcgaGliomaGE, tscapeMelanomaa, tscapeNSCLCa
ABI1	abl-interactor 1 [Source:HGNC Symbol;Acc:11320] locus=10:27035522-27150016	snp3dMetastasis, tcgaBreastMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
ABL1	c-abl oncogene 1, non-receptor tyrosine kinase [Source:HGNC Symbol;Acc:76] locus=9:133589268-133763062	cosmicRecurrent, tcgaColonMethyl, tcgaGliomaGE
ABP1	amiloride binding protein 1 (amine oxidase (copper-containing)) [Source:HGNC Symbol;Acc:80] locus=7:150521715-150558592	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomaa
ACAN	aggrecan [Source:HGNC Symbol;Acc:319] locus=15:89346674-89418585	cosmicMetastasis, tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeNSCLCa
ADH1A	alcohol dehydrogenase 1A (class I), alpha polypeptide [Source:HGNC Symbol;Acc:249] locus=4:100197524-100212185	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianGE, tscapeHCCd
ADH1B	alcohol dehydrogenase 1B (class I), beta polypeptide [Source:HGNC Symbol;Acc:250] locus=4:100226121-100242558	tcgaBreastGE, tcgaOvarianGE, tscapeHCCd
ADH4	alcohol dehydrogenase 4 (class II), pi polypeptide [Source:HGNC Symbol;Acc:252] locus=4:100044808-100078949	tcgaBreastGE, tscapeHCCd
ADH5	alcohol dehydrogenase 5 (class III), chi polypeptide [Source:HGNC Symbol;Acc:253] locus=4:99992132-100009952	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd
ADH6	alcohol dehydrogenase 6 (class V) [Source:HGNC Symbol;Acc:255] locus=4:100123795-100140694	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeHCCd
ADH7	alcohol dehydrogenase 7 (class IV), mu or sigma polypeptide [Source:HGNC Symbol;Acc:256] locus=4:100333418-100356894	cosmicMetastasis, tscapeHCCd
ADRB3	adrenergic, beta-3-, receptor [Source:HGNC Symbol;Acc:288] locus=8:37820516-37824483	snp3dDiabetes, snp3dObesity, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeCRCa, tscapeHCCd, tscapeNSCLCd
ADRBK1	adrenergic, beta, receptor kinase 1 [Source:HGNC Symbol;Acc:289] locus=11:67033881-67054027	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE
AFMID	arylformamidase [Source:HGNC Symbol;Acc:20910] locus=17:76183437-76203782	tcgaColonGE
AGER	advanced glycosylation end product-specific receptor [Source:HGNC Symbol;Acc:320] locus=6:32148745-32152101	tcgaColonGE, tcgaColonMethyl
AGK	acylglycerol kinase [Source:HGNC Symbol;Acc:21869] locus=7:141250989-141355044	tcgaBreastGE, tcgaColonGE, tcgaOvarianGE
AGPAT6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophosphatidic acid acyltransferase, zeta) [Source:HGNC Symbol;Acc:20880] locus=8:41434706-41482520	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeSCLCa
AGPAT9	1-acylglycerol-3-phosphate O-acyltransferase 9 [Source:HGNC Symbol;Acc:28157] locus=4:84457067-84527028	tcgaBreastGE, tcgaColonGE, tscapeHCCd
AHCTF1	AT hook containing transcription factor 1 [Source:HGNC Symbol;Acc:24618] locus=1:247002400-247095280	tscapeBCa, tscapeMelanomaa, tscapeNSCLCa, tscapeOvariana
AKAP12	A kinase (PRKA) anchor protein 12 [Source:HGNC Symbol;Acc:370] locus=6:151561134-151679692	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeOvariand
AKAP5	A kinase (PRKA) anchor protein 5 [Source:HGNC Symbol;Acc:375] locus=14:64932217-64936425	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE
AKT1	v-akt murine thymoma viral oncogene homolog 1 [Source:HGNC Symbol;Acc:391] locus=14:105235686-105262088	tcgaBreastGE, tcgaGliomaGE, tscapeMelanomad
ANPEP	alanyl (membrane) aminopeptidase [Source:HGNC Symbol;Acc:500] locus=15:90328120-90358633	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeNSCLCa
AOC2	amine oxidase, copper containing 2 (retina-specific) [Source:HGNC Symbol;Acc:549] locus=17:40996609-41002722	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand
AOC3	amine oxidase, copper containing 3 (vascular adhesion protein 1) [Source:HGNC Symbol;Acc:550] locus=17:41003201-41010138	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand
APEX1	APEX nuclease (multifunctional DNA repair enzyme) 1 [Source:HGNC Symbol;Acc:587] locus=14:20923350-20925927	snp3dGlioma, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
APITD1	apoptosis-inducing, TAF9-like domain 1 [Source:HGNC Symbol;Acc:23163] locus=1:10490159-10512210	tcgaBreastGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
AR	androgen receptor [Source:HGNC Symbol;Acc:644] locus=X:66763874-66950461	fileAmpOver, snp3dBC, snp3dProstateC, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeProstatea
ARHGEF2	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Source:HGNC Symbol;Acc:682] locus=1:155916645-155966129	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCa, tscapeProstated
ARR3	arrestin 3, retinal (X-arrestin) [Source:HGNC Symbol;Acc:710] locus=X:69488155-69501690	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
ARRB1	arrestin, beta 1 [Source:HGNC Symbol;Acc:711] locus=11:74975226-75062873	tcgaBreastGE, tcgaGliomaGE
ARRB2	arrestin, beta 2 [Source:HGNC Symbol;Acc:712] locus=17:4613784-4624794	snp3dMetastasis, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
ATP5D	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit [Source:HGNC Symbol;Acc:837] locus=19:1241749-1244823	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianGE, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeNSCLCd
AURKB	aurora kinase B [Source:HGNC Symbol;Acc:11390] locus=17:8108051-8113936	fileCIN70, snp3dGlioma, tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
B3GALT4	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4 [Source:HGNC Symbol;Acc:919] locus=6:33244917-33246602	cosmicPrimary
B9D2	B9 protein domain 2 [Source:HGNC Symbol;Acc:28636] locus=19:41860322-41870078	
BACE1	beta-site APP-cleaving enzyme 1 [Source:HGNC Symbol;Acc:933] locus=11:117156402-117186975	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd

Continued on next page...

name	description	studies
BCR	breakpoint cluster region [Source:HGNC Symbol;Acc:1014] locus=22:23521891-23660224	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
BIRC5	baculoviral IAP repeat containing 5 [Source:HGNC Symbol;Acc:593] locus=17:76210277-76221715	snp3dGlioma, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
BRAF	v-raf murine sarcoma viral oncogene homolog B1 [Source:HGNC Symbol;Acc:1097] locus=7:140424943-140624564	cosmicMetastasis, cosmicPrimary, cosmicRecurrent, snp3dCRC, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomaa
BRCA1	breast cancer 1, early onset [Source:HGNC Symbol;Acc:1100] locus=17:41196312-41322290	snp3dBC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeBCd
BUB1	budding uninhibited by benzimidazoles 1 homolog (yeast) [Source:HGNC Symbol;Acc:1148] locus=2:111395275-111435691	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
BUB1B	budding uninhibited by benzimidazoles 1 homolog beta (yeast) [Source:HGNC Symbol;Acc:1149] locus=15:40453224-40513337	tcgaGliomaGE, tscapeCRCd, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand
BUB3	budding uninhibited by benzimidazoles 3 homolog (yeast) [Source:HGNC Symbol;Acc:1151] locus=10:124913793-124924886	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeGliomad, tscapeNSCLCd
C1GALT1	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1 [Source:HGNC Symbol;Acc:24337] locus=7:7196565-7288251	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE
C1GALT1C1	C1GALT1-specific chaperone 1 [Source:HGNC Symbol;Acc:24338] locus=X:119759648-119764005	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
C20orf24	chromosome 20 open reading frame 24 [Source:HGNC Symbol;Acc:15870] locus=20:35234137-35240960	tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa
CACYBP	calcyclin binding protein [Source:HGNC Symbol;Acc:30423] locus=1:174968300-174980851	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeRCCa
CAMKK1	calcium/calmodulin-dependent protein kinase kinase 1, alpha [Source:HGNC Symbol;Acc:1469] locus=17:3763609-3798185	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
CAMKK2	calcium/calmodulin-dependent protein kinase kinase 2, beta [Source:HGNC Symbol;Acc:1470] locus=12:121675497-121736111	tcgaGliomaGE
CARHSP1	calcium regulated heat stable protein 1, 24kDa [Source:HGNC Symbol;Acc:17150] locus=16:8946799-8962866	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
CASC5	cancer susceptibility candidate 5 [Source:HGNC Symbol;Acc:24054] locus=15:40886218-40956540	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tscapeCRCd, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand
CBL	Cbl proto-oncogene, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:1541] locus=11:119076752-119177651	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd
CBLN3	cerebellin 3 precursor [Source:HGNC Symbol;Acc:20146] locus=14:24895738-24900160	tscapeHCCa
CBR3	carbonyl reductase 3 [Source:HGNC Symbol;Acc:1549] locus=21:37507210-37518864	tcgaColonMethyl, tcgaOvarianMethyl
CCDC99	coiled-coil domain containing 99 [Source:HGNC Symbol;Acc:26010] locus=5:169010638-169031782	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianGE, tscapeNSCLCa, tscapeRCCa
CCNT1	cyclin T1 [Source:HGNC Symbol;Acc:1599] locus=12:49082247-49110681	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCa
CD40	CD40 molecule, TNF receptor superfamily member 5 [Source:HGNC Symbol;Acc:11919] locus=20:44746911-44758502	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
CD46	CD46 molecule, complement regulatory protein [Source:HGNC Symbol;Acc:6953] locus=1:207925402-207968858	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
CDC20	cell division cycle 20 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:1723] locus=1:43824599-43828874	fileCIN70, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
CDC37	cell division cycle 37 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:1735] locus=19:10501809-10514271	tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd
CDCA8	cell division cycle associated 8 [Source:HGNC Symbol;Acc:14629] locus=1:38158090-38175391	fileCIN70, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
CDK9	cyclin-dependent kinase 9 [Source:HGNC Symbol;Acc:1780] locus=9:130547958-130553066	tcgaBreastMethyl, tcgaOvarianMethyl
CDS1	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 1 [Source:HGNC Symbol;Acc:1800] locus=4:85504132-85572491	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
CDS2	CDP-diacylglycerol synthase (phosphatidate cytidylyltransferase) 2 [Source:HGNC Symbol;Acc:1801] locus=20:5107432-5178533	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE
CENPA	centromere protein A [Source:HGNC Symbol;Acc:1851] locus=2:26987157-27023935	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
CENPC1	centromere protein C 1 [Source:HGNC Symbol;Acc:1854] locus=4:68337521-68411324	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
CENPE	centromere protein E, 312kDa [Source:HGNC Symbol;Acc:1856] locus=4:104026963-104119566	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
CENPF	centromere protein F, 350/400kDa (mitosin) [Source:HGNC Symbol;Acc:1857] locus=1:214776538-214837931	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
CENPH	centromere protein H [Source:HGNC Symbol;Acc:17268] locus=5:68485375-68506184	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
CENPI	centromere protein I [Source:HGNC Symbol;Acc:3968] locus=X:100353178-100418670	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE
CENPK	centromere protein K [Source:HGNC Symbol;Acc:29479] locus=5:64813593-64858998	tcgaBreastGE, tcgaBreastGESurv, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
CENPL	centromere protein L [Source:HGNC Symbol;Acc:17879] locus=1:173768688-173793858	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tscapeRCCa
CENPM	centromere protein M [Source:HGNC Symbol;Acc:18352] locus=22:42334725-42343168	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
CENPO	centromere protein O [Source:HGNC Symbol;Acc:28152] locus=2:25016005-25045245	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE
CENPP	centromere protein P [Source:HGNC Symbol;Acc:32933] locus=9:95087766-95382815	tcgaBreastGE
CENPQ	centromere protein Q [Source:HGNC Symbol;Acc:21347] locus=6:49431096-49460820	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tscapeNSCLCa
CENPT	centromere protein T [Source:HGNC Symbol;Acc:25787] locus=16:67862060-67881714	tcgaColonGE, tscapeOvariand
CHUK	conserved helix-loop-helix ubiquitous kinase [Source:HGNC Symbol;Acc:1974] locus=10:101948055-101989376	cosmicRecurrent, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeOvariand
CKAP5	cytoskeleton associated protein 5 [Source:HGNC Symbol;Acc:28959] locus=11:46764598-46867847	fileCIN70, tcgaBreastGE, tcgaColonMethyl, tcgaOvarianGE, tcgaOvarianMethyl
CLASP1	cytoplasmic linker associated protein 1 [Source:HGNC Symbol;Acc:17088] locus=2:122095354-122407163	tscapeProstated, tscapeRCCa
CLASP2	cytoplasmic linker associated protein 2 [Source:HGNC Symbol;Acc:17078] locus=3:33537737-33759848	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
CLIP1	CAP-GLY domain containing linker protein 1 [Source:HGNC Symbol;Acc:10461] locus=12:122755979-122907179	
CNBP	CCHC-type zinc finger, nucleic acid binding protein [Source:HGNC Symbol;Acc:13164] locus=3:128888327-128902765	
CNDP1	carnosine dipeptidase 1 (metallopeptidase M20 family) [Source:HGNC Symbol;Acc:20675] locus=18:72201675-72252261	tcgaGliomaGE, tscapeMelanomad, tscapeProstated
CREB1	cAMP responsive element binding protein 1 [Source:HGNC Symbol;Acc:2345] locus=2:208394461-208468155	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl

Continued on next page...

name	description	studies
CS	citrate synthase [Source:HGNC Symbol;Acc:2422] locus=12:56665483-56694176	tcgaOvarianMethyl
CSK	c-src tyrosine kinase [Source:HGNC Symbol;Acc:2444] locus=15:75074398-75095539	tcgaBreastGE, tcgaGliomaGE
CTNNB1	catenin (cadherin-associated protein), beta 1, 88kDa [Source:HGNC Symbol;Acc:2514] locus=3:41236328-41301587	cosmicPrimary, cosmicRecurrent, snp3dCRC, snp3dLungC, snp3dMetastasis, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
CYP19A1	cytochrome P450, family 19, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:2594] locus=15:51500254-51630807	cosmicMetastasis, snp3dBC, tcgaBreastMethyl, tcgaGliomaGE
CYP1A1	cytochrome P450, family 1, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:2595] locus=15:75011883-75017951	cosmicRecurrent, snp3dLungC, tcgaOvarianMethyl
CYP2D6	cytochrome P450, family 2, subfamily D, polypeptide 6 [Source:HGNC Symbol;Acc:2625] locus=22:42522501-42540472	tscapeGliomad
CYP3A4	cytochrome P450, family 3, subfamily A, polypeptide 4 [Source:HGNC Symbol;Acc:2637] locus=7:99354604-99381888	tcgaBreastGE, tscapeNSCLCa
CYP3A43	cytochrome P450, family 3, subfamily A, polypeptide 43 [Source:HGNC Symbol;Acc:17450] locus=7:99425636-99463718	tscapeNSCLCa
CYP3A5	cytochrome P450, family 3, subfamily A, polypeptide 5 [Source:HGNC Symbol;Acc:2638] locus=7:99245817-99277621	tcgaBreastGE, tscapeNSCLCa
CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7 [Source:HGNC Symbol;Acc:2640] locus=7:99293368-99332819	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeNSCLCa
DDB1	damage-specific DNA binding protein 1, 127kDa [Source:HGNC Symbol;Acc:2717] locus=11:61066923-61110068	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
DDR1	discoidin domain receptor tyrosine kinase 1 [Source:HGNC Symbol;Acc:2730] locus=6:30844198-30867933	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
DDX6	DEAD (Asp-Glu-Ala-Asp) box helicase 6 [Source:HGNC Symbol;Acc:2747] locus=11:118620034-118661858	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeRCCd
DEAF1	deformed epidermal autoregulatory factor 1 (Drosophila) [Source:HGNC Symbol;Acc:14677] locus=11:644233-706715	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand
DGKA	diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;Acc:2849] locus=12:56321103-56347811	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
DGKB	diacylglycerol kinase, beta 90kDa [Source:HGNC Symbol;Acc:2850] locus=7:14184674-15014402	cosmicMetastasis, tcgaGliomaGE
DGKD	diacylglycerol kinase, delta 130kDa [Source:HGNC Symbol;Acc:2851] locus=2:234263153-234380750	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
DGKE	diacylglycerol kinase, epsilon 64kDa [Source:HGNC Symbol;Acc:2852] locus=17:54911460-54946036	tcgaBreastGESurv, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa
DGKG	diacylglycerol kinase, gamma 90kDa [Source:HGNC Symbol;Acc:2853] locus=3:185823457-186080026	tcgaBreastMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
DGKH	diacylglycerol kinase, eta [Source:HGNC Symbol;Acc:2854] locus=13:42614176-42830714	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
DGKI	diacylglycerol kinase, iota [Source:HGNC Symbol;Acc:2855] locus=7:137073563-137531838	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
DGKQ	diacylglycerol kinase, theta 110kDa [Source:HGNC Symbol;Acc:2856] locus=4:952675-980683	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd
DGKZ	diacylglycerol kinase, zeta [Source:HGNC Symbol;Acc:2857] locus=11:46354455-46402104	tcgaGliomaGE, tcgaOvarianMethyl
DNAJA1	DnaJ (Hsp40) homolog, subfamily A, member 1 [Source:HGNC Symbol;Acc:5229] locus=9:33025209-33039905	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
DOK1	docking protein 1, 62kDa (downstream of tyrosine kinase 1) [Source:HGNC Symbol;Acc:2990] locus=2:74776153-74784681	cosmicRecurrent, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
DSN1	DSN1, MIND kinetochore complex component, homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:16165] locus=20:35380194-35402230	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE
DVL3	dishevelled, dsh homolog 3 (Drosophila) [Source:HGNC Symbol;Acc:3087] locus=3:183873176-183891398	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
DYNC1H1	dynein, cytoplasmic 1, heavy chain 1 [Source:HGNC Symbol;Acc:2961] locus=14:102430865-102517129	cosmicPrimary, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad
DYNC1I1	dynein, cytoplasmic 1, intermediate chain 1 [Source:HGNC Symbol;Acc:2963] locus=7:95401866-95739634	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2 [Source:HGNC Symbol;Acc:2964] locus=2:172543919-172604930	
DYNC1LI1	dynein, cytoplasmic 1, light intermediate chain 1 [Source:HGNC Symbol;Acc:18745] locus=3:32567463-32612366	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
DYNC1LI2	dynein, cytoplasmic 1, light intermediate chain 2 [Source:HGNC Symbol;Acc:2966] locus=16:66754796-66785701	tcgaColonGE, tscapeOvariand
DYNC2H1	dynein, cytoplasmic 2, heavy chain 1 [Source:HGNC Symbol;Acc:2962] locus=11:102980160-103350591	tcgaBreastGE, tcgaColonGE
DYNLL1	dynein, light chain, LC8-type 1 [Source:HGNC Symbol;Acc:15476] locus=12:120907653-120936296	tcgaBreastGE, tcgaGliomaGE
EAF1	ELL associated factor 1 [Source:HGNC Symbol;Acc:20907] locus=3:15468862-15484120	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
EGF	epidermal growth factor [Source:HGNC Symbol;Acc:3229] locus=4:110834040-110933422	tcgaBreastMethyl, tcgaColonMethyl, tscapeHCCd
EGFR	epidermal growth factor receptor [Source:HGNC Symbol;Acc:3236] locus=7:55086714-55324313	cosmicMetastasis, cosmicPrimary, cosmicRecurrent, fileAmpOver, snp3dBC, snp3dGlioma, snp3dLungC, snp3dMetastasis, snp3dProstateC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHa, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeNSCLCa
EGR1	early growth response 1 [Source:HGNC Symbol;Acc:3238] locus=5:137801169-137805004	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
EIF3F	eukaryotic translation initiation factor 3, subunit F [Source:HGNC Symbol;Acc:3275] locus=11:7991798-8023409	tcgaBreastGE, tcgaOvarianGE
EIF3I	eukaryotic translation initiation factor 3, subunit I [Source:HGNC Symbol;Acc:3272] locus=1:32687529-32697205	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand
ELF1	E74-like factor 1 (ets domain transcription factor) [Source:HGNC Symbol;Acc:3316] locus=13:41506056-41635576	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
ELK1	ELK1, member of ETS oncogene family [Source:HGNC Symbol;Acc:3321] locus=X:47494920-47510003	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
ELL	elongation factor RNA polymerase II [Source:HGNC Symbol;Acc:23114] locus=19:18553475-18632937	tcgaGliomaGE, tcgaOvarianMethyl, tscapeRCCd
EPHB1	EPH receptor B1 [Source:HGNC Symbol;Acc:3392] locus=3:134316643-134979309	cosmicMetastasis, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
ERBB2	v-erb-b2 erythroblastic leukemia viral oncogene homolog 2, neuro/glioblastoma derived oncogene homolog (avian) [Source:HGNC Symbol;Acc:3430] locus=17:37844393-37884915	cosmicRecurrent, fileAmpOver, snp3dBC, snp3dLungC, snp3dMetastasis, snp3dProstateC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeCRCa, tscapeCRCd, tscapeNSCLCa, tscapeOvariand, tscapeSCLCd
ERBB3	v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (avian) [Source:HGNC Symbol;Acc:3431] locus=12:56473641-56497289	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
ERBB4	v-erb-a erythroblastic leukemia viral oncogene homolog 4 (avian) [Source:HGNC Symbol;Acc:3432] locus=2:212240446-213403565	cosmicMetastasis, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd, tscapeRCCd

Continued on next page...

name	description	studies
ERCC6L	excision repair cross-complementing rodent repair deficiency, complementation group 6-like [Source:HGNC Symbol;Acc:20794] locus=X:71424510-71458897	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE
ESR1	estrogen receptor 1 [Source:HGNC Symbol;Acc:3467] locus=6:151977826-152450754	snp3dBC, tcgaBreastMethyl, tcgaColonMethyl, tscapeOvariand
EXOC1	exocyst complex component 1 [Source:HGNC Symbol;Acc:30380] locus=4:56719782-56771200	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
EZR	ezrin [Source:HGNC Symbol;Acc:12691] locus=6:159186773-159240444	tcgaBreastGE, tcgaColonGE, tscapeBCd, tscapeOvariand, tscapeProstated
FAM98B	family with sequence similarity 98, member B [Source:HGNC Symbol;Acc:26773] locus=15:38746328-38779911	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeCRCd, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand
FANCA	Fanconi anemia, complementation group A [Source:HGNC Symbol;Acc:3582] locus=16:89803957-89883065	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeNSCLCd, tscapeProstated
FBL	fibrillarin [Source:HGNC Symbol;Acc:3599] locus=19:40325094-40337054	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd, tscapeNSCLCa, tscapeOvariana, tscapeRCCd
FES	feline sarcoma oncogene [Source:HGNC Symbol;Acc:3657] locus=15:91426925-91439006	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
FHL1	four and a half LIM domains 1 [Source:HGNC Symbol;Acc:3702] locus=X:135229559-135293518	tcgaBreastGE, tcgaGliomaGE, tscapeBCa
FLAD1	FAD1 flavin adenine dinucleotide synthetase homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:24671] locus=1:154955814-154965587	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
FOXO3	forkhead box O3 [Source:HGNC Symbol;Acc:3821] locus=6:108881038-109005977	cosmicRecurrent, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
FSCN1	fascin homolog 1, actin-bundling protein (Strongylocentrotus purpuratus) [Source:HGNC Symbol;Acc:11148] locus=7:5632439-5646286	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeOvariand
FURIN	furin (paired basic amino acid cleaving enzyme) [Source:HGNC Symbol;Acc:8568] locus=15:91411822-91426688	tcgaBreastGE, tcgaBreastMethyl, tscapeNSCLCa
FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group) [Source:HGNC Symbol;Acc:4012] locus=19:49251268-49258647	tscapeNSCLCd, tscapeOvariand
FUT2	fucosyltransferase 2 (secretor status included) [Source:HGNC Symbol;Acc:4013] locus=19:49199228-49209207	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeOvariand
FXYD1	FXYD domain containing ion transport regulator 1 [Source:HGNC Symbol;Acc:4025] locus=19:35629728-35634013	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianGE, tscapeNSCLCa
FXYD7	FXYD domain containing ion transport regulator 7 [Source:HGNC Symbol;Acc:4034] locus=19:35634154-35645205	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
FYN	FYN oncogene related to SRC, FGR, YES [Source:HGNC Symbol;Acc:4037] locus=6:111981535-112194655	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd
GANAB	glucosidase, alpha; neutral AB [Source:HGNC Symbol;Acc:4138] locus=11:62392298-62414104	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
GAPDH	glyceraldehyde-3-phosphate dehydrogenase [Source:HGNC Symbol;Acc:4141] locus=12:6643093-6647537	tcgaOvarianCGHa, tcgaOvarianMethyl
GCH1	GTP cyclohydrolase 1 [Source:HGNC Symbol;Acc:4193] locus=14:55308726-55369570	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
GCNT1	glucosaminyl (N-acetyl) transferase 1, core 2 [Source:HGNC Symbol;Acc:4203] locus=9:79034752-79122332	tcgaOvarianMethyl
GCNT3	glucosaminyl (N-acetyl) transferase 3, mucin type [Source:HGNC Symbol;Acc:4205] locus=15:59887074-59932438	tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2 [Source:HGNC Symbol;Acc:17973] locus=5:74323289-74326724	tcgaBreastGE, tcgaGliomaGE, tscapeNSCLCd, tscapeOvariand, tscapeProstated
GDI2	GDP dissociation inhibitor 2 [Source:HGNC Symbol;Acc:4227] locus=10:5807186-5884095	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
GDNF	glial cell derived neurotrophic factor [Source:HGNC Symbol;Acc:4232] locus=5:37812779-37839788	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
GFRA1	GDNF family receptor alpha 1 [Source:HGNC Symbol;Acc:4243] locus=10:117816444-118033126	tcgaBreastGE, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd
GHR	growth hormone receptor [Source:HGNC Symbol;Acc:4263] locus=5:42423879-42721979	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
GIGYF1	GRB10 interacting GYF protein 1 [Source:HGNC Symbol;Acc:9126] locus=7:100277130-100287071	tcgaColonGE, tscapeNSCLCa
GIGYF2	GRB10 interacting GYF protein 2 [Source:HGNC Symbol;Acc:11960] locus=2:233562009-233725285	cosmicPrimary, tcgaColonGE, tscapeBCd, tscapeNSCLCd, tscapeRCCd
GJA1	gap junction protein, alpha 1, 43kDa [Source:HGNC Symbol;Acc:4274] locus=6:121756791-121770873	fileBC2brain, tcgaBreastMethyl, tcgaColonMethyl
GNA11	guanine nucleotide binding protein (G protein), alpha 11 (Gq class) [Source:HGNC Symbol;Acc:4379] locus=19:3094408-3121452	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd, tscapeRCCd
GNA14	guanine nucleotide binding protein (G protein), alpha 14 [Source:HGNC Symbol;Acc:4382] locus=9:80037995-80263223	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
GNA15	guanine nucleotide binding protein (G protein), alpha 15 (Gq class) [Source:HGNC Symbol;Acc:4383] locus=19:3136191-3163766	cosmicMetastasis, tcgaBreastGE, tcgaColonGE, tcgaOvarianMethyl, tscapeHCCd, tscapeRCCd
GNAL	guanine nucleotide binding protein (G protein), alpha activating activity polypeptide, olfactory type [Source:HGNC Symbol;Acc:4388] locus=18:11689184-11885684	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
GNAS	GNAS complex locus [Source:HGNC Symbol;Acc:4392] locus=20:57414773-57486247	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
GOT1	glutamic-oxaloacetic transaminase 1, soluble (aspartate aminotransferase 1) [Source:HGNC Symbol;Acc:4432] locus=10:101156627-101190393	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeOvariand
GOT2	glutamic-oxaloacetic transaminase 2, mitochondrial (aspartate aminotransferase 2) [Source:HGNC Symbol;Acc:4433] locus=16:58741035-58768261	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
GPAM	glycerol-3-phosphate acyltransferase, mitochondrial [Source:HGNC Symbol;Acc:24865] locus=10:113909624-113975135	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd
GPAT2	glycerol-3-phosphate acyltransferase 2, mitochondrial [Source:HGNC Symbol;Acc:27168] locus=2:96687694-96705199	
GPRASP1	G protein-coupled receptor associated sorting protein 1 [Source:HGNC Symbol;Acc:24834] locus=X:101906294-101914008	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
GRB2	growth factor receptor-bound protein 2 [Source:HGNC Symbol;Acc:4566] locus=17:73314157-73401790	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeNSCLCa
GRIN2B	glutamate receptor, ionotropic, N-methyl D-aspartate 2B [Source:HGNC Symbol;Acc:4586] locus=12:13714144-14133053	cosmicMetastasis, cosmicRecurrent, tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeProstated
GRK5	G protein-coupled receptor kinase 5 [Source:HGNC Symbol;Acc:4544] locus=10:120967101-121215131	tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand
GRK6	G protein-coupled receptor kinase 6 [Source:HGNC Symbol;Acc:4545] locus=5:176830205-176869902	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa, tscapeRCCa
GRM7	glutamate receptor, metabotropic 7 [Source:HGNC Symbol;Acc:4599] locus=3:6811688-7783215	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE

Continued on next page...

name	description	studies
GSK3A	glycogen synthase kinase 3 alpha [Source:HGNC Symbol;Acc:4616] locus=19:42734338-42746777	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeProstated
GSK3B	glycogen synthase kinase 3 beta [Source:HGNC Symbol;Acc:4617] locus=3:119540170-119813264	tcgaBreastGE, tcgaBreastGESurv, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
GSN	gelsolin [Source:HGNC Symbol;Acc:4620] locus=9:123970075-124095121	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
GUSB	glucuronidase, beta [Source:HGNC Symbol;Acc:4696] locus=7:65425671-65447301	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
HDAC1	histone deacetylase 1 [Source:HGNC Symbol;Acc:4852] locus=1:32757687-32799236	tcgaBreastGE, tcgaGliomaGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
HDAC2	histone deacetylase 2 [Source:HGNC Symbol;Acc:4853] locus=6:114254192-114332472	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeNSCLCd
HEMK1	HemK methyltransferase family member 1 [Source:HGNC Symbol;Acc:24923] locus=3:50606583-50622366	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
HEXDC	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing [Source:HGNC Symbol;Acc:26307] locus=17:80376252-80400515	tscapeBCa, tscapeMelanomaa
HJURP	Holliday junction recognition protein [Source:HGNC Symbol;Acc:25444] locus=2:234742062-234763212	tcgaBreastGE, tcgaGliomaGE, tscapeBCd, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand, tscapeRCCd, tscapeSCLCd
HNMT	histamine N-methyltransferase [Source:HGNC Symbol;Acc:5028] locus=2:138721590-138773930	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tscapeProstated
HNRNPAB	heterogeneous nuclear ribonucleoprotein A/B [Source:HGNC Symbol;Acc:5034] locus=5:177631508-177638164	tcgaBreastGE, tcgaGliomaGE
HNRNPL	heterogeneous nuclear ribonucleoprotein L [Source:HGNC Symbol;Acc:5045] locus=19:39327029-39342987	tcgaBreastGE, tscapeOvariana
HNRNPM	heterogeneous nuclear ribonucleoprotein M [Source:HGNC Symbol;Acc:5046] locus=19:8509651-8553885	tcgaGliomaGE
HOXC9	homeobox C9 [Source:HGNC Symbol;Acc:5130] locus=12:54388679-54397121	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeRCCa
HSD17B12	hydroxysteroid (17-beta) dehydrogenase 12 [Source:HGNC Symbol;Acc:18646] locus=11:43577986-43878167	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2 [Source:HGNC Symbol;Acc:5211] locus=16:82068609-82132139	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
HSD17B3	hydroxysteroid (17-beta) dehydrogenase 3 [Source:HGNC Symbol;Acc:5212] locus=9:98997588-99064434	tcgaOvarianMethyl
HSD17B6	hydroxysteroid (17-beta) dehydrogenase 6 homolog (mouse) [Source:HGNC Symbol;Acc:23316] locus=12:57145945-57181574	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
HSD17B8	hydroxysteroid (17-beta) dehydrogenase 8 [Source:HGNC Symbol;Acc:3554] locus=6:33172419-33174608	tcgaOvarianMethyl
HSD3B1	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1 [Source:HGNC Symbol;Acc:5217] locus=1:120049821-120057681	tcgaBreastMethyl, tscapeBCa, tscapeNSCLCd, tscapeSCLCd
HSD3B2	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2 [Source:HGNC Symbol;Acc:5218] locus=1:119957554-119965658	tcgaBreastMethyl, tcgaColonGE, tscapeBCa, tscapeNSCLCd, tscapeSCLCd
HSF1	heat shock transcription factor 1 [Source:HGNC Symbol;Acc:5224] locus=8:145515280-145538385	tcgaBreastGE, tcgaOvarianCGHa
HSP90AA1	heat shock protein 90kDa alpha (cytosolic), class A member 1 [Source:HGNC Symbol;Acc:5253] locus=14:102547106-102606036	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeMelanomad
HSPH1	heat shock 105kDa/110kDa protein 1 [Source:HGNC Symbol;Acc:16969] locus=13:31710762-31736525	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeSCLCd
HTR4	5-hydroxytryptamine (serotonin) receptor 4, G protein-coupled [Source:HGNC Symbol;Acc:5299] locus=5:147830595-148056798	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
HYOU1	hypoxia up-regulated 1 [Source:HGNC Symbol;Acc:16931] locus=11:118914899-118927940	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
IARS	isoleucyl-tRNA synthetase [Source:HGNC Symbol;Acc:5330] locus=9:94972489-95056038	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl
IDO1	indoleamine 2,3-dioxygenase 1 [Source:HGNC Symbol;Acc:6059] locus=8:39759794-39785963	tcgaGliomaGE
IDO2	indoleamine 2,3-dioxygenase 2 [Source:HGNC Symbol;Acc:27269] locus=8:39792133-39873910	
IGF1	insulin-like growth factor 1 (somatomedin C) [Source:HGNC Symbol;Acc:5464] locus=12:102789645-102874423	snp3dBC, snp3dDementia, snp3dObesity, snp3dProstateC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
IGF1R	insulin-like growth factor 1 receptor [Source:HGNC Symbol;Acc:5465] locus=15:99192200-99507759	snp3dBC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCa, tscapeMelanomaa, tscapeNSCLCa
IKBKB	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase beta [Source:HGNC Symbol;Acc:5960] locus=8:42128820-42189973	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa, tscapeHCCd, tscapeNSCLCa, tscapeNSCLCd, tscapeOvariana, tscapeProstatea, tscapeRCCd, tscapeSCLCa
IKBKE	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase epsilon [Source:HGNC Symbol;Acc:14552] locus=1:206643791-206670223	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeProstatea
IKBKG	inhibitor of kappa light polypeptide gene enhancer in B-cells, kinase gamma [Source:HGNC Symbol;Acc:5961] locus=X:153769414-153796782	tcgaBreastGE
IL1B	interleukin 1, beta [Source:HGNC Symbol;Acc:5992] locus=2:113587328-113594480	fileBC2brain, snp3dDementia, tcgaColonMethyl
IL4I1	interleukin 4 induced 1 [Source:HGNC Symbol;Acc:19094] locus=19:50392916-50432796	tcgaBreastGE, tcgaBreastMethyl, tscapeOvariand
INCENP	inner centromere protein antigens 135/155kDa [Source:HGNC Symbol;Acc:6058] locus=11:61891445-61920635	tcgaBreastGE
INMT	indolethylamine N-methyltransferase [Source:HGNC Symbol;Acc:6069] locus=7:30737601-30797218	tcgaOvarianMethyl
INS	insulin [Source:HGNC Symbol;Acc:6081] locus=11:2181009-2182571	snp3dDiabetes, snp3dObesity, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand
INSR	insulin receptor [Source:HGNC Symbol;Acc:6091] locus=19:7112266-7294011	snp3dDiabetes, snp3dObesity
IPO4	importin 4 [Source:HGNC Symbol;Acc:19426] locus=14:24649425-24658170	tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
IRS1	insulin receptor substrate 1 [Source:HGNC Symbol;Acc:6125] locus=2:227599757-227664475	snp3dBC, snp3dDiabetes, snp3dObesity, tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeRCCd
ITGB3BP	integrin beta 3 binding protein (beta3-endonexin) [Source:HGNC Symbol;Acc:6157] locus=1:63906441-64059392	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
ITSN1	intersectin 1 (SH3 domain protein) [Source:HGNC Symbol;Acc:6183] locus=21:35014706-35272165	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
JAK2	Janus kinase 2 [Source:HGNC Symbol;Acc:6192] locus=9:4985033-5128183	tscapeBCd
KCNJ1	potassium inwardly-rectifying channel, subfamily J, member 1 [Source:HGNC Symbol;Acc:6255] locus=11:128706210-128737268	tcgaBreastMethyl, tscapeBCd, tscapeNSCLCd, tscapeRCCd
KCNJ3	potassium inwardly-rectifying channel, subfamily J, member 3 [Source:HGNC Symbol;Acc:6264] locus=2:155554811-155714863	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE
KCNJ6	potassium inwardly-rectifying channel, subfamily J, member 6 [Source:HGNC Symbol;Acc:6267] locus=21:38996789-39288749	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
KCNJ9	potassium inwardly-rectifying channel, subfamily J, member 9 [Source:HGNC Symbol;Acc:6270] locus=1:160051360-160060353	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
KDR	kinase insert domain receptor (a type III receptor tyrosine kinase) [Source:HGNC Symbol;Acc:6307] locus=4:55944644-55991756	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeNSCLCa
KIF18A	kinesin family member 18A [Source:HGNC Symbol;Acc:29441] locus=11:28042167-28129693	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl

Continued on next page…

name	description	studies
KIF2A	kinesin heavy chain member 2A [Source:HGNC Symbol;Acc:6318] locus=5:61601989-61833076	tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
KIF2B	kinesin family member 2B [Source:HGNC Symbol;Acc:29443] locus=17:51900239-51902573	cosmicMetastasis
KIF2C	kinesin family member 2C [Source:HGNC Symbol;Acc:6393] locus=1:45205490-45233439	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tscapeSCLCa
KIF3B	kinesin family member 3B [Source:HGNC Symbol;Acc:6320] locus=20:30865467-30922814	tcgaBreastGE, tcgaBreastGESurv, tcgaGliomaGE
KIT	v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:6342] locus=4:55524085-55606881	cosmicMetastasis, cosmicPrimary, cosmicRecurrent, fileAmpOver, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
KL	klotho [Source:HGNC Symbol;Acc:6344] locus=13:33590207-33640282	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeBCd, tscapeHCCd, tscapeOvariand, tscapeSCLCd
KNTC1	kinetochore associated 1 [Source:HGNC Symbol;Acc:17255] locus=12:123011793-123110926	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianGE
KPNA1	karyopherin alpha 1 (importin alpha 5) [Source:HGNC Symbol;Acc:6394] locus=3:122140796-122233792	tcgaOvarianGE, tcgaOvarianMethyl
KPNA2	karyopherin alpha 2 (RAG cohort 1, importin alpha 1) [Source:HGNC Symbol;Acc:6395] locus=17:66031848-66042969	tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
LAMP2	lysosomal-associated membrane protein 2 [Source:HGNC Symbol;Acc:6501] locus=X:119561682-119603220	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
LDB1	LIM domain binding 1 [Source:HGNC Symbol;Acc:6532] locus=10:103867317-103880210	tcgaColonGE, tcgaGliomaCGHd, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeOvariand
LDB2	LIM domain binding 2 [Source:HGNC Symbol;Acc:6533] locus=4:16503164-16900432	tcgaGliomaGE, tscapeBCd
LETM1	leucine zipper-EF-hand containing transmembrane protein 1 [Source:HGNC Symbol;Acc:6556] locus=4:1813206-1857974	tcgaBreastGE, tcgaBreastGESurv, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
LRIF1	ligand dependent nuclear receptor interacting factor 1 [Source:HGNC Symbol;Acc:30299] locus=1:111489807-111506701	
LTF	lactotransferrin [Source:HGNC Symbol;Acc:6720] locus=3:46477136-46526724	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
MAD1L1	MAD1 mitotic arrest deficient-like 1 (yeast) [Source:HGNC Symbol;Acc:6762] locus=7:1855383-2272878	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
MAD2L1	MAD2 mitotic arrest deficient-like 1 (yeast) [Source:HGNC Symbol;Acc:6763] locus=4:120980577-120988229	fileCIN70, tcgaOvarianMethyl
MAGEA1	melanoma antigen family A, 1 (directs expression of antigen MZ2-E) [Source:HGNC Symbol;Acc:6796] locus=X:152481522-152486115	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
MAOA	monoamine oxidase A [Source:HGNC Symbol;Acc:6833] locus=X:43515467-43606068	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
MAOB	monoamine oxidase B [Source:HGNC Symbol;Acc:6834] locus=X:43625858-43741693	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
MAP2K1	mitogen-activated protein kinase kinase 1 [Source:HGNC Symbol;Acc:6840] locus=15:66679155-66784754	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
MAP3K14	mitogen-activated protein kinase kinase kinase 14 [Source:HGNC Symbol;Acc:6853] locus=17:43340488-43394414	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
MAP3K3	mitogen-activated protein kinase kinase kinase 3 [Source:HGNC Symbol;Acc:6855] locus=17:61699801-61773667	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
MAP3K7	mitogen-activated protein kinase kinase kinase 7 [Source:HGNC Symbol;Acc:6859] locus=6:91223292-91296786	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
MAP3K8	mitogen-activated protein kinase kinase kinase 8 [Source:HGNC Symbol;Acc:6860] locus=10:30722866-30750762	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeProstated
MAPK1	mitogen-activated protein kinase 1 [Source:HGNC Symbol;Acc:6871] locus=22:22108789-22221970	snp3dBC, tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa
MAPK14	mitogen-activated protein kinase 14 [Source:HGNC Symbol;Acc:6876] locus=6:35995488-36079013	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
MAPK6	mitogen-activated protein kinase 6 [Source:HGNC Symbol;Acc:6879] locus=15:52244303-52358462	tcgaGliomaGE
MAPK7	mitogen-activated protein kinase 7 [Source:HGNC Symbol;Acc:6880] locus=17:19281034-19286857	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeHCCa
MAPRE1	microtubule-associated protein, RP/EB family, member 1 [Source:HGNC Symbol;Acc:6890] locus=20:31407699-31438211	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianGESurv
MAPT	microtubule-associated protein tau [Source:HGNC Symbol;Acc:6893] locus=17:43971748-44105700	snp3dDementia, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl, tscapeMelanomad
MBP	myelin basic protein [Source:HGNC Symbol;Acc:6925] locus=18:74690783-74845639	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad, tscapeProstated
MEGF10	multiple EGF-like-domains 10 [Source:HGNC Symbol;Acc:29634] locus=5:126626523-126801429	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeProstated
MEIS1	Meis homeobox 1 [Source:HGNC Symbol;Acc:7000] locus=2:66660584-66799890	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
MERTK	c-mer proto-oncogene tyrosine kinase [Source:HGNC Symbol;Acc:7027] locus=2:112656056-112787138	tcgaBreastGE
MET	met proto-oncogene (hepatocyte growth factor receptor) [Source:HGNC Symbol;Acc:7029] locus=7:116312248-116438440	fileAmpOver, snp3dLungC, snp3dMetastasis, snp3dProstateC, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomaa, tscapeNSCLCa, tscapeOvariand
METTL2B	methyltransferase like 2B [Source:HGNC Symbol;Acc:18272] locus=7:128095894-128146656	
METTL6	methyltransferase like 6 [Source:HGNC Symbol;Acc:28343] locus=3:15422782-15469047	tcgaBreastGE, tcgaColonGE, tscapeOvariand
MIS12	MIS12, MIND kinetochore complex component, homolog (S. pombe) [Source:HGNC Symbol;Acc:24967] locus=17:5389605-5394134	tcgaGliomaGE
MIS18A	MIS18 kinetochore protein homolog A (S. pombe) [Source:HGNC Symbol;Acc:1286] locus=21:33640530-33651380	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
MIS18BP1	MIS18 binding protein 1 [Source:HGNC Symbol;Acc:20190] locus=14:45672393-45722743	tcgaGliomaGE, tcgaOvarianGE
MLF1IP	MLF1 interacting protein [Source:HGNC Symbol;Acc:21348] locus=4:185615772-185655287	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeRCCd
MLLT3	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 3 [Source:HGNC Symbol;Acc:7136] locus=9:20341663-20622542	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
MOB1A	MOB kinase activator 1A [Source:HGNC Symbol;Acc:16015] locus=2:74382165-74406025	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
MOK	MOK protein kinase [Source:HGNC Symbol;Acc:9833] locus=14:102690837-102771537	cosmicRecurrent, tcgaColonGE
MTA1	metastasis associated 1 [Source:HGNC Symbol;Acc:7410] locus=14:105886157-105937066	snp3dMetastasis, snp3dProstateC, tcgaOvarianMethyl, tscapeMelanomad
MYC	v-myc myelocytomatosis viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:7553] locus=8:128747680-128753674	fileAmpOver, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa, tscapeBCd, tscapeCRCa, tscapeHCCa, tscapeMelanomaa, tscapeOvariana, tscapeOvariand, tscapeRCCa, tscapeSCLCa

Continued on next page. . .

name	description	studies
MYH1	myosin, heavy chain 1, skeletal muscle, adult [Source:HGNC Symbol;Acc:7567] locus=17:10395629-10421859	cosmicMetastasis, cosmicPrimary, cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
MYH9	myosin, heavy chain 9, non-muscle [Source:HGNC Symbol;Acc:7579] locus=22:36677323-36784063	cosmicRecurrent, tcgaColonGE, tcgaColonMethyl
NASP	nuclear autoantigenic sperm protein (histone-binding) [Source:HGNC Symbol;Acc:7644] locus=1:46049518-46084566	tcgaGliomaGE, tcgaOvarianMethyl, tscapeSCLCa
NDC80	NDC80 kinetochore complex component homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:16909] locus=18:2571510-2616634	tcgaBreastGE, tcgaGliomaGE
NDE1	nudE nuclear distribution E homolog 1 (A. nidulans) [Source:HGNC Symbol;Acc:17619] locus=16:15737124-15820210	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
NDEL1	nudE nuclear distribution E homolog (A. nidulans)-like 1 [Source:HGNC Symbol;Acc:17620] locus=17:8339179-8383942	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
NEDD4	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:7727] locus=15:56119120-56285944	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
NEDD4L	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:7728] locus=18:55711619-56068772	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
NEK6	NIMA (never in mitosis gene a)-related kinase 6 [Source:HGNC Symbol;Acc:7749] locus=9:127019885-127115586	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
NEUROD1	neuronal differentiation 1 [Source:HGNC Symbol;Acc:7762] locus=2:182537815-182545603	snp3dDiabetes, tcgaBreastMethyl
NFKB1	nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 [Source:HGNC Symbol;Acc:7794] locus=4:103422486-103538459	cosmicRecurrent, snp3dMetastasis, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
NFKB2	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) [Source:HGNC Symbol;Acc:7795] locus=10:104154229-104162281	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd
NFKBIA	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha [Source:HGNC Symbol;Acc:7797] locus=14:35870717-35873955	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
NFKBIB	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, beta [Source:HGNC Symbol;Acc:7798] locus=19:39390340-39399533	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariana
NFKBIE	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon [Source:HGNC Symbol;Acc:7799] locus=6:44225919-44233500	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCa, tscapeOvariana
NFYC	nuclear transcription factor Y, gamma [Source:HGNC Symbol;Acc:7806] locus=1:41157320-41237275	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeBCa, tscapeOvariana
NHLH1	nescient helix loop helix 1 [Source:HGNC Symbol;Acc:7817] locus=1:160336857-160342638	tcgaColonMethyl
NMI	N-myc (and STAT) interactor [Source:HGNC Symbol;Acc:7854] locus=2:152126979-152146571	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
NOS1	nitric oxide synthase 1 (neuronal) [Source:HGNC Symbol;Acc:7872] locus=12:117636114-117889975	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
NR3C1	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor) [Source:HGNC Symbol;Acc:7978] locus=5:142657496-142815077	tcgaBreastGE
NR5A1	nuclear receptor subfamily 5, group A, member 1 [Source:HGNC Symbol;Acc:7983] locus=9:127243516-127269709	tcgaBreastMethyl, tcgaColonGE
NRAS	neuroblastoma RAS viral (v-ras) oncogene homolog [Source:HGNC Symbol;Acc:7989] locus=1:115247090-115259515	cosmicMetastasis, cosmicRecurrent, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
NSL1	NSL1, MIND kinetochore complex component, homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:24548] locus=1:212899495-212965124	tcgaGliomaGE
NUDC	nuclear distribution C homolog (A. nidulans) [Source:HGNC Symbol;Acc:8045] locus=1:27226729-27273353	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
NUF2	NUF2, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:14621] locus=1:163236366-163325554	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE
NUP107	nucleoporin 107kDa [Source:HGNC Symbol;Acc:29914] locus=12:69080514-69136785	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeRCCa
NUP133	nucleoporin 133kDa [Source:HGNC Symbol;Acc:18016] locus=1:229577044-229644103	tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeMelanomad, tscapeOvariana, tscapeProstated
NUP160	nucleoporin 160kDa [Source:HGNC Symbol;Acc:18017] locus=11:47799639-47870107	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
NUP37	nucleoporin 37kDa [Source:HGNC Symbol;Acc:29929] locus=12:102467967-102513902	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
NUP43	nucleoporin 43kDa [Source:HGNC Symbol;Acc:21182] locus=6:150045451-150070801	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
NUP62	nucleoporin 62kDa [Source:HGNC Symbol;Acc:8066] locus=19:50410086-50432786	tcgaBreastGE, tcgaGliomaGE, tscapeOvariand
NUP85	nucleoporin 85kDa [Source:HGNC Symbol;Acc:8734] locus=17:73201597-73231854	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tscapeNSCLCa
OIP5	Opa interacting protein 5 [Source:HGNC Symbol;Acc:20300] locus=15:41601466-41624819	fileCIN70, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeCRCd, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand
OLA1	Obg-like ATPase 1 [Source:HGNC Symbol;Acc:28833] locus=2:174937175-175113426	tcgaColonGE
OPRD1	opioid receptor, delta 1 [Source:HGNC Symbol;Acc:8153] locus=1:29138654-29190208	cosmicPrimary, cosmicRecurrent, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
OTOF	otoferlin [Source:HGNC Symbol;Acc:8515] locus=2:26680071-26781566	cosmicPrimary, tcgaColonGE, tcgaOvarianMethyl
PA2G4	proliferation-associated 2G4, 38kDa [Source:HGNC Symbol;Acc:8550] locus=12:56498103-56509935	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
PABPC1	poly(A) binding protein, cytoplasmic 1 [Source:HGNC Symbol;Acc:8554] locus=8:101698044-101735037	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeNSCLCa
PAFAH1B1	platelet-activating factor acetylhydrolase 1b, regulatory subunit 1 (45kDa) [Source:HGNC Symbol;Acc:8574] locus=17:2496504-2588888	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PAH	phenylalanine hydroxylase [Source:HGNC Symbol;Acc:8582] locus=12:103230663-103352188	cosmicPrimary, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PAICS	phosphoribosylaminoimidazole carboxylase, phosphoribosylaminoimidazole succinocarboxamide synthetase [Source:HGNC Symbol;Acc:8587] locus=4:57301907-57327534	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
PDGFB	platelet-derived growth factor beta polypeptide [Source:HGNC Symbol;Acc:8800] locus=22:39619364-39640756	snp3dGlioma, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomaa
PDGFRB	platelet-derived growth factor receptor, beta polypeptide [Source:HGNC Symbol;Acc:8804] locus=5:149493400-149535423	tcgaBreastMethyl, tcgaGliomaGE
PDPK1	3-phosphoinositide dependent protein kinase-1 [Source:HGNC Symbol;Acc:8816] locus=16:2587965-2653189	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeHCCd, tscapeOvariand
PEMT	phosphatidylethanolamine N-methyltransferase [Source:HGNC Symbol;Acc:8830] locus=17:17408877-17495022	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
PFAS	phosphoribosylformylglycinamidine synthase [Source:HGNC Symbol;Acc:8863] locus=17:8152604-8173809	cosmicPrimary, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PGR	progesterone receptor [Source:HGNC Symbol;Acc:8910] locus=11:100900355-101001255	snp3dBC, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl

Continued on next page...

name	description	studies
PHLPP1	PH domain and leucine rich repeat protein phosphatase 1 [Source:HGNC Symbol;Acc:20610] locus=18:60382672-60647666	
PIGR	polymeric immunoglobulin receptor [Source:HGNC Symbol;Acc:8968] locus=1:207101863-207119811	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeBCa, tscapeProstatea
PIK3CA	phosphoinositide-3-kinase, catalytic, alpha polypeptide [Source:HGNC Symbol;Acc:8975] locus=3:178865902-178957881	cosmicPrimary, fileAmpOver, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianGE, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
PIK3R1	phosphoinositide-3-kinase, regulatory subunit 1 (alpha) [Source:HGNC Symbol;Acc:8979] locus=5:67511548-67597649	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated, tscapeSCLCd
PIP	prolactin-induced protein [Source:HGNC Symbol;Acc:8993] locus=7:142829170-142836839	tcgaBreastMethyl, tcgaColonMethyl, tscapeBCd, tscapeMelanomaa, tscapeMelanomad, tscapeOvariand
PISD	phosphatidylserine decarboxylase [Source:HGNC Symbol;Acc:8999] locus=22:32014477-32058418	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
PITPNB	phosphatidylinositol transfer protein, beta [Source:HGNC Symbol;Acc:9002] locus=22:28202413-28316122	tcgaColonMethyl, tcgaOvarianMethyl
PLAUR	plasminogen activator, urokinase receptor [Source:HGNC Symbol;Acc:9053] locus=19:44150271-44174502	snp3dLungC, snp3dMetastasis, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeProstated
PLK1	polo-like kinase 1 [Source:HGNC Symbol;Acc:9077] locus=16:23688977-23701688	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PMF1	polyamine-modulated factor 1 [Source:HGNC Symbol;Acc:9112] locus=1:156182784-156212874	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tscapeHCCa
POU1F1	POU class 1 homeobox 1 [Source:HGNC Symbol;Acc:9210] locus=3:87308554-87325737	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeSCLCa
PPP1CC	protein phosphatase 1, catalytic subunit, gamma isozyme [Source:HGNC Symbol;Acc:9283] locus=12:111157485-111180744	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PPP2CA	protein phosphatase 2, catalytic subunit, alpha isozyme [Source:HGNC Symbol;Acc:9299] locus=5:133530025-133561833	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
PPP3CA	protein phosphatase 3, catalytic subunit, alpha isozyme [Source:HGNC Symbol;Acc:9314] locus=4:101944566-102269435	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
PPP5C	protein phosphatase 5, catalytic subunit [Source:HGNC Symbol;Acc:9322] locus=19:46850251-46896238	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
PRDX6	peroxiredoxin 6 [Source:HGNC Symbol;Acc:16753] locus=1:173446405-173457946	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCa
PRKCD	protein kinase C, delta [Source:HGNC Symbol;Acc:9399] locus=3:53190025-53226733	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
PRKCQ	protein kinase C, theta [Source:HGNC Symbol;Acc:9410] locus=10:6469105-6622263	tcgaBreastMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeRCCd
PSMA6	proteasome (prosome, macropain) subunit, alpha type, 6 [Source:HGNC Symbol;Acc:9535] locus=14:35747839-35786699	tcgaOvarianMethyl, tscapeBCa, tscapeHCCa, tscapeProstatea
PSMD6	proteasome (prosome, macropain) 26S subunit, non-ATPase, 6 [Source:HGNC Symbol;Acc:9564] locus=3:63996225-64009658	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeSCLCd
PXN	paxillin [Source:HGNC Symbol;Acc:9718] locus=12:120648250-120703574	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
RAF1	v-raf-1 murine leukemia viral oncogene homolog 1 [Source:HGNC Symbol;Acc:9829] locus=3:12625100-12705725	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
RANBP2	RAN binding protein 2 [Source:HGNC Symbol;Acc:9848] locus=2:109335937-109402267	cosmicRecurrent, tcgaBreastMethyl
RANGAP1	Ran GTPase activating protein 1 [Source:HGNC Symbol;Acc:9854] locus=22:41641615-41698963	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
RBBP4	retinoblastoma binding protein 4 [Source:HGNC Symbol;Acc:9887] locus=1:33116743-33146258	tcgaBreastMethyl, tscapeBCd, tscapeOvariand
RBBP7	retinoblastoma binding protein 7 [Source:HGNC Symbol;Acc:9890] locus=X:16857406-16888537	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
RBBP8	retinoblastoma binding protein 8 [Source:HGNC Symbol;Acc:9891] locus=18:20513290-20606449	tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
RBPMS	RNA binding protein with multiple splicing [Source:HGNC Symbol;Acc:19097] locus=8:30241944-30429778	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHd, tcgaOvarianGE, tcgaOvarianMethyl
RCC2	regulator of chromosome condensation 2 [Source:HGNC Symbol;Acc:30297] locus=1:17733256-17766220	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
REL	v-rel reticuloendotheliosis viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:9954] locus=2:61108656-61150645	fileAmpOver, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
RELA	v-rel reticuloendotheliosis viral oncogene homolog A (avian) [Source:HGNC Symbol;Acc:9955] locus=11:65421067-65430565	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
RELB	v-rel reticuloendotheliosis viral oncogene homolog B [Source:HGNC Symbol;Acc:9956] locus=19:45504695-45541452	tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeOvariand
RELT	RELT tumor necrosis factor receptor [Source:HGNC Symbol;Acc:13764] locus=11:73087309-73108519	tcgaBreastGE, tcgaColonGE
RET	ret proto-oncogene [Source:HGNC Symbol;Acc:9967] locus=10:43572475-43625799	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeOvariand
RHOXF2	Rhox homeobox family, member 2 [Source:HGNC Symbol;Acc:30011] locus=X:119292467-119297945	cosmicPrimary
RIF1	RAP1 interacting factor homolog (yeast) [Source:HGNC Symbol;Acc:23207] locus=2:152266397-152364527	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
RIPK1	receptor (TNFRSF)-interacting serine-threonine kinase 1 [Source:HGNC Symbol;Acc:10019] locus=6:3064092-3115421	tcgaGliomaGE, tscapeOvariana, tscapeSCLCd
RIPK2	receptor-interacting serine-threonine kinase 2 [Source:HGNC Symbol;Acc:10020] locus=8:90769975-90803291	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianGE, tcgaOvarianMethyl
RIPK3	receptor-interacting serine-threonine kinase 3 [Source:HGNC Symbol;Acc:10021] locus=14:24805227-24809251	cosmicRecurrent, tcgaGliomaGE, tscapeHCCa
RP11-1286E23.8	Ubiquitin carboxyl-terminal hydrolase 17 [Source:UniProtKB/Swiss-Prot;Acc:Q0WX57] locus=4:9212383-9228214	cosmicMetastasis
RPL3	ribosomal protein L3 [Source:HGNC Symbol;Acc:10332] locus=22:39708887-39716394	tscapeMelanomaa
RPLP1	ribosomal protein, large, P1 [Source:HGNC Symbol;Acc:10372] locus=15:69745123-69748255	tcgaBreastMethyl, tcgaOvarianMethyl
RPS27	ribosomal protein S27 [Source:HGNC Symbol;Acc:10416] locus=1:153963235-153964626	tcgaOvarianMethyl, tscapeHCCa, tscapeMelanomaa, tscapeNSCLCa, tscapeProstatea
RPS3A	ribosomal protein S3A [Source:HGNC Symbol;Acc:10421] locus=4:152020725-152025804	tcgaOvarianMethyl, tscapeRCCd
RSF1	remodeling and spacing factor 1 [Source:HGNC Symbol;Acc:18118] locus=11:77371041-77532063	tscapeOvariana
RUVBL1	RuvB-like 1 (E. coli) [Source:HGNC Symbol;Acc:10474] locus=3:127783625-127872757	fileAmpOver, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
S100A1	S100 calcium binding protein A1 [Source:HGNC Symbol;Acc:10486] locus=1:153600402-153604513	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa, tscapeHCCa, tscapeMelanomaa, tscapeNSCLCa
S100A2	S100 calcium binding protein A2 [Source:HGNC Symbol;Acc:10492] locus=1:153533584-153540366	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa, tscapeHCCa, tscapeMelanomaa, tscapeNSCLCa

Continued on next page...

name	description	studies
S100A4	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:10494] locus=1:153516089-153522612	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tscapeCRCa, tscapeHCCa, tscapeMelanomaa, tscapeNSCLCa
S100Z	S100 calcium binding protein Z [Source:HGNC Symbol;Acc:30367] locus=5:76145826-76217475	tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
SDCBP2	syndecan binding protein (syntenin) 2 [Source:HGNC Symbol;Acc:15756] locus=20:1290619-1309883	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
SEC13	SEC13 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:10697] locus=3:10334815-10362862	tcgaBreastGE, tcgaGliomaGE
SEC24D	SEC24 family, member D (S. cerevisiae) [Source:HGNC Symbol;Acc:10706] locus=4:119643978-119759838	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
SERPINA3	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 [Source:HGNC Symbol;Acc:16] locus=14:95058395-95090983	tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
SF3B2	splicing factor 3b, subunit 2, 145kDa [Source:HGNC Symbol;Acc:10769] locus=11:65818200-65836779	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl
SFN	stratifin [Source:HGNC Symbol;Acc:10773] locus=1:27189633-27190947	tcgaBreastGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
SGOL1	shugoshin-like 1 (S. pombe) [Source:HGNC Symbol;Acc:25088] locus=3:20202085-20227784	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
SGOL2	shugoshin-like 2 (S. pombe) [Source:HGNC Symbol;Acc:30812] locus=2:201374731-201448505	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE
SHBG	sex hormone-binding globulin [Source:HGNC Symbol;Acc:10839] locus=17:7517382-7536700	tcgaBreastGE
SHC1	SHC (Src homology 2 domain containing) transforming protein 1 [Source:HGNC Symbol;Acc:10840] locus=1:154934774-154946871	fileAmpOver, tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
SIAH1	siah E3 ubiquitin protein ligase 1 [Source:HGNC Symbol;Acc:10857] locus=16:48390275-48482313	tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
SKA1	spindle and kinetochore associated complex subunit 1 [Source:HGNC Symbol;Acc:28109] locus=18:47901365-47920543	tcgaBreastGE, tcgaGliomaGE
SKA2	spindle and kinetochore associated complex subunit 2 [Source:HGNC Symbol;Acc:28006] locus=17:57187308-57232800	tcgaBreastGE, tcgaGliomaGE
SKIL	SKI-like oncogene [Source:HGNC Symbol;Acc:10897] locus=3:170075466-170114623	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianGE, tcgaOvarianMethyl, tscapeBCa, tscapeNSCLCa, tscapeOvariana
SLC12A1	solute carrier family 12 (sodium/potassium/chloride transporters), member 1 [Source:HGNC Symbol;Acc:10910] locus=15:48483861-48596275	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianGE, tscapeMelanomad
SLC12A2	solute carrier family 12 (sodium/potassium/chloride transporters), member 2 [Source:HGNC Symbol;Acc:10911] locus=5:127419458-127525380	cosmicRecurrent, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand, tscapeProstated
SLC12A6	solute carrier family 12 (potassium/chloride transporters), member 6 [Source:HGNC Symbol;Acc:10914] locus=15:34525460-34630261	tcgaBreastMethyl, tcgaGliomaGE
SLC1A3	solute carrier family 1 (glial high affinity glutamate transporter), member 3 [Source:HGNC Symbol;Acc:10941] locus=5:36606457-36688436	tcgaBreastMethyl
SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1 [Source:HGNC Symbol;Acc:11068] locus=2:40339286-40838193	cosmicPrimary, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
SLC9A3R1	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1 [Source:HGNC Symbol;Acc:11075] locus=17:72744763-72765498	tcgaGliomaGE, tcgaOvarianMethyl
SLC9A3R2	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 2 [Source:HGNC Symbol;Acc:11076] locus=16:2075357-2089027	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
SMAD2	SMAD family member 2 [Source:HGNC Symbol;Acc:6768] locus=18:45357922-45457515	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
SMAD3	SMAD family member 3 [Source:HGNC Symbol;Acc:6769] locus=15:67356101-67487533	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
SMAD9	SMAD family member 9 [Source:HGNC Symbol;Acc:6774] locus=13:37418968-37494902	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianGE, tscapeBCd, tscapeProstated, tscapeSCLCd
SMARCA2	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2 [Source:HGNC Symbol;Acc:11098] locus=9:2015342-2193624	cosmicPrimary, tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd, tscapeSCLCa
SMARCA5	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5 [Source:HGNC Symbol;Acc:11101] locus=4:144434616-144478639	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
SOCS1	suppressor of cytokine signaling 1 [Source:HGNC Symbol;Acc:19383] locus=16:11348262-11350036	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
SOS1	son of sevenless homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:11187] locus=2:39208537-39351486	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
SPC24	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:26913] locus=19:11257444-11266484	
SPC25	SPC25, NDC80 kinetochore complex component, homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:24031] locus=2:169690642-169769881	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
SRC	v-src sarcoma (Schmidt-Ruppin A-2) viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:11283] locus=20:35973088-36034453	tcgaBreastGE
ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5 [Source:HGNC Symbol;Acc:19342] locus=1:77333126-77531396	fileBC2brain, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
ST6GALNAC	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 6 [Source:HGNC Symbol;Acc:23364] locus=9:130647600-130667687	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
ST8SIA1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1 [Source:HGNC Symbol;Acc:10869] locus=12:22216707-22589975	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl
ST8SIA5	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 5 [Source:HGNC Symbol;Acc:17827] locus=18:44259081-44337132	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl
STIP1	stress-induced-phosphoprotein 1 [Source:HGNC Symbol;Acc:11387] locus=11:63952744-63972015	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
STK11	serine/threonine kinase 11 [Source:HGNC Symbol;Acc:11389] locus=19:1205798-1228434	tcgaBreastGE, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeRCCd
SUGT1	SGT1, suppressor of G2 allele of SKP1 (S. cerevisiae) [Source:HGNC Symbol;Acc:16987] locus=13:53226844-53262433	tcgaBreastMethyl, tscapeBCd, tscapeGliomad, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
TAB1	TGF-beta activated kinase 1/MAP3K7 binding protein 1 [Source:HGNC Symbol;Acc:18157] locus=22:39795746-39913596	tcgaBreastGE
TAB2	TGF-beta activated kinase 1/MAP3K7 binding protein 2 [Source:HGNC Symbol;Acc:17075] locus=6:149539777-149732749	tcgaBreastGE, tcgaColonGE
TANK	TRAF family member-associated NFKB activator [Source:HGNC Symbol;Acc:11562] locus=2:161993419-162092732	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
TAOK1	TAO kinase 1 [Source:HGNC Symbol;Acc:29259] locus=17:27717943-27871502	
TAT	tyrosine aminotransferase [Source:HGNC Symbol;Acc:11573] locus=16:71599563-71611033	tcgaBreastGE, tcgaBreastMethyl, tscapeOvariand
TBK1	TANK-binding kinase 1 [Source:HGNC Symbol;Acc:11584] locus=12:64845660-64895888	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCa
TCEA1	transcription elongation factor A (SII), 1 [Source:HGNC Symbol;Acc:11612] locus=8:54879112-54935089	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd, tscapeRCCd
TCEA2	transcription elongation factor A (SII), 2 [Source:HGNC Symbol;Acc:11614] locus=20:62681189-62703700	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeNSCLCa
TCF21	transcription factor 21 [Source:HGNC Symbol;Acc:11632] locus=6:134210276-134216691	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeBCa, tscapeCRCa
TFPT	TCF3 (E2A) fusion partner (in childhood Leukemia) [Source:HGNC Symbol;Acc:13630] locus=19:54610320-54619055	tcgaBreastGE, tcgaOvarianMethyl
TH	tyrosine hydroxylase [Source:HGNC Symbol;Acc:11782] locus=11:2185159-2193107	tcgaBreastMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand

Continued on next page...

name	description	studies
TINAGL1	tubulointerstitial nephritis antigen-like 1 [Source:HGNC Symbol;Acc:19168] locus=1:32042116-32053288	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand
TNFRSF1A	tumor necrosis factor receptor superfamily, member 1A [Source:HGNC Symbol;Acc:11916] locus=12:6437923-6451280	snp3dDiabetes, snp3dObesity, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl
TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:11917] locus=1:12227060-12269285	snp3dObesity, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
TPH1	tryptophan hydroxylase 1 [Source:HGNC Symbol;Acc:12008] locus=11:18039111-18063973	tcgaBreastMethyl, tcgaGliomaGE
TPH2	tryptophan hydroxylase 2 [Source:HGNC Symbol;Acc:20692] locus=12:72332626-72580398	tcgaGliomaGE
TRADD	TNFRSF1A-associated via death domain [Source:HGNC Symbol;Acc:12030] locus=16:67188083-67194201	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
TRAF1	TNF receptor-associated factor 1 [Source:HGNC Symbol;Acc:12031] locus=9:123664671-123691451	tcgaBreastGE, tcgaColonGE
TRAF2	TNF receptor-associated factor 2 [Source:HGNC Symbol;Acc:12032] locus=9:139776364-139821059	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeCRCa
TRAF6	TNF receptor-associated factor 6, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:12036] locus=11:36508577-36531822	tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa
TSEN15	tRNA splicing endonuclease 15 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:16791] locus=1:184020811-184043346	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
TTN	titin [Source:HGNC Symbol;Acc:12403] locus=2:179390716-179695529	tcgaBreastGE
TUBA4A	tubulin, alpha 4a [Source:HGNC Symbol;Acc:12407] locus=2:220114433-220142892	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeOvariand, tscapeRCCd
TUBB	tubulin, beta class I [Source:HGNC Symbol;Acc:20778] locus=6:30687978-30693203	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianGE, tcgaOvarianMethyl
TUBB1	tubulin, beta 1 class VI [Source:HGNC Symbol;Acc:16257] locus=20:57594309-57601709	tcgaColonMethyl
TUBB2A	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412] locus=6:3153903-3157809	snp3dLungC, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tscapeOvariana, tscapeSCLCd
TUBB2B	tubulin, beta 2B class IIb [Source:HGNC Symbol;Acc:30829] locus=6:3224517-3231964	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariana, tscapeSCLCd
TUBB3	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:20772] locus=16:89987800-90005169	tcgaOvarianMethyl, tscapeCRCd, tscapeNSCLCd, tscapeProstated
TUBB4A	tubulin, beta 4A class IVa [Source:HGNC Symbol;Acc:20774] locus=19:6494331-6502330	tcgaGliomaGE
TUBB4B	tubulin, beta 4B class IVb [Source:HGNC Symbol;Acc:20771] locus=9:140135665-140138159	tcgaBreastGE
TUBB6	tubulin, beta 6 class V [Source:HGNC Symbol;Acc:20776] locus=18:12308070-12326568	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
TUBB8	tubulin, beta 8 class VIII [Source:HGNC Symbol;Acc:20773] locus=10:92828-96053	tcgaOvarianMethyl
TUBG1	tubulin, gamma 1 [Source:HGNC Symbol;Acc:12417] locus=17:40761358-40767254	tcgaBreastGE, tcgaColonGE, tscapeBCd
TUFM	Tu translation elongation factor, mitochondrial [Source:HGNC Symbol;Acc:12420] locus=16:28853732-28857729	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd
TYR	tyrosinase (oculocutaneous albinism IA) [Source:HGNC Symbol;Acc:12442] locus=11:88910620-89028908	
UBQLN4	ubiquilin 4 [Source:HGNC Symbol;Acc:1237] locus=1:156005092-156023585	tcgaOvarianMethyl, tscapeHCCa, tscapeProstated
UGDH	UDP-glucose 6-dehydrogenase [Source:HGNC Symbol;Acc:12525] locus=4:39500375-39529931	tcgaGliomaGE, tcgaOvarianMethyl
USP20	ubiquitin specific peptidase 20 [Source:HGNC Symbol;Acc:12619] locus=9:132596977-132644107	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
USP33	ubiquitin specific peptidase 33 [Source:HGNC Symbol;Acc:20059] locus=1:78161672-78225537	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
USP49	ubiquitin specific peptidase 49 [Source:HGNC Symbol;Acc:20078] locus=6:41762107-41863099	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCa, tscapeOvariana
VARS	valyl-tRNA synthetase [Source:HGNC Symbol;Acc:12651] locus=6:31745295-31763730	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
VCAN	versican [Source:HGNC Symbol;Acc:2464] locus=5:82767284-82878122	cosmicMetastasis, tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGESurv, tscapeNSCLCd, tscapeOvariand
VCP	valosin containing protein [Source:HGNC Symbol;Acc:12666] locus=9:35056061-35073246	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
VEGFA	vascular endothelial growth factor A [Source:HGNC Symbol;Acc:12680] locus=6:43737921-43754224	snp3dBC, snp3dGlioma, snp3dLungC, snp3dMetastasis, snp3dProstateC, tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeHCCa, tscapeNSCLCa
WBSCR22	Williams Beuren syndrome chromosome region 22 [Source:HGNC Symbol;Acc:16405] locus=7:73097355-73119491	tcgaBreastGE, tcgaGliomaGE
WNK4	WNK lysine deficient protein kinase 4 [Source:HGNC Symbol;Acc:14544] locus=17:40932649-40949061	tcgaBreastMethyl, tscapeBCd, tscapeOvariand
XPO1	exportin 1 (CRM1 homolog, yeast) [Source:HGNC Symbol;Acc:12825] locus=2:61704984-61765761	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
YWHAQ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, theta polypeptide [Source:HGNC Symbol;Acc:12854] locus=2:9724101-9771143	fileAmpOver, tcgaColonMethyl, tcgaOvarianMethyl
ZNF675	zinc finger protein 675 [Source:HGNC Symbol;Acc:30768] locus=19:23835708-23870017	tcgaOvarianGE, tscapeNSCLCd
ZW10	ZW10, kinetochore associated, homolog (Drosophila) [Source:HGNC Symbol;Acc:13194] locus=11:113603909-113644533	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeMelanomad, tscapeProstated
ZWILCH	Zwilch, kinetochore associated, homolog (Drosophila) [Source:HGNC Symbol;Acc:25468] locus=15:66797297-66842115	fileCIN70, tcgaBreastGE, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
ZWINT	ZW10 interactor [Source:HGNC Symbol;Acc:13195] locus=10:58116989-58121036	fileCIN70, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl

Table 24: List of KEGG [6] pathways supporting the relationships between the genes shown in Figure 49. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Phagosome	90	COLEC12, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, LAMP2, NOS1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8
Steroid hormone biosynthesis	90	CYP19A1, CYP1A1, CYP3A4, CYP3A43, CYP3A5, CYP3A7, HSD17B12, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, UGT2B17
Endocytosis	78	ADRB2, ADRB3, ADRBK1, ARRB1, ARRB2, CBL, EGF, EGFR, ERBB3, ERBB4, GRK5, GRK6, IGF1R, KDR, KIT, MET, NEDD4, NEDD4L, RET, SMAD2, SMAD3, SRC, TRAF6
Prostate cancer	74	AKT1, AR, BRAF, CHUK, CREB1, CTNNB1, EGF, EGFR, ERBB2, GRB2, GSK3B, HSP90AA1, IGF1, IGF1R, IKBKB, IKBKG, INS, MAP2K1, MAPK1, NFKB1, NFKBIA, NRAS, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, RAF1, RELA, SOS1
Pathways in cancer	64	ABL1, AKT1, AR, BCR, BIRC5, BRAF, CBL, CHUK, CTNNB1, DVL3, EGF, EGFR, ERBB2, GRB2, GSK3B, HDAC1, HDAC2, HSP90AA1, IGF1, IGF1R, IKBKB, IKBKG, KIT, MAP2K1, MAPK1, MET, MYC, NFKB1, NFKB2, NFKBIA, NRAS, PDGFB, PDGFRB, PIK3CA, PIK3R1, RAF1, RELA, RET, SMAD2, SMAD3, SOS1, TRAF1, TRAF2, TRAF6, VEGFA
Focal adhesion	63	AKT1, BRAF, CTNNB1, EGF, EGFR, ELK1, ERBB2, FYN, GRB2, GSK3B, IGF1, IGF1R, KDR, MAP2K1, MAPK1, MET, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PPP1CC, PXN, RAF1, SHC1, SOS1, SRC, VEGFA
Neurotrophin signaling pathway	57	ABL1, AKT1, BRAF, FOXO3, GRB2, GSK3B, IKBKB, IRS1, MAP2K1, MAP3K3, MAPK1, MAPK14, MAPK7, NFKB1, NFKBIA, NFKBIB, NFKBIE, NRAS, PIK3CA, PIK3R1, PRKCD, RAF1, RELA, RIPK2, SHC1, SOS1, TRAF6, YWHAQ

Continued on next page...

name	edges	genes
Chemokine signaling pathway	49	ADRBK1, AKT1, ARRB1, ARRB2, BRAF, CHUK, FOXO3, GRB2, GRK5, GRK6, GSK3A, GSK3B, IKBKB, IKBKG, JAK2, MAP2K1, MAPK1, NFKB1, NFKBIA, NFKBIB, NRAS, PIK3CA, PIK3R1, PRKCD, PXN, RAF1, RELA, SHC1, SOS1, SRC
Tyrosine metabolism	49	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7, AOC2, AOC3, DDC, GOT1, GOT2, HEMK1, IL4I1, MAOA, MAOB, METTL2B, METTL6, NUP62, TAT, TH, TYR, WBSCR22
Tryptophan metabolism	48	ABP1, AFMID, CYP1A1, DDC, IDO1, IDO2, IL4I1, INMT, MAOA, MAOB, NUP62, TPH1, TPH2
Epstein-Barr virus infection	45	AKT1, CD40, CHUK, GSK3B, HDAC1, HDAC2, IKBKB, IKBKG, MAP3K14, MAP3K7, MAPK14, MYC, NEDD4, NFKB1, NFKB2, NFKBIA, NFKBIB, NFKBIE, PIK3CA, PIK3R1, PSMD6, RELA, RELB, RIPK1, TAB1, TAB2, TBK1, TRADD, TRAF1, TRAF2, TRAF6, XPO1, YWHAQ
Adipocytokine signaling pathway	45	AKT1, CAMKK1, CAMKK2, CHUK, IKBKB, IKBKG, IRS1, JAK2, NFKB1, NFKBIA, NFKBIB, NFKBIE, PRKCQ, RELA, STK11, TNFRSF1A, TNFRSF1B, TRADD, TRAF2
Gap junction	41	EGF, EGFR, GJA1, GNA11, GNAS, GRB2, MAP2K1, MAPK1, MAPK7, NRAS, PDGFB, PDGFRB, RAF1, SOS1, SRC, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8
Insulin signaling pathway	37	AKT1, BRAF, CBL, ELK1, GRB2, GSK3B, IKBKB, INS, INSR, IRS1, MAP2K1, MAPK1, NRAS, PDPK1, PIK3CA, PIK3R1, PPP1CC, RAF1, SHC1, SOCS1, SOS1
Chronic myeloid leukemia	36	ABL1, AKT1, BCR, BRAF, CBL, CHUK, GRB2, HDAC1, HDAC2, IKBKB, IKBKG, MAP2K1, MAPK1, MYC, NFKB1, NFKBIA, NRAS, PIK3CA, PIK3R1, RAF1, RELA, SHC1, SMAD3, SOS1
Glycerophospholipid metabolism	36	AGPAT6, AGPAT9, CDS1, CDS2, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, GPAM, GPAT2, MBOAT2, PEMT, PISD
MAPK signaling pathway	35	AKT1, ARRB1, ARRB2, BRAF, CHUK, EGF, EGFR, ELK1, GRB2, IKBKB, IKBKG, IL1B, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK7, MAPT, MYC, NFKB1, NFKB2, NRAS, PDGFB, PDGFRB, PPP3CA, PPP5C, RAF1, RELA, RELB, SOS1, TAB1, TAB2, TAOK1, TNFRSF1A, TRAF2, TRAF6
Drug metabolism - cytochrome P450	34	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, MAOA, MAOB, UGT2B17
T cell receptor signaling pathway	32	AKT1, CBL, CHUK, FYN, GRB2, GSK3B, IKBKB, IKBKG, MAP2K1, MAP3K14, MAP3K7, MAP3K8, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, NFKBIE, NRAS, PIK3CA, PIK3R1, PPP3CA, PRKCQ, RAF1, RELA, SOS1
Non-small cell lung cancer	32	AKT1, BRAF, EGF, EGFR, ERBB2, FOXO3, GRB2, MAP2K1, MAPK1, NRAS, PDPK1, PIK3CA, PIK3R1, RAF1, SOS1
Melanoma	32	AKT1, BRAF, EGF, EGFR, IGF1, IGF1R, MAP2K1, MAPK1, MET, NRAS, PDGFB, PDGFRB, PIK3CA, PIK3R1, RAF1
Toxoplasmosis	31	AKT1, CD40, CHUK, IKBKB, IKBKG, JAK2, MAP3K7, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, PIK3CA, PIK3R1, RELA, SOCS1, TAB1, TAB2, TNFRSF1A, TRAF6
Glioma	28	AKT1, BRAF, EGF, EGFR, GRB2, IGF1, IGF1R, MAP2K1, MAPK1, NRAS, PDGFB, PDGFRB, PIK3CA, PIK3R1, RAF1, SHC1, SOS1
ErbB signaling pathway	28	ABL1, AKT1, BRAF, CBL, EGF, EGFR, ELK1, ERBB2, ERBB3, ERBB4, GRB2, GSK3B, MAP2K1, MAPK1, MYC, NRAS, PIK3CA, PIK3R1, RAF1, SHC1, SOS1, SRC
HTLV-I infection	27	AKT1, BUB1B, BUB3, CD40, CDC20, CHUK, CREB1, CTNNB1, DVL3, EGR1, ELK1, GSK3B, IKBKB, IKBKG, MAD2L1, MAP3K14, MAP3K3, MYC, NFKB1, NFKB2, NFKBIA, NRAS, PDGFB, PDGFRB, PIK3CA, PIK3R1, PPP3CA, RELA, RELB, SMAD2, SMAD3, TNFRSF1A, XPO1
Cytosolic DNA-sensing pathway	26	CHUK, IKBKB, IKBKE, IKBKG, IL1B, NFKB1, NFKBIA, NFKBIB, RELA, RIPK1, RIPK3, TBK1
Small cell lung cancer	26	AKT1, CHUK, IKBKB, IKBKG, MYC, NFKB1, NFKBIA, PIK3CA, PIK3R1, RELA, TRAF1, TRAF2, TRAF6
Chagas disease (American trypanosomiasis)	26	AKT1, CHUK, GNA11, GNA14, GNA15, GNAL, GNAS, IKBKB, IKBKG, IL1B, MAPK1, MAPK14, NFKB1, NFKBIA, PIK3CA, PIK3R1, PPP2CA, RELA, SMAD2, SMAD3, TNFRSF1A, TRAF6
Influenza A	26	AKT1, FURIN, GSK3B, IKBKB, IKBKE, IL1B, JAK2, KPNA1, KPNA2, MAP2K1, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, PIK3CA, PIK3R1, RAF1, RELA, TBK1, TNFRSF1A, XPO1
B cell receptor signaling pathway	25	AKT1, CHUK, GRB2, GSK3B, IKBKB, IKBKG, MAP2K1, MAPK1, NFKB1, NFKBIA, NFKBIB, NFKBIE, NRAS, PIK3CA, PIK3R1, PPP3CA, RAF1, RELA, SOS1
Acute myeloid leukemia	25	AKT1, BRAF, CHUK, GRB2, IKBKB, IKBKG, KIT, MAP2K1, MAPK1, MYC, NFKB1, NRAS, PIK3CA, PIK3R1, RAF1, RELA, SOS1
Apoptosis	24	AKT1, CHUK, IKBKB, IKBKG, IL1B, MAP3K14, NFKB1, NFKBIA, PIK3CA, PIK3R1, PPP3CA, RELA, RIPK1, TNFRSF1A, TRADD, TRAF2
Endometrial cancer	24	AKT1, BRAF, CTNNB1, EGF, EGFR, ELK1, ERBB2, FOXO3, GRB2, GSK3B, MAP2K1, MAPK1, MYC, NRAS, PDPK1, PIK3CA, PIK3R1, RAF1, SOS1
Hepatitis C	24	AKT1, BRAF, CHUK, EGF, EGFR, GRB2, GSK3B, IKBKB, IKBKE, IKBKG, MAPK1, MAPK14, NFKB1, NFKBIA, NRAS, PIK3CA, PIK3R1, PPP2CA, RAF1, RELA, RIPK1, SOS1, TBK1, TNFRSF1A, TRADD, TRAF2, TRAF6
Pancreatic cancer	23	AKT1, BRAF, CHUK, EGF, EGFR, ERBB2, IKBKB, IKBKG, MAP2K1, MAPK1, NFKB1, PIK3CA, PIK3R1, RAF1, RELA, SMAD2, SMAD3, VEGFA
Phenylalanine metabolism	22	AOC2, AOC3, DDC, GOT1, GOT2, IL4I1, MAOA, MAOB, NUP62, PAH, PRDX6, TAT
Osteoclast differentiation	21	AKT1, CHUK, CREB1, FYN, GRB2, IKBKB, IKBKG, IL1B, MAP2K1, MAP3K14, MAP3K7, MAPK1, MAPK14, NFKB1, NFKB2, NFKBIA, PIK3CA, PIK3R1, PPP3CA, RELA, RELB, SOCS1, TAB1, TAB2, TNFRSF1A, TRAF2, TRAF6
Jak-STAT signaling pathway	20	AKT1, CBL, GHR, GRB2, JAK2, MYC, PIK3CA, PIK3R1, SOCS1, SOS1
Phosphatidylinositol signaling system	18	CDS1, CDS2, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, PIK3CA, PIK3R1
Glycerolipid metabolism	18	AGK, AGPAT6, AGPAT9, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, GPAM, GPAT2, MBOAT2
RIG-I-like receptor signaling pathway	18	CHUK, IKBKB, IKBKE, IKBKG, MAP3K7, MAPK14, NFKB1, NFKBIA, NFKBIB, RELA, RIPK1, TANK, TBK1, TRADD, TRAF2, TRAF6
VEGF signaling pathway	18	AKT1, KDR, MAP2K1, MAPK1, MAPK14, NRAS, PIK3CA, PIK3R1, PPP3CA, PXN, RAF1, SRC, VEGFA
Measles	17	AKT1, CD46, CHUK, DOK1, FYN, GSK3B, IKBKE, IL1B, JAK2, MAP3K7, NFKB1, NFKBIA, NFKBIB, PIK3CA, PIK3R1, PRKCQ, RELA, TAB2, TBK1, TRAF6
Tuberculosis	16	AKT1, CREB1, IL1B, JAK2, LAMP2, MAPK1, MAPK14, NFKB1, NFYC, PPP3CA, RAF1, RELA, RIPK2, SRC, TNFRSF1A, TRADD, TRAF6
Mucin type O-Glycan biosynthesis	16	C1GALT1, C1GALT1C1, GALNTL4, GCNT1, GCNT3, GCNT4, ST3GAL1
Toll-like receptor signaling pathway	15	AKT1, CD40, CHUK, IKBKB, IKBKE, IKBKG, IL1B, MAP2K1, MAP3K7, MAP3K8, MAPK1, MAPK14, NFKB1, NFKBIA, PIK3CA, PIK3R1, RELA, RIPK1, TAB1, TAB2, TBK1, TRAF6
RNA transport	14	EIF3F, EIF3I, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, PABPC1, RANBP2, RANGAP1, SEC13, XPO1
GnRH signaling pathway	14	EGFR, ELK1, GNA11, GNAS, GRB2, MAP2K1, MAP3K3, MAPK1, MAPK14, MAPK7, NRAS, PRKCD, RAF1, SOS1, SRC
Histidine metabolism	14	ABP1, CNDP1, DDC, HEMK1, HNMT, MAOA, MAOB, METTL2B, METTL6, WBSCR22
Retinol metabolism	13	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7, CYP1A1, CYP3A4, CYP3A43, CYP3A5, CYP3A7, HSD17B6, UGT2B17
Cholinergic synapse	13	AKT1, CREB1, FYN, GNA11, JAK2, KCNJ3, KCNJ6, MAP2K1, MAPK1, NRAS, PIK3CA, PIK3R1
Alcoholism	12	BRAF, CAMKK1, CAMKK2, CREB1, DDC, GNAS, GRB2, GRIN2B, HDAC1, HDAC2, MAOA, MAOB, MAP2K1, MAPK1, NRAS, PPP1CC, RAF1, SHC1, SOS1, TH
Pathogenic Escherichia coli infection	12	ABL1, ARHGEF2, CTNNB1, EZR, FYN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, YWHAQ
Shigellosis	12	ABL1, CHUK, IKBKB, IKBKG, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, RELA, RIPK2, SRC
Aldosterone-regulated sodium reabsorption	12	ATP1B1, IGF1, INS, INSR, IRS1, KCNJ1, MAPK1, NEDD4L, PDPK1, PIK3CA, PIK3R1, SFN, SGK1, SLC9A3R2
Herpes simplex infection	12	IKBKE, IKBKG, IL1B, JAK2, MAP3K7, NFKB1, NFKBIA, NFKBIB, PPP1CC, RELA, TAB1, TAB2, TBK1, TNFRSF1A, TRAF1, TRAF2, TRAF6
Adherens junction	12	CTNNB1, EGFR, ERBB2, FYN, IGF1R, INSR, MAP3K7, MAPK1, MET, SMAD2, SMAD3, SRC
Long-term depression	11	BRAF, GNA11, GNAS, IGF1, IGF1R, MAP2K1, MAPK1, NOS1, NRAS, PPP2CA, RAF1
Fc gamma R-mediated phagocytosis	11	AKT1, GSN, MAP2K1, MAPK1, PIK3CA, PIK3R1, PRKCD, RAF1
Glycosphingolipid biosynthesis - ganglio series	11	B3GALT4, ST3GAL1, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5
NOD-like receptor signaling pathway	11	CHUK, HSP90AA1, IKBKB, IKBKG, IL1B, MAP3K7, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, RELA, RIPK2, SUGT1, TAB1, TAB2, TRAF6
Natural killer cell mediated cytotoxicity	11	BRAF, FYN, GRB2, MAP2K1, MAPK1, NRAS, PIK3CA, PIK3R1, PPP3CA, RAF1, SHC1, SOS1
Vascular smooth muscle contraction	10	BRAF, GNA11, GNAS, MAP2K1, MAPK1, PPP1CC, PRKCD, PRKCQ, RAF1
Dopaminergic synapse	10	AKT1, ARRB2, CREB1, DDC, GNAL, GNAS, GRIN2B, GSK3A, GSK3B, KCNJ3, KCNJ6, KCNJ9, MAOA, MAOB, MAPK14, PPP1CC, PPP2CA, PPP3CA, TH
Bladder cancer	10	BRAF, EGF, EGFR, ERBB2, MAP2K1, MAPK1, MYC, NRAS, RAF1, VEGFA
Type II diabetes mellitus	10	IKBKB, INS, INSR, IRS1, MAPK1, PIK3CA, PIK3R1, PRKCD, SOCS1
Regulation of actin cytoskeleton	10	BRAF, EGF, EGFR, EZR, GSN, INS, MAP2K1, MAPK1, MYH9, NRAS, PDGFB, PDGFRB, PIK3CA, PIK3R1, PPP1CC, PXN, RAF1, SOS1, SRC
Melanogenesis	10	CREB1, CTNNB1, DVL3, GNAS, GSK3B, KIT, MAP2K1, MAPK1, NRAS, RAF1, TUBB3, TYR
Leishmaniasis	10	ELK1, IL1B, JAK2, MAP3K7, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, RELA, TAB1, TAB2, TRAF6
Metabolism of xenobiotics by cytochrome P450	9	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7, CBR3, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, UGT2B17
Epithelial cell signaling in Helicobacter pylori infection	9	CHUK, CSK, EGFR, IKBKB, IKBKG, MAP3K14, MAPK14, MET, NFKB1, NFKBIA, RELA, SRC
Renal cell carcinoma	8	AKT1, BRAF, GRB2, MAP2K1, MAPK1, MET, NRAS, PDGFB, PIK3CA, PIK3R1, RAF1, SOS1, VEGFA
Phenylalanine, tyrosine and tryptophan biosynthesis	8	GOT1, GOT2, IL4I1, NUP62, PAH, TAT
Progesterone-mediated oocyte maturation	7	AKT1, BRAF, BUB1, HSP90AA1, IGF1, IGF1R, INS, MAD1L1, MAD2L1, MAP2K1, MAPK1, MAPK14, PGR, PIK3CA, PIK3R1, PLK1, RAF1
Colorectal cancer	7	AKT1, BIRC5, BRAF, CTNNB1, GSK3B, MAP2K1, MAPK1, MYC, PIK3CA, PIK3R1, RAF1, SMAD2, SMAD3

Continued on next page...

name	edges	genes
Serotonergic synapse	7	BRAF, CYP2D6, DDC, GNAS, HTR4, KCNJ3, KCNJ6, KCNJ9, MAOA, MAOB, MAP2K1, MAPK1, NRAS, RAF1, TPH1, TPH2
Calcium signaling pathway	6	ADRB2, ADRB3, EGFR, ERBB2, ERBB3, ERBB4, GNA11, GNA14, GNA15, GNAL, GNAS, HTR4, NOS1, PDGFRB, PPP3CA, SLC8A1
Fc epsilon RI signaling pathway	6	AKT1, FYN, GRB2, MAP2K1, MAPK1, MAPK14, NRAS, PIK3CA, PIK3R1, PRKCD, RAF1, SOS1
Thyroid cancer	5	BRAF, CTNNB1, MAP2K1, MAPK1, MYC, NRAS, RET
Oocyte meiosis	5	AR, BUB1, CDC20, IGF1, IGF1R, INS, MAD2L1, MAP2K1, MAPK1, PGR, PLK1, PPP1CC, PPP2CA, PPP3CA, SGOL1, YWHAQ
mTOR signaling pathway	5	AKT1, BRAF, IGF1, INS, MAPK1, PDPK1, PIK3CA, PIK3R1, STK11, VEGFA
Wnt signaling pathway	5	CACYBP, CTNNB1, DVL3, GSK3B, MAP3K7, MYC, PPP2CA, PPP3CA, RUVBL1, SIAH1, SMAD2, SMAD3
Long-term potentiation	5	BRAF, GRIN2B, MAP2K1, MAPK1, NRAS, PPP1CC, PPP3CA, RAF1
Pertussis	4	IL1B, MAPK1, MAPK14, NFKB1, RELA, TRAF6
Salmonella infection	4	DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, IL1B, MAPK1, MAPK14, MYH9, NFKB1, RELA
Dorso-ventral axis formation	4	EGFR, GRB2, MAP2K1, MAPK1, SOS1
Legionellosis	4	HSF1, IL1B, NFKB1, NFKB2, NFKBIA, RELA, VCP
Starch and sucrose metabolism	3	GUSB, KL, UGDH, UGT2B17
Endocrine and other factor-regulated calcium reabsorption	3	ATP1B1, ESR1, GNAS, KL, SLC8A1
Glycosphingolipid biosynthesis - globo series	3	FUT1, FUT2, ST3GAL1, ST8SIA1
Prion diseases	3	EGR1, ELK1, FYN, IL1B, MAP2K1, MAPK1, STIP1
Pentose and glucuronate interconversions	3	GUSB, KL, UGDH, UGT2B17
Cytokine-cytokine receptor interaction	3	CD40, EGF, EGFR, GHR, IL1B, KDR, KIT, MET, PDGFB, PDGFRB, RELT, TNFRSF1A, TNFRSF1B, VEGFA
Cell cycle	3	ABL1, BUB1, BUB1B, BUB3, CDC20, GSK3B, HDAC1, HDAC2, MAD1L1, MAD2L1, MYC, PLK1, SFN, SMAD2, SMAD3, YWHAQ
Bacterial invasion of epithelial cells	2	CBL, CTNNB1, MET, PIK3CA, PIK3R1, PXN, SHC1, SRC
Salivary secretion	2	ADRB2, ADRB3, ATP1B1, GNAS, NOS1, SLC12A2
Basal cell carcinoma	2	CTNNB1, DVL3, GSK3B
Protein processing in endoplasmic reticulum	2	DNAJA1, GANAB, HSP90AA1, HSPH1, HYOU1, SEC13, SEC24D, TRAF2, UBQLN4, VCP
Amphetamine addiction	2	CREB1, DDC, GNAS, GRIN2B, HDAC1, MAOA, MAOB, PPP1CC, PPP3CA, TH
Drug metabolism - other enzymes	1	CYP3A4, CYP3A43, CYP3A5, CYP3A7, GUSB, UGT2B17
Porphyrin and chlorophyll metabolism	1	GUSB, UGT2B17
Riboflavin metabolism	1	ACPP, FLAD1, TYR
Axon guidance	1	ABL1, EPHB1, FES, FYN, GSK3B, MAPK1, MET, NRAS, PPP3CA
Maturity onset diabetes of the young	1	INS, NEUROD1
Fatty acid elongation	1	ELOVL5, HSD17B12
Alzheimer's disease	1	ATP5D, BACE1, GAPDH, GRIN2B, GSK3B, IL1B, MAPK1, MAPT, NOS1, PPP3CA, TNFRSF1A

Table 25: List of WikiPathways [7] pathways supporting the relationships between the genes shown in Figure 49. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Apoptosis	43	AKT1, BIRC5, CHUK, IGF1, IGF1R, IKBKB, IKBKG, MYC, NFKB1, NFKBIA, NFKBIB, NFKBIE, PIK3R1, RELA, RIPK1, TNFRSF1A, TNFRSF1B, TRADD, TRAF1, TRAF2
Focal Adhesion	39	AKT1, BRAF, EGF, EGFR, ELK1, ERBB2, FYN, GRB2, GSK3B, IGF1, IGF1R, KDR, MAP2K1, MAPK1, MAPK6, MAPK7, MET, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PXN, RAF1, SHC1, SOS1, SRC
TNF alpha Signaling Pathway	33	AKT1, CDC37, CHUK, GRB2, HSP90AA1, IKBKB, IKBKG, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, NFKB1, NFKB2, NFKBIA, NFKBIB, NFKBIE, PLK1, PPP2CA, RAF1, REL, RIPK1, RIPK3, SOS1, TAB1, TAB2, TANK, TBK1, TNFRSF1A, TNFRSF1B, TRADD, TRAF1, TRAF2
EBV LMP1 signaling	31	CHUK, HSP90AA1, IKBKB, IKBKG, MAP3K14, MAP3K3, MAP3K7, MAPK1, NFKB1, NFKB2, RELA, TRADD, TRAF1, TRAF6
MicroRNAs in cardiomyocyte hypertrophy	14	AKT1, CDK9, CHUK, CTNNB1, EGF, GSK3B, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, MAP2K1, MAP3K14, MAPK1, MAPK14, MAPK7, NFKB1, PDPK1, PIK3CA, PIK3R1, PPP3CA, RAF1, TAB1
EGF/EGFR Signaling Pathway	11	ABI1, ABL1, AKT1, BRAF, CREB1, CSK, EGF, EGFR, ELK1, ERBB2, GJA1, GRB2, JAK2, MAP2K1, MAP3K3, MAPK1, MAPK14, MAPK7, PDPK1, PIK3R1, PRKCD, RAF1, SHC1, SOS1
Estrogen signaling pathway	9	AKT1, BRAF, CREB1, ELK1, ESR1, GNAS, MAP2K1, MAPK1, MAPK14, NFKB1, PIK3CA
MAPK Cascade	8	BRAF, ELK1, MAP2K1, MAP3K3, MAPK1, MAPK14, MBP, NRAS, RAF1
Cell cycle	8	ABL1, BUB1, BUB1B, BUB3, CDC20, GSK3B, HDAC1, HDAC2, MAD1L1, MAD2L1, PLK1, SMAD3, YWHAQ
MAPK signaling pathway	7	AKT1, ARRB1, ARRB2, BRAF, EGF, EGFR, ELK1, GRB2, IKBKB, IKBKG, IL1B, MAP2K1, MAP3K14, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MAPT, MYC, NFKB1, NRAS, PDGFB, PDGFRB, PPP3CA, PPP5C, PRKCD, RAF1, TAB1, TAB2, TAOK1, TRAF2, TRAF6
ErbB signaling pathway	7	ABL1, EGF, EGFR, ELK1, ERBB2, ERBB3, ERBB4, GRB2, GSK3B, MAP2K1, MAPK1, MYC, SOS1, SRC
IL-2 Signaling pathway	7	AKT1, CBL, FOXO3, FYN, GRB2, MAP2K1, MAPK1, MAPT, MYC, NMI, PIK3R1, RAF1, SHC1, SOS1
TCR Signaling Pathway	7	AKT1, CBL, CHUK, CREB1, FYN, GRB2, IKBKB, IKBKG, IL1B, MAP2K1, MAP3K14, MAP3K7, MAP3K8, MAPK1, MAPK14, NFKB1, NFKBIA, PDPK1, PIK3R1, PRKCD, PRKCQ, RAF1, REL, RELA, RIPK2, SHC1, SOS1, TRAF6
EPO Receptor Signaling	6	AKT1, GRB2, IRS1, JAK2, MAP2K1, MAPK1, RAF1, SHC1, SOCS1, SOS1, SRC
Integrated Breast Cancer Pathway	6	ABL1, AKT1, AR, BRAF, BRCA1, CHUK, CREB1, CTNNB1, CYP19A1, EGFR, ESR1, GSK3A, HDAC1, IRS1, MAPK1, MYC, NFKB1, NUP85, PIGR, PLK1, SMAD2, STK11, TAB1, TRADD, VEGFA
angiogenesis overview	6	AKT1, ELK1, GRB2, KDR, MAP2K1, MAP3K7, MAPK1, MAPK14, PDPK1, PXN, RAF1, SHC1, SOS1, SRC, VEGFA
NLR proteins	6	CD40, CHUK, IKBKB, IKBKG, MAP3K7
Osteopontin Signaling	6	CHUK, IKBKB, MAP2K1, MAP3K14, MAPK1, NFKB1, RELA
IL-3 Signaling Pathway	5	AKT1, CBL, FYN, GRB2, JAK2, MAP2K1, MAPK1, PIK3R1, RAF1, SHC1, SOS1, SRC, YWHAQ
IL-1 signaling pathway	5	AKT1, CHUK, IKBKB, IKBKG, IL1B, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAPK1, MAPK14, NFKB1, NFKBIA, NFKBIB, PIK3R1, REL, RELA, TAB1, TAB2, TRAF6
RANKL/RANK Signaling Pathway	4	AKT1, CBL, CHUK, IKBKB, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, NFKB1, NFKB2, NFKBIA, PIK3R1, RELA, RELB, SRC, TAB1, TAB2, TRAF1, TRAF2, TRAF6
Prolactin Signaling Pathway	4	AKT1, CBL, ELK1, ERBB2, FYN, GRB2, GSK3B, IRS1, JAK2, MAP2K1, MAPK1, MAPK14, MYC, NFKB1, NFKBIA, NFKBIB, PIK3CA, PIK3R1, PXN, RAF1, RELA, SHC1, SOCS1, SOS1, SRC
AMPK signaling	4	AKT1, CAMKK1, CAMKK2, INSR, PIK3CA, PIK3R1, STK11
DNA damage response (only ATM dependent)	4	ABL1, CTNNB1, DVL3, ERBB2, FOXO3, GRB2, GSK3B, INSR, IRS1, MAP3K7, MAPK1, MYC, SHC1, SMAD3, SOS1
B Cell Receptor Signaling Pathway	4	AKT1, BRAF, CBL, CHUK, CREB1, ELK1, FYN, GRB2, GSK3A, GSK3B, IKBKB, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MYC, NFKB1, NFKBIA, PDPK1, PIK3R1, PRKCD, RAF1, REL, RELA, SHC1, SOS1
TGF beta Signaling Pathway	4	AKT1, GRB2, HDAC1, MAP2K1, MAP3K7, MAPK1, MAPK14, MYC, NEDD4L, PIK3R1, RAF1, SHC1, SKIL, SMAD2, SMAD3, SOS1, SRC, TAB1, TRAF6
Ovarian Infertility Genes	3	CYP19A1, EGR1, NR5A1, PGR, SMAD3
Angiogenesis	3	AKT1, KDR, MAPK1, PDGFB, PIK3CA, SRC, VEGFA
Regulation of Microtubule Cytoskeleton	3	ABL1, AKT1, AURKB, CLASP1, CLIP1, GSK3B, KIF2C, MAPRE1, MAPT, PIK3CA, SRC, TAOK1
TWEAK Signaling Pathway	3	AKT1, CHUK, CTNNB1, GSK3B, HDAC1, IKBKB, MAP3K7, MAPK1, MAPK14, NFKB1, NFKB2, NFKBIA, NFKBIB, RAF1, RELA, RELB, RIPK1, TRAF1, TRAF2
Leptin signaling pathway	3	AKT1, CHUK, CREB1, ELK1, ERBB2, ESR1, FYN, GRB2, IKBKB, IKBKG, IRS1, JAK2, MAP2K1, MAPK1, MAPK14, NFKB1, PIK3R1, RAF1, REL, RELA, SHC1, SOS1, SRC
Regulation of Actin Cytoskeleton	3	BRAF, CSK, EGF, EGFR, EZR, GSN, MAP2K1, MAPK1, MAPK6, NRAS, PDGFB, PDGFRB, PIK3CA, PIK3R1, PXN, RAF1, SOS1
Regulation of toll-like receptor signaling pathway	3	AKT1, CD40, CHUK, IKBKB, IKBKE, IKBKG, IL1B, MAP2K1, MAP3K7, MAP3K8, MAPK1, MAPK14, NFKB1, NFKB2, NFKBIA, PIK3CA, PIK3R1, PLK1, RELA, RIPK1, SOCS1, TAB1, TAB2, TBK1, TRAF6
Signaling of Hepatocyte Growth Factor Receptor	3	ELK1, GRB2, MAP2K1, MAPK1, PIK3CA, PXN, RAF1, SOS1, SRC
IL-4 signaling pathway	2	AKT1, BIRC5, CBL, CHUK, ELK1, GRB2, IKBKB, JAK2, MAPK1, MAPK14, NFKB1, NFKBIA, PIK3CA, PIK3R1, RELA, SHC1, SOCS1, SOS1
IL-6 signaling pathway	2	A2M, AKT1, GRB2, GSK3B, HDAC1, JAK2, MAP2K1, MAPK1, PIK3R1, PRKCD, SHC1, SOS1
Endochondral Ossification	2	ACAN, ADAMTS1, AKT1, GHR, IGF1, IGF1R, VEGFA
IL-5 signaling pathway	2	AKT1, ELK1, FOXO3, GRB2, GSK3A, GSK3B, JAK2, MAP2K1, MAPK1, MAPT, MYC, PIK3R1, RAF1, SHC1, SOS1
Kit receptor signaling pathway	2	AKT1, CBL, DOK1, FOXO3, GRB10, JAK2, KIT, MAP2K1, MAPK1, MAPK14, MAPT, PIK3R1, RAF1, SHC1, SOCS1, SOS1, SRC
Integrin-mediated cell adhesion	2	AKT1, BRAF, CSK, FYN, GRB2, MAP2K1, MAPK1, MAPK6, MAPK7, PDPK1, PXN, RAF1, SHC1, SOS1, SRC
SREBP signalling	2	CREB1, GPAM, GSK3A, INS, SEC13, SEC24D
IL17 signaling pathway	2	AKT1, GSK3B, IKBKB, IKBKG, JAK2, MAP3K14, MAP3K7, MAPK1, NFKB1, NFKBIB, RELA, TRAF6
Toll-like receptor signaling pathway	2	AKT1, CD40, CHUK, IKBKB, IKBKE, IKBKG, IL1B, MAP2K1, MAP3K7, MAP3K8, MAPK1, MAPK14, NFKB1, NFKB2, NFKBIA, PIK3CA, PIK3R1, RELA, RIPK1, TAB1, TAB2, TBK1, TRAF6

Continued on next page...

name	**edges**	**genes**
Serotonin HTR1 Group and FOS Pathway	2	BRAF, CREB1, ELK1, MAP2K1, MAPK14, PDPK1, PIK3CA
Neural Crest Differentiation	1	CTNNB1, DVL3, GSK3B, HDAC1, HDAC2, MBP, MYC, NFKB1, NFKB2
Alzheimers Disease	1	BACE1, GAPDH, GRIN2B, GSK3B, IL1B, MAPK1, MAPT, NOS1, PPP3CA, TNFRSF1A
IL-7 signaling pathway	1	AKT1, FYN, GSK3B, MAP2K1, MAPK1, MYC, PIK3R1
FSH signaling pathway	1	AKT1, CREB1, CYP19A1, GRK6, MAPK1, MAPK14, RAF1, SGK1, SRC
IL-9 signaling pathway	1	CDK9, GRB2, MAP2K1, MAPK1, PIK3R1
Osteoblast Signaling	1	PDGFB, PDGFRB
Interferon type I	1	CBL, CREB1, FYN, IRS1, MAPK14, PIK3R1, SOCS1
Hypothetical Network for Drug Addiction	1	CREB1, GRIN2B, MAP2K1, MAPK1
Epigenetic Stress Regulation	1	EGR1, NR3C1
Heart Development	1	CTNNB1, ERBB3, MAPK1, VEGFA
SIDS Susceptibility Pathways	1	AR, CREB1, DDC, DEAF1, MAOA, NFKB1, NR3C1, RET, TPH1, TPH2
Type II diabetes mellitus	1	IKBKB, INSR, IRS1, MAPK1, PRKCD
Androgen receptor signaling pathway	1	AKT1, AR, BRCA1, CREB1, CTNNB1, EGFR, GSK3B, HDAC1, PIK3R1, RELA, SMAD3, SRC
AhR pathway	1	CDC37, CYP1A1, EGFR, HSP90AA1, SRC
Integrated Cancer pathway	1	AKT1, BRCA1, PLK1, SMAD2, SMAD3

11.1.1 GO enrichment of the candidate pathway

Table 26: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.01$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.154	BP	mitotic prometaphase	AHCTF1, APITD1, AURKB, B9D2, BIRC5, BUB1, BUB1B, BUB3, CASC5, CCDC99, CDC20, CDCA8, CENPA, CENPC1, CENPE, CENPH, CENPI, CENPK, CENPL, CENPM, CENPN, CENPO, CENPP, CENPQ, CENPT, CKAP5, CLASP1, CLASP2, CLIP1, DSN1, ERCC6L, INCENP, ITGB3BP, KIF18A, KIF2A, KIF2B, KIF2C, KNTC1, MAD1L1, MAD2L1, MAPRE1, MIS12, MLF1IP, NDC80, NDE1, NDEL1, NSL1, NUDC, NUF2, NUP107, NUP133, NUP160, NUP37, NUP43, NUP85, PAFAH1B1, PLK1, PMF1, PPP1CC, RANBP2, RANGAP1, RCC2, RPS27, SEC13, SGOL1, SGOL2, SKA1, SKA2, SPC24, SPC25, TAOK1, XPO1, ZW10, ZWILCH, ZWINT
0.448	CC	cytosol	A2M, ABI1, ABL1, ADH1A, ADH1B, ADH4, ADH6, ADH7, ADRBK1, AFMID, AHCTF1, AKAP5, AKT1, ANPEP, APITD1, ARHGEF2, ARRB1, ARRB2, AURKB, B9D2, BCR, BIRC5, BRAF, BUB1, BUB1B, BUB3, CAMKK1, CARHSP1, CASC5, CBL, CBR3, CCDC99, CDC20, CDC37, CDCA8, CENPA, CENPC1, CENPE, CENPH, CENPI, CENPK, CENPL, CENPM, CENPN, CENPO, CENPP, CENPQ, CENPT, CHUK, CKAP5, CLASP1, CLASP2, CLIP1, CNBP, CSK, CTNNB1, CYP19A1, DDC, DDX6, DGKA, DGKQ, DOK1, DSN1, DYNC1H1, DYNC1I2, DYNLL1, EIF3F, EIF3I, ERBB4, ERCC6L, EZR, FES, FHL1, FLAD1, FOXO3, FYN, GAPDH, GCH1, GDI2, GJA1, GOT1, GRB10, GRB2, GSK3A, GSK3B, GSN, HDAC1, HSP90AA1, IARS, IDO1, IDO2, IKBKB, IKBKE, IKBKG, IL1B, INCENP, INSR, IRS1, ITGB3BP, ITSN1, JAK2, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KNTC1, KPNA1, KPNA2, MAD1L1, MAD2L1, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK7, MAPRE1, MAPT, MIS12, MLF1IP, MYBPC1, MYH9, NDC80, NDE1, NDEL1, NEDD4, NFKB1, NFKB2, NFKBIA, NFKBIB, NOS1, NR3C1, NSL1, NUDC, NUF2, NUP107, NUP133, NUP160, NUP37, NUP43, NUP85, OTOF, PABPC1, PAFAH1B1, PAH, PAICS, PDPK1, PFAS, PHLPP1, PIK3CA, PIK3R1, PLK1, PMF1, PPP1CC, PPP2CA, PPP3CA, PPP5C, PRDX6, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RANBP2, RANGAP1, RCC2, RELA, RELB, RILPL2, RIPK1, RIPK2, RPL3, RPLP1, RPS27, RPS3A, SEC13, SEC24D, SGOL1, SGOL2, SHC1, SIAH1, SKA1, SKA2, SMAD2, SMAD3, SMAD9, SOCS1, SOS1, SPC24, SPC25, SRC, STK11, SUGT1, TAB1, TAB2, TANK, TAOK1, TAT, TBK1, TH, TPH1, TPH2, TRADD, TRAF2, TRAF6, TTN, TUBA4A, TUBB, TUBB4A, TUBB4B, TUBG1, UBQLN4, UGDH, VARS, VCP, XPO1, ZW10, ZWILCH, ZWINT
0.147	CC	chromosome, centromeric region	AHCTF1, APITD1, AURKB, BIRC5, BUB1, BUB1B, BUB3, CASC5, CCDC99, CDCA8, CENPA, CENPC1, CENPE, CENPH, CENPI, CENPK, CENPL, CENPM, CENPN, CENPO, CENPP, CENPQ, CENPT, CLASP1, CLASP2, CLIP1, DSN1, DYNC1I1, DYNC1LI1, ERCC6L, HJURP, INCENP, ITGB3BP, KIF2B, KIF2C, KNTC1, MAD1L1, MAD2L1, MIS12, MIS18A, MIS18BP1, MLF1IP, NDC80, NDE1, NDEL1, NSL1, NUF2, NUP107, NUP133, NUP160, NUP37, NUP43, NUP85, OIP5, PAFAH1B1, PLK1, PMF1, PPP1CC, PPP2CA, RANGAP1, RCC2, SEC13, SGOL1, SGOL2, SKA1, SKA2, SPC24, SPC25, SUGT1, XPO1, ZW10, ZWILCH, ZWINT
0.123	CC	kinetochore	AHCTF1, BIRC5, BUB1, BUB1B, BUB3, CASC5, CCDC99, CENPA, CENPC1, CENPE, CENPH, CENPI, CENPK, CENPM, CENPN, CENPO, CENPT, CLASP1, CLASP2, CLIP1, DSN1, DYNC1I1, DYNC1LI1, ERCC6L, HJURP, INCENP, KIF2B, KIF2C, KNTC1, MAD1L1, MAD2L1, MIS12, MLF1IP, NDC80, NDE1, NDEL1, NSL1, NUF2, NUP107, NUP133, NUP160, NUP37, NUP43, NUP85, PAFAH1B1, PLK1, PMF1, PPP1CC, RANGAP1, SEC13, SGOL1, SGOL2, SKA1, SKA2, SPC24, SPC25, SUGT1, XPO1, ZW10, ZWILCH, ZWINT
0.111	CC	condensed chromosome, centromeric region	AHCTF1, AURKB, BIRC5, BUB1, BUB1B, BUB3, CASC5, CCDC99, CENPA, CENPC1, CENPE, CENPH, CENPK, CENPM, CENPN, CENPO, CENPT, CLASP1, CLASP2, DSN1, DYNC1I1, DYNC1LI1, ERCC6L, HJURP, INCENP, KIF2B, KIF2C, KNTC1, MAD1L1, MAD2L1, MIS12, MLF1IP, NDC80, NDE1, NDEL1, NSL1, NUF2, NUP107, NUP133, NUP37, NUP43, NUP85, PLK1, PMF1, PPP1CC, RANGAP1, SGOL1, SGOL2, SKA1, SKA2, SPC24, SPC25, ZW10, ZWILCH, ZWINT
0.109	CC	condensed chromosome kinetochore	AHCTF1, BIRC5, BUB1, BUB1B, BUB3, CASC5, CCDC99, CENPA, CENPC1, CENPE, CENPH, CENPK, CENPM, CENPN, CENPO, CENPT, CLASP1, CLASP2, DSN1, DYNC1I1, DYNC1LI1, ERCC6L, HJURP, INCENP, KIF2B, KIF2C, KNTC1, MAD1L1, MAD2L1, MIS12, MLF1IP, NDC80, NDE1, NDEL1, NSL1, NUF2, NUP107, NUP133, NUP37, NUP43, NUP85, PLK1, PMF1, PPP1CC, RANGAP1, SGOL1, SGOL2, SKA1, SKA2, SPC24, SPC25, ZW10, ZWILCH, ZWINT
0.045	BP	TRIF-dependent toll-like receptor signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKE, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK1, RIPK2, TAB1, TAB2, TBK1, TRAF6
0.195	BP	intracellular protein kinase cascade	ADRB2, ADRB3, AGER, AKAP12, AKAP5, AKT1, AR, ARRB1, ARRB2, BRAF, CAMKK2, CD40, CHUK, CREB1, CTNNB1, DGKQ, DOK1, DVL3, EGF, EGFR, ELK1, EPHB1, ERBB2, ERBB4, ESR1, FYN, GHR, GJA1, GRB2, GRIN2B, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KDR, KIT, KL, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MYC, NEK6, NEUROD1, NFKBIA, NFKBIB, NMI, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PIK3CA, PPP2CA, PPP5C, PXN, RAF1, REL, RELA, RET, RIPK1, RIPK2, RIPK3, S100A4, SHC1, SLC9A3R1, SOCS1, SRC, STK11, TAB1, TAB2, TANK, TAOK1, TBK1, TNFRSF1A, TRADD, TRAF1, TRAF2, TRAF6, VEGFA, WNK4, ZNF675
0.242	BP	protein phosphorylation	AATK, ABI1, ABL1, ADRB2, ADRBK1, AGK, AKAP5, AKT1, ARR3, ARRB1, ARRB2, AURKB, BCR, BIRC5, BRAF, BUB1, BUB1B, CAMKK1, CAMKK2, CCNT1, CD40, CDC37, CDK9, CENPE, CHUK, CREB1, CSK, DDR1, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, FES, FYN, GHR, GRK5, GRK6, GSK3A, GSK3B, HSF1, HYOU1, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, INSR, JAK2, KDR, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MOK, NEK6, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLK1, PPP2CA, PRKCD, PRKCQ, PXN, RAF1, RBPMS, RET, RIPK1, RIPK2, RIPK3, SFN, SGK1, SHC1, SLC9A3R1, SMAD2, SMAD3, SMAD9, SOCS1, SRC, ST3GAL1, STK11, STK39, TAB1, TAB2, TAOK1, TBK1, TNFRSF1A, TRAF2, TRAF6, TTN, VEGFA, WNK4, ZNF675
0.164	BP	transmembrane receptor protein tyrosine kinase signaling pathway	ABI1, ADRB2, ADRBK1, AKT1, AR, ARHGEF2, BRAF, CBL, CHUK, CREB1, CSK, CTNNB1, DDR1, DGKD, DOK1, EGF, EGFR, ELK1, EPHB1, ERBB2, ERBB3, ERBB4, ESR1, FOXO3, FURIN, GFRA1, GHR, GIGYF1, GIGYF2, GRB10, GRB2, GSK3A, GSK3B, HDAC1, HDAC2, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, ITGB3BP, ITSN1, JAK2, KDR, KIT, KL, MAP2K1, MAPK1, MAPK14, MAPK7, MET, NEDD4, NFKB1, NFKBIA, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PHLPP1, PIK3CA, PIK3R1, POU1F1, PPP2CA, PRKCD, PRKCQ, PXN, RAF1, RELA, RIPK2, SHC1, SLC9A3R1, SOCS1, SOS1, SRC, STK11, TRAF6, VEGFA
0.236	BP	regulation of protein metabolic process	A2M, ABI1, ABL1, ADRB2, AGK, AKAP5, AKT1, APITD1, ARR3, ARRB1, ARRB2, BRAF, BRCA1, BUB1B, BUB3, CAMKK1, CAMKK2, CCNT1, CD40, CD46, CDC20, CDC37, CDK9, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, EGR1, ERBB2, ERBB3, ERBB4, FOXO3, FURIN, FYN, GHR, GJA1, GSK3A, GSK3B, HDAC2, HYOU1, IGF1, IGF1R, IKBKG, IL1B, INS, INSR, JAK2, KIT, LDB1, MAD2L1, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK7, MET, NEDD4, NEDD4L, NFKB1, NFKBIA, NOS1, NRAS, NUP62, PA2G4, PABPC1, PDGFB, PDGFRB, PDPK1, PEMT, PIK3CA, PIK3R1, PLAUR, PLK1, PPP2CA, PRKCD, PRKCQ, PSMA6, PSMD6, PXN, RAF1, RBPMS, REL, RELA, RIPK1, RIPK2, SERPINA3, SFN, SHC1, SLC9A3R1, SMAD3, SOCS1, STK11, TAB1, TAB2, TAOK1, TBK1, TNFRSF1A, TRAF2, TRAF6, TTN, UBQLN4, VCP, VEGFA, XPO1, ZNF675
0.264	BP	response to organic substance	ABP1, ACAN, ADH5, ADH6, ADH7, ADRBK1, AKT1, AR, ARRB1, BCR, BRAF, BRCA1, CACYBP, CDC37, CDK9, COLEC12, CREB1, CTNNB1, CYP19A1, CYP1A1, DDC, DGKD, DGKQ, DNAJA1, DOK1, EGR1, ERBB2, ERBB3, ERBB4, ESR1, FOXO3, FYN, GCH1, GCNT1, GHR, GJA1, GNAL, GNAS, GOT1, GOT2, GPAM, GRB10, GRB2, GRIN2B, GSK3A, GSN, HNMT, HSD17B3, HSF1, HSP90AA1, HSPH1, HYOU1, IDO1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, KL, KPNA1, KPNA2, MAOB, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEDD4, NEUROD1, NFKB1, NFKB2, NFKBIA, NOS1, NR3C1, NR5A1, NRAS, NUDC, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, OPRD1, PDGFB, PDGFRB, PDPK1, PEMT, PGR, PIK3CA, PIK3R1, PPP2CA, PPP3CA, PPP5C, PRKCD, PRKCQ, PXN, RAF1, RANBP2, RELA, RIPK1, RIPK2, S100P, SHC1, SKIL, SLC8A1, SMAD2, SMAD3, SMAD9, SOCS1, SOS1, SRC, STK11, TAT, TH, TNFRSF1A, TNFRSF1B, TPH2, TRADD, TRAF2, TRAF6, VCP, VEGFA, ZNF675
0.123	BP	microtubule-based process	ARHGEF2, AURKB, BIRC5, BRCA1, BUB1B, BUB3, CASC5, CCDC99, CENPA, CENPE, CKAP5, CLASP1, CLASP2, CLIP1, CTNNB1, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC2H1, DYNLL1, ERBB2, FES, GSK3B, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KPNA2, MAP2K1, MAPRE1, MAPT, MYH9, NDC80, NDE1, NDEL1, NEK6, PAFAH1B1, PLK1, SGOL1, SKA1, SKA2, SPC25, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, XPO1, ZW10, ZWINT
0.191	MF	enzyme binding	A2M, ABL1, ADRB2, AKAP12, AKAP5, AKT1, AR, ARHGEF2, ARRB1, ARRB2, BACE1, BIRC5, BRAF, BRCA1, CAMK2N1, CARHSP1, CCNT1, CD40, CDC20, CDC37, CSK, CTNNB1, CYP1A1, CYP3A4, DGKI, DGKQ, DVL3, DYNLL1, EGFR, EGR1, ELL, ERBB2, ESR1, FOXO3, FURIN, FXYD7, FYN, GHR, GRB2, GRK5, GSK3A, GSK3B, HDAC1, HDAC2, IGF1R, INSR, IRS1, JAK2, KIF3B, KIT, KPNA2, LDB1, LDB2, MAGEA1, MAP2K1, MAPK1, MAPK6, MAPT, MBP, MET, NEDD4, NEK6, NFKBIA, NR5A1, PA2G4, PAFAH1B1, PDPK1, PGR, PIK3R1, PLAUR, PLK1, PPP1CC, PPP3CA, PRKCD, RAF1, RANBP2, RBBP4, RELA, S100A1, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SOCS1, STK39, TAOK1, TCF21, TNFRSF1A, TRADD, TRAF2, TRAF6, TTN, VCP, ZNF675
0.089	CC	spindle	AKT1, ARHGEF2, AURKB, BIRC5, BUB1B, CCDC99, CDC20, CDCA8, CENPE, CKAP5, CLASP1, CLASP2, CTNNB1, DYNC1I1, DYNC1LI1, INCENP, KIF18A, KIF2A, KIF2B, KIF3B, KNTC1, MAD1L1, MAD2L1, MAP2K1, MAPK14, MAPRE1, MYC, MYH9, NDE1, NDEL1, NEK6, NUP62, NUP85, PAFAH1B1, PLK1, PPP2CA, RANGAP1, RCC2, RIF1, SGOL1, SKA1, SKA2, TUBG1, ZW10

Continued on next page. . .

Ratio	Type	Description	Genes
0.163	MF	phosphotransferase activity, alcohol group as acceptor	AATK, ABL1, ADRBK1, AGK, AKT1, AURKB, BCR, BRAF, BUB1, BUB1B, CAMKK1, CAMKK2, CDK9, CHUK, CSK, DDR1, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, FES, FYN, GRK5, GRK6, GSK3A, GSK3B, HSP90AA1, IGF1R, IKBKB, IKBKE, INSR, IRS1, JAK2, KDR, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MOK, NEK6, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLK1, PRKCD, PRKCQ, RAF1, RET, RIPK1, RIPK2, RIPK3, SGK1, SHC1, SRC, STK11, STK39, TAOK1, TBK1, TTN, WNK4
0.234	BP	cellular response to chemical stimulus	ABP1, ADH1A, ADH1B, ADH4, ADH6, ADH7, AKAP5, AKT1, AR, ARRB1, ARRB2, BRCA1, CACYBP, CDC37, CDK9, COLEC12, CREB1, CTNNB1, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, DDC, DOK1, EGR1, EPHB1, ERBB3, ESR1, FOXO3, FYN, GHR, GNAS, GOT1, GPAM, GRB10, GRB2, GRIN2B, GSK3A, GSN, HSD17B2, HSD17B3, HYOU1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, KL, KPNA1, KPNA2, MAOA, MAOB, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEDD4, NFKB1, NOS1, NR3C1, NR5A1, NRAS, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, OPRD1, PDGFB, PDGFRB, PDPK1, PGR, PIK3CA, PIK3R1, PPP3CA, PRDX6, PRKCD, PRKCQ, PXN, RAF1, RANBP2, RELA, RET, RIPK1, RIPK2, SHC1, SLC8A1, SMAD2, SMAD3, SMAD9, SOCS1, SOS1, STK11, TH, TNFRSF1A, TNFRSF1B, TPH2, TRADD, TRAF2, TRAF6, UGDH, VCP, VEGFA, ZNF675
0.130	MF	protein tyrosine kinase activity	AATK, ABL1, ADRBK1, AKT1, AURKB, BRAF, CAMKK1, CAMKK2, CDK9, CHUK, CSK, DDR1, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, FES, FYN, GRK5, GRK6, GSK3A, GSK3B, IGF1R, IKBKB, IKBKE, INSR, IRS1, JAK2, KDR, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MOK, NEK6, PDGFB, PDGFRB, PDPK1, PLK1, PRKCD, PRKCQ, RAF1, RET, RIPK1, RIPK2, RIPK3, SGK1, SHC1, SRC, STK11, STK39, TAOK1, TBK1, TTN, WNK4
0.129	BP	cell division	AHCTF1, ARHGEF2, AURKB, BIRC5, BUB1, BUB1B, BUB3, CASC5, CCDC99, CCNT1, CDC20, CDCA8, CENPE, CENPH, CENPO, CKAP5, CLASP1, CLASP2, DSN1, DYNC1LI1, ERCC6L, IGF1R, IL1B, INCENP, KIF2A, KIF2B, KIF2C, KNTC1, MAD1L1, MAD2L1, MAPRE1, MIS12, MIS18A, MIS18BP1, MYC, MYH9, NDC80, NDE1, NEK6, NSL1, NUDC, NUF2, NUP37, NUP43, OIP5, PAFAH1B1, PDGFB, PLK1, PMF1, PPP1CC, RCC2, RUVBL1, SGOL1, SGOL2, SKA1, SKA2, SPC24, SPC25, TUBB, VEGFA, ZW10, ZWILCH, ZWINT
0.139	BP	regulation of intracellular protein kinase cascade	ADRB2, ADRB3, AKAP12, AKAP5, AKT1, AR, ARRB1, ARRB2, BRAF, CD40, CHUK, CTNNB1, DVL3, EGFR, EPHB1, ERBB2, ERBB4, ESR1, GHR, GJA1, GRB2, GRIN2B, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, INSR, ITSN1, JAK2, KDR, KIT, KL, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAPK1, MYC, NEK6, NEUROD1, NUP62, PDGFB, PDGFRB, PDPK1, PPP2CA, PPP5C, REL, RELA, RIPK1, RIPK2, S100A4, SLC9A3R1, SOCS1, STK11, TAB1, TAB2, TAOK1, TBK1, TNFRSF1A, TRADD, TRAF1, TRAF2, TRAF6, VEGFA, ZNF675
0.172	BP	regulation of phosphorylation	ABI1, ABL1, ADRB2, AGK, AKAP5, AKT1, AR, ARR3, ARRB1, ARRB2, BRAF, CAMKK1, CAMKK2, CCNT1, CD40, CDC37, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, DYNLL1, EGF, EGFR, ERBB2, ERBB3, ERBB4, GHR, GRB10, GSK3A, GSK3B, HYOU1, IGF1, IGF1R, IKBKG, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLK1, PPP2CA, PRKCD, PXN, RAF1, RBPMS, RIPK1, RIPK2, SFN, SHC1, SLC9A3R1, SMAD3, SOCS1, STK11, TAB1, TAB2, TAOK1, TNFRSF1A, TRAF2, TRAF6, TTN, VEGFA, ZNF675
0.205	BP	positive regulation of molecular function	ABI1, ABL1, ADRB2, ADRB3, ADRBK1, AGER, AGK, AKT1, AR, ARHGEF2, ARRB1, BCR, BRAF, CAMKK1, CD40, CDC20, CENPE, CHUK, CREB1, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, ERBB2, ERBB3, ERBB4, ESR1, GCH1, GDI2, GDNF, GHR, GNA11, GNA14, GNA15, GNAL, GNAS, GSK3A, GSK3B, HTR4, HYOU1, IGF1, IKBKB, IKBKG, IL1B, INS, INSR, IRS1, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, MYC, NDEL1, NEUROD1, NFKB1, NFKB2, NFKBIA, NFKBIB, NRAS, OPRD1, PDGFB, PDGFRB, PDPK1, PLK1, PPP2CA, PRKCD, PRKCQ, PSMA6, PSMD6, PXN, RAF1, RANGAP1, RELA, RIPK1, RIPK2, SGK1, SHC1, SLC9A3R1, SMAD3, SOS1, TAB1, TAB2, TRADD, TRAF1, TRAF2, TRAF6, VCP, VEGFA
0.184	BP	regulation of protein modification process	ABI1, ABL1, ADRB2, AGK, AKAP5, AKT1, APITD1, ARR3, ARRB1, ARRB2, BRAF, BRCA1, BUB1B, BUB3, CAMKK1, CAMKK2, CCNT1, CD40, CDC20, CDC37, CDK9, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, EGR1, ERBB2, ERBB3, ERBB4, GHR, GSK3A, GSK3B, HYOU1, IGF1, IGF1R, IKBKG, IL1B, INS, INSR, JAK2, KIT, MAD2L1, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NOS1, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLK1, PPP2CA, PRKCD, PSMA6, PSMD6, PXN, RAF1, RBPMS, RIPK1, RIPK2, SFN, SHC1, SLC9A3R1, SMAD3, SOCS1, STK11, TAB1, TAB2, TAOK1, TNFRSF1A, TRAF2, TRAF6, TTN, VEGFA, ZNF675
0.074	BP	chromosome segregation	APITD1, AURKB, BIRC5, BRCA1, BUB1, BUB3, CASC5, CCDC99, CENPE, CENPH, CENPO, CTNNB1, DSN1, HJURP, INCENP, KIF18A, KIF2B, KIF2C, MAD2L1, MIS12, NDC80, NDEL1, NEK6, NSL1, NUF2, NUP37, NUP43, PMF1, SGOL1, SGOL2, SKA1, SKA2, SPC25, TTN, ZW10, ZWINT
0.162	BP	regulation of protein phosphorylation	ABI1, ABL1, ADRB2, AGK, AKAP5, AKT1, ARR3, ARRB1, ARRB2, BRAF, CAMKK1, CAMKK2, CCNT1, CD40, CDC37, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, ERBB2, ERBB3, ERBB4, GHR, GSK3A, GSK3B, HYOU1, IGF1, IGF1R, IKBKG, IL1B, INS, INSR, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLK1, PPP2CA, PRKCD, PXN, RAF1, RBPMS, RIPK1, RIPK2, SFN, SHC1, SLC9A3R1, SMAD3, SOCS1, STK11, TAB1, TAB2, TAOK1, TNFRSF1A, TRAF2, TRAF6, TTN, VEGFA, ZNF675
0.184	BP	cellular response to organic substance	ABP1, AKT1, AR, ARRB1, BRCA1, CDC37, CDK9, COLEC12, CREB1, CTNNB1, CYP19A1, DDC, DOK1, EGR1, ERBB3, ESR1, FOXO3, FYN, GHR, GNAS, GOT1, GPAM, GRB10, GRB2, GRIN2B, GSK3A, HSD17B3, HYOU1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, KL, KPNA1, KPNA2, MAP2K1, MAPK1, MAPK14, MAPK7, MET, NEDD4, NFKB1, NOS1, NR3C1, NR5A1, NRAS, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, OPRD1, PDGFB, PDGFRB, PDPK1, PGR, PIK3CA, PIK3R1, PPP3CA, PRKCD, PRKCQ, PXN, RAF1, RANBP2, RELA, RIPK1, RIPK2, SHC1, SLC8A1, SMAD2, SMAD3, SMAD9, SOCS1, SOS1, STK11, TH, TNFRSF1A, TNFRSF1B, TRADD, TRAF2, TRAF6, VCP, VEGFA, ZNF675
0.099	CC	microtubule	ARHGEF2, BIRC5, CENPE, CKAP5, CLASP1, CLASP2, CLIP1, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, DYNLL1, HSPH1, INCENP, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KNTC1, MAP2K1, MAPRE1, MAPT, NDE1, NDEL1, NEK6, NUDC, PAFAH1B1, PLK1, RCC2, SKA1, SKA2, SLC8A1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, ZW10
0.308	MF	nucleotide binding	AATK, ABL1, ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7, ADRBK1, AGK, AKT1, ATP5D, AURKB, BCR, BRAF, BUB1, BUB1B, CAMKK1, CAMKK2, CBR3, CDK9, CENPE, CHUK, CSK, DDR1, DDX6, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DNAJA1, DYNC1H1, DYNC1LI1, DYNC1LI2, DYNC2H1, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, ERCC6L, FES, FLAD1, FYN, GAPDH, GCH1, GNA11, GNA14, GNA15, GNAL, GNAS, GRK5, GRK6, GSK3A, GSK3B, HNRNPAB, HNRNPL, HNRNPM, HSD17B12, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, HSP90AA1, HSPH1, HYOU1, IARS, IGF1R, IKBKB, IKBKE, INSR, JAK2, KCNJ1, KDR, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MOK, MYH1, MYH9, NEK6, NMI, NOS1, NRAS, OLA1, PABPC1, PAICS, PDGFRB, PDPK1, PFAS, PIK3CA, PLK1, PRKCD, PRKCQ, PSMA6, RAF1, RBPMS, RET, RIPK1, RIPK2, RIPK3, RUVBL1, SGK1, SKIL, SMARCA2, SMARCA5, SRC, STK11, STK39, TAOK1, TBK1, TTN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, TUFM, UGDH, VARS, VCP, WNK4
0.139	BP	regulation of kinase activity	ABI1, ABL1, ADRB2, AGK, AKT1, BRAF, CAMKK1, CAMKK2, CCNT1, CD40, CDC37, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, ERBB2, ERBB3, ERBB4, GHR, GSK3A, GSK3B, HYOU1, IGF1R, IKBKG, IL1B, INS, INSR, IRS1, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PIK3R1, PLK1, PPP2CA, PRKCD, PXN, RAF1, RIPK1, RIPK2, SFN, SHC1, SLC9A3R1, TAB1, TAB2, TRAF2, TRAF6, TTN, VEGFA, ZNF675
0.259	MF	purine ribonucleoside triphosphate binding	AATK, ABL1, ADRBK1, AGK, AKT1, ATP5D, AURKB, BCR, BRAF, BUB1, BUB1B, CAMKK1, CAMKK2, CDK9, CENPE, CHUK, CSK, DDR1, DDX6, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DNAJA1, DYNC1H1, DYNC1LI1, DYNC1LI2, DYNC2H1, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, ERCC6L, FES, FLAD1, FYN, GCH1, GNA11, GNA14, GNA15, GNAL, GNAS, GRK5, GRK6, GSK3A, GSK3B, HSP90AA1, HSPH1, HYOU1, IARS, IGF1R, IKBKB, IKBKE, INSR, JAK2, KCNJ1, KDR, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MOK, MYH1, MYH9, NEK6, NRAS, OLA1, PAICS, PDGFRB, PDPK1, PFAS, PIK3CA, PLK1, PRKCD, PRKCQ, PSMA6, RAF1, RET, RIPK1, RIPK2, RIPK3, RUVBL1, SGK1, SMARCA2, SMARCA5, SRC, STK11, STK39, TAOK1, TBK1, TTN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, TUFM, VARS, VCP, WNK4
0.111	BP	positive regulation of kinase activity	ABI1, ADRB2, AGK, AKT1, BRAF, CAMKK1, CD40, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, ERBB2, ERBB3, ERBB4, GHR, GSK3A, HYOU1, IKBKG, IL1B, INS, INSR, IRS1, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NRAS, PDGFB, PDGFRB, PDPK1, PPP2CA, PXN, RAF1, RIPK1, RIPK2, SHC1, TAB1, TAB2, TRAF2, TRAF6, VEGFA

Continued on next page...

Ratio	Type	Description	Genes
0.322	BP	regulation of biological quality	A2M, ABL1, ADH4, ADH5, ADH7, ADRB2, ADRB3, ADRBK1, AGER, AGPAT6, AKAP5, AKT1, ANPEP, APEX1, ARRB1, ARRB2, ATP1B1, AURKB, BUB3, CASC5, CBLN2, CD40, CDC20, CENPE, CHUK, CLASP1, CLASP2, CREB1, CSK, CTNNB1, CYP19A1, CYP1A1, CYP3A4, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, EGF, EGR1, EPHB1, ERBB2, ERBB4, ESR1, EZR, FES, FOXO3, FURIN, FXYD1, FYN, GAPDH, GCH1, GCNT4, GDNF, GIGYF2, GNA11, GNA14, GNA15, GNAS, GOT1, GPAM, GRB2, GRIN2B, GSK3A, GSK3B, GSN, HDAC1, HDAC2, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, IGF1, IGF1R, IKBKB, IKBKG, IL1B, INS, INSR, IRS1, JAK2, KDR, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, LAMP2, LDB1, LDB2, LTF, MAOA, MAP2K1, MAPK1, MAPK14, MAPT, MBP, MERTK, MET, MYC, MYH9, NDC80, NDEL1, NEDD4L, NEUROD1, NFKBIA, NFKBIB, NFKBIE, NOS1, NR3C1, NR5A1, NRAS, OTOF, PAFAH1B1, PAH, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLAUR, PLK1, PPP3CA, PRKCD, PRKCQ, RAF1, SERPINA3, SGK1, SGOL1, SHBG, SHC1, SIAH1, SKIL, SLC12A1, SLC1A3, SLC8A1, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SOS1, SRC, STK11, TCEA1, TH, TRAF6, TTN, TUBA4A, VEGFA, WNK4, ZNF675
0.107	BP	positive regulation of intracellular protein kinase cascade	ADRB2, ADRB3, AKAP12, AKAP5, AR, ARRB1, ARRB2, BRAF, CD40, CHUK, CTNNB1, EGFR, ERBB2, ERBB4, ESR1, GHR, GJA1, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, INSR, ITSN1, JAK2, KDR, KIT, KL, MAP3K14, MAP3K3, MAP3K7, NEK6, NUP62, PDGFB, PDGFRB, PPP5C, REL, RELA, RIPK1, RIPK2, S100A4, TAB1, TAB2, TAOK1, TBK1, TNFRSF1A, TRADD, TRAF1, TRAF6, VEGFA
0.133	BP	regulation of protein kinase activity	ABI1, ABL1, ADRB2, AGK, AKT1, BRAF, CAMKK1, CAMKK2, CCNT1, CD40, CDC37, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, ERBB2, ERBB3, GHR, GSK3A, GSK3B, HYOU1, IGF1R, IKBKG, IL1B, INS, INSR, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NRAS, NUP62, PDGFB, PDGFRB, PDPK1, PLK1, PPP2CA, PRKCD, PXN, RAF1, RIPK1, RIPK2, SFN, SHC1, SLC9A3R1, TAB1, TAB2, TRAF2, TRAF6, TTN, VEGFA, ZNF675
0.107	BP	positive regulation of protein kinase activity	ABI1, ADRB2, AGK, AKT1, BRAF, CAMKK1, CD40, CENPE, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DVL3, EGF, EGFR, ERBB2, ERBB3, GHR, GSK3A, HYOU1, IKBKG, IL1B, INS, INSR, JAK2, KIT, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MET, NRAS, PDGFB, PDGFRB, PDPK1, PPP2CA, PXN, RAF1, RIPK1, RIPK2, SHC1, TAB1, TAB2, TRAF2, TRAF6, VEGFA
0.092	BP	microtubule cytoskeleton organization	ARHGEF2, AURKB, BIRC5, BRCA1, BUB1B, BUB3, CASC5, CCDC99, CENPA, CKAP5, CLASP1, CLASP2, CLIP1, CTNNB1, DYNC1H1, DYNC1LI1, FES, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, MAPRE1, MAPT, MYH9, NDC80, NDE1, NDEL1, NEK6, PAFAH1B1, PLK1, SGOL1, SKA1, SKA2, SPC25, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB4B, TUBG1, XPO1, ZW10, ZWINT
0.043	BP	histone exchange	CASC5, CENPA, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, HJURP, ITGB3BP, MIS18A, MIS18BP1, MLF1IP, NASP, OIP5, RBBP4, RBBP7, RSF1, RUVBL1, SMARCA5
0.041	BP	CenH3-containing nucleosome assembly at centromere	CASC5, CENPA, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, HJURP, ITGB3BP, MIS18A, MIS18BP1, MLF1IP, OIP5, RBBP4, RBBP7, RSF1, RUVBL1, SMARCA5
0.041	BP	DNA replication-independent nucleosome assembly	CASC5, CENPA, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, HJURP, ITGB3BP, MIS18A, MIS18BP1, MLF1IP, OIP5, RBBP4, RBBP7, RSF1, RUVBL1, SMARCA5
0.059	BP	epidermal growth factor receptor signaling pathway	ADRBK1, AKT1, CBL, CHUK, CREB1, CSK, DGKD, EGF, EGFR, ERBB2, ESR1, FOXO3, GRB2, GSK3A, GSK3B, MAP2K1, MAPK1, NRAS, NUP62, PDPK1, PHLPP1, PIK3CA, PIK3R1, PRKCD, PXN, RAF1, SHC1, SOS1, SRC
0.115	BP	MAPKKK cascade	ADRB2, ADRB3, AKT1, AR, ARRB1, ARRB2, BRAF, CAMKK2, CREB1, CTNNB1, DVL3, EGF, ELK1, EPHB1, ERBB2, ERBB4, ESR1, GHR, GRB2, GRIN2B, IGF1, IGF1R, IKBKG, IL1B, INS, INSR, JAK2, KDR, KIT, KL, MAP2K1, MAP3K3, MAP3K7, MAPK1, MAPK14, MAPK6, MAPK7, MET, MYC, NRAS, PDGFB, PDGFRB, PPP2CA, PXN, RAF1, RET, RIPK1, RIPK2, SHC1, SLC9A3R1, TAB1, TAB2, TAOK1, TRAF2, TRAF6, ZNF675
0.286	CC	nuclear part	ABL1, ADH7, AHCTF1, AKT1, APEX1, APITD1, AR, AURKB, BIRC5, BRCA1, BUB1, BUB1B, CACYBP, CASC5, CCNT1, CDC20, CDCA8, CDK9, CENPA, CENPC1, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, CREB1, CTNNB1, DDB1, DEAF1, DGKH, DGKQ, DYNLL1, EAF1, EAF2, EGFR, EGR1, ELL, ELL2, ERBB4, ESR1, EZR, FANCA, FBL, FOXO3, GCH1, HDAC1, HDAC2, HJURP, HNRNPL, HNRNPM, IKBKE, IL4I1, INCENP, IPO4, ITGB3BP, JAK2, KIF2B, KPNA1, KPNA2, LDB1, LDB2, LMO4, LRIF1, MAD1L1, MAD2L1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPT, MEIS1, MIS18A, MIS18BP1, MLF1IP, MTA1, MYC, MYH9, NDC80, NDEL1, NEK6, NEUROD1, NFKB1, NFKB2, NFYC, NR3C1, NR5A1, NUDC, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, OIP5, PA2G4, PABPC1, PAFAH1B1, PDPK1, PGC, PGR, PITX1, PLK1, PMF1, PPP1CC, PRKCD, PSMA6, PSMD6, RANBP2, RANGAP1, RBBP4, RBBP7, RBBP8, RCC2, RELA, RP11-1286E23.8, RPL3, RPS3A, RSF1, RUVBL1, SEC13, SF3B2, SGOL1, SGOL2, SKIL, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TCEA1, TCEA2, TFPT, TRAF6, TSEN15, TTN, TUBB, TUBG1, UBQLN4, XPO1
0.214	MF	ATP binding	AATK, ABL1, ADRBK1, AGK, AKT1, ATP5D, AURKB, BCR, BRAF, BUB1, BUB1B, CAMKK1, CAMKK2, CDK9, CENPE, CHUK, CSK, DDR1, DDX6, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, DNAJA1, DYNC1H1, DYNC1LI1, DYNC1LI2, DYNC2H1, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, ERCC6L, FES, FLAD1, FYN, GRK5, GRK6, GSK3A, GSK3B, HSP90AA1, HSPH1, HYOU1, IARS, IGF1R, IKBKB, IKBKE, INSR, JAK2, KCNJ1, KDR, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MERTK, MET, MOK, MYH1, MYH9, NEK6, OLA1, PAICS, PDGFRB, PDPK1, PFAS, PIK3CA, PLK1, PRKCD, PRKCQ, RAF1, RET, RIPK1, RIPK2, RIPK3, RUVBL1, SGK1, SMARCA2, SMARCA5, SRC, STK11, STK39, TAOK1, TBK1, TTN, VARS, VCP, WNK4
0.184	BP	cellular component movement	ABI1, ABL1, ACAN, AGER, AKT1, ARRB2, ATP1B1, BCR, BRCA1, CENPE, CLASP2, DDR1, DGKZ, DNAJA1, DYNC1H1, DYNC1I1, DYNC1I2, DYNC2H1, EGFR, EPHB1, ERBB4, FES, FSCN1, FURIN, FYN, GDNF, GJA1, GRB2, GSK3A, GSK3B, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KIT, MAP2K1, MAPK1, MAPK14, MAPT, MERTK, MET, MYBPC1, MYH9, NDE1, NDEL1, NRAS, NUP85, PAFAH1B1, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, PLAUR, PXN, RAF1, RET, S100A2, S100P, SGK1, SHC1, SLC9A3R1, SMAD3, SOS1, SRC, TTN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, USP33, VCAN, VEGFA
0.184	BP	response to wounding	A2M, ABL1, ADRB2, AGER, AKT1, AOC3, ARRB1, ARRB2, ATP1B1, BCR, CD40, CD46, CENPE, CHUK, CSK, CYP1A1, DDR1, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, EGF, ERBB2, ERBB3, ERBB4, FYN, GJA1, GNA11, GNA14, GNA15, GNAS, GRB2, GSN, HDAC1, HDAC2, IDO1, IGF1, IKBKB, IKBKG, IL1B, INS, JAK2, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, KL, LAMP2, MAP2K1, MAPK1, MAPK14, MAPK7, MERTK, MET, NDEL1, NFKB1, NMI, NOS1, NRAS, PDGFB, PDPK1, PIK3CA, PIK3R1, PLAUR, PRKCD, PRKCQ, PSMA6, RAF1, RELA, RIPK2, SERPINA3, SHC1, SLC1A3, SLC8A1, SMAD3, SOS1, SRC, TBK1, TNFRSF1A, TNFRSF1B, TTN, TUBA4A, VCAN, VEGFA
0.133	BP	wound healing	A2M, ABL1, ADRB2, AKT1, ARRB1, ARRB2, ATP1B1, CD40, CENPE, CSK, DDR1, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, EGF, ERBB2, ERBB3, ERBB4, FYN, GJA1, GNA11, GNA14, GNA15, GNAS, GRB2, GSN, HDAC1, HDAC2, IGF1, IL1B, INS, JAK2, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, LAMP2, MAPK1, MAPK14, MERTK, NOS1, NRAS, PDGFB, PDPK1, PIK3CA, PIK3R1, PLAUR, PRKCD, PRKCQ, RAF1, SHC1, SLC8A1, SMAD3, SOS1, SRC, TTN, TUBA4A, VEGFA
0.236	BP	positive regulation of metabolic process	ADRB2, AKAP12, AKAP5, AKT1, APEX1, APITD1, AR, ARRB1, BRAF, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDC20, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, FURIN, GDNF, GHR, GJA1, GPAM, GRB10, GRB2, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSP90AA1, HSPH1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KDR, KIT, LDB1, LMO4, MAOB, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEDD4, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PABPC1, PDGFB, PDGFRB, PEMT, PIK3CA, PIK3R1, PITX1, PLAUR, PLK1, POU1F1, PPP3CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RBPMS, REL, RELA, RELB, RET, RIPK1, RIPK2, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, STK11, TAB1, TAOK1, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VCP, VEGFA
0.080	BP	platelet activation	A2M, AKT1, ARRB1, ARRB2, CD40, CSK, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, EGF, FYN, GNA11, GNA14, GNA15, GRB2, IGF1, LAMP2, MAPK1, MAPK14, MERTK, PDGFB, PDPK1, PIK3CA, PIK3R1, PRKCD, PRKCQ, RAF1, SHC1, SOS1, SRC, TTN, TUBA4A, VEGFA
0.053	BP	fibroblast growth factor receptor signaling pathway	ADRBK1, AKT1, BRAF, CBL, CHUK, CREB1, CTNNB1, FOXO3, GRB2, GSK3A, GSK3B, KL, MAP2K1, MAPK1, NRAS, PDGFB, PDPK1, PHLPP1, PIK3CA, PIK3R1, PPP2CA, PRKCD, RAF1, SHC1, SOS1, SRC
0.076	BP	nerve growth factor receptor signaling pathway	ADRBK1, AKT1, ARHGEF2, BRAF, CHUK, CREB1, ELK1, FOXO3, FURIN, GRB2, GSK3A, GSK3B, HDAC1, HDAC2, IKBKB, IRS1, ITGB3BP, ITSN1, MAP2K1, MAPK1, MAPK14, MAPK7, NFKB1, NFKBIA, NRAS, PDPK1, PHLPP1, PIK3CA, PIK3R1, PRKCD, RAF1, RELA, RIPK2, SHC1, SOS1, SRC, TRAF6
0.160	BP	regulation of transport	ABL1, ADRB2, ADRBK1, AKAP5, AKT1, ANPEP, ARRB1, BCR, CBL, CD40, CREB1, CTNNB1, EGF, EGFR, ERBB3, ERBB4, FES, FXYD7, GDNF, GJA1, GNAS, GPAM, GRB10, GRIN2B, GRM7, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, IRS1, JAK2, MAOB, MAP2K1, MAPK1, MAPK7, MAPT, MET, NEDD4, NEDD4L, NEUROD1, NFKB1, NFKBIA, NFKBIB, NFKBIE, NOS1, NR3C1, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, OPRD1, PDGFB, PDGFRB, PDPK1, PIK3R1, PPP1CC, PPP3CA, PRKCQ, RANBP2, RANGAP1, RBPMS, RIPK1, SFN, SGK1, SLC8A1, SLC9A3R1, SMAD3, STK39, TNFRSF1A, TRAF2, TRAF6, WNK4, XPO1
0.223	BP	positive regulation of cellular metabolic process	ADRB2, AKAP12, AKAP5, AKT1, APEX1, APITD1, AR, ARRB1, BRAF, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDC20, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, FURIN, GDNF, GHR, GPAM, GRB10, GRB2, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSP90AA1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KIT, LDB1, LMO4, MAOB, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PABPC1, PDGFB, PDGFRB, PEMT, PIK3CA, PIK3R1, PITX1, PLK1, POU1F1, PPP3CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RBPMS, REL, RELA, RET, RIPK1, RIPK2, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, STK11, TAB1, TAOK1, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VCP, VEGFA
0.045	BP	toll-like receptor 3 signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKE, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK1, RIPK2, TAB1, TAB2, TBK1, TRAF6

Continued on next page...

Ratio	Type	Description	Genes
0.219	BP	positive regulation of macromolecule metabolic process	ADRB2, AKAP5, AKT1, APEX1, APITD1, AR, ARRB1, BRAF, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDC20, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, FURIN, GDNF, GHR, GJA1, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSPH1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, LDB1, LMO4, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEDD4, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PABPC1, PDGFB, PDGFRB, PEMT, PIK3CA, PIK3R1, PITX1, PLAUR, PLK1, POU1F1, PPP3CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RBPMS, REL, RELA, RELB, RET, RIPK1, RIPK2, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, STK11, TAOK1, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VCP, VEGFA
0.064	BP	activation of protein kinase activity	ADRB2, AGK, BRAF, CAMKK1, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ, EGF, GHR, IKBKG, INS, INSR, JAK2, MAP2K1, MAP3K3, MAP3K7, MAPK1, NRAS, PDGFB, PDPK1, RAF1, TAB1, TRAF2, TRAF6, VEGFA
0.051	MF	receptor signaling protein activity	BRAF, DOK1, EGFR, ERBB2, ERBB3, ERBB4, IKBKE, INSR, KDR, KIT, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, RAF1, RIPK3, SMAD2, SMAD3, SMAD9, STK39
0.049	BP	positive regulation of NF-kappaB transcription factor activity	AGER, AR, ARHGEF2, CD40, CHUK, IKBKB, IKBKG, IL1B, INS, MAP3K7, NFKB1, NFKB2, NFKBIA, NFKBIB, PRKCQ, PSMA6, RELA, RIPK1, RIPK2, TAB1, TAB2, TRAF1, TRAF2, TRAF6
0.070	BP	I-kappaB kinase/NF-kappaB cascade	CD40, CHUK, CTNNB1, ESR1, GJA1, IKBKB, IKBKE, IKBKG, IL1B, MAP3K14, MAP3K3, MAP3K7, NEK6, NFKBIA, NFKBIB, NUP62, PDPK1, PPP5C, REL, RELA, RIPK1, RIPK2, RIPK3, S100A4, TAB1, TAB2, TANK, TBK1, TNFRSF1A, TRADD, TRAF1, TRAF2, TRAF6, ZNF675
0.179	CC	cell fraction	ABI1, ADH7, ADRB2, ADRB3, ADRBK1, AGPAT6, AKT1, ANPEP, ARR3, ARRB1, BACE1, BRAF, CACYBP, CAMK2N1, CAMKK1, CARHSP1, CTNNB1, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, DDC, DGKB, DYNLL1, EGF, FOXO3, FUT1, FYN, GCH1, GCNT3, GJA1, GNA11, GNAS, GOT1, GRIN2B, GRK5, GSK3B, GUSB, HNMT, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, HTR4, IARS, IDO1, IGF1R, IKBKB, INSR, IRS1, ITGB3BP, ITSN1, JAK2, KL, LAMP2, MAOA, MAP2K1, MAPK1, MAPK14, MERTK, MET, NEDD4, NR3C1, NRAS, OPRD1, OTOF, PAFAH1B1, PEMT, PIK3R1, PPP2CA, PPP3CA, PRKCQ, RAF1, RANGAP1, SIAH1, SLC12A1, SLC12A2, SLC1A3, SLC8A1, STK39, TH, TRAF6, UGT2B17, VCP
0.094	BP	response to peptide hormone stimulus	AKT1, AR, BRAF, CACYBP, DOK1, EGR1, ERBB3, FOXO3, FYN, GCNT1, GHR, GJA1, GNAS, GOT1, GPAM, GRB10, GRB2, GRIN2B, GSK3A, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KL, MAP2K1, MAPK1, MET, NR3C1, NRAS, NUDC, PDGFB, PDPK1, PIK3CA, PIK3R1, PRKCD, PRKCQ, PXN, RAF1, RELA, SHC1, SOCS1, SOS1, STK11, TH
0.334	BP	negative regulation of biological process	A2M, ABI1, ACAN, ADAMTS1, ADRB2, ADRBK1, AKAP5, AKT1, ANPEP, APEX1, AR, ARHGEF2, ARRB1, ARRB2, AURKB, BCR, BIRC5, BRAF, BRCA1, BUB1, BUB1B, BUB3, CACYBP, CASC5, CBL, CD46, CDC20, CDK9, CLASP1, CLASP2, CREB1, CSK, CTNNB1, CYP2D6, DDB1, DDR1, DGKZ, DYNC1LI1, DYNLL1, EAF2, EGF, EGFR, EGR1, ELF1, ERBB2, ERBB3, ERBB4, ESR1, FHL1, FOXO3, FURIN, FYN, GDNF, GJA1, GPAM, GRB10, GRB2, GRK5, GRM7, GSK3A, GSK3B, GSN, HDAC1, HDAC2, HSF1, IDO1, IGF1, IGF1R, IKBKB, IKBKE, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KDR, KIT, KNTC1, LDB1, LDB2, LMO4, MAD1L1, MAD2L1, MAGEA1, MAOB, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPRE1, MAPT, MBP, MET, MYC, NEDD4, NEDD4L, NEK6, NEUROD1, NFKB1, NFKBIA, NFKBIB, NFKBIE, NOS1, NR3C1, NR5A1, NUP62, OPRD1, PA2G4, PABPC1, PAFAH1B1, PDGFB, PDPK1, PEMT, PGR, PIK3CA, PIK3R1, PLAUR, PLK1, POU1F1, PPP2CA, PPP3CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RANGAP1, RBBP4, RBBP7, RBBP8, RELA, RIF1, RIPK1, RIPK2, RSF1, S100A1, SFN, SKIL, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SMARCA2, SMARCA5, SOCS1, STK11, TAOK1, TBK1, TCF21, TNFRSF1A, TNFRSF1B, TRAF2, TRAF6, VEGFA, WNK4, XPO1, YWHAQ, ZNF675, ZW10, ZWILCH, ZWINT
0.141	BP	protein complex subunit organization	ADRB2, AHCTF1, AKAP5, ARHGEF2, AURKB, CD40, CENPA, CENPE, CLASP1, CLASP2, CLIP1, COLEC12, DGKD, DGKH, EGF, FANCA, FES, GCH1, GJA1, GRB2, GSK3B, GSN, HJURP, HSP90AA1, IGF1R, INSR, IRS1, JAK2, KIF18A, KIF2B, KIF2C, KNTC1, LMO4, MAPRE1, MAPT, MIS12, PPP2CA, PRKCD, PXN, RAF1, RPL3, RPLP1, RPS27, RPS3A, SKIL, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SRC, STK11, TRAF1, TRAF2, TTN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP, ZW10
0.182	BP	positive regulation of biosynthetic process	ADRB2, AKAP12, AKAP5, AKT1, AR, ARRB1, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GPAM, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSP90AA1, HSPH1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, JAK2, KDR, LDB1, LMO4, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PABPC1, PDGFB, PDGFRB, PIK3R1, PITX1, POU1F1, PPP3CA, PRKCD, PRKCQ, REL, RELA, RET, RIPK1, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, STK11, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.189	BP	regulation of cell death	ABL1, ADRB2, AGER, AKT1, APEX1, AR, ARHGEF2, ARRB1, ARRB2, AURKB, BIRC5, BRAF, BRCA1, CACYBP, CBL, CD40, CREB1, CTNNB1, DYNLL1, EAF2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FOXO3, FURIN, GCH1, GDNF, GHR, GPAM, GRIN2B, GRK5, GSK3B, HDAC1, HDAC2, IDO1, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, ITGB3BP, ITSN1, JAK2, KDR, KIT, MAD2L1, MAP3K7, MAPK1, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NR3C1, NUP62, PDPK1, PIK3CA, PIK3R1, PLAUR, PLK1, PPP2CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RELA, RIPK1, RIPK2, RIPK3, RPS3A, SFN, SGK1, SIAH1, SKIL, SMAD3, SOS1, STK11, TFPT, TNFRSF1A, TRADD, TRAF1, TRAF2, TRAF6, TUBB, TUBB4B, VCP, VEGFA
0.045	BP	Toll signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKE, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK1, RIPK2, TAB1, TAB2, TBK1, TRAF6
0.280	CC	membrane-enclosed lumen	A2M, ABL1, ADH7, AHCTF1, AKT1, ANPEP, APEX1, APITD1, AR, ATP5D, AURKB, BIRC5, BRCA1, BUB1, CACYBP, CASC5, CCNT1, CDC20, CDCA8, CDK9, CENPA, CENPC1, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, CREB1, CS, CTNNB1, DDB1, DEAF1, DGKQ, EAF1, EAF2, ECI2, EGF, EGR1, ELL, ELL2, ERBB4, ESR1, EZR, FANCA, FBL, FOXO3, FURIN, GANAB, GOT2, HDAC1, HDAC2, HJURP, HNRNPL, HNRNPM, HSD17B8, HSD3B1, HSD3B2, HYOU1, IGF1, IKBKE, INCENP, INS, ITGB3BP, JAK2, KIF2B, KPNA1, KPNA2, LDB1, LDB2, LMO4, LRIF1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPT, MEIS1, MIS18A, MIS18BP1, MLF1IP, MTA1, MYC, NDC80, NEK6, NEUROD1, NFKB1, NFKB2, NFYC, NR3C1, NR5A1, NUDC, OIP5, PA2G4, PDGFB, PDGFRB, PDPK1, PGC, PGR, PITX1, PLAUR, PLK1, PMF1, PPP1CC, PRKCD, PSMA6, PSMD6, RBBP4, RBBP7, RBBP8, RCC2, RELA, RP11-1286E23.8, RPL3, RPS3A, RSF1, RUVBL1, SF3B2, SGOL1, SGOL2, SHC1, SKIL, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TCEA1, TCEA2, TFPT, TSEN15, TTN, TUBB, TUBG1, TUFM, UBQLN4, VEGFA, XPO1
0.078	BP	positive regulation of phosphate metabolic process	AKAP5, AKT1, AR, ARRB1, BRAF, CD40, DVL3, EGF, EGFR, ERBB2, ERBB4, GHR, GRB10, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KIT, MAPK1, MET, PDGFB, PIK3CA, PIK3R1, PLK1, PRKCD, RAF1, RBPMS, RIPK1, STK11, TAB1, TAOK1, TNFRSF1A, VEGFA
0.078	BP	positive regulation of phosphorus metabolic process	AKAP5, AKT1, AR, ARRB1, BRAF, CD40, DVL3, EGF, EGFR, ERBB2, ERBB4, GHR, GRB10, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KIT, MAPK1, MET, PDGFB, PIK3CA, PIK3R1, PLK1, PRKCD, RAF1, RBPMS, RIPK1, STK11, TAB1, TAOK1, TNFRSF1A, VEGFA
0.096	MF	protein serine/threonine kinase activity	AATK, ADRBK1, AKT1, AURKB, BCR, BRAF, BUB1, BUB1B, CAMKK1, CAMKK2, CDK9, CHUK, EGFR, GRK5, GRK6, GSK3A, GSK3B, HSP90AA1, IKBKB, IKBKE, MAP2K1, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, MOK, NEK6, PDPK1, PIK3CA, PLK1, PRKCD, PRKCQ, RAF1, RIPK1, RIPK2, RIPK3, SGK1, STK11, STK39, TAOK1, TBK1, TTN, WNK4
0.184	BP	regulation of programmed cell death	ABL1, ADRB2, AGER, AKT1, APEX1, AR, ARHGEF2, ARRB1, ARRB2, AURKB, BIRC5, BRAF, BRCA1, CBL, CD40, CREB1, CTNNB1, DYNLL1, EAF2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FOXO3, FURIN, GCH1, GDNF, GHR, GPAM, GRK5, GSK3B, HDAC1, HDAC2, IDO1, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, ITGB3BP, ITSN1, JAK2, KDR, KIT, MAD2L1, MAP3K7, MAPK1, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NR3C1, NUP62, PDPK1, PIK3CA, PIK3R1, PLAUR, PLK1, PPP2CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RELA, RIPK1, RIPK2, RIPK3, RPS3A, SFN, SGK1, SIAH1, SKIL, SMAD3, SOS1, STK11, TFPT, TNFRSF1A, TRADD, TRAF1, TRAF2, TRAF6, TUBB, TUBB4B, VCP, VEGFA
0.076	BP	positive regulation of phosphorylation	AKAP5, AKT1, AR, ARRB1, BRAF, CD40, DVL3, EGF, EGFR, ERBB2, ERBB4, GHR, GRB10, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KIT, MAPK1, MET, PDGFB, PIK3CA, PIK3R1, PLK1, RAF1, RBPMS, RIPK1, STK11, TAB1, TAOK1, TNFRSF1A, VEGFA
0.178	BP	positive regulation of cellular biosynthetic process	ADRB2, AKAP12, AKAP5, AKT1, AR, ARRB1, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GPAM, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSP90AA1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, JAK2, LDB1, LMO4, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PABPC1, PDGFB, PDGFRB, PIK3R1, PITX1, POU1F1, PPP3CA, PRKCD, PRKCQ, REL, RELA, RET, RIPK1, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, STK11, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.045	BP	toll-like receptor 4 signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKE, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK1, RIPK2, TAB1, TAB2, TBK1, TRAF6
0.061	BP	protein autophosphorylation	AATK, AKT1, AURKB, CAMKK2, DDR1, EGFR, EPHB1, ERBB2, ERBB4, FES, FYN, GRK5, IGF1R, INS, INSR, JAK2, KDR, KIT, MAP3K3, MAPK14, MAPK7, MET, NEK6, PDGFB, PDGFRB, PDPK1, PPP2CA, RIPK1, STK11, VEGFA
0.182	BP	regulation of apoptosis	ABL1, ADRB2, AGER, AKT1, APEX1, AR, ARHGEF2, ARRB1, ARRB2, AURKB, BIRC5, BRAF, BRCA1, CBL, CD40, CREB1, CTNNB1, DYNLL1, EAF2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FOXO3, FURIN, GCH1, GDNF, GHR, GPAM, GRK5, GSK3B, HDAC1, HDAC2, IDO1, IGF1, IGF1R, IKBKB, IKBKE, IKBKG, IL1B, INS, ITGB3BP, ITSN1, JAK2, KDR, MAD2L1, MAP3K7, MAPK1, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NR3C1, NUP62, PDPK1, PIK3CA, PIK3R1, PLAUR, PLK1, PPP2CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RELA, RIPK1, RIPK2, RIPK3, RPS3A, SFN, SGK1, SIAH1, SKIL, SMAD3, SOS1, STK11, TFPT, TNFRSF1A, TRADD, TRAF1, TRAF2, TRAF6, TUBB, TUBB4B, VCP, VEGFA

Continued on next page...

Ratio	Type	Description	Genes
0.272	CC	organelle lumen	A2M, ABL1, ADH7, AHCTF1, AKT1, ANPEP, APEX1, APITD1, AR, ATP5D, AURKB, BIRC5, BRCA1, BUB1, CASC5, CCNT1, CDC20, CDCA8, CDK9, CENPA, CENPC1, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, CREB1, CS, CTNNB1, DDB1, DEAF1, DGKQ, EAF1, EAF2, ECI2, EGF, EGR1, ELL, ELL2, ERBB4, ESR1, EZR, FANCA, FBL, FOXO3, FURIN, GANAB, GOT2, HDAC1, HDAC2, HJURP, HNRNPL, HNRNPM, HSD17B8, HYOU1, IGF1, IKBKE, INCENP, INS, ITGB3BP, JAK2, KIF2B, KPNA1, KPNA2, LDB1, LDB2, LMO4, LRIF1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPT, MEIS1, MIS18A, MIS18BP1, MLF1IP, MTA1, MYC, NDC80, NEK6, NEUROD1, NFKB1, NFKB2, NFYC, NR3C1, NR5A1, NUDC, OIP5, PA2G4, PDGFB, PDGFRB, PDPK1, PGC, PGR, PITX1, PLAUR, PLK1, PMF1, PPP1CC, PRKCD, PSMA6, PSMD6, RBBP4, RBBP7, RBBP8, RCC2, RELA, RP11-1286E23.8, RPL3, RPS3A, RSF1, RUVBL1, SF3B2, SGOL1, SGOL2, SHC1, SKIL, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TCEA1, TCEA2, TFPT, TSEN15, TTN, TUBG1, TUFM, UBQLN4, VEGFA, XPO1
0.109	BP	positive regulation of protein metabolic process	AKAP5, AKT1, APITD1, ARRB1, BRAF, BRCA1, CD40, CDC20, DVL3, EGF, ERBB2, ERBB4, FURIN, GHR, GJA1, GSK3A, GSK3B, HDAC2, IGF1, IL1B, INS, INSR, JAK2, KIT, LDB1, MAPK1, MAPK7, MET, NEDD4, NFKBIA, NOS1, PABPC1, PDGFB, PEMT, PIK3CA, PIK3R1, PLK1, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RBPMS, REL, RELA, RIPK2, STK11, TAOK1, TBK1, TNFRSF1A, TRAF6, VCP, VEGFA
0.170	BP	regulation of cellular component organization	ABL1, AKAP5, AKT1, AR, ARHGEF2, ARRB1, BCR, BRCA1, BUB1, BUB1B, BUB3, CBL, CBLN2, CDC20, CDK9, CLASP1, CLASP2, CLIP1, CTNNB1, DDR1, DYNC1LI1, EAF2, EGF, EPHB1, ERBB2, EZR, FES, FHL1, FYN, GDNF, GRB2, GSK3A, GSK3B, GSN, HDAC2, HJURP, IGF1, IL1B, INS, INSR, KDR, LMO4, MAD1L1, MAD2L1, MAP2K1, MAPK1, MAPRE1, MAPT, MBP, MET, MYC, MYH9, NDEL1, NEDD4, NEDD4L, NEK6, NOS1, PAFAH1B1, PDGFB, PDGFRB, PDPK1, PIK3R1, PLK1, PPP2CA, PRKCD, PRKCQ, RAF1, RBBP7, RET, SFN, SGK1, SKA1, SKA2, SKIL, SMAD2, SMAD3, SMARCA2, SRC, STK11, TAOK1, VCP, VEGFA, XPO1
0.170	BP	positive regulation of nitrogen compound metabolic process	ADRB2, AKAP12, AKAP5, AKT1, APEX1, AR, ARRB1, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSP90AA1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, JAK2, LDB1, LMO4, MAOB, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PDGFB, PDGFRB, PIK3R1, PITX1, POU1F1, PPP3CA, REL, RELA, RET, RIPK1, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.234	CC	nuclear lumen	ABL1, ADH7, AHCTF1, AKT1, APEX1, APITD1, AR, AURKB, BIRC5, BRCA1, BUB1, CASC5, CCNT1, CDC20, CDCA8, CDK9, CENPA, CENPC1, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, CREB1, CTNNB1, DDB1, DEAF1, DGKQ, EAF1, EAF2, EGR1, ELL, ELL2, ERBB4, ESR1, EZR, FANCA, FBL, FOXO3, HDAC1, HDAC2, HJURP, HNRNPL, HNRNPM, IKBKE, INCENP, ITGB3BP, JAK2, KIF2B, KPNA1, KPNA2, LDB1, LDB2, LMO4, LRIF1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPT, MEIS1, MIS18A, MIS18BP1, MLF1IP, MTA1, MYC, NDC80, NEK6, NEUROD1, NFKB1, NFKB2, NFYC, NR3C1, NR5A1, NUDC, OIP5, PA2G4, PDPK1, PGC, PGR, PITX1, PLK1, PMF1, PPP1CC, PRKCD, PSMA6, PSMD6, RBBP4, RBBP7, RBBP8, RCC2, RELA, RP11-1286E23.8, RPL3, RPS3A, RSF1, RUVBL1, SF3B2, SGOL1, SGOL2, SKIL, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TCEA1, TCEA2, TFPT, TSEN15, TTN, TUBG1, UBQLN4, XPO1
0.053	BP	microtubule-based movement	CENPE, DYNC1H1, DYNC1I1, DYNC1I2, DYNC2H1, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, MAP2K1, MAPT, NDEL1, PAFAH1B1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8
0.072	BP	response to insulin stimulus	AKT1, AR, DOK1, EGR1, ERBB3, FOXO3, GCNT1, GHR, GOT1, GPAM, GRB10, GRB2, GSK3A, IGF1R, IL1B, INS, INSR, IRS1, KL, MAP2K1, MAPK1, NR3C1, NRAS, PDGFB, PDPK1, PIK3CA, PIK3R1, PRKCD, PRKCQ, RAF1, RELA, SHC1, SOCS1, SOS1, STK11
0.092	BP	cellular response to hormone stimulus	AKT1, AR, CYP19A1, DOK1, ERBB3, ESR1, FOXO3, FYN, GHR, GNAS, GOT1, GPAM, GRB10, GRB2, GSK3A, HSD17B3, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KIT, KL, MAP2K1, MAPK1, MET, NR3C1, NR5A1, NRAS, NUP62, PDPK1, PGR, PIK3CA, PIK3R1, PRKCD, PRKCQ, PXN, RAF1, RELA, SHC1, SOCS1, SOS1, STK11, TNFRSF1A
0.078	BP	regulation of MAPKKK cascade	ADRB2, ADRB3, AKT1, AR, ARRB1, ARRB2, BRAF, CTNNB1, DVL3, EPHB1, ERBB2, ERBB4, ESR1, GRB2, GRIN2B, IGF1, IGF1R, IL1B, INS, INSR, KDR, KIT, KL, MAP2K1, MAP3K7, MAPK1, MYC, PDGFB, PDGFRB, PPP2CA, RIPK1, RIPK2, SLC9A3R1, TAB1, TAOK1, TRAF2, TRAF6, ZNF675
0.236	BP	cellular localization	A2M, ADRB2, ADRBK1, AKAP12, AKAP5, AKT1, AR, ARHGEF2, ARRB1, ATP5D, AURKB, BCR, BIRC5, BUB1B, BUB3, CASC5, CCDC99, CD40, CDC37, CENPA, CENPE, CLASP1, CLASP2, CREB1, CTNNB1, DYNC1I1, EGF, EGFR, ERBB4, EXOC1, EZR, FES, FURIN, GDNF, GNAS, GPAM, GRIN2B, GRM7, GSK3B, HSP90AA1, IGF1, IL1B, INS, IPO4, IRS1, JAK2, KIF18A, KIF3B, KPNA1, KPNA2, LAMP2, MAOA, MAOB, MAP2K1, MAPK1, MAPK7, MAPRE1, MAPT, MERTK, MYH9, NDC80, NDE1, NDEL1, NEDD4, NEUROD1, NFKBIA, NFKBIB, NFKBIE, NR3C1, NR5A1, NUDC, NUP107, NUP133, NUP160, NUP62, OPRD1, OTOF, PAFAH1B1, PDGFB, PDPK1, PIK3R1, PLK1, PPP1CC, PPP3CA, PRKCQ, RANBP2, RANGAP1, RBPMS, RPL3, RPLP1, RPS27, RPS3A, SDCBP2, SEC13, SEC24D, SFN, SGOL1, SLC1A3, SLC9A3R1, SMAD2, SMAD3, STK11, TINAGL1, TNFRSF1A, TRAF2, TRAF6, TTN, TUBA4A, TUBB, VCP, VEGFA, XPO1, YWHAQ, ZW10, ZWINT
0.041	BP	regulation of glucose transport	AKT1, ERBB3, ERBB4, GRB10, GSK3A, IGF1, IL1B, INS, INSR, IRS1, MET, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, PIK3R1, RANBP2
0.301	BP	negative regulation of cellular process	ABI1, ACAN, ADAMTS1, ADRB2, ADRBK1, AKT1, APEX1, AR, ARHGEF2, ARRB1, ARRB2, AURKB, BCR, BIRC5, BRAF, BRCA1, BUB1, BUB1B, BUB3, CACYBP, CASC5, CBL, CDC20, CDK9, CLASP1, CLASP2, CREB1, CSK, CTNNB1, CYP2D6, DDB1, DDR1, DGKZ, DYNC1LI1, DYNLL1, EAF2, EGF, EGFR, EGR1, ELF1, ERBB2, ERBB3, ERBB4, ESR1, FHL1, FOXO3, FURIN, GDNF, GJA1, GPAM, GRB10, GRB2, GRK5, GRM7, GSK3A, GSK3B, GSN, HDAC1, HDAC2, HSF1, IDO1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, ITSN1, JAK2, KDR, KIT, KNTC1, LDB1, LDB2, MAD1L1, MAD2L1, MAGEA1, MAOB, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPRE1, MAPT, MBP, MET, MYC, NEDD4, NEK6, NEUROD1, NFKB1, NFKBIA, NFKBIB, NFKBIE, NOS1, NR3C1, NUP62, PA2G4, PABPC1, PAFAH1B1, PDGFB, PDPK1, PEMT, PIK3CA, PIK3R1, PLAUR, PLK1, POU1F1, PPP2CA, PPP3CA, PRKCD, PRKCQ, PSMA6, PSMD6, RAF1, RBBP4, RBBP7, RBBP8, RELA, RIF1, RIPK1, RIPK2, RSF1, S100A1, SFN, SKIL, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SMARCA2, SMARCA5, SOCS1, STK11, TAOK1, TCF21, TRAF2, TRAF6, VEGFA, XPO1, YWHAQ, ZNF675, ZW10, ZWILCH, ZWINT
0.164	BP	positive regulation of nucleobase-containing compound metabolic process	ADRB2, AKAP12, AKAP5, AKT1, APEX1, AR, ARRB1, BRCA1, CACYBP, CAMKK2, CCNT1, CD40, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, LDB1, LMO4, MAP2K1, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PDGFB, PDGFRB, PIK3R1, PITX1, POU1F1, PPP3CA, REL, RELA, RET, RIPK1, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.040	CC	spindle pole	CCDC99, CDC20, CKAP5, CTNNB1, DYNC1I1, DYNC1LI1, KIF2A, KNTC1, MAD2L1, MAP2K1, MAPK14, NDE1, NEK6, NUP62, PLK1, PPP2CA, RANGAP1, SGOL1, TUBG1, ZW10
0.072	BP	cellular response to peptide hormone stimulus	AKT1, DOK1, ERBB3, FOXO3, FYN, GHR, GNAS, GOT1, GPAM, GRB10, GRB2, GSK3A, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KL, MAP2K1, MAPK1, MET, NRAS, PDPK1, PIK3CA, PIK3R1, PRKCD, PRKCQ, PXN, RAF1, RELA, SHC1, SOCS1, SOS1, STK11
0.162	BP	positive regulation of macromolecule biosynthetic process	ADRB2, AKT1, AR, ARRB1, BRCA1, CACYBP, CAMKK2, CD40, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGFR, EGR1, ELF1, ELK1, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, HSPH1, IGF1, IGF1R, IKBKB, IL1B, INS, INSR, IRS1, JAK2, KDR, LDB1, LMO4, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PABPC1, PDGFB, PDGFRB, PIK3R1, PITX1, POU1F1, PPP3CA, PRKCQ, REL, RELA, RET, RIPK1, RSF1, SHC1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.039	BP	toll-like receptor 1 signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK2, TAB1, TAB2, TRAF6
0.074	BP	gland development	AGPAT6, AKT1, AR, CHUK, CREB1, CTNNB1, CYP19A1, DDR1, DEAF1, EAF2, EGFR, ERBB2, ERBB3, ERBB4, ESR1, IGF1, IGF1R, IRS1, JAK2, MAPK1, MET, NR3C1, NR5A1, PDGFB, PDGFRB, PGR, PITX1, PLAUR, POU1F1, SLC12A2, SMAD3, SRC, STK11, TCF21, TPH1, VEGFA
0.242	BP	anatomical structure morphogenesis	ABI1, ABL1, ACAN, ADAMTS1, AKAP5, ANPEP, AR, ARHGEF2, B9D2, BCR, BRAF, BRCA1, C1GALT1, CASC5, CHUK, CLASP1, CLASP2, CREB1, CTNNB1, DDR1, DEAF1, DVL3, DYNC2H1, DYNLL1, EGF, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, ESR1, EZR, FES, FHL1, FYN, GCNT4, GDNF, GFRA1, GHR, GJA1, GNAS, GRB2, GSK3A, GSK3B, GSN, HDAC1, HDAC2, HNRNPAB, HOXC13, HOXC9, HSP90AA1, HSPH1, HYOU1, IGF1, IGF1R, IL1B, INSR, JAK2, KDR, LDB1, LMO4, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, MAPT, MBP, MEIS1, MERTK, MET, MYC, MYH9, NDEL1, NEDD4, NEUROD1, NOS1, NR3C1, NRAS, PAFAH1B1, PDGFB, PDGFRB, PGR, PIK3CA, PITX1, PLAUR, PPP2CA, PRKCQ, PXN, RAF1, RELA, RET, S100A4, SHC1, SIAH1, SKIL, SLC12A2, SLC12A6, SLC1A3, SMAD2, SMAD3, SMAD9, SOCS1, SOS1, SRC, STIP1, STK11, TAB1, TCF21, TH, TNFRSF1A, TRAF6, TTN, TUBB3, UGDH, USP33, VCAN, VEGFA
0.119	BP	protein complex assembly	ADRB2, AHCTF1, AURKB, CD40, CENPA, CENPE, CLIP1, COLEC12, DGKD, DGKH, EGF, FANCA, FES, GCH1, GJA1, GRB2, GSK3B, GSN, HJURP, HSP90AA1, IGF1R, INSR, IRS1, JAK2, KNTC1, LMO4, MAPRE1, MAPT, MIS12, PPP2CA, PRKCD, PXN, RAF1, SKIL, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SRC, STK11, TRAF1, TRAF2, TTN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP, ZW10
0.055	BP	regulation of I-kappaB kinase/NF-kappaB cascade	CD40, CHUK, CTNNB1, ESR1, GJA1, IKBKB, IKBKE, IKBKG, IL1B, MAP3K14, MAP3K3, MAP3K7, NEK6, NUP62, PDPK1, PPP5C, REL, RELA, RIPK1, RIPK2, S100A4, TAB2, TBK1, TNFRSF1A, TRADD, TRAF1, TRAF6
0.139	CC	insoluble fraction	ABI1, ADRB2, ADRB3, ADRBK1, AGPAT6, AKT1, ARRB1, BACE1, BRAF, CAMK2N1, CTNNB1, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, DGKB, DYNLL1, FOXO3, FUT1, FYN, GCNT3, GJA1, GNA11, GNAS, GRIN2B, GUSB, HNMT, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, HTR4, IGF1R, IKBKB, INSR, IRS1, ITGB3BP, ITSN1, JAK2, KL, LAMP2, MAPK1, MET, NEDD4, NR3C1, NRAS, OPRD1, OTOF, PAFAH1B1, PEMT, PIK3R1, PPP3CA, PRKCQ, RAF1, SIAH1, SLC12A1, SLC12A2, SLC1A3, SLC8A1, STK39, TH, TRAF6, UGT2B17, VCP

Continued on next page...

Ratio	Type	Description	Genes
0.039	BP	toll-like receptor 2 signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK2, TAB1, TAB2, TRAF6
0.051	BP	positive regulation of I-kappaB kinase/NF-kappaB cascade	CD40, CHUK, CTNNB1, GJA1, IKBKB, IKBKE, IKBKG, IL1B, MAP3K14, MAP3K3, MAP3K7, NEK6, NUP62, PPP5C, REL, RELA, RIPK1, RIPK2, S100A4, TAB2, TBK1, TNFRSF1A, TRADD, TRAF1, TRAF6
0.072	BP	cellular protein complex assembly	ADRB2, AHCTF1, AURKB, CENPA, CENPE, CLIP1, EGF, FES, GRB2, GSN, HSP90AA1, JAK2, MAPRE1, MAPT, MIS12, PRKCD, PXN, SMAD2, SMAD3, SRC, TRAF2, TTN, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1
0.197	BP	cell proliferation	ABI1, ADAMTS1, ADRB2, AGER, AKT1, AR, ARHGEF2, AURKB, BIRC5, BRCA1, BUB1, BUB1B, CD40, CDC20, CDK9, CHUK, CNBP, CSK, CTNNB1, CYP1A1, DDR1, DEAF1, EAF2, EGF, EGFR, EGR1, EPHB1, ERBB2, ERBB3, ERBB4, ESR1, FANCA, FES, FOXO3, FSCN1, FURIN, FYN, GJA1, GPAM, HDAC1, HDAC2, HSF1, HTR4, IDO1, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIF2C, KIT, MAP2K1, MAPK1, MAPRE1, MET, MYC, NASP, NDE1, NDEL1, NFKBIA, NR3C1, NRAS, NUDC, NUP62, PA2G4, PAFAH1B1, PDGFB, PDGFRB, PEMT, PGR, PIK3R1, PLK1, POU1F1, PRKCD, PRKCQ, RAF1, RBBP4, RBBP7, RELA, RIPK2, RPS27, SFN, SGK1, SHC1, SLC9A3R1, SMAD2, SMAD3, SMARCA2, ST8SIA1, STK11, TRAF6, TYR, VEGFA
0.061	BP	cellular response to insulin stimulus	AKT1, DOK1, ERBB3, FOXO3, GHR, GOT1, GPAM, GRB10, GRB2, GSK3A, IGF1R, IL1B, INS, INSR, IRS1, KL, MAP2K1, MAPK1, NRAS, PDPK1, PIK3CA, PIK3R1, PRKCD, PRKCQ, RAF1, RELA, SHC1, SOCS1, SOS1, STK11
0.135	CC	membrane fraction	ABI1, ADRB2, ADRB3, ADRBK1, AGPAT6, AKT1, ARRB1, BACE1, BRAF, CAMK2N1, CTNNB1, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, DGKB, DYNLL1, FOXO3, FUT1, FYN, GCNT3, GJA1, GNA11, GNAS, GRIN2B, GUSB, HNMT, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, HTR4, IGF1R, IKBKB, INSR, IRS1, ITGB3BP, ITSN1, JAK2, KL, LAMP2, MET, NEDD4, NR3C1, NRAS, OPRD1, OTOF, PAFAH1B1, PEMT, PIK3R1, PPP3CA, PRKCQ, SIAH1, SLC12A1, SLC12A2, SLC1A3, SLC8A1, STK39, TH, TRAF6, UGT2B17, VCP
0.109	BP	peptidyl-amino acid modification	ABI1, ABL1, ADH5, ADRBK1, AKT1, ARRB1, BRAF, BRCA1, CD40, DDR1, EGF, EGFR, ERBB4, FES, FKBP5, FURIN, FYN, GANAB, GAPDH, GHR, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, JAK2, KDR, KIT, LDB1, MAP3K7, MAPK1, MAPK14, MAPK7, MET, NEK6, NOS1, PDGFB, PDGFRB, PDPK1, PIK3CA, PLK1, PPP2CA, PRKCD, PXN, RAF1, RUVBL1, SEC13, SEC24D, SOCS1, SRC, TNFRSF1A, VEGFA
0.039	BP	MyD88-dependent toll-like receptor signaling pathway	CHUK, CREB1, ELK1, IKBKB, IKBKG, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, NFKB1, NFKB2, NFKBIA, NFKBIB, RELA, RIPK2, TAB1, TAB2, TRAF6
0.179	CC	nucleoplasm	AHCTF1, AKT1, APEX1, APITD1, AR, BRCA1, CASC5, CCNT1, CDC20, CDK9, CENPA, CENPH, CENPI, CENPK, CENPN, CENPO, CENPP, CENPQ, CREB1, CTNNB1, DDB1, DEAF1, DGKQ, EAF1, EAF2, EGR1, ELL, ELL2, ERBB4, ESR1, FANCA, FBL, FOXO3, HDAC1, HDAC2, HJURP, HNRNPL, HNRNPM, IKBKE, ITGB3BP, KPNA1, KPNA2, LDB1, LDB2, LMO4, MAP3K7, MAPK1, MAPK14, MAPK7, MEIS1, MIS18A, MIS18BP1, MLF1IP, MTA1, MYC, NEK6, NEUROD1, NFKB1, NFKB2, NFYC, NR3C1, NR5A1, NUDC, OIP5, PDPK1, PGR, PITX1, PLK1, PMF1, PPP1CC, PRKCD, PSMA6, PSMD6, RBBP4, RBBP7, RBBP8, RELA, RSF1, RUVBL1, SF3B2, SKIL, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TCEA1, TCEA2, XPO1
0.082	BP	protein localization to organelle	AKAP5, AKT1, AURKB, BUB1B, CCDC99, CENPA, EGF, EGFR, ERBB4, GSK3B, HSP90AA1, IGF1, IL1B, IRS1, JAK2, KPNA1, KPNA2, MAPK1, MAPK7, MAPRE1, NEDD4, NFKBIA, NFKBIB, NFKBIE, NR5A1, OPRD1, PIK3R1, PLK1, PPP3CA, PRKCQ, RANBP2, RBPMS, RPL3, RPLP1, RPS27, RPS3A, SMAD3, TNFRSF1A, XPO1, ZW10
0.111	BP	negative regulation of programmed cell death	AKT1, APEX1, AR, ARRB1, AURKB, BIRC5, BRAF, CBL, CTNNB1, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FURIN, GDNF, GPAM, GRK5, GSK3B, HDAC1, HDAC2, IDO1, IGF1, IGF1R, IKBKB, IL1B, INS, ITSN1, KDR, KIT, MAD2L1, MAP3K7, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NR3C1, NUP62, PDPK1, PIK3CA, PIK3R1, PLAUR, PLK1, PRKCD, PRKCQ, RAF1, RELA, RIPK1, RIPK2, SMAD3, TRAF2, TRAF6, VEGFA
0.079	MF	kinase binding	ABL1, AKAP5, AKT1, ARRB1, ARRB2, BRAF, CAMK2N1, CCNT1, CDC37, CTNNB1, DGKQ, FOXO3, FYN, GHR, GRK5, GSK3A, GSK3B, IGF1R, INSR, IRS1, JAK2, MAP2K1, MAPK1, MAPK6, MET, NEK6, PDPK1, PIK3R1, PLK1, PPP1CC, RAF1, RELA, SMAD3, SOCS1, STK39, TAOK1, TRADD, TRAF2, TRAF6
0.053	BP	insulin receptor signaling pathway	AKT1, DOK1, FOXO3, GRB10, GRB2, GSK3A, IGF1R, IL1B, INS, INSR, IRS1, KL, MAP2K1, MAPK1, NRAS, PDPK1, PIK3CA, PIK3R1, PRKCD, PRKCQ, RAF1, RELA, SHC1, SOCS1, SOS1, STK11
0.209	BP	regulation of multicellular organismal process	ADRB2, ADRBK1, AGPAT6, AKAP5, AKT1, ANPEP, AR, ARHGEF2, ARRB1, ARRB2, CBLN2, CD40, CDC20, CENPF, CREB1, CTNNB1, DEAF1, DVL3, EAF2, EGF, EGR1, ELF1, EPHB1, ERBB2, ERBB4, ESR1, FES, FOXO3, FURIN, GDNF, GHR, GJA1, GNAS, GPAM, GRIN2B, GSK3A, GSK3B, HDAC2, HSF1, IDO1, IGF1, IKBKE, IL1B, INS, INSR, JAK2, KDR, KL, LDB1, MAP2K1, MAP3K7, MAPK14, MAPK7, MAPT, MBP, MET, MYC, NDEL1, NEDD4, NEUROD1, NFKB1, NFKBIA, NOS1, NR5A1, NRAS, OPRD1, PAFAH1B1, PDGFB, PDGFRB, PIK3CA, PIK3R1, PLAUR, POU1F1, PPP2CA, PPP3CA, PRKCD, PRKCQ, REL, RELA, RET, RIPK1, RIPK2, S100A1, SGK1, SHC1, SKIL, SLC1A3, SLC8A1, SLC9A3R1, SMAD2, SMAD3, SRC, STK11, TBK1, TH, TNFRSF1A, TRADD, TRAF2, TRAF6, VEGFA, WNK4, ZNF675
0.109	BP	negative regulation of apoptosis	AKT1, APEX1, AR, ARRB1, AURKB, BIRC5, BRAF, CBL, CTNNB1, EGFR, ERBB2, ERBB3, ERBB4, ESR1, FURIN, GDNF, GPAM, GRK5, GSK3B, HDAC1, HDAC2, IDO1, IGF1, IGF1R, IKBKB, IL1B, INS, ITSN1, KDR, MAD2L1, MAP3K7, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NR3C1, NUP62, PDPK1, PIK3CA, PIK3R1, PLAUR, PLK1, PRKCD, PRKCQ, RAF1, RELA, RIPK1, RIPK2, SMAD3, TRAF2, TRAF6, VEGFA
0.088	BP	regulation of organelle organization	ABL1, AKT1, ARHGEF2, ARRB1, BRCA1, BUB1, BUB1B, BUB3, CDC20, CDK9, CLASP1, CLASP2, CLIP1, CTNNB1, DYNC1LI1, EGF, FES, GRB2, GSN, IGF1, IL1B, INS, INSR, MAD1L1, MAD2L1, MAP2K1, MAPK1, MAPRE1, MAPT, MET, MYC, NEK6, NOS1, PDGFB, PDGFRB, PLK1, PRKCD, PRKCQ, SKA1, SKA2, SMAD3, TAOK1, XPO1
0.064	BP	regulation of MAP kinase activity	CD40, DVL3, EGF, EGFR, ERBB2, GHR, GSK3B, IKBKG, IL1B, INSR, KIT, MAP2K1, MAP3K7, MAPK1, MAPK14, MET, NUP62, PDGFB, PDGFRB, PPP2CA, PRKCD, PXN, RIPK1, RIPK2, SHC1, TAB1, TAB2, TRAF2, TRAF6, VEGFA, ZNF675
0.123	BP	carbohydrate metabolic process	ADRB3, AKT1, B3GALT4, C1GALT1, C1GALT1C1, CS, EGF, FUT1, FUT2, GANAB, GAPDH, GCNT1, GCNT3, GCNT4, GOT1, GOT2, GPAT2, GRB10, GSK3A, GSK3B, GUSB, HEXDC, HSD3B1, HSD3B2, IGF1, IKBKB, IL1B, INS, INSR, IRS1, KL, MAPK14, MAPK7, MYC, NFKB1, NR3C1, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, PDGFB, PIK3CA, PIK3R1, POU1F1, PPP1CC, RANBP2, SEC13, SEC24D, ST3GAL1, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5, STK11, TH, UGDH, UGT2B17
0.053	BP	positive regulation of MAP kinase activity	CD40, DVL3, EGF, EGFR, ERBB2, GHR, IKBKG, IL1B, INSR, KIT, MAP2K1, MAP3K7, MAPK1, MAPK14, MET, PDGFB, PDGFRB, PXN, RIPK1, RIPK2, SHC1, TAB1, TAB2, TRAF2, TRAF6, VEGFA
0.020	MF	diacylglycerol kinase activity	AGK, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ
0.039	BP	phosphatidylinositol-mediated signaling	AKT1, BUB1B, CHUK, CREB1, ERBB2, FOXO3, GSK3A, GSK3B, GSN, IGF1, IGF1R, IRS1, NDC80, PDGFRB, PDPK1, PHLPP1, PIK3CA, PIK3R1, ZWINT
0.012	BP	signal transduction via phosphorylation event	ERBB2, INSR, KDR, KIT, MAP2K1, STK39
0.033	BP	phosphatidylinositol 3-kinase cascade	CBL, ERBB2, ERBB3, IGF1, IGF1R, INS, IRS1, JAK2, KDR, KIT, NEDD4, PDGFB, PDGFRB, PIK3R1, SLC9A3R1, SLC9A3R2
0.182	BP	cell development	ABL1, ACAN, AGER, AGPAT6, AKAP5, AKT1, ARHGEF2, BRCA1, CASC5, CDC20, CLASP1, CLASP2, CREB1, CTNNB1, DEAF1, DGKG, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, ESR1, EZR, FES, FOXO3, FYN, GDNF, GFRA1, GJA1, GRB2, GSK3A, GSK3B, GSN, HDAC2, HNRNPAB, HSP90AA1, IGF1, IGF1R, INS, JAK2, KDR, KIT, LDB1, LDB2, MAP2K1, MAPK1, MAPT, MBP, MERTK, MET, MYH9, NDEL1, NEDD4, NEUROD1, NRAS, PAFAH1B1, PDGFB, PDGFRB, PDPK1, PGR, PIK3R1, POU1F1, PPP2CA, PPP3CA, PRKCQ, RAF1, RELA, RET, RIF1, S100A4, SHBG, SHC1, SIAH1, SKIL, SLC1A3, SLC8A1, SMAD2, SMAD3, SOS1, SRC, STIP1, STK11, TH, TRAF6, TTN, TUBB3, USP33, VCAN, VEGFA
0.090	BP	positive regulation of cellular protein metabolic process	AKAP5, AKT1, APITD1, ARRB1, BRAF, BRCA1, CD40, CDC20, DVL3, EGF, ERBB2, ERBB4, FURIN, GHR, GSK3A, GSK3B, HDAC2, IGF1, IL1B, INS, INSR, JAK2, KIT, MAPK1, MET, NFKBIA, NOS1, PABPC1, PDGFB, PEMT, PIK3CA, PIK3R1, PLK1, PRKCD, PSMA6, PSMD6, RAF1, RBPMS, RIPK2, STK11, TAOK1, TNFRSF1A, VCP, VEGFA
0.129	BP	cell motility	ABL1, ACAN, AGER, AKT1, ARRB2, ATP1B1, BCR, BRCA1, CLASP2, DDR1, DGKZ, DNAJA1, EGFR, EPHB1, ERBB4, FES, FSCN1, FURIN, FYN, GDNF, GJA1, GRB2, GSK3A, GSK3B, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, MAP2K1, MAPK1, MAPT, MERTK, MET, MYH9, NDE1, NDEL1, NRAS, NUP85, PAFAH1B1, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, RAF1, RET, S100A2, S100P, SGK1, SHC1, SLC9A3R1, SMAD3, SOS1, SRC, TUBB2B, USP33, VCAN, VEGFA
0.047	BP	mammary gland development	AGPAT6, AKT1, AR, CHUK, CREB1, DDR1, DEAF1, ERBB2, ERBB3, ERBB4, ESR1, IGF1, IGF1R, IRS1, JAK2, MAPK1, MET, NR3C1, PGR, SLC12A2, SRC, TPH1, VEGFA
0.051	BP	peptidyl-tyrosine phosphorylation	ABI1, ABL1, CD40, DDR1, EGF, EGFR, ERBB4, FES, FYN, GHR, IGF1, INS, INSR, JAK2, KDR, KIT, PDGFB, PDGFRB, PPP2CA, PRKCD, PXN, SOCS1, SRC, TNFRSF1A, VEGFA
0.084	BP	positive regulation of cellular component organization	AKAP5, AKT1, AR, ARRB1, BCR, BRCA1, CBL, CBLN2, CDC20, CLIP1, CTNNB1, EGF, EPHB1, FES, GDNF, GRB2, GSK3B, IGF1, IL1B, INS, INSR, KDR, MAPT, MET, NDEL1, NEDD4L, NOS1, PAFAH1B1, PDGFB, PDGFRB, PDPK1, PIK3R1, PLK1, PRKCQ, RET, SKIL, SMAD2, SMAD3, SRC, STK11, VCP
0.083	CC	microtubule organizing center	APEX1, B9D2, BIRC5, BRCA1, BUB1B, CCDC99, CDC20, CKAP5, CLASP1, CLASP2, CLIP1, CSK, CTNNB1, DYNC1H1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNLL1, EZR, GSK3B, KIF18A, KIF2A, KIF2B, KIF3B, MAD1L1, MAP2K1, MAPK1, MAPRE1, MLF1IP, NDE1, NDEL1, NEK6, PAFAH1B1, PLK1, RELB, RUVBL1, SGOL1, SKA1, SLC9A3R1, TUBG1, YWHAQ
0.061	BP	positive regulation of protein phosphorylation	AKAP5, AKT1, ARRB1, BRAF, CD40, DVL3, EGF, ERBB2, ERBB4, GHR, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, JAK2, KIT, MAPK1, MET, PDGFB, PIK3CA, PIK3R1, PLK1, RAF1, RBPMS, STK11, TAOK1, TNFRSF1A, VEGFA
0.098	BP	regulation of cellular localization	ADRBK1, AKAP5, AKT1, AR, ARRB1, BCR, CD40, CREB1, CTNNB1, EGF, EGFR, ERBB4, FES, GDNF, GNAS, GPAM, GRIN2B, GRM7, GSK3B, IGF1, IL1B, INS, IRS1, JAK2, MAOB, MAP2K1, MAPK1, MAPK7, MAPT, NEDD4, NEUROD1, NFKBIA, NFKBIB, NFKBIE, NR3C1, PDPK1, PIK3R1, PPP1CC, PPP3CA, PRKCQ, RANGAP1, RBPMS, SFN, SMAD3, TNFRSF1A, TRAF2, TRAF6, XPO1
0.053	BP	intracellular receptor mediated signaling pathway	AR, BRCA1, CHUK, CTNNB1, DNAJA1, ESR1, HDAC1, IGF1, IKBKB, IKBKG, JAK2, MAP3K7, NEDD4, NFKBIA, NR3C1, NR5A1, PGR, PMEPA1, RELA, RIPK2, SRC, SUGT1, TAB1, TAB2, TCF21, TRAF6

Continued on next page. . .

Ratio	Type	Description	Genes
0.205	BP	establishment of localization in cell	A2M, ADRB2, ADRBK1, AKAP12, AKAP5, AKT1, ARHGEF2, ARRB1, ATP5D, BCR, BIRC5, CCDC99, CD40, CDC37, CENPA, CENPE, CREB1, DYNC1I1, EGF, EGFR, ERBB4, EXOC1, FES, FURIN, GDNF, GNAS, GPAM, GRIN2B, GRM7, GSK3B, HSP90AA1, IGF1, IL1B, INS, IPO4, IRS1, JAK2, KIF18A, KIF3B, KPNA1, KPNA2, LAMP2, MAOA, MAOB, MAP2K1, MAPK1, MAPK7, MAPT, MERTK, MYH9, NDC80, NDE1, NDEL1, NEDD4, NEUROD1, NFKBIA, NFKBIB, NFKBIE, NR3C1, NUDC, NUP107, NUP133, NUP160, NUP62, OPRD1, OTOF, PAFAH1B1, PDGFB, PDPK1, PIK3R1, PPP1CC, PPP3CA, PRKCQ, RANBP2, RANGAP1, RBPMS, RPL3, RPLP1, RPS27, RPS3A, SDCBP2, SEC13, SEC24D, SFN, SLC1A3, SMAD2, SMAD3, TINAGL1, TNFRSF1A, TRAF2, TRAF6, TTN, TUBA4A, TUBB, VCP, VEGFA, XPO1, YWHAQ, ZW10, ZWINT
0.145	BP	positive regulation of gene expression	ADRB2, AKT1, AR, ARRB1, BRAF, BRCA1, CAMKK2, CD40, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGR1, ELF1, ELK1, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GJA1, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, IGF1, IKBKB, IL1B, KIT, LDB1, LMO4, MAPK1, MAPK14, MAPK7, MET, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PDGFB, PIK3R1, PITX1, PLAUR, POU1F1, PPP3CA, REL, RELA, RELB, RET, RIPK1, RSF1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.082	BP	regulation of cell cycle process	AKT1, AURKB, BIRC5, BRCA1, BUB1, BUB1B, BUB3, CASC5, CDC20, CDK9, CTNNB1, CYP1A1, DDB1, DGKZ, DYNC1LI1, EGF, FHL1, IGF1, IL1B, INS, INSR, KNTC1, MAD1L1, MAD2L1, MAPK14, MET, NEK6, NEUROD1, PDGFB, PDGFRB, PLK1, PRKCQ, PSMA6, PSMD6, RBBP8, TAOK1, XPO1, ZW10, ZWILCH, ZWINT
0.069	MF	protein kinase binding	ABL1, AKAP5, AKT1, ARRB1, ARRB2, BRAF, CAMK2N1, CCNT1, CDC37, CTNNB1, FOXO3, GHR, GRK5, GSK3A, GSK3B, INSR, IRS1, JAK2, MAP2K1, MAPK1, MAPK6, NEK6, PDPK1, PIK3R1, PLK1, PPP1CC, RAF1, RELA, SMAD3, SOCS1, STK39, TAOK1, TRAF2, TRAF6
0.061	BP	negative regulation of transport	ADRB2, AKAP5, AKT1, ANPEP, BCR, EGF, ERBB3, GRB10, GRM7, GSK3A, GSK3B, IL1B, INS, INSR, IRS1, MAOB, MAPK7, MAPT, NEDD4, NEDD4L, NFKB1, NFKBIA, NFKBIB, NFKBIE, NOS1, OPRD1, PPP3CA, RANGAP1, SLC9A3R1, WNK4
0.141	BP	positive regulation of RNA metabolic process	ADRB2, AKT1, AR, ARRB1, BRCA1, CAMKK2, CCNT1, CD40, CDK9, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGR1, ELF1, ELK1, ELL, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, IGF1, IKBKB, IL1B, LDB1, LMO4, MAP2K1, MAPK1, MAPK14, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PDGFB, PIK3R1, PITX1, POU1F1, PPP3CA, REL, RELA, RET, RIPK1, RSF1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.026	CC	spindle microtubule	BIRC5, CLASP1, CLASP2, KIF18A, KIF2A, KIF3B, KNTC1, PAFAH1B1, PLK1, SKA1, SKA2, TUBG1, ZW10
0.029	MF	receptor signaling protein serine/threonine kinase activity	BRAF, EGFR, IKBKE, MAP3K14, MAP3K3, MAP3K7, MAP3K8, MAPK1, MAPK14, MAPK6, MAPK7, RAF1, RIPK3, STK39
0.030	CC	nuclear pore	AHCTF1, IPO4, KPNA1, MAD1L1, MAD2L1, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, RANBP2, RANGAP1, SEC13
0.230	BP	catabolic process	ABL1, ADH4, ADH5, ADH7, AFMID, AKT1, ARRB1, ARRB2, ATP5D, AURKB, BCR, BUB1B, BUB3, CBR3, CD40, CDC20, CS, CYP1A1, CYP2D6, CYP3A4, CYP3A5, DDB1, DDX6, DGKI, ECI2, EGF, EGFR, ERBB2, FURIN, FUT1, FUT2, FYN, GAPDH, GCH1, GDI2, GJA1, GNA11, GNA14, GNA15, GNAL, GNAS, GOT1, GOT2, GSK3A, GSK3B, GUSB, HSD17B6, HSP90AA1, IDO1, IDO2, IGF1, IL1B, INS, INSR, IRS1, KPNA1, MAD2L1, MAOA, MAP2K1, MAPT, MYC, MYH9, NDEL1, NEDD4, NEDD4L, NOS1, NRAS, OLA1, PABPC1, PAFAH1B1, PAH, PLK1, PPP1CC, PPP2CA, PRDX6, PRKCD, PSMA6, PSMD6, RANGAP1, RBBP8, RELA, RP11-1286E23.8, RPL3, RPLP1, RPS27, RPS3A, SIAH1, SMAD3, SMARCA5, SOS1, STK11, TAT, TRAF2, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, UBQLN4, USP20, USP33, USP49, VCP, XPO1
0.048	CC	membrane raft	ADRB2, ADRBK1, ATP1B1, CBL, EGFR, EPHB1, ERBB2, ERBB4, FURIN, GJA1, GSK3B, IGF1R, IKBKB, INSR, IRS1, JAK2, KIF18A, MAPK1, OPRD1, RIPK1, SRC, TNFRSF1A, TNFRSF1B, TRAF2
0.049	BP	regulation of intracellular transport	AKAP5, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, MAP2K1, MAPK1, MAPK7, MAPT, NEDD4, NFKBIA, NFKBIB, NFKBIE, PPP1CC, PRKCQ, RANGAP1, RBPMS, SFN, SMAD3, TNFRSF1A, XPO1
0.037	BP	T cell receptor signaling pathway	CHUK, CSK, ELF1, FYN, IKBKB, IKBKG, MAP3K7, MAPK1, NFKB1, NFKBIA, PDPK1, PIK3CA, PIK3R1, PRKCQ, RELA, RIPK2, TAB2, TRAF6
0.166	BP	response to external stimulus	A2M, ABL1, ABP1, ACAN, ADRB2, AGER, AKT1, ARRB1, ARRB2, BCR, BRCA1, CD40, CD46, CDS1, CLASP1, CLASP2, CREB1, CYP1A1, EGFR, EPHB1, ERBB2, EZR, FES, FYN, GDNF, GFRA1, GHR, GPAM, GRB2, GRIN2B, GSK3B, GSN, HSD17B2, HSD17B3, HSP90AA1, IDO1, IGF1R, IL1B, INS, INSR, JAK2, KDR, MAP2K1, MAP3K14, MAPK1, MAPK14, MAPK7, MET, MYC, MYH9, NDEL1, NFKB1, NRAS, NUP85, PDGFB, PDGFRB, PEMT, PIK3R1, PLAUR, PRKCD, PRKCQ, PSMA6, RAF1, RELA, RET, SIAH1, SLC12A2, SLC1A3, SLC8A1, SMAD3, SOS1, SRC, STIP1, TH, TNFRSF1A, TNFRSF1B, TPH2, TUBB3, TULP4, USP33, VEGFA
0.119	BP	cell migration	ACAN, AGER, AKT1, ARRB2, ATP1B1, BCR, CLASP2, DDR1, DGKZ, EGFR, EPHB1, ERBB4, FSCN1, FURIN, FYN, GDNF, GJA1, GRB2, GSK3A, GSK3B, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, MAP2K1, MAPK1, MAPT, MERTK, MET, MYH9, NDE1, NDEL1, NRAS, NUP85, PAFAH1B1, PDGFB, PDGFRB, PDPK1, PIK3CA, PIK3R1, RET, S100A2, S100P, SGK1, SHC1, SLC9A3R1, SMAD3, SOS1, SRC, TUBB2B, USP33, VCAN, VEGFA
0.080	BP	response to cytokine stimulus	CDC37, CDK9, CTNNB1, EGR1, GCH1, GHR, GRIN2B, HNMT, IL1B, INSR, JAK2, KIT, KPNA1, KPNA2, MAPK7, MET, NEDD4, NFKB1, NFKB2, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, PRKCD, RANBP2, RELA, RIPK1, RIPK2, SOCS1, SRC, TNFRSF1A, TNFRSF1B, TRADD, TRAF2, TRAF6, ZNF675
0.141	CC	cell projection	ABI1, ACPP, ADRB2, ADRBK1, AGER, AKAP5, AKT1, AR, ARHGEF2, ARR3, ARRB1, B9D2, BACE1, BRCA1, CACYBP, CAMK2N1, CLASP2, CLIP1, CTNNB1, CYP19A1, DDC, DGKZ, DYNC2H1, EPHB1, ERBB2, ERBB4, ESR1, EZR, FSCN1, GNAS, GOT1, GRIN2B, GRM7, GSK3B, GSN, IGF1R, ITSN1, KCNJ6, KIF18A, MAP2K1, MAPK1, MAPRE1, MAPT, MBP, MEGF10, MERTK, MET, MYC, MYH9, NDEL1, NOS1, NR3C1, OPRD1, PAFAH1B1, PEMT, PIK3CA, PPP5C, PXN, RAF1, S100A4, SLC12A6, SLC1A3, SLC8A1, SLC9A3R1, TH, TNFRSF1A, TPH1, TPH2, TUBB3, TUBB4A
0.074	BP	protein targeting	AKAP12, AKAP5, AKT1, CDC37, EGF, EGFR, ERBB4, GSK3B, HSP90AA1, IGF1, IL1B, JAK2, KPNA1, KPNA2, MAPK1, MAPK7, NEDD4, NFKBIA, NFKBIB, NFKBIE, OPRD1, PIK3R1, PPP3CA, PRKCQ, RANBP2, RANGAP1, RBPMS, RPL3, RPLP1, RPS27, RPS3A, SFN, SMAD3, TNFRSF1A, XPO1, YWHAQ
0.016	CC	Nup107-160 complex	AHCTF1, NUP107, NUP133, NUP160, NUP37, NUP43, NUP85, SEC13
0.031	MF	transmembrane receptor protein tyrosine kinase activity	DDR1, EGFR, EPHB1, ERBB2, ERBB3, ERBB4, IGF1R, INSR, IRS1, KDR, KIT, MERTK, MET, PDGFRB, RET
0.043	BP	regulation of nucleocytoplasmic transport	AKAP5, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, MAPK7, NEDD4, NFKBIA, NFKBIB, NFKBIE, PPP1CC, PRKCQ, RANGAP1, RBPMS, SFN, SMAD3, TNFRSF1A, XPO1
0.201	BP	cellular catabolic process	ABL1, ADH5, AFMID, AKT1, ARRB1, ARRB2, ATP5D, AURKB, BCR, BUB1B, BUB3, CBR3, CD40, CDC20, CS, CYP1A1, CYP2D6, CYP3A4, CYP3A5, DDB1, DDX6, DGKI, ECI2, EGF, ERBB2, FURIN, GCH1, GDI2, GNA11, GNA14, GNA15, GNAL, GNAS, GOT1, GOT2, GSK3A, GSK3B, HSP90AA1, IDO1, IDO2, IGF1, IL1B, INS, INSR, IRS1, KPNA1, MAD2L1, MAOA, MAP2K1, MAPT, MYC, MYH9, NDEL1, NEDD4, NEDD4L, NOS1, NRAS, OLA1, PABPC1, PAFAH1B1, PAH, PLK1, PPP1CC, PPP2CA, PRDX6, PRKCD, PSMA6, PSMD6, RANGAP1, RBBP8, RP11-1286E23.8, RPL3, RPLP1, RPS27, RPS3A, SIAH1, SMARCA5, SOS1, STK11, TAT, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, UBQLN4, USP20, USP33, USP49, VCP
0.059	MF	protein complex binding	ABP1, AKAP5, ATP5D, DOK1, ESR1, FYN, GFRA1, GNA11, GNA14, GNA15, GNAL, GNAS, GRB10, GSK3B, IGF1, IGF1R, INS, INSR, IRS1, KDR, MET, MYC, PDPK1, PIK3R1, PLK1, SHC1, SKIL, SRC, TUBB
0.133	BP	positive regulation of transcription, DNA-dependent	ADRB2, AKT1, AR, ARRB1, BRCA1, CAMKK2, CD40, CENPK, CNBP, CREB1, CTNNB1, DVL3, EAF2, EGF, EGR1, ELF1, ELK1, ERBB2, ERBB4, ESR1, FOXO3, GDNF, GSK3A, GSK3B, HDAC1, HDAC2, HNRNPAB, IGF1, IKBKB, IL1B, LDB1, LMO4, MAPK1, MAPK14, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NFYC, NOS1, NR3C1, NR5A1, NUP62, PDGFB, PIK3R1, PITX1, POU1F1, PPP3CA, REL, RELA, RET, RIPK1, RSF1, SMAD2, SMAD3, SMAD9, SMARCA2, SMARCA5, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.055	BP	protein localization to nucleus	AKAP5, AKT1, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, IRS1, JAK2, KPNA1, KPNA2, MAPK1, MAPK7, NFKBIA, NFKBIB, NFKBIE, NR5A1, OPRD1, PIK3R1, PPP3CA, PRKCQ, RANBP2, RBPMS, SMAD3, TNFRSF1A, XPO1
0.047	BP	response to growth factor stimulus	AKT1, CREB1, CTNNB1, CYP19A1, DDC, FYN, GRB10, GRIN2B, IL1B, INSR, KDR, MAPK14, MAPK7, MET, MYC, NEDD4, NOS1, OPRD1, PDGFRB, PIK3R1, SKIL, TH, VEGFA
0.016	CC	condensed chromosome outer kinetochore	BUB1B, CCDC99, CENPE, NDC80, NUP133, PLK1, SKA1, SKA2
0.023	BP	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	CHUK, IKBKB, IKBKG, MAP3K7, NFKBIA, RELA, RIPK2, SUGT1, TAB1, TAB2, TRAF6
0.166	BP	regulation of developmental process	ABL1, ADRB2, AKAP5, AKT1, AR, ARHGEF2, CBLN2, CD40, CDC20, CENPF, CREB1, CTNNB1, DEAF1, DVL3, EAF2, EGF, EGR1, EPHB1, ERBB2, ERBB4, ESR1, EZR, FES, FOXO3, FYN, GDNF, GHR, GJA1, GNA11, GNAS, GSK3A, GSK3B, HDAC2, IDO1, IGF1, IL1B, INS, INSR, JAK2, KDR, KIT, KL, LDB1, LDB2, LMO4, MAP2K1, MAPK1, MAPK14, MAPK7, MAPT, MBP, MET, MYC, MYH9, NDEL1, NEDD4, NEK6, NEUROD1, NFKB1, NFKBIA, NR5A1, PAFAH1B1, PDGFB, PDGFRB, PIK3R1, PPP2CA, RAF1, RELA, RET, RIF1, RIPK2, SKIL, SMAD2, SMAD3, SMAD9, STK11, TNFRSF1A, TRADD, TRAF6, VEGFA, ZNF675
0.100	BP	negative regulation of response to stimulus	A2M, ADRB2, ADRBK1, AKT1, ARRB1, ARRB2, BCR, CBL, CD46, DGKZ, EGF, EGFR, EGR1, ELF1, ERBB3, ESR1, GRB10, GRB2, GSK3A, GSK3B, HDAC1, HDAC2, IGF1, IGF1R, IL1B, INS, IRS1, MAGEA1, MAPK7, MYC, NEDD4, NEUROD1, NFKBIA, NR3C1, NUP62, PDPK1, PPP2CA, PRKCD, PRKCQ, RELA, SKIL, SLC9A3R1, SLC9A3R2, SMAD3, SOCS1, TCF21, TNFRSF1B, TRAF6, ZNF675
0.047	BP	positive regulation of MAPKKK cascade	ADRB2, ADRB3, AR, ARRB1, ARRB2, BRAF, CTNNB1, ERBB2, ERBB4, ESR1, IGF1, IGF1R, IL1B, INS, INSR, KDR, KIT, KL, PDGFB, PDGFRB, RIPK2, TAB1, TAOK1
0.053	BP	regulation of transmembrane transport	ADRB2, AKAP5, AKT1, CTNNB1, EGF, EGFR, ERBB4, GRM7, GSK3B, IGF1, IL1B, INS, JAK2, MAPK7, NFKBIA, NFKBIB, NFKBIE, OPRD1, PDGFB, PDGFRB, PRKCQ, RBPMS, RIPK1, SLC9A3R1, SMAD3, TNFRSF1A

Continued on next page...

Ratio	Type	Description	Genes
0.035	BP	regulation of mitosis	BUB1, BUB1B, BUB3, CDC20, DYNC1LI1, EGF, IGF1, IL1B, INS, INSR, MAD1L1, MAD2L1, MET, NEK6, PDGFB, PDGFRB, PLK1
0.088	MF	protein domain specific binding	ABL1, AKAP5, AR, ARR3, CBL, DDC, DYNLL1, GHR, GJA1, GRB2, GRM7, HNRNPM, HSP90AA1, IKBKG, IL1B, INSR, IRS1, JAK2, LDB1, LDB2, MAPT, NEDD4, NUP62, PIK3R1, PMEPA1, PMF1, PXN, RELA, RIPK1, RIPK2, SFN, SKIL, SLC9A3R1, SLC9A3R2, SRC, STK11, TH, TRADD, TUBA3D, TUBA3E, VCP, XPO1, YWHAQ
0.055	BP	cellular aromatic compound metabolic process	ACPP, AFMID, ANPEP, AOC2, CYP19A1, CYP1A1, CYP2D6, DDC, FLAD1, GCH1, GCNT4, HSD17B3, IDO1, IDO2, IL4I1, MAOA, MAOB, MAPK1, PAH, PAICS, PFAS, TAT, TH, TNFRSF1A, TPH1, TPH2, TYR
0.037	BP	establishment or maintenance of cell polarity	ARHGEF2, CCDC99, CENPA, CKAP5, CLASP1, CLASP2, EPHB1, EZR, GSK3B, IGF1, IGF1R, KIF2C, MYH9, NDC80, NDE1, PAFAH1B1, STK11, ZW10
0.023	BP	insulin-like growth factor receptor signaling pathway	AKT1, AR, GHR, GIGYF1, GIGYF2, GRB10, IGF1, IGF1R, IRS1, PIK3R1, POU1F1
0.027	BP	regulation of phosphatidylinositol 3-kinase cascade	CBL, ERBB2, ERBB3, IGF1, INS, JAK2, KDR, KIT, NEDD4, PDGFB, PDGFRB, SLC9A3R1, SLC9A3R2
0.041	MF	tubulin binding	ARHGEF2, B9D2, BIRC5, BRCA1, CLASP1, CLASP2, CLIP1, DYNC1I1, FYN, HSPH1, KIF18A, KIF2C, MAPRE1, MAPT, NDE1, NDEL1, PAFAH1B1, PLK1, SKA1, SKA2
0.022	CC	cytoplasmic microtubule	BIRC5, CLASP1, CLASP2, CLIP1, KIF2C, MAPRE1, PAFAH1B1, TUBA3D, TUBA3E, TUBA4A, TUBG1
0.154	BP	tissue development	ACAN, ADRB2, AGPAT6, AKT1, AR, CACYBP, CENPF, CHUK, CTNNB1, DDR1, DEAF1, DVL3, EGFR, ERBB2, ERBB3, ERBB4, ESR1, EZR, FOXO3, GCNT4, GDNF, GHR, GJA1, GNAS, GRB2, GSK3A, GSK3B, GSN, HDAC1, HDAC2, HNRNPAB, HOXC13, IGF1, IGF1R, JAK2, KDR, KL, LDB1, LDB2, LMO4, MAP2K1, MAP3K7, MAPK1, MAPK14, MET, MYC, MYH9, NOS1, NR3C1, NR5A1, NUP133, PDGFB, PDGFRB, PGR, PIK3R1, PITX1, PLAUR, PPP2CA, PPP3CA, PRKCQ, RELA, RET, S100A4, SFN, SKIL, SLC12A2, SLC8A1, SMAD2, SMAD3, SRC, TCF21, TRADD, TRAF6, TTN, VEGFA
0.043	BP	protein polymerization	CLIP1, FES, GRB2, GSN, JAK2, MAPRE1, MAPT, PRKCD, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1
0.033	MF	microtubule binding	ARHGEF2, BIRC5, CLASP1, CLASP2, CLIP1, DYNC1I1, KIF18A, KIF2C, MAPRE1, MAPT, NDE1, NDEL1, PAFAH1B1, PLK1, SKA1, SKA2
0.016	CC	condensed nuclear chromosome, centromeric region	AURKB, BUB1, CENPA, CENPC1, NDC80, PLK1, SGOL1, SGOL2
0.145	BP	regulation of cell proliferation	ABI1, ADAMTS1, ADRB2, AGER, AR, ARHGEF2, BIRC5, BRCA1, CD40, CDC20, CNBP, CSK, CTNNB1, DDR1, DEAF1, EAF2, EGF, EGFR, EGR1, ERBB2, ERBB3, ERBB4, ESR1, FANCA, FES, FOXO3, GJA1, GPAM, HDAC1, HDAC2, HSF1, HTR4, IDO1, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KIT, MAP2K1, MAPK1, MYC, NFKBIA, NR3C1, NRAS, NUP62, PDGFB, PDGFRB, PEMT, PGR, PIK3R1, POU1F1, PRKCQ, RAF1, RBBP4, RELA, RIPK2, SFN, SGK1, SHC1, SLC9A3R1, SMAD2, SMAD3, SMARCA2, ST8SIA1, STK11, TRAF6, VEGFA
0.031	BP	stress-activated MAPK cascade	CREB1, ELK1, IKBKG, IL1B, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, MYC, RIPK2, TAB1, TAB2, TAOK1, TRAF6
0.098	BP	positive regulation of developmental process	ABL1, ADRB2, AKAP5, AKT1, AR, CBLN2, CDC20, CREB1, CTNNB1, EPHB1, ERBB4, FES, FOXO3, GDNF, GHR, GJA1, GNAS, HDAC2, IGF1, IL1B, INS, INSR, JAK2, KDR, KL, MAP2K1, MAPK14, MAPT, MET, MYC, NDEL1, NEUROD1, NFKB1, NR5A1, PAFAH1B1, PIK3R1, RELA, RET, RIPK2, SKIL, SMAD2, SMAD3, SMAD9, STK11, TNFRSF1A, TRADD, TRAF6, VEGFA
0.086	BP	negative regulation of signal transduction	ADRB2, ADRBK1, AKT1, ARRB1, ARRB2, CBL, DGKZ, EGF, EGFR, EGR1, ELF1, ERBB3, ESR1, GRB10, GRB2, GSK3A, GSK3B, HDAC1, HDAC2, IGF1, IGF1R, IL1B, IRS1, MAGEA1, MYC, NEDD4, NEUROD1, NFKBIA, NR3C1, NUP62, PDPK1, PPP2CA, PRKCD, PRKCQ, RELA, SKIL, SLC9A3R1, SLC9A3R2, SOCS1, TCF21, TRAF6, ZNF675
0.051	BP	aging	ACAN, ADH5, ADRB3, ADRBK1, AURKB, CACYBP, DDC, FURIN, GRB2, GSN, IL1B, KL, MAP2K1, MAPK14, MET, NEK6, NFKB2, NR3C1, NUP62, POU1F1, PRKCD, PRKCQ, RELA, SHC1, TH
0.035	MF	phosphatase binding	AKAP5, CARHSP1, CSK, CTNNB1, EGFR, ELL, ERBB2, GHR, GRB2, INSR, MAPK1, PIK3R1, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, VCP
0.136	MF	receptor binding	ADH7, ADRB2, ADRB3, ADRBK1, AKAP5, APITD1, AR, ARRB1, ARRB2, BRCA1, CBL, CTNNB1, DNAJA1, DOK1, DVL3, EGF, ERBB2, ERBB4, ESR1, FES, FYN, GDNF, GFRA1, GJA1, GNA11, GNA14, GNA15, GNAL, GNAS, GRB10, GRB2, GRIN2B, GSK3B, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, KL, NEDD4, NR3C1, NUP62, PDGFB, PDGFRB, PDPK1, PGR, PIK3R1, RIPK1, S100A4, SHC1, SLC9A3R1, SLC9A3R2, SMAD2, SMAD3, SOCS1, SRC, TCF21, TRAF2, TUBB, TUBB4B, USP20, USP33, VCP, VEGFA
0.041	BP	regulation of protein catabolic process	AKT1, EGF, EGFR, FURIN, FYN, GJA1, GSK3A, GSK3B, IL1B, INS, MAD2L1, NEDD4, NEDD4L, PLK1, PPP2CA, RELA, SMAD3, UBQLN4, VCP, XPO1
0.016	MF	insulin-like growth factor receptor binding	ARRB1, IGF1, INS, INSR, IRS1, PIK3R1, SHC1, SOCS1
0.057	BP	regulation of establishment of protein localization	AKAP5, AKT1, AR, CD40, EGF, EGFR, ERBB4, GPAM, GSK3B, IGF1, IL1B, INS, JAK2, MAPK7, NFKBIA, NFKBIB, NFKBIE, PDPK1, PIK3R1, PRKCQ, RANGAP1, RBPMS, SFN, SMAD3, TNFRSF1A, TRAF2, TRAF6, XPO1
0.089	CC	neuron projection	ABI1, ADRB2, ADRBK1, AGER, AKAP5, AR, ARHGEF2, BACE1, CACYBP, CAMK2N1, CTNNB1, CYP19A1, DDC, EPHB1, ERBB4, ESR1, GOT1, GRIN2B, GRM7, GSK3B, IGF1R, KCNJ6, MAP2K1, MAPK1, MAPT, MBP, MET, MYC, NDEL1, NOS1, NR3C1, OPRD1, PAFAH1B1, PPP5C, S100A4, SLC12A6, SLC1A3, SLC8A1, TH, TNFRSF1A, TPH1, TPH2, TUBB3, TUBB4A
0.049	BP	protein import into nucleus	AKAP5, AKT1, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, KPNA1, KPNA2, MAPK1, MAPK7, NFKBIA, NFKBIB, NFKBIE, OPRD1, PIK3R1, PPP3CA, PRKCQ, RANBP2, RBPMS, SMAD3, TNFRSF1A
0.106	MF	protein dimerization activity	ABP1, ADH5, ADH7, ADRB2, ADRB3, AOC3, AR, BIRC5, BRAF, CACYBP, CENPF, CLIP1, CREB1, DGKD, DVL3, DYNLL1, EGFR, ERBB2, ERBB3, ERBB4, GCH1, GDNF, GHR, GRIN2B, HSP90AA1, IKBKB, KIT, LDB1, MAD2L1, MAOB, MAPK6, MEIS1, MET, MYC, MYH9, NEUROD1, NFKB1, NR3C1, PAFAH1B1, PAH, PDGFB, PPP2CA, PPP3CA, RAF1, RIPK2, S100A1, SDCBP2, SHBG, SMAD3, TCF21, TYR, VEGFA
0.094	BP	response to abiotic stimulus	ACAN, ADRB3, AKAP5, AKT1, ARRB1, AURKB, BRCA1, CD40, CDS1, CYP19A1, DNAJA1, EGFR, EGR1, EPHB1, FYN, GJA1, GRB2, GRIN2B, HNMT, HSF1, IL1B, KCNJ3, KCNJ6, KIT, MAP3K14, MAPK14, MYC, NEDD4, NFKB1, NFKBIA, NOS1, NR3C1, NRAS, PDPK1, PIK3R1, PRKCQ, RBBP7, RELA, SLC12A2, SLC12A6, SLC1A3, ST8SIA1, STK11, TH, TNFRSF1A, VEGFA
0.031	BP	spindle organization	AURKB, BUB1B, CKAP5, DYNC1H1, KIF2A, KIF3B, MYH9, NDC80, NEK6, SPC25, TUBB, TUBB1, TUBB4B, TUBG1, ZWINT
0.020	BP	aromatic amino acid family metabolic process	AFMID, IDO1, IDO2, IL4I1, PAH, TAT, TH, TPH1, TPH2, TYR
0.055	BP	cytokine-mediated signaling pathway	CDC37, EGR1, IL1B, JAK2, KIT, KPNA1, KPNA2, NEDD4, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, PRKCD, RANBP2, RELA, RIPK1, RIPK2, SOCS1, TNFRSF1A, TNFRSF1B, TRADD, TRAF2, TRAF6, ZNF675
0.012	BP	O-glycan processing	C1GALT1, C1GALT1C1, GCNT1, GCNT3, GCNT4, ST3GAL1
0.025	BP	microtubule polymerization or depolymerization	ARHGEF2, CLASP1, CLASP2, CLIP1, FES, KIF18A, KIF2B, KIF2C, MAPRE1, MAPT, SKA1, SKA2
0.041	BP	cellular response to growth factor stimulus	AKT1, CREB1, CTNNB1, CYP19A1, DDC, FYN, GRB10, GRIN2B, IL1B, INSR, KDR, MAPK14, MAPK7, MET, NEDD4, NOS1, OPRD1, PDGFRB, TH, VEGFA
0.100	BP	cell morphogenesis involved in differentiation	ABL1, AKAP5, BRCA1, CLASP1, CLASP2, CREB1, CTNNB1, EGFR, EPHB1, ERBB2, ERBB3, EZR, FES, FYN, GDNF, GFRA1, GRB2, GSK3B, HNRNPAB, HSP90AA1, IGF1R, JAK2, MAP2K1, MAPK1, MAPT, MBP, MERTK, MET, MYH9, NDEL1, NEDD4, NRAS, PAFAH1B1, PPP2CA, PRKCQ, RAF1, S100A4, SIAH1, SKIL, SLC1A3, SMAD2, SMAD3, SOS1, SRC, STIP1, STK11, TUBB3, USP33, VCAN
0.020	BP	cytoplasmic pattern recognition receptor signaling pathway	CHUK, IKBKB, IKBKG, MAP3K7, NFKBIA, RELA, RIPK2, TAB1, TAB2, TRAF6
0.020	BP	nucleotide-binding oligomerization domain containing signaling pathway	CHUK, IKBKB, IKBKG, MAP3K7, NFKBIA, RELA, RIPK2, TAB1, TAB2, TRAF6
0.014	MF	receptor signaling protein tyrosine kinase activity	EGFR, ERBB2, ERBB3, ERBB4, INSR, KDR, KIT
0.096	BP	positive regulation of transcription from RNA polymerase II promoter	ADRB2, AKT1, AR, ARRB1, BRCA1, CD40, CENPK, CNBP, CREB1, CTNNB1, EGR1, ELF1, ELK1, ESR1, FOXO3, GDNF, GSK3A, GSK3B, HDAC1, HDAC2, IGF1, IL1B, LDB1, LMO4, MAPK14, MAPK7, MYC, NEUROD1, NFKB1, NFKBIA, NOS1, NR5A1, PIK3R1, PITX1, POU1F1, PPP3CA, RELA, RIPK1, SMAD2, SMAD3, SMARCA2, TBK1, TCEA1, TCF21, TNFRSF1A, TRAF6, VEGFA
0.032	CC	microtubule associated complex	AURKB, BIRC5, CDCA8, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, DYNLL1, KIF2C, KIF3B, MAPT, NDEL1, PAFAH1B1, PXN
0.039	BP	regulation of intracellular protein transport	AKAP5, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, MAPK7, NFKBIA, NFKBIB, NFKBIE, PRKCQ, RANGAP1, RBPMS, SFN, SMAD3, TNFRSF1A, XPO1
0.054	CC	basolateral plasma membrane	ADRBK1, AGER, AKAP5, ATP1B1, BRCA1, CD46, CTNNB1, DDR1, EGFR, ERBB2, ERBB3, ERBB4, EZR, FES, MAP2K1, MAPK1, MEGF10, MET, OTOF, PDGFB, PDPK1, PXN, SLC12A2, SLC12A6, SLC1A3, SLC8A1, STK39
0.023	BP	positive regulation of phosphatidylinositol 3-kinase cascade	CBL, ERBB2, ERBB3, IGF1, INS, JAK2, KDR, KIT, NEDD4, PDGFB, PDGFRB
0.037	BP	cellular biogenic amine metabolic process	AFMID, AGPAT6, AOC2, CDS1, CYP19A1, DDC, GCH1, GOT1, IDO1, IDO2, MAOA, MAOB, PAFAH1B1, PAH, PEMT, TH, TPH1, TPH2
0.068	BP	response to drug	ABP1, ACAN, CREB1, CTNNB1, CYP19A1, CYP1A1, CYP3A4, DDC, DVL3, ERBB2, ERBB3, ERBB4, FYN, GNAS, GRK5, GSK3B, IKBKB, IL1B, MAOB, MET, MYC, NEUROD1, NOS1, PDGFB, PEMT, PIK3R1, PPP3CA, RELA, SLC1A3, SLC8A1, SOCS1, TH, XPO1
0.084	BP	lipid biosynthetic process	AGK, AGPAT6, AGPAT9, AKT1, BRCA1, CDS1, CDS2, CNBP, CREB1, CYP19A1, CYP1A1, DGKE, ELOVL5, GPAM, GPAT2, HSD17B12, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2, IGF1R, IKBKB, INS, MAPK14, MAPK7, MBOAT2, NFKB1, NR3C1, NR5A1, PDGFB, PEMT, PISD, PLAUR, PRKCD, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5, STK11
0.076	BP	positive regulation of multicellular organismal process	ADRB2, ARRB2, CD40, CREB1, CTNNB1, ERBB4, GDNF, GHR, GPAM, GRIN2B, GSK3A, HDAC2, HSF1, IDO1, IGF1, IL1B, INS, JAK2, KL, MAP3K7, MYC, NOS1, PDGFB, POU1F1, PRKCQ, RET, RIPK1, RIPK2, SHC1, SLC1A3, SMAD3, TBK1, TNFRSF1A, TRADD, TRAF2, TRAF6, VEGFA

Continued on next page...

Ratio	Type	Description	Genes
0.074	BP	positive regulation of transport	ADRB2, ADRBK1, AKAP5, AKT1, ARRB1, BCR, CBL, CREB1, EGF, EGFR, ERBB3, ERBB4, GDNF, GRIN2B, GSK3B, IGF1, IL1B, INS, INSR, IRS1, JAK2, MET, NEDD4, NEDD4L, NFKBIA, NR3C1, PDGFB, PDGFRB, PIK3R1, PRKCQ, RBPMS, SFN, SGK1, SMAD3, STK39, TNFRSF1A
0.041	BP	organelle localization	ARHGEF2, BIRC5, CCDC99, CENPA, CENPE, DYNC1I1, KIF18A, KIF3B, MAP2K1, MAPT, MYH9, NDC80, NDE1, NDEL1, NUDC, PAFAH1B1, SEC13, SEC24D, STK11, ZW10
0.104	MF	identical protein binding	ABP1, ADH5, ADH7, ADRB2, ADRB3, AKT1, AOC3, BIRC5, CACYBP, CENPF, CLIP1, DGKD, DYNLL1, EGFR, ERBB2, ERBB3, ERBB4, ESR1, GCH1, GDNF, GHR, HSP90AA1, IGF1R, KIT, LDB1, MAD2L1, MAOB, MYH9, NDE1, NFKB1, NFKBIA, NR3C1, PAFAH1B1, PAH, PAICS, PDGFB, PPP5C, RELA, RILPL2, RIPK2, S100A1, S100A4, SDCBP2, SHBG, SMAD3, TRADD, TRAF2, TTN, TYR, VCP, VEGFA
0.053	BP	carbohydrate biosynthetic process	AKT1, EGF, GAPDH, GOT1, GOT2, GRB10, GSK3A, GSK3B, HSD3B1, HSD3B2, IGF1, IKBKB, IL1B, INS, INSR, IRS1, MAPK14, MAPK7, NFKB1, NR3C1, PDGFB, POU1F1, ST6GALNAC5, ST6GALNAC6, STK11, UGDH
0.068	BP	response to inorganic substance	ABP1, ADRBK1, ATP5D, CACYBP, CTNNB1, CYP19A1, CYP1A1, ERBB4, GPAM, GRIN2B, GSK3A, GSK3B, GSN, HSD17B2, HSD17B3, INSR, MAOB, MET, NEDD4, NEDD4L, NFKB1, NR3C1, PIK3R1, PRDX6, PXN, RELA, SHC1, SLC1A3, SLC8A1, TAT, TH, TPH2, TTN
0.018	BP	androgen metabolic process	CYP19A1, CYP3A4, ESR1, HSD17B2, HSD17B3, HSD17B6, HSD17B8, HSD3B1, HSD3B2
0.031	BP	regulation of microtubule-based process	ARHGEF2, BRCA1, CLASP1, CLASP2, CLIP1, CTNNB1, DYNC1LI1, ERBB2, FES, GSK3B, MAPRE1, MAPT, SKA1, SKA2, XPO1
0.018	BP	response to growth hormone stimulus	CACYBP, GHR, GRIN2B, IRS1, JAK2, MAPK1, PIK3R1, PXN, SOCS1
0.052	CC	axon	ADRB2, ADRBK1, AGER, AR, BACE1, CYP19A1, DDC, EPHB1, ESR1, GOT1, GRIN2B, GRM7, KCNJ6, MAP2K1, MAPK1, MAPT, MBP, MYC, NDEL1, OPRD1, PAFAH1B1, SLC12A6, TH, TNFRSF1A, TUBB3, TUBB4A
0.029	BP	positive regulation of intracellular transport	AKAP5, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, NEDD4, PRKCQ, RBPMS, SFN, SMAD3, TNFRSF1A
0.024	CC	caveola	ADRB2, ADRBK1, ATP1B1, CBL, ERBB4, IGF1R, INSR, IRS1, JAK2, KIF18A, MAPK1, SRC
0.037	BP	polysaccharide biosynthetic process	AKT1, EGF, GRB10, GSK3A, GSK3B, HSD3B1, HSD3B2, IGF1, IKBKB, IL1B, INS, INSR, IRS1, MAPK14, MAPK7, NFKB1, PDGFB, UGDH
0.067	CC	soluble fraction	ABI1, ADH7, ADRBK1, AKT1, ANPEP, ARR3, ARRB1, BRAF, CACYBP, CAMKK1, CARHSP1, DDC, EGF, GCH1, GOT1, GRK5, GSK3B, GUSB, IARS, IDO1, INSR, KL, MAOA, MAP2K1, MAPK1, MAPK14, MERTK, PAFAH1B1, PIK3R1, PPP2CA, PPP3CA, PRKCQ, RANGAP1
0.016	BP	establishment of spindle localization	ARHGEF2, CCDC99, CENPA, MYH9, NDC80, NDE1, PAFAH1B1, ZW10
0.014	MF	insulin receptor substrate binding	GRB2, IGF1R, INSR, JAK2, PIK3CA, PIK3R1, PRKCD
0.012	MF	alcohol dehydrogenase (NAD) activity	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7
0.031	BP	JAK-STAT cascade	AGER, CD40, EGF, ERBB4, GHR, IGF1, IRS1, JAK2, KIT, MAPK1, NEUROD1, NMI, PPP2CA, SOCS1, TNFRSF1A
0.020	BP	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway	AGK, DGKA, DGKB, DGKD, DGKE, DGKG, DGKH, DGKI, DGKQ, DGKZ
0.096	BP	neuron projection development	ABL1, AGER, AKAP5, AKT1, CDC20, CLASP1, CLASP2, CREB1, EGFR, EPHB1, ERBB2, ERBB3, EZR, FES, FYN, GDNF, GFRA1, GJA1, GRB2, GSK3B, HDAC2, HSP90AA1, IGF1R, JAK2, MAP2K1, MAPK1, MAPT, MBP, MET, MYH9, NDEL1, NEDD4, NRAS, PAFAH1B1, PRKCQ, RAF1, RET, SHC1, SIAH1, SKIL, SOS1, SRC, STIP1, STK11, TUBB3, USP33, VCAN
0.018	BP	regulation of insulin receptor signaling pathway	GRB10, GSK3A, IL1B, INS, IRS1, PRKCD, PRKCQ, RELA, SOCS1
0.018	MF	insulin receptor binding	DOK1, GRB10, IGF1, IGF1R, INS, IRS1, PDPK1, PIK3R1, SHC1
0.033	BP	peptidyl-serine phosphorylation	ADRBK1, AKT1, ARRB1, BRAF, GSK3A, GSK3B, MAPK1, MAPK14, MAPK7, MET, NEK6, PDGFB, PIK3CA, PLK1, RAF1, VEGFA
0.143	BP	heterocycle metabolic process	ACPP, ADRB2, ADRB3, AFMID, AKAP12, AKAP5, ARRB1, ATP1B1, ATP5D, BCR, CD40, CYP19A1, CYP1A1, CYP2D6, CYP3A4, DDC, DGKI, ERBB2, FLAD1, GCH1, GDI2, GHR, GNA11, GNA14, GNA15, GNAL, GNAS, GRM7, GSK3A, GSK3B, HSP90AA1, HTR4, IDO1, IDO2, MAOA, MAP2K1, MAPK1, MYH9, NDEL1, NRAS, OLA1, OPRD1, PAFAH1B1, PAH, PAICS, PEMT, PFAS, PSMD6, RANGAP1, SLC9A3R1, SMARCA5, SOS1, TH, TNFRSF1A, TPH1, TPH2, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP
0.090	BP	positive regulation of cell death	ABL1, ADRB2, AGER, AKT1, ARHGEF2, ARRB2, BRCA1, CD40, CTNNB1, DYNLL1, EAF2, FOXO3, GCH1, GRIN2B, GSK3B, IDO1, IKBKE, IKBKG, IL1B, ITGB3BP, ITSN1, JAK2, MAPK1, MYC, NEUROD1, NR3C1, PIK3R1, PPP2CA, RIPK1, RIPK2, RIPK3, RPS3A, SFN, SIAH1, SMAD3, SOS1, STK11, TFPT, TNFRSF1A, TRADD, TRAF2, TRAF6, TUBB, TUBB4B
0.125	BP	small molecule catabolic process	ADH4, ADH5, ADH7, AFMID, AKT1, ARRB1, ATP5D, BCR, CBR3, CD40, DGKI, ECI2, ERBB2, FUT1, FUT2, GAPDH, GCH1, GDI2, GNA11, GNA14, GNA15, GNAL, GNAS, GOT1, GOT2, GSK3B, HSP90AA1, IDO1, IDO2, IGF1, INS, INSR, IRS1, MAOA, MAP2K1, MYH9, NDEL1, NOS1, NRAS, OLA1, PAFAH1B1, PAH, PSMD6, RANGAP1, SMARCA5, SOS1, TAT, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP
0.043	BP	regulation of DNA metabolic process	APEX1, BRCA1, CACYBP, CD40, CDK9, EGFR, GSK3A, GSK3B, IGF1, IGF1R, INS, INSR, KPNA1, KPNA2, MET, MYC, PDGFB, PDGFRB, PIK3CA, PPP2CA, SHC1
0.025	BP	establishment of cell polarity	ARHGEF2, CCDC99, CENPA, EPHB1, GSK3B, IGF1R, MYH9, NDC80, NDE1, PAFAH1B1, STK11, ZW10
0.014	MF	oxidoreductase activity, acting on the CH-NH2 group of donors, oxygen as acceptor	ABP1, AOC2, AOC3, IL4I1, MAOA, MAOB, NUP62
0.053	BP	regulation of cell cycle arrest	AKT1, BIRC5, BRCA1, BUB1, BUB1B, BUB3, CASC5, CDC20, CDK9, DDB1, DGKZ, DYNC1LI1, KNTC1, MAD1L1, MAD2L1, MAPK14, NEK6, NEUROD1, PLK1, PSMA6, PSMD6, RBBP8, TAOK1, ZW10, ZWILCH, ZWINT
0.018	BP	positive regulation of glucose transport	AKT1, ERBB3, ERBB4, IGF1, INS, INSR, IRS1, MET, PIK3R1
0.033	BP	tissue homeostasis	ADRB2, CTNNB1, ERBB4, GIGYF2, GNAS, KDR, LDB1, LDB2, NEUROD1, PDGFRB, SERPINA3, SRC, STK11, TRAF6, VEGFA, ZNF675
0.088	BP	positive regulation of apoptosis	ABL1, ADRB2, AGER, AKT1, ARHGEF2, ARRB2, BRCA1, CD40, CTNNB1, DYNLL1, EAF2, FOXO3, GCH1, GSK3B, IDO1, IKBKE, IKBKG, IL1B, ITGB3BP, ITSN1, JAK2, MAPK1, MYC, NEUROD1, NR3C1, PIK3R1, PPP2CA, RIPK1, RIPK2, RIPK3, RPS3A, SFN, SIAH1, SMAD3, SOS1, STK11, TFPT, TNFRSF1A, TRADD, TRAF2, TRAF6, TUBB, TUBB4B
0.016	BP	negative regulation of insulin receptor signaling pathway	GRB10, GSK3A, IL1B, IRS1, PRKCD, PRKCQ, RELA, SOCS1
0.023	BP	regulation of carbohydrate biosynthetic process	AKT1, GRB10, GSK3A, GSK3B, IGF1, INS, INSR, IRS1, NR3C1, POU1F1, STK11
0.033	BP	regulation of protein import into nucleus	AKAP5, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, MAPK7, NFKBIA, NFKBIB, NFKBIE, PRKCQ, RBPMS, SMAD3, TNFRSF1A
0.027	BP	mammary gland epithelium development	AKT1, AR, CHUK, DDR1, DEAF1, ERBB4, ESR1, JAK2, MAPK1, NR3C1, PGR, SLC12A2, SRC
0.014	BP	establishment of mitotic spindle orientation	ARHGEF2, CCDC99, CENPA, NDC80, NDE1, PAFAH1B1, ZW10
0.014	BP	growth hormone receptor signaling pathway	GHR, IRS1, JAK2, MAPK1, PIK3R1, PXN, SOCS1
0.020	BP	regulation of glucose import	AKT1, ERBB3, ERBB4, GRB10, GSK3A, IGF1, INS, INSR, IRS1, PIK3R1
0.084	BP	alcohol metabolic process	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7, AGPAT6, AKT1, AOC2, CDS1, CNBP, DDC, FUT1, FUT2, GAPDH, GCH1, GCNT4, GOT1, GOT2, GPAT2, GRB10, GSK3A, GSK3B, HSD17B3, IGF1, INS, INSR, IRS1, MAOA, MAOB, MAPK14, MYC, NR3C1, PAFAH1B1, PAH, PEMT, PIK3CA, PIK3R1, STK11, TH, UGDH
0.035	BP	activation of MAPK activity	GHR, IKBKG, IL1B, INSR, KIT, MAP2K1, MAP3K7, MAPK1, MAPK14, MET, PXN, RIPK1, RIPK2, SHC1, TAB1, TAB2, TRAF6
0.027	BP	positive regulation of intracellular protein transport	AKAP5, EGF, EGFR, ERBB4, GSK3B, IGF1, IL1B, JAK2, PRKCQ, RBPMS, SFN, SMAD3, TNFRSF1A
0.127	BP	regulation of multicellular organismal development	ADRB2, AKAP5, AKT1, AR, ARHGEF2, CBLN2, CD40, CDC20, CENPF, CTNNB1, DEAF1, DVL3, EAF2, EGF, EGR1, EPHB1, ERBB2, ERBB4, ESR1, FES, FOXO3, GDNF, GJA1, GNAS, GSK3A, GSK3B, HDAC2, IDO1, IGF1, IL1B, INSR, KDR, KL, LDB1, MAPK14, MAPK7, MAPT, MBP, MET, MYC, NDEL1, NEDD4, NEUROD1, NFKBIA, NR5A1, PAFAH1B1, PDGFB, PDGFRB, PIK3R1, PPP2CA, RELA, RET, RIPK2, SKIL, SMAD2, SMAD3, STK11, TNFRSF1A, TRADD, TRAF6, VEGFA, ZNF675
0.058	CC	centrosome	APEX1, B9D2, BIRC5, CDC20, CKAP5, CLASP1, CLIP1, CSK, CTNNB1, DYNC1H1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNLL1, GSK3B, KIF2A, KIF3B, MAD1L1, MAPRE1, MLF1IP, NDE1, NDEL1, PAFAH1B1, PLK1, SGOL1, SKA1, SLC9A3R1, TUBG1, YWHAQ
0.053	BP	anti-apoptosis	AKT1, APEX1, ARRB1, BIRC5, BRAF, CTNNB1, ERBB4, ESR1, GDNF, GSK3B, HDAC1, IGF1, IGF1R, IKBKB, IL1B, MYC, NFKB1, NFKBIA, NR3C1, PIK3CA, PIK3R1, RELA, RIPK1, RIPK2, TRAF6, VEGFA
0.084	BP	cell morphogenesis involved in neuron differentiation	ABL1, AKAP5, CLASP1, CLASP2, CREB1, EGFR, EPHB1, ERBB2, ERBB3, EZR, FES, FYN, GDNF, GFRA1, GRB2, GSK3B, HSP90AA1, IGF1R, JAK2, MAP2K1, MAPK1, MAPT, MBP, MET, MYH9, NDEL1, NEDD4, NRAS, PAFAH1B1, PRKCQ, RAF1, SIAH1, SKIL, SLC1A3, SOS1, SRC, STIP1, STK11, TUBB3, USP33, VCAN
0.039	BP	regulation of binding	ADRB2, ARRB1, ARRB2, CYP2D6, EGF, GSK3B, HJURP, IGF1, JAK2, MYC, NEUROD1, NFKBIA, PLK1, PRKCD, RSF1, SMAD2, SMAD3, TRAF6, ZNF675
0.039	BP	positive regulation of T cell activation	AKT1, CSK, FYN, GPAM, GRB2, HSPH1, IGF1, IL1B, MAP3K14, MAP3K7, MAP3K8, PDPK1, PIK3CA, PIK3R1, PRKCQ, RIPK2, SRC, TRAF2, TRAF6
0.027	BP	regulation of microtubule cytoskeleton organization	ARHGEF2, BRCA1, CLASP1, CLASP2, CLIP1, CTNNB1, DYNC1LI1, FES, MAPRE1, MAPT, SKA1, SKA2, XPO1
0.084	BP	neuron projection morphogenesis	ABL1, AKAP5, CLASP1, CLASP2, CREB1, EGFR, EPHB1, ERBB2, ERBB3, EZR, FES, FYN, GDNF, GFRA1, GJA1, GRB2, GSK3B, HSP90AA1, IGF1R, JAK2, MAP2K1, MAPK1, MAPT, MBP, MET, MYH9, NDEL1, NEDD4, NRAS, PAFAH1B1, PRKCQ, RAF1, SIAH1, SKIL, SOS1, SRC, STIP1, STK11, TUBB3, USP33, VCAN
0.037	BP	G2/M transition of mitotic cell cycle	BIRC5, CKAP5, CLASP1, DYNC1H1, DYNC1I2, DYNLL1, FHL1, HSP90AA1, MAPRE1, NDE1, PAFAH1B1, PLK1, PRKCQ, TUBA4A, TUBB, TUBB4A, TUBB4B, TUBG1

Continued on next page...

Ratio	Type	Description	Genes
0.115	BP	embryo development	ABI1, AKT1, AR, BCR, BIRC5, BRCA1, CTNNB1, CYP1A1, DEAF1, DVL3, DYNC2H1, EGFR, ELL, ERBB4, FOXO3, GDNF, GJA1, GNAS, GRB2, GRIN2B, HDAC1, HDAC2, HOXC9, HSF1, IL1B, INSR, KDR, LDB1, LMO4, MAP2K1, MAP3K7, MAPK1, MAPK7, MYC, MYH9, NASP, NDEL1, NEUROD1, PDGFB, PDGFRB, PITPNB, PITX1, RBBP8, RET, SKIL, SLC8A1, SMAD2, SMAD3, SMARCA5, TAB1, TCF21, TH, TRAF6, TTN, UGDH, VEGFA
0.016	BP	indolalkylamine metabolic process	AFMID, CYP19A1, DDC, IDO1, IDO2, MAOA, TPH1, TPH2
0.025	BP	microtubule organizing center organization	BRCA1, CKAP5, CLASP1, CLASP2, CTNNB1, DYNC1LI1, KIF3B, NDE1, PAFAH1B1, PLK1, SGOL1, XPO1
0.010	CC	kinetochore microtubule	CLASP1, CLASP2, KIF18A, KNTC1, ZW10
0.037	MF	protein C-terminus binding	ABL1, CDC20, CSK, CTNNB1, DGKZ, DYNLL1, ERBB2, ITGB3BP, MAPK14, MAPRE1, PABPC1, PIK3R1, PPP2CA, PRKCD, SDCBP2, SIAH1, SLC9A3R2, STIP1
0.010	MF	primary amine oxidase activity	ABP1, AOC2, AOC3, MAOA, MAOB
0.098	BP	cardiovascular system development	ADAMTS1, ADRBK1, AKT1, ANPEP, C1GALT1, CACYBP, CTNNB1, DVL3, EGF, EGR1, EPHB1, ERBB2, ERBB3, ERBB4, GJA1, GNA11, GSK3A, IGF1, IL1B, INSR, KDR, LMO4, MAP2K1, MAP3K7, MAPK1, MAPK14, MAPK7, MEIS1, MYH9, PDGFB, PDGFRB, PIK3CA, RAF1, SHC1, SLC12A6, SLC8A1, SMAD2, SMAD3, SMARCA2, STK11, TAB1, TAB2, TCF21, TH, TNFRSF1A, TTN, VCAN, VEGFA
0.049	BP	cell cycle checkpoint	AKT1, BIRC5, BRCA1, BUB1, BUB1B, BUB3, CASC5, CDC20, DDB1, DGKZ, DYNC1LI1, KNTC1, MAD1L1, MAD2L1, MAPK14, NEK6, PLK1, PSMA6, PSMD6, RBBP8, TAOK1, ZW10, ZWILCH, ZWINT
0.018	BP	positive regulation of mitosis	EGF, IGF1, IL1B, INS, INSR, MET, PDGFB, PDGFRB, PLK1
0.033	BP	ERK1 and ERK2 cascade	ARRB1, ARRB2, BRAF, EGF, EPHB1, ERBB2, ERBB4, ESR1, IGF1, IL1B, KDR, MAPK1, PDGFB, PDGFRB, RIPK2, SLC9A3R1
0.070	BP	regulation of system process	ADRB2, ADRBK1, ANPEP, ARRB2, CDC20, CTNNB1, EGR1, ERBB4, GDNF, GJA1, GRIN2B, GSK3A, GSK3B, IGF1, IL1B, INS, JAK2, MAP2K1, NEUROD1, NOS1, NRAS, OPRD1, PDGFB, PIK3R1, PPP3CA, PRKCQ, S100A1, SGK1, SHC1, SLC1A3, SLC8A1, SLC9A3R1, TH, WNK4
0.020	MF	phosphoprotein binding	ARR3, CBL, GRB2, MAPK1, NEDD4, PAFAH1B1, PIK3R1, SFN, SHC1, TBK1
0.078	BP	axonogenesis	ABL1, CLASP1, CLASP2, CREB1, EGFR, EPHB1, ERBB2, ERBB3, EZR, FES, FYN, GDNF, GFRA1, GRB2, GSK3B, HSP90AA1, IGF1R, JAK2, MAP2K1, MAPK1, MAPT, MBP, MET, MYH9, NDEL1, NRAS, PAFAH1B1, PRKCQ, RAF1, SIAH1, SKIL, SOS1, SRC, STIP1, STK11, TUBB3, USP33, VCAN
0.012	BP	ethanol metabolic process	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7
0.012	BP	ethanol oxidation	ADH1A, ADH1B, ADH4, ADH5, ADH6, ADH7
0.049	BP	response to metal ion	ABP1, ATP5D, CACYBP, CTNNB1, CYP19A1, CYP1A1, GPAM, GRIN2B, GSK3A, GSK3B, GSN, HSD17B2, HSD17B3, INSR, MAOB, NEDD4, NEDD4L, NFKB1, NR3C1, PIK3R1, TAT, TH, TPH2, TTN
0.125	BP	multi-organism process	ADH5, ADH7, AKAP5, ANPEP, AR, BCR, BUB1, CCNT1, CD40, CD46, CENPA, CHUK, CREB1, CYP1A1, DDB1, DDR1, DYNC1I2, DYNC1LI1, DYNLL1, ESR1, FYN, GCH1, GCNT4, GNAS, GPAM, GRB2, GRIN2B, HDAC1, HSF1, IDO1, IKBKB, IKBKG, IL1B, INSR, JAK2, KDR, KPNA1, KPNA2, LTF, MAOB, MAPK1, MAPK14, MLF1IP, NEDD4, NEDD4L, NFKB1, NFKB2, NFKBIA, PGR, PIK3R1, RELA, RIPK2, SF3B2, SMAD3, SOCS1, SRC, TBK1, TH, TNFRSF1A, TRAF6, XPO1
0.029	BP	positive regulation of DNA metabolic process	APEX1, BRCA1, CACYBP, CD40, EGFR, IGF1, IGF1R, INS, INSR, MET, MYC, PDGFB, PDGFRB, SHC1
0.047	BP	regulation of cellular response to stress	ABL1, AKT1, APEX1, BRCA1, CDK9, DVL3, EGFR, EPHB1, IGF1R, IL1B, MAP2K1, MAP3K7, MAPK1, MYC, NDEL1, NEK6, PRKCD, RIPK1, RIPK2, TAOK1, TRAF2, TRAF6, ZNF675
0.010	BP	JAK-STAT cascade involved in growth hormone signaling pathway	GHR, IRS1, JAK2, MAPK1, SOCS1
0.044	CC	cell leading edge	ABI1, AKAP5, AKT1, ARHGEF2, BRCA1, CLASP2, CLIP1, CTNNB1, DGKZ, EZR, GNAS, GSN, ITSN1, KIF18A, MYH9, NDEL1, OPRD1, PAFAH1B1, PIK3CA, PXN, SLC9A3R1, TUBG1
0.029	BP	steroid hormone receptor signaling pathway	AR, BRCA1, CTNNB1, DNAJA1, ESR1, HDAC1, IGF1, JAK2, NEDD4, NR3C1, PGR, PMEPA1, SRC, TCF21
0.016	BP	positive regulation of glucose import	AKT1, ERBB3, ERBB4, IGF1, INS, INSR, IRS1, PIK3R1
0.012	MF	microtubule plus-end binding	CLASP1, CLASP2, CLIP1, KIF18A, KIF2C, MAPRE1
0.069	MF	lipid binding	ADH4, ADH5, ADH7, ADRBK1, AKT1, AR, ARHGEF2, BCR, CYP3A4, DGKA, DGKD, DGKH, DOK1, ECI2, ESR1, FES, GRB10, GRK5, IRS1, ITSN1, KL, NR3C1, NR5A1, PEMT, PGR, PHLPP1, PIK3R1, PITPNB, SGK1, SHBG, SHC1, SOS1, TRAF2, VCP
0.033	BP	regulation of peptidyl-tyrosine phosphorylation	CD40, EGF, EGFR, ERBB4, GHR, IGF1, INS, JAK2, KIT, PDGFB, PDGFRB, PPP2CA, PRKCD, SOCS1, TNFRSF1A, VEGFA
0.010	MF	nitric-oxide synthase regulator activity	AKT1, DYNLL1, EGFR, ESR1, HSP90AA1
0.035	BP	response to carbohydrate stimulus	ACAN, ARRB1, COLEC12, CYP19A1, EGR1, GPAM, GRIN2B, INSR, MAPK14, MET, NEUROD1, PIK3R1, PPP3CA, PRKCQ, SLC8A1, SMAD2, TH
0.014	MF	MAP kinase kinase kinase activity	BRAF, EGFR, MAP3K14, MAP3K3, MAP3K7, MAP3K8, RAF1
0.014	MF	phosphatidylinositol 3-kinase binding	FYN, IGF1R, INSR, IRS1, JAK2, MET, PIK3R1
0.064	BP	interspecies interaction between organisms	ANPEP, BUB1, CCNT1, CD46, CENPA, CREB1, DDB1, DYNC1I2, DYNC1LI1, DYNLL1, FYN, GRB2, HDAC1, IKBKG, INSR, KDR, KPNA1, KPNA2, MAPK1, MLF1IP, NEDD4, NEDD4L, NFKBIA, PIK3R1, RELA, SF3B2, SMAD3, SRC, TBK1, TNFRSF1A, XPO1
0.141	BP	negative regulation of metabolic process	A2M, AKT1, AR, ARRB1, ARRB2, AURKB, BIRC5, BRCA1, BUB1B, BUB3, CD46, CDC20, CDK9, CREB1, CTNNB1, CYP2D6, DYNLL1, EGFR, EGR1, ESR1, FOXO3, FURIN, FYN, GJA1, GRB10, GRM7, GSK3A, GSK3B, HDAC1, HDAC2, IL1B, INS, INSR, LDB1, MAD2L1, MAGEA1, MET, MYC, NEDD4, NFKB1, PA2G4, PABPC1, PDGFB, PGR, PIK3R1, PLAUR, PLK1, PPP2CA, PRKCD, PSMA6, PSMD6, RBBP7, RBBP8, RELA, RSF1, S100A1, SKIL, SMAD2, SMAD3, SMARCA2, SMARCA5, SOCS1, TBK1, TCF21, TNFRSF1A, TRAF6, XPO1, YWHAQ, ZNF675
0.020	BP	nitric oxide biosynthetic process	AKT1, EGFR, ESR1, GCH1, HSP90AA1, IL1B, INS, INSR, JAK2, NOS1
0.016	BP	regulation of glycogen biosynthetic process	AKT1, GRB10, GSK3A, GSK3B, IGF1, INS, INSR, IRS1
0.018	MF	activating transcription factor binding	CREB1, DGKQ, HDAC1, LDB1, NEUROD1, POU1F1, RELA, SMAD2, SMAD3
0.016	BP	positive regulation of nitric oxide biosynthetic process	AKT1, EGFR, ESR1, HSP90AA1, IL1B, INS, INSR, JAK2
0.031	BP	response to hexose stimulus	ACAN, ARRB1, CYP19A1, EGR1, GPAM, INSR, MAPK14, MET, NEUROD1, PIK3R1, PPP3CA, PRKCQ, SLC8A1, SMAD2, TH
0.034	CC	receptor complex	ADRB2, ADRB3, CD40, CHUK, ERBB2, ERBB3, GHR, GRIN2B, IKBKB, INSR, IRS1, MYH9, RIPK1, SMAD3, TRADD, TRAF2, TRAF6
0.008	BP	hyaluronan biosynthetic process	EGF, IL1B, NFKB1, PDGFB
0.102	BP	secretion	A2M, ADRBK1, AGPAT6, AKAP5, ANPEP, ARRB1, BCR, CD40, CHUK, CREB1, EGF, ERBB3, ERBB4, EXOC1, FES, FURIN, GDNF, GNAS, GPAM, GRIN2B, GRM7, IGF1, IL1B, INS, IRS1, JAK2, KCNJ1, LAMP2, MAOA, MAOB, MERTK, MET, NEDD4L, NEUROD1, NR3C1, OTOF, PDGFB, PDPK1, PPP3CA, PRKCQ, SGK1, SLC12A1, SLC9A3R1, SMAD2, TRAF2, TRAF6, TTN, TUBA4A, VEGFA, WNK4
0.014	BP	mammary gland alveolus development	AR, CHUK, DDR1, ERBB4, ESR1, TPH1, VEGFA
0.026	MF	monooxygenase activity	CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, NOS1, PAH, TH, TPH1, TPH2, TYR
0.018	BP	regulation of microtubule polymerization or depolymerization	ARHGEF2, CLASP1, CLASP2, CLIP1, FES, MAPRE1, MAPT, SKA1, SKA2
0.018	BP	regulation of mitotic metaphase/anaphase transition	BUB1, BUB1B, BUB3, CDC20, DYNC1LI1, MAD1L1, MAD2L1, NEK6, PLK1
0.020	BP	'de novo' posttranslational protein folding	HSPH1, TUBA3D, TUBA4A, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6
0.090	BP	negative regulation of molecular function	ABL1, ADRB2, AKT1, ARRB1, ARRB2, BIRC5, BUB1B, BUB3, CASC5, CD46, CDC20, CYP2D6, DGKZ, ELL, ESR1, GNAL, GRM7, GSK3A, GSK3B, HDAC2, IGF1R, IL1B, INS, INSR, JAK2, MAD2L1, MYC, NFKB1, NFKBIA, NOS1, NUP62, OPRD1, PDPK1, PLK1, PPP2CA, PRKCD, PSMA6, PSMD6, RAF1, RSF1, SERPINA3, SFN, SLC9A3R1, ZNF675
0.062	CC	perinuclear region of cytoplasm	AATK, ABL1, AKAP5, APEX1, BUB1B, CDC20, CTNNB1, DGKI, DOK1, DYNC1I1, EGFR, ERBB2, ESR1, GAPDH, GSN, MAD2L1, MAP2K1, NEDD4, NFKBIE, NOS1, PAFAH1B1, PRKCD, RANGAP1, S100A4, SEC24D, TRAF6, TYR, UBQLN4, USP20, USP33, ZNF675
0.029	BP	regulation of ERK1 and ERK2 cascade	ARRB1, ARRB2, BRAF, EPHB1, ERBB2, ERBB4, ESR1, IGF1, IL1B, KDR, PDGFB, PDGFRB, RIPK2, SLC9A3R1
0.059	BP	regulation of cell motility	ABL1, ACAN, AGER, AKT1, BCR, BRCA1, EGFR, ERBB4, FES, FURIN, IGF1, IGF1R, INS, INSR, IRS1, JAK2, KDR, MAP2K1, MAPK1, PDGFB, PDGFRB, PDPK1, PIK3R1, RAF1, RET, SGK1, SLC9A3R1, SMAD3, VEGFA
0.023	BP	negative regulation of catabolic process	AKT1, EGFR, FURIN, FYN, GSK3A, IL1B, INS, MAD2L1, PABPC1, RELA, SMAD3
0.018	BP	membrane protein proteolysis	BACE1, FURIN, IL1B, MYH9, NFKB1, PRKCQ, RELA, RET, TRAF6
0.018	BP	regulation of monooxygenase activity	AKT1, EGFR, ESR1, GCH1, GDNF, HSP90AA1, IL1B, INS, NFKB1
0.018	BP	spindle checkpoint	BIRC5, BUB1, BUB1B, BUB3, CASC5, CDC20, DYNC1LI1, MAD1L1, MAD2L1
0.071	MF	protein homodimerization activity	ABP1, ADH5, ADH7, ADRB2, ADRB3, AOC3, BIRC5, CACYBP, CENPF, CLIP1, DGKD, DYNLL1, ERBB3, ERBB4, GCH1, GDNF, GHR, HSP90AA1, KIT, LDB1, MAD2L1, MAOB, MYH9, NFKB1, NR3C1, PAFAH1B1, PAH, PDGFB, RIPK2, S100A1, SDCBP2, SHBG, SMAD3, TYR, VEGFA
0.027	BP	maintenance of protein location in cell	AURKB, BUB3, CASC5, CLASP1, CLASP2, CTNNB1, EZR, NDC80, NFKBIA, NFKBIB, NFKBIE, NR5A1, SGOL1
0.027	BP	response to alkaloid	CYP19A1, DDC, GHR, GNAL, GRIN2B, HNMT, IL1B, MYC, PPP5C, RELA, SHC1, TH, TNFRSF1A
0.064	BP	induction of apoptosis	ABL1, AKT1, ARHGEF2, ARRB2, BRCA1, DYNLL1, EAF2, FOXO3, GCH1, IKBKE, IKBKG, ITGB3BP, ITSN1, JAK2, MAPK1, MYC, PPP2CA, RIPK1, RIPK3, RPS3A, SFN, SMAD3, SOS1, STK11, TFPT, TNFRSF1A, TRADD, TRAF2, TRAF6, TUBB, TUBB4B
0.047	BP	reproductive structure development	ADAMTS1, ADRBK1, AR, CENPI, CTNNB1, CYP19A1, EAF2, ESR1, FANCA, FOXO3, HSD17B3, IGF1, IGF1R, KDR, KIT, MET, NR5A1, PGR, PLAUR, SRC, STK11, TCF21, VEGFA
0.025	BP	secondary metabolic process	ADH4, ADH5, ADH7, CYP1A1, CYP2D6, CYP3A4, CYP3A5, DDC, HSD17B3, TH, TNFRSF1A, TYR
0.020	MF	beta-catenin binding	AR, DVL3, ESR1, GRIN2B, GSK3B, MET, PXN, SLC9A3R1, SLC9A3R2, SMAD3
0.057	BP	response to steroid hormone stimulus	AR, BRCA1, CTNNB1, CYP19A1, ERBB2, ERBB4, ESR1, GHR, GOT1, HNMT, HSD17B3, IL1B, INSR, MAOB, MAP2K1, MAPK1, NR3C1, NR5A1, PDGFB, PGR, PIK3R1, RELA, SHC1, SOCS1, TAT, TH, TNFRSF1A, TPH2
0.049	BP	striated muscle tissue development	ADRB2, CACYBP, CENPF, ERBB2, ERBB3, ERBB4, GJA1, GSK3A, GSK3B, IGF1, MAPK14, MET, MYH9, NOS1, PDGFRB, PIK3R1, PITX1, PPP3CA, SKIL, SLC8A1, SMAD3, TCF21, TTN, VEGFA

Continued on next page...

Ratio	Type	Description	Genes
0.024	MF	amino acid binding	DDC, GRIN2B, GRM7, IDO1, NEDD4, NOS1, PAH, SLC1A3, TAT, TH, TPH1, TPH2
0.051	BP	negative regulation of cellular component organization	AKT1, AR, ARHGEF2, BRCA1, BUB1, BUB1B, BUB3, CDC20, CLASP1, CLASP2, DYNC1LI1, GSK3B, GSN, HDAC2, IGF1, LMO4, MAD1L1, MAD2L1, MAPRE1, MAPT, MBP, PAFAH1B1, PPP2CA, PRKCD, RAF1
0.049	MF	cofactor binding	ABP1, ADH4, ADH7, AOC2, AOC3, BIRC5, CBR3, DDC, ECI2, GAPDH, GCH1, GOT1, GOT2, HSD3B1, HSD3B2, IL4I1, INSR, MAOA, MAOB, NOS1, PAH, TAT, TH, UGDH
0.035	BP	negative regulation of organelle organization	AKT1, ARHGEF2, BRCA1, BUB1, BUB1B, BUB3, CDC20, CLASP1, CLASP2, DYNC1LI1, GSN, IGF1, MAD1L1, MAD2L1, MAPRE1, MAPT, PRKCD
0.012	BP	positive regulation of peptidyl-threonine phosphorylation	EGF, GSK3A, GSK3B, MAPK1, MET, PLK1
0.051	BP	tube morphogenesis	AR, CTNNB1, DDR1, DEAF1, DVL3, EGF, ESR1, GDNF, GJA1, IGF1, KDR, LMO4, MAP3K7, MET, MYC, NR3C1, PGR, PXN, RET, SLC12A2, SMAD3, SRC, TCF21, TRAF6, VEGFA
0.031	MF	motor activity	CENPE, DYNC1H1, DYNC1I1, DYNC1I2, DYNC1LI1, DYNC1LI2, DYNC2H1, DYNLL1, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B, MYH1, MYH9
0.018	BP	positive regulation of peptidyl-serine phosphorylation	AKT1, ARRB1, BRAF, GSK3A, GSK3B, MET, PIK3CA, RAF1, VEGFA
0.102	BP	cellular lipid metabolic process	ADH4, ADH5, ADH7, AGK, AGPAT6, AGPAT9, AKT1, BRCA1, CDS1, CDS2, CYP1A1, CYP2D6, CYP3A4, DGKD, DGKE, DGKZ, ECI2, ELOVL5, GHR, GPAM, GPAT2, HSD17B12, HSD17B8, IKBKB, INS, IRS1, KIT, MAPK14, MAPK7, MBOAT2, PAFAH1B1, PDGFB, PDGFRB, PEMT, PIK3CA, PIK3R1, PISD, PLAUR, PPP1CC, PPP2CA, PRDX6, PRKCD, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5, STK11, TH, TNFRSF1A, UGT2B17
0.023	BP	positive regulation of nucleocytoplasmic transport	AKAP5, EGF, EGFR, ERBB4, GSK3B, IL1B, NEDD4, PRKCQ, RBPMS, SFN, SMAD3
0.029	BP	response to glucose stimulus	ACAN, ARRB1, CYP19A1, EGR1, GPAM, INSR, MAPK14, MET, NEUROD1, PPP3CA, PRKCQ, SLC8A1, SMAD2, TH
0.016	BP	spindle assembly checkpoint	BUB1, BUB1B, BUB3, CASC5, CDC20, DYNC1LI1, MAD1L1, MAD2L1
0.131	BP	negative regulation of macromolecule metabolic process	A2M, AR, ARRB1, ARRB2, AURKB, BIRC5, BRCA1, BUB1B, BUB3, CD46, CDC20, CDK9, CREB1, CTNNB1, EGFR, EGR1, ESR1, FOXO3, FURIN, FYN, GJA1, GRB10, GSK3A, GSK3B, HDAC1, HDAC2, INS, INSR, LDB1, MAD2L1, MAGEA1, MET, MYC, NEDD4, NFKB1, PA2G4, PABPC1, PDGFB, PGR, PIK3R1, PLAUR, PLK1, PPP2CA, PRKCD, PSMA6, PSMD6, RBBP7, RBBP8, RELA, RSF1, S100A1, SKIL, SMAD2, SMAD3, SMARCA2, SMARCA5, SOCS1, TBK1, TCF21, TNFRSF1A, TRAF6, XPO1, YWHAQ, ZNF675
0.018	BP	positive regulation of DNA replication	CACYBP, EGFR, IGF1, IGF1R, INS, INSR, MET, PDGFB, SHC1
0.026	CC	internal side of plasma membrane	ARRB1, CHUK, CTNNB1, FES, GNA11, GNA14, GNA15, GNAL, GNAS, IKBKB, TH, TRAF2, TRAF6
0.041	BP	positive regulation of cell migration	AGER, AKT1, EGFR, ERBB4, FURIN, IGF1, IGF1R, INS, INSR, IRS1, JAK2, KDR, MAP2K1, MAPK1, PDGFB, PDGFRB, PIK3R1, RET, SMAD3, VEGFA
0.057	BP	axon guidance	ABL1, CLASP1, CLASP2, CREB1, EGFR, EPHB1, ERBB2, EZR, FES, FYN, GDNF, GFRA1, GRB2, GSK3B, HSP90AA1, MAP2K1, MAPK1, MET, MYH9, NRAS, PRKCQ, RAF1, SIAH1, SOS1, SRC, STIP1, TUBB3, USP33
0.012	BP	positive regulation of monooxygenase activity	AKT1, ESR1, GCH1, GDNF, IL1B, INS
0.048	CC	cell body	ADRB2, AGER, AKAP5, ARHGEF2, CACYBP, CAMK2N1, CYP19A1, DDC, ESR1, GHR, GSK3B, KCNJ6, MAP2K1, MAPK1, MBP, MET, NDEL1, PAFAH1B1, PPP5C, SLC1A3, TH, TUBB, TUBB4A, USP33
0.039	BP	regulation of lipid metabolic process	AKT1, BRCA1, CREB1, ERBB4, GPAM, IGF1R, IL1B, INS, IRS1, KIT, NFKB1, NR3C1, NR5A1, PDGFB, PDGFRB, PIK3R1, PRKCD, SERPINA3, STK11
0.096	BP	growth	ADRB2, AGPAT6, AKT1, AR, CREB1, CYP19A1, DDR1, DGKD, EAF2, ERBB2, ERBB4, ESR1, FHL1, FOXO3, GHR, GIGYF2, GJA1, GNAS, GPAM, GSK3A, GSN, HSF1, IGF1, INS, INSR, MAPT, NDEL1, PAFAH1B1, PDGFB, PIK3CA, PLAUR, POU1F1, PPP2CA, PRKCQ, RBBP7, RUVBL1, SFN, SGK1, SHBG, SHC1, SLC12A2, SMAD2, SMAD3, SMARCA2, SOCS1, STK11, VEGFA
0.014	BP	microtubule depolymerization	ARHGEF2, CLASP1, CLASP2, KIF18A, KIF2B, KIF2C, MAPT
0.092	BP	cellular nitrogen compound catabolic process	AFMID, ARRB1, ATP5D, BCR, CD40, CYP2D6, CYP3A4, CYP3A5, DGKI, ERBB2, GCH1, GDI2, GNA11, GNA14, GNA15, GNAL, GNAS, GSK3B, HSP90AA1, IDO1, IDO2, MAP2K1, MYH9, NDEL1, NRAS, OLA1, PAFAH1B1, PSMD6, RANGAP1, SMARCA5, SOS1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP
0.018	BP	mitotic sister chromatid segregation	BUB3, CCDC99, CENPE, KIF18A, MAD2L1, NDC80, TTN, ZW10, ZWINT
0.008	CC	MIS12/MIND type complex	DSN1, MIS12, NSL1, PMF1
0.008	CC	Ndc80 complex	NDC80, NUF2, SPC24, SPC25
0.008	MF	alcohol dehydrogenase activity, zinc-dependent	ADH1A, ADH1B, ADH4, ADH7
0.008	MF	kinetochore binding	CCDC99, CENPE, CENPH, CLASP1
0.055	BP	morphogenesis of an epithelium	AR, CHUK, CTNNB1, DDR1, DEAF1, DVL3, EGFR, ESR1, GDNF, GJA1, GRB2, IGF1, IGF1R, LMO4, MAP3K7, MET, MYC, NR3C1, PDGFB, PGR, RET, SLC12A2, SMAD3, SRC, TCF21, TRAF6, VEGFA
0.033	BP	xenobiotic metabolic process	ADH1A, ADH1B, ADH4, ADH6, ADH7, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, HSD17B3, MAOA, MAOB, UGDH
0.010	BP	alkaloid metabolic process	CYP2D6, CYP3A4, CYP3A5, DDC, TH
0.029	BP	gland morphogenesis	AR, DDR1, EGFR, ERBB2, ERBB3, ESR1, IGF1, IGF1R, MET, NR3C1, PDGFB, PGR, SLC12A2, SRC
0.109	BP	regulation of cell differentiation	ABL1, AKAP5, AKT1, AR, ARHGEF2, CDC20, CREB1, CTNNB1, ERBB2, FES, FOXO3, GDNF, GHR, GNA11, GNAS, GSK3A, GSK3B, HDAC2, IGF1, INS, JAK2, KIT, LDB1, LDB2, LMO4, MAP2K1, MAPK1, MAPK14, MAPT, MBP, MET, MYC, NDEL1, NEDD4, NEUROD1, NFKB1, NFKBIA, PAFAH1B1, PIK3R1, PPP2CA, RAF1, RELA, RET, RIF1, RIPK2, SKIL, SMAD2, SMAD3, SMAD9, STK11, TRAF6, VEGFA, ZNF675
0.041	MF	phospholipid binding	ADRBK1, AKT1, ARHGEF2, BCR, DGKA, DGKD, DGKH, DOK1, FES, GRB10, GRK5, IRS1, ITSN1, NR5A1, PEMT, PHLPP1, PIK3R1, SGK1, SHC1, SOS1
0.023	BP	benzene-containing compound metabolic process	AOC2, CYP19A1, CYP1A1, DDC, GCH1, GCNT4, HSD17B3, MAOA, MAOB, PAH, TH
0.014	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen	CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7
0.080	BP	purine ribonucleoside triphosphate catabolic process	ARRB1, ATP5D, BCR, CD40, DGKI, ERBB2, GCH1, GDI2, GNA11, GNA14, GNA15, GNAL, GNAS, GSK3B, HSP90AA1, MAP2K1, MYH9, NDEL1, NRAS, OLA1, PAFAH1B1, PSMD6, RANGAP1, SMARCA5, SOS1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP
0.080	BP	ribonucleoside triphosphate catabolic process	ARRB1, ATP5D, BCR, CD40, DGKI, ERBB2, GCH1, GDI2, GNA11, GNA14, GNA15, GNAL, GNAS, GSK3B, HSP90AA1, MAP2K1, MYH9, NDEL1, NRAS, OLA1, PAFAH1B1, PSMD6, RANGAP1, SMARCA5, SOS1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, VCP
0.043	BP	response to organic cyclic compound	ACAN, ADRBK1, CTNNB1, CYP19A1, CYP1A1, GHR, GNAL, GRIN2B, GSK3A, HNMT, HSD17B3, IL1B, MET, PDGFB, PPP5C, PRKCQ, RELA, SHC1, SMAD9, TAT, TH
0.066	BP	positive regulation of cell differentiation	ABL1, AKAP5, AKT1, CREB1, CTNNB1, FES, FOXO3, GDNF, GHR, GNAS, HDAC2, IGF1, INS, JAK2, MAP2K1, MAPK14, MAPT, MET, NDEL1, NEUROD1, NFKB1, PAFAH1B1, PIK3R1, RELA, RIPK2, SKIL, SMAD2, SMAD3, SMAD9, STK11, TRAF6, VEGFA
0.061	BP	regulation of secretion	ADRBK1, AKAP5, ANPEP, ARRB1, BCR, CD40, CREB1, EGF, ERBB3, FES, GDNF, GNAS, GPAM, GRIN2B, GRM7, IL1B, INS, IRS1, JAK2, MAOB, NEUROD1, NR3C1, PDPK1, PPP3CA, PRKCQ, SGK1, SLC9A3R1, TRAF2, TRAF6, WNK4
0.025	BP	protein kinase B signaling cascade	ARRB2, EGFR, IGF1, IGF1R, IL1B, INS, INSR, ITSN1, MERTK, PIK3CA, SLC9A3R1, STK11
0.010	CC	CD40 receptor complex	CD40, CHUK, IKBKB, TRAF2, TRAF6
0.010	CC	cytoplasmic dynein complex	DYNC1H1, DYNC1I1, DYNC1LI1, DYNC1LI2, DYNLL1
0.051	BP	in utero embryonic development	AKT1, AR, CTNNB1, EGFR, ELL, GJA1, GRB2, GRIN2B, HSF1, MAP2K1, MAPK1, MYH9, NASP, NDEL1, PDGFB, PDGFRB, PITPNB, RBBP8, SKIL, SLC8A1, SMAD2, SMAD3, TAB1, TTN, VEGFA
0.029	BP	positive regulation of catabolic process	AKT1, FURIN, GJA1, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, IRS1, NEDD4, PLK1, PRKCD, VCP
0.016	BP	response to antibiotic	ABP1, AOC3, CYP1A1, HSD17B3, JAK2, PLK1, SKIL, SLC1A3
0.020	BP	transcription factor import into nucleus	AKAP5, GSK3B, IL1B, MAPK7, NFKBIA, NFKBIB, NFKBIE, PIK3R1, PRKCQ, SMAD3
0.033	BP	regulation of inflammatory response	A2M, ADRB2, AGER, BCR, CD46, IDO1, IL1B, INS, JAK2, MAPK7, PRKCD, PSMA6, RELA, SMAD3, TNFRSF1A, TNFRSF1B
0.016	MF	kinase activator activity	ABI1, EGF, ERBB3, ITSN1, PIK3CA, STK11, TAB1, TAOK1
0.018	BP	activation of MAPKK activity	BRAF, EGF, JAK2, MAP2K1, MAP3K3, MAP3K7, MAPK1, NRAS, RAF1
0.018	BP	prostate gland development	AR, CTNNB1, CYP19A1, EAF2, ESR1, IGF1, IGF1R, PLAUR, STK11
0.043	BP	regulation of cell adhesion	ABL1, DDR1, ERBB2, ERBB3, FES, GSK3B, GSN, HSD17B12, IL1B, JAK2, KDR, LDB1, MAP2K1, MAPK7, PIK3R1, PPP2CA, PRKCD, PRKCQ, RET, SMAD3, VEGFA
0.012	BP	regulation of metanephros development	EGR1, GDNF, MYC, PDGFB, PDGFRB, RET
0.008	MF	glycerol-3-phosphate O-acyltransferase activity	AGPAT6, AGPAT9, GPAM, GPAT2
0.008	MF	testosterone 17-beta-dehydrogenase (NAD+) activity	HSD17B2, HSD17B3, HSD17B6, HSD17B8
0.016	BP	interleukin-12 production	ARRB2, CD40, IDO1, NFKB1, PRKCD, REL, RELA, TRAF6
0.064	BP	positive regulation of hydrolase activity	ADRBK1, ARRB1, BCR, CD40, CREB1, EGFR, ERBB2, GDI2, GNA11, GNA14, GNA15, GSK3A, GSK3B, HYOU1, JAK2, KIT, MAP2K1, MYC, NDEL1, OPRD1, PDGFRB, PRKCD, RANGAP1, RIPK1, SHC1, SLC9A3R1, SMAD3, SOS1, TRADD, TRAF2, VCP
0.027	BP	response to ethanol	ADH6, ADH7, FYN, GOT2, GRIN2B, GSN, HSD17B3, INSR, MAOB, PEMT, PIK3R1, TH, TNFRSF1A
0.018	BP	regulation of tyrosine phosphorylation of STAT protein	CD40, ERBB4, GHR, IGF1, JAK2, KIT, PPP2CA, SOCS1, TNFRSF1A
0.020	BP	positive regulation of transmembrane transport	AKAP5, EGF, EGFR, ERBB4, IL1B, PDGFB, PDGFRB, PRKCQ, RBPMS, SMAD3

Continued on next page...

Ratio	Type	Description	Genes
0.025	BP	positive regulation of lipid metabolic process	AKT1, CREB1, ERBB4, GPAM, IGF1R, IL1B, INS, IRS1, KIT, PDGFB, PDGFRB, PRKCD
0.025	BP	regulation of lipid biosynthetic process	AKT1, BRCA1, CREB1, GPAM, IGF1R, INS, NFKB1, NR3C1, NR5A1, PDGFB, PRKCD, STK11
0.010	MF	estradiol 17-beta-dehydrogenase activity	HSD17B12, HSD17B2, HSD17B3, HSD17B6, HSD17B8
0.029	BP	cellular response to abiotic stimulus	AURKB, CD40, CYP19A1, EGR1, GRB2, IL1B, MAP3K14, MAPK14, MYC, NEDD4, NFKB1, PIK3R1, SLC12A6, TNFRSF1A
0.080	BP	positive regulation of cell proliferation	ADRB2, AGER, AR, BIRC5, CD40, CDC20, CNBP, CTNNB1, EGF, EGFR, EGR1, ERBB2, ERBB4, ESR1, GPAM, HDAC1, HDAC2, HTR4, IGF1, IGF1R, IL1B, INS, INSR, IRS1, JAK2, KDR, MAPK1, MYC, NRAS, PDGFB, PDGFRB, POU1F1, PRKCQ, RELA, RIPK2, SHC1, ST8SIA1, TRAF6, VEGFA
0.039	BP	response to lipopolysaccharide	ADH5, BCR, CYP1A1, GCH1, HSF1, IDO1, IL1B, JAK2, MAOB, MAPK1, MAPK14, NFKB2, NFKBIA, RELA, RIPK2, SOCS1, TH, TNFRSF1A, TRAF6
0.033	BP	branching morphogenesis of a tube	AR, CTNNB1, DDR1, EGF, ESR1, GDNF, IGF1, KDR, MET, MYC, PGR, PXN, SLC12A2, SRC, TCF21, VEGFA
0.020	BP	T cell costimulation	AKT1, CSK, FYN, GRB2, MAP3K14, MAP3K8, PDPK1, PIK3CA, PIK3R1, SRC
0.020	BP	lymphocyte costimulation	AKT1, CSK, FYN, GRB2, MAP3K14, MAP3K8, PDPK1, PIK3CA, PIK3R1, SRC
0.020	BP	negative regulation of binding	ADRB2, ARRB2, CYP2D6, GSK3B, JAK2, MYC, NFKBIA, PRKCD, RSF1, ZNF675
0.049	BP	negative regulation of protein metabolic process	A2M, ARRB1, ARRB2, BRCA1, BUB1B, BUB3, CD46, CDC20, EGFR, FURIN, FYN, INS, INSR, MAD2L1, MET, NFKB1, PIK3R1, PPP2CA, PRKCD, PSMA6, PSMD6, RELA, SMAD3, SOCS1
0.031	BP	regulation of stress-activated protein kinase signaling cascade	AKT1, DVL3, EPHB1, IGF1R, IL1B, MAP2K1, MAP3K7, MAPK1, MYC, RIPK1, RIPK2, TAOK1, TRAF2, TRAF6, ZNF675
0.044	CC	vesicular fraction	ADRB2, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, FYN, GUSB, HSD17B2, HSD17B3, HSD17B6, HSD3B1, HSD3B2, IGF1R, IKBKB, INSR, IRS1, PAFAH1B1, PPP3CA, UGT2B17, VCP
0.008	CC	beta-catenin destruction complex	CACYBP, GSK3A, GSK3B, SIAH1
0.012	BP	tongue development	CTNNB1, ERBB2, ERBB3, HDAC1, HDAC2, HOXC13
0.062	CC	endosome	ACPP, ADRB2, BACE1, CLIP1, DGKH, EGFR, EPHB1, ERBB2, FYN, GJA1, GRB2, HSD17B6, HTR4, IKBKE, INS, INSR, JAK2, KDR, LAMP2, MAP2K1, MAP3K7, MAPK1, PIGR, RET, RIPK1, SHC1, SIAH1, TAB1, TAB2, TBK1, TRAF6
0.020	MF	protein phosphatase binding	AKAP5, CSK, CTNNB1, EGFR, ERBB2, GHR, GRB2, INSR, PIK3R1, VCP
0.010	BP	androgen biosynthetic process	HSD17B2, HSD17B3, HSD17B6, HSD3B1, HSD3B2
0.061	BP	muscle structure development	ABL1, ADRB2, AKT1, CACYBP, CENPF, CTNNB1, ERBB2, ERBB3, ERBB4, FHL1, GJA1, GSK3A, GSK3B, IGF1, MAPK14, MET, MYH9, NOS1, NRAS, PDGFRB, PIK3R1, PITX1, PPP3CA, SKIL, SLC8A1, SMAD3, SMARCA2, TCF21, TTN, VEGFA
0.022	MF	heat shock protein binding	CDC37, DNAJA1, ERBB2, FKBP5, KDR, NASP, NFKB1, NFKBIA, NR3C1, SLC8A1, STIP1
0.016	MF	non-membrane spanning protein tyrosine kinase activity	ABL1, CSK, FES, FYN, JAK2, PRKCD, RIPK2, SRC
0.025	BP	carbohydrate homeostasis	AKT1, ARRB1, CYP19A1, FOXO3, INS, INSR, IRS1, MET, NEUROD1, PPP3CA, STK11, TH
0.025	BP	glucose homeostasis	AKT1, ARRB1, CYP19A1, FOXO3, INS, INSR, IRS1, MET, NEUROD1, PPP3CA, STK11, TH
0.014	BP	microtubule anchoring	AURKB, BUB3, CASC5, CLASP1, CLASP2, NDC80, SGOL1
0.014	BP	mitotic cell cycle spindle assembly checkpoint	BUB1, BUB1B, BUB3, CDC20, DYNC1LI1, MAD1L1, MAD2L1
0.012	BP	chromosome localization	BIRC5, CCDC99, CENPE, KIF18A, NDE1, ZW10
0.012	BP	establishment of chromosome localization	BIRC5, CCDC99, CENPE, KIF18A, NDE1, ZW10
0.012	BP	regulation of chromosome segregation	AURKB, BUB1, BUB3, CTNNB1, KIF2B, KIF2C
0.090	BP	anatomical structure formation involved in morphogenesis	ABI1, ADAMTS1, ANPEP, AR, B9D2, C1GALT1, CASC5, CTNNB1, DEAF1, DVL3, DYNC2H1, EGF, EPHB1, ERBB2, GDNF, GJA1, GRB2, GSK3B, HDAC1, HDAC2, IL1B, KDR, LDB1, LMO4, MAP3K7, MAPK14, MAPK7, MEIS1, MYH9, NOS1, PAFAH1B1, PDGFRB, PIK3CA, RET, SHC1, SKIL, SLC12A6, SMAD2, SMAD3, TCF21, TNFRSF1A, TRAF6, TTN, VEGFA
0.068	BP	regulation of growth	ADRB2, AGPAT6, AKT1, AR, CREB1, DDR1, EAF2, ERBB2, ERBB4, FHL1, GHR, GPAM, GSK3A, HSF1, IGF1, INS, INSR, MAPT, NDEL1, PAFAH1B1, PIK3CA, POU1F1, PPP2CA, PRKCQ, RBBP7, RUVBL1, SFN, SGK1, SHC1, SMAD3, SMARCA2, SOCS1, STK11
0.051	BP	regulation of cytokine production	ARRB1, ARRB2, CD40, CREB1, ELF1, FURIN, GPAM, HSF1, IDO1, IKBKE, IL1B, INS, JAK2, MAP3K7, NFKB1, PRKCQ, REL, RELA, RIPK1, RIPK2, SMAD3, TBK1, TNFRSF1A, TRAF2, TRAF6
0.025	BP	pallium development	AKAP5, CYP19A1, EGFR, GRIN2B, GSK3B, HDAC2, HSD17B3, NDE1, NDEL1, NEUROD1, PAFAH1B1, TH
0.041	BP	epithelial tube morphogenesis	AR, CTNNB1, DDR1, DEAF1, DVL3, ESR1, GDNF, GJA1, LMO4, MAP3K7, MYC, NR3C1, PGR, RET, SLC12A2, SMAD3, SRC, TCF21, TRAF6, VEGFA
0.008	BP	SRP-dependent cotranslational protein targeting to membrane	RPL3, RPLP1, RPS27, RPS3A
0.035	MF	G-protein-coupled receptor binding	ADRB3, ADRBK1, AKAP5, ARRB1, ARRB2, DVL3, ESR1, GNA11, GNA14, GNA15, GNAL, GNAS, GRIN2B, NEDD4, SLC9A3R1, USP20, USP33
0.018	BP	mammary gland morphogenesis	AR, DDR1, ERBB2, ERBB3, ESR1, NR3C1, PGR, SLC12A2, SRC
0.020	MF	microtubule motor activity	CENPE, DYNC1H1, DYNC1I1, DYNC1I2, DYNC2H1, KIF18A, KIF2A, KIF2B, KIF2C, KIF3B
0.043	BP	muscle cell differentiation	ABL1, AKT1, CACYBP, CTNNB1, ERBB2, GSK3A, GSK3B, IGF1, MAPK14, MET, MYH9, NOS1, NRAS, PDGFRB, PIK3R1, PITX1, PPP3CA, SLC8A1, SMARCA2, TTN, VEGFA
0.010	BP	positive regulation of glycogen biosynthetic process	AKT1, IGF1, INS, INSR, IRS1
0.012	MF	aromatase activity	CYP19A1, CYP1A1, CYP2D6, CYP3A43, CYP3A5, CYP3A7
0.037	BP	rhythmic process	ADAMTS1, ADRBK1, CENPI, CREB1, DDC, ERBB2, ERBB3, ESR1, FOXO3, GRIN2B, KDR, NR3C1, NR5A1, PGR, PHLPP1, TH, TPH2, VEGFA
0.041	MF	chromatin binding	APEX1, APITD1, AR, CCNT1, CENPA, CTNNB1, ESR1, HDAC2, LDB1, MEIS1, NEUROD1, NR3C1, NR5A1, NUP62, POU1F1, RELA, SKIL, SMAD2, SMAD3, SMARCA5
0.032	CC	cell cortex	AKAP12, CLASP1, CLASP2, CTNNB1, DVL3, EXOC1, EZR, GRM7, MAP2K1, MAPRE1, MYH9, NEDD4, PAFAH1B1, PXN, TRAF2, TRAF6
0.008	MF	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced pteridine as one donor, and incorporation of one atom of oxygen	PAH, TH, TPH1, TPH2
0.010	CC	NuRD complex	HDAC1, HDAC2, MTA1, RBBP4, RBBP7
0.010	MF	ionotropic glutamate receptor binding	ADRB2, CTNNB1, GNAS, GRIN2B, GSK3B
0.010	MF	proline-rich region binding	ABL1, CSK, GHR, ITSN1, NEDD4
0.014	BP	activation of pro-apoptotic gene products	AKT1, DYNLL1, MYC, RIPK1, SMAD3, TRADD, TRAF2
0.014	BP	negative regulation of protein catabolic process	EGFR, FURIN, FYN, INS, MAD2L1, RELA, SMAD3
0.042	CC	microsome	ADRB2, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, FYN, GUSB, HSD17B2, HSD17B3, HSD17B6, HSD3B1, HSD3B2, IGF1R, IKBKB, INSR, IRS1, PPP3CA, UGT2B17, VCP
0.093	CC	vesicle	A2M, ACPP, ADAMTS1, ANPEP, ARRB1, ARRB2, BACE1, CASC5, CD46, CLIP1, CYP19A1, DDC, DGKD, DYNC1I1, DYNC1I2, EGF, EGFR, FES, FURIN, GANAB, GCH1, GJA1, GNAS, GRB2, GRIN2B, HSP90AA1, IGF1, IL1B, INS, ITSN1, KDR, LAMP2, LTF, OPRD1, OTOF, PDGFB, PDGFRB, PDPK1, PIGR, PRDX6, SEC13, SEC24D, SOCS1, TH, TYR, VEGFA
0.022	MF	growth factor receptor binding	EGF, ERBB4, GRB2, IL1B, JAK2, KL, PDGFB, PDGFRB, SHC1, SLC9A3R1, VEGFA
0.014	MF	oxygen binding	CYP19A1, CYP1A1, CYP3A4, CYP3A5, CYP3A7, IDO1, TH
0.014	BP	regulation of sodium ion transport	ADRB2, AKT1, NEDD4, NEDD4L, NOS1, SLC8A1, SLC9A3R1
0.018	BP	centrosome organization	BRCA1, CKAP5, CTNNB1, DYNC1LI1, KIF3B, NDE1, PLK1, SGOL1, XPO1
0.018	BP	regulation of transcription factor import into nucleus	AKAP5, GSK3B, IL1B, MAPK7, NFKBIA, NFKBIB, NFKBIE, PRKCQ, SMAD3
0.008	BP	estrogen biosynthetic process	CYP19A1, HSD17B2, HSD17B8, HSD3B1
0.008	BP	kinetochore organization	CENPA, CENPE, CENPH, MIS12
0.008	BP	protein localization to kinetochore	AURKB, BUB1B, CCDC99, ZW10
0.029	BP	positive regulation of growth	ADRB2, AKT1, CREB1, ERBB2, GHR, GPAM, HSF1, INS, INSR, MAPT, NDEL1, PAFAH1B1, POU1F1, SFN
0.006	BP	activation of signaling protein activity involved in unfolded protein response	GSK3A, HYOU1, SHC1
0.014	BP	tumor necrosis factor-mediated signaling pathway	JAK2, RIPK1, TNFRSF1A, TNFRSF1B, TRADD, TRAF2, ZNF675
0.025	BP	response to estradiol stimulus	BRCA1, CTNNB1, CYP19A1, ESR1, GHR, IL1B, INSR, PDGFB, PIK3R1, SOCS1, TH, TNFRSF1A
0.069	CC	cell projection part	ABI1, ADRB2, ADRBK1, AKAP5, ARHGEF2, B9D2, CAMK2N1, CLASP2, CTNNB1, CYP19A1, DYNC2H1, ERBB4, ESR1, EZR, GOT1, GRIN2B, GRM7, GSK3B, MAP2K1, MAPK1, MAPRE1, MAPT, MBP, MET, NOS1, NR3C1, OPRD1, PAFAH1B1, PEMT, SLC1A3, SLC8A1, SLC9A3R1, TH, TUBB4A
0.090	BP	organ morphogenesis	ACAN, ADAMTS1, AR, BCR, BRAF, CHUK, CTNNB1, DDR1, DVL3, EPHB1, ERBB3, ESR1, FHL1, GDNF, GHR, GJA1, GNAS, GSK3A, GSK3B, HDAC1, HDAC2, HOXC13, HOXC9, IGF1, IGF1R, INSR, MAPK1, MEIS1, MET, MYC, NEUROD1, PAFAH1B1, PDGFRB, RELA, SHC1, SMAD2, SMAD3, SOCS1, TAB1, TCF21, TH, TRAF6, TTN, VEGFA
0.024	MF	ubiquitin protein ligase binding	ARRB1, ARRB2, BRCA1, ERBB2, GSK3B, NFKBIA, PA2G4, PIK3R1, RELA, SMAD2, SMAD3, ZNF675
0.043	BP	developmental growth	ADRB2, AKT1, AR, CYP19A1, ERBB4, ESR1, FOXO3, GJA1, GSK3A, GSN, IGF1, INSR, MAPT, NDEL1, PAFAH1B1, PLAUR, PRKCQ, SHBG, SLC12A2, SMAD2, SMAD3
0.029	BP	response to glucocorticoid stimulus	GHR, GOT1, HNMT, HSD17B3, IL1B, INSR, MAOB, MAP2K1, NR3C1, PIK3R1, SHC1, TAT, TH, TPH2
0.016	BP	hippocampus development	AKAP5, CYP19A1, GRIN2B, GSK3B, HDAC2, HSD17B3, NEUROD1, PAFAH1B1

Continued on next page...

Ratio	Type	Description	Genes
0.185	CC	organelle membrane	ABL1, ACPP, AGK, AGPAT6, AGPAT9, AHCTF1, ANPEP, ARRB1, ATP5D, B3GALT4, BACE1, C1GALT1, C1GALT1C1, CD46, CDS1, CDS2, CLIP1, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, DGKH, EGFR, ELOVL5, EPHB1, ERBB2, FURIN, FUT1, FUT2, GALNTL4, GCH1, GCNT1, GCNT3, GCNT4, GJA1, GNAS, GOT2, GPAM, GPAT2, GRB2, HSD17B12, HSD17B2, HSD17B3, HSD17B6, HSD3B1, HSD3B2, IKBKE, IL4I1, INSR, LAMP2, LETM1, MAOA, MAOB, MAP3K7, NRAS, NUP62, NUP85, OTOF, PAFAH1B1, PDGFB, PEMT, PIGR, PLAUR, PPP1CC, RAF1, RANGAP1, RET, RIPK1, SEC13, SEC24D, SGK1, SHC1, SLC1A3, SMAD3, SRC, ST3GAL1, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5, TAB1, TAB2, TBK1, TH, TRAF6, TYR, UBQLN4, UGT2B17, ZW10
0.027	BP	transforming growth factor beta receptor signaling pathway	ARRB2, CREB1, FURIN, MAP3K7, NR3C1, PDGFB, PDPK1, SKIL, SMAD2, SMAD3, SMAD9, STK11, TAB1
0.010	MF	Hsp90 protein binding	CDC37, ERBB2, KDR, NASP, NR3C1
0.012	BP	branching involved in mammary gland duct morphogenesis	AR, DDR1, ESR1, PGR, SLC12A2, SRC
0.012	BP	positive regulation of reactive oxygen species metabolic process	GRB2, MAPK14, PDGFB, PDGFRB, PRKCD, RIPK1
0.053	BP	heart development	ADAMTS1, ADRBK1, CACYBP, CTNNB1, DVL3, ERBB2, ERBB3, ERBB4, GJA1, GNA11, GSK3A, INSR, LMO4, PDGFB, PDGFRB, RAF1, SHC1, SLC8A1, SMAD2, SMAD3, TAB1, TAB2, TH, TTN, VCAN, VEGFA
0.018	BP	phenol-containing compound metabolic process	AOC2, DDC, GCH1, GCNT4, HSD17B3, MAOA, MAOB, PAH, TH
0.018	BP	response to interleukin-1	EGR1, GHR, HNMT, NFKB1, RELA, RIPK2, SRC, TRAF6, ZNF675
0.043	BP	organophosphate metabolic process	AGPAT6, AGPAT9, CDS1, CDS2, DGKE, GNA15, GPAM, GPAT2, GSK3A, MBOAT2, PAFAH1B1, PDGFB, PDGFRB, PEMT, PIK3CA, PIK3R1, PISD, PLAUR, POU1F1, PRDX6, PRKCD
0.016	BP	dicarboxylic acid metabolic process	CS, CYP19A1, GHR, GOT1, GOT2, PAH, TAT, TH
0.043	MF	protein heterodimerization activity	BIRC5, BRAF, DGKD, DVL3, EGFR, ERBB2, ERBB3, GRIN2B, IKBKB, MAPK6, MEIS1, MET, MYC, NEUROD1, NR3C1, PDGFB, PPP3CA, RAF1, SDCBP2, TYR, VEGFA
0.020	BP	positive regulation of ERK1 and ERK2 cascade	ARRB1, ARRB2, BRAF, ERBB4, ESR1, IL1B, KDR, PDGFB, PDGFRB, RIPK2
0.047	BP	blood circulation	ADH5, ADRB2, ADRB3, ADRBK1, GCH1, GJA1, GSK3A, INS, JAK2, MAP2K1, NOS1, NR3C1, PDGFB, PIK3CA, PIK3R1, PRKCQ, S100A1, SGK1, SHC1, SLC8A1, SRC, TH, VEGFA
0.008	BP	activation of phospholipase C activity by dopamine receptor signaling pathway	GNA11, GNA14, GNA15, SLC9A3R1
0.029	MF	double-stranded DNA binding	APITD1, CREB1, CTNNB1, DEAF1, EGFR, EGR1, FOXO3, MYC, NEUROD1, NFKB1, NR3C1, NR5A1, SMAD2, SMAD3
0.010	BP	attachment of spindle microtubules to kinetochore	AURKB, BUB3, CASC5, NDC80, SGOL1
0.010	BP	metanephric glomerulus development	EGR1, PDGFB, PDGFRB, RET, TCF21
0.010	BP	positive regulation of tyrosine phosphorylation of Stat5 protein	ERBB4, GHR, IGF1, JAK2, KIT
0.014	BP	regulation of interleukin-12 production	ARRB2, CD40, IDO1, NFKB1, REL, RELA, TRAF6
0.012	BP	regulation of stress-activated MAPK cascade	IL1B, MAP2K1, MAPK1, MYC, RIPK2, TAOK1
0.006	MF	IkappaB kinase activity	CHUK, IKBKB, IKBKE
0.006	MF	L-phenylalanine:2-oxoglutarate aminotransferase activity	GOT1, GOT2, TAT
0.006	MF	beta-1,3-galactosyl-O-glycosyl-glycoprotein beta-1,6-N-acetylglucosaminyltransferase activity	GCNT1, GCNT3, GCNT4
0.006	MF	galactoside 2-alpha-L-fucosyltransferase activity	CLASP2, FUT1, FUT2
0.014	BP	regulation of RNA stability	APEX1, CARHSP1, GDNF, MAPK14, PABPC1, TNFRSF1B, VEGFA
0.066	BP	GTP catabolic process	ARRB1, BCR, CD40, DGKI, ERBB2, GCH1, GDI2, GNA11, GNA14, GNA15, GNAL, GNAS, GSK3B, MAP2K1, NDEL1, NRAS, PAFAH1B1, RANGAP1, SOS1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1
0.031	BP	JNK cascade	AKT1, DVL3, EPHB1, IGF1R, IKBKG, IL1B, MAP3K7, RIPK1, RIPK2, TAB1, TAB2, TAOK1, TRAF2, TRAF6, ZNF675
0.043	BP	regulation of cell morphogenesis	AKAP5, CTNNB1, EZR, FES, FYN, GDNF, GSK3B, KDR, MAPT, MBP, MET, MYH9, NDEL1, NEDD4, PAFAH1B1, PPP2CA, SKIL, SMAD2, SMAD3, STK11, VEGFA
0.033	MF	electron carrier activity	ADH5, ADH6, AOC2, CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, HSD17B6, IDO1, IL4I1, MAOA, MAOB, UGDH
0.012	BP	positive regulation of Ras protein signal transduction	ARRB1, DGKI, ERBB2, IGF1, MAP2K1, NRAS
0.012	BP	regulation of phosphatidylinositol 3-kinase activity	ERBB4, IRS1, KIT, PDGFB, PDGFRB, PIK3R1
0.020	BP	hair follicle development	AKT1, CTNNB1, EGFR, HDAC1, HDAC2, HOXC13, LDB1, LDB2, RELA, TRADD
0.010	BP	regulation of protein export from nucleus	GSK3B, IL1B, RANGAP1, SFN, XPO1
0.068	BP	negative regulation of catalytic activity	ABL1, AKT1, ARRB1, BIRC5, BUB1B, BUB3, CASC5, CD46, CDC20, DGKZ, ELL, GNAL, GRM7, GSK3A, GSK3B, IGF1R, IL1B, INS, MAD2L1, NFKB1, NOS1, NUP62, OPRD1, PDPK1, PLK1, PPP2CA, PRKCD, PSMA6, PSMD6, RAF1, SERPINA3, SFN, ZNF675
0.008	CC	IkappaB kinase complex	CHUK, IKBKB, IKBKG, MAP3K7
0.018	BP	regulation of DNA binding	EGF, HJURP, IGF1, JAK2, NEUROD1, NFKBIA, RSF1, TRAF6, ZNF675
0.018	BP	regulation of protein kinase B signaling cascade	ARRB2, EGFR, IGF1, IGF1R, INS, INSR, ITSN1, SLC9A3R1, STK11
0.018	BP	regulation of smooth muscle cell proliferation	AGER, CTNNB1, IGF1, PDGFB, PDGFRB, PIK3R1, SHC1, TRAF6, VEGFA
0.008	BP	NFAT protein import into nucleus	AKAP5, GSK3B, MAPK7, PIK3R1
0.020	BP	cellular response to inorganic substance	ABP1, CACYBP, GRIN2B, GSK3A, GSN, HSD17B2, MET, NR3C1, TH, TPH2
0.024	CC	extrinsic to membrane	ARRB1, CTNNB1, EZR, FES, GFRA1, GHR, GNA11, GNA14, GNA15, GNAL, GNAS, PLAUR
0.008	BP	interleukin-12 biosynthetic process	NFKB1, REL, RELA, TRAF6
0.008	BP	metanephric glomerulus vasculature development	EGR1, PDGFB, PDGFRB, TCF21
0.008	BP	regulation of calcium ion import	CTNNB1, EGF, PDGFB, PDGFRB
0.008	BP	regulation of interleukin-12 biosynthetic process	NFKB1, REL, RELA, TRAF6
0.008	BP	serotonin metabolic process	DDC, MAOA, TPH1, TPH2
0.008	MF	adrenergic receptor binding	ADRB3, ADRBK1, NEDD4, SLC9A3R1
0.008	MF	nucleocytoplasmic transporter activity	NUP107, NUP133, NUP160, NUP62
0.035	MF	iron ion binding	CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, IDO1, IDO2, JAK2, LTF, NOS1, PAH, SRC, TH, TPH1, TPH2
0.076	BP	synaptic transmission	ADRB2, AKAP5, ARRB2, BRAF, CAMKK1, CBLN2, CDC20, CREB1, CTNNB1, CYP19A1, DDC, EGR1, EPHB1, ERBB4, GDNF, GNAL, GRIN2B, GRM7, GSK3B, ITSN1, KCNJ1, KCNJ3, KCNJ6, KCNJ9, MAOA, MAPK1, MBP, NOS1, NRAS, OTOF, PAFAH1B1, PAH, PDPK1, PPP3CA, RAF1, SLC1A3, TH
0.029	BP	positive regulation of cell development	AKAP5, CTNNB1, GDNF, HDAC2, MAPT, MET, NDEL1, PAFAH1B1, RELA, SKIL, SMAD2, SMAD3, STK11, VEGFA
0.006	BP	alkaloid catabolic process	CYP2D6, CYP3A4, CYP3A5
0.006	BP	fungiform papilla formation	CTNNB1, HDAC1, HDAC2
0.006	BP	fungiform papilla morphogenesis	CTNNB1, HDAC1, HDAC2
0.006	BP	isoquinoline alkaloid metabolic process	CYP2D6, DDC, TH
0.006	BP	serotonin biosynthetic process	DDC, TPH1, TPH2
0.041	MF	GTPase activity	GNA11, GNA14, GNA15, GNAL, GNAS, NRAS, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, TUFM
0.037	BP	epithelial cell proliferation	AR, CHUK, CTNNB1, DEAF1, EAF2, EGFR, ERBB2, ERBB4, ESR1, IGF1, KDR, MAPK1, MYC, PDGFB, PGR, SMAD3, STK11, VEGFA
0.025	BP	response to temperature stimulus	ADRB3, AKT1, DNAJA1, EPHB1, HSF1, IL1B, NFKBIA, NOS1, PRKCQ, RBBP7, ST8SIA1, VEGFA
0.033	BP	striated muscle cell differentiation	AKT1, CACYBP, ERBB2, GSK3A, GSK3B, IGF1, MET, MYH9, NOS1, NRAS, PDGFRB, PIK3R1, PPP3CA, SLC8A1, TTN, VEGFA
0.016	BP	regulation of anti-apoptosis	AKT1, APEX1, ARRB1, CTNNB1, ERBB4, IGF1R, PIK3R1, RIPK1
0.014	BP	negative regulation of ion transport	ADRB2, AKAP5, NEDD4, NEDD4L, NOS1, OPRD1, SLC9A3R1
0.029	BP	mesenchyme development	CTNNB1, ERBB3, ERBB4, GDNF, GSK3B, HNRNPAB, MYC, PLAUR, PPP2CA, RET, S100A4, SMAD2, SMAD3, TCF21
0.117	BP	negative regulation of cellular metabolic process	AKT1, ARRB1, ARRB2, AURKB, BIRC5, BRCA1, BUB1B, BUB3, CDC20, CDK9, CREB1, CTNNB1, CYP2D6, DYNLL1, EGR1, FOXO3, FURIN, GRB10, GRM7, GSK3A, GSK3B, HDAC1, HDAC2, INS, INSR, LDB1, MAD2L1, MAGEA1, MET, MYC, NEDD4, NFKB1, PA2G4, PABPC1, PDGFB, PIK3R1, PLK1, PPP2CA, PRKCD, PSMA6, PSMD6, RBBP7, RBBP8, RELA, RSF1, S100A1, SKIL, SMAD2, SMAD3, SMARCA2, SMARCA5, SOCS1, TCF21, TRAF6, XPO1, YWHAQ, ZNF675
0.044	CC	dendrite	ADRB2, ADRBK1, AKAP5, AR, ARHGEF2, CAMK2N1, CTNNB1, CYP19A1, EPHB1, ERBB4, GRIN2B, GRM7, GSK3B, KCNJ6, MAP2K1, MAPK1, MET, NOS1, NR3C1, SLC1A3, SLC8A1, TH
0.010	MF	protein phosphorylated amino acid binding	CBL, GRB2, MAPK1, NEDD4, SHC1
0.010	MF	sialyltransferase activity	ST3GAL1, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5
0.018	BP	negative regulation of defense response	A2M, ADRB2, ARRB2, BCR, INS, MAPK7, PRKCD, SMAD3, TNFRSF1B
0.040	CC	neuronal cell body	ADRB2, AGER, AKAP5, ARHGEF2, CAMK2N1, CYP19A1, DDC, ESR1, GHR, GSK3B, KCNJ6, MAP2K1, MAPK1, MBP, MET, PAFAH1B1, PPP5C, SLC1A3, TH, TUBB4A

Continued on next page...

Ratio	Type	Description	Genes
0.027	BP	myeloid leukocyte differentiation	CHUK, CTNNB1, CYP19A1, GNAS, KIT, MAPK14, MYC, MYH9, PIK3R1, RELB, TRAF6, VEGFA, ZNF675
0.014	BP	catecholamine metabolic process	AOC2, DDC, GCH1, MAOA, MAOB, PAH, TH
0.014	BP	positive regulation of smooth muscle cell proliferation	AGER, IGF1, PDGFB, PDGFRB, SHC1, TRAF6, VEGFA
0.014	BP	response to activity	AKAP5, GPAM, HSD17B3, INSR, NR3C1, TH, TPH2
0.012	BP	aromatic compound catabolic process	AFMID, CYP1A1, IDO1, IDO2, PAH, TAT
0.014	MF	RNA polymerase II transcription factor binding	CREB1, GSK3B, LDB1, NEUROD1, POU1F1, RBBP8, SMAD3
0.018	BP	cellular response to metal ion	ABP1, CACYBP, GRIN2B, GSK3A, GSN, HSD17B2, NR3C1, TH, TPH2
0.031	BP	regulation of cell morphogenesis involved in differentiation	AKAP5, CTNNB1, GDNF, GSK3B, MAPT, MBP, MET, NDEL1, NEDD4, PAFAH1B1, PPP2CA, SKIL, SMAD2, SMAD3, STK11
0.008	BP	activation of protein kinase B activity	INS, INSR, PDGFB, PDPK1
0.008	BP	metaphase	CDCA8, CENPE, MAD1L1, MYH9
0.008	BP	mitotic anaphase	MAD1L1, PLK1, SKA1, SKA2
0.008	BP	negative regulation of glycogen metabolic process	GRB10, GSK3A, GSK3B, INS
0.008	BP	positive regulation of interleukin-2 production	MAP3K7, RIPK2, TRAF2, TRAF6
0.008	BP	positive regulation of nitric-oxide synthase activity	AKT1, ESR1, GCH1, INS
0.008	BP	response to herbicide	CYP19A1, CYP1A1, HSD17B3, TH
0.008	BP	tyrosine metabolic process	PAH, TAT, TH, TYR
0.006	CC	chromosome passenger complex	AURKB, BIRC5, CDCA8
0.006	CC	condensed nuclear chromosome kinetochore	CENPA, NDC80, PLK1
0.010	BP	aromatic amino acid family catabolic process	AFMID, IDO1, IDO2, PAH, TAT
0.006	MF	G-protein activated inward rectifier potassium channel activity	KCNJ3, KCNJ6, KCNJ9
0.006	MF	adenylate cyclase binding	ADRB2, AKAP12, AKAP5
0.014	BP	positive regulation of anti-apoptosis	AKT1, APEX1, CTNNB1, ERBB4, IGF1R, PIK3R1, RIPK1
0.014	BP	vascular endothelial growth factor receptor signaling pathway	GRB10, IL1B, KDR, MAPK14, NEDD4, PDGFRB, VEGFA
0.012	CC	dendritic shaft	ADRBK1, AKAP5, ARHGEF2, CTNNB1, GRM7, GSK3B
0.012	MF	SH2 domain binding	GHR, INSR, IRS1, JAK2, NUP62, SRC
0.016	BP	positive regulation of protein import into nucleus	AKAP5, EGF, EGFR, ERBB4, IL1B, PRKCQ, RBPMS, SMAD3
0.016	BP	protein heterooligomerization	GCH1, GRB2, IGF1R, INSR, IRS1, PPP2CA, SKIL, STK11
0.059	BP	regulation of cellular catabolic process	ABL1, AKT1, ARRB1, BCR, CD40, DGKI, EGF, ERBB2, FURIN, GDI2, GSK3A, GSK3B, IGF1, IL1B, INS, INSR, IRS1, MAD2L1, MAP2K1, MAPT, NDEL1, PABPC1, PAFAH1B1, PLK1, PRKCD, RANGAP1, SOS1, UBQLN4, VCP
0.014	BP	cytoskeleton-dependent intracellular transport	DYNC1I1, KIF3B, MAP2K1, MAPT, NDEL1, PAFAH1B1, TUBB
0.045	BP	response to radiation	ACAN, AKT1, ARRB1, AURKB, BRCA1, CDS1, CYP19A1, EGFR, EGR1, GRB2, IL1B, KIT, MAPK14, MYC, NEDD4, NR3C1, NRAS, PIK3R1, RELA, SLC1A3, STK11, TH
0.078	BP	secretion by cell	A2M, ADRBK1, AKAP5, ARRB1, BCR, CD40, CREB1, EGF, EXOC1, FES, FURIN, GDNF, GNAS, GPAM, GRIN2B, GRM7, IGF1, IL1B, INS, IRS1, JAK2, LAMP2, MAOA, MAOB, MERTK, NEUROD1, NR3C1, OTOF, PDGFB, PDPK1, PPP3CA, PRKCQ, SMAD2, TRAF2, TRAF6, TTN, TUBA4A, VEGFA
0.083	CC	membrane-bounded vesicle	A2M, ACPP, ANPEP, ARRB1, ARRB2, BACE1, CASC5, CD46, CLIP1, CYP19A1, DDC, DGKD, EGF, EGFR, FES, FURIN, GANAB, GJA1, GNAS, GRB2, GRIN2B, HSP90AA1, IGF1, IL1B, INS, ITSN1, KDR, LAMP2, LTF, OTOF, PDGFB, PDGFRB, PDPK1, PIGR, PRDX6, SEC13, SEC24D, SOCS1, TH, TYR, VEGFA
0.016	BP	androgen receptor signaling pathway	AR, BRCA1, CTNNB1, DNAJA1, HDAC1, IGF1, PMEPA1, TCF21
0.012	BP	mitotic spindle organization	AURKB, DYNC1H1, KIF2A, KIF3B, NDC80, SPC25
0.010	MF	G-protein beta/gamma-subunit complex binding	GNA11, GNA14, GNA15, GNAL, GNAS
0.006	BP	metanephric glomerular mesangial cell proliferation involved in metanephros development	EGR1, PDGFB, PDGFRB
0.006	BP	metanephric glomerular mesangium development	EGR1, PDGFB, PDGFRB
0.006	BP	peptidyl-cysteine S-nitrosylation	ADH5, GAPDH, NOS1
0.020	BP	positive regulation of cellular catabolic process	AKT1, FURIN, IGF1, IL1B, INS, INSR, IRS1, PLK1, PRKCD, VCP
0.006	BP	protein nitrosylation	ADH5, GAPDH, NOS1
0.008	BP	I-kappaB phosphorylation	CHUK, IKBKB, IKBKE, MAP3K7
0.008	BP	centromere complex assembly	CENPA, CENPE, HJURP, MIS12
0.008	BP	oxaloacetate metabolic process	CS, GHR, GOT1, GOT2
0.014	BP	terpenoid metabolic process	ADH4, ADH5, ADH7, CYP1A1, CYP2D6, CYP3A4, TNFRSF1A
0.025	BP	phospholipid biosynthetic process	AGPAT6, AGPAT9, CDS1, CDS2, DGKE, GPAM, GPAT2, MBOAT2, PDGFB, PEMT, PISD, PLAUR
0.018	BP	positive regulation of protein catabolic process	AKT1, FURIN, GJA1, GSK3A, GSK3B, IL1B, NEDD4, PLK1, VCP
0.026	CC	dendritic spine	ADRB2, ADRBK1, AKAP5, CAMK2N1, CYP19A1, ERBB4, GRIN2B, GSK3B, MET, NOS1, NR3C1, SLC1A3, SLC8A1
0.012	MF	protein kinase activator activity	ABI1, EGF, ERBB3, PIK3CA, STK11, TAOK1
0.012	BP	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	PABPC1, PPP2CA, RPL3, RPLP1, RPS27, RPS3A
0.055	BP	cellular process involved in reproduction	ADRBK1, AKT1, AR, CASC5, CCNT1, CDK9, CENPI, CTNNB1, DEAF1, EAF2, ELL, ESR1, FOXO3, HDAC1, HSD17B3, KIT, PAFAH1B1, PLAUR, RPL3, RPLP1, RPS27, RPS3A, RSF1, SHBG, STK11, TCEA1, TCF21
0.025	BP	regulation of gene expression, epigenetic	APEX1, BRCA1, GNAS, GSK3A, GSK3B, HDAC2, HEMK1, NR3C1, PIK3CA, SMAD2, SMAD3, SMARCA5
0.010	BP	cellular response to drug	DDC, IL1B, MYC, PPP3CA, TH
0.074	BP	cellular membrane organization	ABL1, ADRB2, ADRBK1, AKT1, AR, ARR3, ARRB1, ARRB2, BCR, CBL, COLEC12, DGKD, EGFR, GDNF, GHR, GJA1, GRB2, GRIN2B, HSP90AA1, ITSN1, LETM1, MAPK1, MEGF10, MERTK, NDEL1, NEDD4, NEDD4L, OTOF, PAFAH1B1, PDPK1, PIK3R1, SEC13, SEC24D, SRC, USP20, USP33
0.024	MF	heme binding	CYP19A1, CYP1A1, CYP2D6, CYP3A4, CYP3A43, CYP3A5, CYP3A7, IDO1, IDO2, JAK2, NOS1, SRC
0.023	BP	response to amine stimulus	ABP1, GNAL, GRIN2B, HNMT, PEMT, PIK3R1, PPP3CA, RELA, SOCS1, TH, TNFRSF1A
0.006	CC	I-kappaB/NF-kappaB complex	NFKB1, NFKB2, NFKBIA
0.006	MF	insulin binding	IGF1R, INSR, PIK3R1
0.006	MF	neurotrophin TRK receptor binding	GRB2, PIK3R1, SHC1
0.006	MF	neurotrophin TRKA receptor binding	GRB2, PIK3R1, SHC1
0.006	MF	transforming growth factor beta receptor, pathway-specific cytoplasmic mediator activity	SMAD2, SMAD3, SMAD9
0.014	MF	ubiquitin binding	KIF18A, NEDD4, NUP62, SMAD3, TAB2, UBQLN4, VCP
0.029	BP	skeletal muscle tissue development	ADRB2, ERBB2, ERBB3, GSK3B, IGF1, MAPK14, MET, MYH9, NOS1, PIK3R1, PITX1, PPP3CA, SKIL, TCF21
0.033	BP	gonad development	ADAMTS1, ADRBK1, AR, CENPI, CYP19A1, ESR1, FANCA, FOXO3, HSD17B3, KDR, KIT, MET, NR5A1, PGR, TCF21, VEGFA
0.008	BP	drug catabolic process	CYP2D6, CYP3A4, CYP3A5, NOS1
0.008	BP	prostate gland growth	AR, CYP19A1, ESR1, IGF1
0.008	BP	vesicle transport along microtubule	DYNC1I1, KIF3B, MAP2K1, PAFAH1B1
0.010	MF	RNA polymerase II activating transcription factor binding	CREB1, LDB1, NEUROD1, POU1F1, SMAD3
0.018	BP	regulation of G-protein coupled receptor protein signaling pathway	ADRB2, ADRBK1, ARRB1, ARRB2, GRK5, GRK6, GSK3A, USP20, USP33
0.022	MF	growth factor binding	A2M, ERBB2, ERBB3, FURIN, GHR, IGF1R, INSR, KDR, KL, PDGFB, PDGFRB
0.031	BP	negative regulation of protein modification process	ARRB1, ARRB2, BRCA1, BUB1B, BUB3, CDC20, INSR, MAD2L1, MET, PPP2CA, PRKCD, PSMA6, PSMD6, SMAD3, SOCS1
0.016	BP	response to lipid	BRCA1, EGR1, GRIN2B, HSD17B3, PDGFB, PIK3R1, SMAD2, STK11
0.027	BP	regulation of proteolysis	AKT1, EGF, FURIN, HDAC2, IL1B, INS, MAD2L1, PIK3R1, PLAUR, PLK1, SERPINA3, UBQLN4, VCP
0.025	BP	regulation of JNK cascade	AKT1, DVL3, EPHB1, IGF1R, IL1B, MAP3K7, RIPK1, RIPK2, TAOK1, TRAF2, TRAF6, ZNF675
0.012	BP	glycosphingolipid metabolic process	KIT, PRKCD, ST6GALNAC5, ST6GALNAC6, ST8SIA1, ST8SIA5
0.025	BP	RNA transport	AHCTF1, CKAP5, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, RANBP2, SEC13, XPO1
0.025	BP	nucleic acid transport	AHCTF1, CKAP5, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, RANBP2, SEC13, XPO1
0.025	BP	response to mechanical stimulus	ACAN, CD40, FYN, GRIN2B, IL1B, MAP3K14, MYC, NFKB1, RELA, SLC12A2, SLC1A3, TNFRSF1A
0.055	BP	viral reproduction	CCNT1, CDK9, ELL, FURIN, FYN, HDAC1, INSR, KPNA1, NEDD4, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, PSMA6, PSMD6, RANBP2, RPL3, RPLP1, RPS27, RPS3A, RSF1, SMAD3, TCEA1, XPO1
0.008	MF	phosphotyrosine binding	CBL, GRB2, MAPK1, SHC1
0.006	BP	hair follicle placode formation	CTNNB1, HDAC1, HDAC2
0.006	BP	negative regulation of sodium ion transport	NEDD4, NEDD4L, SLC9A3R1

Continued on next page...

Ratio	Type	Description	Genes
0.014	BP	acylglycerol biosynthetic process	AGPAT6, AGPAT9, CDS1, ELOVL5, GPAM, GPAT2, HSD17B12
0.014	BP	neutral lipid biosynthetic process	AGPAT6, AGPAT9, CDS1, ELOVL5, GPAM, GPAT2, HSD17B12
0.083	CC	cytoplasmic vesicle	A2M, ACPP, ADAMTS1, ARRB1, ARRB2, BACE1, CASC5, CD46, CLIP1, CYP19A1, DDC, DGKD, EGF, EGFR, FES, FURIN, GANAB, GCH1, GJA1, GNAS, GRIN2B, HSP90AA1, IGF1, IL1B, INS, ITSN1, KDR, LAMP2, LTF, OTOF, PDGFB, PDGFRB, PDPK1, PIGR, PRDX6, SEC13, SEC24D, SOCS1, TH, TYR, VEGFA
0.014	CC	extrinsic to internal side of plasma membrane	ARRB1, FES, GNA11, GNA14, GNA15, GNAL, GNAS
0.025	BP	regeneration	DDR1, ERBB4, GJA1, GSN, IGF1, JAK2, NDEL1, PLAUR, PRKCQ, SHC1, SOCS1, VCAN
0.010	BP	negative regulation of cell-cell adhesion	JAK2, MAP2K1, MAPK7, PIK3R1, PRKCD
0.010	BP	regulation of transcription elongation, DNA-dependent	ELL, LDB1, MAP2K1, TCEA1, TCEA2
0.010	BP	sex determination	AR, IGF1R, INSR, NR5A1, TCF21
0.008	BP	catechol biosynthetic process	DDC, GCH1, PAH, TH
0.008	BP	catecholamine biosynthetic process	DDC, GCH1, PAH, TH
0.008	BP	positive regulation of histone acetylation	ARRB1, BRCA1, IL1B, NOS1
0.023	BP	mRNA transport	AHCTF1, NUP107, NUP133, NUP160, NUP37, NUP43, NUP62, NUP85, RANBP2, SEC13, XPO1
0.020	BP	female gonad development	ADAMTS1, ADRBK1, CENPI, ESR1, FANCA, FOXO3, KDR, NR5A1, PGR, VEGFA
0.020	BP	ovulation cycle process	ADAMTS1, ADRBK1, CENPI, ERBB2, ESR1, FOXO3, KDR, NR5A1, PGR, VEGFA
0.012	CC	heterotrimeric G-protein complex	ARRB1, GNA11, GNA14, GNA15, GNAL, GNAS
0.047	MF	GTP binding	GCH1, GNA11, GNA14, GNA15, GNAL, GNAS, INSR, NRAS, OLA1, TUBA3D, TUBA3E, TUBA4A, TUBB, TUBB1, TUBB2A, TUBB2B, TUBB3, TUBB4A, TUBB4B, TUBB6, TUBB8, TUBG1, TUFM
0.079	CC	cytoplasmic membrane-bounded vesicle	A2M, ACPP, ARRB1, ARRB2, BACE1, CASC5, CD46, CLIP1, CYP19A1, DDC, DGKD, EGF, EGFR, FES, FURIN, GANAB, GJA1, GNAS, GRIN2B, HSP90AA1, IGF1, IL1B, INS, ITSN1, KDR, LAMP2, LTF, OTOF, PDGFB, PDGFRB, PDPK1, PIGR, PRDX6, SEC13, SEC24D, SOCS1, TH, TYR, VEGFA
0.014	BP	positive regulation of protein kinase B signaling cascade	ARRB2, EGFR, IGF1, IGF1R, INS, INSR, ITSN1
0.023	BP	G-protein signaling, coupled to cAMP nucleotide second messenger	ADRB2, ADRB3, GNA11, GNA14, GNA15, GNAL, GNAS, GRK5, HTR4, OPRD1, SLC9A3R1
0.023	BP	negative regulation of secretion	ANPEP, BCR, EGF, ERBB3, GRM7, IL1B, INS, IRS1, MAOB, PPP3CA, WNK4
0.025	BP	mesenchymal cell differentiation	CTNNB1, ERBB4, GDNF, GSK3B, HNRNPAB, PLAUR, PPP2CA, RET, S100A4, SMAD2, SMAD3, TCF21
0.012	BP	lipopolysaccharide-mediated signaling pathway	IL1B, MAPK1, MAPK14, NFKBIA, RIPK2, TRAF6
0.012	BP	regulation of mRNA stability	APEX1, CARHSP1, GDNF, MAPK14, PABPC1, VEGFA
0.018	BP	ovum-producing ovary development	ADAMTS1, ADRBK1, CENPI, ESR1, FOXO3, KDR, NR5A1, PGR, VEGFA

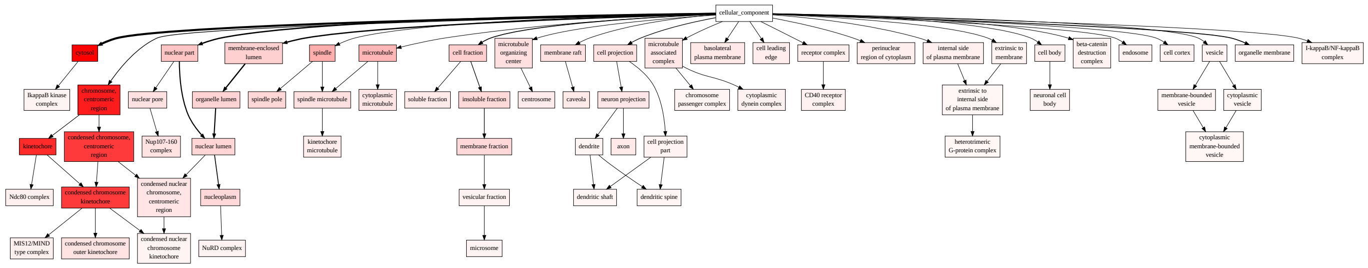


Figure 50: Relationships between the enriched *cellular component* Gene Ontology terms that were listed in Table 26. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

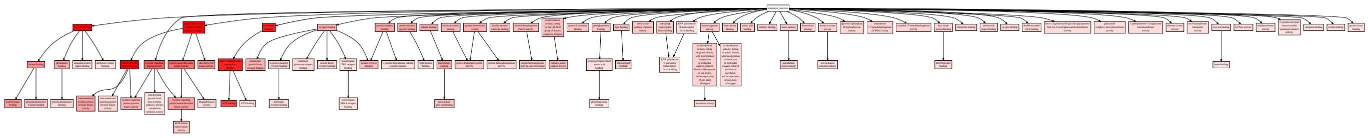


Figure 51: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 26. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

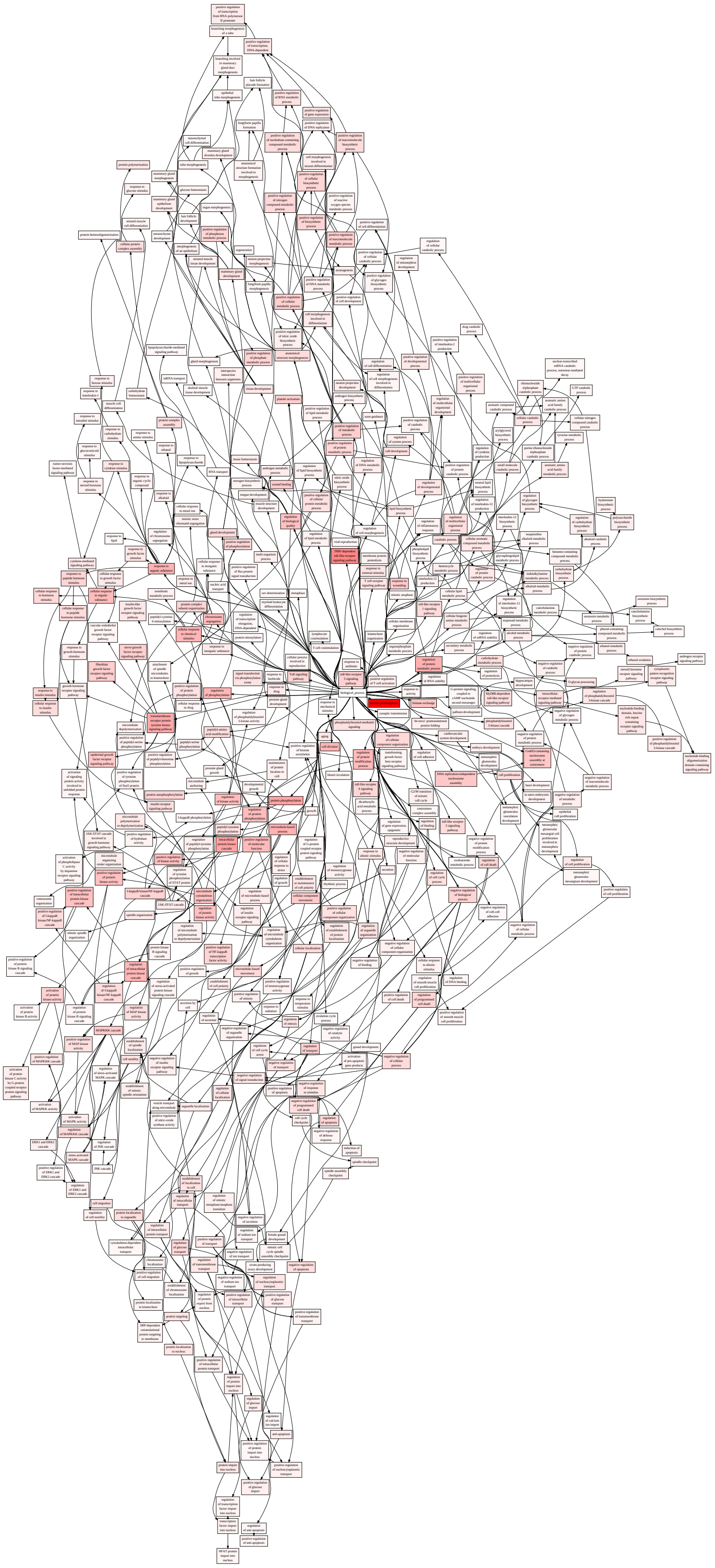


Figure 52: Relationships between the enriched *biological process* Gene Ontology terms that were listed in Table 26. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

11.2 Candidate genes

Table 27: Descriptions of the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. S column contains an at sign if the gene is part of the candidate pathway. The statuses of the genes are shown as: *a*=absent, *d*=down regulated, *u*=up regulated, *s*=stable. This table has 49 rows.

S	name	locus	description	studies
u	ABCC4	13:95672083-95953687 13q32.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:HGNC Symbol;Acc:55], type=processed_transcript,protein_coding, GO=[15-hydroxyprostaglandin dehydrogenase (NAD+) activity; platelet dense granule membrane; chloride channel activity; platelet degranulation; platelet activation; blood coagulation; wound healing]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa
u	AC061975.9	17:26603489-26603579 17q11.2	[undefined], type=miRNA	tcgaBreastGE
d*	ACPP	3:132036211-132087142 3q22.1	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125], type=processed_transcript,protein_coding,retained_intron, GO=[choline binding; adenosine metabolic process; acid phosphatase activity; 5'-nucleotidase activity; multivesicular body; alcohol binding; purine base metabolic process; filopodium; Golgi cisterna; lysosomal membrane; amine binding; apical part of cell; lysosome; lytic vacuole; dephosphorylation]	snp3dProstateC
u*	ADAMTS1	21:28208606-28217728 21q21.3	ADAM metallopeptidase with thrombospondin type 1 motif, 1 [Source:HGNC Symbol;Acc:217], type=protein_coding,retained_intron, GO=[heart trabecula formation; ovulation from ovarian follicle; integrin-mediated signaling pathway; basement membrane; cardiac chamber development; metalloendopeptidase activity; heparin binding; extracellular matrix part; kidney development; endopeptidase activity]	cosmicMetastasis, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
u*	ADRB2	5:148206156-148208196 5q32	adrenergic, beta-2-, receptor, surface [Source:HGNC Symbol;Acc:286], type=protein_coding, GO=[beta2-adrenergic receptor activity; positive regulation of the force of heart contraction by epinephrine; positive regulation of skeletal muscle tissue growth; diaphragm contraction; desensitization of G-protein coupled receptor protein signaling pathway by arrestin; vasodilation by norepinephrine-epinephrine involved in regulation of systemic arterial blood pressure; adenylate cyclase binding; norepinephrine binding; epinephrine binding; positive regulation of potassium ion transport; negative regulation of urine volume; activation of transmembrane receptor protein tyrosine kinase activity; positive regulation of calcium ion transport via voltage-gated calcium channel activity; neuronal cell body membrane; negative regulation of calcium ion transport via voltage-gated calcium channel activity; dopamine binding; positive regulation of sodium ion transport; ionotropic glutamate receptor binding; positive regulation of vasodilation; regulation of sensory perception of pain; endosome to lysosome transport; potassium channel regulator activity; positive regulation of bone mineralization; negative regulation of ossification; positive regulation of transporter activity; regulation of excitatory postsynaptic membrane potential; alcohol binding; bone resorption; synaptic transmission, glutamatergic; activation of adenylate cyclase activity by G-protein signaling pathway; caveola; negative regulation of inflammatory response; sarcolemma; drug binding; receptor-mediated endocytosis; amine binding; dendritic spine; receptor complex; positive regulation of MAPKKK cascade; apical plasma membrane; apical part of cell; axon; lytic vacuole; lysosome; microsome; protein homodimerization activity; positive regulation of apoptosis; positive regulation of cell proliferation; positive regulation of transcription from RNA polymerase II promoter; wound healing; protein complex assembly; identical protein binding]	snp3dObesity, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	ATP1B1	1:169074935-169101960 1q24.2	ATPase, Na+/K+ transporting, beta 1 polypeptide [Source:HGNC Symbol;Acc:804], type=processed_transcript,protein_coding, GO=[sodium:potassium-exchanging ATPase complex; sodium:potassium-exchanging ATPase activity; ATP biosynthetic process; caveola; apical plasma membrane; response to hypoxia; leukocyte migration; apical part of cell; basolateral plasma membrane; blood coagulation; wound healing]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	BRP44	1:167885967-167906278 1q24.2	brain protein 44 [Source:HGNC Symbol;Acc:24515], type=protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	C19orf48	19:51300962-51307974 19q13.33	chromosome 19 open reading frame 48 [Source:HGNC Symbol;Acc:29667], type=protein_coding	tcgaBreastGE, tcgaGliomaGE
d*	CAMK2N1	1:20808884-20812713 1p36.12	calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:24190], type=processed_transcript,protein_coding, GO=[calcium-dependent protein kinase inhibitor activity; postsynaptic density; synaptosome; dendritic spine; postsynaptic membrane; protein kinase binding; cell junction]	tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
d*	CBLN2	18:70203915-70211774 18q22.3	cerebellin 2 precursor [Source:HGNC Symbol;Acc:1544], type=protein_coding, GO=[positive regulation of nervous system development; positive regulation of synapse assembly; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	CENPN	16:81040103-81066719 16q23.2	centromere protein N [Source:HGNC Symbol;Acc:30873], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[CenH3-containing nucleosome assembly at centromere; DNA replication-independent nucleosome assembly; condensed chromosome kinetochore; mitotic prometaphase]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeProstated
d*	COLEC12	18:319355-500729 18p11.32	collectin sub-family member 12 [Source:HGNC Symbol;Acc:16016], type=protein_coding, GO=[carbohydrate mediated signaling; galactose binding; phagocytosis, recognition; pattern recognition receptor activity; low-density lipoprotein particle binding; scavenger receptor activity; collagen; pattern recognition receptor signaling pathway; protein homooligomerization; extracellular matrix part; protein complex assembly]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	DDC	7:50526134-50633154 7p12.1	dopa decarboxylase (aromatic L-amino acid decarboxylase) [Source:HGNC Symbol;Acc:2719], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[aromatic-L-amino-acid decarboxylase activity; phytoalexin metabolic process; synaptic vesicle amine transport; isoquinoline alkaloid metabolic process; serotonin biosynthetic process; response to pyrethroid; dopamine biosynthetic process; cellular response to alkaloid; cellular response to drug; multicellular organismal aging; pyridoxal phosphate binding; amino acid binding; circadian rhythm; synaptic vesicle; amine binding; axon; soluble fraction; cellular amino acid metabolic process]	tcgaColonGE, tscapeGliomaa
u*	EAF2	3:121554030-121605373 3q13.33	ELL associated factor 2 [Source:HGNC Symbol;Acc:23115], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[negative regulation of epithelial cell proliferation involved in prostate gland development; nuclear speck; negative regulation of cell growth; negative regulation of growth; regulation of cell growth; induction of apoptosis; positive regulation of apoptosis]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	ECI2	6:4115923-4135831 6p25.2	enoyl-CoA delta isomerase 2 [Source:HGNC Symbol;Acc:14601], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[dodecenoyl-CoA delta-isomerase activity; fatty-acyl-CoA binding; peroxisomal matrix; fatty acid catabolic process]	tcgaBreastGESurv, tcgaColonGE, tcgaGliomaGE
u*	ELL2	5:95220802-95297775 5q15	elongation factor, RNA polymerase II, 2 [Source:HGNC Symbol;Acc:17064], type=processed_transcript,protein_coding,retained_intron, GO=[transcription elongation factor complex; translation elongation factor activity; transcription elongation from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u	ELL2P1	1:158145640-158147545 1q23.1	elongation factor, RNA polymerase II, 2 pseudogene 1 [Source:HGNC Symbol;Acc:39343], type=processed_pseudogene,pseudogene	
u*	ELOVL5	6:53132196-53213947 6p12.1	ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:21308], type=processed_transcript,protein_coding, GO=[fatty acid elongase activity; fatty acid elongation, monounsaturated fatty acid; fatty acid elongation, polyunsaturated fatty acid; very long-chain fatty acid biosynthetic process; long-chain fatty-acyl-CoA biosynthetic process; triglyceride biosynthetic process; endoplasmic reticulum membrane]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
u*	FKBP5	6:35541362-35696360 6p21.31	FK506 binding protein 5 [Source:HGNC Symbol;Acc:3721], type=protein_coding, GO=[macrolide binding; FK506 binding; protein peptidyl-prolyl isomerization; peptidyl-prolyl cis-trans isomerase activity; heat shock protein binding; drug binding; protein folding]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	GALNTL4	11:11292423-11643552 11p15.3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 [Source:HGNC Symbol;Acc:30488], type=processed_transcript,protein_coding, GO=[polypeptide N-acetylgalactosaminyltransferase activity; UDP-glycosyltransferase activity]	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
d*	GRB10	7:50657760-50861159 7p12.1	growth factor receptor-bound protein 10 [Source:HGNC Symbol;Acc:4564], type=processed_transcript,protein_coding,retained_intron, GO=[negative regulation of glucose import; negative regulation of glycogen biosynthetic process; positive regulation of vascular endothelial growth factor receptor signaling pathway; negative regulation of insulin receptor signaling pathway; insulin receptor binding; insulin-like growth factor receptor signaling pathway; SH3/SH2 adaptor activity; negative regulation of phosphorylation; negative regulation of Wnt receptor signaling pathway; phospholipid binding; positive regulation of phosphorylation]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeGliomaa

Continued on next page. . .

S	name	locus	description	studies
d*	HOXC13	12:54332535-54340328 12q13.13	homeobox C13 [Source:HGNC Symbol;Acc:5125], type=protein_coding, GO=[tongue morphogenesis; hair follicle development; anterior/posterior pattern specification]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeRCCa
u*	KLK4	19:51409608-51413994 19q13.41	kallikrein-related peptidase 4 [Source:HGNC Symbol;Acc:6365], type=protein_coding, GO=[serine-type endopeptidase activity; endopeptidase activity]	snp3dProstateC, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	LMO4	1:87794151-87812788 1p22.3	LIM domain only 4 [Source:HGNC Symbol;Acc:6644], type=processed_transcript,protein_coding, GO=[ventral spinal cord interneuron differentiation; spinal cord association neuron differentiation; regulation of cell fate specification; enhancer sequence-specific DNA binding; spinal cord motor neuron differentiation; thymus development; ventricular septum development; negative regulation of protein complex assembly; neural tube closure; cardiac chamber development; transcription factor complex; regulation of cell activation; transcription factor binding; positive regulation of transcription from RNA polymerase II promoter; protein complex assembly]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeGliomad, tscapeNSCLCd, tscapeOvariand
u*	LRIG1	3:66429221-66551687 3p14.1	leucine-rich repeats and immunoglobulin-like domains 1 [Source:HGNC Symbol;Acc:17360], type=processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
d	LRRC31	3:169556967-169587718 3q26.2	leucine rich repeat containing 31 [Source:HGNC Symbol;Acc:26261], type=processed_transcript,protein_coding	tcgaColonGE, tcgaOvarianCGHa, tscapeBCa, tscapeNSCLCa, tscapeOvariana
d	LRRN1	3:3841121-3889387 3p26.2	leucine rich repeat neuronal 1 [Source:HGNC Symbol;Acc:20980], type=processed_transcript,protein_coding,retained_intron	tcgaGliomaGE, tscapeOvariand
u*	MBOAT2	2:8992820-9143942 2p25.1	membrane bound O-acyltransferase domain containing 2 [Source:HGNC Symbol;Acc:25193], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[1-acylglycerol-3-phosphate O-acyltransferase activity; phospholipid biosynthetic process]	tcgaBreastGE, tcgaColonGE
d	MT1X	16:56716336-56718108 16q13	metallothionein 1X [Source:HGNC Symbol;Acc:7405], type=processed_transcript,protein_coding,retained_intron, GO=[cellular response to zinc ion; cellular response to cadmium ion; negative regulation of growth; perinuclear region of cytoplasm]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeMelanomad
u*	MYBPC1	12:101962131-102079796 12q23.2	myosin binding protein C, slow type [Source:HGNC Symbol;Acc:7549], type=processed_transcript,protein_coding,retained_intron, GO=[titin binding; myosin filament; muscle filament sliding; structural constituent of muscle; myofibril; actin binding]	tcgaBreastGE, tcgaGliomaGE
u*	PGC	6:41704449-41721847 6p21.1	progastricsin (pepsinogen C) [Source:HGNC Symbol;Acc:8890], type=protein_coding, GO=[aspartic-type endopeptidase activity; endopeptidase activity; nucleolus; extracellular space]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeCRCa, tscapeOvariana
d*	PITX1	5:134362615-134370503 5q31.1	paired-like homeodomain 1 [Source:HGNC Symbol;Acc:9004], type=protein_coding,retained_intron, GO=[branchiomeric skeletal muscle development; myoblast cell fate commitment; embryonic hindlimb morphogenesis; pituitary gland development; cartilage development; transcription factor complex; protein binding transcription factor activity; nucleolus; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl
u*	PMEPA1	20:56223448-56286592 20q13.31	prostate transmembrane protein, androgen induced 1 [Source:HGNC Symbol;Acc:14107], type=processed_transcript,protein_coding, GO=[WW domain binding; androgen receptor signaling pathway]	
d*	RILPL2	12:123899936-123921264 12q24.31	Rab interacting lysosomal protein-like 2 [Source:HGNC Symbol;Acc:28787], type=protein_coding, GO=[identical protein binding]	tcgaBreastGE
d	RP11-343H19.2	16:56716382-56721719 16q13	[undefined], type=processed_transcript	
u*	S100P	4:6694796-6698897 4p16.1	S100 calcium binding protein P [Source:HGNC Symbol;Acc:10504], type=processed_transcript,protein_coding, GO=[calcium-dependent protein binding; endothelial cell migration; magnesium ion binding; calcium ion binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
u*	SGK1	6:134490384-134639250 6q23.2	serum/glucocorticoid regulated kinase 1 [Source:HGNC Symbol;Acc:10810], type=processed_transcript,protein_coding,retained_intron, GO=[renal sodium ion absorption; regulation of gastric acid secretion; chloride channel regulator activity; sodium channel regulator activity; calcium channel regulator activity; long-term memory; potassium channel regulator activity; positive regulation of transporter activity; phosphatidylinositol binding; phospholipid binding; regulation of cell growth; regulation of sequence-specific DNA binding transcription factor activity; regulation of cell migration; protein tyrosine kinase activity; response to DNA damage stimulus; endoplasmic reticulum membrane]	cosmicRecurrent, tcgaBreastGE, tcgaColonGE, tscapeBCa, tscapeCRCa
u	SLC45A3	1:205626979-205649587 1q32.1	solute carrier family 45, member 3 [Source:HGNC Symbol;Acc:8642], type=processed_transcript,protein_coding	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa
u	SNORD88B	19:51302289-51302379 19q13.33	small nucleolar RNA, C/D box 88B [Source:HGNC Symbol;Acc:32748], type=snoRNA	
d*	ST3GAL1	8:134467091-134584183 8q24.22	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 [Source:HGNC Symbol;Acc:10862], type=processed_transcript,protein_coding,retained_intron, GO=[beta-galactoside alpha-2,3-sialyltransferase activity; O-glycan processing; integral to Golgi membrane; Golgi cisterna membrane; Golgi cisterna; post-translational protein modification]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
u*	STK39	2:168810530-169104651 2q24.3	serine threonine kinase 39 [Source:HGNC Symbol;Acc:17717], type=processed_transcript,protein_coding, GO=[signal transduction via phosphorylation event; positive regulation of potassium ion transport; receptor signaling protein serine/threonine kinase activity; apical plasma membrane; apical part of cell; basolateral plasma membrane; protein kinase binding; protein tyrosine kinase activity]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	TM4SF1	3:149086809-149095652 3q25.1	transmembrane 4 L six family member 1 [Source:HGNC Symbol;Acc:11853], type=nonsense_mediated_decay,protein_coding	snp3dMetastasis, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
u	TMEFF2	2:192813769-193060435 2q32.3	transmembrane protein with EGF-like and two follistatin-like domains 2 [Source:HGNC Symbol;Acc:11867], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
u	TMPRSS2	21:42836478-42903043 21q22.3	transmembrane protease, serine 2 [Source:HGNC Symbol;Acc:11876], type=processed_transcript,protein_coding,retained_intron, GO=[scavenger receptor activity; serine-type endopeptidase activity; endopeptidase activity]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeProstated
u*	TSKU	11:76493295-76509198 11q13.5	tsukushi small leucine rich proteoglycan homolog (Xenopus laevis) [Source:HGNC Symbol;Acc:28850], type=protein_coding	tscapeOvariana
u*	TUBA3D	2:132233666-132240507 2q21.1	tubulin, alpha 3d [Source:HGNC Symbol;Acc:24071], type=processed_transcript,protein_coding, GO=[cytoplasmic microtubule; 'de novo' posttranslational protein folding; structural constituent of cytoskeleton; microtubule-based movement; protein polymerization; protein folding; GTPase activity; microtubule cytoskeleton organization; GTP binding; GTP catabolic process; protein complex assembly]	tcgaBreastGE, tcgaColonGE, tscapeOvariand, tscapeProstated
u*	TUBA3E	2:130949318-130956034 2q21.1	tubulin, alpha 3e [Source:HGNC Symbol;Acc:20765], type=protein_coding, GO=[cytoplasmic microtubule; structural constituent of cytoskeleton; microtubule-based movement; protein polymerization; GTPase activity; microtubule cytoskeleton organization; GTP binding; GTP catabolic process; protein complex assembly]	tscapeCRCa, tscapeOvariand, tscapeProstated
d*	TULP4	6:158733692-158932860 6q25.3	tubby like protein 4 [Source:HGNC Symbol;Acc:15530], type=protein_coding, GO=[response to nutrient]	tcgaGliomaGE, tscapeBCd, tscapeOvariand, tscapeProstated, tscapeSCLCd
d*	UGT2B17	4:69402902-69434245 4q13.2	UDP glucuronosyltransferase 2 family, polypeptide B17 [Source:HGNC Symbol;Acc:12547], type=protein_coding, GO=[lipid glycosylation; glucuronosyltransferase activity; UDP-glycosyltransferase activity; microsome; steroid metabolic process; endoplasmic reticulum membrane]	tcgaBreastMethyl

12 Candidate report for DHT and DEX

12.1 Moksiskaan candidate pathway

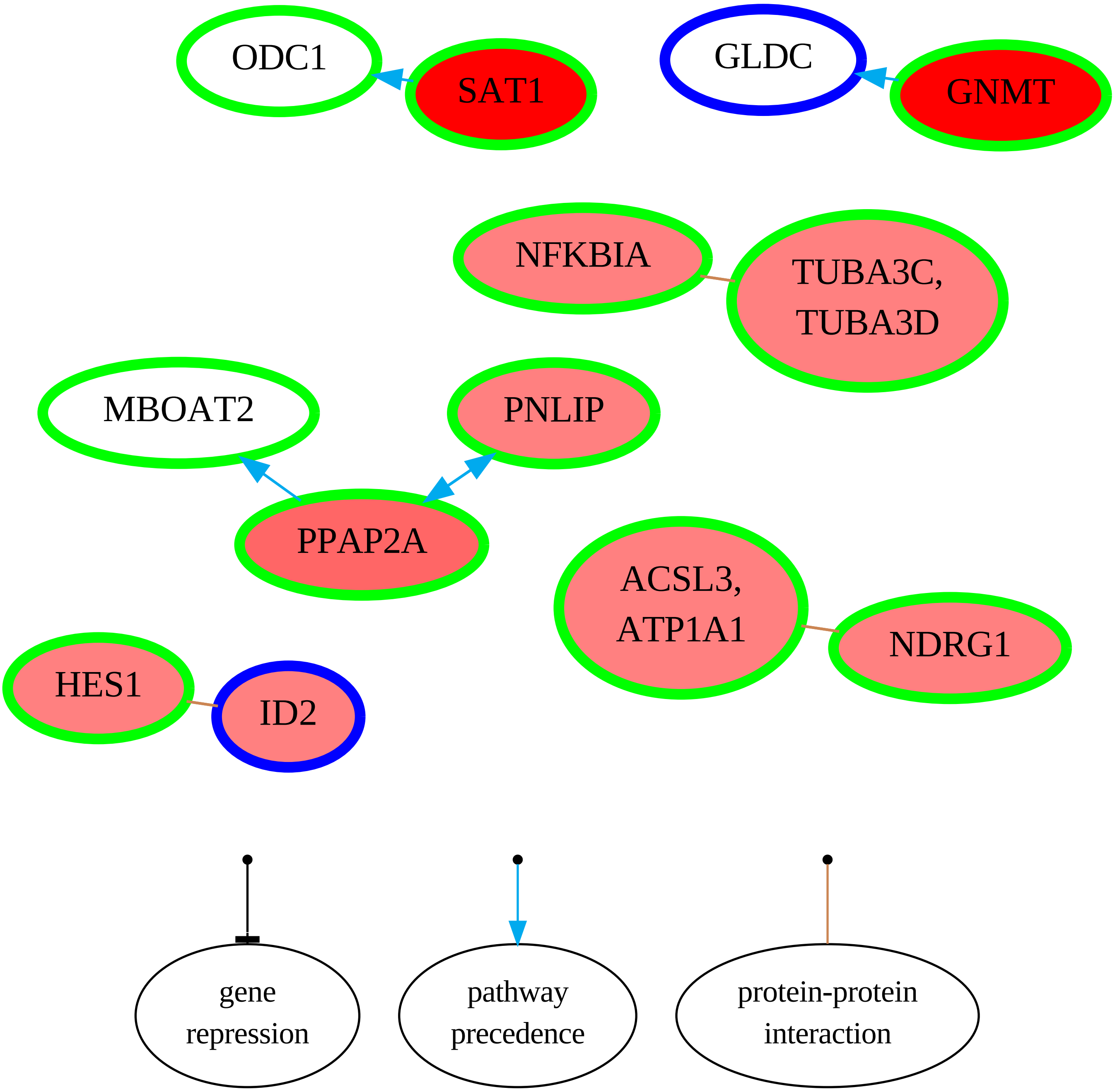


Figure 53: Known relationships between the candidate genes. Candidate genes are shown in red if they have only output connections. The ratio of input and output connections determines how light they are. Completely white genes have only input connections. The maximum of 0 other gene step(s) are allowed between the candidate genes and these intermediate genes are shown on gray. Green and blue borders are referring to up and down regulated genes, respectively. Light grey is used to emphasize stably expressed genes. Known regulations are shown with bold borders whereas the predictions are kept thin.

Table 28: List of KEGG [6] pathways supporting the relationships between the genes shown in Figure 53. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Glycerolipid metabolism	3	MBOAT2, PNLIP, PPAP2A
Glycine, serine and threonine metabolism	1	GLDC, GNMT
Arginine and proline metabolism	1	ODC1, SAT1
Glycerophospholipid metabolism	1	MBOAT2, PPAP2A

12.2 Candidate genes

Table 29: Descriptions of the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. S column contains an at sign if the gene is part of the candidate pathway. The statuses of the genes are shown as: *a*=absent, *d*=down regulated, *u*=up regulated, *s*=stable. This table has 135 rows.

S	name	locus	description	studies
u	AC061975.9	17:26603489-26603579 17q11.2	[undefined], type=miRNA	tcgaBreastGE
d	AC078802.1	3:169484713-169487683 3q26.2	Actin-related protein M1 [Source:UniProtKB/Swiss-Prot;Acc:Q9BYD9], type=protein_coding	tcgaColonGE
u	ACAA1	3:38164201-38178733 3p22.2	acetyl-CoA acyltransferase 1 [Source:HGNC Symbol;Acc:82], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[acetyl-CoA C-acyltransferase activity; fatty acid beta-oxidation using acyl-CoA oxidase; peroxisomal matrix; fatty acid beta-oxidation; peroxisomal part; microbody part; fatty acid metabolic process]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d	ACPP	3:132036211-132087142 3q22.1	acid phosphatase, prostate [Source:HGNC Symbol;Acc:125], type=processed_transcript,protein_coding,retained_intron, GO=[choline binding; adenosine metabolic process; acid phosphatase activity; 5'-nucleotidase activity; multivesicular body; purine base metabolic process; filopodium; purine ribonucleoside metabolic process; Golgi cisterna; lysosomal membrane; amine binding; stored secretory granule; apical part of cell; Golgi apparatus part]	snp3dProstateC
u*	ACSL3	2:223725652-223809357 2q36.1	acyl-CoA synthetase long-chain family member 3 [Source:HGNC Symbol;Acc:3570], type=protein_coding,retained_intron, GO=[long-chain fatty acid-CoA ligase activity; long-chain fatty-acyl-CoA biosynthetic process; peroxisomal membrane; triglyceride biosynthetic process; peroxisomal part; microbody part; triglyceride metabolic process; mitochondrial outer membrane; glycerol ether metabolic process; microsome; fatty acid metabolic process; endoplasmic reticulum membrane; endoplasmic reticulum part]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCd
u	ADRB2	5:148206156-148208196 5q32	adrenergic, beta-2-, receptor, surface [Source:HGNC Symbol;Acc:286], type=protein_coding, GO=[beta2-adrenergic receptor activity; positive regulation of the force of heart contraction by epinephrine; desensitization of G-protein coupled receptor protein signaling pathway by arrestin; diaphragm contraction; positive regulation of skeletal muscle tissue growth; vasodilation by norepinephrine-epinephrine involved in regulation of systemic arterial blood pressure; norepinephrine binding; adenylate cyclase binding; epinephrine binding; negative regulation of urine volume; positive regulation of potassium ion transport; activation of transmembrane receptor protein tyrosine kinase activity; positive regulation of calcium ion transport via voltage-gated calcium channel activity; neuronal cell body membrane; negative regulation of calcium ion transport via voltage-gated calcium channel activity; dopamine binding; positive regulation of sodium ion transport; ionotropic glutamate receptor binding; positive regulation of vasodilation; regulation of sensory perception of pain; positive regulation of heart contraction; glutamate receptor binding; regulation of the force of heart contraction; endosome to lysosome transport; potassium channel regulator activity; musculoskeletal movement; multicellular organismal movement; positive regulation of bone mineralization; negative regulation of ossification; positive regulation of transporter activity; negative regulation of G-protein coupled receptor protein signaling pathway; regulation of excitatory postsynaptic membrane potential; regulation of sodium ion transport; positive regulation of ossification; bone resorption; vasodilation; synaptic transmission, glutamatergic; activation of adenylate cyclase activity by G-protein signaling pathway; caveola; negative regulation of inflammatory response; renal system process; activation of adenylate cyclase activity; negative regulation of binding; sensory perception of pain; sarcolemma; drug binding; regulation of protein binding; G-protein signaling, coupled to cAMP nucleotide second messenger; receptor-mediated endocytosis; regulation of blood pressure; amine binding; dendritic spine; regulation of ossification; regulation of binding; positive regulation of MAPKKK cascade; apical plasma membrane; apical part of cell; axon; negative regulation of transport; microsome; neuronal cell body; regulation of nucleotide metabolic process; MAPKKK cascade; protein homodimerization activity; negative regulation of signal transduction; neuron projection; negative regulation of signaling; negative regulation of cell communication; positive regulation of cell proliferation; wound healing; identical protein binding]	snp3dObesity, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d	AIDA	1:222841355-222886552 1q41	axin interactor, dorsalization associated [Source:HGNC Symbol;Acc:25761], type=processed_transcript,protein_coding, GO=[negative regulation of JUN kinase activity; regulation of protein homodimerization activity; negative regulation of JNK cascade; negative regulation of MAP kinase activity; regulation of protein binding; negative regulation of protein kinase activity; negative regulation of kinase activity; regulation of binding; JNK cascade; stress-activated protein kinase signaling cascade; regionalization; MAPKKK cascade; negative regulation of signal transduction; protein domain specific binding; negative regulation of signaling; negative regulation of cell communication]	tcgaGliomaGE
u	AL162497.1	13:110407168-110407615 13q34	[undefined], type=pseudogene	
u	ANKRD37	4:186317175-186321782 4q35.1	ankyrin repeat domain 37 [Source:HGNC Symbol;Acc:29593], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCd, tscapeHCCd, tscapeMelanomad, tscapeNSCLCd, tscapeProstated, tscapeRCCd
u	APOD	3:195295573-195311076 3q29	apolipoprotein D [Source:HGNC Symbol;Acc:612], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[negative regulation of T cell migration; negative regulation of lipoprotein lipid oxidation; negative regulation of monocyte chemotactic protein-1 production; negative regulation of smooth muscle cell-matrix adhesion; evasion or tolerance of host defense response; negative regulation of chemokine production; negative regulation of focal adhesion assembly; peripheral nervous system axon regeneration; negative regulation of lipoprotein metabolic process; negative regulation of platelet-derived growth factor receptor signaling pathway; negative regulation of leukocyte migration; cholesterol binding; negative regulation of smooth muscle cell proliferation; negative regulation of cell-substrate adhesion; platelet-derived growth factor receptor signaling pathway; negative regulation of protein import into nucleus; tissue regeneration; negative regulation of transmembrane transport; lipid transporter activity; regulation of smooth muscle cell proliferation; interaction with host; negative regulation of protein transport; cytosolic ribosome; symbiosis, encompassing mutualism through parasitism; response to reactive oxygen species; regulation of intracellular protein transport; regulation of lipid metabolic process; aging; glucose metabolic process; leukocyte migration; response to oxidative stress; negative regulation of transport; neuronal cell body; angiogenesis; regulation of cell migration; interspecies interaction between organisms; perinuclear region of cytoplasm; blood vessel morphogenesis; vasculature development; negative regulation of cell proliferation; negative regulation of signal transduction; organic substance transport; neuron projection; negative regulation of signaling; negative regulation of cell communication; wound healing; cell morphogenesis involved in differentiation; extracellular space]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa, tscapeBCa, tscapeNSCLCd, tscapeOvariana
d	ARHGAP10	4:148653214-148993931 4q31.23	Rho GTPase activating protein 10 [Source:HGNC Symbol;Acc:26099], type=processed_transcript,protein_coding,retained_intron, GO=[cytoskeletal adaptor activity; Rho GTPase activator activity; filopodium assembly; positive regulation of Rho GTPase activity; SH3 domain binding; phospholipid binding; regulation of GTPase activity; perinuclear region of cytoplasm; Ras protein signal transduction; regulation of nucleotide metabolic process; regulation of cellular catabolic process; protein domain specific binding; GTP catabolic process; negative regulation of apoptosis; negative regulation of cell death; purine ribonucleoside triphosphate metabolic process]	tcgaBreastGE, tscapeRCCd
u	ATAD2	8:124332090-124428590 8q24.13	ATPase family, AAA domain containing 2 [Source:HGNC Symbol;Acc:30123], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nucleoside-triphosphatase activity]	fileCIN70, tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianGE, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana

Continued on next page...

S	name	locus	description	studies
u*	ATP1A1	1:116915290-116952883 1p13.1	ATPase, Na+/K+ transporting, alpha 1 polypeptide [Source:HGNC Symbol;Acc:799], type=processed_transcript,protein_coding,retained_intron, GO=[4-nitrophenylphosphatase activity; negative regulation of glucocorticoid metabolic process; negative regulation of glucocorticoid biosynthetic process; sodium:potassium-exchanging ATPase complex; positive regulation of striated muscle contraction; sodium:potassium-exchanging ATPase activity; negative regulation of steroid biosynthetic process; negative regulation of heart contraction; positive regulation of heart contraction; regulation of the force of heart contraction; regulation of hormone metabolic process; regulation of sodium ion transport; ATP biosynthetic process; sarcolemma; melanosome; regulation of blood pressure; ATP metabolic process; regulation of lipid metabolic process; basolateral plasma membrane; microsome; purine ribonucleoside triphosphate metabolic process; nucleoside-triphosphatase activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeSCLCa, tscapeSCLCd
d	BAMBI	10:28966271-28971868 10p12.1	BMP and activin membrane-bound inhibitor homolog (Xenopus laevis) [Source:HGNC Symbol;Acc:30251], type=protein_coding,retained_intron, GO=[type II transforming growth factor beta receptor binding; positive regulation of catenin import into nucleus; transforming growth factor beta-activated receptor activity; regulation of catenin import into nucleus; positive regulation of epithelial to mesenchymal transition; frizzled binding; positive regulation of protein binding; negative regulation of transforming growth factor beta receptor signaling pathway; positive regulation of canonical Wnt receptor signaling pathway; positive regulation of binding; regulation of transforming growth factor beta receptor signaling pathway; regulation of protein binding; regulation of cell shape; regulation of canonical Wnt receptor signaling pathway; transforming growth factor beta receptor signaling pathway; regulation of intracellular protein transport; regulation of binding; protein serine/threonine kinase activity; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication; protein kinase activity; positive regulation of cell proliferation; cell morphogenesis involved in differentiation]	tcgaColonGE, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeBCd
d	BCHE	3:165490692-165555260 3q26.1	butyrylcholinesterase [Source:HGNC Symbol;Acc:983], type=nonsense_mediated_decay,protein_coding, GO=[tropane alkaloid metabolic process; cocaine metabolic process; acetylcholinesterase activity; choline binding; choline metabolic process; nuclear envelope lumen; alkaloid metabolic process; response to folic acid; synaptic transmission, cholinergic; beta-amyloid binding; carboxylesterase activity; negative regulation of synaptic transmission; learning; response to alkaloid; endoplasmic reticulum lumen; amine binding; response to glucocorticoid stimulus; negative regulation of signaling; negative regulation of cell communication; endoplasmic reticulum part; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl
u	BRP44	1:167885967-167906278 1q24.2	brain protein 44 [Source:HGNC Symbol;Acc:24515], type=protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	C17orf48	17:10600931-10614550 17p13.1	chromosome 17 open reading frame 48 [Source:HGNC Symbol;Acc:30925], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[CDP-glycerol diphosphatase activity; ADP-sugar diphosphatase activity; ADP-ribose diphosphatase activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	C9orf152	9:112952328-112970469 9q31.3	chromosome 9 open reading frame 152 [Source:HGNC Symbol;Acc:31455], type=processed_transcript,protein_coding	
d	C9orf64	9:86553226-86571901 9q21.32	chromosome 9 open reading frame 64 [Source:HGNC Symbol;Acc:28144], type=protein_coding	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl
d	CAMK2N1	1:20808884-20812713 1p36.12	calcium/calmodulin-dependent protein kinase II inhibitor 1 [Source:HGNC Symbol;Acc:24190], type=processed_transcript,protein_coding, GO=[calcium-dependent protein kinase inhibitor activity; postsynaptic density; synaptosome; dendritic spine; postsynaptic membrane; neuronal cell body; protein kinase binding; synapse part; neuron projection]	tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u	CAP2	6:17393447-17558023 6p22.3	CAP, adenylate cyclase-associated protein, 2 (yeast) [Source:HGNC Symbol;Acc:20039], type=nonsense_mediated_decay,protein_coding, GO=[activation of adenylate cyclase activity; establishment or maintenance of cell polarity; actin binding; regulation of nucleotide metabolic process; cell morphogenesis involved in differentiation]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
d	CBLN2	18:70203915-70211774 18q22.3	cerebellin 2 precursor [Source:HGNC Symbol;Acc:1544], type=protein_coding, GO=[positive regulation of synapse assembly; positive regulation of nervous system development; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	CEBPD	8:48649471-48651648 8q11.21	CCAAT/enhancer binding protein (C/EBP), delta [Source:HGNC Symbol;Acc:1835], type=protein_coding, GO=[sequence-specific DNA binding]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeRCCd
d	COLEC12	18:319355-500729 18p11.32	collectin sub-family member 12 [Source:HGNC Symbol;Acc:16016], type=protein_coding, GO=[carbohydrate mediated signaling; galactose binding; phagocytosis, recognition; pattern recognition receptor activity; low-density lipoprotein particle binding; scavenger receptor activity; phagocytosis; collagen; protein homooligomerization; extracellular matrix]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	CREB3L2	7:137559725-137686813 7q33	cAMP responsive element binding protein 3-like 2 [Source:HGNC Symbol;Acc:23720], type=processed_transcript,protein_coding, GO=[cAMP response element binding; ER to Golgi vesicle-mediated transport; chondrocyte differentiation; endoplasmic reticulum membrane; sequence-specific DNA binding; endoplasmic reticulum part]	tcgaGliomaGE, tscapeMelanomaa
u	CRISPLD2	16:84853590-84954374 16q24.1	cysteine-rich secretory protein LCCL domain containing 2 [Source:HGNC Symbol;Acc:25248], type=processed_transcript,protein_coding,retained_intron, GO=[transport vesicle; heparin binding; extracellular matrix organization; extracellular matrix]	tscapeProstated
u	CTD-2653M23.1	5:36885308-36886599 5p13.2	[undefined], type=processed_pseudogene,pseudogene	tcgaBreastGE
d	CXCR7	2:237476430-237491001 2q37.3	chemokine (C-X-C motif) receptor 7 [Source:HGNC Symbol;Acc:23692], type=protein_coding, GO=[C-X-C chemokine receptor activity; chemokine-mediated signaling pathway; recycling endosome; early endosome; interspecies interaction between organisms; perinuclear region of cytoplasm; negative regulation of apoptosis; negative regulation of cell death]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u	DBI	2:120124497-120130126 2q14.2	diazepam binding inhibitor (GABA receptor modulator, acyl-CoA binding protein) [Source:HGNC Symbol;Acc:2690], type=processed_transcript,protein_coding,retained_intron, GO=[benzodiazepine receptor binding; fatty-acyl-CoA binding; skin development; hair follicle development; triglyceride metabolic process; glycerol ether metabolic process; cofactor binding]	tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa
d	DDC	7:50526134-50633154 7p12.1	dopa decarboxylase (aromatic L-amino acid decarboxylase) [Source:HGNC Symbol;Acc:2719], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[aromatic-L-amino-acid decarboxylase activity; phytoalexin metabolic process; serotonin biosynthetic process; isoquinoline alkaloid metabolic process; synaptic vesicle amine transport; response to pyrethroid; dopamine biosynthetic process; alkaloid metabolic process; cellular response to alkaloid; cellular response to drug; multicellular organismal aging; cellular biogenic amine biosynthetic process; pyridoxal phosphate binding; circadian rhythm; response to alkaloid; synaptic vesicle; amine binding; clathrin-coated vesicle; coated vesicle; aging; axon; neuronal cell body; cofactor binding; synapse part; soluble fraction; protein domain specific binding; organic substance transport; neuron projection]	tcgaColonGE, tscapeGliomaa
d	DEPTOR	8:120885957-121063152 8q24.12	DEP domain containing MTOR-interacting protein [Source:HGNC Symbol;Acc:22953], type=processed_transcript,protein_coding, GO=[negative regulation of cell size; negative regulation of TOR signaling cascade; negative regulation of protein kinase activity; negative regulation of kinase activity; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa
u	DHCR24	1:55315300-55352921 1p32.3	24-dehydrocholesterol reductase [Source:HGNC Symbol;Acc:2859], type=protein_coding, GO=[delta24-sterol reductase activity; UDP-N-acetylmuramate dehydrogenase activity; amyloid precursor protein catabolic process; peptide antigen binding; plasminogen activation; male genitalia development; neuroprotection; cholesterol biosynthetic process; negative regulation of caspase activity; skin development; negative regulation of hydrolase activity; response to oxidative stress; anti-apoptosis; cofactor binding; Ras protein signal transduction; negative regulation of cell proliferation; Golgi apparatus part; negative regulation of apoptosis; endoplasmic reticulum membrane; negative regulation of cell death; endoplasmic reticulum part]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	DNAJB9	7:108210012-108215294 7q31.1	DnaJ (Hsp40) homolog, subfamily B, member 9 [Source:HGNC Symbol;Acc:6968], type=processed_transcript,protein_coding,retained_intron, GO=[activation of signaling protein activity involved in unfolded protein response; misfolded protein binding; ER-associated protein catabolic process; heat shock protein binding; unfolded protein binding; protein folding; nucleolus; endoplasmic reticulum membrane; endoplasmic reticulum part]	tcgaBreastMethyl, tcgaColonMethyl

Continued on next page...

S	name	locus	description	studies
u	EAF2	3:121554030-121605373 3q13.33	ELL associated factor 2 [Source:HGNC Symbol;Acc:23115], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[negative regulation of epithelial cell proliferation involved in prostate gland development; nuclear speck; negative regulation of cell growth; urogenital system development; regulation of cell growth; negative regulation of cell proliferation]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	ELL2	5:95220802-95297775 5q15	elongation factor, RNA polymerase II, 2 [Source:HGNC Symbol;Acc:17064], type=processed_transcript,protein_coding,retained_intron, GO=[transcription elongation factor complex; translation elongation factor activity; transcription elongation from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u	ELL2P1	1:158145640-158147545 1q23.1	elongation factor, RNA polymerase II, 2 pseudogene 1 [Source:HGNC Symbol;Acc:39343], type=processed_pseudogene,pseudogene	
u	ELOVL5	6:53132196-53213947 6p12.1	ELOVL fatty acid elongase 5 [Source:HGNC Symbol;Acc:21308], type=processed_transcript,protein_coding, GO=[fatty acid elongase activity; fatty acid elongation, polyunsaturated fatty acid; fatty acid elongation, monounsaturated fatty acid; very long-chain fatty acid biosynthetic process; long-chain fatty-acyl-CoA biosynthetic process; very long-chain fatty acid metabolic process; triglyceride biosynthetic process; triglyceride metabolic process; glycerol ether metabolic process; fatty acid metabolic process; endoplasmic reticulum membrane; endoplasmic reticulum part]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
u	ERRFI1	1:8064464-8086368 1p36.23	ERBB receptor feedback inhibitor 1 [Source:HGNC Symbol;Acc:18185], type=processed_transcript,protein_coding, GO=[negative regulation of protein autophosphorylation; lung vasculature development; skin morphogenesis; negative regulation of epidermal growth factor-activated receptor activity; negative regulation of peptidyl-tyrosine phosphorylation; regulation of keratinocyte differentiation; lung epithelium development; Rho GTPase activator activity; lung alveolus development; negative regulation of epidermal growth factor receptor signaling pathway; extrinsic to internal side of plasma membrane; skin development; positive regulation of Rho GTPase activity; internal side of plasma membrane; negative regulation of protein kinase activity; negative regulation of kinase activity; regulation of GTPase activity; protein kinase binding; Ras protein signal transduction; regulation of nucleotide metabolic process; regulation of cellular catabolic process; vasculature development; negative regulation of signal transduction; GTP catabolic process; negative regulation of signaling; negative regulation of cell communication; purine ribonucleoside triphosphate metabolic process]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
u	F2RL1	5:76114758-76131140 5q13.3	coagulation factor II (thrombin) receptor-like 1 [Source:HGNC Symbol;Acc:3538], type=protein_coding, GO=[positive regulation of glomerular filtration; chemokine (C-C motif) ligand 2 secretion; regulation of neutrophil mediated killing of bacterium; positive regulation of eosinophil degranulation; positive regulation of neutrophil mediated cytotoxicity; positive regulation of neutrophil mediated killing of symbiont cell; positive regulation of neutrophil mediated killing of bacterium; positive regulation of neutrophil mediated killing of gram-negative bacterium; regulation of neutrophil mediated killing of symbiont cell; interleukin-10 secretion; negative regulation of chemokine secretion; regulation of neutrophil mediated cytotoxicity; regulation of neutrophil mediated killing of gram-negative bacterium; neutrophil mediated killing of gram-negative bacterium; positive regulation of cytokine secretion involved in immune response; positive regulation of toll-like receptor 2 signaling pathway; negative regulation of toll-like receptor 3 signaling pathway; positive regulation of interleukin-6 secretion; mature dendritic cell differentiation; interleukin-6 secretion; G-protein beta-subunit binding; positive regulation of toll-like receptor 3 signaling pathway; negative regulation of chemokine production; positive regulation of phagocytosis, engulfment; regulation of phagocytosis, engulfment; positive regulation of interleukin-8 secretion; regulation of interleukin-8 secretion; interferon-gamma secretion; negative regulation of tumor necrosis factor-mediated signaling pathway; positive regulation of actin filament depolymerization; thrombin receptor activity; positive regulation of toll-like receptor 4 signaling pathway; positive regulation of superoxide anion generation; positive regulation of Rho protein signal transduction; establishment of endothelial barrier; positive regulation of pseudopodium assembly; G-protein alpha-subunit binding; pseudopodium; positive regulation of vasodilation; neutrophil activation; negative regulation of cytokine secretion; negative regulation of JNK cascade; positive regulation of positive chemotaxis; interleukin-1 beta secretion; positive regulation of phagocytosis; actin filament depolymerization; positive regulation of phosphatidylinositol 3-kinase cascade; endothelial cell differentiation; vasodilation; T cell activation involved in immune response; positive regulation of JNK cascade; positive regulation of leukocyte chemotaxis; regulation of blood coagulation; renal system process; toll-like receptor 3 signaling pathway; toll-like receptor 2 signaling pathway; positive regulation of ERK1 and ERK2 cascade; phagocytosis; negative regulation of protein transport; toll-like receptor 4 signaling pathway; defense response to virus; symbiosis, encompassing mutualism through parasitism; ERK1 and ERK2 cascade; regulation of blood pressure; positive regulation of I-kappaB kinase/NF-kappaB cascade; JNK cascade; elevation of cytosolic calcium ion concentration; positive regulation of MAPKKK cascade; leukocyte proliferation; positive regulation of cell migration; stress-activated protein kinase signaling cascade; leukocyte migration; negative regulation of transport; regulation of cell migration; interspecies interaction between organisms; Ras protein signal transduction; MAPKKK cascade; hemopoiesis; negative regulation of signal transduction; blood coagulation; negative regulation of signaling; negative regulation of cell communication; wound healing]	tcgaBreastMethyl, tcgaGliomaGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u	FAM105A	5:14581884-14615073 5p15.2	family with sequence similarity 105, member A [Source:HGNC Symbol;Acc:25629], type=processed_transcript,protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa
d	FAM134B	5:16473147-16617167 5p15.1	family with sequence similarity 134, member B [Source:HGNC Symbol;Acc:25964], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cis-Golgi network; sensory perception of pain; Golgi apparatus part]	tcgaColonGE, tcgaGliomaGE
d	FAM198B	4:159045735-159094202 4q32.1	family with sequence similarity 198, member B [Source:HGNC Symbol;Acc:25312], type=protein_coding, GO=[Golgi apparatus part]	tcgaBreastGE
d	FIGNL1	7:50511831-50518088 7p12.1	fidgetin-like 1 [Source:HGNC Symbol;Acc:13286], type=protein_coding, GO=[osteoblast proliferation; four-way junction helicase activity; osteoblast differentiation; ATP metabolic process; magnesium ion binding; DNA recombination; DNA repair; negative regulation of apoptosis; negative regulation of cell death; purine ribonucleoside triphosphate metabolic process; nucleoside-triphosphatase activity]	tcgaColonGE, tcgaOvarianMethyl, tscapeGliomaa
u	FKBP5	6:35541362-35696360 6p21.31	FK506 binding protein 5 [Source:HGNC Symbol;Acc:3721], type=protein_coding, GO=[FK506 binding; macrolide binding; protein peptidyl-prolyl isomerization; peptidyl-prolyl cis-trans isomerase activity; heat shock protein binding; drug binding; protein folding]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	GLDC	9:6532464-6645650 9p24.1	glycine dehydrogenase (decarboxylating) [Source:HGNC Symbol;Acc:4313], type=processed_transcript,protein_coding, GO=[glycine dehydrogenase (decarboxylating) activity; glycine catabolic process; pyridoxal phosphate binding; electron carrier activity; cofactor binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl, tscapeBCd
u	GLRX	5:95087023-95158709 5q15	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:4330], type=processed_transcript,protein_coding,retained_intron, GO=[glutathione disulfide oxidoreductase activity; nucleobase-containing compound interconversion; protein disulfide oxidoreductase activity; cell redox homeostasis; protein N-terminus binding; electron transport chain; electron carrier activity]	tcgaBreastMethyl, tcgaColonMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u*	GNMT	6:42928496-42931618 6p21.1	glycine N-methyltransferase [Source:HGNC Symbol;Acc:4415], type=protein_coding, GO=[glycine N-methyltransferase activity; S-adenosylmethionine metabolic process; S-adenosylhomocysteine metabolic process; glycine binding; methionine metabolic process; folic acid binding; regulation of gluconeogenesis; purine ribonucleoside metabolic process; protein homotetramerization; regulation of carbohydrate biosynthetic process; glycogen metabolic process; regulation of glucose metabolic process; cellular polysaccharide metabolic process; amine binding; regulation of cellular ketone metabolic process; protein homooligomerization; cellular carbohydrate biosynthetic process; glucose metabolic process]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCa

Continued on next page. . .

S	name	locus	description	studies
u*	HES1	3:193853934-193856521 3q29	hairy and enhancer of split 1, (Drosophila) [Source:HGNC Symbol;Acc:5192], type=protein_coding,retained_intron, GO=[N-box binding; lateral inhibition; regulation of pancreatic A cell differentiation; negative regulation of pancreatic A cell differentiation; regulation of forebrain neuron differentiation; negative regulation of forebrain neuron differentiation; regulation of stomach neuroendocrine cell differentiation; negative regulation of stomach neuroendocrine cell differentiation; trochlear nerve development; negative regulation of auditory receptor cell differentiation; renal interstitial cell differentiation; renal interstitial cell development; auditory receptor cell fate determination; oculomotor nerve development; negative regulation of pro-B cell differentiation; regulation of pro-B cell differentiation; cardiac neural crest cell development involved in outflow tract morphogenesis; vascular smooth muscle cell development; midbrain-hindbrain boundary morphogenesis; forebrain radial glial cell differentiation; common bile duct development; regulation of timing of neuron differentiation; comma-shaped body morphogenesis; negative regulation of stem cell differentiation; S-shaped body morphogenesis; neuronal stem cell maintenance; metanephric nephron tubule morphogenesis; metanephric tubule morphogenesis; positive regulation of astrocyte differentiation; regulation of secondary heart field cardioblast proliferation; negative regulation of glial cell proliferation; regulation of cardioblast proliferation; cardioblast proliferation; STAT protein import into nucleus; negative regulation of oligodendrocyte differentiation; positive regulation of Notch signaling pathway; pharyngeal system development; glomerulus vasculature development; adenohypophysis development; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription; positive regulation of tyrosine phosphorylation of Stat3 protein; regulation of Notch signaling pathway; auditory receptor cell differentiation; positive regulation of BMP signaling pathway; positive regulation of DNA binding; cochlea development; hindbrain morphogenesis; midbrain development; thymus development; ventricular septum development; artery morphogenesis; nephron tubule development; somatic stem cell maintenance; outflow tract morphogenesis; negative regulation of neuron differentiation; regulation of fat cell differentiation; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; histone deacetylase binding; regulation of BMP signaling pathway; positive regulation of T cell proliferation; positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway; regulation of DNA binding; ureteric bud morphogenesis; positive regulation of binding; regulation of JAK-STAT cascade; smoothened signaling pathway; liver development; positive regulation of lymphocyte proliferation; cell maturation; regulation of binding; leukocyte proliferation; kidney development; urogenital system development; regionalization; in utero embryonic development; blood vessel morphogenesis; negative regulation of transcription from RNA polymerase II promoter; embryonic morphogenesis; protein homodimerization activity; vasculature development; hemopoiesis; negative regulation of cell proliferation; positive regulation of cell proliferation; sequence-specific DNA binding; cell morphogenesis involved in differentiation; identical protein binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa, tscapeMelanomad, tscapeNSCLCd, tscapeOvariana
u	HIPK2	7:139246316-139477577 7q34	homeodomain interacting protein kinase 2 [Source:HGNC Symbol;Acc:14402], type=protein_coding, GO=[voluntary musculoskeletal movement; PML body organization; virion binding; lens induction in camera-type eye; iris morphogenesis; embryonic retina morphogenesis in camera-type eye; retina layer formation; DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator; SMAD protein signal transduction; RNA polymerase II transcription coactivator activity; positive regulation of transforming growth factor beta receptor signaling pathway; RNA polymerase II activating transcription factor binding; DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis; embryonic camera-type eye morphogenesis; multicellular organismal movement; musculoskeletal movement; negative regulation of BMP signaling pathway; positive regulation of DNA binding; adult walking behavior; positive regulation of protein binding; virus-host interaction; cellular response to hypoxia; peptidyl-threonine phosphorylation; positive regulation of JNK cascade; lipopolysaccharide biosynthetic process; SMAD binding; PML body; regulation of BMP signaling pathway; positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway; regulation of DNA binding; interaction with host; positive regulation of binding; regulation of transforming growth factor beta receptor signaling pathway; smoothened signaling pathway; positive regulation of angiogenesis; regulation of protein binding; negative regulation of neuron apoptosis; cellular polysaccharide biosynthetic process; peptidyl-serine phosphorylation; symbiosis, encompassing mutualism through parasitism; DNA damage response, signal transduction by p53 class mediator; transforming growth factor beta receptor signaling pathway; cellular polysaccharide metabolic process; nuclear membrane; regulation of binding; transcription corepressor activity; JNK cascade; positive regulation of sequence-specific DNA binding transcription factor activity; positive regulation of MAPKKK cascade; cellular carbohydrate biosynthetic process; stress-activated protein kinase signaling cascade; embryonic organ morphogenesis; regionalization; regulation of sequence-specific DNA binding transcription factor activity; centrosome; angiogenesis; interspecies interaction between organisms; protein serine/threonine kinase activity; blood vessel morphogenesis; negative regulation of transcription from RNA polymerase II promoter; protein tyrosine kinase activity; MAPKKK cascade; embryonic morphogenesis; vasculature development; hemopoiesis; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication; protein kinase activity; negative regulation of apoptosis; positive regulation of cell proliferation; negative regulation of cell death]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tscapeMelanomaa
u	HOMER2	15:83509838-83654661 15q25.2	homer homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:17513], type=processed_transcript,protein_coding,retained_intron, GO=[metabotropic glutamate receptor binding; GKAP/Homer scaffold activity; metabotropic glutamate receptor signaling pathway; glutamate receptor binding; postsynaptic density; dendritic spine; postsynaptic membrane; neuronal cell body; protein heterodimerization activity; actin binding; synapse part; protein homodimerization activity; protein domain specific binding; neuron projection; identical protein binding]	tcgaGliomaGE
d	HOXC13	12:54332535-54340328 12q13.13	homeobox C13 [Source:HGNC Symbol;Acc:5125], type=protein_coding, GO=[tongue morphogenesis; hair follicle development; regionalization; sequence-specific DNA binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeRCCa
u	HPGD	4:175411328-175444305 4q34.1	hydroxyprostaglandin dehydrogenase 15-(NAD) [Source:HGNC Symbol;Acc:5154], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[15-hydroxyprostaglandin dehydrogenase (NAD+) activity; lipoxygenase pathway; ductus arteriosus closure; prostaglandin E receptor activity; thrombin receptor signaling pathway; NAD+ binding; parturition; ovulation; prostaglandin metabolic process; very long-chain fatty acid metabolic process; artery morphogenesis; transforming growth factor beta receptor signaling pathway; female pregnancy; cofactor binding; fatty acid metabolic process; blood vessel morphogenesis; protein homodimerization activity; vasculature development; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeMelanomad, tscapeProstated, tscapeRCCd
d	HTRA1	10:124221041-124274424 10q26.13	HtrA serine peptidase 1 [Source:HGNC Symbol;Acc:9476], type=protein_coding, GO=[insulin-like growth factor binding; negative regulation of BMP signaling pathway; negative regulation of transforming growth factor beta receptor signaling pathway; regulation of BMP signaling pathway; regulation of transforming growth factor beta receptor signaling pathway; transforming growth factor beta receptor signaling pathway; serine-type endopeptidase activity; regulation of cell growth; extracellular matrix; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication; extracellular space]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeGliomad, tscapeNSCLCd
d*	ID2	2:8818975-8824583 2p25.1	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein [Source:HGNC Symbol;Acc:5361], type=protein_coding,retained_intron, GO=[positive regulation of transcription involved in G1/S phase of mitotic cell cycle; epithelial cell differentiation involved in mammary gland alveolus development; bundle of His development; His-Purkinje system development; endodermal digestive tract morphogenesis; negative regulation of B cell differentiation; ion channel binding; positive regulation of astrocyte differentiation; entrainment of circadian clock; Peyer's patch development; negative regulation of oligodendrocyte differentiation; negative regulation of neural precursor cell proliferation; natural killer cell differentiation; cellular response to lithium ion; positive regulation of erythrocyte differentiation; adipose tissue development; embryonic digestive tract morphogenesis; positive regulation of fat cell differentiation; mammary gland epithelial cell proliferation; olfactory bulb development; cellular senescence; oligodendrocyte development; negative regulation of DNA binding; negative regulation of osteoblast differentiation; positive regulation of smooth muscle cell proliferation; negative regulation of neuron differentiation; positive regulation of myeloid cell differentiation; regulation of fat cell differentiation; negative regulation of binding; regulation of smooth muscle cell proliferation; regulation of DNA binding; positive regulation of cell cycle arrest; circadian rhythm; regulation of osteoblast differentiation; regulation of G1/S transition of mitotic cell cycle; negative regulation of sequence-specific DNA binding transcription factor activity; positive regulation of cell cycle; cell maturation; regulation of blood pressure; regulation of myeloid cell differentiation; osteoblast differentiation; regulation of ossification; regulation of binding; kidney development; regulation of lipid metabolic process; aging; embryonic organ morphogenesis; urogenital system development; regulation of sequence-specific DNA binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter; embryonic morphogenesis; hemopoiesis; negative regulation of cell proliferation; positive regulation of cell proliferation]	tcgaBreastGE, tcgaColonGE

Continued on next page...

S	name	locus	description	studies
d	IFIH1	2:163123589-163175213 2q24.2	interferon induced with helicase C domain 1 [Source:HGNC Symbol;Acc:18873], type=protein_coding,retained_intron, GO=[detection of virus; positive regulation of interferon-alpha production; positive regulation of interferon-beta production; negative regulation of type I interferon production; double-stranded RNA binding; ribonucleoprotein binding; ATP-dependent helicase activity; interspecies interaction between organisms; nucleoside-triphosphatase activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	INSIG1	7:155089486-155101945 7q36.2, 7q36.3	insulin induced gene 1 [Source:HGNC Symbol;Acc:6083], type=protein_coding,retained_intron, GO=[ER-nuclear sterol response pathway; cranial suture morphogenesis; negative regulation of fatty acid biosynthetic process; negative regulation of steroid biosynthetic process; middle ear morphogenesis; negative regulation of fat cell differentiation; cholesterol biosynthetic process; regulation of fat cell differentiation; palate development; triglyceride metabolic process; inner ear morphogenesis; glycerol ether metabolic process; regulation of cellular ketone metabolic process; regulation of lipid metabolic process; embryonic organ morphogenesis; fatty acid metabolic process; embryonic morphogenesis; endoplasmic reticulum membrane; endoplasmic reticulum part]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomaa, tscapeNSCLCd, tscapeOvariana, tscapeOvariand
u	IRS2	13:110406184-110438915 13q34	insulin receptor substrate 2 [Source:HGNC Symbol;Acc:6126], type=protein_coding, GO=[negative regulation of plasma membrane long-chain fatty acid transport; JAK-STAT cascade involved in growth hormone signaling pathway; positive regulation of fatty acid beta-oxidation; negative regulation of B cell apoptosis; phosphatidylinositol-4,5-bisphosphate 3-kinase activity; positive regulation of glycogen biosynthetic process; phosphatidylinositol 3-kinase binding; negative regulation of lipid transport; positive regulation of glucose import; insulin receptor binding; positive regulation of mesenchymal cell proliferation; positive regulation of B cell proliferation; positive regulation of insulin secretion; regulation of glucose import; negative regulation of transmembrane transport; regulation of carbohydrate biosynthetic process; fatty acid beta-oxidation; regulation of lipid transport; glycogen metabolic process; regulation of glucose metabolic process; lipid homeostasis; phosphatidylinositol-mediated signaling; positive regulation of lymphocyte proliferation; cellular polysaccharide biosynthetic process; response to glucose stimulus; cellular polysaccharide metabolic process; carbohydrate transport; negative regulation of kinase activity; regulation of cellular ketone metabolic process; insulin receptor signaling pathway; leukocyte proliferation; cellular carbohydrate biosynthetic process; regulation of lipid metabolic process; positive regulation of cell migration; glucose metabolic process; phospholipid binding; negative regulation of transport; microsome; fatty acid metabolic process; protein kinase binding; regulation of cell migration; regulation of cellular catabolic process; organic substance transport; negative regulation of apoptosis; positive regulation of cell proliferation; negative regulation of cell death]	snp3dDiabetes, snp3dObesity, tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCa, tscapeNSCLCa, tscapeSCLCa
u	ITGAV	2:187454790-187545628 2q32.1	integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) [Source:HGNC Symbol;Acc:6150], type=processed_transcript,protein_coding,retained_intron, GO=[entry of bacterium into host cell; antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent; entry of symbiont into host cell by promotion of host phagocytosis; negative regulation of low-density lipoprotein particle receptor biosynthetic process; regulation of apoptotic cell clearance; negative regulation of lipoprotein metabolic process; insulin-like growth factor I binding; opsonin binding; positive regulation of osteoblast proliferation; transforming growth factor beta binding; negative regulation of macrophage derived foam cell differentiation; negative regulation of lipid storage; entry of virus into host cell; phagocytic vesicle; apoptotic cell clearance; osteoblast proliferation; negative regulation of lipid transport; insulin-like growth factor binding; positive regulation of phagocytosis; integrin complex; protein kinase C binding; regulation of lipid transport; interaction with host; phagocytosis; symbiosis, encompassing mutualism through parasitism; positive regulation of cell adhesion; ERK1 and ERK2 cascade; external side of plasma membrane; positive regulation of cell migration; leukocyte migration; negative regulation of transport; protein kinase binding; angiogenesis; regulation of cell migration; interspecies interaction between organisms; blood vessel morphogenesis; MAPKKK cascade; vasculature development; blood coagulation; organic substance transport; negative regulation of apoptosis; positive regulation of cell proliferation; wound healing; negative regulation of cell death; cell morphogenesis involved in differentiation]	snp3dMetastasis, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	JAG1	20:10618332-10654608 20p12.2	jagged 1 [Source:HGNC Symbol;Acc:6188], type=processed_transcript,protein_coding, GO=[negative regulation of stem cell differentiation; neuronal stem cell maintenance; distal tubule development; response to muramyl dipeptide; Notch binding; loop of Henle development; positive regulation of Notch signaling pathway; morphogenesis of an epithelial sheet; Notch receptor processing; regulation of Notch signaling pathway; auditory receptor cell differentiation; negative regulation of fat cell differentiation; nephron tubule development; myoblast differentiation; endothelial cell differentiation; negative regulation of neuron differentiation; positive regulation of myeloid cell differentiation; regulation of fat cell differentiation; regulation of myeloid cell differentiation; growth factor activity; kidney development; urogenital system development; apical part of cell; angiogenesis; regulation of cell migration; blood vessel morphogenesis; vasculature development; hemopoiesis; calcium ion binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	KCNMA1	10:78637355-79398353 10q22.3	potassium large conductance calcium-activated channel, subfamily M, alpha member 1 [Source:HGNC Symbol;Acc:6284], type=processed_transcript,protein_coding, GO=[cellular potassium ion homeostasis; eye blink reflex; large conductance calcium-activated potassium channel activity; response to carbon monoxide; negative regulation of cell volume; smooth muscle contraction involved in micturition; locomotor rhythm; regulation of aldosterone metabolic process; relaxation of vascular smooth muscle; saliva secretion; regulation of hormone metabolic process; auditory receptor cell differentiation; adult walking behavior; terminal button; neuromuscular process controlling balance; vasodilation; response to osmotic stress; caveola; potassium ion transmembrane transport; cellular potassium ion transport; renal system process; digestive system process; voltage-gated potassium channel complex; response to calcium ion; circadian rhythm; voltage-gated potassium channel activity; cell maturation; sensory perception of sound; postsynaptic membrane; protein homooligomerization; external side of plasma membrane; apical plasma membrane; regulation of lipid metabolic process; apical part of cell; axon; actin binding; synapse part; blood coagulation; neuron projection; wound healing]	tcgaBreastGE, tcgaColonGE, tcgaGliomaCGHd, tcgaGliomaGE, tscapeOvariana, tscapeProstatea
u	KIF5C	HSCHR2_2_CTG12:149632819-149889354 HSCHR2_2_CTG12q23.1	kinesin family member 5C [Source:HGNC Symbol;Acc:6325], type=processed_transcript,protein_coding,retained_intron, GO=[apolipoprotein receptor binding; ciliary rootlet; kinesin complex; motor axon guidance; microtubule motor activity; microtubule-based movement; neuron projection; cell morphogenesis involved in differentiation; nucleoside-triphosphatase activity]	
u	KLF15	3:126061478-126076285 3q21.3	Kruppel-like factor 15 [Source:HGNC Symbol;Acc:14536], type=processed_transcript,protein_coding, GO=[RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; carbohydrate transport; nucleolus; organic substance transport]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
u	KRT8	12:53290971-53343738 12q13.13	keratin 8 [Source:HGNC Symbol;Acc:6446], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nuclear matrix; keratin filament; intermediate filament; intermediate filament cytoskeleton; interspecies interaction between organisms]	snp3dLungC, tcgaOvarianMethyl, tscapeRCCa
u	KRT8P33	5:122736616-122738038 5q23.2	keratin 8 pseudogene 33 [Source:HGNC Symbol;Acc:39867], type=processed_pseudogene,pseudogene	tcgaBreastGE
u	LCP1	13:46700061-46786006 13q14.13	lymphocyte cytosolic protein 1 (L-plastin) [Source:HGNC Symbol;Acc:6528], type=processed_transcript,protein_coding, GO=[phagocytic cup; ruffle membrane; T cell activation involved in immune response; actin filament; organ regeneration; actin filament binding; actin filament bundle assembly; regulation of intracellular protein transport; actin binding; calcium ion binding; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
u	LONRF1	8:12579403-12613582 8p23.1	LON peptidase N-terminal domain and ring finger 1 [Source:HGNC Symbol;Acc:26302], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[ATP-dependent peptidase activity; nucleoside-triphosphatase activity]	tcgaBreastGE, tcgaBreastMethyl
u	LRIG1	3:66429221-66551687 3p14.1	leucine-rich repeats and immunoglobulin-like domains 1 [Source:HGNC Symbol;Acc:17360], type=processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
d	LRRC31	3:169556967-169587718 3q26.2	leucine rich repeat containing 31 [Source:HGNC Symbol;Acc:26261], type=processed_transcript,protein_coding	tcgaColonGE, tcgaOvarianCGHa, tscapeBCa, tscapeNSCLCa, tscapeOvariana
u	LRRFIP2	3:37094117-37225180 3p22.2	leucine rich repeat (in FLII) interacting protein 2 [Source:HGNC Symbol;Acc:6703], type=processed_transcript,protein_coding,retained_intron, GO=[LRR domain binding; protein domain specific binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d	LRRN1	3:3841121-3889387 3p26.2	leucine rich repeat neuronal 1 [Source:HGNC Symbol;Acc:20980], type=processed_transcript,protein_coding,retained_intron	tcgaGliomaGE, tscapeOvariand

Continued on next page. . .

S	name	locus	description	studies
d	MAPKAPK3	3:50648951-50686720 3p21.2	mitogen-activated protein kinase-activated protein kinase 3 [Source:HGNC Symbol;Acc:6888], type=processed_transcript,protein_coding, GO=[TRIF-dependent toll-like receptor signaling pathway; macropinocytosis; MAP kinase kinase activity; lipopolysaccharide biosynthetic process; toll-like receptor 3 signaling pathway; toll-like receptor 1 signaling pathway; stress-activated MAPK cascade; toll-like receptor 2 signaling pathway; MyD88-dependent toll-like receptor signaling pathway; Toll signaling pathway; toll-like receptor 4 signaling pathway; cellular polysaccharide biosynthetic process; peptidyl-serine phosphorylation; activation of MAPK activity; cellular polysaccharide metabolic process; cellular carbohydrate biosynthetic process; positive regulation of protein serine/threonine kinase activity; stress-activated protein kinase signaling cascade; protein serine/threonine kinase activity; Ras protein signal transduction; protein tyrosine kinase activity; MAPKKK cascade; protein kinase activity]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	MBOAT2	2:8992820-9143942 2p25.1	membrane bound O-acyltransferase domain containing 2 [Source:HGNC Symbol;Acc:25193], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[1-acylglycerol-3-phosphate O-acyltransferase activity; phospholipid biosynthetic process]	tcgaBreastGE, tcgaColonGE
u	MERTK	2:112656056-112787138 2q13	c-mer proto-oncogene tyrosine kinase [Source:HGNC Symbol;Acc:7027], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[rhabdomere; apoptotic cell clearance; substrate adhesion-dependent cell spreading; photoreceptor outer segment; transmembrane receptor protein tyrosine kinase activity; phagocytosis; protein kinase B signaling cascade; leukocyte migration; platelet activation; soluble fraction; protein tyrosine kinase activity; blood coagulation; protein kinase activity; wound healing; cell morphogenesis involved in differentiation]	tcgaBreastGE
u	MICAL1	6:109765265-109787171 6q21	microtubule associated monoxygenase, calponin and LIM domain containing 1 [Source:HGNC Symbol;Acc:20619], type=processed_transcript,protein_coding,retained_intron, GO=[FAD binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen; actin filament depolymerization; negative regulation of caspase activity; SH3 domain binding; intermediate filament; electron carrier activity; intermediate filament cytoskeleton; negative regulation of hydrolase activity; cofactor binding; actin binding; protein domain specific binding; negative regulation of apoptosis; negative regulation of cell death]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeCRCd, tscapeSCLCd
u	MUM1L1	X:105412298-105452949 Xq22.3	melanoma associated antigen (mutated) 1-like 1 [Source:HGNC Symbol;Acc:26583], type=protein_coding	tcgaGliomaGE
u	MYBPC1	12:101962131-102079796 12q23.2	myosin binding protein C, slow type [Source:HGNC Symbol;Acc:7549], type=processed_transcript,protein_coding,retained_intron, GO=[titin binding; myosin filament; muscle filament sliding; structural constituent of muscle; myofibril; actin binding]	tcgaBreastGE, tcgaGliomaGE
u	NBL1	1:19967048-19984945 1p36.13	neuroblastoma, suppression of tumorigenicity 1 [Source:HGNC Symbol;Acc:7650], type=protein_coding, GO=[morphogen activity; negative regulation of BMP signaling pathway by extracellular sequestering of BMP; determination of dorsal identity; determination of dorsal/ventral asymmetry; negative regulation of BMP signaling pathway; regulation of BMP signaling pathway; positive regulation of neuron differentiation; regionalization; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u*	NDRG1	8:134249414-134314265 8q24.22	N-myc downstream regulated 1 [Source:HGNC Symbol;Acc:7679], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[peripheral nervous system myelin maintenance; positive regulation of spindle checkpoint; gamma-tubulin binding; cadherin binding; recycling endosome membrane; mast cell activation; cellular response to hypoxia; Rab GTPase binding; cell-cell adherens junction; recycling endosome; microtubule binding; DNA damage response, signal transduction by p53 class mediator; cell-cell junction; centrosome; perinuclear region of cytoplasm]	snp3dMetastasis, tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl
u*	NFKBIA	14:35870717-35873955 14q13.2	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha [Source:HGNC Symbol;Acc:7797], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[TRIF-dependent toll-like receptor signaling pathway; cellular response to cold; nucleotide-binding oligomerization domain containing 1 signaling pathway; I-kappaB/NF-kappaB complex; cytoplasmic sequestering of NF-kappaB; nucleotide-binding oligomerization domain containing 2 signaling pathway; response to muramyl dipeptide; nuclear localization sequence binding; negative regulation of Notch signaling pathway; positive regulation of cholesterol efflux; negative regulation of macrophage derived foam cell differentiation; negative regulation of lipid storage; response to exogenous dsRNA; NF-kappaB binding; regulation of Notch signaling pathway; negative regulation of DNA binding; lipopolysaccharide-mediated signaling pathway; negative regulation of protein import into nucleus; protein import into nucleus, translocation; negative regulation of transmembrane transport; negative regulation of NF-kappaB transcription factor activity; regulation of lipid transport; cholesterol transport; negative regulation of binding; regulation of DNA binding; toll-like receptor 3 signaling pathway; negative regulation of myeloid cell differentiation; toll-like receptor 1 signaling pathway; toll-like receptor 2 signaling pathway; MyD88-dependent toll-like receptor signaling pathway; Toll signaling pathway; heat shock protein binding; toll-like receptor 4 signaling pathway; negative regulation of protein transport; T cell receptor signaling pathway; positive regulation of NF-kappaB transcription factor activity; negative regulation of sequence-specific DNA binding transcription factor activity; ubiquitin protein ligase binding; regulation of intracellular protein transport; regulation of myeloid cell differentiation; regulation of binding; positive regulation of sequence-specific DNA binding transcription factor activity; negative regulation of transport; anti-apoptosis; regulation of sequence-specific DNA binding transcription factor activity; interspecies interaction between organisms; hemopoiesis; negative regulation of signal transduction; organic substance transport; negative regulation of signaling; negative regulation of cell communication; negative regulation of apoptosis; negative regulation of cell death; identical protein binding]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	ODC1	2:10580094-10588630 2p25.1	ornithine decarboxylase 1 [Source:HGNC Symbol;Acc:8109], type=processed_transcript,protein_coding, GO=[ornithine decarboxylase activity; polyamine biosynthetic process; cellular biogenic amine biosynthetic process; regulation of cellular amino acid metabolic process; regulation of cellular ketone metabolic process; kidney development; urogenital system development; positive regulation of cell proliferation]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE
u	PACS1	11:65837834-66012218 11q13.1, 11q13.2	phosphofurin acidic cluster sorting protein 1 [Source:HGNC Symbol;Acc:30032], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[protein targeting to plasma membrane; ion channel binding; protein targeting to Golgi; COPI-coated vesicle; regulation of defense response to virus by virus; positive regulation of protein binding; positive regulation of binding; regulation of protein binding; defense response to virus; regulation of binding; coated vesicle; interspecies interaction between organisms; perinuclear region of cytoplasm; Golgi apparatus part]	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	PAK1IP1	6:10694928-10710015 6p24.2	PAK1 interacting protein 1 [Source:HGNC Symbol;Acc:20882], type=protein_coding, GO=[negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication]	tcgaColonGE, tcgaOvarianGE, tscapeBCa, tscapeOvariana, tscapeProstated, tscapeSCLCd
u	PDIA5	3:122785909-122944074 3q21.1	protein disulfide isomerase family A, member 5 [Source:HGNC Symbol;Acc:24811], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[activation of signaling protein activity involved in unfolded protein response; protein disulfide isomerase activity; protein disulfide oxidoreductase activity; antioxidant activity; cell redox homeostasis; endoplasmic reticulum lumen; glycerol ether metabolic process; electron carrier activity; protein folding; endoplasmic reticulum membrane; endoplasmic reticulum part]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	PEA15	1:160175127-160185166 1q23.2	phosphoprotein enriched in astrocytes 15 [Source:HGNC Symbol;Acc:8822], type=processed_transcript,protein_coding, GO=[negative regulation of glucose import; response to isoquinoline alkaloid; response to morphine; regulation of glucose import; response to alkaloid; carbohydrate transport; negative regulation of transport; anti-apoptosis; organic substance transport; negative regulation of apoptosis; negative regulation of cell death]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
u	PGC	6:41704449-41721847 6p21.1	progastricsin (pepsinogen C) [Source:HGNC Symbol;Acc:8890], type=protein_coding, GO=[aspartic-type endopeptidase activity; nucleolus; extracellular space]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeCRCa, tscapeOvariana
u	PHGR1	15:40643234-40648635 15q15.1	proline/histidine/glycine-rich 1 [Source:HGNC Symbol;Acc:37226], type=protein_coding,retained_intron	
u*	PNLIP	10:118305443-118327367 10q25.3	pancreatic lipase [Source:HGNC Symbol;Acc:9155], type=processed_transcript,protein_coding, GO=[retinyl-palmitate esterase activity; intestinal cholesterol absorption; triglyceride lipase activity; retinoid metabolic process; digestive system process; response to lipid; cholesterol transport; post-embryonic development; organic substance transport; extracellular space]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd
u*	PPAP2A	5:54720682-54830878 5q11.2	phosphatidic acid phosphatase type 2A [Source:HGNC Symbol;Acc:9228], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[phosphatidate phosphatase activity; germ cell migration; phospholipid dephosphorylation; activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway; sphingolipid biosynthetic process; androgen receptor signaling pathway; protein dephosphorylation; regulation of lipid metabolic process; negative regulation of cell proliferation]	tcgaBreastGE, tcgaColonGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated

Continued on next page...

S	name	locus	description	studies
d	PRKD1	14:30045687-30661104 14q12	protein kinase D1 [Source:HGNC Symbol;Acc:9407], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[regulation of integrin-mediated signaling pathway; endothelial cell chemotaxis; regulation of keratinocyte proliferation; positive regulation of CREB transcription factor activity; protein kinase C activity; positive regulation of blood vessel endothelial cell migration; negative regulation of endocytosis; Golgi organization; vascular endothelial growth factor receptor signaling pathway; sphingolipid biosynthetic process; positive regulation of osteoblast differentiation; positive regulation of neuron projection development; positive regulation of endothelial cell proliferation; trans-Golgi network; positive regulation of angiogenesis; regulation of osteoblast differentiation; positive regulation of NF-kappaB transcription factor activity; cellular response to oxidative stress; peptidyl-serine phosphorylation; osteoblast differentiation; positive regulation of I-kappaB kinase/NF-kappaB cascade; regulation of ossification; cell cortex; positive regulation of sequence-specific DNA binding transcription factor activity; positive regulation of cell migration; phospholipid binding; response to oxidative stress; cell-cell junction; negative regulation of transport; regulation of sequence-specific DNA binding transcription factor activity; angiogenesis; regulation of cell migration; protein serine/threonine kinase activity; blood vessel morphogenesis; protein tyrosine kinase activity; vasculature development; Golgi apparatus part; protein kinase activity; positive regulation of cell proliferation; negative regulation of cell death]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeHCCa
u	PTGER4	5:40679600-40693837 5p13.1	prostaglandin E receptor 4 (subtype EP4) [Source:HGNC Symbol;Acc:9596], type=processed_transcript,protein_coding, GO=[negative regulation of eosinophil migration; regulation of eosinophil migration; eosinophil extravasation; regulation of eosinophil extravasation; negative regulation of integrin activation; negative regulation of eosinophil extravasation; prostaglandin E receptor activity; negative regulation of leukocyte migration; negative regulation of cytokine secretion; T-helper cell differentiation; CD4-positive, alpha-beta T cell differentiation involved in immune response; regulation of stress fiber assembly; T cell activation involved in immune response; cellular response to mechanical stimulus; negative regulation of inflammatory response; positive regulation of inflammatory response; actin filament bundle assembly; negative regulation of protein transport; G-protein signaling, coupled to cAMP nucleotide second messenger; ERK1 and ERK2 cascade; regulation of ossification; JNK cascade; stress-activated protein kinase signaling cascade; leukocyte migration; negative regulation of transport; regulation of cell migration; MAPKKK cascade; hemopoiesis]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeSCLCa
u	PYGB	20:25228705-25278650 20p11.21	phosphorylase, glycogen; brain [Source:HGNC Symbol;Acc:9723], type=processed_transcript,protein_coding, GO=[glycogen phosphorylase activity; glycogen catabolic process; pyridoxal phosphate binding; glycogen metabolic process; drug binding; cellular polysaccharide metabolic process; glucose metabolic process; axon; cofactor binding; soluble fraction; protein homodimerization activity; neuron projection; identical protein binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	RAB3B	1:52373628-52456436 1p32.3	RAB3B, member RAS oncogene family [Source:HGNC Symbol;Acc:9778], type=protein_coding, GO=[peptidyl-cysteine methylation; synaptic vesicle; clathrin-coated vesicle; coated vesicle; stored secretory granule; GTPase activity; synapse part; GTP binding; GTP catabolic process; purine ribonucleoside triphosphate metabolic process; nucleoside-triphosphatase activity]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	RGS2	1:192778169-192781403 1q31.2	regulator of G-protein signaling 2, 24kDa [Source:HGNC Symbol;Acc:9998], type=processed_transcript,protein_coding, GO=[relaxation of cardiac muscle; negative regulation of phospholipase activity; regulation of adrenergic receptor signaling pathway; positive regulation of cardiac muscle contraction; relaxation of vascular smooth muscle; positive regulation of striated muscle contraction; negative regulation of cardiac muscle hypertrophy; negative regulation of G-protein coupled receptor protein signaling pathway; brown fat cell differentiation; vasodilation; negative regulation of MAP kinase activity; internal side of plasma membrane; calmodulin binding; negative regulation of protein kinase activity; negative regulation of kinase activity; regulation of translation; negative regulation of hydrolase activity; regulation of GTPase activity; regulation of nucleotide metabolic process; regulation of cellular catabolic process; negative regulation of signal transduction; GTP catabolic process; nucleolus; negative regulation of signaling; negative regulation of cell communication; purine ribonucleoside triphosphate metabolic process]	fileBC2brain, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d	RILPL2	12:123899936-123921264 12q24.31	Rab interacting lysosomal protein-like 2 [Source:HGNC Symbol;Acc:28787], type=protein_coding, GO=[identical protein binding]	tcgaBreastGE
d	RP11-124L9.1	HSCHR5_1_CTG1:69151881-69194073 HSCHR5_1_CTG1q13.2	[undefined], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	
d	RP11-124L9.2	HSCHR5_1_CTG1:690509 69144625 HSCHR5_1_CTG1q13.2	[undefined], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	
d	RP11-124L9.6	HSCHR5_1_CTG1:69640521-69650987 HSCHR5_1_CTG1q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
d	RP11-1264N5.1	HSCHR5_1_CTG1:6935987 69430017 HSCHR5_1_CTG1q13.2	[undefined], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	
d	RP11-181C21.4	1:78276507-78277621 1p31.1	[undefined], type=processed_pseudogene,pseudogene,retrotransposed	
u	RP11-18F14.2	16:80631803-80636416 16q23.2	[undefined], type=lincRNA	tcgaBreastGE
d	RP11-195E2.1	5:70370052-70389020 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
d	RP11-279F6.1	15:69755365-69863775 15q23	[undefined], type=lincRNA	tcgaColonGE
d	RP11-510N19.5	1:201980498-201984785 1q32.1	[undefined], type=processed_transcript	
u	RP11-529H2.2	4:88238322-88266362 4q22.1	[undefined], type=processed_transcript	
u	S100P	4:6694796-6698897 4p16.1	S100 calcium binding protein P [Source:HGNC Symbol;Acc:10504], type=processed_transcript,protein_coding, GO=[calcium-dependent protein binding; magnesium ion binding; calcium ion binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
u*	SAT1	X:23801290-23804343 Xp22.11	spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:10540], type=processed_transcript,protein_coding, GO=[spermidine binding; polyamine binding; diamine N-acetyltransferase activity; polyamine biosynthetic process; cellular biogenic amine biosynthetic process; amine binding; angiogenesis; soluble fraction; blood vessel morphogenesis; vasculature development]	tcgaGliomaGE
u	SGK1	6:134490384-134639250 6q23.2	serum/glucocorticoid regulated kinase 1 [Source:HGNC Symbol;Acc:10810], type=processed_transcript,protein_coding,retained_intron, GO=[renal sodium ion absorption; regulation of gastric acid secretion; chloride channel regulator activity; sodium channel regulator activity; calcium channel regulator activity; long-term memory; potassium channel regulator activity; positive regulation of transporter activity; renal system process; digestive system process; regulation of blood pressure; phospholipid binding; regulation of cell growth; regulation of sequence-specific DNA binding transcription factor activity; regulation of cell migration; protein serine/threonine kinase activity; protein tyrosine kinase activity; protein kinase activity; endoplasmic reticulum membrane; endoplasmic reticulum part]	cosmicRecurrent, tcgaBreastGE, tcgaColonGE, tscapeBCa, tscapeCRCa
u	SHROOM3	4:77356253-77704406 4q21.1	shroom family member 3 [Source:HGNC Symbol;Acc:30422], type=processed_transcript,protein_coding,retained_intron, GO=[cellular pigment accumulation; columnar/cuboidal epithelial cell development; apical protein localization; neural tube closure; regulation of cell shape; apical junction complex; apical plasma membrane; cell-cell junction; apical part of cell; actin binding; embryonic morphogenesis]	tscapeHCCd
u	SLC16A3	17:80186293-80197369 17q25.3	solute carrier family 16, member 3 (monocarboxylic acid transporter 4) [Source:HGNC Symbol;Acc:10924], type=protein_coding, GO=[secondary active monocarboxylate transmembrane transporter activity; pyruvate metabolic process; organic anion transport; symporter activity; nuclear membrane; leukocyte migration; blood coagulation; organic substance transport; wound healing]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tscapeBCa, tscapeMelanomaa, tscapeNSCLCa, tscapeOvariana
d	SLC7A5	16:87863629-87903094 16q24.2	solute carrier family 7 (amino acid transporter light chain, L system), member 5 [Source:HGNC Symbol;Acc:11063], type=protein_coding,retained_intron, GO=[peptide antigen binding; neutral amino acid transmembrane transporter activity; neutral amino acid transport; L-amino acid transmembrane transporter activity; amino acid transmembrane transport; apical plasma membrane; leukocyte migration; apical part of cell; blood coagulation; organic substance transport; wound healing]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeProstated
d	SLITRK3	3:164904508-164914897 3q26.1	SLIT and NTRK-like family, member 3 [Source:HGNC Symbol;Acc:23501], type=protein_coding, GO=[cell morphogenesis involved in differentiation]	cosmicMetastasis, cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
u	SNAI2	8:49830249-49834299 8q11.21	snail homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11094], type=protein_coding, GO=[desmosome disassembly; negative regulation of stem cell proliferation; negative regulation of anoikis; negative regulation of vitamin D receptor signaling pathway; negative regulation of cell adhesion involved in substrate-bound cell migration; regulation of tight junction assembly; negative regulation of keratinocyte proliferation; negative regulation of vitamin D biosynthetic process; negative regulation of cell adhesion mediated by integrin; epithelial to mesenchymal transition involved in endocardial cushion formation; negative regulation of catenin import into nucleus; cellular response to epidermal growth factor stimulus; negative regulation of DNA damage response, signal transduction by p53 class mediator; regulation of keratinocyte proliferation; cartilage morphogenesis; negative regulation of chondrocyte differentiation; white fat cell differentiation; positive regulation of survival gene product expression; positive regulation of histone acetylation; negative regulation of steroid biosynthetic process; regulation of catenin import into nucleus; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription; positive regulation of fat cell differentiation; regulation of chondrocyte differentiation; negative regulation of protein import into nucleus; negative regulation of transmembrane transport; regulation of fat cell differentiation; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; negative regulation of canonical Wnt receptor signaling pathway; chondrocyte differentiation; palate development; negative regulation of protein transport; regulation of osteoblast differentiation; sequence-specific distal enhancer binding RNA polymerase II transcription factor activity; regulation of canonical Wnt receptor signaling pathway; nuclear chromatin; DNA damage response, signal transduction by p53 class mediator; sensory perception of sound; regulation of intracellular protein transport; osteoblast differentiation; regulation of ossification; regulation of lipid metabolic process; positive regulation of cell migration; negative regulation of transport; anti-apoptosis; response to radiation; regulation of cell migration; negative regulation of transcription from RNA polymerase II promoter; negative regulation of cell proliferation; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication; negative regulation of apoptosis; negative regulation of cell death; sequence-specific DNA binding; cell morphogenesis involved in differentiation]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeRCCd
u	SOCS2	12:93963590-93977263 12q22	suppressor of cytokine signaling 2 [Source:HGNC Symbol;Acc:19382], type=ambiguous_orf,processed_transcript,protein_coding, GO=[JAK pathway signal transduction adaptor activity; prolactin receptor binding; growth hormone receptor binding; JAK-STAT cascade involved in growth hormone signaling pathway; insulin-like growth factor receptor binding; SH3/SH2 adaptor activity; regulation of JAK-STAT cascade; response to estradiol stimulus; aging; anti-apoptosis; regulation of cell growth; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication; negative regulation of apoptosis; negative regulation of cell death]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE
u	SPOCK1	5:136310987-136934068 5q31.2	sparc/osteonectin, cwcv and kazal-like domains proteoglycan (testican) 1 [Source:HGNC Symbol;Acc:11251], type=processed_transcript,protein_coding,retained_intron, GO=[node of Ranvier; metalloendopeptidase inhibitor activity; negative regulation of cell-substrate adhesion; negative regulation of neuron projection development; neuromuscular junction; cysteine-type endopeptidase inhibitor activity; sarcoplasm; negative regulation of endopeptidase activity; serine-type endopeptidase inhibitor activity; neuron migration; postsynaptic density; dendritic spine; negative regulation of hydrolase activity; axon; regulation of cell growth; synapse part; extracellular matrix; neuron projection; calcium ion binding; extracellular space]	tcgaBreastGE, tcgaGliomaGE
u	SPRY2	13:80910111-80915086 13q31.1	sprouty homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:11270], type=protein_coding, GO=[lung growth; negative regulation of nerve growth factor receptor signaling pathway; negative regulation of Ras GTPase activity; protein serine/threonine kinase activator activity; negative regulation of fibroblast growth factor receptor signaling pathway; negative regulation of ERK1 and ERK2 cascade; negative regulation of Ras protein signal transduction; positive regulation of peptidyl-serine phosphorylation; negative regulation of epidermal growth factor receptor signaling pathway; lung morphogenesis; ruffle membrane; positive regulation of protein kinase B signaling cascade; negative regulation of MAP kinase activity; positive regulation of ERK1 and ERK2 cascade; protein kinase B signaling cascade; inner ear morphogenesis; peptidyl-serine phosphorylation; ERK1 and ERK2 cascade; sensory perception of sound; negative regulation of protein kinase activity; negative regulation of kinase activity; branching morphogenesis of a tube; positive regulation of MAPKKK cascade; positive regulation of protein serine/threonine kinase activity; embryonic organ morphogenesis; negative regulation of hydrolase activity; regulation of GTPase activity; Ras protein signal transduction; regulation of nucleotide metabolic process; regulation of cellular catabolic process; MAPKKK cascade; embryonic morphogenesis; negative regulation of cell proliferation; negative regulation of signal transduction; GTP catabolic process; negative regulation of signaling; negative regulation of cell communication; negative regulation of apoptosis; negative regulation of cell death; purine ribonucleoside triphosphate metabolic process]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
u	ST3GAL4	11:126225535-126310239 11q24.2	ST3 beta-galactoside alpha-2,3-sialyltransferase 4 [Source:HGNC Symbol;Acc:10864], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[monosialoganglioside sialyltransferase activity; beta-galactoside alpha-2,3-sialyltransferase activity; O-glycan processing; integral to Golgi membrane; Golgi cisterna membrane; Golgi cisterna; peptidyl-asparagine modification; protein N-linked glycosylation via asparagine; post-translational protein modification; Golgi apparatus part]	tcgaBreastGE, tscapeBCd, tscapeNSCLCd
u	STK39	2:168810530-169104651 2q24.3	serine threonine kinase 39 [Source:HGNC Symbol;Acc:17717], type=processed_transcript,protein_coding, GO=[signal transduction via phosphorylation event; positive regulation of potassium ion transport; receptor signaling protein serine/threonine kinase activity; apical plasma membrane; apical part of cell; basolateral plasma membrane; protein kinase binding; protein serine/threonine kinase activity; protein tyrosine kinase activity; protein kinase activity]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	SUSD4	1:223394161-223537544 1q41	sushi domain containing 4 [Source:HGNC Symbol;Acc:25470], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaGliomaGE
u	TBC1D8	2:101624079-101869328 2q11.2	TBC1 domain family, member 8 (with GRAM domain) [Source:HGNC Symbol;Acc:17791], type=processed_transcript,protein_coding,retained_intron, GO=[Rab GTPase activator activity; regulation of Rab GTPase activity; regulation of GTPase activity; Ras protein signal transduction; regulation of nucleotide metabolic process; regulation of cellular catabolic process; GTP catabolic process; positive regulation of cell proliferation; calcium ion binding; purine ribonucleoside triphosphate metabolic process]	
u	TIPARP	3:156391024-156424559 3q25.31	TCDD-inducible poly(ADP-ribose) polymerase [Source:HGNC Symbol;Acc:23696], type=protein_coding, GO=[estrogen metabolic process; smooth muscle tissue development; NAD+ ADP-ribosyltransferase activity; protein ADP-ribosylation; androgen metabolic process; face morphogenesis; platelet-derived growth factor receptor signaling pathway; vasculogenesis; multicellular organismal metabolic process; palate development; female gonad development; post-embryonic development; kidney development; urogenital system development; blood vessel morphogenesis; vasculature development; hemopoiesis]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
d	TMEM144	4:159122756-159176563 4q32.1	transmembrane protein 144 [Source:HGNC Symbol;Acc:25633], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[carbohydrate transmembrane transport; carbohydrate transmembrane transporter activity; carbohydrate transport; organic substance transport]	tcgaGliomaGE, tscapeRCCd
d	TRIB1	8:126442563-126450647 8q24.13	tribbles homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:16891], type=processed_transcript,protein_coding, GO=[ubiquitin-protein ligase regulator activity; ligase regulator activity; negative regulation of lipopolysaccharide-mediated signaling pathway; negative regulation of smooth muscle cell migration; mitogen-activated protein kinase kinase binding; negative regulation of smooth muscle cell proliferation; positive regulation of proteasomal ubiquitin-dependent protein catabolic process; lipopolysaccharide-mediated signaling pathway; regulation of smooth muscle cell proliferation; negative regulation of sequence-specific DNA binding transcription factor activity; ubiquitin protein ligase binding; negative regulation of protein kinase activity; negative regulation of kinase activity; JNK cascade; stress-activated protein kinase signaling cascade; protein kinase binding; regulation of sequence-specific DNA binding transcription factor activity; regulation of cell migration; regulation of cellular catabolic process; MAPKKK cascade; negative regulation of cell proliferation; negative regulation of signal transduction; negative regulation of signaling; negative regulation of cell communication; protein kinase activity]	fileAmpOver, tcgaBreastMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeHCCa, tscapeOvariana
u	TSC22D1	13:45007655-45151283 13q14.11	TSC22 domain family, member 1 [Source:HGNC Symbol;Acc:16826], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[negative regulation of apoptosis; positive regulation of cell proliferation; negative regulation of cell death]	tcgaBreastGE, tcgaGliomaGE, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
u	TSKU	11:76493295-76509198 11q13.5	tsukushi small leucine rich proteoglycan homolog (Xenopus laevis) [Source:HGNC Symbol;Acc:28850], type=protein_coding	tscapeOvariana
u*	TUBA3C	13:19747910-19755992 13q12.11	tubulin, alpha 3c [Source:HGNC Symbol;Acc:12408], type=processed_transcript,protein_coding, GO=[cytoplasmic microtubule; 'de novo' posttranslational protein folding; structural constituent of cytoskeleton; microtubule-based movement; protein polymerization; protein folding; GTPase activity; microtubule cytoskeleton organization; GTP binding; protein domain specific binding; GTP catabolic process; purine ribonucleoside triphosphate metabolic process; nucleoside-triphosphatase activity]	tcgaBreastGE, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd

Continued on next page...

S	name	locus	description	studies
u*	TUBA3D	2:132233666-132240507 2q21.1	tubulin, alpha 3d [Source:HGNC Symbol;Acc:24071], type=processed_transcript,protein_coding, GO=[cytoplasmic microtubule; 'de novo' posttranslational protein folding; structural constituent of cytoskeleton; microtubule-based movement; protein polymerization; protein folding; GTPase activity; microtubule cytoskeleton organization; GTP binding; protein domain specific binding; GTP catabolic process; purine ribonucleoside triphosphate metabolic process; nucleoside-triphosphatase activity]	tcgaBreastGE, tcgaColonGE, tscapeOvariand, tscapeProstated
u	TUBA3E	2:130949318-130956034 2q21.1	tubulin, alpha 3e [Source:HGNC Symbol;Acc:20765], type=protein_coding, GO=[cytoplasmic microtubule; structural constituent of cytoskeleton; microtubule-based movement; protein polymerization; GTPase activity; microtubule cytoskeleton organization; GTP binding; protein domain specific binding; GTP catabolic process; purine ribonucleoside triphosphate metabolic process; nucleoside-triphosphatase activity]	tscapeCRCa, tscapeOvariand, tscapeProstated
d	UGT2B17	4:69402902-69434245 4q13.2	UDP glucuronosyltransferase 2 family, polypeptide B17 [Source:HGNC Symbol;Acc:12547], type=protein_coding, GO=[lipid glycosylation; glucuronosyltransferase activity; microsome; endoplasmic reticulum membrane; endoplasmic reticulum part]	tcgaBreastMethyl
u	USP10	16:84733584-84813528 16q24.1	ubiquitin specific peptidase 10 [Source:HGNC Symbol;Acc:12608], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cystic fibrosis transmembrane conductance regulator binding; ubiquitin-specific protease activity; p53 binding; protein deubiquitination; ubiquitin thiolesterase activity; DNA damage response, signal transduction by p53 class mediator; early endosome; intermediate filament cytoskeleton; DNA repair]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeProstated
u	WDYHV1	8:124428965-124479470 8q24.13	WDYHV motif containing 1 [Source:HGNC Symbol;Acc:25490], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[protein N-terminal glutamine amidohydrolase activity]	tcgaBreastGE, tcgaColonGE, tcgaOvarianCGHa
u	WIPI1	17:66417423-66453653 17q24.2	WD repeat domain, phosphoinositide interacting 1 [Source:HGNC Symbol;Acc:25471], type=protein_coding, GO=[vesicle targeting, trans-Golgi to endosome; PAS complex; activation of signaling protein activity involved in unfolded protein response; pre-autophagosomal structure membrane; phosphatidylinositol-3,5-bisphosphate binding; phosphatidylinositol-3-phosphate binding; autophagic vacuole membrane; estrogen receptor binding; androgen receptor binding; macroautophagy; trans-Golgi network; clathrin-coated vesicle; coated vesicle; phospholipid binding; Golgi apparatus part]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	ZBTB16	11:113930315-114121398 11q23.2	zinc finger and BTB domain containing 16 [Source:HGNC Symbol;Acc:12930], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[germ-line stem cell division; male germ-line stem cell division; positive regulation of cartilage development; positive regulation of chondrocyte differentiation; mesonephros development; positive regulation of fat cell differentiation; regulation of chondrocyte differentiation; embryonic hindlimb morphogenesis; forelimb morphogenesis; positive regulation of ossification; transcriptional repressor complex; regulation of fat cell differentiation; PML body; embryonic pattern specification; negative regulation of myeloid cell differentiation; chondrocyte differentiation; nuclear speck; regulation of myeloid cell differentiation; regulation of ossification; kidney development; urogenital system development; regionalization; embryonic morphogenesis; protein homodimerization activity; hemopoiesis; negative regulation of cell proliferation; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeBCd, tscapeMelanomad, tscapeProstated
u	ZBTB24	6:109783797-109804440 6q21	zinc finger and BTB domain containing 24 [Source:HGNC Symbol;Acc:21143], type=protein_coding	
d	ZIC2	13:100634026-100639018 13q32.3	Zic family member 2 [Source:HGNC Symbol;Acc:12873], type=processed_transcript,protein_coding, GO=[retinal ganglion cell axon guidance; chromatin DNA binding; developmental pigmentation; neural tube closure; positive regulation of sequence-specific DNA binding transcription factor activity; visual perception; regulation of sequence-specific DNA binding transcription factor activity; embryonic morphogenesis; cell morphogenesis involved in differentiation]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tscapeSCLCa
u	ZNF18	17:11880762-11900785 17p12	zinc finger protein 18 [Source:HGNC Symbol;Acc:12969], type=protein_coding	tcgaBreastGE

12.2.1 GO enrichment of all candidates

Table 30: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.05$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.173	BP	negative regulation of cell communication	ADRB2, AIDA, APOD, BAMBI, BCHE, DEPTOR, ERRFI1, F2RL1, HIPK2, HTRA1, NBL1, NFKBIA, PAK1IP1, RGS2, SNAI2, SOCS2, SPRY2, TRIB1
0.173	BP	negative regulation of signaling	ADRB2, AIDA, APOD, BAMBI, BCHE, DEPTOR, ERRFI1, F2RL1, HIPK2, HTRA1, NBL1, NFKBIA, PAK1IP1, RGS2, SNAI2, SOCS2, SPRY2, TRIB1
0.163	BP	negative regulation of signal transduction	ADRB2, AIDA, APOD, BAMBI, DEPTOR, ERRFI1, F2RL1, HIPK2, HTRA1, NBL1, NFKBIA, PAK1IP1, RGS2, SNAI2, SOCS2, SPRY2, TRIB1
0.221	BP	cellular component movement	APOD, BAMBI, F2RL1, HES1, IRS2, ITGAV, JAG1, KIF5C, MERTK, MYBPC1, PPAP2A, PRKD1, PTGER4, S100P, SGK1, SLC16A3, SLC7A5, SNAI2, SPOCK1, TRIB1, TUBA3C, TUBA3D, TUBA3E
0.221	BP	regulation of cell proliferation	ADRB2, APOD, BAMBI, DHCR24, EAF2, HES1, HIPK2, ID2, IRS2, ITGAV, JAG1, NFKBIA, ODC1, PPAP2A, PRKD1, SAT1, SGK1, SNAI2, SPRY2, TBC1D8, TRIB1, TSC22D1, ZBTB16
0.029	BP	activation of signaling protein activity involved in unfolded protein response	DNAJB9, PDIA5, WIPI1
0.058	BP	regulation of fat cell differentiation	HES1, ID2, INSIG1, JAG1, SNAI2, ZBTB16
0.173	BP	cell migration	APOD, BAMBI, F2RL1, HES1, IRS2, ITGAV, JAG1, MERTK, PPAP2A, PRKD1, PTGER4, S100P, SGK1, SLC16A3, SLC7A5, SNAI2, SPOCK1, TRIB1
0.096	BP	negative regulation of transport	ADRB2, APOD, F2RL1, IRS2, ITGAV, NFKBIA, PEA15, PRKD1, PTGER4, SNAI2
0.784	MF	protein binding	ACAA1, ADRB2, AIDA, ANKRD37, APOD, ARHGAP10, ATAD2, ATP1A1, BAMBI, BCHE, CAMK2N1, CAP2, CBLN2, CEBPD, CREB3L2, CXCR7, DBI, DDC, DEPTOR, DHCR24, DNAJB9, EAF2, ELOVL5, ERRFI1, F2RL1, FKBP5, GLRX, GNMT, HES1, HIPK2, HOMER2, HOXC13, HPGD, HTRA1, ID2, IFIH1, INSIG1, IRS2, ITGAV, JAG1, KCNMA1, KIF5C, KLF15, KRT8, LCP1, LONRF1, LRIG1, LRRC31, LRRFIP2, LRRN1, MAPKAPK3, MERTK, MICAL1, MYBPC1, NDRG1, NFKBIA, PACS1, PAK1IP1, PEA15, PNLIP, PRKD1, PTGER4, PYGB, RAB3B, RGS2, RILPL2, S100P, SAT1, SGK1, SHROOM3, SLITRK3, SOCS2, SPOCK1, SPRY2, ST3GAL4, STK39, TRIB1, TSKU, TUBA3C, TUBA3D, TUBA3E, USP10, WDYHV1, WIPI1, ZBTB16, ZBTB24, ZIC2
0.567	BP	multicellular organismal process	ACSL3, ADRB2, AIDA, APOD, ATP1A1, BAMBI, BCHE, CAP2, CBLN2, COLEC12, CREB3L2, CXCR7, DBI, DDC, DHCR24, EAF2, ERRFI1, F2RL1, FAM134B, FIGNL1, HES1, HIPK2, HOXC13, HPGD, ID2, IFIH1, INSIG1, IRS2, ITGAV, JAG1, KCNMA1, KIF5C, KLF15, LCP1, MERTK, MYBPC1, NBL1, NDRG1, NFKBIA, ODC1, PGC, PNLIP, PPAP2A, PRKD1, PTGER4, RGS2, SAT1, SGK1, SHROOM3, SLC16A3, SLC7A5, SLITRK3, SNAI2, SPOCK1, SPRY2, TBC1D8, TIPARP, ZBTB16, ZIC2
0.077	BP	regulation of binding	ADRB2, AIDA, BAMBI, HES1, HIPK2, ID2, NFKBIA, PACS1
0.404	BP	system development	ACSL3, ADRB2, APOD, BAMBI, CAP2, CBLN2, CREB3L2, DBI, DHCR24, EAF2, ERRFI1, F2RL1, HES1, HIPK2, HOXC13, HPGD, ID2, INSIG1, IRS2, ITGAV, JAG1, KCNMA1, KIF5C, KLF15, LCP1, MERTK, NBL1, NDRG1, NFKBIA, ODC1, PRKD1, PTGER4, SAT1, SHROOM3, SLC7A5, SLITRK3, SNAI2, SPOCK1, SPRY2, TIPARP, ZBTB16, ZIC2
0.714	CC	cytoplasm	AC078802.1, ACAA1, ACPP, ACSL3, ADRB2, AIDA, ANKRD37, APOD, ARHGAP10, ATP1A1, BAMBI, BCHE, BRP44, CREB3L2, CRISPLD2, CXCR7, DBI, DDC, DHCR24, DNAJB9, ELOVL5, ERRFI1, F2RL1, FAM134B, FAM198B, FIGNL1, FKBP5, GLDC, GLRX, GNMT, HES1, HIPK2, HOMER2, HPGD, HTRA1, ID2, IFIH1, INSIG1, IRS2, ITGAV, KCNMA1, KIF5C, KRT8, LCP1, MAPKAPK3, MERTK, MICAL1, MYBPC1, NDRG1, NFKBIA, ODC1, PACS1, PDIA5, PEA15, PRKD1, PYGB, RAB3B, RGS2, RILPL2, S100P, SAT1, SGK1, SHROOM3, SLC7A5, SNAI2, SOCS2, SPOCK1, SPRY2, ST3GAL4, STK39, TRIB1, TSC22D1, TUBA3C, TUBA3D, TUBA3E, UGT2B17, USP10, WDYHV1, WIPI1, ZIC2
0.144	BP	negative regulation of cell death	ARHGAP10, CXCR7, DHCR24, FIGNL1, HIPK2, IRS2, ITGAV, MICAL1, NFKBIA, PEA15, PRKD1, SNAI2, SOCS2, SPRY2, TSC22D1
0.202	BP	lipid metabolic process	ACAA1, ACSL3, APOD, ATP1A1, DBI, DHCR24, ELOVL5, HIPK2, HPGD, ID2, INSIG1, IRS2, KCNMA1, MAPKAPK3, MBOAT2, PNLIP, PPAP2A, PRKD1, SNAI2, TIPARP, UGT2B17
0.019	BP	TRIF-dependent toll-like receptor signaling pathway	MAPKAPK3, NFKBIA
0.077	BP	regulation of lipid metabolic process	APOD, ATP1A1, ID2, INSIG1, IRS2, KCNMA1, PPAP2A, SNAI2
0.135	BP	negative regulation of apoptosis	ARHGAP10, CXCR7, DHCR24, FIGNL1, HIPK2, IRS2, ITGAV, MICAL1, NFKBIA, PEA15, SNAI2, SOCS2, SPRY2, TSC22D1
0.202	BP	regulation of apoptosis	ADRB2, ARHGAP10, CXCR7, DEPTOR, DHCR24, EAF2, FIGNL1, HIPK2, IFIH1, IRS2, ITGAV, KCNMA1, MICAL1, NFKBIA, PEA15, SGK1, SNAI2, SOCS2, SPRY2, TSC22D1, ZBTB16
0.067	BP	negative regulation of kinase activity	AIDA, DEPTOR, ERRFI1, IRS2, RGS2, SPRY2, TRIB1
0.096	BP	regulation of cell migration	APOD, F2RL1, IRS2, ITGAV, JAG1, PRKD1, PTGER4, SGK1, SNAI2, TRIB1
0.154	BP	enzyme linked receptor protein signaling pathway	ADRB2, APOD, BAMBI, ERRFI1, HES1, HIPK2, HPGD, HTRA1, IRS2, MAPKAPK3, NBL1, NFKBIA, PRKD1, SOCS2, SPRY2, TIPARP
0.029	BP	negative regulation of steroid biosynthetic process	ATP1A1, INSIG1, SNAI2
0.231	BP	regulation of multicellular organismal process	ADRB2, APOD, ATP1A1, BAMBI, BCHE, CBLN2, EAF2, ERRFI1, F2RL1, HES1, HIPK2, ID2, IFIH1, JAG1, KCNMA1, NBL1, NFKBIA, PRKD1, PTGER4, RGS2, SGK1, SNAI2, SPOCK1, ZBTB16
0.048	BP	regulation of protein binding	ADRB2, AIDA, BAMBI, HIPK2, PACS1
0.048	BP	negative regulation of protein transport	APOD, F2RL1, NFKBIA, PTGER4, SNAI2
0.038	BP	negative regulation of transmembrane transport	APOD, IRS2, NFKBIA, SNAI2
0.038	BP	vasodilation	ADRB2, F2RL1, KCNMA1, RGS2
0.144	BP	intracellular protein kinase cascade	ADRB2, AIDA, F2RL1, HES1, HIPK2, IRS2, ITGAV, MAPKAPK3, MERTK, NFKBIA, PRKD1, PTGER4, SOCS2, SPRY2, TRIB1
0.019	BP	negative regulation of chemokine production	APOD, F2RL1
0.144	BP	cellular lipid metabolic process	ACAA1, ACSL3, APOD, DBI, ELOVL5, HIPK2, HPGD, INSIG1, IRS2, MAPKAPK3, MBOAT2, PNLIP, PPAP2A, PRKD1, UGT2B17
0.250	CC	cytosol	APOD, ARHGAP10, DDC, DHCR24, GLRX, GNMT, HPGD, HTRA1, ID2, IFIH1, IRS2, LCP1, MAPKAPK3, MYBPC1, NDRG1, NFKBIA, ODC1, PACS1, PRKD1, RAB3B, RGS2, RILPL2, SAT1, SLC7A5, SOCS2, SPRY2, WDYHV1, WIPI1
0.058	BP	negative regulation of protein kinase activity	AIDA, DEPTOR, ERRFI1, RGS2, SPRY2, TRIB1
0.054	MF	amine binding	ACPP, ADRB2, BCHE, DDC, GNMT, SAT1
0.058	BP	regulation of ossification	ADRB2, ID2, PRKD1, PTGER4, SNAI2, ZBTB16
0.029	BP	positive regulation of fat cell differentiation	ID2, SNAI2, ZBTB16
0.019	BP	JAK-STAT cascade involved in growth hormone signaling pathway	IRS2, SOCS2
0.018	MF	choline binding	ACPP, BCHE
0.019	BP	negative regulation of lipoprotein metabolic process	APOD, ITGAV
0.019	BP	negative regulation of stem cell differentiation	HES1, JAG1
0.018	MF	prostaglandin E receptor activity	HPGD, PTGER4
0.038	BP	regulation of BMP signaling pathway	HES1, HIPK2, HTRA1, NBL1
0.029	BP	regulation of Notch signaling pathway	HES1, JAG1, NFKBIA
0.038	BP	renal system process	ADRB2, F2RL1, KCNMA1, SGK1
0.029	BP	auditory receptor cell differentiation	HES1, JAG1, KCNMA1
0.067	BP	leukocyte migration	APOD, F2RL1, ITGAV, MERTK, PTGER4, SLC16A3, SLC7A5
0.019	BP	positive regulation of potassium ion transport	ADRB2, STK39
0.019	BP	relaxation of vascular smooth muscle	KCNMA1, RGS2
0.192	BP	cell development	APOD, BAMBI, CAP2, F2RL1, HES1, ID2, ITGAV, JAG1, KCNMA1, KIF5C, MERTK, NBL1, NDRG1, PRKD1, SHROOM3, SLITRK3, SNAI2, SPOCK1, ZBTB16, ZIC2
0.029	BP	negative regulation of BMP signaling pathway	HIPK2, HTRA1, NBL1
0.106	BP	organic substance transport	APOD, DDC, IRS2, ITGAV, KLF15, NFKBIA, PEA15, PNLIP, SLC16A3, SLC7A5, TMEM144
0.038	BP	regulation of DNA binding	HES1, HIPK2, ID2, NFKBIA
0.038	BP	positive regulation of binding	BAMBI, HES1, HIPK2, PACS1
0.067	BP	urogenital system development	EAF2, HES1, ID2, JAG1, ODC1, TIPARP, ZBTB16
0.087	BP	interspecies interaction between organisms	APOD, CXCR7, F2RL1, HIPK2, IFIH1, ITGAV, KRT8, NFKBIA, PACS1
0.019	BP	neuronal stem cell maintenance	HES1, JAG1
0.019	BP	positive regulation of striated muscle contraction	ATP1A1, RGS2
0.240	BP	anatomical structure morphogenesis	APOD, BAMBI, CAP2, ERRFI1, HES1, HIPK2, HOXC13, HPGD, ID2, INSIG1, ITGAV, JAG1, KIF5C, LCP1, MERTK, NBL1, PRKD1, SAT1, SHROOM3, SLITRK3, SNAI2, SPRY2, TIPARP, ZBTB16, ZIC2
0.144	BP	purine-containing compound metabolic process	ACPP, ADRB2, ARHGAP10, ATP1A1, CAP2, ERRFI1, FIGNL1, GNMT, RAB3B, RGS2, SPRY2, TBC1D8, TUBA3C, TUBA3D, TUBA3E
0.048	BP	glycerol ether metabolic process	ACSL3, DBI, ELOVL5, INSIG1, PDIA5
0.029	BP	positive regulation of protein binding	BAMBI, HIPK2, PACS1
0.018	MF	ion channel binding	ID2, PACS1
0.027	CC	cytoplasmic microtubule	TUBA3C, TUBA3D, TUBA3E

Continued on next page...

Ratio	Type	Description	Genes
0.019	BP	positive regulation of astrocyte differentiation	HES1, ID2
0.019	BP	response to muramyl dipeptide	JAG1, NFKBIA
0.058	BP	kidney development	HES1, ID2, JAG1, ODC1, TIPARP, ZBTB16
0.087	BP	blood vessel morphogenesis	APOD, HES1, HIPK2, HPGD, ITGAV, JAG1, PRKD1, SAT1, TIPARP
0.029	BP	cellular biogenic amine biosynthetic process	DDC, ODC1, SAT1
0.048	BP	regulation of blood pressure	ADRB2, ATP1A1, F2RL1, ID2, SGK1
0.096	BP	vasculature development	APOD, ERRFI1, HES1, HIPK2, HPGD, ITGAV, JAG1, PRKD1, SAT1, TIPARP
0.019	BP	alkaloid metabolic process	BCHE, DDC
0.029	BP	negative regulation of protein import into nucleus	APOD, NFKBIA, SNAI2
0.048	BP	regulation of intracellular protein transport	APOD, BAMBI, LCP1, NFKBIA, SNAI2

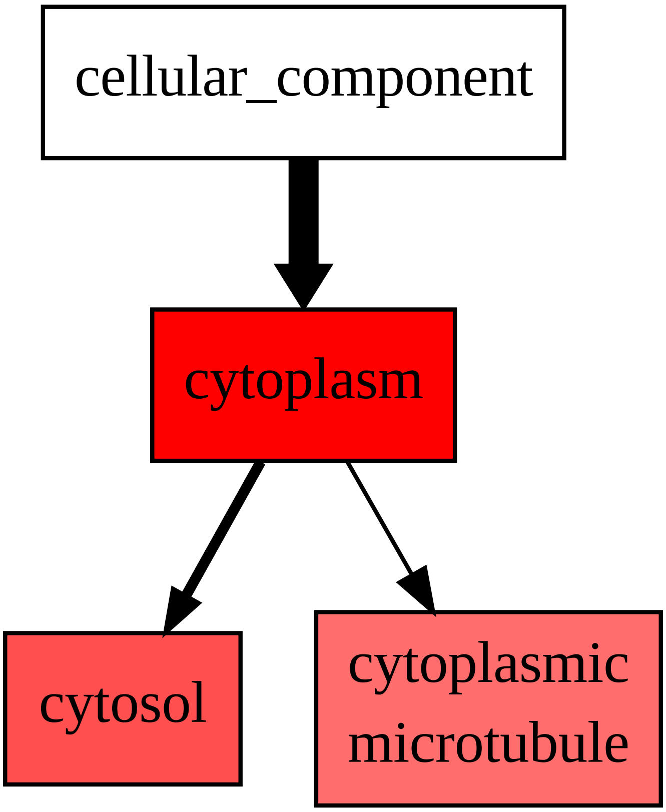


Figure 54: Relationships between the enriched *cellular component* Gene Ontology terms that were listed in Table 30. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

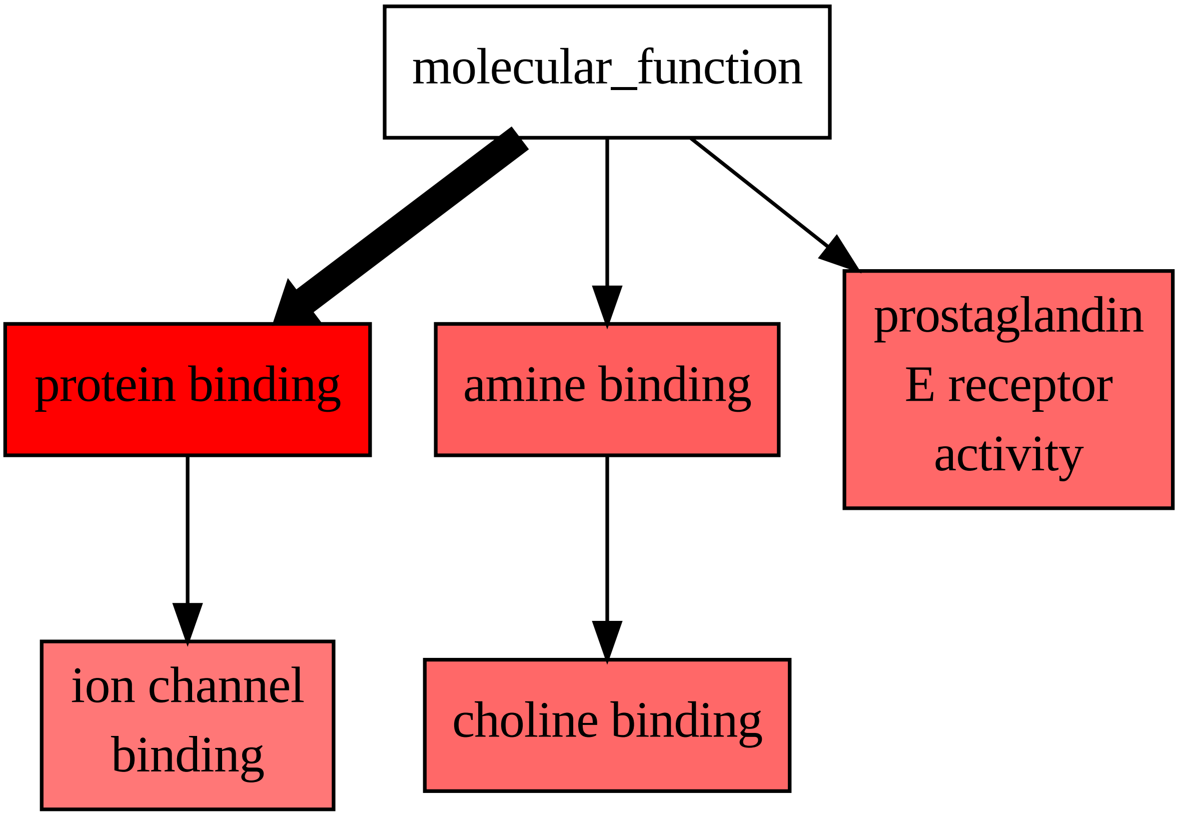


Figure 55: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 30. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

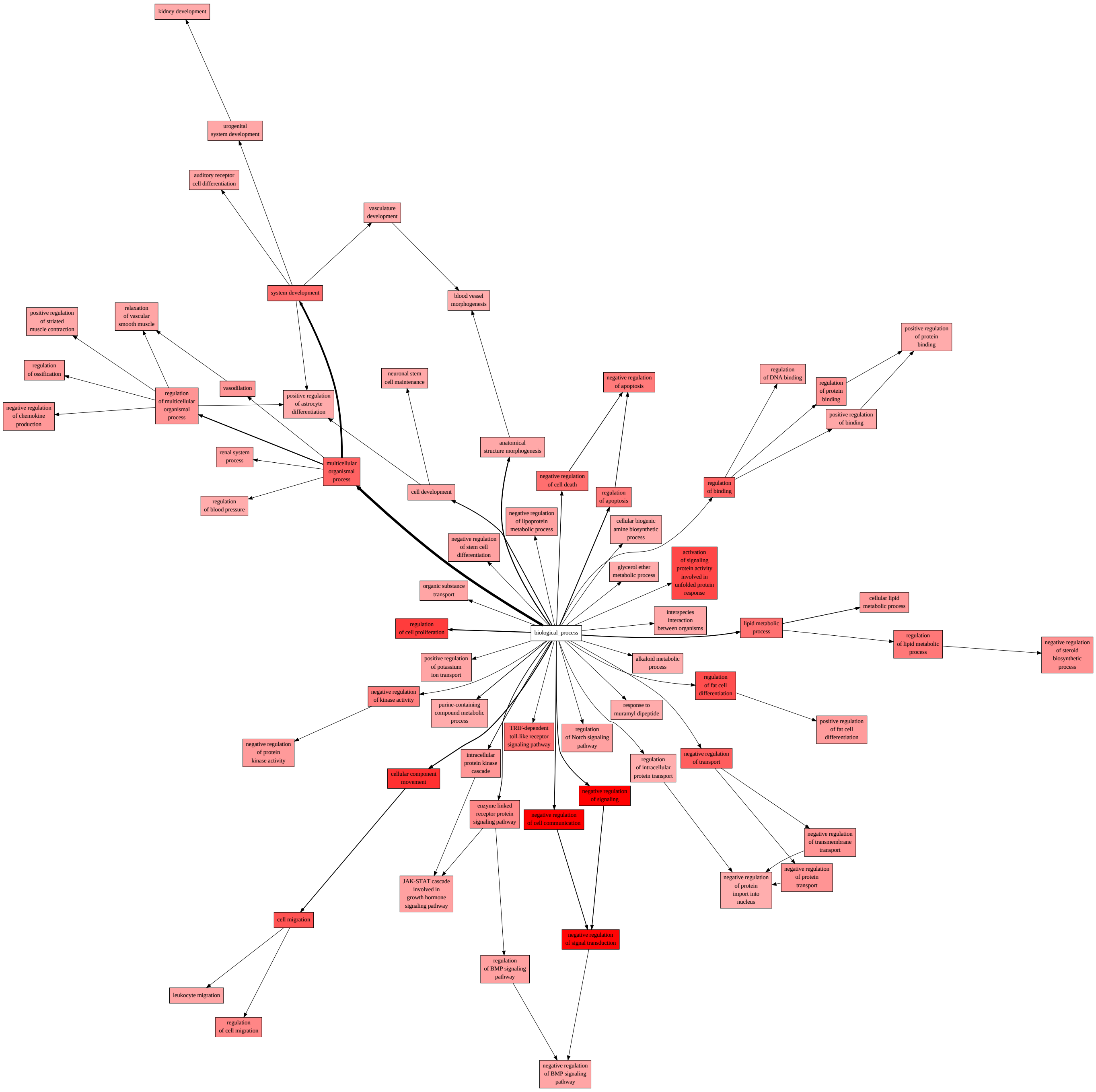


Figure 56: Relationships between the enriched *biological process* Gene Ontology terms that were listed in Table 30. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

13 Candidate report for DHT no DEX

13.1 Moksiskaan candidate pathway

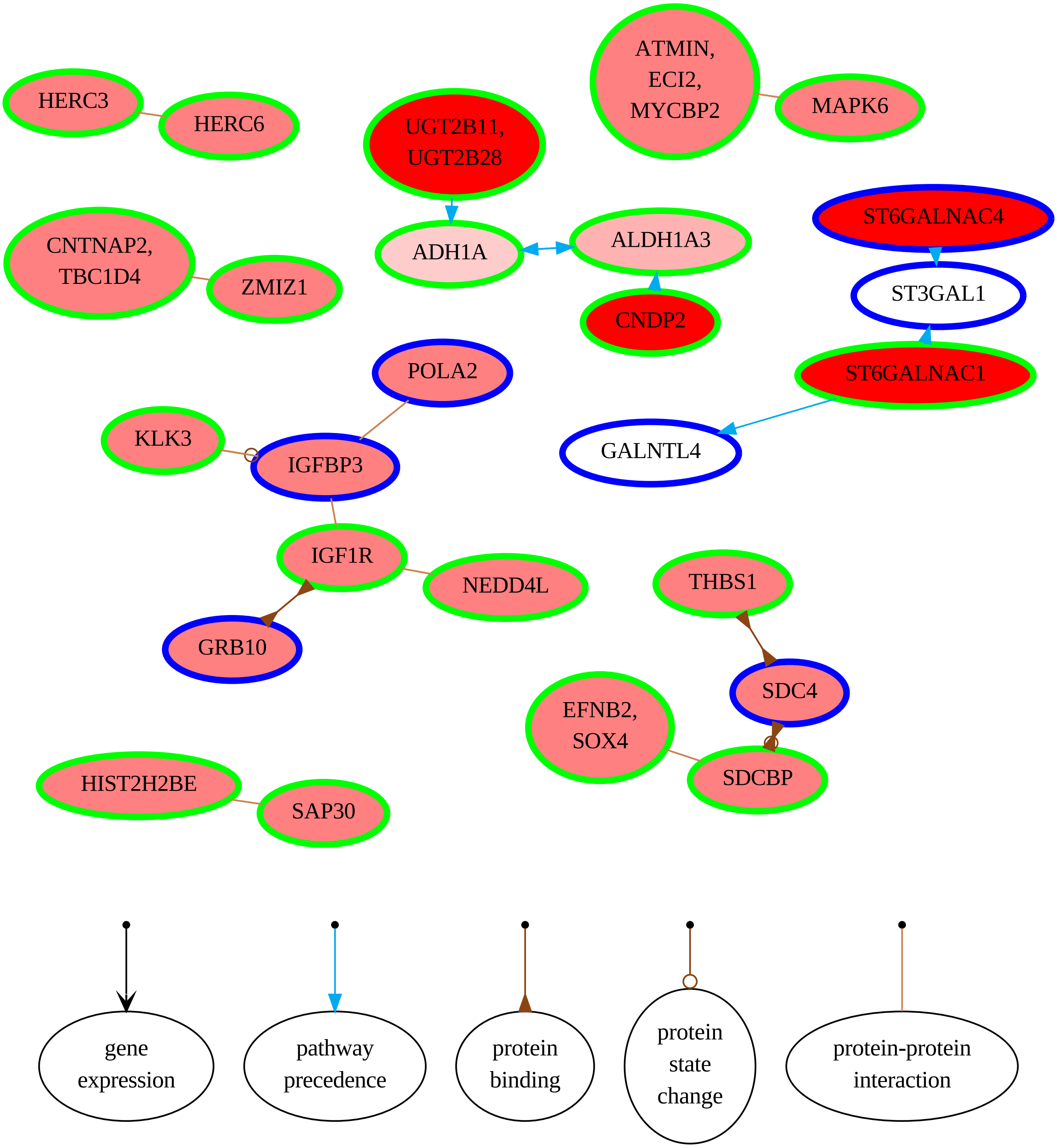


Figure 57: Known relationships between the candidate genes. Candidate genes are shown in red if they have only output connections. The ratio of input and output connections determines how light they are. Completely white genes have only input connections. The maximum of 0 other gene step(s) are allowed between the candidate genes and these intermediate genes are shown on gray. Green and blue borders are referring to up and down regulated genes, respectively. Light grey is used to emphasize stably expressed genes. Known regulations are shown with bold borders whereas the predictions are kept thin.

Table 31: List of KEGG [6] pathways supporting the relationships between the genes shown in Figure 57. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Metabolism of xenobiotics by cytochrome P450	3	ADH1A, ALDH1A3, UGT2B11, UGT2B28

Continued on next page...

name	edges	genes
Mucin type O-Glycan biosynthesis	2	GALNTL4, ST3GAL1, ST6GALNAC1
Drug metabolism - cytochrome P450	2	ADH1A, ALDH1A3, UGT2B11, UGT2B28
Endocytosis	2	IGF1R, NEDD4L
Glycolysis / Gluconeogenesis	1	ADH1A, ALDH1A3
Tyrosine metabolism	1	ADH1A, ALDH1A3
beta-Alanine metabolism	1	ALDH1A3, CNDP2
Glycosphingolipid biosynthesis - ganglio series	1	ST3GAL1, ST6GALNAC4

13.1.1 GO enrichment of the candidate pathway

Table 32: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.01$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.097	MF	fibronectin binding	IGFBP3, SDC4, THBS1
0.097	MF	sialyltransferase activity	ST3GAL1, ST6GALNAC1, ST6GALNAC4
0.194	MF	transferase activity, transferring glycosyl groups	GALNTL4, ST3GAL1, ST6GALNAC1, ST6GALNAC4, UGT2B11, UGT2B28

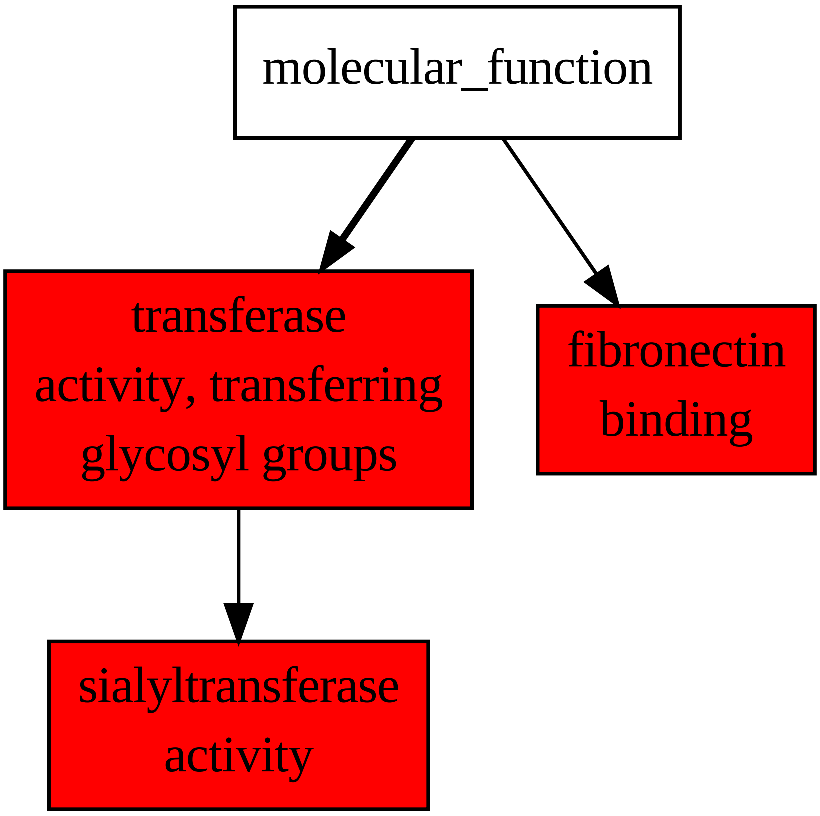


Figure 58: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 32. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

13.2 Candidate genes

Table 33: Descriptions of the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. S column contains an at sign if the gene is part of the candidate pathway. The statuses of the genes are shown as: *a*=absent, *d*=down regulated, *u*=up regulated, *s*=stable. This table has 257 rows.

S	name	locus	description	studies
d	ABCB9	12:123405498-123466196 12q24.31	ATP-binding cassette, sub-family B (MDR/TAP), member 9 [Source:HGNC Symbol;Acc:50], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[TAP complex; TAP2 binding; TAP1 binding; tapasin binding; TAP binding; oligopeptide-transporting ATPase activity; MHC class I protein binding; peptide antigen binding; positive regulation of T cell mediated cytotoxicity; T cell mediated cytotoxicity; regulation of T cell mediated immunity; lysosomal membrane; lytic vacuole; lysosome; protein homodimerization activity; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	ABCC4	13:95672083-95953687 13q32.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 4 [Source:HGNC Symbol;Acc:55], type=processed_transcript,protein_coding, GO=[15-hydroxyprostaglandin dehydrogenase (NAD+) activity; platelet dense granule membrane; platelet degranulation; platelet activation; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa
d	AC010170.1	3:45266617-45267519 3p21.31	[undefined], type=pseudogene	
u	AC020915.4	19:58816715-58827023 19q13.43	[undefined], type=lincRNA,retained_intron	
d	AC073869.2	2:132109787-132110812 2q21.1	[undefined], type=processed_pseudogene,pseudogene	
u	ACAD8	11:134123389-134135749 11q25	acyl-CoA dehydrogenase family, member 8 [Source:HGNC Symbol;Acc:87], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[acyl-CoA dehydrogenase activity; branched chain family amino acid catabolic process; flavin adenine dinucleotide binding; mitochondrial matrix]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd
u	ADAMTS1	21:28208606-28217728 21q21.3	ADAM metallopeptidase with thrombospondin type 1 motif, 1 [Source:HGNC Symbol;Acc:217], type=protein_coding,retained_intron, GO=[ovulation from ovarian follicle; heart trabecula formation; integrin-mediated signaling pathway; basement membrane; metalloendopeptidase activity; heparin binding; metallopeptidase activity; urogenital system development; carbohydrate binding; cytoplasmic vesicle]	cosmicMetastasis, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
d	ADCY1	7:45613739-45762715 7p12.3	adenylate cyclase 1 (brain) [Source:HGNC Symbol;Acc:232], type=protein_coding,retained_intron, GO=[calcium- and calmodulin-responsive adenylate cyclase activity; activation of protein kinase A activity; phosphorus-oxygen lyase activity; cyclase activity; long-term memory; response to lithium ion; water transport; cellular response to glucagon stimulus; inhibition of adenylate cyclase activity by G-protein signaling pathway; activation of adenylate cyclase activity by G-protein signaling pathway; memory; circadian rhythm; epidermal growth factor receptor signaling pathway; G-protein signaling, coupled to cAMP nucleotide second messenger; calmodulin binding; nerve growth factor receptor signaling pathway; GTPase activity; cellular response to peptide hormone stimulus; positive regulation of protein kinase activity; response to drug; response to peptide hormone stimulus]	tcgaGliomaGE, tcgaOvarianMethyl
d	ADD3	10:111756126-111895323 10q25.1	adducin 3 (gamma) [Source:HGNC Symbol;Acc:245], type=processed_transcript,protein_coding, GO=[protein kinase C binding; structural constituent of cytoskeleton; calmodulin binding; actin binding; response to drug; soluble fraction]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand
u*	ADH1A	4:100197524-100212185 4q23	alcohol dehydrogenase 1A (class I), alpha polypeptide [Source:HGNC Symbol;Acc:249], type=processed_transcript,protein_coding,retained_intron, GO=[alcohol dehydrogenase activity, zinc-dependent; ethanol oxidation; ethanol metabolic process; xenobiotic metabolic process]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianGE, tscapeHCCd
u	ADH1C	4:100257649-100274184 4q23	alcohol dehydrogenase 1C (class I), gamma polypeptide [Source:HGNC Symbol;Acc:251], type=polymorphic_pseudogene,processed_transcript	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tscapeHCCd
u*	ALDH1A3	15:101402129-101456831 15q26.3	aldehyde dehydrogenase 1 family, member A3 [Source:HGNC Symbol;Acc:409], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nucleus accumbens development; retinoic acid biosynthetic process; olfactory pit development; thyroid hormone binding; aldehyde dehydrogenase [NAD(P)+] activity; optic cup morphogenesis involved in camera-type eye development; retinal metabolic process; aldehyde dehydrogenase (NAD) activity; NAD+ binding; striatum development; embryonic camera-type eye development; face development; pituitary gland development; NAD binding; limbic system development; diencephalon development; respiratory system development; urogenital system development; response to drug; protein homodimerization activity; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeMelanomaa, tscapeNSCLCa
u	APIP	11:34874641-34938046 11p13	APAF1 interacting protein [Source:HGNC Symbol;Acc:17581], type=processed_transcript,protein_coding, GO=[methylthioribulose 1-phosphate dehydratase activity; L-methionine salvage from methylthioadenosine; methionine metabolic process; polyamine metabolic process; sulfur amino acid metabolic process; sulfur compound biosynthetic process; identical protein binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa
d	ARHGEF3	3:56761446-57113357 3p14.3	Rho guanine nucleotide exchange factor (GEF) 3 [Source:HGNC Symbol;Acc:683], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[Rho guanyl-nucleotide exchange factor activity; induction of apoptosis by extracellular signals; phospholipid binding; nerve growth factor receptor signaling pathway]	tscapeHCCd
u*	ATMIN	16:81069452-81080963 16q23.2	ATM interactor [Source:HGNC Symbol;Acc:29034], type=processed_transcript,protein_coding,retained_intron	tcgaColonGE, tcgaGliomaGE, tscapeProstated
d	ATP12A	13:25254549-25285921 13q12.12	ATPase, H+/K+ transporting, nongastric, alpha polypeptide [Source:HGNC Symbol;Acc:13816], type=protein_coding, GO=[hydrogen:potassium-exchanging ATPase complex; hydrogen:potassium-exchanging ATPase activity; potassium ion homeostasis; potassium-transporting ATPase activity; ATP biosynthetic process; proton transport; potassium ion transport; apical plasma membrane; apical part of cell]	tcgaOvarianMethyl, tscapeBCd, tscapeSCLCd
d	ATP1B1	1:169074935-169101960 1q24.2	ATPase, Na+/K+ transporting, beta 1 polypeptide [Source:HGNC Symbol;Acc:804], type=processed_transcript,protein_coding, GO=[sodium:potassium-exchanging ATPase complex; sodium:potassium-exchanging ATPase activity; potassium-transporting ATPase activity; ATP biosynthetic process; caveola; potassium ion transport; apical plasma membrane; apical part of cell]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	B2M	15:45003675-45011075 15q21.1	beta-2-microglobulin [Source:HGNC Symbol;Acc:914], type=TEC,nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[early endosome lumen; antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent; antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent; antigen processing and presentation of peptide antigen via MHC class Ib; antigen processing and presentation of exogenous peptide antigen via MHC class Ib; antigen processing and presentation of exogenous protein antigen via MHC class Ib, TAP-dependent; phagocytic vesicle membrane; protein refolding; positive regulation of T cell mediated cytotoxicity; MHC class I protein complex; T cell mediated cytotoxicity; ER to Golgi transport vesicle membrane; regulation of defense response to virus by virus; regulation of T cell mediated immunity; regulation of defense response to virus; early endosome membrane; T cell differentiation in thymus; interferon-gamma-mediated signaling pathway; external side of plasma membrane; cytokine-mediated signaling pathway; response to bacterium; cell surface; viral reproduction; Golgi membrane; cytoplasmic membrane-bounded vesicle; endoplasmic reticulum part; cytoplasmic vesicle]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeMelanomad, tscapeNSCLCd
d	BARD1	2:215590370-215674428 2q35	BRCA1 associated RING domain 1 [Source:HGNC Symbol;Acc:952], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[negative regulation of mRNA 3'-end processing; BRCA1-BARD1 complex; negative regulation of protein export from nucleus; BRCA1-A complex; protein K6-linked ubiquitination; positive regulation of protein catabolic process; tissue homeostasis; regulation of protein catabolic process; ubiquitin-protein ligase activity; protein heterodimerization activity; DNA repair; protein homodimerization activity; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeRCCd

Continued on next page...

S	name	locus	description	studies
u	BBS4	15:72978527-73030817 15q24.1	Bardet-Biedl syndrome 4 [Source:HGNC Symbol;Acc:969], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[leptin-mediated signaling pathway; regulation of flagellum assembly; positive regulation of flagellum assembly; sensory processing; regulation of cilium movement; convergent extension involved in gastrulation; regulation of cilium movement involved in cell motility; cilium movement involved in cell motility; pigment granule aggregation in cell center; regulation of cilium beat frequency involved in ciliary motility; microtubule anchoring at centrosome; dynactin binding; retinal rod cell development; negative regulation of appetite; nonmotile primary cilium assembly; retina homeostasis; BBSome; centriolar satellite; motile cilium; melanosome transport; negative regulation of systemic arterial blood pressure; negative regulation of response to nutrient levels; negative regulation of response to extracellular stimulus; regulation of response to food; pericentriolar material; cilium membrane; striatum development; maintenance of protein location in nucleus; melanosome localization; alpha-tubulin binding; beta-tubulin binding; brain morphogenesis; regulation of cytokinesis; photoreceptor cell maintenance; cell cycle cytokinesis; positive regulation of multicellular organism growth; heart looping; centriole; hippocampus development; microtubule basal body; nonmotile primary cilium; centrosome organization; sensory perception of smell; limbic system development; microtubule motor activity; neural tube closure; spermatid development; neural tube formation; adult behavior; dendrite development; tissue homeostasis; germ cell development; cytokine-mediated signaling pathway]	snp3dObesity, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	BCAP29	7:107220422-107269615 7q22.3	B-cell receptor-associated protein 29 [Source:HGNC Symbol;Acc:24131], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaOvarianMethyl
d	C11orf92	11:111164114-111175770 11q23.1	chromosome 11 open reading frame 92 [Source:HGNC Symbol;Acc:33789], type=processed_transcript,protein_coding	tcgaBreastGE
u	C19orf48	19:51300962-51307974 19q13.33	chromosome 19 open reading frame 48 [Source:HGNC Symbol;Acc:29667], type=protein_coding	tcgaBreastGE, tcgaGliomaGE
u	C1QTNF9B-AS1	13:24463028-24471402 13q12.12	C1QTNF9B antisense RNA 1 (non-protein coding) [Source:HGNC Symbol;Acc:39839], type=antisense	
u	C1orf116	1:207191866-207206101 1q32.1, 1q32.2	chromosome 1 open reading frame 116 [Source:HGNC Symbol;Acc:28667], type=protein_coding	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeProstatea
u	C1orf21	1:184356192-184598154 1q25.3	chromosome 1 open reading frame 21 [Source:HGNC Symbol;Acc:15494], type=ambiguous_orf,processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeProstated
d	C1orf53	1:197871777-197876497 1q31.3	chromosome 1 open reading frame 53 [Source:HGNC Symbol;Acc:30003], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE
u	C2orf76	2:120059801-120124404 2q14.2	chromosome 2 open reading frame 76 [Source:HGNC Symbol;Acc:27017], type=processed_transcript,protein_coding	tcgaColonGE
u	C3orf58	3:143690640-143767561 3q24	chromosome 3 open reading frame 58 [Source:HGNC Symbol;Acc:28490], type=processed_transcript,protein_coding,retained_intron, GO=[COPI vesicle coat; vesicle coat; Golgi membrane; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
u	C4orf34	4:39552541-39640710 4p14	chromosome 4 open reading frame 34 [Source:HGNC Symbol;Acc:27321], type=nonsense_mediated_decay,processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE
d	C5orf30	5:102594403-102614361 5q21.1	chromosome 5 open reading frame 30 [Source:HGNC Symbol;Acc:25052], type=protein_coding, GO=[ciliary transition zone; nonmotile primary cilium]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
u	C6orf52	6:10671651-10695030 6p24.2	chromosome 6 open reading frame 52 [Source:HGNC Symbol;Acc:20881], type=processed_transcript,protein_coding	tcgaBreastGE
d	C7orf49	7:134777115-134855547 7q33	chromosome 7 open reading frame 49 [Source:HGNC Symbol;Acc:22432], type=processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaGliomaGE
d	CALD1	7:134429003-134655479 7q33	caldesmon 1 [Source:HGNC Symbol;Acc:1441], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[actin cap; tropomyosin binding; positive regulation of protein binding; actin filament; postsynaptic density; calmodulin binding; dendritic spine; dendrite; actin binding]	snp3dGlioma, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
u	CALU	7:128379346-128411861 7q32.1	calumenin [Source:HGNC Symbol;Acc:1458], type=protein_coding, GO=[sarcoplasmic reticulum lumen; platelet degranulation; melanosome; platelet activation; calcium ion binding; cytoplasmic membrane-bounded vesicle; endoplasmic reticulum part; cytoplasmic vesicle]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	CAPZB	1:19665267-19812066 1p36.13	capping protein (actin filament) muscle Z-line, beta [Source:HGNC Symbol;Acc:1491], type=processed_transcript,protein_coding, GO=[F-actin capping protein complex; WASH complex; actin filament capping; lamellipodium assembly; negative regulation of protein complex assembly; regulation of actin filament polymerization; lamellipodium; actin binding]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u	CBLL1	7:107384142-107401142 7q22.3, 7q31.1	Cbl proto-oncogene, E3 ubiquitin protein ligase-like 1 [Source:HGNC Symbol;Acc:21225], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[positive regulation of endocytosis; ubiquitin-protein ligase activity]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
d	CCDC28B	1:32665987-32670988 1p35.1	coiled-coil domain containing 28B [Source:HGNC Symbol;Acc:28163], type=nonsense_mediated_decay,processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand
d	CDR2L	17:72983727-73001895 17q25.1	cerebellar degeneration-related protein 2-like [Source:HGNC Symbol;Acc:29999], type=protein_coding	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa
u	CDYL2	16:80637609-80838226 16q23.2	chromodomain protein, Y-like 2 [Source:HGNC Symbol;Acc:23030], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaGliomaGE, tscapeProstated
u	CENPN	16:81040103-81066719 16q23.2	centromere protein N [Source:HGNC Symbol;Acc:30873], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[CenH3-containing nucleosome assembly at centromere; DNA replication-independent nucleosome assembly; condensed chromosome kinetochore; mitotic prometaphase; nucleosome assembly]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeProstated
u	CHRNA2	8:27317279-27337400 8p21.2	cholinergic receptor, nicotinic, alpha 2 (neuronal) [Source:HGNC Symbol;Acc:1956], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[nicotinic acetylcholine-gated receptor-channel complex; nicotinic acetylcholine-activated cation-selective channel activity; acetylcholine receptor activity; postsynaptic membrane]	tcgaGliomaGE, tcgaOvarianCGHd, tscapeOvariand
d	CHST13	3:126243126-126262134 3q21.3	carbohydrate (chondroitin 4) sulfotransferase 13 [Source:HGNC Symbol;Acc:21755], type=protein_coding, GO=[chondroitin 4-sulfotransferase activity; N-acetylgalactosamine 4-O-sulfotransferase activity; chondroitin sulfate biosynthetic process; sulfur compound biosynthetic process; carbohydrate biosynthetic process; Golgi membrane]	tcgaBreastMethyl, tcgaOvarianGE, tcgaOvarianMethyl
d	CHST15	10:125767184-125853206 10q26.13	carbohydrate (N-acetylgalactosamine 4-sulfate 6-O) sulfotransferase 15 [Source:HGNC Symbol;Acc:18137], type=processed_transcript,protein_coding, GO=[N-acetylgalactosamine 4-sulfate 6-O-sulfotransferase activity; 3'-phosphoadenosine 5'-phosphosulfate binding; carbohydrate biosynthetic process; Golgi membrane]	tcgaBreastGE, tcgaColonGE, tcgaGliomaCGHd, tcgaGliomaGE
u	CLCN2	3:184063973-184079439 3q27.1	chloride channel, voltage-sensitive 2 [Source:HGNC Symbol;Acc:2020], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cell differentiation involved in salivary gland development; voltage-gated chloride channel activity; perikaryon; chloride channel complex; chloride transport; retina development in camera-type eye; inorganic anion transport; respiratory system development; dendrite]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
u	CLDN8	21:31586324-31588391 21q22.11	claudin 8 [Source:HGNC Symbol;Acc:2050], type=protein_coding, GO=[calcium-independent cell-cell adhesion; tight junction; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	CMC2	16:81009698-81053875 16q23.2	COX assembly mitochondrial protein 2 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:24447], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl

Continued on next page...

S	name	locus	description	studies
u*	CNDP2	18:72163443-72190687 18q22.3	CNDP dipeptidase 2 (metallopeptidase M20 family) [Source:HGNC Symbol;Acc:24437], type=protein_coding, GO=[tripeptidase activity; dipeptidase activity; glutathione biosynthetic process; sulfur amino acid metabolic process; carboxypeptidase activity; glutathione metabolic process; sulfur compound biosynthetic process; xenobiotic metabolic process; metallopeptidase activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad, tscapeProstated
u*	CNTNAP2	7:145813453-148118090 7q35, 7q36.1	contactin associated protein-like 2 [Source:HGNC Symbol;Acc:13830], type=processed_transcript,protein_coding, GO=[superior temporal gyrus development; clustering of voltage-gated potassium channels; protein localization to juxtaparanode region of axon; vocalization behavior; juxtaparanode region of axon; axolemma; thalamus development; striatum development; neuron projection membrane; neuron recognition; perikaryon; limbic system development; diencephalon development; voltage-gated potassium channel complex; dendrite; cell surface]	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tscapeMelanomaa, tscapeNSCLCd, tscapeOvariana
u	CORO1B	11:67205519-67211292 11q13.2	coronin, actin binding protein, 1B [Source:HGNC Symbol;Acc:2253], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[actin filament binding; actin binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	CPNE3	8:87497059-87573726 8q21.3	copine III [Source:HGNC Symbol;Acc:2316], type=protein_coding,retained_intron, GO=[calcium-dependent phospholipid binding; phospholipid binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
u	CREB3L4	1:153940010-153946839 1q21.3	cAMP responsive element binding protein 3-like 4 [Source:HGNC Symbol;Acc:18854], type=processed_transcript,protein_coding, GO=[response to unfolded protein; Golgi membrane; positive regulation of transcription from RNA polymerase II promoter; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeHCCa, tscapeMelanomaa, tscapeNSCLCa, tscapeProstatea
u	CRIP2	14:105939299-105946499 14q32.33	cysteine-rich protein 2 [Source:HGNC Symbol;Acc:2361], type=processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaOvarianMethyl, tscapeMelanomad
u	CROT	7:86974997-87029111 7q21.12	carnitine O-octanoyltransferase [Source:HGNC Symbol;Acc:2366], type=protein_coding,retained_intron, GO=[carnitine O-octanoyltransferase activity; fatty acid beta-oxidation using acyl-CoA oxidase; peroxisomal matrix; fatty acid beta-oxidation; fatty acid catabolic process; response to organic nitrogen; response to drug; soluble fraction]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeNSCLCa
u	CTD-2008A1.2	15:45118569-45176892 15q21.1	[undefined], type=processed_transcript,pseudogene,retained_intron,transcribed_unprocessed_pseudogene	
d	CTSH	15:79213400-79241916 15q25.1	cathepsin H [Source:HGNC Symbol;Acc:2535], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[HLA-A specific activating MHC class I receptor activity; neuropeptide catabolic process; kininogen binding; dichotomous subdivision of terminal units involved in lung branching; thyroid hormone binding; bradykinin catabolic process; lamellar body; cellular response to thyroid hormone stimulus; surfactant homeostasis; positive regulation of epithelial cell migration; protein destabilization; apoptotic protease activator activity; zymogen activation; T cell mediated cytotoxicity; aminopeptidase activity; membrane protein proteolysis; cysteine-type endopeptidase activity; positive regulation of angiogenesis; metanephros development; response to retinoic acid; response to vitamin A; tissue homeostasis; positive regulation of peptidase activity; ERK1 and ERK2 cascade; serine-type endopeptidase activity; respiratory system development; urogenital system development; lytic vacuole; lysosome; MAPKKK cascade; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
u	CTSO	4:156845270-156875069 4q32.1	cathepsin O [Source:HGNC Symbol;Acc:2542], type=protein_coding, GO=[cysteine-type endopeptidase activity; lysosome; lytic vacuole]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE
u	CYP11A1	15:74630100-74660081 15q24.1	cytochrome P450, family 11, subfamily A, polypeptide 1 [Source:HGNC Symbol;Acc:2590], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[response to genistein; cholesterol monooxygenase (side-chain-cleaving) activity; fractalkine metabolic process; testosterone biosynthetic process; phthalate metabolic process; granulosa cell differentiation; progesterone biosynthetic process; mitochondrial crista; dibenzo-p-dioxin metabolic process; biphenyl metabolic process; estrogen biosynthetic process; cellular response to follicle-stimulating hormone stimulus; response to L-ascorbic acid; cellular response to antibiotic; response to vitamin E; response to fungicide; cellular response to cadmium ion; cellular response to fibroblast growth factor stimulus; Leydig cell differentiation; vitamin D metabolic process; mating behavior; estrogen metabolic process; response to insecticide; cellular response to cAMP; response to salt stress; cholesterol binding; Schwann cell differentiation; maternal process involved in female pregnancy; response to corticosterone stimulus; cellular response to transforming growth factor beta stimulus; cellular response to interleukin-1; response to gamma radiation; perikaryon; hippocampus development; phenol-containing compound metabolic process; cerebellum development; cellular response to tumor necrosis factor; limbic system development; steroid binding; peripheral nervous system development; cellular response to lipopolysaccharide; cellular response to molecule of bacterial origin; response to hydrogen peroxide; response to alkaloid; response to acid; male gonad development; response to toxin; heme binding; response to glucocorticoid stimulus; xenobiotic metabolic process; response to estrogen stimulus; electron carrier activity; mitochondrial matrix; cellular response to peptide hormone stimulus; response to bacterium; response to drug; response to peptide hormone stimulus; mitochondrial envelope]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
u	CYP2U1	4:108852525-108874613 4q25	cytochrome P450, family 2, subfamily U, polypeptide 1 [Source:HGNC Symbol;Acc:20582], type=processed_transcript,protein_coding, GO=[aromatase activity; heme binding; xenobiotic metabolic process; electron carrier activity; microsome; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastGE, tcgaGliomaGE, tscapeHCCd
u	DNM1L	12:32832134-32905700 12p11.21	dynamin 1-like [Source:HGNC Symbol;Acc:2973], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[membrane fission involved in mitochondrial fission; dynamin polymerization involved in mitochondrial fission; dynamin polymerization involved in membrane fission; positive regulation of mitochondrial fission; peroxisome fission; mitochondrial fragmentation involved in apoptosis; positive regulation of protein secretion; cellular component disassembly involved in apoptosis; mitochondrial outer membrane; ubiquitin protein ligase binding; organelle outer membrane; GTPase activity; GTP binding; perinuclear region of cytoplasm; mitochondrial envelope; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl, tscapeNSCLCa
u*	ECI2	6:4115923-4135831 6p25.2	enoyl-CoA delta isomerase 2 [Source:HGNC Symbol;Acc:14601], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[dodecenoyl-CoA delta-isomerase activity; fatty-acyl-CoA binding; peroxisomal matrix; fatty acid catabolic process]	tcgaBreastGESurv, tcgaColonGE, tcgaGliomaGE
d	EDN2	1:41944446-41950344 1p34.2	endothelin 2 [Source:HGNC Symbol;Acc:3177], type=processed_transcript,protein_coding, GO=[hormonal regulation of the force of heart contraction; endothelin B receptor binding; ovarian follicle rupture; regulation of prostaglandin-endoperoxide synthase activity; positive regulation of prostaglandin-endoperoxide synthase activity; vein smooth muscle contraction; artery smooth muscle contraction; regulation of systemic arterial blood pressure by endothelin; positive regulation of the force of heart contraction by chemical signal; ovulation from ovarian follicle; positive regulation of heart rate; phasic smooth muscle contraction; macrophage chemotaxis; prostaglandin biosynthetic process; positive regulation of smooth muscle contraction; activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway; macrophage activation; neutrophil chemotaxis; negative regulation of hormone secretion; regulation of vasoconstriction; positive regulation of hormone secretion; calcium-mediated signaling; hormone activity; cytokine-mediated signaling pathway; positive regulation of protein kinase activity]	tcgaBreastGE, tcgaColonGE, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
d	EFHD1	2:233470767-233547491 2q37.1	EF-hand domain family, member D1 [Source:HGNC Symbol;Acc:29556], type=nonsense_mediated_decay,protein_coding, GO=[mitochondrial envelope; calcium ion binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tscapeBCd, tscapeRCCd
u*	EFNB2	13:107142093-107187462 13q33.3	ephrin-B2 [Source:HGNC Symbol;Acc:3227], type=protein_coding, GO=[lymph vessel development; cell migration involved in sprouting angiogenesis; ephrin receptor binding; ephrin receptor signaling pathway; sprouting angiogenesis; blood vessel endothelial cell migration; endothelial cell migration]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCa, tscapeSCLCa
u	ELOVL2	6:10980992-11044547 6p24.2	ELOVL fatty acid elongase 2 [Source:HGNC Symbol;Acc:14416], type=protein_coding, GO=[fatty acid elongase activity; fatty acid elongation, polyunsaturated fatty acid; very long-chain fatty acid biosynthetic process; long-chain fatty-acyl-CoA biosynthetic process; triglyceride biosynthetic process; triglyceride metabolic process; microsome; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastMethyl, tcgaGliomaGE, tscapeBCa, tscapeOvariana, tscapeSCLCd
u	ENDOD1	11:94822974-94865809 11q21	endonuclease domain containing 1 [Source:HGNC Symbol;Acc:29129], type=protein_coding, GO=[endonuclease activity]	tcgaColonGE
u	ENDOD1	HG348_PATCH:94822976-94865811 HG348_PATCHq21	endonuclease domain containing 1 [Source:HGNC Symbol;Acc:29129], type=protein_coding, GO=[endonuclease activity]	

Continued on next page...

S	name	locus	description	studies
d	EPHX1	1:225997794-226033260 1q42.12	epoxide hydrolase 1, microsomal (xenobiotic) [Source:HGNC Symbol;Acc:3401], type=processed_transcript,protein_coding, GO=[cis-stilbene-oxide hydrolase activity; epoxide hydrolase activity; cellular response to glucocorticoid stimulus; cellular response to corticosteroid stimulus; aromatic compound catabolic process; liver development; response to toxin; response to glucocorticoid stimulus; microsome; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tscapeBCa, tscapeProstated
d	EXOG	3:38537618-38583652 3p22.2	endo/exonuclease (5'-3'), endonuclease G-like [Source:HGNC Symbol;Acc:3347], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[endonuclease activity; mitochondrial envelope]	tcgaColonGE
u	EXTL2	1:101337943-101361554 1p21.2	exostoses (multiple)-like 2 [Source:HGNC Symbol;Acc:3516], type=processed_transcript,protein_coding, GO=[alpha-1,4-N-acetylgalactosaminyltransferase activity; glucuronyl-galactosyl-proteoglycan 4-alpha-N-acetylglucosaminyltransferase activity; UDP-N-acetylgalactosamine metabolic process; glucosamine metabolic process; N-acetylglucosamine metabolic process; nucleotide-sugar metabolic process; UDP-glycosyltransferase activity; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeProstated
d	FAM113B	12:47473386-47630443 12q13.11	family with sequence similarity 113, member B [Source:HGNC Symbol;Acc:28255], type=protein_coding	tcgaBreastGE, tcgaBreastGESurv, tcgaColonGE, tcgaColonMethyl, tscapeRCCa, tscapeSCLCa
d	FAM217B	20:58508819-58523735 20q13.33	family with sequence similarity 217, member B [Source:HGNC Symbol;Acc:16170], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
d	FAM46C	1:118148556-118170994 1p12	family with sequence similarity 46, member C [Source:HGNC Symbol;Acc:24712], type=protein_coding	tcgaOvarianMethyl, tscapeNSCLCd, tscapeSCLCa, tscapeSCLCd
d	FBXO2	1:11708424-11715842 1p36.22	F-box protein 2 [Source:HGNC Symbol;Acc:13581], type=processed_transcript,protein_coding, GO=[SCF-dependent proteasomal ubiquitin-dependent protein catabolic process; glycoprotein catabolic process; SCF ubiquitin ligase complex; beta-amyloid binding; ER-associated protein catabolic process; glycoprotein binding; dendritic spine; regulation of protein ubiquitination; ubiquitin-protein ligase activity; microsome; dendrite; carbohydrate binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
u	FDFT1	8:11653082-11696818 8p23.1	farnesyl-diphosphate farnesyltransferase 1 [Source:HGNC Symbol;Acc:3629], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[squalene synthase activity; farnesyl-diphosphate farnesyltransferase activity; farnesyl diphosphate metabolic process; isoprenoid biosynthetic process; cholesterol biosynthetic process; microsome; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHd, tcgaOvarianMethyl
d	FFAR2	19:35940617-35942667 19q13.12	free fatty acid receptor 2 [Source:HGNC Symbol;Acc:4501], type=protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeNSCLCa
d	FZD2	17:42634827-42636907 17q21.31	frizzled family receptor 2 [Source:HGNC Symbol;Acc:4040], type=protein_coding, GO=[hard palate development; G-protein signaling, coupled to cGMP nucleotide second messenger; positive regulation of cGMP metabolic process; Wnt receptor signaling pathway, calcium modulating pathway; cellular response to vitamin D; cGMP-mediated signaling; Wnt-activated receptor activity; inner ear receptor cell development; cochlea morphogenesis; ventricular septum morphogenesis; neuron projection membrane; Wnt-protein binding; ventricular septum development; outflow tract morphogenesis; sensory perception of smell; PDZ domain binding; inner ear morphogenesis; canonical Wnt receptor signaling pathway; positive regulation of sequence-specific DNA binding transcription factor activity; apical part of cell; cellular response to peptide hormone stimulus; protein heterodimerization activity; response to peptide hormone stimulus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeProstated
u	FZD5	2:208627310-208634287 2q33.3	frizzled family receptor 5 [Source:HGNC Symbol;Acc:4043], type=protein_coding, GO=[Spemann organizer formation; Wnt receptor signaling pathway involved in dorsal/ventral axis specification; post-embryonic camera-type eye development; apoptosis involved in morphogenesis; labyrinthine layer blood vessel development; anterior/posterior axis specification, embryo; tripartite regional subdivision; Wnt-activated receptor activity; Wnt-protein binding; positive regulation of interferon-gamma production; embryonic camera-type eye development; positive regulation of JUN kinase activity; T cell differentiation in thymus; embryonic placenta development; PDZ domain binding; cellular response to molecule of bacterial origin; regulation of JNK cascade; JNK cascade; canonical Wnt receptor signaling pathway; regulation of MAPKKK cascade; response to bacterium; positive regulation of protein kinase activity; cell surface; Golgi membrane; MAPKKK cascade; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	FZD8	10:35927177-35930362 10p11.21	frizzled family receptor 8 [Source:HGNC Symbol;Acc:4046], type=protein_coding, GO=[Wnt-activated receptor activity; Wnt-protein binding; positive regulation of JUN kinase activity; T cell differentiation in thymus; PDZ domain binding; regulation of JNK cascade; JNK cascade; canonical Wnt receptor signaling pathway; positive regulation of phosphorylation; regulation of MAPKKK cascade; positive regulation of protein kinase activity; negative regulation of transcription from RNA polymerase II promoter; MAPKKK cascade; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaCGHd, tcgaOvarianMethyl
d	GALK1	17:73754018-73761307 17q25.1	galactokinase 1 [Source:HGNC Symbol;Acc:4118], type=protein_coding, GO=[galactitol metabolic process; galactokinase activity; hexitol metabolic process; galactose binding; galactose catabolic process; carbohydrate phosphorylation; carbohydrate binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
d*	GALNTL4	11:11292423-11643552 11p15.3	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase-like 4 [Source:HGNC Symbol;Acc:30488], type=processed_transcript,protein_coding, GO=[polypeptide N-acetylgalactosaminyltransferase activity; UDP-glycosyltransferase activity; carbohydrate binding; Golgi membrane]	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
d	GATA2	3:128198270-128212028 3q21.3	GATA binding protein 2 [Source:HGNC Symbol;Acc:4171], type=processed_transcript,protein_coding, GO=[negative regulation of fat cell proliferation; eosinophil fate commitment; negative regulation of macrophage differentiation; positive regulation of megakaryocyte differentiation; negative regulation of Notch signaling pathway; semicircular canal development; C2H2 zinc finger domain binding; ventral spinal cord interneuron differentiation; negative regulation of neural precursor cell proliferation; RNA polymerase II distal enhancer sequence-specific DNA binding; cell differentiation in hindbrain; positive regulation of erythrocyte differentiation; definitive hemopoiesis; enhancer sequence-specific DNA binding; homeostasis of number of cells within a tissue; positive regulation of phagocytosis; regulation of histone acetylation; negative regulation of fat cell differentiation; ventral spinal cord development; somatic stem cell maintenance; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription; cell fate determination; pituitary gland development; central nervous system neuron development; neuron fate commitment; positive regulation of endocytosis; diencephalon development; embryonic placenta development; positive regulation of angiogenesis; inner ear morphogenesis; tissue homeostasis; chromatin binding; urogenital system development; negative regulation of transcription from RNA polymerase II promoter; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
d	GC	4:72607410-72669758 4q13.3	group-specific component (vitamin D binding protein) [Source:HGNC Symbol;Acc:4187], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[vitamin D binding; lysosomal lumen; vitamin transporter activity; vitamin D metabolic process; vitamin transport; lactation; steroid binding; response to estradiol stimulus; response to estrogen stimulus; lytic vacuole; lysosome; actin binding; perinuclear region of cytoplasm]	cosmicPrimary, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
d	GCG	2:162999392-163008914 2q24.2	glucagon [Source:HGNC Symbol;Acc:4191], type=protein_coding,retained_intron, GO=[glucagon receptor binding; positive regulation of calcium ion import; positive regulation of insulin secretion involved in cellular response to glucose stimulus; negative regulation of appetite; negative regulation of response to nutrient levels; negative regulation of response to extracellular stimulus; regulation of response to food; protein kinase A signaling cascade; positive regulation of peptidyl-threonine phosphorylation; positive regulation of protein binding; positive regulation of cAMP metabolic process; positive regulation of cAMP biosynthetic process; cellular response to glucagon stimulus; positive regulation of peptidyl-serine phosphorylation; peptidyl-threonine phosphorylation; positive regulation of hormone secretion; positive regulation of ERK1 and ERK2 cascade; feeding behavior; hormone activity; peptidyl-serine phosphorylation; response to glucose stimulus; G-protein signaling, coupled to cAMP nucleotide second messenger; response to hexose stimulus; ERK1 and ERK2 cascade; positive regulation of MAPKKK cascade; positive regulation of phosphorylation; cellular response to peptide hormone stimulus; regulation of MAPKKK cascade; positive regulation of protein kinase activity; soluble fraction; response to peptide hormone stimulus; MAPKKK cascade; cytoplasmic membrane-bounded vesicle; endoplasmic reticulum part; cytoplasmic vesicle]	snp3dObesity, tcgaBreastMethyl

Continued on next page...

S	name	locus	description	studies
u	GLRX2	1:193065598-193075244 1q31.2	glutaredoxin 2 [Source:HGNC Symbol;Acc:16065], type=processed_transcript,protein_coding, GO=[arsenate reductase (glutaredoxin) activity; DNA protection; glutathione disulfide oxidoreductase activity; protein thiol-disulfide exchange; response to redox state; 2 iron, 2 sulfur cluster binding; protein disulfide oxidoreductase activity; glutathione metabolic process; cell redox homeostasis; response to hydrogen peroxide; electron transport chain; electron carrier activity]	tcgaBreastGE
u	GOLGB1	3:121382046-121468602 3q13.33	golgin B1 [Source:HGNC Symbol;Acc:4429], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[Golgi organization; endoplasmic reticulum-Golgi intermediate compartment; Golgi stack; Golgi membrane]	cosmicPrimary, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d	GOLIM4	3:167726465-167813763 3q26.2	golgi integral membrane protein 4 [Source:HGNC Symbol;Acc:15448], type=protein_coding,retained_intron, GO=[Golgi lumen; cis-Golgi network; Golgi cisterna membrane; Golgi cisterna; Golgi stack; Golgi membrane; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa
d	GPER	7:1121844-1133451 7p22.3	G protein-coupled estrogen receptor 1 [Source:HGNC Symbol;Acc:4485], type=protein_coding, GO=[estrogen receptor activity; positive regulation of epidermal growth factor receptor signaling pathway; steroid hormone mediated signaling pathway; steroid binding; positive regulation of ERK1 and ERK2 cascade; steroid hormone receptor signaling pathway; epidermal growth factor receptor signaling pathway; ERK1 and ERK2 cascade; positive regulation of MAPKKK cascade; regulation of MAPKKK cascade; Golgi membrane; MAPKKK cascade; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastGE, tcgaColonGE, tscapeOvariand
d*	GRB10	7:50657760-50861159 7p12.1	growth factor receptor-bound protein 10 [Source:HGNC Symbol;Acc:4564], type=processed_transcript,protein_coding,retained_intron, GO=[negative regulation of glycogen biosynthetic process; negative regulation of glucose import; positive regulation of vascular endothelial growth factor receptor signaling pathway; negative regulation of insulin receptor signaling pathway; regulation of glycogen biosynthetic process; insulin receptor binding; insulin-like growth factor receptor signaling pathway; SH3/SH2 adaptor activity; negative regulation of phosphorylation; negative regulation of Wnt receptor signaling pathway; phospholipid binding; carbohydrate biosynthetic process; response to insulin stimulus; positive regulation of phosphorylation; cellular response to peptide hormone stimulus; response to peptide hormone stimulus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeGliomaa
u	GUCY1A3	4:156587863-156653501 4q32.1	guanylate cyclase 1, soluble, alpha 3 [Source:HGNC Symbol;Acc:4685], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[guanylate cyclase complex, soluble; response to defense-related nitric oxide production by other organism involved in symbiotic interaction; response to defense-related host nitric oxide production; relaxation of vascular smooth muscle; positive regulation of cGMP biosynthetic process; guanylate cyclase activity; positive regulation of cGMP metabolic process; response to herbicide; nitric oxide mediated signal transduction; phosphorus-oxygen lyase activity; cyclase activity; response to toxin; heme binding; protein heterodimerization activity; GTP binding]	tcgaBreastGE, tcgaGliomaGE, tscapeRCCd
d	GUSBP2	6:26839263-26924333 6p22.2	glucuronidase, beta pseudogene 2 [Source:HGNC Symbol;Acc:18792], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	
d	GUSBP3	5:68790040-69006341 5q13.2	glucuronidase, beta pseudogene 3 [Source:HGNC Symbol;Acc:37301], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	tcgaBreastGE
d	GUSBP9	5:70435716-70585611 5q13.2	glucuronidase, beta pseudogene 9 [Source:HGNC Symbol;Acc:42323], type=pseudogene,unprocessed_pseudogene	
d	HBQ1	16:230452-231180 16p13.3	hemoglobin, theta 1 [Source:HGNC Symbol;Acc:4833], type=protein_coding, GO=[hemoglobin complex; oxygen transport; oxygen transporter activity; oxygen binding; heme binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeHCCd, tscapeNSCLCd
u	HEBP2	6:138724668-138734310 6q23.3	heme binding protein 2 [Source:HGNC Symbol;Acc:15716], type=nonsense_mediated_decay,protein_coding	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa
u*	HERC3	4:89444961-89629693 4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase 3 [Source:HGNC Symbol;Acc:4876], type=processed_transcript,protein_coding,retained_intron, GO=[protein ubiquitination involved in ubiquitin-dependent protein catabolic process; ubiquitin-protein ligase activity; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
u	HERC5	4:89378268-89427314 4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase 5 [Source:HGNC Symbol;Acc:24368], type=processed_transcript,protein_coding,retained_intron, GO=[ISG15 ligase activity; ISG15-protein conjugation; negative regulation of type I interferon production; regulation of defense response to virus; protein ubiquitination involved in ubiquitin-dependent protein catabolic process; regulation of cyclin-dependent protein kinase activity; ubiquitin-protein ligase activity; cytokine-mediated signaling pathway; perinuclear region of cytoplasm]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tscapeHCCd
u*	HERC6	4:89299891-89364263 4q22.1	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6 [Source:HGNC Symbol;Acc:26072], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[protein ubiquitination involved in ubiquitin-dependent protein catabolic process; ubiquitin-protein ligase activity]	tcgaBreastGE, tscapeHCCd
u	HES6	2:239146908-239149303 2q37.3	hairy and enhancer of split 6 (Drosophila) [Source:HGNC Symbol;Acc:18254], type=protein_coding, GO=[transcription factor complex; transcription cofactor activity; protein binding transcription factor activity]	tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeMelanomad, tscapeOvariand, tscapeRCCd
u*	HIST2H2BE	1:149856010-149858232 1q21.2	histone cluster 2, H2be [Source:HGNC Symbol;Acc:4760], type=protein_coding, GO=[nucleosome; nucleosome assembly; response to bacterium]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeBCa, tscapeHCCa
u	HMGCS1	5:43289497-43313614 5p12	3-hydroxy-3-methylglutaryl-CoA synthase 1 (soluble) [Source:HGNC Symbol;Acc:5007], type=protein_coding,retained_intron, GO=[organic acid binding; response to low light intensity stimulus; response to tellurium ion; hydroxymethylglutaryl-CoA synthase activity; cellular response to follicle-stimulating hormone stimulus; cellular response to cholesterol; response to vitamin E; response to lipoprotein stimulus; response to purine-containing compound; isoprenoid biosynthetic process; cholesterol biosynthetic process; cellular response to organic cyclic compound; drug binding; liver development; response to acid; male gonad development; response to organic nitrogen; response to drug; soluble fraction; protein homodimerization activity; identical protein binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeSCLCa
u	HMGXB3	5:149379884-149432386 5q32	HMG box domain containing 3 [Source:HGNC Symbol;Acc:28982], type=nonsense_mediated_decay,protein_coding,retained_intron	tcgaGliomaGE
d	HOXC9	12:54388679-54397121 12q13.13	homeobox C9 [Source:HGNC Symbol;Acc:5130], type=processed_transcript,protein_coding, GO=[embryonic skeletal system morphogenesis]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeRCCa
d	HSPA12A	10:118430703-118502085 10q25.3	heat shock 70kDa protein 12A [Source:HGNC Symbol;Acc:19022], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaGliomaCGHd, tcgaGliomaGE
d	IFI35	17:41158742-41166473 17q21.31	interferon-induced protein 35 [Source:HGNC Symbol;Acc:5399], type=processed_transcript,protein_coding,retained_intron, GO=[type I interferon-mediated signaling pathway; cytokine-mediated signaling pathway]	tcgaBreastGE, tcgaGliomaGE, tscapeBCd
u*	IGF1R	15:99192200-99507759 15q26.3	insulin-like growth factor 1 receptor [Source:HGNC Symbol;Acc:5465], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[inactivation of MAPKK activity; insulin-like growth factor-activated receptor activity; insulin binding; positive regulation of steroid hormone biosynthetic process; insulin-like growth factor I binding; exocrine pancreas development; response to vitamin E; insulin receptor substrate binding; male sex determination; positive regulation of cytokinesis; negative regulation of protein kinase B signaling cascade; phosphatidylinositol 3-kinase binding; regulation of cytokinesis; insulin receptor binding; prostate gland epithelium morphogenesis; insulin-like growth factor receptor signaling pathway; positive regulation of anti-apoptosis; positive regulation of DNA replication; positive regulation of protein kinase B signaling cascade; caveola; protein heterooligomerization; phosphatidylinositol 3-kinase cascade; establishment of cell polarity; protein tetramerization; phosphatidylinositol-mediated signaling; regulation of JNK cascade; JNK cascade; positive regulation of MAPKKK cascade; protein autophosphorylation; urogenital system development; response to insulin stimulus; microsome; cellular response to peptide hormone stimulus; regulation of MAPKKK cascade; response to peptide hormone stimulus; MAPKKK cascade; identical protein binding]	snp3dBC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCa, tscapeMelanomaa, tscapeNSCLCa
d*	IGFBP3	7:45951850-45961473 7p12.3	insulin-like growth factor binding protein 3 [Source:HGNC Symbol;Acc:5472], type=processed_transcript,protein_coding,retained_intron, GO=[insulin-like growth factor binary complex; insulin-like growth factor ternary complex; protein tyrosine phosphatase activator activity; insulin-like growth factor II binding; insulin-like growth factor I binding; negative regulation of smooth muscle cell migration; positive regulation of myoblast differentiation; fibronectin binding; negative regulation of smooth muscle cell proliferation; negative regulation of protein phosphorylation; negative regulation of phosphorylation; regulation of cell growth; cell growth]	snp3dBC, snp3dLungC, snp3dProstateC, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
d	IL27RA	19:14142262-14164026 19p13.12	interleukin 27 receptor, alpha [Source:HGNC Symbol;Acc:17290], type=protein_coding, GO=[interleukin-27 receptor activity; interleukin-27-mediated signaling pathway; negative regulation of type 2 immune response; positive regulation of T-helper 1 type immune response; regulation of isotype switching to IgG isotypes; positive regulation of interferon-gamma production; T-helper 1 type immune response; defense response to Gram-positive bacterium; cytokine-mediated signaling pathway; response to bacterium]	fileBC2brain, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHa
u	INPP4B	4:142944313-143768585 4q31.21	inositol polyphosphate-4-phosphatase, type II, 105kDa [Source:HGNC Symbol;Acc:6075], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[phosphatidylinositol-4,5-bisphosphate 4-phosphatase activity; phosphatidylinositol-3,4-bisphosphate 4-phosphatase activity]	tcgaGliomaGE
d	INSIG2	2:118846028-118868573 2q14.2	insulin induced gene 2 [Source:HGNC Symbol;Acc:20452], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[SREBP-SCAP-Insig complex; ER-nuclear sterol response pathway; negative regulation of fatty acid biosynthetic process; cranial suture morphogenesis; negative regulation of steroid biosynthetic process; middle ear morphogenesis; response to fatty acid; cholesterol biosynthetic process; triglyceride metabolic process; inner ear morphogenesis; response to insulin stimulus; response to peptide hormone stimulus; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	IQGAP2	5:75699074-76003957 5q13.3	IQ motif containing GTPase activating protein 2 [Source:HGNC Symbol;Acc:6111], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[GTPase inhibitor activity; microvillus; Ras GTPase activator activity; calmodulin binding; actin binding]	cosmicPrimary, tcgaBreastMethyl, tcgaGliomaGE, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
d	ITPK1	14:93403259-93582665 14q32.12	inositol-tetrakisphosphate 1-kinase [Source:HGNC Symbol;Acc:6177], type=processed_transcript,protein_coding, GO=[inositol-1,3,4-trisphosphate 5-kinase activity; inositol-1,3,4-trisphosphate 6-kinase activity; inositol tetrakisphosphate 1-kinase activity; inositol trisphosphate metabolic process; magnesium ion binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad
u	KCNN2	5:113696666-113832321 5q22.3	potassium intermediate/small conductance calcium-activated channel, subfamily N, member 2 [Source:HGNC Symbol;Acc:6291], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[small conductance calcium-activated potassium channel activity; calcium activated cation channel activity; potassium ion transmembrane transport; cellular potassium ion transport; calmodulin binding; potassium ion transport]	tcgaBreastMethyl, tcgaColonMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
d	KIAA1467	12:13197218-13295455 12p13.1	KIAA1467 [Source:HGNC Symbol;Acc:29288], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaGliomaGE, tscapeBCd, tscapeProstated
u	KLHL29	2:23608088-23931481 2p24.1	kelch-like 29 (Drosophila) [Source:HGNC Symbol;Acc:29404], type=protein_coding,retained_intron	cosmicMetastasis, tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
u	KLK2	19:51376689-51383822 19q13.33	kallikrein-related peptidase 2 [Source:HGNC Symbol;Acc:6363], type=protein_coding, GO=[serine-type endopeptidase activity]	snp3dProstateC, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	KLK3	19:51358171-51364020 19q13.33	kallikrein-related peptidase 3 [Source:HGNC Symbol;Acc:6364], type=protein_coding, GO=[negative regulation of angiogenesis; serine-type endopeptidase activity]	snp3dProstateC, tcgaBreastGE, tcgaBreastMethyl
u	KLK4	19:51409608-51413994 19q13.41	kallikrein-related peptidase 4 [Source:HGNC Symbol;Acc:6365], type=protein_coding, GO=[serine-type endopeptidase activity]	snp3dProstateC, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	KRT19	17:39679869-39684560 17q21.2	keratin 19 [Source:HGNC Symbol;Acc:6436], type=protein_coding,retained_intron, GO=[costamere; cell differentiation involved in embryonic placenta development; dystrophin-associated glycoprotein complex; sarcomere organization; structural constituent of muscle; actomyosin structure organization; Z disc; embryonic placenta development; structural constituent of cytoskeleton; sarcolemma; response to estrogen stimulus; intermediate filament]	snp3dMetastasis, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand
d	LGI2	4:25000469-25032501 4p15.2	leucine-rich repeat LGI family, member 2 [Source:HGNC Symbol;Acc:18710], type=protein_coding	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd
u	LIMCH1	4:41361624-41702061 4p13	LIM and calponin homology domains 1 [Source:HGNC Symbol;Acc:29191], type=processed_transcript,protein_coding, GO=[actomyosin structure organization; actin binding]	tcgaBreastGE, tcgaGliomaGE
d	LMO4	1:87794151-87812788 1p22.3	LIM domain only 4 [Source:HGNC Symbol;Acc:6644], type=processed_transcript,protein_coding, GO=[ventral spinal cord interneuron differentiation; spinal cord association neuron differentiation; regulation of cell fate specification; enhancer sequence-specific DNA binding; spinal cord motor neuron differentiation; regulation of cell fate commitment; ventral spinal cord development; ventricular septum development; thymus development; negative regulation of protein complex assembly; neural tube closure; neural tube formation; transcription factor complex; positive regulation of transcription from RNA polymerase II promoter]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeGliomad, tscapeNSCLCd, tscapeOvariand
u	LPAR3	1:85277285-85358896 1p22.3	lysophosphatidic acid receptor 3 [Source:HGNC Symbol;Acc:14298], type=processed_transcript,protein_coding, GO=[lysophosphatidic acid receptor activity; lysosphingolipid and lysophosphatidic acid receptor activity; bleb assembly; G-protein alpha-subunit binding; elevation of cytosolic calcium ion concentration involved in G-protein signaling coupled to IP3 second messenger; activation of MAPK activity; positive regulation of MAPKKK cascade; phospholipid binding; regulation of MAPKKK cascade; positive regulation of protein kinase activity; MAPKKK cascade]	tcgaGliomaGE
u	LYPLAL1	1:219347186-219386207 1q41	lysophospholipase-like 1 [Source:HGNC Symbol;Acc:20440], type=processed_transcript,protein_coding, GO=[lysophospholipase activity]	tcgaBreastGE
u	MAK	6:10762956-10838764 6p24.2	male germ cell-associated kinase [Source:HGNC Symbol;Acc:6816], type=processed_transcript,protein_coding, GO=[mitotic spindle; photoreceptor inner segment; photoreceptor cell maintenance; cyclin-dependent protein kinase activity; photoreceptor outer segment; nonmotile primary cilium; midbody; protein autophosphorylation; transcription coactivator activity; transcription cofactor activity; protein binding transcription factor activity]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeBCa, tscapeOvariana, tscapeProstated, tscapeSCLCd
u	MAP7D1	1:36621180-36646450 1p34.3	MAP7 domain containing 1 [Source:HGNC Symbol;Acc:25514], type=processed_transcript,protein_coding,retained_intron	tcgaColonGE, tcgaGliomaGE
u*	MAPK6	15:52244303-52358462 15q21.2	mitogen-activated protein kinase 6 [Source:HGNC Symbol;Acc:6879], type=processed_transcript,protein_coding, GO=[MAP kinase activity; protein heterodimerization activity; MAPKKK cascade]	tcgaGliomaGE
u	MCEE	2:71336814-71357369 2p13.3	methylmalonyl CoA epimerase [Source:HGNC Symbol;Acc:16732], type=processed_transcript,protein_coding, GO=[methylmalonyl-CoA epimerase activity; short-chain fatty acid catabolic process; L-methylmalonyl-CoA metabolic process; fatty acid beta-oxidation; fatty acid catabolic process; mitochondrial matrix]	tcgaBreastMethyl, tcgaOvarianMethyl
u	MCPH1	8:6264113-6501144 8p23.1	microcephalin 1 [Source:HGNC Symbol;Acc:6954], type=processed_transcript,protein_coding	tcgaOvarianCGHd, tscapeHCCd
d	MECOM	3:168801287-169381406 3q26.2	MDS1 and EVI1 complex locus [Source:HGNC Symbol;Acc:3498], type=processed_transcript,protein_coding,retained_intron, GO=[neutrophil homeostasis; hemopoietic stem cell proliferation; pericardium development; negative regulation of JNK cascade; embryonic forelimb morphogenesis; embryonic hindlimb morphogenesis; histone deacetylase complex; nuclear speck; regulation of JNK cascade; JNK cascade; regulation of MAPKKK cascade; response to bacterium; MAPKKK cascade; protein homodimerization activity; positive regulation of transcription from RNA polymerase II promoter; identical protein binding]	cosmicMetastasis, tcgaGliomaGE, tcgaOvarianCGHa
d	METRN	16:765115-769499 16p13.3	meteorin, glial cell differentiation regulator [Source:HGNC Symbol;Acc:14151], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[positive regulation of axonogenesis]	tcgaBreastGE, tcgaOvarianMethyl, tscapeHCCd
u	MGAT2	14:50087489-50090198 14q21.3	mannosyl (alpha-1,6-)-glycoprotein beta-1,2-N-acetylglucosaminyltransferase [Source:HGNC Symbol;Acc:7045], type=protein_coding, GO=[alpha-1,6-mannosylglycoprotein 2-beta-N-acetylglucosaminyltransferase activity; oligosaccharide biosynthetic process; protein N-linked glycosylation via asparagine; peptidyl-asparagine modification; Golgi stack; UDP-glycosyltransferase activity; post-translational protein modification; carbohydrate biosynthetic process; carbohydrate binding; Golgi membrane]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeProstatea
u	MLPH	2:238394071-238463961 2q37.3	melanophilin [Source:HGNC Symbol;Acc:29643], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[myosin V binding; microtubule plus-end binding; melanosome localization; melanocyte differentiation; Rab GTPase binding; melanosome; actin binding; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
u	MOB4	2:198380295-198418423 2q33.1	MOB family member 4, phocein [Source:HGNC Symbol;Acc:17261], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[Golgi cisterna membrane; Golgi cisterna; Golgi stack; perinuclear region of cytoplasm; Golgi membrane]	

Continued on next page...

S	name	locus	description	studies
u	MPHOSPH9	12:123636867-123728561 12q24.31	M-phase phosphoprotein 9 [Source:HGNC Symbol;Acc:7215], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[centriole; Golgi membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
u	MPZL1	1:167690429-167761156 1q24.2	myelin protein zero-like 1 [Source:HGNC Symbol;Acc:7226], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE
d	MT1A	16:56672578-56673999 16q12.2	metallothionein 1A [Source:HGNC Symbol;Acc:7393], type=protein_coding, GO=[cellular response to chromate; cadmium ion binding; cellular response to zinc ion; cellular response to cadmium ion; cellular zinc ion homeostasis; nitric oxide mediated signal transduction; copper ion binding; negative regulation of growth; lysosome; lytic vacuole; perinuclear region of cytoplasm]	
d	MT1F	16:56691606-56694610 16q12.2	metallothionein 1F [Source:HGNC Symbol;Acc:7398], type=processed_transcript,protein_coding,retained_intron, GO=[cadmium ion binding; cellular response to cadmium ion; copper ion binding; negative regulation of growth; perinuclear region of cytoplasm]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
d	MT1X	16:56716336-56718108 16q13	metallothionein 1X [Source:HGNC Symbol;Acc:7405], type=processed_transcript,protein_coding,retained_intron, GO=[cellular response to zinc ion; cellular response to cadmium ion; negative regulation of growth; perinuclear region of cytoplasm]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeMelanomad
u	MTOR	1:11166592-11322608 1p36.22	mechanistic target of rapamycin (serine/threonine kinase) [Source:HGNC Symbol;Acc:3942], type=processed_transcript,protein_coding, GO=[mTOR-FKBP12-rapamycin complex; carbohydrate utilization; regulation of carbohydrate utilization; TFIIIC-class transcription factor binding; RNA polymerase III transcription factor binding; TORC2 complex; TORC1 complex; RNA polymerase III type 3 promoter DNA binding; RNA polymerase III type 2 promoter DNA binding; RNA polymerase III type 1 promoter DNA binding; RNA polymerase III regulatory region DNA binding; negative regulation of macroautophagy; negative regulation of NFAT protein import into nucleus; negative regulation of cell size; positive regulation of lamellipodium assembly; positive regulation of transcription from RNA polymerase III promoter; negative regulation of response to nutrient levels; negative regulation of response to extracellular stimulus; regulation of response to food; phosphatidylinositol 3-kinase complex; regulation of fatty acid beta-oxidation; regulation of Rac GTPase activity; ruffle organization; ribosome binding; positive regulation of stress fiber assembly; regulation of glycogen biosynthetic process; lamellipodium assembly; positive regulation of actin filament polymerization; TOR signaling cascade; cellular response to hypoxia; phosphoprotein binding; peptidyl-threonine phosphorylation; positive regulation of translation; positive regulation of protein kinase B signaling cascade; fatty acid beta-oxidation; positive regulation of endothelial cell proliferation; PML body; T cell costimulation; fatty acid catabolic process; lymphocyte costimulation; response to amino acid stimulus; regulation of endothelial cell proliferation; regulation of actin filament polymerization; phosphatidylinositol-mediated signaling; response to acid; positive regulation of peptidyl-tyrosine phosphorylation; mitochondrial outer membrane; peptidyl-serine phosphorylation; epidermal growth factor receptor signaling pathway; organelle outer membrane; germ cell development; response to organic nitrogen; protein autophosphorylation; nerve growth factor receptor signaling pathway; carbohydrate biosynthetic process; lytic vacuole; lysosome; response to insulin stimulus; positive regulation of phosphorylation; cellular response to peptide hormone stimulus; dendrite; cell growth; soluble fraction; response to peptide hormone stimulus; Golgi membrane; mitochondrial envelope; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	cosmicRecurrent, tcgaBreastGE
u*	MYCBP2	13:77618792-77901185 13q22.3	MYC binding protein 2, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:23386], type=processed_transcript,protein_coding, GO=[branchiomotor neuron axon guidance; central nervous system projection neuron axonogenesis; central nervous system neuron development; protein homodimerization activity; identical protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd
u	MYOF	10:95066186-95242074 10q23.33	myoferlin [Source:HGNC Symbol;Acc:3656], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[plasma membrane repair; cellular response to heat; caveola; nuclear membrane; phospholipid binding; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaColonGE, tcgaGliomaCGHd, tcgaGliomaGE
d	MYT1	20:62783144-62873604 20q13.33	myelin transcription factor 1 [Source:HGNC Symbol;Acc:7622], type=protein_coding	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeNSCLCa
d	NAP1L3	X:92925929-92928567 Xq21.32	nucleosome assembly protein 1-like 3 [Source:HGNC Symbol;Acc:7639], type=processed_transcript,protein_coding, GO=[chromatin assembly complex; nucleosome assembly]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
u	NCAPD3	11:134020014-134095348 11q25	non-SMC condensin II complex, subunit D3 [Source:HGNC Symbol;Acc:28952], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nuclear condensin complex; nuclear centromeric heterochromatin; mitotic chromosome condensation; methylated histone residue binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tscapeBCd, tscapeNSCLCd
d	NCOA7	6:126102307-126252266 6q22.32	nuclear receptor coactivator 7 [Source:HGNC Symbol;Acc:21081], type=processed_transcript,protein_coding, GO=[cell wall macromolecule catabolic process; ligand-dependent nuclear receptor transcription coactivator activity; transcription coactivator activity; transcription cofactor activity; protein binding transcription factor activity; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
u*	NEDD4L	18:55711619-56068772 18q21.31	neural precursor cell expressed, developmentally down-regulated 4-like, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:7728], type=protein_coding, GO=[sodium channel inhibitor activity; cellular sodium ion homeostasis; negative regulation of sodium ion transport; water homeostasis; protein ubiquitination involved in ubiquitin-dependent protein catabolic process; positive regulation of endocytosis; excretion; regulation of protein catabolic process; ubiquitin-protein ligase activity]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
d	NETO1	18:70409671-70535184 18q22.3	neuropilin (NRP) and tolloid (TLL)-like 1 [Source:HGNC Symbol;Acc:13823], type=protein_coding, GO=[excitatory synapse; regulation of long-term neuronal synaptic plasticity; visual learning; memory; postsynaptic density; dendritic spine; postsynaptic membrane; dendrite]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeProstated
d	NIPSNAP3A	9:107509969-107522403 9q31.1	nipsnap homolog 3A (C. elegans) [Source:HGNC Symbol;Acc:23619], type=processed_transcript,protein_coding	tcgaColonMethyl, tcgaOvarianMethyl
u	NRIP1	21:16333556-16437321 21q11.2, 21q21.1	nuclear receptor interacting protein 1 [Source:HGNC Symbol;Acc:8001], type=protein_coding, GO=[ovarian follicle rupture; glucocorticoid receptor binding; ovulation from ovarian follicle; retinoid X receptor binding; estrogen receptor binding; androgen receptor binding; histone deacetylase complex; lipid storage; androgen receptor signaling pathway; histone deacetylase binding; steroid hormone receptor signaling pathway; transcription corepressor activity; transcription coactivator activity; transcription cofactor activity; protein binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
d	NUCB2	11:17229700-17371521 11p15.1	nucleobindin 2 [Source:HGNC Symbol;Acc:8044], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[Golgi medial cisterna; nuclear outer membrane; tumor necrosis factor receptor binding; endoplasmic reticulum-Golgi intermediate compartment; Golgi cisterna; Golgi stack; organelle outer membrane; nuclear membrane; calcium ion binding; nuclear outer membrane-endoplasmic reticulum membrane network]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	NUDT9	4:88343734-88380606 4q22.1	nudix (nucleoside diphosphate linked moiety X)-type motif 9 [Source:HGNC Symbol;Acc:8056], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[adenosine-diphosphatase activity; IDP catabolic process; IDP metabolic process; ADP catabolic process; ADP-sugar diphosphatase activity; ADP-ribose diphosphatase activity]	tcgaColonGE, tcgaColonMethyl, tscapeHCCd
d	NUP93	16:56764017-56880792 16q13	nucleoporin 93kDa [Source:HGNC Symbol;Acc:28958], type=TEC,processed_transcript,protein_coding,retained_intron, GO=[nuclear pore; mRNA transport; nuclear membrane; cytokine-mediated signaling pathway; viral reproduction]	tcgaBreastGE, tcgaColonMethyl, tscapeMelanomad
d	NUPR1	16:28548606-28550495 16p11.2	nuclear protein, transcriptional regulator, 1 [Source:HGNC Symbol;Acc:29990], type=nonsense_mediated_decay,protein_coding, GO=[regulation of female gonad development; DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis; negative regulation of fibroblast proliferation; skeletal muscle cell differentiation; acute inflammatory response; male gonad development; response to toxin; chromatin binding; cell growth]	cosmicPrimary, tcgaColonGE, tcgaGliomaGE, tscapeHCCd
u	ODZ1	X:123509753-124097666 Xq25	odz, odd Oz/ten-m homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:8117], type=processed_transcript,protein_coding, GO=[heparin binding; carbohydrate binding]	tcgaGliomaGE
u	ORM1	9:117085336-117088755 9q32	orosomucoid 1 [Source:HGNC Symbol;Acc:8498], type=processed_transcript,protein_coding, GO=[acute-phase response; acute inflammatory response]	tcgaBreastGE

Continued on next page...

S	name	locus	description	studies
u	ORM2	9:117092149-117095532 9q32	orosomucoid 2 [Source:HGNC Symbol;Acc:8499], type=protein_coding, GO=[acute-phase response; acute inflammatory response]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	PAQR4	16:3019246-3023490 16p13.3	progestin and adipoQ receptor family member IV [Source:HGNC Symbol;Acc:26386], type=protein_coding	tcgaBreastGE, tcgaColonGE, tscapeHCCd, tscapeOvariand
u	PCDH20	13:61983991-62002220 13q21.2	protocadherin 20 [Source:HGNC Symbol;Acc:14257], type=processed_transcript,protein_coding, GO=[homophilic cell adhesion; calcium ion binding]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeProstated
d	PDGFRL	8:17433942-17501580 8p22	platelet-derived growth factor receptor-like [Source:HGNC Symbol;Acc:8805], type=processed_transcript,protein_coding, GO=[platelet-derived growth factor beta-receptor activity; platelet activating factor receptor activity; platelet-derived growth factor receptor-beta signaling pathway; platelet-derived growth factor receptor signaling pathway]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianCGHd, tcgaOvarianMethyl
d	PELI2	14:56584532-56768244 14q22.3	pellino E3 ubiquitin protein ligase family member 2 [Source:HGNC Symbol;Acc:8828], type=protein_coding, GO=[toll-like receptor 1 signaling pathway; toll-like receptor 2 signaling pathway; MyD88-dependent toll-like receptor signaling pathway; Toll signaling pathway; toll-like receptor 4 signaling pathway; positive regulation of I-kappaB kinase/NF-kappaB cascade; positive regulation of MAPKKK cascade; positive regulation of phosphorylation; regulation of MAPKKK cascade; MAPKKK cascade]	fileBC2brain, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
d	PITX1	5:134362615-134370503 5q31.1	paired-like homeodomain 1 [Source:HGNC Symbol;Acc:9004], type=protein_coding,retained_intron, GO=[branchiomeric skeletal muscle development; myoblast cell fate commitment; embryonic hindlimb morphogenesis; pituitary gland development; diencephalon development; transcription factor complex; protein binding transcription factor activity; nucleolus; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl
d	PLCH1	3:155093369-155462856 3q25.31	phospholipase C, eta 1 [Source:HGNC Symbol;Acc:29185], type=protein_coding,retained_intron, GO=[calcium-dependent phospholipase C activity; phosphatidylinositol phospholipase C activity; phosphatidylinositol-mediated signaling; nuclear membrane; phospholipid binding; calcium ion binding]	tcgaGliomaGE
u	PMEPA1	20:56223448-56286592 20q13.31	prostate transmembrane protein, androgen induced 1 [Source:HGNC Symbol;Acc:14107], type=processed_transcript,protein_coding, GO=[WW domain binding; androgen receptor signaling pathway; steroid hormone receptor signaling pathway]	
d	PNMA6A	X:152240839-152340864 Xq28	paraneoplastic Ma antigen family member 6A [Source:HGNC Symbol;Acc:28248], type=protein_coding	
d	PNMA6C	X:152240819-152243401 Xq28	paraneoplastic Ma antigen family member 6C [Source:HGNC Symbol;Acc:41914], type=protein_coding	
d*	POLA2	11:65029233-65073060 11q13.1	polymerase (DNA directed), alpha 2 (70kD subunit) [Source:HGNC Symbol;Acc:30073], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[alpha DNA polymerase:primase complex; telomere maintenance via semi-conservative replication; telomere maintenance via recombination; DNA-directed DNA polymerase activity; DNA-dependent DNA replication initiation; DNA strand elongation involved in DNA replication; protein import into nucleus, translocation; M/G1 transition of mitotic cell cycle; S phase of mitotic cell cycle; protein heterodimerization activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
u	PPAPDC2	9:4662298-4665256 9p24.1	phosphatidic acid phosphatase type 2 domain containing 2 [Source:HGNC Symbol;Acc:23682], type=protein_coding	tcgaColonGE, tscapeBCd
u	PPFIBP2	11:7534529-7678358 11p15.4	PTPRF interacting protein, binding protein 2 (liprin beta 2) [Source:HGNC Symbol;Acc:9250], type=processed_transcript,protein_coding,retained_intron, GO=[integrase activity; DNA integration]	tcgaColonGE
d	PPP1R14C	6:150464212-150571493 6q25.1	protein phosphatase 1, regulatory (inhibitor) subunit 14C [Source:HGNC Symbol;Acc:14952], type=protein_coding, GO=[protein serine/threonine phosphatase inhibitor activity]	tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeOvariand
u	PRAGMIN	8:8175258-8244008 8p23.1	Tyrosine-protein kinase SgK223 [Source:UniProtKB/Swiss-Prot;Acc:Q86YV5], type=protein_coding, GO=[non-membrane spanning protein tyrosine kinase activity]	tcgaColonGE
u	PRKCH	14:61654277-62017694 14q23.1	protein kinase C, eta [Source:HGNC Symbol;Acc:9403], type=processed_transcript,protein_coding, GO=[regulation of tight junction assembly; positive regulation of B cell receptor signaling pathway; Ral GTPase binding; negative regulation of glial cell apoptosis; regulation of glial cell apoptosis; positive regulation of glial cell proliferation; positive regulation of keratinocyte differentiation; positive regulation of macrophage derived foam cell differentiation; protein kinase C activity; glial cell proliferation; positive regulation of NF-kappaB transcription factor activity; positive regulation of sequence-specific DNA binding transcription factor activity; platelet activation]	tcgaBreastMethyl, tcgaOvarianMethyl
u	PTPRCAP	11:67202981-67205538 11q13.2	protein tyrosine phosphatase, receptor type, C-associated protein [Source:HGNC Symbol;Acc:9667], type=protein_coding	tcgaBreastGE, tcgaBreastMethyl
u	RAB4A	1:229406822-229441641 1q42.13	RAB4A, member RAS oncogene family [Source:HGNC Symbol;Acc:9781], type=processed_transcript,protein_coding,retained_intron, GO=[insulin-responsive compartment; ATPase activator activity; ionotropic glutamate receptor binding; positive regulation of ATPase activity; ATPase binding; GDP binding; syntaxin binding; recycling endosome; protein transporter activity; microsome; GTPase activity; GTP binding; soluble fraction; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastMethyl, tscapeBCa, tscapeOvariana, tscapeProstated
d	RAI14	5:34656342-34832732 5p13.2	retinoic acid induced 14 [Source:HGNC Symbol;Acc:14873], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	RASL11A	13:27844464-27847827 13q12.2	RAS-like, family 11, member A [Source:HGNC Symbol;Acc:23802], type=processed_transcript,protein_coding, GO=[positive regulation of transcription from RNA polymerase I promoter; GTPase activity; GTP binding; nucleolus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeSCLCd
d	RASL11B	4:53728457-53733000 4q12	RAS-like, family 11, member B [Source:HGNC Symbol;Acc:23804], type=processed_transcript,protein_coding,retained_intron, GO=[ferrous iron transmembrane transporter activity; ferrous iron transport; GTPase activity; GTP binding]	tcgaGliomaGE
u	RASSF3	12:65004293-65091347 12q14.2	Ras association (RalGDS/AF-6) domain family member 3 [Source:HGNC Symbol;Acc:14271], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[microtubule; identical protein binding]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCa
d	REEP1	2:86441116-86565206 2p11.2	receptor accessory protein 1 [Source:HGNC Symbol;Acc:25786], type=processed_transcript,protein_coding,retained_intron, GO=[olfactory receptor binding; protein insertion into membrane; mitochondrial envelope]	cosmicRecurrent, tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
u	REP15	12:27849428-27850566 12p11.22	RAB15 effector protein [Source:HGNC Symbol;Acc:33748], type=protein_coding, GO=[early endosome membrane]	tscapeCRCa, tscapeSCLCa
u	RHOBTB3	5:95049226-95160087 5q15	Rho-related BTB domain containing 3 [Source:HGNC Symbol;Acc:18757], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[retrograde transport, endosome to Golgi; Rab GTPase binding; ATP catabolic process; GTP binding]	tcgaBreastGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
d	RNF144B	6:18368779-18469105 6p22.3	ring finger protein 144B [Source:HGNC Symbol;Acc:21578], type=processed_transcript,protein_coding, GO=[positive regulation of anti-apoptosis; protein ubiquitination involved in ubiquitin-dependent protein catabolic process; ubiquitin-protein ligase activity; mitochondrial envelope]	tcgaColonGE, tcgaGliomaGE, tscapeBCa, tscapeOvariana
d	RP11-1198D22.1	5:70516183-70555065 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
u	RP11-1267H10.4	4:69570318-69578216 4q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
d	RP11-1415C14.3	5:69515745-69580686 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
d	RP11-1415C14.4	5:69435402-69503572 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
u	RP11-312J18.5	1:160864770-160865866 1q23.3	[undefined], type=processed_pseudogene,pseudogene	
d	RP11-343H19.2	16:56716382-56721719 16q13	[undefined], type=processed_transcript	
d	RP11-497H16.5	5:69812214-69851093 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
d	RP11-589F5.4	5:70046954-70149508 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
d	RP11-823P9.1	5:21341942-21544886 5p14.3	[undefined], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	

Continued on next page...

S	name	locus	description	studies
d	RP11-98J23.2	5:69171098-69274436 5q13.2	[undefined], type=pseudogene,unprocessed_pseudogene	
u*	SAP30	4:174291120-174298683 4q34.1	Sin3A-associated protein, 30kDa [Source:HGNC Symbol;Acc:10532], type=processed_transcript,protein_coding, GO=[histone deacetylase complex; transcription corepressor activity; transcription cofactor activity; protein binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad, tscapeProstated, tscapeRCCd
u	SASH1	6:148593440-148873186 6q24.3	SAM and SH3 domain containing 1 [Source:HGNC Symbol;Acc:19182], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
d*	SDC4	20:43953928-43977064 20q13.12	syndecan 4 [Source:HGNC Symbol;Acc:10661], type=protein_coding, GO=[thrombospondin receptor activity; positive regulation of focal adhesion assembly; costamere; regulation of focal adhesion assembly; fibronectin binding; positive regulation of stress fiber assembly; protein kinase C binding; ureteric bud development; focal adhesion; positive regulation of protein kinase activity; cell surface]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd
u*	SDCBP	8:59465483-59495419 8q12.1	syndecan binding protein (syntenin) [Source:HGNC Symbol;Acc:10662], type=processed_transcript,protein_coding,retained_intron, GO=[interleukin-5 receptor complex; interleukin-5 receptor binding; syndecan binding; substrate-dependent cell migration, cell extension; cytoskeletal adaptor activity; frizzled binding; ephrin receptor binding; protein targeting to membrane; positive regulation of JNK cascade; cell adhesion molecule binding; glycoprotein binding; protein N-terminus binding; melanosome; focal adhesion; regulation of JNK cascade; protein C-terminus binding; JNK cascade; positive regulation of MAPKKK cascade; positive regulation of phosphorylation; protein heterodimerization activity; regulation of MAPKKK cascade; MAPKKK cascade; protein homodimerization activity; nuclear outer membrane-endoplasmic reticulum membrane network; cytoplasmic membrane-bounded vesicle; endoplasmic reticulum part; identical protein binding; cytoplasmic vesicle]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd, tscapeRCCd
u	SEC24B	4:110354928-110461612 4q25	SEC24 family, member B (S. cerevisiae) [Source:HGNC Symbol;Acc:10704], type=protein_coding, GO=[COPII vesicle coat; COPII vesicle coating; vesicle targeting, rough ER to cis-Golgi; ER to Golgi transport vesicle membrane; vesicle coat; peptidyl-asparagine modification; protein N-linked glycosylation via asparagine; post-translational protein modification; perinuclear region of cytoplasm; Golgi membrane; nuclear outer membrane-endoplasmic reticulum membrane network; cytoplasmic membrane-bounded vesicle; endoplasmic reticulum part; cytoplasmic vesicle]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd
d	SELENBP1	1:151336778-151345209 1q21.3	selenium binding protein 1 [Source:HGNC Symbol;Acc:10719], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[selenium binding; nucleolus]	tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa, tscapeMelanomaa, tscapeOvariana, tscapeSCLCa
u	SEMA4A	1:156117157-156147543 1q22	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:HGNC Symbol;Acc:10729], type=processed_transcript,protein_coding, GO=[semaphorin-plexin signaling pathway; T-helper 1 cell differentiation; T-helper 1 type immune response; negative regulation of angiogenesis; endothelial cell migration; regulation of cell shape]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
d	SERPINI1	3:167453031-167543356 3q26.1	serpin peptidase inhibitor, clade I (neuroserpin), member 1 [Source:HGNC Symbol;Acc:8943], type=processed_transcript,protein_coding,retained_intron, GO=[negative regulation of endopeptidase activity; peripheral nervous system development; serine-type endopeptidase inhibitor activity; negative regulation of peptidase activity; regulation of proteolysis]	fileBC2brain, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl
d	SI	3:164696686-164796283 3q26.1	sucrase-isomaltase (alpha-glucosidase) [Source:HGNC Symbol;Acc:10856], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[oligo-1,6-glucosidase activity; beta-fructofuranosidase activity; sucrose alpha-glucosidase activity; polysaccharide digestion; response to fructose stimulus; response to sucrose stimulus; brush border; response to vitamin A; response to hexose stimulus; response to glucocorticoid stimulus; apical plasma membrane; aging; apical part of cell; response to insulin stimulus; response to peptide hormone stimulus; carbohydrate binding]	cosmicPrimary, tcgaColonGE, tcgaOvarianCGHa, tscapeMelanomad, tscapeProstated
u	SLC16A6	17:66263167-66287405 17q24.2	solute carrier family 16, member 6 (monocarboxylic acid transporter 7) [Source:HGNC Symbol;Acc:10927], type=protein_coding, GO=[monocarboxylic acid transmembrane transporter activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	SLC26A3	7:107405912-107443670 7q31.1	solute carrier family 26, member 3 [Source:HGNC Symbol;Acc:3018], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[secondary active sulfate transmembrane transporter activity; sulfate transport; anion:anion antiporter activity; excretion; inorganic anion transport; transcription cofactor activity; protein binding transcription factor activity]	cosmicPrimary, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl
u	SLC2A12	6:134309835-134373774 6q23.2	solute carrier family 2 (facilitated glucose transporter), member 12 [Source:HGNC Symbol;Acc:18067], type=protein_coding, GO=[perinuclear region of cytoplasm]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tscapeBCa, tscapeCRCa
d	SLC30A3	2:27476552-27498685 2p23.3	solute carrier family 30 (zinc transporter), member 3 [Source:HGNC Symbol;Acc:11014], type=protein_coding,retained_intron, GO=[zinc transporting ATPase activity; regulation of sequestering of zinc ion; sequestering of zinc ion; cellular zinc ion homeostasis; zinc ion transport; synaptic vesicle membrane; late endosome; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	SLC30A7	1:101361632-101447309 1p21.2	solute carrier family 30 (zinc transporter), member 7 [Source:HGNC Symbol;Acc:19306], type=protein_coding, GO=[sequestering of zinc ion; cellular zinc ion homeostasis; zinc ion transport; perinuclear region of cytoplasm; Golgi membrane; cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd
u	SLC35F2	11:107661717-107799019 11q22.3	solute carrier family 35, member F2 [Source:HGNC Symbol;Acc:23615], type=nonsense_mediated_decay,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeMelanomad
u	SLC41A1	1:205758221-205782876 1q32.1	solute carrier family 41, member 1 [Source:HGNC Symbol;Acc:19429], type=processed_transcript,protein_coding	tcgaColonGE, tscapeBCa
u	SLC43A1	11:57252007-57283259 11q12.1	solute carrier family 43, member 1 [Source:HGNC Symbol;Acc:9225], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[neutral amino acid transmembrane transporter activity; neutral amino acid transport; L-amino acid transport; L-amino acid transmembrane transporter activity]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d	SLC44A1	9:108006903-108201452 9q31.1, 9q31.2	solute carrier family 44, member 1 [Source:HGNC Symbol;Acc:18798], type=nonsense_mediated_decay,protein_coding, GO=[choline transmembrane transporter activity; choline transport; mitochondrial outer membrane; organelle outer membrane; mitochondrial envelope]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	SLC45A3	1:205626979-205649587 1q32.1	solute carrier family 45, member 3 [Source:HGNC Symbol;Acc:8642], type=processed_transcript,protein_coding	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa
u	SLC4A4	4:72053003-72437804 4q13.3	solute carrier family 4, sodium bicarbonate cotransporter, member 4 [Source:HGNC Symbol;Acc:11030], type=processed_transcript,protein_coding, GO=[sodium:bicarbonate symporter activity; inorganic anion exchanger activity; bicarbonate transport; anion:anion antiporter activity; inorganic anion transport]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE
u	SMPD2	6:109761966-109765122 6q21	sphingomyelin phosphodiesterase 2, neutral membrane (neutral sphingomyelinase) [Source:HGNC Symbol;Acc:11121], type=protein_coding,retained_intron, GO=[sphingomyelin phosphodiesterase activity; sphingomyelin metabolic process; ceramide biosynthetic process; glycosphingolipid metabolic process; glycolipid metabolic process; caveola; sphingolipid metabolic process; membrane lipid metabolic process; induction of apoptosis by extracellular signals; response to mechanical stimulus; nerve growth factor receptor signaling pathway]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
u	SMS	X:21958691-22025798 Xp22.11	spermine synthase [Source:HGNC Symbol;Acc:11123], type=processed_transcript,protein_coding, GO=[spermine synthase activity; spermidine synthase activity; spermine biosynthetic process; methionine metabolic process; polyamine metabolic process; sulfur amino acid metabolic process]	tcgaOvarianMethyl
u	SNORD88B	19:51302289-51302379 19q13.33	small nucleolar RNA, C/D box 88B [Source:HGNC Symbol;Acc:32748], type=snoRNA	
u	SNORD88C	19:51305585-51305675 19q13.33	small nucleolar RNA, C/D box 88C [Source:HGNC Symbol;Acc:32749], type=snoRNA	

Continued on next page...

S	name	locus	description	studies
u	SORD	15:45315302-45369383 15q21.1	sorbitol dehydrogenase [Source:HGNC Symbol;Acc:11184], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[L-iditol 2-dehydrogenase activity; sorbitol metabolic process; sorbitol catabolic process; pentitol metabolic process; pentitol catabolic process; L-xylitol catabolic process; fructose biosynthetic process; hexitol metabolic process; sperm motility; NAD binding; flagellum; carbohydrate biosynthetic process; soluble fraction; carbohydrate binding; mitochondrial envelope]	tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad, tscapeNSCLCd
u*	SOX4	6:21593972-21598847 6p22.3	SRY (sex determining region Y)-box 4 [Source:HGNC Symbol;Acc:11200], type=protein_coding, GO=[positive regulation of N-terminal peptidyl-lysine acetylation; regulation of N-terminal peptidyl-lysine acetylation; ascending aorta development; ascending aorta morphogenesis; atrial septum primum morphogenesis; septum primum development; mitral valve morphogenesis; mitral valve development; negative regulation of protein export from nucleus; neuroepithelial cell differentiation; noradrenergic neuron differentiation; pro-B cell differentiation; DNA damage response, detection of DNA damage; cardiac ventricle formation; limb bud formation; cardiac right ventricle morphogenesis; RNA polymerase II transcription coactivator activity; glial cell proliferation; ventricular septum morphogenesis; spinal cord motor neuron differentiation; core promoter sequence-specific DNA binding; sympathetic nervous system development; ventral spinal cord development; ventricular septum development; somatic stem cell maintenance; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription; kidney morphogenesis; positive regulation of canonical Wnt receptor signaling pathway; positive regulation of translation; protein stabilization; glial cell development; DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest; positive regulation of hormone secretion; neural tube formation; negative regulation of protein ubiquitination; response to glucose stimulus; response to hexose stimulus; endocrine pancreas development; regulation of protein ubiquitination; canonical Wnt receptor signaling pathway; urogenital system development; transcription coactivator activity; transcription cofactor activity; protein binding transcription factor activity; positive regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
u	SPDEF	6:34505579-34524110 6p21.31	SAM pointed domain containing ets transcription factor [Source:HGNC Symbol;Acc:17257], type=protein_coding, GO=[lung goblet cell differentiation; positive regulation of cell fate commitment; intestinal epithelial cell development; negative regulation of survival gene product expression; negative regulation of cell fate commitment; regulation of cell fate commitment; respiratory system development; negative regulation of transcription from RNA polymerase II promoter; positive regulation of transcription from RNA polymerase II promoter]	snp3dProstateC, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE
u	SPHAR	1:229440129-229441248 1q42.13	S-phase response (cyclin related) [Source:HGNC Symbol;Acc:16957], type=protein_coding	tscapeBCa, tscapeMelanomad, tscapeOvariana, tscapeProstated
u	SPON2	4:1160720-1202750 4p16.3	spondin 2, extracellular matrix protein [Source:HGNC Symbol;Acc:11253], type=processed_transcript,protein_coding,retained_intron	snp3dLungC, tcgaBreastMethyl, tcgaColonGE
d	SQRDL	15:45923346-45983492 15q21.1	sulfide quinone reductase-like (yeast) [Source:HGNC Symbol;Acc:20390], type=protein_coding, GO=[sulfide:quinone oxidoreductase activity; sulfide oxidation, using sulfide:quinone oxidoreductase; sulfide oxidation; sulfur amino acid catabolic process; sulfur amino acid metabolic process; mitochondrial envelope]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl, tscapeMelanomad, tscapeNSCLCd
d	SRPX	X:38008589-38080696 Xp11.4	sushi-repeat containing protein, X-linked [Source:HGNC Symbol;Acc:11309], type=processed_transcript,protein_coding, GO=[cell surface]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
d*	ST3GAL1	8:134467091-134584183 8q24.22	ST3 beta-galactoside alpha-2,3-sialyltransferase 1 [Source:HGNC Symbol;Acc:10862], type=processed_transcript,protein_coding,retained_intron, GO=[beta-galactoside alpha-2,3-sialyltransferase activity; O-glycan processing; sialyltransferase activity; integral to Golgi membrane; Golgi cisterna membrane; Golgi cisterna; Golgi stack; post-translational protein modification; Golgi membrane]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
u*	ST6GALNAC1	17:74620847-74639894 17q25.1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1 [Source:HGNC Symbol;Acc:23614], type=protein_coding, GO=[alpha-N-acetylgalactosaminide alpha-2,6-sialyltransferase activity; sialyltransferase activity; integral to Golgi membrane; oligosaccharide biosynthetic process; carbohydrate biosynthetic process; Golgi membrane]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	ST6GALNAC	9:130670114-130679317 9q34.11	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4 [Source:HGNC Symbol;Acc:17846], type=processed_transcript,protein_coding, GO=[(alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetyl-galactosaminide 6-alpha-sialyltransferase activity; O-glycan processing; sialyltransferase activity; glycolipid metabolic process; integral to Golgi membrane; membrane lipid metabolic process; post-translational protein modification; soluble fraction; Golgi membrane]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u*	TBC1D4	13:75858808-76056250 13q22.2	TBC1 domain family, member 4 [Source:HGNC Symbol;Acc:19165], type=processed_transcript,protein_coding, GO=[Rab GTPase activator activity; regulation of Rab GTPase activity; Ras GTPase activator activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeProstated
u	TEX2	17:62224796-62340653 17q23.3	testis expressed 2 [Source:HGNC Symbol;Acc:30884], type=protein_coding, GO=[sphingolipid metabolic process; membrane lipid metabolic process; phospholipid binding]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	TEX2	HG183_PATCH:62224796-62340653 HG183_PATCHq23.3	testis expressed 2 [Source:HGNC Symbol;Acc:30884], type=protein_coding, GO=[sphingolipid metabolic process; membrane lipid metabolic process; phospholipid binding]	
d	TGM3	20:2276647-2321724 20p13	transglutaminase 3 (E polypeptide, protein-glutamine-gamma-glutamyltransferase) [Source:HGNC Symbol;Acc:11779], type=processed_transcript,protein_coding, GO=[cell envelope organization; protein-glutamine gamma-glutamyltransferase activity; hair follicle morphogenesis; GDP binding; peptide cross-linking; keratinization; extrinsic to internal side of plasma membrane; protein tetramerization; hair follicle development; magnesium ion binding; GTPase activity; GTP binding; calcium ion binding]	cosmicMetastasis, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE
u*	THBS1	15:39873280-39891667 15q14	thrombospondin 1 [Source:HGNC Symbol;Acc:11785], type=protein_coding,retained_intron, GO=[regulation of nitric oxide mediated signal transduction; negative regulation of nitric oxide mediated signal transduction; regulation of cGMP-mediated signaling; negative regulation of cGMP-mediated signaling; negative regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II; negative regulation of dendritic cell antigen processing and presentation; engulfment of apoptotic cell; regulation of antigen processing and presentation of peptide or polysaccharide antigen via MHC class II; fibrinogen binding; collagen V binding; positive regulation of transforming growth factor beta1 production; negative regulation of plasma membrane long-chain fatty acid transport; negative regulation of plasminogen activation; negative regulation of focal adhesion assembly; positive regulation of fibroblast migration; regulation of fibroblast migration; fibrinogen complex; positive regulation of macrophage chemotaxis; positive regulation of macrophage activation; negative regulation of fibroblast growth factor receptor signaling pathway; negative regulation of interleukin-12 production; growth plate cartilage development; positive regulation of tumor necrosis factor biosynthetic process; negative regulation of fibrinolysis; transforming growth factor beta binding; phosphatidylserine binding; negative regulation of blood vessel endothelial cell migration; response to magnesium ion; cGMP-mediated signaling; proteoglycan binding; nitric oxide mediated signal transduction; fibroblast growth factor binding; cellular response to heat; regulation of focal adhesion assembly; zymogen activation; chronic inflammatory response; positive regulation of blood vessel endothelial cell migration; macrophage chemotaxis; low-density lipoprotein particle binding; positive regulation of transforming growth factor beta receptor signaling pathway; laminin binding; fibronectin binding; eukaryotic cell surface binding; negative regulation of endothelial cell proliferation; positive regulation of reactive oxygen species metabolic process; response to progesterone stimulus; peptide cross-linking; sprouting angiogenesis; macrophage activation; platelet alpha granule lumen; positive regulation of translation; positive regulation of protein kinase B signaling cascade; blood vessel endothelial cell migration; negative regulation of angiogenesis; negative regulation of caspase activity; glycoprotein binding; regulation of endothelial cell proliferation; integrin binding; positive regulation of angiogenesis; response to calcium ion; platelet degranulation; endothelial cell migration; response to glucose stimulus; response to hexose stimulus; heparin binding; negative regulation of peptidase activity; activation of MAPK activity; external side of plasma membrane; phospholipid binding; platelet activation; positive regulation of phosphorylation; positive regulation of protein kinase activity; response to drug; carbohydrate binding; cell surface; MAPKKK cascade; calcium ion binding; cytoplasmic membrane-bounded vesicle; identical protein binding; cytoplasmic vesicle]	cosmicRecurrent, snp3dGlioma, tcgaBreastGE, tcgaOvarianMethyl, tscapeCRCd, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand

Continued on next page...

S	name	locus	description	studies
u	TM4SF1	3:149086809-149095652 3q25.1	transmembrane 4 L six family member 1 [Source:HGNC Symbol;Acc:11853], type=nonsense_mediated_decay,protein_coding	snp3dMetastasis, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
u	TM4SF18	3:149036285-149052201 3q25.1	transmembrane 4 L six family member 18 [Source:HGNC Symbol;Acc:25181], type=protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl
u	TMEFF2	2:192813769-193060435 2q32.3	transmembrane protein with EGF-like and two follistatin-like domains 2 [Source:HGNC Symbol;Acc:11867], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
d	TMEM140	7:134832824-134850650 7q33	transmembrane protein 140 [Source:HGNC Symbol;Acc:21870], type=processed_transcript,protein_coding	tcgaColonGE, tcgaGliomaGE
d	TMEM158	3:45265958-45267770 3p21.31	transmembrane protein 158 (gene/pseudogene) [Source:HGNC Symbol;Acc:30293], type=protein_coding	tcgaGliomaGE
u	TMEM79	1:156252726-156262976 1q22	transmembrane protein 79 [Source:HGNC Symbol;Acc:28196], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
u	TMPRSS2	21:42836478-42903043 21q22.3	transmembrane protease, serine 2 [Source:HGNC Symbol;Acc:11876], type=processed_transcript,protein_coding,retained_intron, GO=[scavenger receptor activity; serine-type endopeptidase activity]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeProstated
u	TNFRSF19	13:24144509-24250232 13q12.12	tumor necrosis factor receptor superfamily, member 19 [Source:HGNC Symbol;Acc:11915], type=processed_transcript,protein_coding, GO=[tumor necrosis factor receptor activity; tumor necrosis factor-mediated signaling pathway; cellular response to tumor necrosis factor; hair follicle development; positive regulation of I-kappaB kinase/NF-kappaB cascade; JNK cascade; cytokine-mediated signaling pathway; MAPKKK cascade]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeBCd, tscapeOvariand, tscapeSCLCd
u	TNS3	7:47314752-47622156 7p12.3	tensin 3 [Source:HGNC Symbol;Acc:21616], type=processed_transcript,protein_coding,retained_intron, GO=[lung alveolus development; focal adhesion; respiratory system development; dephosphorylation]	tcgaColonGE, tcgaColonMethyl
u	TP53TG1	7:86954541-86974831 7q21.12	TP53 target 1 (non-protein coding) [Source:HGNC Symbol;Acc:17026], type=lincRNA,processed_transcript	tcgaColonGE
d	TRNP1	1:27320198-27327147 1p36.11	TMF1-regulated nuclear protein 1 [Source:HGNC Symbol;Acc:34348], type=protein_coding	tcgaBreastGE, tcgaColonGE
u	TRPM4	19:49661052-49715091 19q13.33	transient receptor potential cation channel, subfamily M, member 4 [Source:HGNC Symbol;Acc:17993], type=protein_coding, GO=[regulation of T cell cytokine production; dendritic cell chemotaxis; calcium activated cation channel activity; protein sumoylation; regulation of T cell mediated immunity; positive regulation of canonical Wnt receptor signaling pathway; calcium channel activity; calmodulin binding; canonical Wnt receptor signaling pathway]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd, tscapeOvariand
d	TSHZ3	19:31765851-31840453 19q12	teashirt zinc finger homeobox 3 [Source:HGNC Symbol;Acc:30700], type=processed_transcript,protein_coding, GO=[ureter smooth muscle contraction; ureteric peristalsis; sensory perception of touch; kidney smooth muscle cell differentiation; positive regulation of smooth muscle cell differentiation; ureter smooth muscle cell differentiation; ureter smooth muscle development; regulation of respiratory gaseous exchange by neurological system process; phasic smooth muscle contraction; musculoskeletal movement; multicellular organismal movement; kidney morphogenesis; growth cone; metanephros development; ureteric bud development; respiratory system development; chromatin binding; urogenital system development]	cosmicPrimary, tcgaBreastGE, tcgaColonGE
d	TULP4	6:158733692-158932860 6q25.3	tubby like protein 4 [Source:HGNC Symbol;Acc:15530], type=protein_coding	tcgaGliomaGE, tscapeBCd, tscapeOvariand, tscapeProstated, tscapeSCLCd
d	TXNIP	1:145438469-145442635 1q21.1	thioredoxin interacting protein [Source:HGNC Symbol;Acc:16952], type=processed_transcript,protein_coding,retained_intron, GO=[cellular response to tumor cell; negative regulation of cell division; response to progesterone stimulus; nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway; platelet-derived growth factor receptor signaling pathway; mitochondrial intermembrane space; response to calcium ion; response to hydrogen peroxide; response to estradiol stimulus; ubiquitin protein ligase binding; response to glucose stimulus; response to hexose stimulus; response to mechanical stimulus; response to estrogen stimulus; response to drug; mitochondrial envelope]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	UAP1	1:162531321-162569627 1q23.3	UDP-N-acteylglucosamine pyrophosphorylase 1 [Source:HGNC Symbol;Acc:12457], type=processed_transcript,protein_coding, GO=[UDP-N-acetylglucosamine diphosphorylase activity; UDP-N-acetylglucosamine biosynthetic process; N-acetylglucosamine biosynthetic process; glucosamine biosynthetic process; glucosamine metabolic process; N-acetylglucosamine metabolic process; nucleotide-sugar metabolic process; dolichol-linked oligosaccharide biosynthetic process; oligosaccharide biosynthetic process; peptidyl-asparagine modification; protein N-linked glycosylation via asparagine; post-translational protein modification; carbohydrate biosynthetic process]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	UGT2B11	4:70065669-70080449 4q13.2	UDP glucuronosyltransferase 2 family, polypeptide B11 [Source:HGNC Symbol;Acc:12545], type=protein_coding,retained_intron, GO=[estrogen metabolic process; lipid glycosylation; glucuronosyltransferase activity; UDP-glycosyltransferase activity; xenobiotic metabolic process; microsome; carbohydrate binding; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	tcgaOvarianMethyl
u*	UGT2B28	4:70146217-70160768 4q13.2	UDP glucuronosyltransferase 2 family, polypeptide B28 [Source:HGNC Symbol;Acc:13479], type=protein_coding, GO=[lipid glycosylation; glucuronosyltransferase activity; UDP-glycosyltransferase activity; xenobiotic metabolic process; microsome; carbohydrate binding; nuclear outer membrane-endoplasmic reticulum membrane network; endoplasmic reticulum part]	
u	VPS26B	11:134094539-134117686 11q25	vacuolar protein sorting 26 homolog B (S. pombe) [Source:HGNC Symbol;Acc:28119], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[retromer complex; vacuolar transport]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd
u	WWC1	5:167718656-167899308 5q34	WW and C2 domain containing 1 [Source:HGNC Symbol;Acc:29435], type=TEC,processed_transcript,protein_coding,retained_intron, GO=[regulation of hippo signaling cascade; ruffle membrane; positive regulation of MAPKKK cascade; transcription coactivator activity; regulation of MAPKKK cascade; perinuclear region of cytoplasm; transcription cofactor activity; protein binding transcription factor activity; MAPKKK cascade]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa, tscapeRCCa
u	YIPF1	1:54317392-54356407 1p32.3	Yip1 domain family, member 1 [Source:HGNC Symbol;Acc:25231], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[cytoplasmic membrane-bounded vesicle; cytoplasmic vesicle]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
u	ZBTB10	8:81397854-81438500 8q21.13	zinc finger and BTB domain containing 10 [Source:HGNC Symbol;Acc:30953], type=protein_coding, GO=[negative regulation of transcription from RNA polymerase II promoter]	tcgaGliomaGE, tscapeBCa, tscapeNSCLCa
u*	ZMIZ1	10:80828792-81076285 10q22.3	zinc finger, MIZ-type containing 1 [Source:HGNC Symbol;Acc:16493], type=processed_transcript,protein_coding, GO=[nuclear speck]	tcgaColonGE, tcgaGliomaCGHd, tscapeBCa
u	ZNF385B	2:180306709-180726232 2q31.2, 2q31.3	zinc finger protein 385B [Source:HGNC Symbol;Acc:26332], type=processed_transcript,protein_coding	cosmicPrimary, tcgaBreastGE, tcgaBreastGESurv, tcgaGliomaGE
d	ZNF467	7:149461271-149470568 7q36.1	zinc finger protein 467 [Source:HGNC Symbol;Acc:23154], type=protein_coding	tcgaBreastGE, tcgaBreastMethyl, tscapeMelanomaa, tscapeOvariana
d	ZNF503	10:77039484-77161664 10q22.2	zinc finger protein 503 [Source:HGNC Symbol;Acc:23589], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeOvariana, tscapeProstatea

14 Candidate report for DEX no DHT

14.1 Moksiskaan candidate pathway

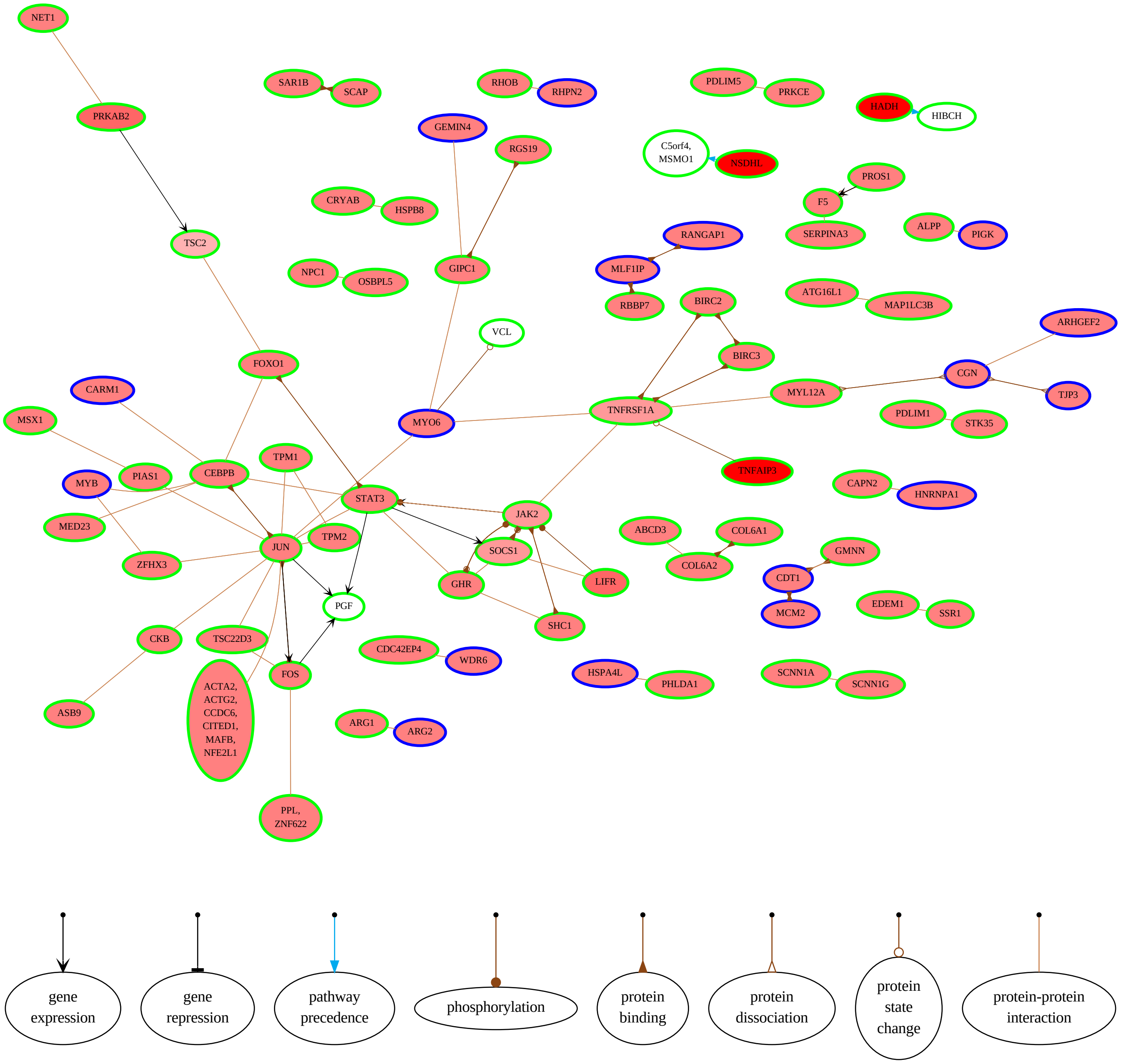


Figure 59: Known relationships between the candidate genes. Candidate genes are shown in red if they have only output connections. The ratio of input and output connections determines how light they are. Completely white genes have only input connections. The maximum of 0 other gene step(s) are allowed between the candidate genes and these intermediate genes are shown on gray. Green and blue borders are referring to up and down regulated genes, respectively. Light grey is used to emphasize stably expressed genes. Known regulations are shown with bold borders whereas the predictions are kept thin.

Table 34: List of KEGG [6] pathways supporting the relationships between the genes shown in Figure 59. Number of edges taken from each pathway is shown on edges column.

name	edges	genes
Jak-STAT signaling pathway	10	GHR, JAK2, LIFR, PIAS1, SOCS1, STAT3
Tight junction	4	CGN, MYL12A, PRKCE, TJP3
Pathways in cancer	3	BIRC2, BIRC3, CCDC6, FOS, FOXO1, JUN, PGF, PIAS1, STAT3
Steroid biosynthesis	2	C5orf4, MSMO1, NSDHL
Chemokine signaling pathway	2	JAK2, SHC1, STAT3
Adipocytokine signaling pathway	2	JAK2, PRKAB2, STAT3, TNFRSF1A
Toxoplasmosis	2	BIRC2, BIRC3, JAK2, SOCS1, STAT3, TNFRSF1A
Valine, leucine and isoleucine degradation	1	HADH, HIBCH
Pancreatic cancer	1	PGF, STAT3

Table 35: List of WikiPathways [7] pathways supporting the relationships between the genes shown in Figure 59. Number of edges taken from each pathway is shown on edges column.

name	**edges**	**genes**
SREBP signalling	2	SAR1B, SCAP
EGF/EGFR Signaling Pathway	2	FOS, FOXO1, JAK2, JUN, SHC1, STAT3
AMPK signaling	1	PRKAB2, TSC2
TOR signaling	1	PRKAB2, TSC2
Leptin signaling pathway	1	FOXO1, JAK2, SHC1, STAT3
Complement and Coagulation Cascades	1	F5, PROS1
TGF Beta Signaling Pathway	1	FOS, JUN, STAT3

14.1.1 GO enrichment of the candidate pathway

Table 36: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.01$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.506	BP	response to stress	ARG1, ARG2, ATG16L1, BIRC2, BIRC3, CAPN2, CEBPB, CITED1, CRYAB, EDEM1, F5, FOS, FOXO1, HSPA4L, HSPB8, JAK2, JUN, MAP1LC3B, MSX1, MYB, MYO6, NET1, NFE2L1, NPC1, PDLIM1, PGF, PIAS1, PRKCE, PROS1, RBBP7, RHOB, SCAP, SCNN1G, SERPINA3, SHC1, SOCS1, SSR1, STAT3, TNFAIP3, TNFRSF1A, TPM1, TSC2, TSC22D3, VCL, ZNF622
0.400	CC	cytosol	ABCD3, ACTA2, ACTG2, ARG1, ARHGEF2, BIRC2, CARM1, CDT1, CITED1, CKB, CRYAB, FOXO1, GEMIN4, GIPC1, GMNN, JAK2, JUN, MLF1IP, MYO6, NET1, OSBPL5, PDLIM5, PRKAB2, PRKCE, RANGAP1, RGS19, RHOB, SAR1B, SHC1, SOCS1, STAT3, TNFAIP3, TPM1, TPM2, TSC2, VCL
0.667	CC	organelle part	ABCD3, ACTA2, ARG2, ARHGEF2, CAPN2, CARM1, CDT1, CEBPB, CGN, CRYAB, EDEM1, F5, FOS, FOXO1, GEMIN4, GIPC1, GMNN, HADH, HIBCH, HNRNPA1, JAK2, JUN, MAFB, MAP1LC3B, MCM2, MED23, MLF1IP, MSMO1, MSX1, MYB, MYL12A, MYO6, NPC1, NSDHL, PDLIM1, PDLIM5, PHLDA1, PIAS1, PIGK, PRKAB2, PRKCE, PROS1, RANGAP1, RBBP7, RHOB, SAR1B, SCAP, SCNN1A, SHC1, SSR1, STAT3, STK35, TNFAIP3, TPM1, TPM2, TSC2, VCL, WDR6, ZFHX3, ZNF622
0.337	BP	response to organic substance	ARG1, ARG2, CARM1, CEBPB, CITED1, COL6A1, COL6A2, CRYAB, EDEM1, FOS, FOXO1, GHR, HADH, HSPA4L, JAK2, JUN, LIFR, NPC1, PGF, PIAS1, PRKAB2, PRKCE, SCAP, SHC1, SOCS1, SSR1, STAT3, TNFAIP3, TNFRSF1A, TSC2
0.180	BP	cellular response to endogenous stimulus	ARG1, ARG2, CEBPB, COL6A1, FOS, FOXO1, GHR, JAK2, NPC1, PGF, PRKAB2, SHC1, SOCS1, STAT3, TNFRSF1A, TSC2
0.644	CC	intracellular organelle part	ABCD3, ARG2, ARHGEF2, CAPN2, CARM1, CDT1, CEBPB, CGN, CRYAB, EDEM1, F5, FOS, FOXO1, GEMIN4, GMNN, HADH, HIBCH, HNRNPA1, JAK2, JUN, MAFB, MAP1LC3B, MCM2, MED23, MLF1IP, MSMO1, MSX1, MYB, MYL12A, MYO6, NPC1, NSDHL, PDLIM1, PDLIM5, PHLDA1, PIAS1, PIGK, PRKAB2, PRKCE, PROS1, RANGAP1, RBBP7, RHOB, SAR1B, SCAP, SCNN1A, SHC1, SSR1, STAT3, STK35, TNFAIP3, TPM1, TPM2, TSC2, VCL, WDR6, ZFHX3, ZNF622
0.124	BP	response to lipopolysaccharide	ARG1, ARG2, CEBPB, CITED1, FOS, JAK2, JUN, PRKCE, SOCS1, TNFAIP3, TNFRSF1A
0.258	BP	response to wounding	ARG1, ARG2, BIRC2, BIRC3, CEBPB, F5, FOS, JAK2, JUN, MYB, NFE2L1, PRKCE, PROS1, RHOB, SCNN1G, SERPINA3, SHC1, STAT3, TNFAIP3, TNFRSF1A, TPM1, TSC2, VCL
0.236	BP	cellular response to organic substance	ARG1, ARG2, CEBPB, COL6A1, EDEM1, FOS, FOXO1, GHR, JAK2, LIFR, NPC1, PGF, PIAS1, PRKAB2, PRKCE, SHC1, SOCS1, SSR1, STAT3, TNFRSF1A, TSC2
0.124	BP	response to hypoxia	ARG2, CAPN2, CRYAB, PDLIM1, PGF, PRKCE, SCAP, SCNN1G, SHC1, TNFRSF1A, TSC2
0.438	BP	negative regulation of biological process	ARG2, ARHGEF2, BIRC2, BIRC3, CDT1, CEBPB, CITED1, CRYAB, FOXO1, GIPC1, GMNN, HADH, JAK2, JUN, LIFR, MAFB, MCM2, MSX1, MYB, NPC1, PIAS1, PRKAB2, PRKCE, PROS1, RANGAP1, RBBP7, RGS19, RHOB, SCAP, SOCS1, STAT3, TNFAIP3, TNFRSF1A, TPM1, TSC2, TSC22D3, VCL, WDR6, ZFHX3
0.045	BP	JAK-STAT cascade involved in growth hormone signaling pathway	GHR, JAK2, SOCS1, STAT3
0.844	MF	protein binding	ABCD3, ARG2, ARHGEF2, ASB9, ATG16L1, BIRC2, BIRC3, CAPN2, CARM1, CCDC6, CDC42EP4, CDT1, CEBPB, CGN, CITED1, CKB, COL6A1, COL6A2, CRYAB, EDEM1, F5, FOS, FOXO1, GEMIN4, GHR, GIPC1, GMNN, HSPB8, JAK2, JUN, LIFR, MAFB, MAP1LC3B, MCM2, MED23, MLF1IP, MSX1, MYB, MYO6, NET1, NFE2L1, NPC1, OSBPL5, PDLIM1, PDLIM5, PGF, PHLDA1, PIAS1, PIGK, PPL, PRKAB2, PRKCE, PROS1, RANGAP1, RBBP7, RGS19, RHOB, RHPN2, SCAP, SCNN1A, SCNN1G, SERPINA3, SHC1, SOCS1, STAT3, TJP3, TNFAIP3, TNFRSF1A, TPM1, TPM2, TSC2, TSC22D3, VCL, WDR6, ZFHX3, ZNF622
0.337	BP	anatomical structure morphogenesis	ARG1, ARHGEF2, CAPN2, CARM1, CDC42EP4, CITED1, COL6A1, COL6A2, CRYAB, GHR, GMNN, HSPA4L, JAK2, JUN, LIFR, MAFB, MSX1, MYO6, NFE2L1, PDLIM5, PGF, RHOB, SHC1, SOCS1, STAT3, TNFAIP3, TNFRSF1A, TPM1, TSC2, VCL
0.202	BP	regulation of hydrolase activity	BIRC2, BIRC3, CRYAB, EDEM1, JAK2, JUN, NET1, PRKCE, PROS1, RANGAP1, RGS19, SERPINA3, SHC1, SSR1, TNFAIP3, TPM1, TPM2, TSC2
0.236	BP	cellular response to stress	ARG1, ATG16L1, CRYAB, EDEM1, FOS, FOXO1, JAK2, JUN, MAP1LC3B, MSX1, MYO6, NET1, NPC1, PRKCE, RBBP7, RHOB, SCAP, SHC1, SSR1, TPM1, ZNF622
0.090	BP	response to reactive oxygen species	ARG1, CRYAB, FOS, JUN, NET1, RHOB, SHC1, TPM1
0.356	CC	organelle lumen	ARG2, CARM1, CDT1, CEBPB, F5, FOS, FOXO1, GEMIN4, GMNN, HADH, HIBCH, HNRNPA1, JAK2, JUN, MAFB, MCM2, MED23, MLF1IP, MSX1, MYB, MYO6, PDLIM1, PHLDA1, PIAS1, PRKAB2, PROS1, RBBP7, SHC1, STAT3, STK35, ZFHX3, ZNF622
0.034	BP	activation of signaling protein activity involved in unfolded protein response	EDEM1, SHC1, SSR1
0.034	BP	regulation of nucleotide-binding oligomerization domain containing signaling pathway	BIRC2, BIRC3, TNFAIP3
0.344	CC	intracellular organelle lumen	ARG2, CARM1, CDT1, CEBPB, FOS, FOXO1, GEMIN4, GMNN, HADH, HIBCH, HNRNPA1, JAK2, JUN, MAFB, MCM2, MED23, MLF1IP, MSX1, MYB, MYO6, PDLIM1, PHLDA1, PIAS1, PRKAB2, PROS1, RBBP7, SHC1, STAT3, STK35, ZFHX3, ZNF622
0.122	CC	actin cytoskeleton	ACTA2, CDC42EP4, CGN, CRYAB, MYL12A, MYO6, PDLIM5, SCNN1A, TPM1, TPM2, VCL
0.067	BP	response to amino acid stimulus	ARG1, ARG2, CEBPB, COL6A1, SOCS1, TNFRSF1A
0.281	BP	regulation of multicellular organismal process	ARG2, ARHGEF2, CARM1, CEBPB, CITED1, GHR, GIPC1, JAK2, JUN, MAFB, MSX1, MYB, MYO6, PDLIM5, PGF, PRKCE, PROS1, RHOB, SHC1, STAT3, TNFAIP3, TNFRSF1A, TPM1, TSC22D3, ZFHX3
0.124	BP	response to steroid hormone stimulus	ARG1, ARG2, CITED1, CRYAB, FOS, GHR, NPC1, SHC1, SOCS1, STAT3, TNFRSF1A
0.200	MF	enzyme binding	ARG2, ARHGEF2, CDC42EP4, FOXO1, GHR, GMNN, JAK2, PDLIM5, PIAS1, PRKAB2, PRKCE, SOCS1, STAT3, TNFAIP3, TNFRSF1A, TSC2, VCL, ZFHX3
0.371	BP	negative regulation of cellular process	ARHGEF2, BIRC2, BIRC3, CDT1, CEBPB, CITED1, CRYAB, FOXO1, GIPC1, GMNN, HADH, JAK2, JUN, LIFR, MAFB, MCM2, MSX1, MYB, NPC1, PIAS1, PRKAB2, RBBP7, RGS19, RHOB, SOCS1, STAT3, TNFAIP3, TPM1, TSC2, TSC22D3, VCL, WDR6, ZFHX3
0.124	BP	response to drug	ABCD3, ARG1, ARG2, FOS, HADH, JUN, MYO6, NPC1, PGF, SOCS1, STAT3
0.322	CC	nuclear part	CARM1, CDT1, CEBPB, FOS, FOXO1, GEMIN4, GMNN, HNRNPA1, JAK2, JUN, MAFB, MCM2, MED23, MLF1IP, MSX1, MYB, MYO6, NPC1, PDLIM1, PHLDA1, PIAS1, PRKAB2, RANGAP1, RBBP7, STAT3, STK35, WDR6, ZFHX3, ZNF622
0.427	BP	system development	ACTA2, ARG1, ARG2, ARHGEF2, BIRC2, CAPN2, CARM1, CEBPB, CITED1, CKB, COL6A1, COL6A2, CRYAB, FOS, FOXO1, GHR, GMNN, JAK2, JUN, LIFR, MAFB, MSX1, MYB, MYO6, NSDHL, PDLIM5, PGF, PPL, RHOB, SHC1, SOCS1, STAT3, TNFAIP3, TNFRSF1A, TPM1, TSC2, TSC22D3, ZFHX3
0.067	BP	response to hydrogen peroxide	ARG1, CRYAB, JUN, NET1, RHOB, SHC1
0.289	CC	nuclear lumen	CARM1, CDT1, CEBPB, FOS, FOXO1, GEMIN4, GMNN, HNRNPA1, JAK2, JUN, MAFB, MCM2, MED23, MLF1IP, MSX1, MYB, MYO6, PDLIM1, PHLDA1, PIAS1, PRKAB2, RBBP7, STAT3, STK35, ZFHX3, ZNF622
0.382	BP	positive regulation of cellular process	ARG1, ARHGEF2, BIRC2, BIRC3, CARM1, CDC42EP4, CEBPB, CITED1, FOS, FOXO1, GHR, GIPC1, JAK2, JUN, LIFR, MAFB, MSX1, MYB, MYO6, NET1, PGF, PHLDA1, PIAS1, PRKCE, RHOB, SCAP, SHC1, SSR1, STAT3, TNFAIP3, TNFRSF1A, TPM1, ZFHX3, ZNF622
0.213	BP	regulation of transcription from RNA polymerase II promoter	CDT1, CEBPB, CITED1, FOS, FOXO1, JUN, MAFB, MED23, MSX1, MYB, MYO6, PHLDA1, PIAS1, RBBP7, SCAP, STAT3, TNFRSF1A, TSC22D3, ZFHX3
0.233	CC	nucleoplasm	CARM1, CDT1, FOS, FOXO1, GEMIN4, GMNN, HNRNPA1, JUN, MAFB, MCM2, MED23, MLF1IP, MSX1, MYO6, PDLIM1, PHLDA1, PIAS1, PRKAB2, RBBP7, STAT3, ZFHX3
0.225	BP	regulation of apoptosis	ARHGEF2, BIRC2, BIRC3, CEBPB, CITED1, CRYAB, FOXO1, GHR, JAK2, JUN, LIFR, MSX1, NET1, PHLDA1, PRKCE, RHOB, TNFAIP3, TNFRSF1A, TSC22D3, ZNF622
0.101	BP	response to insulin stimulus	CITED1, FOXO1, GHR, HADH, PRKAB2, SCAP, SHC1, SOCS1, TSC2
0.337	BP	organ development	ACTA2, ARG1, ARG2, BIRC2, CAPN2, CARM1, CEBPB, CITED1, CKB, CRYAB, FOXO1, GHR, GMNN, JAK2, JUN, LIFR, MAFB, MSX1, MYB, MYO6, NSDHL, PPL, SHC1, SOCS1, STAT3, TNFAIP3, TPM1, TSC2, TSC22D3, ZFHX3
0.022	BP	TRIF-dependent toll-like receptor signaling pathway	FOS, JUN
0.124	BP	response to cytokine stimulus	ARG2, CITED1, FOS, GHR, JAK2, JUN, LIFR, PIAS1, SOCS1, STAT3, TNFRSF1A
0.101	BP	anti-apoptosis	BIRC2, BIRC3, CEBPB, CITED1, CRYAB, FOXO1, LIFR, TNFAIP3, TSC22D3
0.202	BP	intracellular transport	ARHGEF2, CITED1, CRYAB, GIPC1, HNRNPA1, JAK2, JUN, MYO6, NPC1, OSBPL5, PRKAB2, RANGAP1, RHOB, SAR1B, SSR1, STAT3, TNFRSF1A, TSC2
0.056	BP	cellular response to reactive oxygen species	ARG1, FOS, NET1, RHOB, TPM1
0.135	BP	regulation of catabolic process	ASB9, GIPC1, JUN, NET1, NPC1, PRKCE, RANGAP1, RGS19, TNFAIP3, TPM1, TPM2, TSC2
0.124	BP	inflammatory response	BIRC2, BIRC3, CEBPB, FOS, JAK2, NFE2L1, SERPINA3, STAT3, TNFAIP3, TNFRSF1A, TSC2
0.156	CC	nucleoplasm part	FOS, FOXO1, GEMIN4, JUN, MAFB, MCM2, MED23, MSX1, MYO6, PDLIM1, PHLDA1, PIAS1, RBBP7, ZFHX3
0.213	BP	negative regulation of metabolic process	BIRC3, CEBPB, CITED1, CRYAB, GIPC1, GMNN, JUN, MSX1, MYB, NPC1, PIAS1, RBBP7, SCAP, SOCS1, STAT3, TNFAIP3, TNFRSF1A, TSC22D3, ZFHX3
0.067	CC	contractile fiber part	ACTA2, CRYAB, PDLIM5, TPM1, TPM2, VCL
0.356	CC	protein complex	ARHGEF2, BIRC2, CGN, COL6A1, COL6A2, FOS, FOXO1, GHR, JUN, MAFB, MAP1LC3B, MCM2, MED23, MLF1IP, MSX1, MYL12A, MYO6, PDLIM1, PHLDA1, PIGK, PRKAB2, RANGAP1, RBBP7, RGS19, SCAP, SHC1, TNFRSF1A, TPM1, TSC2, VCL, WDR6, ZFHX3
0.213	BP	regulation of cell communication	BIRC2, BIRC3, CITED1, FOXO1, GHR, GIPC1, HADH, JAK2, MSX1, MYO6, NPC1, PRKCE, RGS19, SOCS1, STAT3, TNFAIP3, TNFRSF1A, TSC2, ZNF622
0.022	MF	arginase activity	ARG1, ARG2
0.157	BP	organ morphogenesis	CARM1, CITED1, GHR, GMNN, JUN, LIFR, MAFB, MSX1, MYO6, SHC1, SOCS1, STAT3, TNFAIP3, TPM1

Continued on next page...

Ratio	Type	Description	Genes
0.111	MF	transcription cofactor activity	BIRC2, CARM1, CITED1, GMNN, JUN, MED23, NFE2L1, PDLIM1, PHLDA1, PIAS1
0.034	BP	SMAD protein signal transduction	CITED1, FOS, JUN
0.225	BP	cellular component assembly	ARG1, ATG16L1, CDC42EP4, COL6A1, COL6A2, CRYAB, GEMIN4, GMNN, JAK2, MAP1LC3B, MCM2, MLF1IP, MYO6, PDLIM5, PRKCE, RBBP7, TNFAIP3, TPM1, TSC2, VCL
0.167	CC	insoluble fraction	CAPN2, CRYAB, FOS, GIPC1, JAK2, MYO6, NPC1, PDLIM5, PRKCE, RGS19, RHOB, SCAP, SCNN1A, SCNN1G, TSC2
0.022	BP	regulation of L-arginine import	ARG1, ARG2
0.022	BP	regulation of amino acid import	ARG1, ARG2
0.213	BP	regulation of developmental process	ARHGEF2, BIRC2, CARM1, CDC42EP4, CEBPB, CITED1, GHR, JAK2, JUN, MAFB, MSX1, MYB, PDLIM5, PGF, RHOB, TNFAIP3, TNFRSF1A, TSC22D3, ZFHX3
0.089	CC	transcription factor complex	FOS, FOXO1, JUN, MAFB, MED23, MSX1, PDLIM1, ZFHX3
0.045	BP	acute-phase response	CEBPB, SERPINA3, STAT3, TSC2
0.100	MF	kinase binding	FOXO1, GHR, JAK2, PDLIM5, PRKAB2, PRKCE, SOCS1, STAT3, TNFAIP3
0.191	BP	negative regulation of cellular metabolic process	BIRC3, CEBPB, CITED1, CRYAB, GIPC1, GMNN, JUN, MSX1, MYB, NPC1, PIAS1, RBBP7, SOCS1, STAT3, TNFAIP3, TSC22D3, ZFHX3
0.034	BP	regulation of toll-like receptor signaling pathway	BIRC2, BIRC3, TNFAIP3
0.045	BP	regulation of tyrosine phosphorylation of STAT protein	GHR, JAK2, SOCS1, TNFRSF1A
0.022	BP	necroptosis	BIRC2, BIRC3
0.144	MF	protein dimerization activity	CAPN2, CARM1, CEBPB, CITED1, CRYAB, FOS, GHR, GIPC1, JUN, NFE2L1, PGF, STAT3, TSC2
0.101	BP	protein targeting	GIPC1, JAK2, JUN, MYO6, RANGAP1, SSR1, STAT3, TNFRSF1A, TSC2
0.146	BP	cardiovascular system development	ACTA2, CITED1, FOXO1, JUN, MSX1, NSDHL, PGF, RHOB, SHC1, TNFAIP3, TNFRSF1A, TPM1, TSC2
0.122	MF	cytoskeletal protein binding	ARHGEF2, CAPN2, CGN, CRYAB, GIPC1, MYO6, PDLIM5, PRKCE, SCNN1A, TPM1, TPM2
0.045	BP	response to axon injury	ARG1, ARG2, JAK2, JUN
0.056	BP	response to interferon-gamma	ARG2, CITED1, JAK2, PIAS1, SOCS1
0.022	CC	muscle thin filament tropomyosin	TPM1, TPM2
0.079	BP	nerve growth factor receptor signaling pathway	ARHGEF2, FOXO1, NET1, PRKCE, SHC1, STAT3, TSC2
0.202	BP	response to external stimulus	ARG1, ARG2, ATG16L1, BIRC2, BIRC3, COL6A1, COL6A2, FOS, GHR, JAK2, JUN, MAP1LC3B, NPC1, PROS1, RHOB, TNFAIP3, TNFRSF1A, TSC2
0.056	BP	response to estradiol stimulus	CRYAB, GHR, SOCS1, STAT3, TNFRSF1A
0.112	BP	blood vessel development	ACTA2, CITED1, FOXO1, JUN, NSDHL, PGF, RHOB, SHC1, TNFAIP3, TNFRSF1A
0.079	BP	regulation of endopeptidase activity	BIRC2, BIRC3, CRYAB, JAK2, PROS1, SERPINA3, TNFAIP3
0.034	BP	cellular amide metabolic process	ARG1, ARG2, GHR
0.034	BP	regulation of interferon-gamma-mediated signaling pathway	JAK2, PIAS1, SOCS1
0.089	MF	protein kinase binding	FOXO1, GHR, JAK2, PDLIM5, PRKAB2, PRKCE, SOCS1, STAT3
0.191	BP	tissue development	CAPN2, CARM1, CEBPB, CITED1, FOXO1, GHR, JAK2, JUN, MSX1, NSDHL, PGF, PPL, TPM1, TSC2, TSC22D3, VCL, ZFHX3
0.089	MF	actin binding	CGN, GIPC1, MYO6, PDLIM5, PRKCE, SCNN1A, TPM1, TPM2
0.326	BP	cellular developmental process	ACTA2, ARHGEF2, BIRC2, CAPN2, CARM1, CDC42EP4, CEBPB, CITED1, COL6A1, COL6A2, CRYAB, GHR, HSPA4L, JAK2, JUN, LIFR, MAFB, MSX1, MYB, MYO6, PDLIM5, PGF, PPL, RHOB, SHC1, SOCS1, STAT3, TPM1, ZFHX3
0.078	MF	transcription coactivator activity	BIRC2, CARM1, CITED1, JUN, MED23, PDLIM1, PIAS1

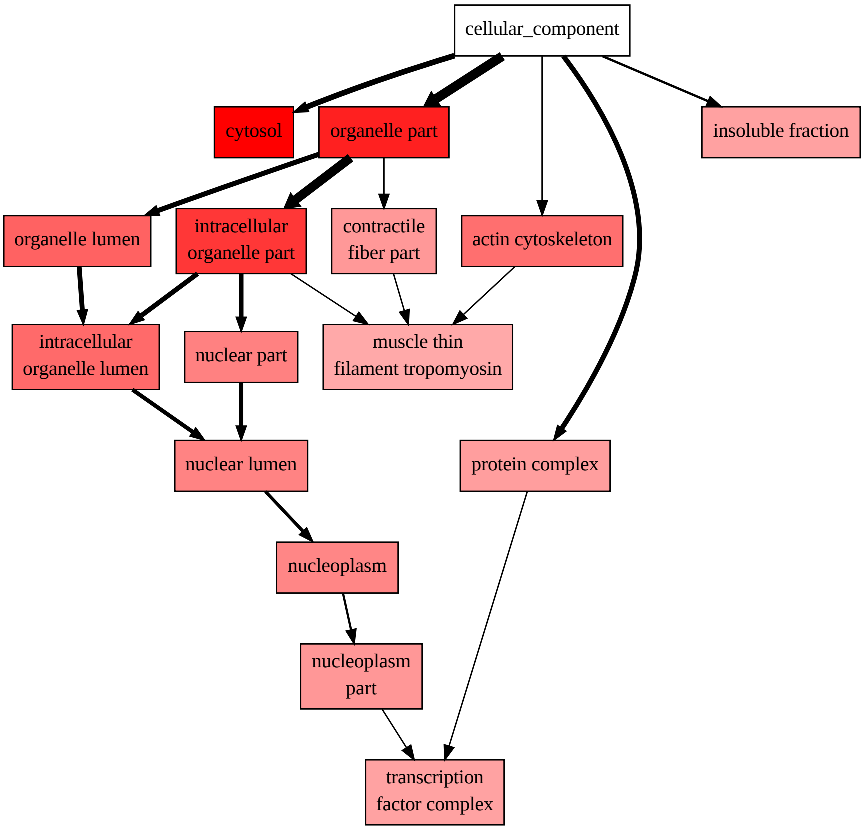


Figure 60: Relationships between the enriched *cellular component* Gene Ontology terms that were listed in Table 36. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

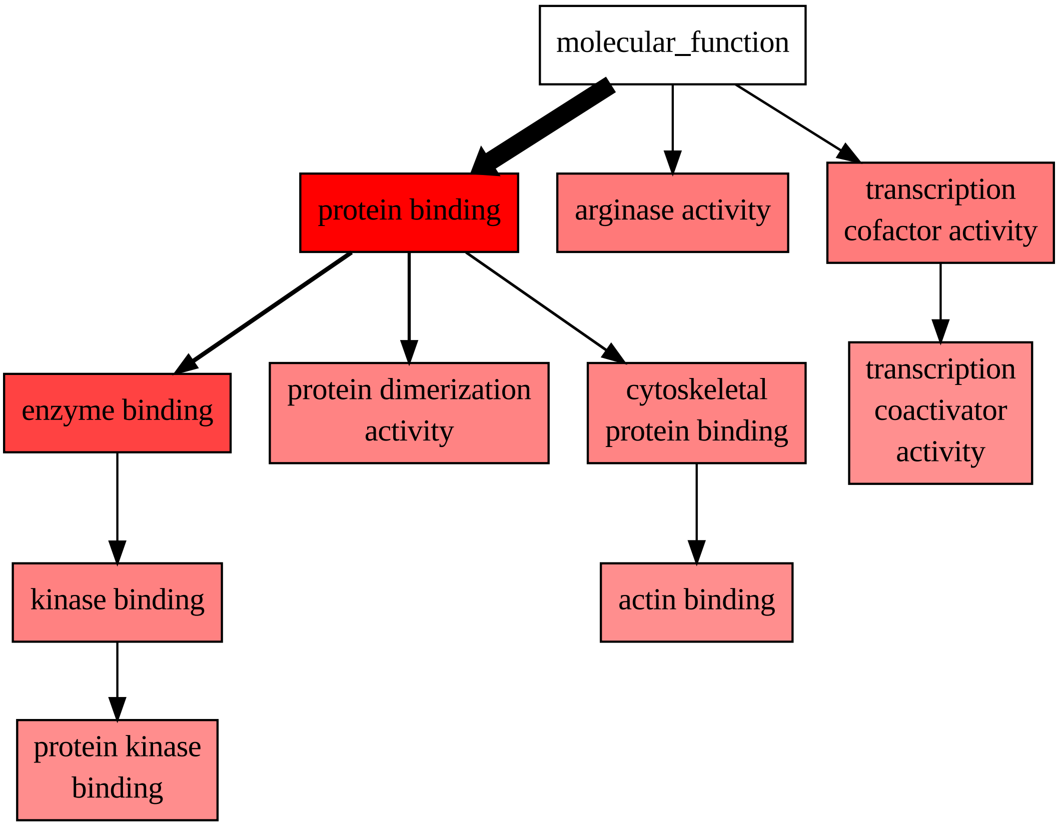


Figure 61: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 36. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

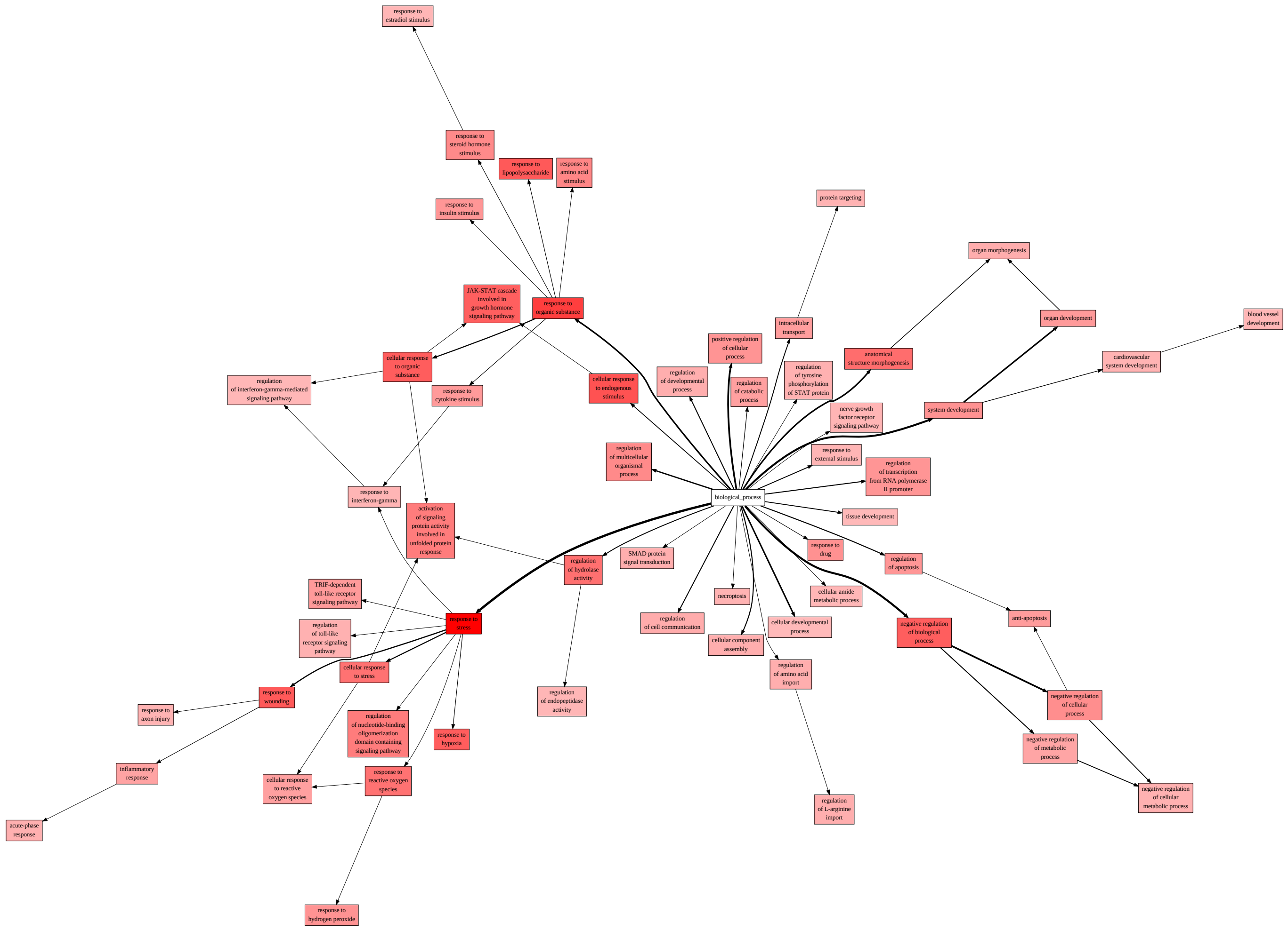


Figure 62: Relationships between the enriched *biological process* Gene Ontology terms that were listed in Table 36. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

14.2 Candidate genes

Table 37: Descriptions of the candidate genes. Studies that have reported results about the candidate genes are listed so that those with negative evidence have been prefixed with a hyphen. S column contains an at sign if the gene is part of the candidate pathway. The statuses of the genes are shown as: *a*=absent, *d*=down regulated, *u*=up regulated, *s*=stable. This table has 402 rows.

S	name	locus	description	studies
u	AASS	7:121715701-121784334 7q31.32	aminoadipate-semialdehyde synthase [Source:HGNC Symbol;Acc:17366], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[saccharopine dehydrogenase (NAD+, L-glutamate-forming) activity; saccharopine dehydrogenase (NADP+, L-lysine-forming) activity; saccharopine dehydrogenase activity; L-lysine catabolic process; protein tetramerization; mitochondrial matrix]	tcgaBreastGE, tcgaGliomaGE
u	ABCC8	11:17414432-17498449 11p15.1	ATP-binding cassette, sub-family C (CFTR/MRP), member 8 [Source:HGNC Symbol;Acc:59], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[sulfonylurea receptor activity; positive regulation of potassium ion transport; potassium ion transmembrane transporter activity; response to pH; inward rectifier potassium channel activity; negative regulation of insulin secretion; syntaxin binding; response to zinc ion; synaptic vesicle membrane; potassium ion transmembrane transport; cellular potassium ion transport; sarcolemma; clathrin coated vesicle membrane; synaptic vesicle; ATPase activity, coupled to transmembrane movement of substances; metal ion transmembrane transporter activity; response to lipopolysaccharide; response to insulin stimulus; response to drug; response to hormone stimulus]	snp3dDiabetes, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
u*	ABCD3	1:94883933-94984222 1p21.3	ATP-binding cassette, sub-family D (ALD), member 3 [Source:HGNC Symbol;Acc:67], type=processed_transcript,protein_coding, GO=[protein self-association; peroxisomal membrane; peroxisomal part; microbody part; ATP catabolic process; ATPase activity, coupled to transmembrane movement of substances; mitochondrial inner membrane; response to drug]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad, tscapeNSCLCd
u	ABHD3	18:19230858-19284766 18q11.2	abhydrolase domain containing 3 [Source:HGNC Symbol;Acc:18718], type=protein_coding, GO=[carboxylesterase activity]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeNSCLCa
d	AC010296.1	5:115780104-115780830 5q23.1	[undefined], type=pseudogene	
u	AC093162.5	2:85542164-85543652 2p11.2	[undefined], type=pseudogene,unprocessed_pseudogene	
u	AC093323.3	4:6675178-6677774 4p16.1	[undefined], type=lincRNA,processed_transcript	tcgaBreastGE
u	ACPL2	3:140947568-141013748 3q23	acid phosphatase-like 2 [Source:HGNC Symbol;Acc:26303], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[acid phosphatase activity]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	ACSL1	4:185676749-185747972 4q35.1	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:3569], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[adiponectin-mediated signaling pathway; response to oleic acid; xenobiotic catabolic process; long-chain fatty acid-CoA ligase activity; long-chain fatty-acyl-CoA biosynthetic process; response to fatty acid; regulation of fatty acid oxidation; peroxisomal membrane; triglyceride biosynthetic process; neutral lipid biosynthetic process; acylglycerol biosynthetic process; peroxisomal part; microbody part; fatty acid oxidation; mitochondrial outer membrane; glycerolipid biosynthetic process; positive regulation of protein serine/threonine kinase activity; response to organic cyclic compound; microsome; fatty acid metabolic process; regulation of protein serine/threonine kinase activity; response to drug; soluble fraction; monocarboxylic acid metabolic process; lipid biosynthetic process; endoplasmic reticulum membrane]	tcgaOvarianMethyl, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeRCCd
u*	ACTA2	10:90694831-90751147 10q23.31	actin, alpha 2, smooth muscle, aorta [Source:HGNC Symbol;Acc:130], type=processed_transcript,protein_coding, GO=[glomerular mesangial cell development; glomerular mesangial cell differentiation; smooth muscle contractile fiber; vascular smooth muscle contraction; blood vessel development; vasculature development]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeSCLCd
u*	ACTG2	2:74119441-74146992 2p13.1	actin, gamma 2, smooth muscle, enteric [Source:HGNC Symbol;Acc:145], type=nonsense_mediated_decay,protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	AGT	1:230838269-230850043 1q42.2	angiotensinogen (serpin peptidase inhibitor, clade A, member 8) [Source:HGNC Symbol;Acc:333], type=protein_coding, GO=[type 2 angiotensin receptor binding; regulation of extracellular matrix constituent secretion; angiotensin mediated vasoconstriction involved in regulation of systemic arterial blood pressure; positive regulation of extracellular matrix constituent secretion; response to muscle activity involved in regulation of muscle adaptation; acetyltransferase activator activity; positive regulation of NAD(P)H oxidase activity; extracellular matrix constituent secretion; renal response to blood flow involved in circulatory renin-angiotensin regulation of systemic arterial blood pressure; establishment of blood-nerve barrier; angiotensin-mediated drinking behavior; astrocyte activation; physiological cardiac muscle hypertrophy; regulation of renal output by angiotensin; renin-angiotensin regulation of aldosterone production; ovarian follicle rupture; cell growth involved in cardiac muscle cell development; artery smooth muscle contraction; cellular sodium ion homeostasis; negative regulation of nerve growth factor receptor signaling pathway; positive regulation of superoxide anion generation; type 1 angiotensin receptor binding; positive regulation of activation of JAK2 kinase activity; regulation of activation of JAK2 kinase activity; positive regulation of cholesterol esterification; response to muscle activity; positive regulation of cardiac muscle hypertrophy; positive regulation of calcium ion transport via voltage-gated calcium channel activity; G-protein signaling, coupled to cGMP nucleotide second messenger; activation of JAK2 kinase activity; peristalsis; positive regulation of renal sodium excretion; vascular smooth muscle contraction; regulation of norepinephrine secretion; positive regulation of systemic arterial blood pressure; low-density lipoprotein particle remodeling; ovulation from ovarian follicle; negative regulation of tissue remodeling; positive regulation of macrophage derived foam cell differentiation; nitric oxide mediated signal transduction; positive regulation of fatty acid biosynthetic process; positive regulation of organ growth; activation of NF-kappaB-inducing kinase activity; positive regulation of epidermal growth factor receptor signaling pathway; response to salt stress; positive regulation of branching involved in ureteric bud morphogenesis; catenin import into nucleus; positive regulation of protein tyrosine kinase activity; regulation of long-term neuronal synaptic plasticity; positive regulation of multicellular organism growth; regulation of fatty acid biosynthetic process; response to cold; positive regulation of endothelial cell migration; positive regulation of fibroblast proliferation; positive regulation of phosphatidylinositol 3-kinase cascade; regulation of protein tyrosine kinase activity; vasodilation; regulation of morphogenesis of a branching structure; regulation of vasoconstriction; regulation of phosphatidylinositol 3-kinase cascade; response to osmotic stress; cellular response to mechanical stimulus; activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger; regulation of endothelial cell migration; branching involved in ureteric bud morphogenesis; positive regulation of inflammatory response; excretion; smooth muscle cell proliferation; negative regulation of endopeptidase activity; stress-activated MAPK cascade; cytokine secretion; ovum-producing ovary development; serine-type endopeptidase inhibitor activity; negative regulation of neuron apoptosis; endothelial cell migration; positive regulation of NF-kappaB transcription factor activity; regulation of synaptic plasticity; hormone activity; development of primary female sexual characteristics; activation of phospholipase C activity; reactive oxygen species metabolic process; epidermal growth factor receptor signaling pathway; ERK1 and ERK2 cascade; cellular response to abiotic stimulus; regulation of peptidyl-tyrosine phosphorylation; response to mechanical stimulus; regulation of organ morphogenesis; negative regulation of cell growth; fatty acid biosynthetic process; cell-matrix adhesion; endopeptidase inhibitor activity; growth factor activity; regulation of inflammatory response; positive regulation of MAPKKK cascade; rhythmic process; positive regulation of protein serine/threonine kinase activity; I-kappaB kinase/NF-kappaB cascade; nerve growth factor receptor signaling pathway; regulation of endopeptidase activity; enzyme inhibitor activity; regulation of cell growth; fatty acid metabolic process; regulation of sequence-specific DNA binding transcription factor activity; regulation of protein serine/threonine kinase activity; regulation of cell motility; soluble fraction; regulation of cellular component movement; monocarboxylic acid metabolic process; nucleocytoplasmic transport; MAPKKK cascade; blood vessel development; vasculature development; lipid biosynthetic process; extracellular space]	snp3dObesity, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeBCd, tscapeOvariana, tscapeProstated
u	AL163636.6	14:21152746-21168735 14q11.2	[undefined], type=processed_transcript	
u*	ALPP	2:233243244-233247599 2q37.1	alkaline phosphatase, placental [Source:HGNC Symbol;Acc:439], type=protein_coding,retained_intron, GO=[alkaline phosphatase activity; anchored to membrane; cell surface]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeNSCLCd, tscapeRCCd

Continued on next page...

S	name	locus	description	studies
u	ANG	14:21152336-21167130 14q11.2	angiogenin, ribonuclease, RNase A family, 5 [Source:HGNC Symbol;Acc:483], type=processed_transcript,protein_coding, GO=[angiogenin-PRI complex; activation of phospholipase A2 activity; diacylglycerol biosynthetic process; activation of protein kinase B activity; pancreatic ribonuclease activity; oocyte maturation; basal lamina; rRNA transcription; negative regulation of smooth muscle cell proliferation; rRNA binding; acylglycerol biosynthetic process; neutral lipid biosynthetic process; negative regulation of translation; copper ion binding; positive regulation of endothelial cell proliferation; ovarian follicle development; regulation of smooth muscle cell proliferation; smooth muscle cell proliferation; positive regulation of protein secretion; ovum-producing ovary development; growth cone; basement membrane; actin filament polymerization; development of primary female sexual characteristics; activation of phospholipase C activity; actin polymerization or depolymerization; placenta development; heparin binding; glycerolipid biosynthetic process; glycosaminoglycan binding; polysaccharide binding; pattern binding; actin filament organization; rhythmic process; response to hypoxia; epithelial cell proliferation; response to oxygen levels; neuronal cell body; actin binding; actin filament-based process; blood vessel development; vasculature development; lipid biosynthetic process; cytoskeletal protein binding; nucleolus; neuron projection; response to hormone stimulus; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	ANO6	12:45609770-45834187 12q12	anoctamin 6 [Source:HGNC Symbol;Acc:25240], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[phosphatidylserine exposure on blood platelet; activation of blood coagulation via clotting cascade; chloride channel complex; chloride channel activity; chloride transport; inorganic anion transport; anion transport]	tcgaBreastGE, tcgaGliomaGE
u	AP000442.4	11:59328572-59333547 11q12.1	[undefined], type=lincRNA	
u	AP001468.1	21:47609638-47613673 21q22.3	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:E7EVC9], type=protein_coding	
u	AP3S1	5:115177178-115249778 5q22.3, 5q23.1	adaptor-related protein complex 3, sigma 1 subunit [Source:HGNC Symbol;Acc:2013], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[AP-type membrane coat adaptor complex; insulin receptor signaling pathway; cellular response to insulin stimulus; response to insulin stimulus; response to hormone stimulus]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u	ARCN1	11:118443105-118473730 11q23.3	archain 1 [Source:HGNC Symbol;Acc:649], type=processed_transcript,protein_coding, GO=[COPI vesicle coat; COPI coating of Golgi vesicle; Golgi transport vesicle coating; COPI-coated vesicle budding; COPI coated vesicle membrane; vesicle targeting, to, from or within Golgi; retrograde vesicle-mediated transport, Golgi to ER; clathrin adaptor complex; vesicle coating; AP-type membrane coat adaptor complex]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
u*	ARG1	6:131894284-131905472 6q23.2	arginase, liver [Source:HGNC Symbol;Acc:663], type=processed_transcript,protein_coding, GO=[arginase activity; regulation of L-arginine import; regulation of amino acid import; arginine catabolic process; response to herbicide; response to vitamin E; response to methylmercury; urea cycle; response to selenium ion; arginine metabolic process; cellular response to dexamethasone stimulus; response to manganese ion; mammary gland involution; protein homotrimerization; maternal process involved in female pregnancy; cellular amide metabolic process; collagen biosynthetic process; cellular response to transforming growth factor beta stimulus; response to transforming growth factor beta stimulus; response to cadmium ion; manganese ion binding; cellular response to glucagon stimulus; response to zinc ion; cellular response to hydrogen peroxide; collagen metabolic process; positive regulation of endothelial cell proliferation; response to axon injury; cellular response to reactive oxygen species; multicellular organismal metabolic process; response to amino acid stimulus; response to hydrogen peroxide; liver development; response to vitamin A; response to toxin; response to reactive oxygen species; female pregnancy; protein homooligomerization; response to lipopolysaccharide; epithelial cell proliferation; neuronal cell body; response to drug; neuron projection; response to hormone stimulus; extracellular space]	tscapeBCa
d*	ARG2	14:68086515-68118437 14q24.1	arginase, type II [Source:HGNC Symbol;Acc:664], type=processed_transcript,protein_coding,retained_intron, GO=[arginase activity; regulation of L-arginine import; regulation of amino acid import; negative regulation of nitric-oxide synthase activity; nitric-oxide synthase binding; negative regulation of striated muscle contraction; response to herbicide; response to vitamin E; response to selenium ion; urea cycle; arginine metabolic process; cellular response to dexamethasone stimulus; response to mercury ion; midgut development; maternal process involved in female pregnancy; cellular amide metabolic process; response to cadmium ion; regulation of nitric oxide biosynthetic process; response to axon injury; response to amino acid stimulus; cellular response to interferon-gamma; response to interferon-gamma; response to glucose stimulus; response to toxin; response to carbohydrate stimulus; female pregnancy; response to lipopolysaccharide; response to hypoxia; response to oxygen levels; mitochondrial matrix; response to drug; response to hormone stimulus]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
d*	ARHGEF2	1:155916645-155966129 1q22	Rho/Rac guanine nucleotide exchange factor (GEF) 2 [Source:HGNC Symbol;Acc:682], type=processed_transcript,protein_coding, GO=[Rac guanyl-nucleotide exchange factor activity; Rac GTPase binding; establishment of mitotic spindle orientation; negative regulation of microtubule depolymerization; dendritic shaft; Rho GTPase binding; ruffle membrane; negative regulation of protein complex disassembly; microtubule polymerization or depolymerization; protein depolymerization; microtubule binding; tight junction; negative regulation of neurogenesis; positive regulation of NF-kappaB transcription factor activity; induction of apoptosis by extracellular signals; spindle; actin filament organization; Rho protein signal transduction; phospholipid binding; nerve growth factor receptor signaling pathway; neuronal cell body; microtubule; regulation of sequence-specific DNA binding transcription factor activity; actin filament-based process; Ras protein signal transduction; cytoskeletal protein binding; neuron projection; small GTPase mediated signal transduction; microtubule cytoskeleton]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCa, tscapeProstated
u	ARPC5	1:183592401-183604892 1q25.3	actin related protein 2/3 complex, subunit 5, 16kDa [Source:HGNC Symbol;Acc:708], type=processed_transcript,protein_coding, GO=[Arp2/3 protein complex; structural constituent of cytoskeleton; regulation of actin filament polymerization; actin filament polymerization; actin polymerization or depolymerization; regulation of actin filament-based process; actin filament organization; actin binding; actin filament-based process; cytoskeletal protein binding]	tcgaBreastGE, tcgaBreastGESurv, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	ARSA	22:51063446-51066607 22q13.33	arylsulfatase A [Source:HGNC Symbol;Acc:713], type=protein_coding,retained_intron, GO=[cerebroside-sulfatase activity; arylsulfatase activity; lysosomal lumen; binding of sperm to zona pellucida; integral to membrane of membrane fraction; calcium ion binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
u	ASB13	10:5680830-5708768 10p15.1	ankyrin repeat and SOCS box containing 13 [Source:HGNC Symbol;Acc:19765], type=nonsense_mediated_decay,processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
u*	ASB9	X:15252900-15288589 Xp22.2	ankyrin repeat and SOCS box containing 9 [Source:HGNC Symbol;Acc:17184], type=processed_transcript,protein_coding, GO=[positive regulation of protein catabolic process; regulation of catabolic process]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCa
u	ASIP	20:32782375-32857150 20q11.22	agouti signaling protein [Source:HGNC Symbol;Acc:745], type=protein_coding, GO=[regulation of molecular function, epigenetic; type 3 melanocortin receptor binding; type 4 melanocortin receptor binding; melanocortin receptor binding; adult feeding behavior; melanin biosynthetic process; melanosome transport; melanosome organization; genetic imprinting; hormone-mediated signaling pathway; secondary metabolic process; response to hormone stimulus; extracellular space]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv
d	ASNS	7:97481430-97501854 7q21.3	asparagine synthetase (glutamine-hydrolyzing) [Source:HGNC Symbol;Acc:753], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[activation of signaling protein activity involved in unfolded protein response; response to methotrexate; asparagine synthase (glutamine-hydrolyzing) activity; asparagine biosynthetic process; response to follicle-stimulating hormone stimulus; cellular response to glucose starvation; glutamine metabolic process; positive regulation of mitotic cell cycle; response to amino acid stimulus; cellular response to starvation; liver development; response to toxin; response to mechanical stimulus; response to organic cyclic compound; soluble fraction; protein homodimerization activity; regulation of cell cycle; response to hormone stimulus]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
u*	ATG16L1	2:234118697-234204320 2q37.1	ATG16 autophagy related 16-like 1 (S. cerevisiae) [Source:HGNC Symbol;Acc:21498], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[pre-autophagosomal structure membrane; autophagic vacuole; autophagic vacuole assembly; macroautophagy; vacuole organization; cellular response to starvation; autophagy; protein homooligomerization]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u	ATOH8	2:85978467-86015189 2p11.2	atonal homolog 8 (Drosophila) [Source:HGNC Symbol;Acc:24126], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaColonMethyl

Continued on next page...

S	name	locus	description	studies
u	AZGP1	7:99564343-99573780 7q22.1	alpha-2-glycoprotein 1, zinc-binding [Source:HGNC Symbol;Acc:910], type=processed_transcript,protein_coding,retained_intron, GO=[protein transmembrane transporter activity; MHC class I protein complex; fatty acid binding; antigen processing and presentation]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeNSCLCa
u	AZI2	3:28356494-28390618 3p24.1	5-azacytidine induced 2 [Source:HGNC Symbol;Acc:24002], type=processed_transcript,protein_coding,retained_intron, GO=[I-kappaB kinase/NF-kappaB cascade]	tcgaBreastGE, tcgaOvarianMethyl
u	B3GALT4	6:33244917-33246602 6p21.32	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4 [Source:HGNC Symbol;Acc:919], type=protein_coding, GO=[ganglioside galactosyltransferase activity; UDP-galactose:beta-N-acetylglucosamine beta-1,3-galactosyltransferase activity]	cosmicPrimary
u	BBX	3:107241783-107530171 3q13.12	bobby sox homolog (Drosophila) [Source:HGNC Symbol;Acc:14422], type=processed_transcript,protein_coding,retained_intron	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	BCL7C	16:30844947-30906281 16p11.2	B-cell CLL/lymphoma 7C [Source:HGNC Symbol;Acc:1006], type=nonsense_mediated_decay,processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	BEST2	19:12862516-12869272 19p13.2	bestrophin 2 [Source:HGNC Symbol;Acc:17107], type=protein_coding, GO=[chloride channel complex; sensory perception of smell; chloride channel activity; membrane depolarization; chloride transport; inorganic anion transport; anion transport; cilium]	tcgaColonGE
u*	BIRC2	11:102217942-102249401 11q22.2	baculoviral IAP repeat containing 2 [Source:HGNC Symbol;Acc:590], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[regulation of nucleotide-binding oligomerization domain containing signaling pathway; necroptosis; CD40 receptor complex; regulation of toll-like receptor signaling pathway; protein N-terminus binding; placenta development; positive regulation of I-kappaB kinase/NF-kappaB cascade; regulation of inflammatory response; regulation of cysteine-type endopeptidase activity; regulation of I-kappaB kinase/NF-kappaB cascade; I-kappaB kinase/NF-kappaB cascade; ubiquitin-protein ligase activity; regulation of endopeptidase activity; transcription coactivator activity; anti-apoptosis; transcription cofactor activity; protein binding transcription factor activity; regulation of cell cycle]	fileAmpOver, snp3dLungC, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa, tscapeRCCd
u*	BIRC3	11:102188215-102210134 11q22.2	baculoviral IAP repeat containing 3 [Source:HGNC Symbol;Acc:591], type=processed_transcript,protein_coding,retained_intron, GO=[negative regulation of necroptosis; regulation of nucleotide-binding oligomerization domain containing signaling pathway; necroptosis; negative regulation of reactive oxygen species metabolic process; regulation of toll-like receptor signaling pathway; reactive oxygen species metabolic process; positive regulation of I-kappaB kinase/NF-kappaB cascade; regulation of inflammatory response; regulation of cysteine-type endopeptidase activity; regulation of I-kappaB kinase/NF-kappaB cascade; I-kappaB kinase/NF-kappaB cascade; ubiquitin-protein ligase activity; regulation of endopeptidase activity; anti-apoptosis]	snp3dLungC, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa, tscapeRCCd
u	BTD	3:15642848-15687329 3p25.1	biotinidase [Source:HGNC Symbol;Acc:1122], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[biotinidase activity; biotin carboxylase activity; perikaryon; apical part of cell; neuronal cell body; nucleolus; extracellular space]	tcgaColonGE, tcgaOvarianMethyl, tscapeOvariand
u	BTG1	12:92536286-92539673 12q21.33	B-cell translocation gene 1, anti-proliferative [Source:HGNC Symbol;Acc:1130], type=protein_coding, GO=[positive regulation of myoblast differentiation; positive regulation of endothelial cell differentiation; myoblast differentiation; positive regulation of angiogenesis; negative regulation of cell growth; regulation of cell growth; kinase binding; transcription cofactor activity; protein binding transcription factor activity; blood vessel development; vasculature development; response to hormone stimulus]	tcgaGliomaGE, tcgaOvarianMethyl
d	C12orf52	12:113623331-113630173 12q24.13	chromosome 12 open reading frame 52 [Source:HGNC Symbol;Acc:25925], type=protein_coding, GO=[negative regulation of Notch signaling pathway; regulation of Notch signaling pathway; nucleocytoplasmic transport; negative regulation of transcription from RNA polymerase II promoter; cytoskeletal protein binding; microtubule cytoskeleton]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
u	C14orf132	14:96505661-96560417 14q32.2	chromosome 14 open reading frame 132 [Source:HGNC Symbol;Acc:20346], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
d	C16orf59	16:2510081-2514964 16p13.3	chromosome 16 open reading frame 59 [Source:HGNC Symbol;Acc:25849], type=nonsense_mediated_decay,protein_coding,retained_intron	tcgaBreastGE, tcgaColonGE, tscapeHCCd, tscapeOvariand
u	C17orf80	17:71228372-71245091 17q25.1	chromosome 17 open reading frame 80 [Source:HGNC Symbol;Acc:29601], type=protein_coding	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
u	C18orf8	18:21083462-21111771 18q11.2	chromosome 18 open reading frame 8 [Source:HGNC Symbol;Acc:24326], type=protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
u	C1orf122	1:38272651-38275126 1p34.3	chromosome 1 open reading frame 122 [Source:HGNC Symbol;Acc:24789], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	C1orf172	1:27276053-27286897 1p36.11	chromosome 1 open reading frame 172 [Source:HGNC Symbol;Acc:26624], type=protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u	C1orf198	1:230972865-231005335 1q42.2	chromosome 1 open reading frame 198 [Source:HGNC Symbol;Acc:25900], type=protein_coding,retained_intron	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana, tscapeProstated
d	C20orf27	20:3734155-3749034 20p13	chromosome 20 open reading frame 27 [Source:HGNC Symbol;Acc:15873], type=processed_transcript,protein_coding	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	C5orf4	5:154198051-154238812 5q33.2	chromosome 5 open reading frame 4 [Source:HGNC Symbol;Acc:1334], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[fatty acid biosynthetic process; iron ion binding; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tscapeRCCa
u	C5orf46	5:147260289-147286101 5q32	chromosome 5 open reading frame 46 [Source:HGNC Symbol;Acc:33768], type=processed_transcript,protein_coding	tcgaBreastGE
u	C6orf89	6:36839646-36892331 6p21.2	chromosome 6 open reading frame 89 [Source:HGNC Symbol;Acc:21114], type=processed_transcript,protein_coding, GO=[epithelial cell proliferation; regulation of cell cycle]	tcgaBreastGE
u	C8orf42	8:439803-495781 8p23.3	chromosome 8 open reading frame 42 [Source:HGNC Symbol;Acc:26951], type=processed_transcript,protein_coding	tcgaBreastGE, tscapeCRCd, tscapeHCCd, tscapeOvariand, tscapeRCCd
u	C8orf84	8:73976775-74036323 8q21.11	chromosome 8 open reading frame 84 [Source:HGNC Symbol;Acc:30362], type=processed_transcript,protein_coding, GO=[scavenger receptor activity; polysaccharide binding; pattern binding]	tcgaBreastGE, tcgaColonGE
u	CA12	15:63613577-63674360 15q22.2	carbonic anhydrase XII [Source:HGNC Symbol;Acc:1371], type=processed_transcript,protein_coding,retained_intron, GO=[carbonate dehydratase activity]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	CAPN13	2:30945637-31043408 2p23.1	calpain 13 [Source:HGNC Symbol;Acc:16663], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[calcium-dependent cysteine-type endopeptidase activity; calcium ion binding]	tcgaBreastGE, tcgaColonGE
u*	CAPN2	1:223889295-223963720 1q41	calpain 2, (m/II) large subunit [Source:HGNC Symbol;Acc:1479], type=processed_transcript,protein_coding, GO=[myoblast fusion; calcium-dependent cysteine-type endopeptidase activity; blastocyst development; response to hypoxia; response to oxygen levels; protein heterodimerization activity; soluble fraction; cytoskeletal protein binding; calcium ion binding]	snp3dDementia, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE
d	CAPN5	11:76777979-76837201 11q13.5	calpain 5 [Source:HGNC Symbol;Acc:1482], type=processed_transcript,protein_coding,retained_intron, GO=[granulosa cell differentiation; luteinization; calcium-dependent cysteine-type endopeptidase activity; ovarian follicle development; ovum-producing ovary development; development of primary female sexual characteristics; rhythmic process]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
d*	CARM1	19:10982253-11033448 19p13.2	coactivator-associated arginine methyltransferase 1 [Source:HGNC Symbol;Acc:23393], type=protein_coding, GO=[histone methyltransferase activity (H3-R17 specific); histone H3-R17 methylation; histone H3-R2 methylation; regulation of growth plate cartilage chondrocyte proliferation; pathogenesis; protein-arginine omega-N asymmetric methyltransferase activity; peptidyl-arginine methylation, to asymmetrical-dimethyl arginine; tRNA (uracil) methyltransferase activity; histone acetyl-lysine binding; tRNA wobble base modification; tRNA wobble uridine modification; regulation of estrogen receptor signaling pathway; positive regulation of fat cell differentiation; negative regulation of protein binding; ligand-dependent nuclear receptor transcription coactivator activity; beta-catenin binding; negative regulation of binding; response to cAMP; steroid hormone receptor signaling pathway; regulation of organ morphogenesis; cartilage development; transcription coactivator activity; transcription cofactor activity; protein binding transcription factor activity; protein homodimerization activity]	tcgaOvarianMethyl
u*	CCDC6	10:61548521-61666414 10q21.2	coiled-coil domain containing 6 [Source:HGNC Symbol;Acc:18782], type=protein_coding,retained_intron, GO=[structural constituent of cytoskeleton; SH3 domain binding]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl, tscapeOvariand
d	CCDC92	12:124403207-124457378 12q24.31	coiled-coil domain containing 92 [Source:HGNC Symbol;Acc:29563], type=processed_transcript,protein_coding	tcgaColonGE, tcgaGliomaGE
u	CD68	17:7482922-7485431 17p13.1	CD68 molecule [Source:HGNC Symbol;Acc:1693], type=protein_coding, GO=[lysosomal membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeProstated
u	CD99	X:2609220-2659350 Xp22.33	CD99 molecule [Source:HGNC Symbol;Acc:7082], type=processed_transcript,protein_coding	cosmicMetastasis, tcgaGliomaGE
u*	CDC42EP4	17:71279764-71308143 17q25.1	CDC42 effector protein (Rho GTPase binding) 4 [Source:HGNC Symbol;Acc:17147], type=protein_coding, GO=[GTP-Rho binding; positive regulation of pseudopodium assembly; Rho GTPase binding; regulation of cell shape; Rho protein signal transduction; Ras protein signal transduction; small GTPase mediated signal transduction; microtubule cytoskeleton]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	CDCA7L	7:21940518-21985702 7p15.3	cell division cycle associated 7-like [Source:HGNC Symbol;Acc:30777], type=processed_transcript,protein_coding,retained_intron, GO=[nucleolus]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	CDKN1C	11:2904443-2907111 11p15.4	cyclin-dependent kinase inhibitor 1C (p57, Kip2) [Source:HGNC Symbol;Acc:1786], type=protein_coding,retained_intron, GO=[cyclin-dependent protein kinase inhibitor activity; positive regulation of transforming growth factor beta receptor signaling pathway; neuron maturation; G1 phase of mitotic cell cycle; protein kinase inhibitor activity; regulation of cyclin-dependent protein kinase activity; negative regulation of kinase activity; epithelial cell proliferation; enzyme inhibitor activity; regulation of protein serine/threonine kinase activity; negative regulation of cell cycle; negative regulation of transcription from RNA polymerase II promoter; regulation of cell cycle]	snp3dGlioma, tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand
d*	CDT1	16:88869621-88875666 16q24.3	chromatin licensing and DNA replication factor 1 [Source:HGNC Symbol;Acc:24576], type=protein_coding,retained_intron, GO=[regulation of DNA-dependent DNA replication initiation; DNA replication checkpoint; regulation of S phase of mitotic cell cycle; regulation of transcription involved in G1/S phase of mitotic cell cycle; M/G1 transition of mitotic cell cycle; regulation of DNA replication; negative regulation of cell cycle; regulation of cell cycle]	tcgaBreastGE, tcgaGliomaGE, tscapeProstated
u*	CEBPB	20:48807376-48809212 20q13.13	CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:1834], type=protein_coding, GO=[glucocorticoid receptor binding; regulation of interleukin-6 biosynthetic process; mammary gland epithelial cell differentiation; mammary gland epithelial cell proliferation; brown fat cell differentiation; cellular response to amino acid stimulus; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription; cellular response to acid; cellular response to amine stimulus; positive regulation of osteoblast differentiation; acute-phase response; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; nuclear matrix; response to amino acid stimulus; mammary gland epithelium development; sequence-specific distal enhancer binding RNA polymerase II transcription factor activity; placenta development; sequence-specific DNA binding RNA polymerase II transcription factor activity; response to lipopolysaccharide; epithelial cell proliferation; protein heterodimerization activity; anti-apoptosis; protein homodimerization activity]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
d*	CGN	1:151482986-151511168 1q21.3	cingulin [Source:HGNC Symbol;Acc:17429], type=protein_coding,retained_intron, GO=[tight junction; actin binding; cytoskeletal protein binding]	tcgaBreastGE, tcgaOvarianMethyl, tscapeBCd, tscapeHCCa, tscapeMelanomaa, tscapeOvariana
u	CH17-12M21.1	5:97674448-97675536 5q15	[undefined], type=processed_pseudogene,pseudogene	
u	CHN2	7:29186185-29553944 7p14.3	chimerin (chimaerin) 2 [Source:HGNC Symbol;Acc:1944], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[acrosome assembly; Rac GTPase activator activity; positive regulation of Rac GTPase activity; Rho GTPase activator activity; SH3/SH2 adaptor activity; positive regulation of Rho GTPase activity; regulation of Rho GTPase activity; Ras GTPase activator activity; Rho protein signal transduction; regulation of Ras GTPase activity; GTPase activator activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaBreastMethyl, tcgaGliomaGE
u	CHST3	10:73724123-73773322 10q22.1	carbohydrate (chondroitin 6) sulfotransferase 3 [Source:HGNC Symbol;Acc:1971], type=protein_coding, GO=[chondroitin 6-sulfotransferase activity; proteoglycan sulfotransferase activity; peripheral nervous system axon regeneration; chondroitin sulfate biosynthetic process; chondroitin sulfate metabolic process; axon regeneration; T cell homeostasis; response to axon injury; regeneration; regulation of cellular component movement]	tcgaGliomaCGHd
u	CHSY1	15:101715928-101792137 15q26.3	chondroitin sulfate synthase 1 [Source:HGNC Symbol;Acc:17198], type=processed_transcript,protein_coding, GO=[glucuronosyl-N-acetylgalactosaminyl-proteoglycan 4-beta-N-acetylgalactosaminyltransferase activity; N-acetylgalactosaminyl-proteoglycan 3-beta-glucuronosyltransferase activity; chondroitin sulfate biosynthetic process; chondroitin sulfate metabolic process; negative regulation of ossification; Golgi cisterna membrane; Golgi cisterna]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCa, tscapeMelanomaa, tscapeNSCLCa
u*	CITED1	X:71521488-71527037 Xq13.1	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 1 [Source:HGNC Symbol;Acc:1986], type=protein_coding, GO=[response to interleukin-11; response to interleukin-9; negative regulation of mesenchymal to epithelial transition involved in metanephros morphogenesis; LBD domain binding; response to interleukin-2; response to parathyroid hormone stimulus; spongiotrophoblast layer development; co-SMAD binding; melanin biosynthetic process; response to interleukin-4; negative regulation of cell morphogenesis involved in differentiation; SMAD protein signal transduction; response to interleukin-6; positive regulation of transforming growth factor beta receptor signaling pathway; response to transforming growth factor beta stimulus; negative regulation of osteoblast differentiation; melanocyte differentiation; embryonic axis specification; positive regulation of anti-apoptosis; response to interleukin-1; branching involved in ureteric bud morphogenesis; vasculogenesis; response to cAMP; secondary metabolic process; negative regulation of neuron apoptosis; response to interferon-gamma; placenta development; regulation of organ morphogenesis; protein C-terminus binding; response to lipopolysaccharide; chromatin binding; transcription coactivator activity; response to insulin stimulus; anti-apoptosis; nucleocytoplasmic transport; transcription cofactor activity; protein binding transcription factor activity; blood vessel development; protein homodimerization activity; vasculature development; response to hormone stimulus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
u*	CKB	14:103985996-103989448 14q32.32	creatine kinase, brain [Source:HGNC Symbol;Acc:1991], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[cellular monovalent inorganic anion homeostasis; cellular chloride ion homeostasis; creatine kinase activity; creatine metabolic process; phosphagen metabolic process]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl, tscapeMelanomad
d	CLDND2	19:51870352-51872257 19q13.41	claudin domain containing 2 [Source:HGNC Symbol;Acc:28511], type=protein_coding	tcgaBreastGE
u	CLEC16A	16:11038345-11276046 16p13.13	C-type lectin domain family 16, member A [Source:HGNC Symbol;Acc:29013], type=processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaGliomaGE
u	CLGN	4:141309609-141349122 4q31.1	calmegin [Source:HGNC Symbol;Acc:2060], type=protein_coding, GO=[binding of sperm to zona pellucida; unfolded protein binding; calcium ion binding; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonGE

Continued on next page...

S	name	locus	description	studies
u	CNN2	19:1026580-1039063 19p13.3	calponin 2 [Source:HGNC Symbol;Acc:2156], type=protein_coding,retained_intron, GO=[negative regulation of phagocytosis; negative regulation of endocytosis; stress fiber; actin filament bundle; actomyosin structure organization; cellular response to mechanical stimulus; negative regulation of cell migration; cellular response to abiotic stimulus; response to mechanical stimulus; calmodulin binding; regulation of actin filament-based process; actin binding; regulation of cell motility; regulation of cellular component movement; actin filament-based process; cytoskeletal protein binding]	tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeHCCd, tscapeNSCLCd
u	CNST	1:246729746-246831886 1q44	consortin, connexin sorting protein [Source:HGNC Symbol;Acc:26486], type=processed_transcript,protein_coding, GO=[positive regulation of Golgi to plasma membrane protein transport; connexin binding; negative regulation of phosphatase activity; trans-Golgi network; phosphatase binding]	tcgaBreastGE, tcgaGliomaGE
u	CNTN3	3:74311719-74570291 3p12.3	contactin 3 (plasmacytoma associated) [Source:HGNC Symbol;Acc:2173], type=processed_transcript,protein_coding, GO=[anchored to membrane]	cosmicPrimary, tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
u*	COL6A1	21:47401651-47424964 21q22.3	collagen, type VI, alpha 1 [Source:HGNC Symbol;Acc:2211], type=processed_transcript,protein_coding,retained_intron, GO=[collagen type VI; protein heterotrimerization; platelet-derived growth factor binding; cellular response to amino acid stimulus; cellular response to acid; cellular response to amine stimulus; response to amino acid stimulus; sarcolemma]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
u*	COL6A2	21:47518011-47552763 21q22.3	collagen, type VI, alpha 2 [Source:HGNC Symbol;Acc:2212], type=processed_transcript,protein_coding,retained_intron, GO=[protein heterotrimerization; extracellular matrix structural constituent; sarcolemma; response to glucose stimulus; response to carbohydrate stimulus; extracellular space]	cosmicRecurrent, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeBCa
u	CPEB4	5:173315283-173388979 5q35.2	cytoplasmic polyadenylation element binding protein 4 [Source:HGNC Symbol;Acc:21747], type=processed_transcript,protein_coding,retained_intron	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeNSCLCa, tscapeRCCa
u	CRY2	11:45868669-45904798 11p11.2	cryptochrome 2 (photolyase-like) [Source:HGNC Symbol;Acc:2385], type=processed_transcript,protein_coding,retained_intron, GO=[DNA photolyase activity; blue light photoreceptor activity; blue light signaling pathway; protein-chromophore linkage; regulation of circadian rhythm; damaged DNA binding; single-stranded DNA binding; cellular response to abiotic stimulus; rhythmic process; structure-specific DNA binding; DNA repair; nucleocytoplasmic transport; protein binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	CRYAB	11:111779289-111794446 11q23.1	crystallin, alpha B [Source:HGNC Symbol;Acc:2389], type=protein_coding, GO=[tubulin complex assembly; negative regulation of reactive oxygen species metabolic process; apoptosis involved in morphogenesis; structural constituent of eye lens; developmental programmed cell death; actin filament bundle; microtubule polymerization or depolymerization; negative regulation of caspase activity; Z disc; lens development in camera-type eye; stress-activated MAPK cascade; microtubule binding; response to hydrogen peroxide; response to estradiol stimulus; unfolded protein binding; reactive oxygen species metabolic process; response to reactive oxygen species; negative regulation of cell growth; regulation of cysteine-type endopeptidase activity; protein homooligomerization; response to hypoxia; regulation of endopeptidase activity; response to oxygen levels; anti-apoptosis; regulation of cell growth; soluble fraction; cell surface; MAPKKK cascade; protein homodimerization activity; cytoskeletal protein binding; response to hormone stimulus; microtubule cytoskeleton]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE
u	CSRNP1	3:39183346-39196053 3p22.2	cysteine-serine-rich nuclear protein 1 [Source:HGNC Symbol;Acc:14300], type=protein_coding, GO=[face morphogenesis; platelet-derived growth factor receptor signaling pathway; palate development; post-embryonic development]	tcgaBreastGE
u	CST1	20:23728190-23731905 20p11.21	cystatin SN [Source:HGNC Symbol;Acc:2473], type=protein_coding, GO=[cysteine-type endopeptidase inhibitor activity; endopeptidase inhibitor activity; enzyme inhibitor activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeNSCLCa
u	CST3	20:23608534-23619110 20p11.21	cystatin C [Source:HGNC Symbol;Acc:2475], type=protein_coding, GO=[elastin catabolic process; negative regulation of blood vessel remodeling; regulation of elastin catabolic process; negative regulation of elastin catabolic process; histolysis; regulation of histolysis; regulation of collagen catabolic process; negative regulation of histolysis; negative regulation of collagen catabolic process; negative regulation of extracellular matrix disassembly; fibril organization; circadian sleep/wake cycle, REM sleep; Sertoli cell development; negative regulation of tissue remodeling; multivesicular body; beta-amyloid binding; embryo implantation; negative regulation of cellular catabolic process; positive regulation of DNA replication; cysteine-type endopeptidase inhibitor activity; protease binding; cellular response to hydrogen peroxide; collagen metabolic process; response to axon injury; cellular response to reactive oxygen species; multicellular organismal metabolic process; negative regulation of endopeptidase activity; basement membrane; response to hydrogen peroxide; regulation of DNA replication; response to estradiol stimulus; axon part; response to toxin; response to reactive oxygen species; response to carbohydrate stimulus; female pregnancy; endopeptidase inhibitor activity; nuclear membrane; rhythmic process; response to hypoxia; regulation of endopeptidase activity; response to organic cyclic compound; response to oxygen levels; neuronal cell body; enzyme inhibitor activity; response to drug; perinuclear region of cytoplasm; regulation of cellular catabolic process; regulation of catabolic process; neuron projection; response to hormone stimulus; extracellular space]	snp3dDementia, tcgaOvarianGE, tcgaOvarianMethyl, tscapeCRCa, tscapeNSCLCa
u	CTDSPL	3:37903451-38025960 3p22.2	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase-like [Source:HGNC Symbol;Acc:16890], type=nonsense_mediated_decay,processed_transcript,protein_coding	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
u	CTGF	6:132269316-132272513 6q23.2	connective tissue growth factor [Source:HGNC Symbol;Acc:2500], type=protein_coding, GO=[organ senescence; extracellular matrix constituent secretion; response to anoxia; positive regulation of G0 to G1 transition; positive regulation of cardiac muscle contraction; positive regulation of collagen metabolic process; positive regulation of collagen biosynthetic process; cartilage condensation; fibronectin binding; insulin-like growth factor binding; positive regulation of stress fiber assembly; response to fatty acid; collagen biosynthetic process; cis-Golgi network; response to mineralocorticoid stimulus; positive regulation of JNK cascade; collagen metabolic process; multicellular organismal metabolic process; response to amino acid stimulus; integrin binding; cytosolic calcium ion transport; integrin-mediated signaling pathway; positive regulation of ERK1 and ERK2 cascade; fibroblast growth factor receptor signaling pathway; regulation of ERK1 and ERK2 cascade; response to estradiol stimulus; response to glucose stimulus; reactive oxygen species metabolic process; heparin binding; ERK1 and ERK2 cascade; response to carbohydrate stimulus; cell-matrix adhesion; growth factor activity; cartilage development; glycosaminoglycan binding; regulation of cysteine-type endopeptidase activity; regulation of actin filament-based process; positive regulation of MAPKKK cascade; pattern binding; polysaccharide binding; actin filament organization; regulation of endopeptidase activity; response to organic cyclic compound; response to oxygen levels; regulation of cell growth; perinuclear region of cytoplasm; actin filament-based process; MAPKKK cascade; blood vessel development; vasculature development; regulation of cell cycle; response to hormone stimulus; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa
d	CXCL16	17:4636821-4643217 17p13.2	chemokine (C-X-C motif) ligand 16 [Source:HGNC Symbol;Acc:16642], type=processed_transcript,protein_coding,retained_intron, GO=[low-density lipoprotein receptor activity; lymphocyte chemotaxis; scavenger receptor activity; chemokine activity; response to tumor necrosis factor; response to interferon-gamma; regulation of cell growth; regulation of cell motility; regulation of cellular component movement; extracellular space]	tcgaGliomaGE
u	CYR61	1:86046444-86049645 1p22.3	cysteine-rich, angiogenic inducer, 61 [Source:HGNC Symbol;Acc:2654], type=processed_transcript,protein_coding, GO=[intussusceptive angiogenesis; positive regulation of sphingolipid biosynthetic process; apoptosis involved in heart morphogenesis; positive regulation of ceramide biosynthetic process; chondroblast differentiation; chorio-allantoic fusion; atrioventricular valve morphogenesis; positive regulation of osteoblast proliferation; atrial septum morphogenesis; wound healing, spreading of cells; positive regulation of cartilage development; apoptosis involved in morphogenesis; labyrinthine layer blood vessel development; insulin-like growth factor binding; developmental programmed cell death; positive regulation of BMP signaling pathway; ventricular septum development; extracellular matrix binding; positive regulation of osteoblast differentiation; positive regulation of cell-substrate adhesion; integrin binding; regulation of ERK1 and ERK2 cascade; reactive oxygen species metabolic process; placenta development; heparin binding; ERK1 and ERK2 cascade; cartilage development; glycosaminoglycan binding; regulation of cysteine-type endopeptidase activity; pattern binding; polysaccharide binding; regulation of endopeptidase activity; regulation of cell growth; regulation of cell motility; regulation of cellular component movement; MAPKKK cascade; blood vessel development; vasculature development; lipid biosynthetic process]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeGliomad

Continued on next page...

S	name	locus	description	studies
u	DAPK3	19:3958452-3971038 19p13.3	death-associated protein kinase 3 [Source:HGNC Symbol;Acc:2676], type=protein_coding, GO=[leucine zipper domain binding; regulation of actin cytoskeleton reorganization; positive regulation of canonical Wnt receptor signaling pathway; regulation of smooth muscle contraction; lipopolysaccharide biosynthetic process; PML body; autophagy; cytokinesis; regulation of mitosis; cellular polysaccharide biosynthetic process; regulation of actin filament-based process; regulation of cell motility; regulation of cellular component movement; actin filament-based process; regulation of cellular catabolic process; protein homodimerization activity; regulation of catabolic process; lipid biosynthetic process; regulation of cell cycle; microtubule cytoskeleton]	tcgaOvarianMethyl, tscapeHCCd, tscapeRCCd
u	DCUN1D3	16:20869396-20911706 16p12.3	DCN1, defective in cullin neddylation 1, domain containing 3 (S. cerevisiae) [Source:HGNC Symbol;Acc:28734], type=protein_coding, GO=[response to UV-C; negative regulation of S phase of mitotic cell cycle; regulation of S phase of mitotic cell cycle; response to gamma radiation; negative regulation of cell growth; regulation of cell growth; perinuclear region of cytoplasm; negative regulation of cell cycle; regulation of cell cycle]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
u	DDIT4	10:74033678-74035794 10q22.1	DNA-damage-inducible transcript 4 [Source:HGNC Symbol;Acc:24944], type=processed_transcript,protein_coding, GO=[negative regulation of glycolysis; 14-3-3 protein binding; negative regulation of TOR signaling cascade; regulation of TOR signaling cascade; negative regulation of cellular catabolic process; reactive oxygen species metabolic process; response to hypoxia; response to oxygen levels; regulation of cellular catabolic process; regulation of catabolic process]	tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl
u	DDX19A	16:70380732-70407286 16q22.1	DEAD (Asp-Glu-Ala-Asp) box polypeptide 19A [Source:HGNC Symbol;Acc:25628], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nuclear pore; mRNA export from nucleus; RNA export from nucleus; ATP-dependent helicase activity; mRNA transport; nuclear membrane; helicase activity; nucleocytoplasmic transport]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
u	DERA	12:16064106-16190220 12p12.3	deoxyribose-phosphate aldolase (putative) [Source:HGNC Symbol;Acc:24269], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[deoxyribose-phosphate aldolase activity; deoxyribonucleoside catabolic process; deoxyribonucleotide catabolic process]	tcgaGliomaGE, tscapeHCCd
u	DLG5	10:79550549-79686378 10q22.3	discs, large homolog 5 (Drosophila) [Source:HGNC Symbol;Acc:2904], type=processed_transcript,protein_coding, GO=[receptor signaling complex scaffold activity; cell-cell adherens junction; beta-catenin binding; cytoskeletal protein binding]	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
u	DNAJC3	13:96329411-96443301 13q32.1	DnaJ (Hsp40) homolog, subfamily C, member 3 [Source:HGNC Symbol;Acc:9439], type=protein_coding, GO=[activation of signaling protein activity involved in unfolded protein response; endoplasmic reticulum Sec complex; misfolded protein binding; protein kinase inhibitor activity; chaperone binding; heat shock protein binding; endoplasmic reticulum lumen; unfolded protein binding; enzyme inhibitor activity; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaOvarianMethyl, tscapeBCa
u	DNER	2:230222345-230579274 2q36.3	delta/notch-like EGF repeat containing [Source:HGNC Symbol;Acc:24456], type=processed_transcript,protein_coding, GO=[Notch binding; clathrin binding; Notch receptor processing; synapse assembly; neuron migration; early endosome; neuronal cell body; neuron projection; calcium ion binding]	tcgaBreastGE, tcgaColonGE, tscapeNSCLCd, tscapeRCCd, tscapeSCLCd
u	DOCK5	8:25042238-25275598 8p21.2	dedicator of cytokinesis 5 [Source:HGNC Symbol;Acc:23476], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[GTP binding]	tcgaBreastGE, tcgaOvarianCGHd, tscapeBCd, tscapeHCCd, tscapeOvariand, tscapeProstated
u	DPH3	3:16299485-16306479 3p25.1	DPH3, KTI11 homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:27717], type=processed_transcript,protein_coding, GO=[peptidyl-diphthamide metabolic process; peptidyl-diphthamide biosynthetic process from peptidyl-histidine; negative regulation of protein secretion; positive regulation of binding]	
u	DUSP1	5:172195093-172198198 5q35.1	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:3064], type=protein_coding, GO=[protein tyrosine/threonine phosphatase activity; non-membrane spanning protein tyrosine phosphatase activity; MAP kinase tyrosine/serine/threonine phosphatase activity; inactivation of MAPK activity; positive regulation of anti-apoptosis; negative regulation of MAP kinase activity; response to cAMP; response to hydrogen peroxide; negative regulation of protein serine/threonine kinase activity; response to retinoic acid; response to estradiol stimulus; negative regulation of intracellular protein kinase cascade; response to vitamin A; response to reactive oxygen species; negative regulation of kinase activity; anti-apoptosis; regulation of protein serine/threonine kinase activity; soluble fraction; MAPKKK cascade; response to hormone stimulus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCa, tscapeOvariand, tscapeRCCa
d	E2F2	1:23832922-23857712 1p36.12	E2F transcription factor 2 [Source:HGNC Symbol;Acc:3114], type=processed_transcript,protein_coding, GO=[G1 phase of mitotic cell cycle; core promoter binding; transcription initiation from RNA polymerase II promoter; transcription factor complex; regulation of cell cycle]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u*	EDEM1	3:5229331-5261642 3p26.1	ER degradation enhancer, mannosidase alpha-like 1 [Source:HGNC Symbol;Acc:18967], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[activation of signaling protein activity involved in unfolded protein response; misfolded protein binding; mannosyl-oligosaccharide 1,2-alpha-mannosidase activity; ER-associated protein catabolic process; intrinsic to endoplasmic reticulum membrane; peptidyl-asparagine modification; protein N-linked glycosylation via asparagine; calcium ion binding; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	EFNA1	1:155099936-155107333 1q22	ephrin-A1 [Source:HGNC Symbol;Acc:3221], type=processed_transcript,protein_coding, GO=[notochord formation; negative regulation of dendritic spine development; negative regulation of dendritic spine morphogenesis; endocardial cushion to mesenchymal transition involved in heart valve formation; mitral valve development; mitral valve morphogenesis; aortic valve morphogenesis; aortic valve development; regulation of dendritic spine morphogenesis; negative regulation of epithelial to mesenchymal transition; cardiac epithelial to mesenchymal transition; negative regulation of cell morphogenesis involved in differentiation; substrate adhesion-dependent cell spreading; ephrin receptor binding; ephrin receptor signaling pathway; anchored to plasma membrane; regulation of blood vessel endothelial cell migration; regulation of cell adhesion mediated by integrin; regulation of endothelial cell migration; endothelial cell migration; anchored to membrane; regulation of peptidyl-tyrosine phosphorylation; activation of MAPK activity; positive regulation of MAP kinase activity; positive regulation of protein serine/threonine kinase activity; regulation of protein serine/threonine kinase activity; regulation of cell motility; regulation of cellular component movement; negative regulation of transcription from RNA polymerase II promoter; MAPKKK cascade; blood vessel development; vasculature development]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCa, tscapeProstatea
u	EGFLAM	5:38258511-38465123 5p13.1, 5p13.2	EGF-like, fibronectin type III and laminin G domains [Source:HGNC Symbol;Acc:26810], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[peptide cross-linking via chondroitin 4-sulfate glycosaminoglycan; interstitial matrix; chondroitin sulfate metabolic process; positive regulation of cell-substrate adhesion; basement membrane; glycosaminoglycan binding; pattern binding; polysaccharide binding; calcium ion binding]	tcgaBreastGE, tcgaColonGE, tcgaOvarianGE
u	ELF1	13:41506056-41635576 13q14.11	E74-like factor 1 (ets domain transcription factor) [Source:HGNC Symbol;Acc:3316], type=processed_transcript,protein_coding, GO=[negative regulation of T cell receptor signaling pathway]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd
u	ELOVL1	1:43829068-43833697 1p34.2	ELOVL fatty acid elongase 1 [Source:HGNC Symbol;Acc:14418], type=processed_transcript,protein_coding, GO=[fatty acid elongase activity; fatty acid elongation, monounsaturated fatty acid; fatty acid elongation, saturated fatty acid; very long-chain fatty acid biosynthetic process; fatty acid synthase activity; long-chain fatty-acyl-CoA biosynthetic process; very long-chain fatty acid metabolic process; triglyceride biosynthetic process; neutral lipid biosynthetic process; acylglycerol biosynthetic process; intrinsic to endoplasmic reticulum membrane; glycerolipid biosynthetic process; fatty acid biosynthetic process; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
d	ENHO	9:34521038-34523039 9p13.3	energy homeostasis associated [Source:HGNC Symbol;Acc:24838], type=protein_coding	tcgaGliomaGE
u	ENPP3	6:131949582-132068553 6q23.2	ectonucleotide pyrophosphatase/phosphodiesterase 3 [Source:HGNC Symbol;Acc:3358], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[NADH pyrophosphatase activity; phosphodiesterase I activity; nucleoside-triphosphate diphosphatase activity; scavenger receptor activity; polysaccharide binding; pattern binding; perinuclear region of cytoplasm]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tscapeBCa
u	ETNK2	1:204100190-204121307 1q32.1	ethanolamine kinase 2 [Source:HGNC Symbol;Acc:25575], type=processed_transcript,protein_coding,retained_intron, GO=[ethanolamine kinase activity; ethanolamine metabolic process; phosphatidylethanolamine biosynthetic process; post-embryonic development; placenta development; glycerolipid biosynthetic process; lipid biosynthetic process]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeProstatea

Continued on next page...

S	name	locus	description	studies
u*	F5	1:169483404-169555826 1q24.2	coagulation factor V (proaccelerin, labile factor) [Source:HGNC Symbol;Acc:3542], type=processed_transcript,protein_coding, GO=[platelet alpha granule lumen; copper ion binding; platelet degranulation; platelet activation; extracellular space]	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	FADS1	11:61567098-61647626 11q12.2	fatty acid desaturase 1 [Source:HGNC Symbol;Acc:3574], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[C-5 sterol desaturase activity; response to sucrose stimulus; arachidonic acid metabolic process; very long-chain fatty acid metabolic process; icosanoid biosynthetic process; cellular response to starvation; response to vitamin A; heme binding; fatty acid biosynthetic process; response to carbohydrate stimulus; electron transport chain; iron ion binding; response to organic cyclic compound; response to insulin stimulus; microsome; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process; endoplasmic reticulum membrane; response to hormone stimulus]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	FAIM3	1:207077731-207096592 1q32.1	Fas apoptotic inhibitory molecule 3 [Source:HGNC Symbol;Acc:14315], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cellular defense response; anti-apoptosis]	tcgaBreastGE, tcgaColonMethyl, tscapeBCa, tscapeProstatea
u	FAM107A	3:58549844-58613337 3p14.2, 3p14.3	family with sequence similarity 107, member A [Source:HGNC Symbol;Acc:30827], type=processed_transcript,protein_coding, GO=[regulation of cell growth]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE
d	FAM108C1	15:80972025-81047962 15q25.1	family with sequence similarity 108, member C1 [Source:HGNC Symbol;Acc:26925], type=processed_transcript,protein_coding, GO=[serine-type peptidase activity]	tcgaBreastGE, tcgaColonGE
u	FAM129B	9:130267618-130341268 9q33.3, 9q34.11	family with sequence similarity 129, member B [Source:HGNC Symbol;Acc:25282], type=processed_transcript,protein_coding, GO=[phospholipid binding]	tcgaBreastGE, tcgaGliomaGE
u	FAM177A1	14:35514113-35582336 14q13.2	family with sequence similarity 177, member A1 [Source:HGNC Symbol;Acc:19829], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaColonGE
u	FAM214B	9:35104109-35115999 9p13.3	family with sequence similarity 214, member B [Source:HGNC Symbol;Acc:25666], type=processed_transcript,protein_coding	
d	FAM216A	12:110906169-110928190 12q24.11	family with sequence similarity 216, member A [Source:HGNC Symbol;Acc:30180], type=nonsense_mediated_decay,protein_coding	tcgaOvarianMethyl
u	FAM58A	X:152853377-152864707 Xq28	family with sequence similarity 58, member A [Source:HGNC Symbol;Acc:28434], type=processed_transcript,protein_coding, GO=[regulation of cyclin-dependent protein kinase activity; protein kinase binding; regulation of protein serine/threonine kinase activity; kinase binding; regulation of cell cycle]	tscapeBCa
d	FAM65A	16:67552321-67580689 16q22.1	family with sequence similarity 65, member A [Source:HGNC Symbol;Acc:25836], type=nonsense_mediated_decay,protein_coding,retained_intron	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tscapeOvariand
u	FAM65B	6:24797601-25042238 6p22.3	family with sequence similarity 65, member B [Source:HGNC Symbol;Acc:13872], type=processed_transcript,protein_coding,retained_intron, GO=[filopodium]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
d	FANCG	9:35073832-35080013 9p13.3	Fanconi anemia, complementation group G [Source:HGNC Symbol;Acc:3588], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[Fanconi anaemia nuclear complex; damaged DNA binding; ovarian follicle development; ovum-producing ovary development; development of primary female sexual characteristics; rhythmic process; DNA repair; negative regulation of cell cycle; regulation of cell cycle]	tcgaGliomaGE, tcgaOvarianMethyl
u	FBRSL1	12:133066137-133161774 12q24.33	fibrosin-like 1 [Source:HGNC Symbol;Acc:29308], type=processed_transcript,protein_coding,retained_intron	tcgaGliomaGE
u	FBXO31	16:87362942-87425748 16q24.2	F-box protein 31 [Source:HGNC Symbol;Acc:16510], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[cyclin catabolic process; cyclin binding; SCF-dependent proteasomal ubiquitin-dependent protein catabolic process; SCF ubiquitin ligase complex; mitotic cell cycle G1/S transition DNA damage checkpoint; negative regulation of cell cycle; regulation of cell cycle]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeProstated
u	FERMT2	14:53323986-53419153 14q22.1	fermitin family member 2 [Source:HGNC Symbol;Acc:15767], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[filamentous actin; stress fiber; actin filament bundle; actin filament; regulation of cell shape; focal adhesion; phospholipid binding; actin filament-based process]	tcgaBreastGE, tcgaGliomaGE, tscapeBCa
d	FJX1	11:35639735-35642419 11p13	four jointed box 1 (Drosophila) [Source:HGNC Symbol;Acc:17166], type=processed_transcript,protein_coding, GO=[extracellular space]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeNSCLCa
u	FLVCR2	14:76044960-76129557 14q24.3	feline leukemia virus subgroup C cellular receptor family, member 2 [Source:HGNC Symbol;Acc:20105], type=processed_transcript,protein_coding,retained_intron, GO=[heme transporter activity; heme transport; heme binding; iron ion binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
u	FMO4	1:171283347-171311223 1q24.3	flavin containing monooxygenase 4 [Source:HGNC Symbol;Acc:3772], type=processed_transcript,protein_coding, GO=[flavin-containing monooxygenase activity; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen; intrinsic to endoplasmic reticulum membrane; microsome; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeRCCa
u*	FOS	14:75745477-75748933 14q24.3	FBJ murine osteosarcoma viral oncogene homolog [Source:HGNC Symbol;Acc:3796], type=processed_transcript,protein_coding, GO=[TRIF-dependent toll-like receptor signaling pathway; conditioned taste aversion; response to gravity; R-SMAD binding; SMAD protein signal transduction; cellular response to calcium ion; response to corticosterone stimulus; response to progesterone stimulus; response to mineralocorticoid stimulus; response to cold; DNA methylation; DNA alkylation; cellular response to reactive oxygen species; toll-like receptor 1 signaling pathway; stress-activated MAPK cascade; response to cAMP; MyD88-dependent toll-like receptor signaling pathway; Toll signaling pathway; synaptosome; response to toxin; response to reactive oxygen species; response to mechanical stimulus; female pregnancy; double-stranded DNA binding; structure-specific DNA binding; response to lipopolysaccharide; response to organic cyclic compound; transcription factor complex; regulation of sequence-specific DNA binding transcription factor activity; response to drug; MAPKKK cascade; response to hormone stimulus]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	FOXO1	13:41129817-41240734 13q14.11	forkhead box O1 [Source:HGNC Symbol;Acc:3819], type=processed_transcript,protein_coding, GO=[positive regulation of gluconeogenesis; negative regulation of stress-activated MAPK cascade; DNA bending activity; stress-activated MAPK cascade; phosphatidylinositol-mediated signaling; sequence-specific distal enhancer binding RNA polymerase II transcription factor activity; fibroblast growth factor receptor signaling pathway; negative regulation of intracellular protein kinase cascade; epidermal growth factor receptor signaling pathway; endocrine pancreas development; double-stranded DNA binding; insulin receptor signaling pathway; sequence-specific DNA binding RNA polymerase II transcription factor activity; structure-specific DNA binding; cellular response to insulin stimulus; nerve growth factor receptor signaling pathway; response to insulin stimulus; transcription factor complex; anti-apoptosis; protein kinase binding; regulation of sequence-specific DNA binding transcription factor activity; kinase binding; MAPKKK cascade; blood vessel development; vasculature development; response to hormone stimulus]	tcgaBreastGE, tcgaColonGE, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated, tscapeSCLCd
u	FOXO3	6:108881038-109005977 6q21	forkhead box O3 [Source:HGNC Symbol;Acc:3821], type=protein_coding, GO=[initiation of primordial ovarian follicle growth; antral ovarian follicle growth; ovulation from ovarian follicle; oocyte maturation; positive regulation of erythrocyte differentiation; regulation of erythrocyte differentiation; DNA bending activity; ovarian follicle development; ovum-producing ovary development; phosphatidylinositol-mediated signaling; sequence-specific distal enhancer binding RNA polymerase II transcription factor activity; fibroblast growth factor receptor signaling pathway; development of primary female sexual characteristics; epidermal growth factor receptor signaling pathway; double-stranded DNA binding; insulin receptor signaling pathway; sequence-specific DNA binding RNA polymerase II transcription factor activity; rhythmic process; structure-specific DNA binding; cellular response to insulin stimulus; nerve growth factor receptor signaling pathway; response to insulin stimulus; transcription factor complex; protein kinase binding; regulation of sequence-specific DNA binding transcription factor activity; kinase binding; negative regulation of transcription from RNA polymerase II promoter; response to hormone stimulus]	cosmicRecurrent, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
d	FRAT2	10:99092255-99094458 10q24.1	frequently rearranged in advanced T-cell lymphomas 2 [Source:HGNC Symbol;Acc:16048], type=protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeCRCd
u	FTH1P3	2:27615651-27616234 2p23.3	ferritin, heavy polypeptide 1 pseudogene 3 [Source:HGNC Symbol;Acc:3990], type=processed_pseudogene,pseudogene	
u	FXYD3	19:35606732-35615227 19q13.12	FXYD domain containing ion transport regulator 3 [Source:HGNC Symbol;Acc:4027], type=protein_coding, GO=[ATPase binding; chloride channel complex; chloride channel activity; chloride transport; inorganic anion transport; anion transport; microsome; endoplasmic reticulum membrane]	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeNSCLCa

Continued on next page...

S	name	locus	description	studies
u	GADD45B	19:2476123-2478257 19p13.3	growth arrest and DNA-damage-inducible, beta [Source:HGNC Symbol;Acc:4096], type=protein_coding, GO=[activation of MAPKKK activity; activation of MAPKK activity; negative regulation of kinase activity; positive regulation of MAPKKK cascade; MAPKKK cascade; regulation of cell cycle]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd, tscapeRCCd
u	GATSL3	22:30681106-30685616 22q12.2	GATS protein-like 3 [Source:HGNC Symbol;Acc:34423], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	
u	GBA	1:155204239-155214653 1q22	glucosidase, beta, acid [Source:HGNC Symbol;Acc:4177], type=processed_transcript,protein_coding, GO=[glucosylceramidase activity; termination of signal transduction; glucosylceramide catabolic process; sphingosine biosynthetic process; positive regulation of protein dephosphorylation; lysosomal lumen; negative regulation of interleukin-6 production; lysosome organization; negative regulation of inflammatory response; vacuole organization; cellular response to tumor necrosis factor; negative regulation of MAP kinase activity; response to tumor necrosis factor; negative regulation of protein serine/threonine kinase activity; lysosomal membrane; regulation of inflammatory response; negative regulation of kinase activity; regulation of protein serine/threonine kinase activity; lipid biosynthetic process]	tcgaGliomaGE, tcgaOvarianMethyl
u	GBA	HSCHR1_2_CTG31:155219647- 155229865 HSCHR1_2_CTG31q22	Glucocerebrosidase [Source:UniProtKB/TrEMBL;Acc:Q9UQU9], type=processed_transcript,protein_coding, GO=[glucosylceramidase activity; lysosome organization; vacuole organization]	
u	GBAP1	1:155183616-155197214 1q22	glucosidase, beta, acid pseudogene 1 [Source:HGNC Symbol;Acc:4178], type=processed_transcript,pseudogene,retained_intron,transcribed_unprocessed_pseudogene	tcgaBreastGE, tcgaColonGE
u	GBAP1	HSCHR1_2_CTG31:155199568- 155204076 HSCHR1_2_CTG31q22	[undefined], type=pseudogene,unprocessed_pseudogene	
u	GBE1	3:81538850-81811312 3p12.2	glucan (1,4-alpha-), branching enzyme 1 [Source:HGNC Symbol;Acc:4180], type=processed_transcript,protein_coding,retained_intron, GO=[1,4-alpha-glucan branching enzyme activity; glycogen biosynthetic process; cellular polysaccharide biosynthetic process]	cosmicPrimary, tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd, tscapeSCLCd
u	GBF1	10:104005289-104142656 10q24.32	golgi brefeldin A resistant guanine nucleotide exchange factor 1 [Source:HGNC Symbol;Acc:4181], type=processed_transcript,protein_coding, GO=[Golgi transport vesicle coating; COPI-coated vesicle budding; COPI coating of Golgi vesicle; ARF guanyl-nucleotide exchange factor activity; vesicle targeting, to, from or within Golgi; retrograde vesicle-mediated transport, Golgi to ER; vesicle coating; ARF protein signal transduction; regulation of ARF protein signal transduction; Ras protein signal transduction; small GTPase mediated signal transduction]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd
u	GBP1	1:89518002-89531043 1p22.2	guanylate binding protein 1, interferon-inducible [Source:HGNC Symbol;Acc:4182], type=processed_transcript,protein_coding, GO=[cellular response to interferon-gamma; response to interferon-gamma; GTPase activity; GTP binding]	tcgaGliomaGE, tscapeBCd, tscapeGliomad, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand
u	GBP2	1:89571815-89616139 1p22.2	guanylate binding protein 2, interferon-inducible [Source:HGNC Symbol;Acc:4183], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[type I interferon-mediated signaling pathway; cellular response to interferon-gamma; response to interferon-gamma; GTPase activity; GTP binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeBCd, tscapeGliomad, tscapeMelanomad, tscapeNSCLCd, tscapeOvariand
d*	GEMIN4	17:647654-657239 17p13.3	gem (nuclear organelle) associated protein 4 [Source:HGNC Symbol;Acc:15717], type=protein_coding, GO=[small nuclear ribonucleoprotein complex; spliceosomal snRNP assembly; Cajal body; rRNA processing; ribosome biogenesis; nucleolus]	tcgaColonGE
u*	GHR	5:42423879-42721979 5p12, 5p13.1	growth hormone receptor [Source:HGNC Symbol;Acc:4263], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[growth hormone receptor complex; growth hormone receptor activity; response to cycloheximide; creatinine metabolic process; response to cycloalkane; allantoin metabolic process; isoleucine metabolic process; JAK-STAT cascade involved in growth hormone signaling pathway; taurine metabolic process; valine metabolic process; citrate metabolic process; activation of JAK2 kinase activity; succinate metabolic process; oxaloacetate metabolic process; creatine metabolic process; phosphagen metabolic process; proline-rich region binding; positive regulation of tyrosine phosphorylation of Stat5 protein; 2-oxoglutarate metabolic process; response to food; branched chain family amino acid metabolic process; cellular amide metabolic process; positive regulation of tyrosine phosphorylation of Stat3 protein; response to morphine; response to isoquinoline alkaloid; neuroprotection; positive regulation of multicellular organism growth; regulation of tyrosine phosphorylation of Stat3 protein; SH2 domain binding; peptide hormone binding; insulin-like growth factor receptor signaling pathway; receptor internalization; regulation of tyrosine phosphorylation of STAT protein; hormone binding; response to interleukin-1; protein phosphatase binding; multicellular organismal metabolic process; hormone-mediated signaling pathway; response to alkaloid; phosphatase binding; response to estradiol stimulus; extrinsic to membrane; regulation of peptidyl-tyrosine phosphorylation; activation of MAPK activity; cartilage development; positive regulation of MAP kinase activity; positive regulation of protein serine/threonine kinase activity; cellular response to insulin stimulus; response to organic cyclic compound; response to insulin stimulus; neuronal cell body; fatty acid metabolic process; protein kinase binding; regulation of protein serine/threonine kinase activity; kinase binding; monocarboxylic acid metabolic process; cell surface; MAPKKK cascade; protein homodimerization activity; response to hormone stimulus; extracellular space]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
u*	GIPC1	19:14588572-14606944 19p13.12	GIPC PDZ domain containing family, member 1 [Source:HGNC Symbol;Acc:1226], type=protein_coding, GO=[negative regulation of proteasomal ubiquitin-dependent protein catabolic process; positive regulation of transforming growth factor beta receptor signaling pathway; myosin binding; dendritic shaft; glutamate secretion; negative regulation of cellular catabolic process; brush border; PDZ domain binding; regulation of protein stability; synaptic vesicle; endothelial cell migration; regulation of synaptic plasticity; dendritic spine; actin binding; soluble fraction; regulation of cellular catabolic process; protein homodimerization activity; regulation of catabolic process; cytoskeletal protein binding; neuron projection]	tcgaBreastGE, tcgaOvarianCGHa, tcgaOvarianMethyl
u*	GMNN	6:24775159-24786327 6p22.3	geminin, DNA replication inhibitor [Source:HGNC Symbol;Acc:17493], type=protein_coding,retained_intron, GO=[repressing transcription factor binding; negative regulation of DNA replication; histone deacetylase binding; M/G1 transition of mitotic cell cycle; regulation of DNA replication; transcription cofactor activity; protein binding transcription factor activity; negative regulation of cell cycle; regulation of cell cycle]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	GOLGA5	14:93260576-93306308 14q32.12	golgin A5 [Source:HGNC Symbol;Acc:4428], type=protein_coding,retained_intron, GO=[Golgi trans cisterna; Golgi cis cisterna; Golgi medial cisterna; COPI coated vesicle membrane; retrograde transport, vesicle recycling within Golgi; cis-Golgi network; Golgi organization; Rab GTPase binding; Golgi cisterna; protein homodimerization activity]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
u	GOLPH3	5:32124810-32174456 5p13.3	golgi phosphoprotein 3 (coat-protein) [Source:HGNC Symbol;Acc:15452], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[positive regulation of TOR signaling cascade; regulation of mitochondrion organization; regulation of TOR signaling cascade; mitochondrial intermembrane space; Golgi cisterna membrane; trans-Golgi network; Golgi cisterna; nuclear membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	GORASP1	3:39138150-39149854 3p22.2	golgi reassembly stacking protein 1, 65kDa [Source:HGNC Symbol;Acc:16769], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[mitotic prophase; Golgi organization]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	GPER	7:1121844-1133451 7p22.3	G protein-coupled estrogen receptor 1 [Source:HGNC Symbol;Acc:4485], type=protein_coding, GO=[estrogen receptor activity; positive regulation of epidermal growth factor receptor signaling pathway; steroid hormone mediated signaling pathway; hormone binding; hormone-mediated signaling pathway; positive regulation of ERK1 and ERK2 cascade; steroid hormone receptor signaling pathway; regulation of ERK1 and ERK2 cascade; epidermal growth factor receptor signaling pathway; ERK1 and ERK2 cascade; positive regulation of MAPKKK cascade; MAPKKK cascade; endoplasmic reticulum membrane; response to hormone stimulus]	tcgaBreastGE, tcgaColonGE, tscapeOvariand
u	GPR153	1:6307406-6321035 1p36.31	G protein-coupled receptor 153 [Source:HGNC Symbol;Acc:23618], type=protein_coding	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeGliomad, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
d	GULP1	2:189156396-189460653 2q32.1, 2q32.2	GULP, engulfment adaptor PTB domain containing 1 [Source:HGNC Symbol;Acc:18649], type=processed_transcript,protein_coding,retained_intron, GO=[phagocytosis, engulfment]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
u*	HADH	4:108910870-108956331 4q25	hydroxyacyl-CoA dehydrogenase [Source:HGNC Symbol;Acc:4799], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[3-hydroxyacyl-CoA dehydrogenase activity; NAD+ binding; negative regulation of insulin secretion; fatty acid oxidation; mitochondrial matrix; response to insulin stimulus; fatty acid metabolic process; mitochondrial inner membrane; response to drug; monocarboxylic acid metabolic process; response to hormone stimulus]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeHCCd
u	HARS	5:140052758-140071609 5q31.3	histidyl-tRNA synthetase [Source:HGNC Symbol;Acc:4816], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[histidine-tRNA ligase activity; histidyl-tRNA aminoacylation]	tcgaBreastGE, tcgaGliomaGE
u*	HIBCH	2:191054461-191208919 2q32.2	3-hydroxyisobutyryl-CoA hydrolase [Source:HGNC Symbol;Acc:4908], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[3-hydroxyisobutyryl-CoA hydrolase activity; branched chain family amino acid catabolic process; branched chain family amino acid metabolic process; mitochondrial matrix]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
d	HIST3H2A	1:228645065-228645560 1q42.13	histone cluster 3, H2a [Source:HGNC Symbol;Acc:20507], type=protein_coding, GO=[nucleosome; nucleosome assembly]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeProstated
d*	HNRNPA1	12:54673977-54680872 12q13.13	heterogeneous nuclear ribonucleoprotein A1 [Source:HGNC Symbol;Acc:5031], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[heterogeneous nuclear ribonucleoprotein complex; alternative nuclear mRNA splicing, via spliceosome; single-stranded RNA binding; single-stranded DNA binding; RNA export from nucleus; catalytic step 2 spliceosome; mRNA transport; structure-specific DNA binding; nucleocytoplasmic transport; nucleolus]	tcgaBreastGE, tscapeRCCa
d	HS3ST1	4:11394774-11431389 4p15.33	heparan sulfate (glucosamine) 3-O-sulfotransferase 1 [Source:HGNC Symbol;Acc:5194], type=protein_coding, GO=[[heparan sulfate]-glucosamine 3-sulfotransferase 1 activity; Golgi lumen]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	HSD11B2	16:67464555-67471456 16q22.1	hydroxysteroid (11-beta) dehydrogenase 2 [Source:HGNC Symbol;Acc:5209], type=processed_transcript,protein_coding,retained_intron, GO=[11-beta-hydroxysteroid dehydrogenase [NAD(P)] activity; regulation of blood volume by renal aldosterone; positive regulation of systemic arterial blood pressure; glucocorticoid biosynthetic process; response to food; steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; steroid dehydrogenase activity; C21-steroid hormone metabolic process; female pregnancy; steroid biosynthetic process; response to hypoxia; response to oxygen levels; response to insulin stimulus; microsome; response to drug; lipid biosynthetic process; response to hormone stimulus]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
u	HSD17B11	4:88257762-88312538 4q22.1	hydroxysteroid (17-beta) dehydrogenase 11 [Source:HGNC Symbol;Acc:22960], type=processed_transcript,protein_coding,retained_intron, GO=[androgen catabolic process; estradiol 17-beta-dehydrogenase activity; steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; steroid dehydrogenase activity; steroid biosynthetic process; lipid biosynthetic process]	tcgaBreastGE, tcgaColonGE, tscapeHCCd
u	HSD17B4	5:118788138-118878028 5q23.1	hydroxysteroid (17-beta) dehydrogenase 4 [Source:HGNC Symbol;Acc:5213], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[3alpha,7alpha,12alpha-trihydroxy-5beta-cholest-24-enoyl-CoA hydratase activity; long-chain-enoyl-CoA hydratase activity; 3-hydroxyacyl-CoA dehydrogenase activity; Sertoli cell development; estradiol 17-beta-dehydrogenase activity; fatty acid beta-oxidation using acyl-CoA oxidase; sterol transporter activity; bile acid biosynthetic process; peroxisomal matrix; steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; steroid dehydrogenase activity; very long-chain fatty acid metabolic process; bile acid metabolic process; peroxisomal part; microbody part; sterol transport; fatty acid oxidation; steroid biosynthetic process; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
d*	HSPA4L	4:128702976-128755226 4q28.1	heat shock 70kDa protein 4-like [Source:HGNC Symbol;Acc:17041], type=processed_transcript,protein_coding	tcgaColonGE, tcgaGliomaGE
u*	HSPB8	12:119616447-119658936 12q24.23	heat shock 22kDa protein 8 [Source:HGNC Symbol;Acc:30171], type=processed_transcript,protein_coding	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
d	IGSF9	1:159896829-159915394 1q23.2	immunoglobulin superfamily, member 9 [Source:HGNC Symbol;Acc:18132], type=processed_transcript,protein_coding, GO=[neuron projection]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
u	IP6K3	6:33689444-33714762 6p21.31	inositol hexakisphosphate kinase 3 [Source:HGNC Symbol;Acc:17269], type=protein_coding, GO=[inositol hexakisphosphate 6-kinase activity; inositol hexakisphosphate 1-kinase activity; inositol hexakisphosphate 3-kinase activity; inositol hexakisphosphate 5-kinase activity; inositol trisphosphate 3-kinase activity; inositol phosphate biosynthetic process]	
d	IRF2BPL	14:77490888-77495034 14q24.3	interferon regulatory factor 2 binding protein-like [Source:HGNC Symbol;Acc:14282], type=protein_coding	tcgaBreastGE, tcgaColonGE
u	IRX3	16:54317216-54320675 16q12.2	iroquois homeobox 3 [Source:HGNC Symbol;Acc:14360], type=processed_transcript,protein_coding, GO=[specification of loop of Henle identity; segment specification; negative regulation of neuron differentiation; positive regulation of neuron differentiation; neuron projection]	
u	ISG20	15:89179384-89199714 15q26.1	interferon stimulated exonuclease gene 20kDa [Source:HGNC Symbol;Acc:6130], type=processed_transcript,protein_coding,retained_intron, GO=[single-stranded DNA specific 3'-5' exodeoxyribonuclease activity; exoribonuclease II activity; DNA catabolic process, exonucleolytic; 3'-5'-exoribonuclease activity; PML body; type I interferon-mediated signaling pathway; rRNA processing; ribosome biogenesis]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCa
u*	JAK2	9:4985033-5128183 9p24.1	Janus kinase 2 [Source:HGNC Symbol;Acc:6192], type=processed_transcript,protein_coding, GO=[histone kinase activity (H3-Y41 specific); histone tyrosine kinase activity; histone H3-Y41 phosphorylation; histone-tyrosine phosphorylation; activation of caspase activity by protein phosphorylation; positive regulation of growth hormone receptor signaling pathway; mineralocorticoid receptor signaling pathway; endosome lumen; interleukin-12-mediated signaling pathway; acetylcholine receptor binding; growth hormone receptor binding; interleukin-12 receptor binding; JAK-STAT cascade involved in growth hormone signaling pathway; positive regulation of phosphoprotein phosphatase activity; positive regulation of nitric-oxide synthase biosynthetic process; activation of JAK2 kinase activity; STAT protein import into nucleus; response to hydroperoxide; positive regulation of protein import into nucleus, translocation; induction of apoptosis by oxidative stress; insulin receptor substrate binding; peptide hormone receptor binding; tyrosine phosphorylation of Stat1 protein; negative regulation of heart contraction; positive regulation of tyrosine phosphorylation of Stat5 protein; phosphatidylinositol 3-kinase binding; positive regulation of interleukin-1 beta production; negative regulation of cell-cell adhesion; positive regulation of tyrosine phosphorylation of Stat3 protein; regulation of interferon-gamma-mediated signaling pathway; positive regulation of nitric oxide biosynthetic process; neuroprotection; axon regeneration; positive regulation of tumor necrosis factor production; regulation of tyrosine phosphorylation of Stat3 protein; positive regulation of DNA binding; SH2 domain binding; regulation of interleukin-1 beta production; platelet-derived growth factor receptor signaling pathway; negative regulation of DNA binding; tumor necrosis factor-mediated signaling pathway; response to antibiotic; regulation of nitric oxide biosynthetic process; positive regulation of insulin secretion; positive regulation of phosphatidylinositol 3-kinase cascade; non-membrane spanning protein tyrosine kinase activity; activation of MAPKK activity; regulation of phosphatidylinositol 3-kinase cascade; regulation of tyrosine phosphorylation of STAT protein; positive regulation of cell-substrate adhesion; caveola; response to axon injury; tumor necrosis factor production; regulation of tumor necrosis factor production; negative regulation of binding; cellular response to tumor necrosis factor; nuclear matrix; positive regulation of inflammatory response; positive regulation of binding; hormone-mediated signaling pathway; mammary gland epithelium development; response to tumor necrosis factor; cellular response to interferon-gamma; actin filament polymerization; steroid hormone receptor signaling pathway; response to interferon-gamma; actin polymerization or depolymerization; heme binding; regulation of peptidyl-tyrosine phosphorylation; regeneration; regulation of inflammatory response; regulation of cysteine-type endopeptidase activity; membrane raft; actin filament organization; iron ion binding; response to lipopolysaccharide; regulation of endopeptidase activity; protein kinase binding; regulation of sequence-specific DNA binding transcription factor activity; kinase binding; regulation of cell motility; regulation of cellular component movement; nucleocytoplasmic transport; actin filament-based process; MAPKKK cascade; response to hormone stimulus]	tscapeBCd

Continued on next page...

S	name	locus	description	studies
u*	JUN	1:59246465-59249785 1p32.1	jun proto-oncogene [Source:HGNC Symbol;Acc:6204], type=protein_coding, GO=[TRIF-dependent toll-like receptor signaling pathway; leading edge cell differentiation; cellular response to potassium ion starvation; positive regulation of monocyte differentiation; cAMP response element binding; negative regulation of protein autophosphorylation; positive regulation by host of viral transcription; microglial cell activation; nuclear euchromatin; negative regulation by host of viral transcription; RNA polymerase II distal enhancer sequence-specific DNA binding; SMAD protein import into nucleus; R-SMAD binding; SMAD protein signal transduction; cellular response to calcium ion; RNA polymerase II activating transcription factor binding; RNA polymerase II transcription factor binding transcription factor activity involved in positive regulation of transcription; enhancer binding; axon regeneration; Rho GTPase activator activity; negative regulation of DNA binding; macrophage activation; positive regulation of neuron apoptosis; release of cytochrome c from mitochondria; positive regulation of fibroblast proliferation; positive regulation of smooth muscle cell proliferation; outflow tract morphogenesis; positive regulation of DNA replication; positive regulation of endothelial cell proliferation; response to axon injury; membrane depolarization; negative regulation of binding; regulation of smooth muscle cell proliferation; smooth muscle cell proliferation; toll-like receptor 1 signaling pathway; RNA polymerase II transcription factor binding transcription factor activity; stress-activated MAPK cascade; positive regulation of Rho GTPase activity; response to cAMP; cellular response to starvation; MyD88-dependent toll-like receptor signaling pathway; Toll signaling pathway; response to hydrogen peroxide; liver development; negative regulation of neuron apoptosis; regulation of DNA replication; sequence-specific distal enhancer binding RNA polymerase II transcription factor activity; regulation of Rho GTPase activity; Ras GTPase activator activity; response to reactive oxygen species; response to mechanical stimulus; regeneration; double-stranded DNA binding; sequence-specific DNA binding RNA polymerase II transcription factor activity; Rho protein signal transduction; rhythmic process; structure-specific DNA binding; response to lipopolysaccharide; regulation of Ras GTPase activity; epithelial cell proliferation; response to organic cyclic compound; GTPase activator activity; transcription coactivator activity; transcription factor complex; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; regulation of sequence-specific DNA binding transcription factor activity; response to drug; nucleocytoplasmic transport; transcription cofactor activity; Ras protein signal transduction; protein binding transcription factor activity; regulation of cellular catabolic process; MAPKKK cascade; blood vessel development; protein homodimerization activity; vasculature development; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction; regulation of cell cycle]	fileAmpOver, tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	KAZALD1	10:102820999-102827888 10q24.31	Kazal-type serine peptidase inhibitor domain 1 [Source:HGNC Symbol;Acc:25460], type=processed_transcript,protein_coding, GO=[interstitial matrix; insulin-like growth factor binding; regulation of cell growth]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeCRCd
d	KBTBD11	8:1922044-1955102 8p23.3	kelch repeat and BTB (POZ) domain containing 11 [Source:HGNC Symbol;Acc:29104], type=protein_coding	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHd, tscapeCRCd, tscapeHCCd, tscapeOvariand
u	KCNG1	20:49620193-49639666 20q13.13	potassium voltage-gated channel, subfamily G, member 1 [Source:HGNC Symbol;Acc:6248], type=protein_coding, GO=[potassium ion transmembrane transport; cellular potassium ion transport; voltage-gated potassium channel complex]	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	KCNK1	1:233749750-233808258 1q42.2	potassium channel, subfamily K, member 1 [Source:HGNC Symbol;Acc:6272], type=processed_transcript,protein_coding, GO=[inward rectifier potassium channel activity; response to nicotine; brush border membrane; brush border; cellular potassium ion transport; potassium ion transmembrane transport; voltage-gated potassium channel complex; response to alkaloid; apical plasma membrane; response to organic cyclic compound; apical part of cell]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariana, tscapeProstated
u	KIAA0040	1:175126123-175162224 1q25.1	KIAA0040 [Source:HGNC Symbol;Acc:28950], type=lincRNA	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl
u	KIAA0232	4:6783102-6885897 4p16.1	KIAA0232 [Source:HGNC Symbol;Acc:28992], type=processed_transcript,protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	KIAA0513	16:85061375-85127836 16q24.1	KIAA0513 [Source:HGNC Symbol;Acc:29058], type=protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeProstated
u	KIAA1324L	7:86506222-86689015 7q21.12	KIAA1324-like [Source:HGNC Symbol;Acc:21945], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaColonGE, tcgaGliomaGE, tcgaOvarianGE, tscapeNSCLCa
u	KIAA1522	1:33207486-33240571 1p35.1	KIAA1522 [Source:HGNC Symbol;Acc:29301], type=protein_coding,retained_intron	tcgaBreastGE, tcgaGliomaGE, tscapeBCd, tscapeOvariand
u	KIF13B	8:28924796-29120641 8p12	kinesin family member 13B [Source:HGNC Symbol;Acc:14405], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[microtubule motor activity; microtubule; microtubule cytoskeleton]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHd, tcgaOvarianMethyl, tscapeOvariand, tscapeRCCd
d	KIF20A	5:137514408-137523404 5q31.2	kinesin family member 20A [Source:HGNC Symbol;Acc:9787], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[microtubule motor activity; cytokinesis; spindle; microtubule; protein kinase binding; kinase binding; microtubule cytoskeleton]	fileCIN70, tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
u	KLF6	10:3818188-3827473 10p15.1	Kruppel-like factor 6 [Source:HGNC Symbol;Acc:2235], type=processed_transcript,protein_coding, GO=[double-stranded DNA binding; structure-specific DNA binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
u	KLF9	9:72999503-73029540 9q21.12	Kruppel-like factor 9 [Source:HGNC Symbol;Acc:1123], type=protein_coding, GO=[progesterone receptor signaling pathway; cellular response to thyroid hormone stimulus; embryo implantation; steroid hormone receptor signaling pathway; female pregnancy; response to hormone stimulus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
u	KLHL36	16:84682131-84701292 16q24.1	kelch-like 36 (Drosophila) [Source:HGNC Symbol;Acc:17844], type=protein_coding,retained_intron	
u	KRT16	17:39766030-39769005 17q21.2	keratin 16 [Source:HGNC Symbol;Acc:6423], type=protein_coding, GO=[intermediate filament cytoskeleton organization; structural constituent of cytoskeleton]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tscapeBCd, tscapeOvariand
u	KRT6A	12:52880958-52887041 12q13.13	keratin 6A [Source:HGNC Symbol;Acc:6443], type=protein_coding,retained_intron, GO=[ectoderm development; structural constituent of cytoskeleton; keratin filament]	cosmicMetastasis, cosmicPrimary, tcgaOvarianMethyl, tscapeRCCa
u	KRT72	12:52979373-52995322 12q13.13	keratin 72 [Source:HGNC Symbol;Acc:28932], type=nonsense_mediated_decay,protein_coding, GO=[keratin filament]	tscapeRCCa
u	KRT73	12:53001354-53012343 12q13.13	keratin 73 [Source:HGNC Symbol;Acc:28928], type=protein_coding,retained_intron, GO=[keratin filament]	tscapeRCCa
u	LEPREL1	3:189674517-189840226 3q28	leprecan-like 1 [Source:HGNC Symbol;Acc:19317], type=protein_coding,retained_intron, GO=[procollagen-proline 3-dioxygenase activity; peptidyl-proline hydroxylation; L-ascorbic acid binding; collagen metabolic process; multicellular organismal metabolic process; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; basement membrane; iron ion binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa, tscapeOvariana
u	LGALSL	2:64681103-64688515 2p14	lectin, galactoside-binding-like [Source:HGNC Symbol;Acc:25012], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[sugar binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE

Continued on next page...

S	name	locus	description	studies
u*	LIFR	5:38475065-38608456 5p13.1	leukemia inhibitory factor receptor alpha [Source:HGNC Symbol;Acc:6597], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[leukemia inhibitory factor receptor activity; oncostatin-M receptor activity; leukemia inhibitory factor signaling pathway; ciliary neurotrophic factor receptor binding; ciliary neurotrophic factor-mediated signaling pathway; positive regulation of anti-apoptosis; organ regeneration; regeneration; anti-apoptosis]	cosmicRecurrent, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
d	LIN7A	12:81186299-81331704 12q21.31	lin-7 homolog A (C. elegans) [Source:HGNC Symbol;Acc:17787], type=nonsense_mediated_decay,protein_coding, GO=[L27 domain binding; synaptic vesicle transport; PDZ domain binding; tight junction; postsynaptic density; synaptosome; dendritic spine; postsynaptic membrane; synaptic membrane; neuron projection]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE
u	LIN7B	19:49617581-49621717 19q13.33	lin-7 homolog B (C. elegans) [Source:HGNC Symbol;Acc:17788], type=processed_transcript,protein_coding,retained_intron, GO=[tight junction; postsynaptic density; synaptosome; dendritic spine; postsynaptic membrane; synaptic membrane; neuron projection]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd, tscapeOvariand
u	LNX2	13:28120050-28194541 13q12.2	ligand of numb-protein X 2 [Source:HGNC Symbol;Acc:20421], type=protein_coding, GO=[PDZ domain binding; protein homooligomerization]	tcgaBreastGE, tcgaBreastMethyl, tscapeBCd, tscapeSCLCd
u	LRRC16A	6:25279306-25620758 6p22.2	leucine rich repeat containing 16A [Source:HGNC Symbol;Acc:21581], type=processed_transcript,protein_coding, GO=[urate metabolic process; ruffle organization; lamellipodium assembly; lamellipodium; actin filament organization; actin filament-based process]	tcgaColonGE, tcgaGliomaGE
u	LRRC8A	9:131644391-131680318 9q34.11	leucine rich repeat containing 8 family, member A [Source:HGNC Symbol;Acc:19027], type=processed_transcript,protein_coding, GO=[pre-B cell differentiation; immature B cell differentiation]	
d	LYSMD2	15:52015208-52043782 15q21.2	LysM, putative peptidoglycan-binding, domain containing 2 [Source:HGNC Symbol;Acc:28571], type=protein_coding, GO=[cell wall macromolecule catabolic process]	tcgaBreastMethyl, tcgaGliomaGE
u*	MAFB	20:39314488-39317880 20q12	v-maf musculoaponeurotic fibrosarcoma oncogene homolog B (avian) [Source:HGNC Symbol;Acc:6408], type=protein_coding, GO=[rhombomere 6 development; rhombomere 5 development; central nervous system segmentation; brain segmentation; negative regulation of erythrocyte differentiation; segment specification; regulation of erythrocyte differentiation; respiratory gaseous exchange; inner ear morphogenesis; transcription factor complex]	tcgaGliomaGE
u	MAOA	X:43515467-43606068 Xp11.3	monoamine oxidase A [Source:HGNC Symbol;Acc:6833], type=processed_transcript,protein_coding, GO=[phenylethylamine metabolic process; dopamine catabolic process; primary amine oxidase activity; serotonin metabolic process; neurotransmitter catabolic process; serotonin binding; neurotransmitter biosynthetic process; mitochondrial outer membrane; electron carrier activity; soluble fraction]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
u*	MAP1LC3B	16:87417601-87438385 16q24.2	microtubule-associated protein 1 light chain 3 beta [Source:HGNC Symbol;Acc:13352], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[autophagic vacuole membrane; autophagic vacuole; autophagic vacuole assembly; macroautophagy; vacuole organization; cellular response to starvation; autophagy; microtubule; microtubule cytoskeleton]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeProstated
d	MAST4	5:65892176-66465423 5q12.3	microtubule associated serine/threonine kinase family member 4 [Source:HGNC Symbol;Acc:19037], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[magnesium ion binding]	tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u	MBNL1	3:151961617-152183569 3q25.1, 3q25.2	muscleblind-like splicing regulator 1 [Source:HGNC Symbol;Acc:6923], type=processed_transcript,protein_coding,retained_intron, GO=[stress granule; mRNA splice site selection; regulation of alternative nuclear mRNA splicing, via spliceosome; alternative nuclear mRNA splicing, via spliceosome; double-stranded RNA binding; myoblast differentiation]	tcgaBreastMethyl, tcgaColonGE
d*	MCM2	3:127317066-127341276 3q21.3	minichromosome maintenance complex component 2 [Source:HGNC Symbol;Acc:6944], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[DNA replication origin binding; magnesium chelatase activity; chlorophyll biosynthetic process; DNA unwinding involved in replication; photosynthesis; origin recognition complex; nuclear origin of replication recognition complex; MCM complex; DNA strand elongation involved in DNA replication; tetrapyrrole metabolic process; M/G1 transition of mitotic cell cycle; nucleosome assembly; helicase activity; negative regulation of cell cycle; regulation of cell cycle]	fileCIN70, tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl
u	MEAF6	1:37958176-37980375 1p34.3	MYST/Esa1-associated factor 6 [Source:HGNC Symbol;Acc:25674], type=processed_transcript,protein_coding, GO=[histone H3-K14 acetylation; histone H4-K8 acetylation; histone H4-K5 acetylation; H3 histone acetyltransferase complex; MOZ/MORF histone acetyltransferase complex; histone H4-K12 acetylation; histone H2A acetylation; NuA4 histone acetyltransferase complex; nucleolus; microtubule cytoskeleton]	tcgaGliomaGE
u*	MED23	6:131895106-131949369 6q23.2	mediator complex subunit 23 [Source:HGNC Symbol;Acc:2372], type=processed_transcript,protein_coding, GO=[mediator complex; transcription initiation from RNA polymerase II promoter; transcription coactivator activity; transcription factor complex; transcription cofactor activity; protein binding transcription factor activity]	cosmicPrimary, tcgaBreastGE, tcgaColonGE, tscapeBCa
d	MESP1	15:90291892-90294541 15q26.1	mesoderm posterior 1 homolog (mouse) [Source:HGNC Symbol;Acc:29658], type=processed_transcript,protein_coding, GO=[cardioblast migration to the midline involved in heart field formation; negative regulation of endodermal cell fate specification; positive regulation of Notch signaling pathway involved in heart induction; regulation of Notch signaling pathway involved in heart induction; cell migration to the midline involved in heart development; cardioblast anterior-lateral migration; sinus venosus morphogenesis; sinus venosus development; Notch signaling pathway involved in heart induction; cardiac atrium formation; sinoatrial node cell differentiation; positive regulation of hepatocyte differentiation; positive regulation of heart induction by negative regulation of canonical Wnt receptor signaling pathway; growth involved in heart morphogenesis; negative regulation of mesodermal cell fate specification; cardiac cell fate determination; cardiac vascular smooth muscle cell differentiation; mesodermal cell migration; secondary heart field specification; lateral mesoderm development; cardiac ventricle formation; positive regulation of Notch signaling pathway; positive regulation of striated muscle cell differentiation; signal transduction involved in regulation of gene expression; enhancer binding; regulation of Notch signaling pathway; heart looping; liver development; regulation of organ morphogenesis; blood vessel development; vasculature development]	tcgaBreastGE, tcgaOvarianMethyl, tscapeNSCLCa
u	MFSD6	2:191273081-191373931 2q32.2	major facilitator superfamily domain containing 6 [Source:HGNC Symbol;Acc:24711], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaGliomaGE
u	MICAL2	11:12115543-12285334 11p15.3	microtubule associated monoxygenase, calponin and LIM domain containing 2 [Source:HGNC Symbol;Acc:24693], type=processed_transcript,protein_coding,retained_intron, GO=[FAD binding; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen; actin filament depolymerization; protein depolymerization; actin polymerization or depolymerization; electron carrier activity; actin filament organization; actin binding; actin filament-based process; cytoskeletal protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	MIR22HG	17:1614805-1620468 17p13.3	MIR22 host gene (non-protein coding) [Source:HGNC Symbol;Acc:28219], type=lincRNA,non_coding	tcgaBreastGE
d*	MLF1IP	4:185615772-185655287 4q35.1	MLF1 interacting protein [Source:HGNC Symbol;Acc:21348], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[CenH3-containing nucleosome assembly at centromere; DNA replication-independent nucleosome assembly; condensed chromosome kinetochore; mitotic prometaphase; nucleosome assembly; microtubule cytoskeleton]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeRCCd
d	MMD	17:53469974-53499353 17q22	monocyte to macrophage differentiation-associated [Source:HGNC Symbol;Acc:7153], type=processed_transcript,protein_coding, GO=[cytolysis; late endosome membrane; lysosomal membrane]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	MMP11	22:24110413-24126503 22q11.23	matrix metallopeptidase 11 (stromelysin 3) [Source:HGNC Symbol;Acc:7157], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[collagen metabolic process; multicellular organismal metabolic process; metalloendopeptidase activity; calcium ion binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
u	MRFAP1	4:6641818-6644472 4p16.1	Morf4 family associated protein 1 [Source:HGNC Symbol;Acc:24549], type=protein_coding,retained_intron, GO=[perinuclear region of cytoplasm]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	MSANTD4	11:105866350-105893130 11q22.3	Myb/SANT-like DNA-binding domain containing 4 with coiled-coils [Source:HGNC Symbol;Acc:29383], type=processed_transcript,protein_coding	tcgaBreastGE
u*	MSMO1	4:166248775-166264312 4q32.3	methylsterol monooxygenase 1 [Source:HGNC Symbol;Acc:10545], type=protein_coding, GO=[C-4 methylsterol oxidase activity; oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NADH or NADPH as one donor, and incorporation of one atom of oxygen; cholesterol biosynthetic process; fatty acid biosynthetic process; steroid biosynthetic process; iron ion binding; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process; endoplasmic reticulum membrane]	

Continued on next page...

S	name	locus	description	studies
u*	MSX1	4:4861393-4865663 4p16.2	msh homeobox 1 [Source:HGNC Symbol;Acc:7391], type=protein_coding, GO=[nail development; embryonic nail plate morphogenesis; BMP signaling pathway involved in heart development; epithelial to mesenchymal transition involved in endocardial cushion formation; negative regulation of transcription regulatory region DNA binding; negative regulation of striated muscle cell differentiation; positive regulation of DNA damage response, signal transduction by p53 class mediator; cartilage morphogenesis; cardiac epithelial to mesenchymal transition; signal transduction involved in regulation of gene expression; regulation of odontogenesis; middle ear morphogenesis; negative regulation of muscle cell differentiation; embryonic forelimb morphogenesis; positive regulation of BMP signaling pathway; face morphogenesis; embryonic hindlimb morphogenesis; midbrain development; apoptotic nuclear change; negative regulation of DNA binding; p53 binding; protein stabilization; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; odontogenesis of dentine-containing tooth; negative regulation of binding; palate development; mammary gland epithelium development; regulation of protein stability; stem cell differentiation; regulation of organ morphogenesis; negative regulation of cell growth; cartilage development; sequence-specific DNA binding RNA polymerase II transcription factor activity; anterior/posterior pattern specification; transcription factor complex; regulation of cell growth; negative regulation of transcription from RNA polymerase II promoter]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
d*	MYB	6:135502453-135540311 6q23.3	v-myb myeloblastosis viral oncogene homolog (avian) [Source:HGNC Symbol;Acc:7545], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[positive regulation of histone H3-K9 methylation; positive regulation of histone H3-K4 methylation; positive regulation of T-helper cell differentiation; embryonic digestive tract development; nuclear matrix; negative regulation of transcription from RNA polymerase II promoter]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa, tscapeCRCa, tscapeNSCLCd, tscapeOvariand
u*	MYL12A	18:3247528-3256234 18p11.31	myosin, light chain 12A, regulatory, non-sarcomeric [Source:HGNC Symbol;Acc:16701], type=protein_coding, GO=[calcium ion binding]	tcgaGliomaGE
d*	MYO6	6:76458909-76629254 6q14.1	myosin VI [Source:HGNC Symbol;Acc:7605], type=processed_transcript,protein_coding, GO=[minus-end directed microfilament motor activity; cellular response to electrical stimulus; unconventional myosin complex; clathrin-coated endocytic vesicle; filamentous actin; ADP binding; auditory receptor cell differentiation; glutamate secretion; ruffle membrane; coated pit; actin filament; actin filament-based movement; actin filament binding; synapse assembly; DNA-directed RNA polymerase II, holoenzyme; clathrin coated vesicle membrane; regulation of synaptic plasticity; inner ear morphogenesis; cellular response to abiotic stimulus; sensory perception of sound; calmodulin binding; nuclear membrane; apical part of cell; microsome; neuronal cell body; actin binding; response to drug; perinuclear region of cytoplasm; actin filament-based process; cytoskeletal protein binding; neuron projection]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
u	NANS	9:100819021-100845357 9q22.33	N-acetylneuraminic acid synthase [Source:HGNC Symbol;Acc:19237], type=processed_transcript,protein_coding, GO=[N-acylneuraminate-9-phosphate synthase activity; N-acetylneuraminate synthase activity; N-acylneuraminate cytidylyltransferase activity; lipopolysaccharide biosynthetic process; cellular polysaccharide biosynthetic process; lipid biosynthetic process]	tcgaBreastGE, tcgaBreastGESurv, tcgaOvarianMethyl
d	NCS1	9:132934857-132999583 9q34.11	neuronal calcium sensor 1 [Source:HGNC Symbol;Acc:3953], type=processed_transcript,protein_coding, GO=[dense core granule; negative regulation of calcium ion transport via voltage-gated calcium channel activity; positive regulation of exocytosis; Golgi cisterna membrane; Golgi cisterna; phosphatidylinositol-mediated signaling; postsynaptic density; dendritic spine; postsynaptic membrane; synaptic membrane; perinuclear region of cytoplasm; neuron projection; calcium ion binding]	tcgaBreastGE, tcgaGliomaGE
u*	NET1	10:5454514-5500426 10p15.1	neuroepithelial cell transforming 1 [Source:HGNC Symbol;Acc:14592], type=processed_transcript,protein_coding, GO=[cellular response to ionizing radiation; cellular response to hydrogen peroxide; cellular response to reactive oxygen species; positive regulation of Rho GTPase activity; response to hydrogen peroxide; regulation of Rho GTPase activity; response to reactive oxygen species; induction of apoptosis by extracellular signals; cellular response to abiotic stimulus; Rho protein signal transduction; phospholipid binding; regulation of Ras GTPase activity; nerve growth factor receptor signaling pathway; regulation of GTPase activity; regulation of cell growth; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaGliomaGESurv
u*	NFE2L1	17:46125686-46138906 17q21.32	nuclear factor (erythroid-derived 2)-like 1 [Source:HGNC Symbol;Acc:7781], type=protein_coding, GO=[heme biosynthetic process; tetrapyrrole metabolic process; transcription cofactor activity; protein binding transcription factor activity]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianGE, tcgaOvarianMethyl
u	NFIB	9:14081842-14398982 9p22.3, 9p23	nuclear factor I/B [Source:HGNC Symbol;Acc:7785], type=processed_transcript,protein_coding, GO=[lung ciliated cell differentiation; negative regulation of epithelial cell proliferation involved in lung morphogenesis; regulation of mesenchymal cell proliferation involved in lung development; negative regulation of mesenchymal cell proliferation involved in lung development; principal sensory nucleus of trigeminal nerve development; trigeminal sensory nucleus development; cerebellar mossy fiber; Clara cell differentiation; Type I pneumocyte differentiation; anterior commissure morphogenesis; commissural neuron axon guidance; Type II pneumocyte differentiation; RNA polymerase II transcription corepressor activity; neural nucleus development; negative regulation of DNA binding; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in positive regulation of transcription; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; negative regulation of binding; chondrocyte differentiation; RNA polymerase II transcription factor binding transcription factor activity; regulation of organ morphogenesis; double-stranded DNA binding; cartilage development; sequence-specific DNA binding RNA polymerase II transcription factor activity; structure-specific DNA binding; epithelial cell proliferation; transcription cofactor activity; protein binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter; nucleolus; neuron projection]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	NFIL3	9:94171327-94186144 9q22.31	nuclear factor, interleukin 3 regulated [Source:HGNC Symbol;Acc:7787], type=protein_coding, GO=[RNA polymerase II core promoter sequence-specific DNA binding; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity involved in negative regulation of transcription; core promoter binding; RNA polymerase II core promoter proximal region sequence-specific DNA binding transcription factor activity; sequence-specific DNA binding RNA polymerase II transcription factor activity; rhythmic process; transcription cofactor activity; protein binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
d	NKD2	5:1008944-1039058 5p15.33	naked cuticle homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:17046], type=protein_coding,retained_intron, GO=[ubiquitin protein ligase binding; calcium ion binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeNSCLCa
u*	NPC1	18:21111401-21166451 18q11.2	Niemann-Pick disease, type C1 [Source:HGNC Symbol;Acc:7897], type=protein_coding, GO=[negative regulation of macroautophagy; cellular response to low-density lipoprotein particle stimulus; hedgehog receptor activity; sterol transporter activity; adult walking behavior; macroautophagy; cholesterol efflux; negative regulation of cellular catabolic process; lysosomal transport; bile acid metabolic process; cholesterol homeostasis; cholesterol transport; late endosome membrane; sterol transport; cellular response to starvation; autophagy; lysosomal membrane; membrane raft; response to drug; perinuclear region of cytoplasm; monocarboxylic acid metabolic process; regulation of cellular catabolic process; regulation of catabolic process; response to hormone stimulus]	tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
d	NPM3	10:103541082- 103543170 10q24.32	nucleophosmin/nucleoplasmin 3 [Source:HGNC Symbol;Acc:7931], type=processed_transcript,protein_coding, GO=[rRNA transcription; rRNA processing; ribosome biogenesis; nucleolus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeOvariand
u*	NSDHL	X:151999511-152038273 Xq28	NAD(P) dependent steroid dehydrogenase-like [Source:HGNC Symbol;Acc:13398], type=protein_coding, GO=[sterol-4-alpha-carboxylate 3-dehydrogenase (decarboxylating) activity; dTDP-4-dehydrorhamnose reductase activity; extracellular polysaccharide biosynthetic process; 3-beta-hydroxy-delta5-steroid dehydrogenase activity; labyrinthine layer blood vessel development; steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor; steroid dehydrogenase activity; cholesterol biosynthetic process; smoothened signaling pathway; hair follicle development; cellular polysaccharide biosynthetic process; placenta development; steroid biosynthetic process; blood vessel development; vasculature development; lipid biosynthetic process; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaBreastMethyl
u	NUDT16	3:131100515-131107674 3q22.1	nudix (nucleoside diphosphate linked moiety X)-type motif 16 [Source:HGNC Symbol;Acc:26442], type=protein_coding, GO=[nucleolus]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	OCEL1	19:17337055-17340027 19p13.11	occludin/ELL domain containing 1 [Source:HGNC Symbol;Acc:26221], type=protein_coding	tcgaBreastGE, tcgaColonGE, tcgaOvarianCGHa

Continued on next page. . .

S	name	locus	description	studies
u	OFD1	X:13752832-13787480 Xp22.2	oral-facial-digital syndrome 1 [Source:HGNC Symbol;Acc:2567], type=processed_transcript,protein_coding, GO=[cilium axoneme assembly; cilium movement involved in determination of left/right asymmetry; alpha-tubulin binding; gamma-tubulin binding; centriole; microtubule basal body; cilium; cytoskeletal protein binding; microtubule cytoskeleton]	tcgaColonMethyl, tcgaOvarianMethyl
u	OGFRL1	6:71998506-72011973 6q13	opioid growth factor receptor-like 1 [Source:HGNC Symbol;Acc:21378], type=processed_transcript,protein_coding	tcgaBreastGE, tcgaBreastGESurv, tcgaColonGE
u	OLAH	10:15074226-15115851 10p13	oleoyl-ACP hydrolase [Source:HGNC Symbol;Acc:25625], type=processed_transcript,protein_coding, GO=[palmitoyl-[acyl-carrier-protein] hydrolase activity; myristoyl-[acyl-carrier-protein] hydrolase activity; oleoyl-[acyl-carrier-protein] hydrolase activity; fatty acid synthase activity; fatty acid biosynthetic process; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process]	tcgaGliomaCGHd
u*	OSBPL5	11:3108346-3187969 11p15.4	oxysterol binding protein-like 5 [Source:HGNC Symbol;Acc:16392], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[oxysterol binding; cholesterol transport; sterol transport; phospholipid binding]	tcgaBreastMethyl, tcgaColonMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand
d	P2RY11	19:10222214-10226048 19p13.2	purinergic receptor P2Y, G-protein coupled, 11 [Source:HGNC Symbol;Acc:8540], type=processed_transcript,protein_coding, GO=[ATP-activated nucleotide receptor activity; neuronal signal transduction; cellular response to ATP; purinergic nucleotide receptor activity, G-protein coupled; nucleotide receptor activity, G-protein coupled; activation of phospholipase C activity by G-protein coupled receptor protein signaling pathway coupled to IP3 second messenger; activation of adenylate cyclase activity; neurotransmitter receptor activity; calcium-mediated signaling; activation of phospholipase C activity]	tscapeHCCd
u	PACSIN2	22:43231418-43411151 22q13.2	protein kinase C and casein kinase substrate in neurons 2 [Source:HGNC Symbol;Acc:8571], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[negative regulation of endocytosis; actin filament-based process; cytoskeletal protein binding]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHd, tcgaOvarianMethyl, tscapeGliomad, tscapeOvariand
u	PALLD	4:169418217-169849608 4q32.3	palladin, cytoskeletal associated protein [Source:HGNC Symbol;Acc:17068], type=protein_coding,retained_intron, GO=[muscle alpha-actinin binding; actinin binding; actin filament; Z disc; lamellipodium; focal adhesion; actin binding; cytoskeletal protein binding]	tcgaColonMethyl, tcgaGliomaGE, tscapeMelanomad, tscapeProstated, tscapeRCCd
d	PAQR4	16:3019246-3023490 16p13.3	progestin and adipoQ receptor family member IV [Source:HGNC Symbol;Acc:26386], type=protein_coding	tcgaBreastGE, tcgaColonGE, tscapeHCCd, tscapeOvariand
u	PDHA1	X:19362011-19379823 Xp22.12	pyruvate dehydrogenase (lipoamide) alpha 1 [Source:HGNC Symbol;Acc:8806], type=processed_transcript,protein_coding, GO=[pyruvate dehydrogenase activity; pyruvate dehydrogenase (acetyl-transferring) activity; acetyl-CoA biosynthetic process from pyruvate; regulation of acetyl-CoA biosynthetic process from pyruvate; mitochondrial matrix; monocarboxylic acid metabolic process]	tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
u*	PDLIM1	10:96997329-97050781 10q23.33, 10q24.1	PDZ and LIM domain 1 [Source:HGNC Symbol;Acc:2067], type=processed_transcript,protein_coding, GO=[response to hypoxia; response to oxygen levels; transcription coactivator activity; transcription factor complex; transcription cofactor activity; protein binding transcription factor activity]	tcgaBreastGE, tcgaColonGE, tcgaGliomaCGHd, tscapeCRCd
u*	PDLIM5	4:95373037-95589377 4q22.3	PDZ and LIM domain 5 [Source:HGNC Symbol;Acc:17468], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[regulation of dendritic spine morphogenesis; actinin binding; regulation of synapse assembly; protein kinase C binding; Z disc; synapse assembly; protein N-terminus binding; postsynaptic density; synaptosome; dendritic spine; postsynaptic membrane; synaptic membrane; protein kinase binding; actin binding; kinase binding; cytoskeletal protein binding; neuron projection]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
u	PEBP4	8:22570769-22857513 8p21.3	phosphatidylethanolamine-binding protein 4 [Source:HGNC Symbol;Acc:28319], type=processed_transcript,protein_coding	tcgaBreastGE, tscapeBCd, tscapeProstated
u*	PGF	14:75408537-75422487 14q24.3	placental growth factor [Source:HGNC Symbol;Acc:8893], type=processed_transcript,protein_coding,retained_intron, GO=[vascular endothelial growth factor receptor signaling pathway; regulation of morphogenesis of a branching structure; positive regulation of endothelial cell proliferation; branching involved in ureteric bud morphogenesis; heparin binding; female pregnancy; growth factor activity; glycosaminoglycan binding; pattern binding; polysaccharide binding; response to hypoxia; epithelial cell proliferation; response to oxygen levels; protein heterodimerization activity; response to drug; blood vessel development; protein homodimerization activity; vasculature development; response to hormone stimulus; extracellular space]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	PHACTR2	6:143857982-144152322 6q24.2	phosphatase and actin regulator 2 [Source:HGNC Symbol;Acc:20956], type=protein_coding,retained_intron, GO=[protein phosphatase inhibitor activity; enzyme inhibitor activity; actin binding; cytoskeletal protein binding]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tscapeOvariand
u	PHACTR3	20:58152564-58422766 20q13.32, 20q13.33	phosphatase and actin regulator 3 [Source:HGNC Symbol;Acc:15833], type=protein_coding,retained_intron, GO=[protein phosphatase inhibitor activity; nuclear matrix; enzyme inhibitor activity; actin binding; cytoskeletal protein binding]	cosmicRecurrent, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	PHLDA1	12:76419227-76427712 12q21.2	pleckstrin homology-like domain, family A, member 1 [Source:HGNC Symbol;Acc:8933], type=protein_coding, GO=[FasL biosynthetic process; mediator complex; RNA polymerase II transcription factor binding transcription factor activity; phospholipid binding; transcription cofactor activity; protein binding transcription factor activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	PHLDA2	11:2949503-2950685 11p15.4	pleckstrin homology-like domain, family A, member 2 [Source:HGNC Symbol;Acc:12385], type=protein_coding, GO=[phospholipid binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand
u*	PIAS1	15:68346517-68483096 15q23	protein inhibitor of activated STAT, 1 [Source:HGNC Symbol;Acc:2752], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[SUMO ligase activity; positive regulation of protein sumoylation; regulation of interferon-gamma-mediated signaling pathway; androgen receptor binding; androgen receptor signaling pathway; cellular response to interferon-gamma; steroid hormone receptor signaling pathway; response to interferon-gamma; ubiquitin protein ligase binding; nuclear speck; transcription coactivator activity; transcription cofactor activity; protein binding transcription factor activity; negative regulation of transcription from RNA polymerase II promoter]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d*	PIGK	1:77554675-77685115 1p31.1	phosphatidylinositol glycan anchor biosynthesis, class K [Source:HGNC Symbol;Acc:8965], type=processed_transcript,protein_coding, GO=[GPI-anchor transamidase complex; GPI-anchor transamidase activity; protein thiol-disulfide exchange; GPI anchor binding; attachment of GPI anchor to protein; C-terminal protein lipidation; intrinsic to endoplasmic reticulum membrane; glycerolipid biosynthetic process; phospholipid binding; lipid biosynthetic process; endoplasmic reticulum membrane]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeOvariand
d	PIGQ	16:616995-634136 16p13.3	phosphatidylinositol glycan anchor biosynthesis, class Q [Source:HGNC Symbol;Acc:14135], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[phosphatidylinositol N-acetylglucosaminyltransferase activity; glycosylphosphatidylinositol-N-acetylglucosaminyltransferase (GPI-GnT) complex; preassembly of GPI anchor in ER membrane; C-terminal protein lipidation; glycerolipid biosynthetic process; lipid biosynthetic process; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeHCCd
u	PITX1	5:134362615-134370503 5q31.1	paired-like homeodomain 1 [Source:HGNC Symbol;Acc:9004], type=protein_coding,retained_intron, GO=[branchiomeric skeletal muscle development; myoblast cell fate commitment; embryonic hindlimb morphogenesis; myoblast differentiation; pituitary gland development; cartilage development; transcription factor complex; protein binding transcription factor activity; nucleolus]	tcgaBreastGE, tcgaBreastMethyl
u	PLCXD1	X:192989-220023 Xp22.33	phosphatidylinositol-specific phospholipase C, X domain containing 1 [Source:HGNC Symbol;Acc:23148], type=processed_transcript,protein_coding, GO=[phospholipase C activity]	tcgaColonGE, tscapeNSCLCd, tscapeSCLCd
u	PLXNA1	3:126707437-126756235 3q21.3	plexin A1 [Source:HGNC Symbol;Acc:9099], type=processed_transcript,protein_coding,retained_intron, GO=[dichotomous subdivision of terminal units involved in salivary gland branching; semaphorin receptor complex; semaphorin receptor activity; semaphorin-plexin signaling pathway]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE

Continued on next page...

S	name	locus	description	studies
u	PLXNB2	22:50713408-50746056 22q13.33	plexin B2 [Source:HGNC Symbol;Acc:9104], type=processed_transcript,protein_coding,retained_intron, GO=[semaphorin receptor activity; semaphorin-plexin signaling pathway; neuroblast proliferation; positive regulation of axonogenesis; neural tube closure; regulation of cell shape; regulation of Rho GTPase activity; Rho protein signal transduction; regulation of Ras GTPase activity; GTPase activator activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianCGHd, tscapeBCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
d	PNMA3	X:152224766-152228827 Xq28	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:18742], type=nonsense_mediated_decay,protein_coding, GO=[nucleolus]	tcgaBreastGE, tcgaBreastGESurv, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	PPA1	10:71962587-71993667 10q22.1	pyrophosphatase (inorganic) 1 [Source:HGNC Symbol;Acc:9226], type=processed_transcript,protein_coding, GO=[diphosphate metabolic process; inorganic diphosphatase activity; magnesium ion binding]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
d	PPAN	19:10216965-10225414 19p13.2	peter pan homolog (Drosophila) [Source:HGNC Symbol;Acc:9227], type=protein_coding,retained_intron	tcgaOvarianMethyl, tscapeHCCd
d	PPAN-P2RY11	19:10216899-10225456 19p13.2	PPAN-P2RY11 readthrough [Source:HGNC Symbol;Acc:33526], type=protein_coding	tscapeHCCd
u*	PPL	16:4932508-4987136 16p13.3	periplakin [Source:HGNC Symbol;Acc:9273], type=protein_coding, GO=[desmosome; keratinization; structural constituent of cytoskeleton]	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
u	PPP1R14C	6:150464212-150571493 6q25.1	protein phosphatase 1, regulatory (inhibitor) subunit 14C [Source:HGNC Symbol;Acc:14952], type=protein_coding, GO=[protein serine/threonine phosphatase inhibitor activity; protein phosphatase inhibitor activity; enzyme inhibitor activity]	tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl, tscapeOvariand
u	PPTC7	12:110969120-111021125 12q24.11	PTC7 protein phosphatase homolog (S. cerevisiae) [Source:HGNC Symbol;Acc:30695], type=protein_coding,retained_intron	tcgaBreastGE, tcgaColonGE, tcgaGliomaGE
u	PQLC1	18:77662420-77711664 18q23	PQ loop repeat containing 1 [Source:HGNC Symbol;Acc:26188], type=processed_transcript,protein_coding,retained_intron	tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomad, tscapeProstated
d	PRAC	17:46799084-46799884 17q21.32	prostate cancer susceptibility candidate [Source:HGNC Symbol;Acc:30591], type=protein_coding	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	PRDX6	1:173446405-173457946 1q25.1	peroxiredoxin 6 [Source:HGNC Symbol;Acc:16753], type=processed_transcript,protein_coding, GO=[peroxiredoxin activity; glutathione peroxidase activity; hydrogen peroxide catabolic process; phospholipase A2 activity; phospholipid catabolic process; cellular response to hydrogen peroxide; cellular response to reactive oxygen species; response to hydrogen peroxide; reactive oxygen species metabolic process; response to reactive oxygen species]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCa
u*	PRKAB2	1:146626685-146644129 1q21.1	protein kinase, AMP-activated, beta 2 non-catalytic subunit [Source:HGNC Symbol;Acc:9379], type=processed_transcript,protein_coding, GO=[AMP-activated protein kinase complex; AMP-activated protein kinase activity; carnitine shuttle; cAMP-dependent protein kinase complex; regulation of fatty acid biosynthetic process; regulation of fatty acid oxidation; fatty acid oxidation; fatty acid biosynthetic process; insulin receptor signaling pathway; apical plasma membrane; cellular response to insulin stimulus; apical part of cell; response to insulin stimulus; fatty acid metabolic process; protein kinase binding; kinase binding; monocarboxylic acid metabolic process; negative regulation of cell cycle; lipid biosynthetic process; regulation of cell cycle; response to hormone stimulus]	cosmicRecurrent, tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeCRCa
u*	PRKCE	2:45878484-46415129 2p21	protein kinase C, epsilon [Source:HGNC Symbol;Acc:9401], type=processed_transcript,protein_coding, GO=[TRAM-dependent toll-like receptor 4 signaling pathway; TRAM-dependent toll-like receptor signaling pathway; ethanol binding; calcium-independent protein kinase C activity; positive regulation of mucus secretion; cellular response to ethanol; locomotory exploration behavior; regulation of fibroblast migration; positive regulation of fibroblast migration; positive regulation of wound healing; positive regulation of synaptic transmission, GABAergic; 14-3-3 protein binding; macrophage activation involved in immune response; actin monomer binding; positive regulation of cell cycle cytokinesis; regulation of cell cycle cytokinesis; positive regulation of epithelial cell migration; insulin secretion involved in cellular response to glucose stimulus; regulation of insulin secretion involved in cellular response to glucose stimulus; positive regulation of receptor activity; receptor activator activity; positive regulation of lipid catabolic process; response to morphine; response to isoquinoline alkaloid; cell cycle cytokinesis; positive regulation of actin filament polymerization; positive regulation of insulin secretion; macrophage activation; cellular response to hypoxia; release of sequestered calcium ion into cytosol; positive regulation of cell-substrate adhesion; cytosolic calcium ion transport; regulation of actin filament polymerization; actin filament polymerization; response to alkaloid; cytokinesis; fibroblast growth factor receptor signaling pathway; response to glucose stimulus; activation of phospholipase C activity; actin polymerization or depolymerization; epidermal growth factor receptor signaling pathway; SH3 domain binding; regulation of peptidyl-tyrosine phosphorylation; response to carbohydrate stimulus; positive regulation of I-kappaB kinase/NF-kappaB cascade; regulation of I-kappaB kinase/NF-kappaB cascade; regulation of actin filament-based process; positive regulation of MAPKKK cascade; actin filament organization; I-kappaB kinase/NF-kappaB cascade; response to lipopolysaccharide; response to hypoxia; nerve growth factor receptor signaling pathway; response to organic cyclic compound; response to oxygen levels; platelet activation; protein kinase binding; actin binding; kinase binding; regulation of cell motility; regulation of cellular component movement; perinuclear region of cytoplasm; actin filament-based process; MAPKKK cascade; regulation of catabolic process; cytoskeletal protein binding; regulation of cell cycle]	snp3dGlioma, snp3dLungC, snp3dProstateC, tcgaBreastMethyl, tcgaColonGE, tcgaGliomaGE, tcgaOvarianMethyl
u*	PROS1	3:93591881-93692910 3q11.1	protein S (alpha) [Source:HGNC Symbol;Acc:9456], type=protein_coding,retained_intron, GO=[peptidyl-glutamic acid carboxylation; fibrinolysis; Golgi lumen; platelet alpha granule lumen; negative regulation of endopeptidase activity; platelet degranulation; endopeptidase inhibitor activity; regulation of endopeptidase activity; platelet activation; enzyme inhibitor activity; calcium ion binding; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	PRPS2	X:12809474-12842341 Xp22.2	phosphoribosyl pyrophosphate synthetase 2 [Source:HGNC Symbol;Acc:9465], type=processed_transcript,protein_coding, GO=[ribose phosphate diphosphokinase activity; AMP biosynthetic process; ribose phosphate metabolic process; ADP binding; GDP binding; AMP binding; organ regeneration; regeneration; magnesium ion binding; sugar binding; soluble fraction; protein homodimerization activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
u	PSCA	8:143751726-143764142 8q24.3	prostate stem cell antigen [Source:HGNC Symbol;Acc:9500], type=processed_transcript,protein_coding, GO=[anchored to membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl
u	PTPLA	10:17631958-17659376 10p12.33	protein tyrosine phosphatase-like (proline instead of catalytic arginine), member A [Source:HGNC Symbol;Acc:9639], type=processed_transcript,protein_coding, GO=[peptidyl-tyrosine dephosphorylation; fatty acid biosynthetic process; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl
d	RAB17	2:238482965-238510257 2q37.3	RAB17, member RAS oncogene family [Source:HGNC Symbol;Acc:16523], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[GTPase activity; GTP binding; nucleocytoplasmic transport; GTP catabolic process; small GTPase mediated signal transduction]	tscapeBCd, tscapeMelanomad, tscapeOvariand, tscapeRCCd
u	RALY	20:32581452-32696114 20q11.22	RNA binding protein, autoantigenic (hnRNP-associated with lethal yellow homolog (mouse)) [Source:HGNC Symbol;Acc:15921], type=processed_transcript,protein_coding,retained_intron, GO=[heterogeneous nuclear ribonucleoprotein complex; catalytic step 2 spliceosome]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d*	RANGAP1	22:41641615-41698963 22q13.2	Ran GTPase activating protein 1 [Source:HGNC Symbol;Acc:9854], type=processed_transcript,protein_coding, GO=[Ran GTPase activator activity; regulation of Ran GTPase activity; regulation of Ran protein signal transduction; Ran protein signal transduction; positive regulation of Ran GTPase activity; negative regulation of protein export from nucleus; nuclear pore; condensed chromosome kinetochore; spindle pole; mitotic prometaphase; Ras GTPase activator activity; nuclear membrane; spindle; regulation of Ras GTPase activity; GTPase activator activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; soluble fraction; perinuclear region of cytoplasm; nucleocytoplasmic transport; Ras protein signal transduction; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction; microtubule cytoskeleton]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
d	RAP1GAP	1:21922708-21995856 1p36.12	RAP1 GTPase activating protein [Source:HGNC Symbol;Acc:9858], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[regulation of Ras GTPase activity; GTPase activator activity; GTPase activity; regulation of GTPase activity; regulation of purine nucleotide catabolic process; regulation of nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; protein homodimerization activity; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaGliomaGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd
u	RASD1	17:17397751-17399707 17p11.2	RAS, dexamethasone-induced 1 [Source:HGNC Symbol;Acc:15828], type=protein_coding, GO=[nitric oxide mediated signal transduction; GTPase activity; GTP binding; soluble fraction; perinuclear region of cytoplasm; nucleocytoplasmic transport; GTP catabolic process; small GTPase mediated signal transduction]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	RBBP7	X:16857406-16888537 Xp22.2	retinoblastoma binding protein 7 [Source:HGNC Symbol;Acc:9890], type=protein_coding,retained_intron, GO=[cellular heat acclimation; heat acclimation; ESC/E(Z) complex; NuRD complex; DNA replication-independent nucleosome assembly; CenH3-containing nucleosome assembly at centromere; negative regulation of cell growth; nucleosome assembly; regulation of cell growth; negative regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
u	RCL1	9:4792869-4861064 9p24.1	RNA terminal phosphate cyclase-like 1 [Source:HGNC Symbol;Acc:17687], type=processed_transcript,protein_coding, GO=[RNA-3'-phosphate cyclase activity; ribosome biogenesis; nucleolus]	tcgaOvarianMethyl, tscapeBCd
u	RETSAT	2:85569211-85581743 2p11.2	retinol saturase (all-trans-retinol 13,14-reductase) [Source:HGNC Symbol;Acc:25991], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[all-trans-retinol 13,14-reductase activity; retinol metabolic process; nuclear outer membrane; diterpenoid metabolic process; secondary metabolic process; nuclear membrane; electron carrier activity; endoplasmic reticulum membrane]	cosmicRecurrent
u	RGCC	13:42031695-42045018 13q14.11	regulator of cell cycle [Source:HGNC Symbol;Acc:20369], type=processed_transcript,protein_coding, GO=[regulation of cyclin-dependent protein kinase activity; regulation of protein serine/threonine kinase activity; nucleolus; regulation of cell cycle; microtubule cytoskeleton]	tcgaBreastGE, tcgaColonGE
u*	RGS19	20:62704534-62711323 20q13.33	regulator of G-protein signaling 19 [Source:HGNC Symbol;Acc:13735], type=processed_transcript,protein_coding, GO=[G-protein alpha-subunit binding; heterotrimeric G-protein complex; brush border; extrinsic to plasma membrane; autophagy; extrinsic to membrane; GTPase activator activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeNSCLCa
u*	RHOB	2:20646835-20649200 2p24.1	ras homolog family member B [Source:HGNC Symbol;Acc:668], type=protein_coding, GO=[transformed cell apoptosis; endosome to lysosome transport; GDP binding; cell cycle cytokinesis; cellular response to ionizing radiation; cleavage furrow; lysosomal transport; cellular response to hydrogen peroxide; late endosome membrane; cellular response to reactive oxygen species; positive regulation of angiogenesis; response to hydrogen peroxide; cytokinesis; response to reactive oxygen species; cellular response to abiotic stimulus; Rho protein signal transduction; platelet activation; GTPase activity; GTP binding; soluble fraction; Ras protein signal transduction; negative regulation of cell cycle; blood vessel development; vasculature development; GTP catabolic process; small GTPase mediated signal transduction; regulation of cell cycle]	tcgaOvarianMethyl, tscapeNSCLCd, tscapeOvariand
d*	RHPN2	19:33469499-33555824 19q13.11	rhophilin, Rho GTPase binding protein 2 [Source:HGNC Symbol;Acc:19974], type=protein_coding, GO=[perinuclear region of cytoplasm]	cosmicPrimary, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	RIT1	1:155867599-155881195 1q22	Ras-like without CAAX 1 [Source:HGNC Symbol;Acc:10023], type=processed_transcript,protein_coding, GO=[calmodulin binding; nerve growth factor receptor signaling pathway; GTPase activity; GTP binding; nucleocytoplasmic transport; GTP catabolic process; small GTPase mediated signal transduction]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl, tscapeHCCa, tscapeProstated
u	RNASE12	14:21058352-21058982 14q11.2	ribonuclease-like protein 12 precursor [Source:RefSeq peptide;Acc:NP_001019993], type=protein_coding, GO=[pancreatic ribonuclease activity]	
u	RNASE12	14:21058439-21058882 14q11.2	ribonuclease, RNase A family, 12 (non-active) [Source:HGNC Symbol;Acc:24211], type=protein_coding, GO=[pancreatic ribonuclease activity]	
u	RNASE4	14:21152259-21168761 14q11.2	Ribonuclease 4 [Source:UniProtKB/Swiss-Prot;Acc:P34096], type=protein_coding, GO=[pancreatic ribonuclease activity; mRNA cleavage]	
u	RNASE4	14:21152372-21168757 14q11.2	ribonuclease, RNase A family, 4 [Source:HGNC Symbol;Acc:10047], type=protein_coding, GO=[pancreatic ribonuclease activity; mRNA cleavage]	
u	RNF115	1:145611036-145690661 1q21.1	ring finger protein 115 [Source:HGNC Symbol;Acc:18154], type=nonsense_mediated_decay,protein_coding, GO=[protein autoubiquitination; ubiquitin-protein ligase activity]	tcgaBreastGE
d	RNF220	1:44870866-45117396 1p34.1	ring finger protein 220 [Source:HGNC Symbol;Acc:25552], type=processed_transcript,protein_coding, GO=[protein autoubiquitination; ubiquitin-protein ligase activity]	tcgaGliomaGE
u	RP1-130H16.18	22:30681227-30695471 22q12.2	Uncharacterized protein [Source:UniProtKB/TrEMBL;Acc:H0Y2U5], type=nonsense_mediated_decay,protein_coding, GO=[Rab GTPase activator activity; regulation of Rab GTPase activity; Ras GTPase activator activity; regulation of Ras GTPase activity; GTPase activator activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	
d	RP1-256G22.1	6:5609460-5610428 6p25.1	[undefined], type=processed_pseudogene,pseudogene	
u	RP11-125K10.4	9:4860454-4885917 9p24.1	[undefined], type=processed_transcript	
d	RP11-167H9.6	3:149956306-149957996 3q25.1	[undefined], type=lincRNA	
u	RP11-259O2.2	5:1963723-1967268 5p15.33	[undefined], type=lincRNA	
d	RP11-350O14.18	9:140063306-140066436 9q34.3	[undefined], type=processed_transcript	
u	RP11-397D21.1	4:114761206-114761392 4q26	[undefined], type=processed_pseudogene,pseudogene	
u	RP11-796E2.3	12:92537962-92539009 12q21.33	[undefined], type=3prime_overlapping_ncrna	
u	RP11-802E16.3	11:67818207-67821229 11q13.2	[undefined], type=processed_transcript	
u	RP5-955M13.3	20:49620194-49624577 20q13.13	[undefined], type=processed_transcript	
d	RPUSD1	16:834974-838397 16p13.3	RNA pseudouridylate synthase domain containing 1 [Source:HGNC Symbol;Acc:14173], type=nonsense_mediated_decay,protein_coding, GO=[pseudouridine synthase activity; pseudouridine synthesis]	tcgaBreastGE, tcgaBreastMethyl, tscapeHCCd
u	RRAS	19:50138552-50143400 19q13.33	related RAS viral (r-ras) oncogene homolog [Source:HGNC Symbol;Acc:10447], type=protein_coding, GO=[GDP binding; negative regulation of cell migration; GTPase activity; GTP binding; regulation of cell motility; regulation of cellular component movement; nucleocytoplasmic transport; Ras protein signal transduction; GTP catabolic process; small GTPase mediated signal transduction]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianGE, tcgaOvarianMethyl, tscapeOvariand
u	S100A10	1:151955391-151966866 1q21.3	S100 calcium binding protein A10 [Source:HGNC Symbol;Acc:10487], type=processed_transcript,protein_coding, GO=[cellular response to acid; positive regulation of binding; extrinsic to plasma membrane; extrinsic to membrane; calcium ion binding]	tcgaColonGE, tcgaGliomaGE, tscapeHCCa, tscapeMelanomaa
u	S1PR3	9:91606362-91619925 9q22.1	sphingosine-1-phosphate receptor 3 [Source:HGNC Symbol;Acc:3167], type=protein_coding, GO=[regulation of interleukin-1 beta production; inhibition of adenylate cyclase activity by G-protein signaling pathway]	tcgaGliomaGE
d	SAPCD2	9:139956581-139965040 9q34.3	suppressor APC domain containing 2 [Source:HGNC Symbol;Acc:28055], type=protein_coding, GO=[nucleolus]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u*	SAR1B	5:133934233-133984961 5q31.1	SAR1 homolog B (S. cerevisiae) [Source:HGNC Symbol;Acc:10535], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[vesicle targeting, rough ER to cis-Golgi; COPII vesicle coating; ER to Golgi transport vesicle membrane; vesicle targeting, to, from or within Golgi; vesicle coating; Golgi cisterna membrane; Golgi cisterna; antigen processing and presentation of peptide antigen via MHC class I; protein N-linked glycosylation via asparagine; peptidyl-asparagine modification; antigen processing and presentation; GTPase activity; GTP binding; GTP catabolic process; endoplasmic reticulum membrane; small GTPase mediated signal transduction]	tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd

Continued on next page...

S	name	locus	description	studies
u*	SCAP	3:47455184-47518616 3p21.31	SREBF chaperone [Source:HGNC Symbol;Acc:30634], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[positive regulation of transcription via sterol regulatory element binding involved in ER-nuclear sterol response pathway; positive regulation of low-density lipoprotein particle receptor biosynthetic process; negative regulation of cholesterol biosynthetic process; hedgehog receptor activity; ER to Golgi transport vesicle membrane; regulation of fatty acid biosynthetic process; cholesterol biosynthetic process; unfolded protein binding; fatty acid biosynthetic process; steroid biosynthetic process; response to hypoxia; response to oxygen levels; response to insulin stimulus; microsome; fatty acid metabolic process; monocarboxylic acid metabolic process; lipid biosynthetic process; endoplasmic reticulum membrane; response to hormone stimulus]	tcgaColonMethyl, tcgaOvarianMethyl
u*	SCNN1A	12:6456009-6486896 12p13.31	sodium channel, non-voltage-gated 1 alpha subunit [Source:HGNC Symbol;Acc:10599], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[ligand-gated sodium channel activity; WW domain binding; sodium ion transmembrane transport; cortical actin cytoskeleton; sensory perception of taste; excretion; external side of plasma membrane; apical plasma membrane; apical part of cell; actin binding; cell surface; cytoskeletal protein binding]	cosmicRecurrent, tcgaBreastGE, tcgaOvarianCGHa, tcgaOvarianMethyl
u*	SCNN1G	16:23194036-23228204 16p12.2	sodium channel, non-voltage-gated 1, gamma subunit [Source:HGNC Symbol;Acc:10602], type=protein_coding, GO=[ligand-gated sodium channel activity; wound healing, spreading of epidermal cells; wound healing, spreading of cells; WW domain binding; sodium ion transmembrane transport; sensory perception of taste; excretion; external side of plasma membrane; apical plasma membrane; response to hypoxia; response to oxygen levels; apical part of cell; cell surface]	
d	SEMA6A	5:115779312-115910630 5q23.1	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A [Source:HGNC Symbol;Acc:10738], type=processed_transcript,protein_coding,retained_intron, GO=[semaphorin receptor binding; centrosome localization; semaphorin-plexin signaling pathway; neuron migration; neuron projection]	tcgaBreastGE, tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated
u	SEPT11	4:77870856-77961537 4q21.1	septin 11 [Source:HGNC Symbol;Acc:25589], type=processed_transcript,protein_coding,retained_intron, GO=[septin complex; stress fiber; actin filament bundle; dendritic spine; GTP binding; neuron projection]	tcgaGliomaGE, tscapeHCCd
d	SEPT3	22:42372276-42394225 22q13.2	septin 3 [Source:HGNC Symbol;Acc:10750], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[septin complex; presynaptic membrane; cytokinesis; synaptosome; synaptic membrane; GTPase activity; GTP binding]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianGE, tscapeGliomad
u*	SERPINA3	14:95058395-95090983 14q32.13	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 [Source:HGNC Symbol;Acc:16], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[maintenance of gastrointestinal epithelium; acute-phase response; negative regulation of endopeptidase activity; serine-type endopeptidase inhibitor activity; endopeptidase inhibitor activity; regulation of endopeptidase activity; enzyme inhibitor activity]	tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
u*	SHC1	1:154934774-154946871 1q21.3	SHC (Src homology 2 domain containing) transforming protein 1 [Source:HGNC Symbol;Acc:10840], type=processed_transcript,protein_coding, GO=[Shc-EGFR complex; activation of signaling protein activity involved in unfolded protein response; neurotrophin TRK receptor binding; neurotrophin TRKA receptor binding; transmembrane receptor protein tyrosine kinase adaptor activity; insulin-like growth factor receptor binding; phosphotyrosine binding; epidermal growth factor receptor binding; positive regulation of vasoconstriction; regulation of epidermal growth factor-activated receptor activity; ephrin receptor binding; insulin receptor binding; response to nicotine; positive regulation of smooth muscle cell proliferation; regulation of protein tyrosine kinase activity; positive regulation of DNA replication; regulation of vasoconstriction; organ regeneration; regulation of smooth muscle cell proliferation; smooth muscle cell proliferation; response to hydrogen peroxide; response to alkaloid; regulation of DNA replication; fibroblast growth factor receptor signaling pathway; epidermal growth factor receptor signaling pathway; response to toxin; response to reactive oxygen species; activation of MAPK activity; regeneration; insulin receptor signaling pathway; positive regulation of MAP kinase activity; positive regulation of protein serine/threonine kinase activity; cellular response to insulin stimulus; phospholipid binding; response to hypoxia; nerve growth factor receptor signaling pathway; response to organic cyclic compound; response to oxygen levels; mitochondrial matrix; platelet activation; response to insulin stimulus; regulation of protein serine/threonine kinase activity; actin filament-based process; Ras protein signal transduction; MAPKKK cascade; blood vessel development; vasculature development; small GTPase mediated signal transduction; response to hormone stimulus]	fileAmpOver, tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCa
u	SIPA1L2	1:232533711-232697304 1q42.2	signal-induced proliferation-associated 1 like 2 [Source:HGNC Symbol;Acc:23800], type=processed_transcript,protein_coding, GO=[GTPase activator activity; small GTPase mediated signal transduction]	tcgaBreastGE, tcgaColonGE, tscapeBCa, tscapeOvariana, tscapeProstated
u	SLC10A1	14:70242134-70264006 14q24.2	solute carrier family 10 (sodium/bile acid cotransporter family), member 1 [Source:HGNC Symbol;Acc:10905], type=protein_coding, GO=[bile acid:sodium symporter activity; bile acid and bile salt transport; bile acid metabolic process; organic anion transport; metal ion transmembrane transporter activity; anion transport; monocarboxylic acid metabolic process]	tcgaBreastMethyl
u	SLC22A23	6:3269196-3457256 6p25.2	solute carrier family 22, member 23 [Source:HGNC Symbol;Acc:21106], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaColonGE, tscapeOvariana, tscapeSCLCd
u	SLC25A18	22:18043139-18073647 22q11.21	solute carrier family 25 (mitochondrial carrier), member 18 [Source:HGNC Symbol;Acc:10988], type=processed_transcript,protein_coding,retained_intron, GO=[mitochondrial inner membrane]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	SLC27A3	1:153746830-153752633 1q21.3	solute carrier family 27 (fatty acid transporter), member 3 [Source:HGNC Symbol;Acc:10997], type=processed_transcript,protein_coding,retained_intron, GO=[fatty-acyl-CoA synthase activity; fatty acid metabolic process; monocarboxylic acid metabolic process]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	SLC2A5	1:9095166-9148537 1p36.23	solute carrier family 2 (facilitated glucose/fructose transporter), member 5 [Source:HGNC Symbol;Acc:11010], type=processed_transcript,protein_coding, GO=[fructose transmembrane transporter activity; fructose transport; glucose transmembrane transporter activity; glucose transport]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
d	SLC2A6	9:136336217-136344259 9q34.2	solute carrier family 2 (facilitated glucose transporter), member 6 [Source:HGNC Symbol;Acc:11011], type=processed_transcript,protein_coding, GO=[glucose transmembrane transporter activity; glucose transport]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE
u	SLC30A1	1:211744910-211752084 1q32.3	solute carrier family 30 (zinc transporter), member 1 [Source:HGNC Symbol;Acc:11012], type=protein_coding, GO=[negative regulation of zinc ion transmembrane transport; regulation of zinc ion transport; regulation of zinc ion transmembrane transport; regulation of zinc ion import; negative regulation of zinc ion transport; negative regulation of zinc ion import; negative regulation of calcium ion import; negative regulation of neurotransmitter secretion; detoxification of cadmium ion; zinc ion import; cadmium ion transport; cadmium ion transmembrane transport; calcium channel inhibitor activity; zinc ion transmembrane transporter activity; cellular zinc ion homeostasis; T-tubule; response to cadmium ion; sarcolemma; response to toxin; metal ion transmembrane transporter activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	SLC31A2	9:115913222-115926417 9q32	solute carrier family 31 (copper transporters), member 2 [Source:HGNC Symbol;Acc:11017], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[copper ion transmembrane transporter activity; copper ion transmembrane transport; metal ion transmembrane transporter activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaOvarianMethyl
u	SLC38A2	12:46751972-46766650 12q13.11	solute carrier family 38, member 2 [Source:HGNC Symbol;Acc:13448], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[glutamate secretion]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeRCCa, tscapeSCLCa
u	SLC39A11	17:70642086-71088853 17q24.3, 17q25.1	solute carrier family 39 (metal ion transporter), member 11 [Source:HGNC Symbol;Acc:14463], type=protein_coding, GO=[metal ion transmembrane transporter activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	SLC39A14	8:22224762-22291642 8p21.3	solute carrier family 39 (zinc transporter), member 14 [Source:HGNC Symbol;Acc:20858], type=protein_coding,retained_intron, GO=[zinc ion import; zinc ion transmembrane transporter activity; cellular zinc ion homeostasis; ferrous iron transmembrane transporter activity; ferrous iron transport; lamellipodium; metal ion transmembrane transporter activity]	tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHd, tscapeProstated
u	SLC44A3	1:95285898-95360802 1p21.3	solute carrier family 44, member 3 [Source:HGNC Symbol;Acc:28689], type=nonsense_mediated_decay,processed_transcript,protein_coding	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad, tscapeNSCLCd

Continued on next page...

S	name	locus	description	studies
u	SLC4A7	3:27414214-27525911 3p24.1	solute carrier family 4, sodium bicarbonate cotransporter, member 7 [Source:HGNC Symbol;Acc:11033], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[cochlear nucleus development; sodium:bicarbonate symporter activity; retina vasculature morphogenesis in camera-type eye; retinal cell programmed cell death; auditory receptor cell development; inorganic anion exchanger activity; neural nucleus development; bicarbonate transport; stereocilium; developmental programmed cell death; auditory receptor cell differentiation; organic anion transport; inorganic anion transport; metal ion transmembrane transporter activity; anion transport; apical plasma membrane; apical part of cell; vasculature development]	tcgaColonGE, tcgaGliomaGE
u	SLC5A6	2:27422455-27435826 2p23.3	solute carrier family 5 (sodium-dependent vitamin transporter), member 6 [Source:HGNC Symbol;Acc:11041], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[pantothenate transmembrane transport; biotin transport; sodium-dependent multivitamin transmembrane transporter activity; biotin metabolic process; modified amino acid transport; pantothenate metabolic process; cellular amide metabolic process; brush border membrane; brush border; metal ion transmembrane transporter activity; monocarboxylic acid metabolic process]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	SLCO4A1	20:61273797-61317137 20q13.33	solute carrier organic anion transporter family, member 4A1 [Source:HGNC Symbol;Acc:10953], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[thyroid hormone transmembrane transporter activity; thyroid hormone transport; modified amino acid transport; sodium-independent organic anion transport; thyroid hormone metabolic process; organic anion transport; anion transport]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianCGHa, tcgaOvarianMethyl, tscapeBCa
u	SLPI	20:43880880-43883205 20q13.12	secretory leukocyte peptidase inhibitor [Source:HGNC Symbol;Acc:11092], type=protein_coding, GO=[negative regulation of viral genome replication; negative regulation of protein binding; negative regulation of binding; negative regulation of endopeptidase activity; serine-type endopeptidase inhibitor activity; endopeptidase inhibitor activity; regulation of endopeptidase activity; enzyme inhibitor activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCd
d	SNORD97	11:10823014-10823155 11p15.3	small nucleolar RNA, C/D box 97 [Source:HGNC Symbol;Acc:32760], type=snoRNA	
u	SNX33	15:75940247-75954642 15q24.2	sorting nexin 33 [Source:HGNC Symbol;Acc:28468], type=protein_coding, GO=[phospholipid binding]	tcgaColonGE, tcgaGliomaGE
u*	SOCS1	16:11348262-11350036 16p13.13	suppressor of cytokine signaling 1 [Source:HGNC Symbol;Acc:19383], type=protein_coding, GO=[negative regulation of tyrosine phosphorylation of Stat3 protein; JAK-STAT cascade involved in growth hormone signaling pathway; insulin-like growth factor receptor binding; negative regulation of insulin receptor signaling pathway; regulation of interferon-gamma-mediated signaling pathway; response to progesterone stimulus; regulation of insulin receptor signaling pathway; regulation of tyrosine phosphorylation of Stat3 protein; regulation of type I interferon-mediated signaling pathway; cellular response to amino acid stimulus; protein kinase inhibitor activity; cellular response to acid; cellular response to amine stimulus; regulation of tyrosine phosphorylation of STAT protein; organ regeneration; response to amino acid stimulus; type I interferon-mediated signaling pathway; cellular response to interferon-gamma; response to interferon-gamma; response to estradiol stimulus; negative regulation of intracellular protein kinase cascade; regulation of peptidyl-tyrosine phosphorylation; regeneration; insulin receptor signaling pathway; cellular response to insulin stimulus; response to lipopolysaccharide; response to insulin stimulus; enzyme inhibitor activity; protein kinase binding; kinase binding; response to drug; response to hormone stimulus]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	SPINK13	5:147647743-147665817 5q32	serine peptidase inhibitor, Kazal type 13 (putative) [Source:HGNC Symbol;Acc:27200], type=protein_coding, GO=[serine-type endopeptidase inhibitor activity; endopeptidase inhibitor activity; enzyme inhibitor activity]	
u	SPRYD5	11:55650773-55659286 11q11	SPRY domain containing 5 [Source:HGNC Symbol;Acc:19023], type=protein_coding	cosmicPrimary
u	SPSB1	1:9352939-9429591 1p36.22	splA/ryanodine receptor domain and SOCS box containing 1 [Source:HGNC Symbol;Acc:30628], type=protein_coding	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeCRCd, tscapeHCCd, tscapeNSCLCd, tscapeOvariana, tscapeOvariand, tscapeRCCd
u	SRD5A1	5:6633456-6669675 5p15.31	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) [Source:HGNC Symbol;Acc:11284], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[amide binding; 3-oxo-5-alpha-steroid 4-dehydrogenase activity; cellular response to epinephrine stimulus; response to epinephrine stimulus; cellular response to testosterone stimulus; cell body fiber; female genitalia development; NADPH binding; response to muscle activity; cellular response to estradiol stimulus; serotonin metabolic process; circadian sleep/wake cycle, REM sleep; response to follicle-stimulating hormone stimulus; response to fungicide; thalamus development; progesterone metabolic process; androgen biosynthetic process; cellular response to dexamethasone stimulus; hypothalamus development; cellular response to cAMP; sex determination; male genitalia development; myelin sheath; steroid dehydrogenase activity; diterpenoid metabolic process; C21-steroid hormone metabolic process; cellular response to amine stimulus; pituitary gland development; cellular response to organic cyclic compound; hippocampus development; cerebral cortex development; cellular response to starvation; response to cAMP; secondary metabolic process; spinal cord development; liver development; response to estradiol stimulus; development of primary female sexual characteristics; response to toxin; steroid biosynthetic process; electron carrier activity; rhythmic process; cellular response to insulin stimulus; response to organic cyclic compound; response to insulin stimulus; microsome; neuronal cell body; response to drug; perinuclear region of cytoplasm; lipid biosynthetic process; neuron projection; endoplasmic reticulum membrane; response to hormone stimulus]	tcgaColonMethyl
u*	SSR1	6:7268539-7347679 6p24.3	signal sequence receptor, alpha [Source:HGNC Symbol;Acc:11323], type=processed_transcript,protein_coding, GO=[activation of signaling protein activity involved in unfolded protein response; SRP-dependent cotranslational protein targeting to membrane; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariana, tscapeProstated, tscapeSCLCd
u	SSX2IP	1:85109390-85156486 1p22.3	synovial sarcoma, X breakpoint 2 interacting protein [Source:HGNC Symbol;Acc:16509], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[cell-cell adherens junction]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeGliomad
u*	STAT3	17:40465342-40540449 17q21.2	signal transducer and activator of transcription 3 (acute-phase response factor) [Source:HGNC Symbol;Acc:11364], type=processed_transcript,protein_coding,retained_intron, GO=[CCR5 chemokine receptor binding; JAK-STAT cascade involved in growth hormone signaling pathway; radial glial cell differentiation; interleukin-6-mediated signaling pathway; glucocorticoid receptor binding; positive regulation of Notch signaling pathway; response to interleukin-6; regulation of Notch signaling pathway; eating behavior; temperature homeostasis; eye photoreceptor cell differentiation; non-membrane spanning protein tyrosine kinase activity; acute-phase response; response to estradiol stimulus; nerve growth factor receptor signaling pathway; response to organic cyclic compound; protein kinase binding; kinase binding; response to drug; nucleocytoplasmic transport; negative regulation of transcription from RNA polymerase II promoter; calcium ion binding; response to hormone stimulus]	snp3dGlioma, snp3dMetastasis, tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaGliomaGESurv, tcgaOvarianMethyl, tscapeBCd, tscapeOvariand
d	STC2	5:172741716-172756506 5q35.1	stanniocalcin 2 [Source:HGNC Symbol;Acc:11374], type=processed_transcript,protein_coding,retained_intron, GO=[decidualization; response to vitamin D; embryo implantation; cellular response to hypoxia; hormone activity; placenta development; female pregnancy; response to hypoxia; response to oxygen levels; response to hormone stimulus]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tscapeNSCLCa, tscapeOvariand, tscapeRCCa
u*	STK35	20:2082257-2157684 20p13	serine/threonine kinase 35 [Source:HGNC Symbol;Acc:16254], type=nonsense_mediated_decay,protein_coding, GO=[nucleolus]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	STX12	1:28099694-28150963 1p35.3	syntaxin 12 [Source:HGNC Symbol;Acc:11430], type=processed_transcript,protein_coding, GO=[phagocytic vesicle; SNAP receptor activity; cholesterol efflux; protein stabilization; cholesterol transport; sterol transport; regulation of protein stability; membrane raft]	tcgaBreastGE, tcgaColonGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeRCCd

Continued on next page...

S	name	locus	description	studies
u	TBC1D16	17:77906142-78009647 17q25.3	TBC1 domain family, member 16 [Source:HGNC Symbol;Acc:28356], type=processed_transcript,protein_coding, GO=[Rab GTPase activator activity; regulation of Rab GTPase activity; Ras GTPase activator activity; regulation of Ras GTPase activity; GTPase activator activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaOvarianMethyl
u	TBC1D22A	22:47158518-47571336 22q13.31	TBC1 domain family, member 22A [Source:HGNC Symbol;Acc:1309], type=nonsense_mediated_decay,processed_transcript,protein_coding, GO=[Rab GTPase activator activity; regulation of Rab GTPase activity; Ras GTPase activator activity; regulation of Ras GTPase activity; GTPase activator activity; regulation of GTPase activity; regulation of purine nucleotide catabolic process; regulation of nucleotide catabolic process; Ras protein signal transduction; regulation of cellular catabolic process; protein homodimerization activity; GTP catabolic process; regulation of catabolic process; small GTPase mediated signal transduction]	tcgaColonMethyl, tcgaOvarianCGHd, tcgaOvarianMethyl, tscapeBCd, tscapeGliomad, tscapeNSCLCd, tscapeOvariand, tscapeSCLCd
d	TCEA3	1:23707554-23751233 1p36.12	transcription elongation factor A (SII), 3 [Source:HGNC Symbol;Acc:11615], type=processed_transcript,protein_coding, GO=[translation elongation factor activity; regulation of transcription elongation, DNA-dependent]	tcgaBreastGE, tcgaColonGE, tscapeBCd, tscapeCRCd, tscapeNSCLCd, tscapeOvariand, tscapeProstated, tscapeRCCd
u	TDRD9	14:104394799-104519004 14q32.33	tudor domain containing 9 [Source:HGNC Symbol;Acc:20122], type=processed_transcript,protein_coding,retained_intron, GO=[piP-body; piRNA metabolic process; DNA methylation involved in gamete generation; male meiosis; DNA methylation; DNA alkylation; ATP-dependent helicase activity; helicase activity]	tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl, tscapeMelanomad
d*	TJP3	19:3708382-3750810 19p13.3	tight junction protein 3 (zona occludens 3) [Source:HGNC Symbol;Acc:11829], type=protein_coding, GO=[tight junction; apical plasma membrane; apical part of cell]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tscapeHCCd
d	TLE2	19:2997637-3045786 19p13.3	transducin-like enhancer of split 2 (E(sp1) homolog, Drosophila) [Source:HGNC Symbol;Acc:11838], type=protein_coding, GO=[transcription cofactor activity; protein binding transcription factor activity]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeHCCd
u	TMED5	1:93615299-93646285 1p22.1	transmembrane emp24 protein transport domain containing 5 [Source:HGNC Symbol;Acc:24251], type=processed_transcript,protein_coding, GO=[endoplasmic reticulum exit site; Golgi ribbon formation; endoplasmic reticulum-Golgi intermediate compartment membrane; cis-Golgi network; Golgi organization; endoplasmic reticulum membrane]	tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeGliomad, tscapeMelanomad, tscapeNSCLCd
u	TMEM37	2:120187477-120196096 2q14.2	transmembrane protein 37 [Source:HGNC Symbol;Acc:18216], type=processed_transcript,protein_coding, GO=[calcium channel activity]	tcgaBreastGE, tcgaGliomaGE, tscapeCRCa
u	TMEM43	3:14166440-14185179 3p25.1	transmembrane protein 43 [Source:HGNC Symbol;Acc:28472], type=nonsense_mediated_decay,protein_coding, GO=[nuclear inner membrane; nuclear membrane]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	TMEM56	1:95582894-95663163 1p21.3	transmembrane protein 56 [Source:HGNC Symbol;Acc:26477], type=processed_transcript,protein_coding	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeNSCLCd
u	TMEM61	1:55446465-55457966 1p32.3	transmembrane protein 61 [Source:HGNC Symbol;Acc:27296], type=protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl
u*	TNFAIP3	6:138188351-138204449 6q23.3	tumor necrosis factor, alpha-induced protein 3 [Source:HGNC Symbol;Acc:11896], type=processed_transcript,protein_coding, GO=[negative regulation of nucleotide-binding oligomerization domain containing signaling pathway; negative regulation of nucleotide-binding oligomerization domain containing 1 signaling pathway; tolerance induction to lipopolysaccharide; regulation of osteoclast proliferation; negative regulation of osteoclast proliferation; negative regulation of CD40 signaling pathway; negative regulation of nucleotide-binding oligomerization domain containing 2 signaling pathway; negative regulation of toll-like receptor 5 signaling pathway; toll-like receptor 5 signaling pathway; regulation of toll-like receptor 5 signaling pathway; negative regulation of toll-like receptor 3 signaling pathway; regulation of nucleotide-binding oligomerization domain containing signaling pathway; negative regulation of toll-like receptor 2 signaling pathway; positive regulation of hepatocyte proliferation; regulation of vascular wound healing; B-1 B cell homeostasis; negative regulation of endothelial cell apoptosis; negative regulation of interleukin-1 beta production; regulation of lipopolysaccharide-mediated signaling pathway; response to muramyl dipeptide; negative regulation of bone resorption; negative regulation of interleukin-2 production; regulation of germinal center formation; negative regulation of tissue remodeling; protein K63-linked deubiquitination; negative regulation of interleukin-6 production; negative regulation of cyclin-dependent protein kinase activity; negative regulation of I-kappaB kinase/NF-kappaB cascade; caspase inhibitor activity; regulation of toll-like receptor signaling pathway; regulation of defense response to virus by host; negative regulation of smooth muscle cell proliferation; negative regulation of tumor necrosis factor production; negative regulation of B cell activation; protein self-association; regulation of interleukin-1 beta production; negative regulation of type I interferon production; protein K48-linked ubiquitination; caspase regulator activity; ubiquitin-specific protease activity; cysteine-type endopeptidase inhibitor activity; protease binding; ubiquitin binding; negative regulation of NF-kappaB transcription factor activity; negative regulation of caspase activity; negative regulation of inflammatory response; tumor necrosis factor production; regulation of tumor necrosis factor production; regulation of smooth muscle cell proliferation; smooth muscle cell proliferation; positive regulation of protein catabolic process; ubiquitin thiolesterase activity; regulation of cyclin-dependent protein kinase activity; negative regulation of protein serine/threonine kinase activity; liver development; negative regulation of protein ubiquitination; negative regulation of intracellular protein kinase cascade; regulation of organ morphogenesis; endopeptidase inhibitor activity; regulation of inflammatory response; negative regulation of kinase activity; regulation of cysteine-type endopeptidase activity; regulation of I-kappaB kinase/NF-kappaB cascade; I-kappaB kinase/NF-kappaB cascade; response to lipopolysaccharide; epithelial cell proliferation; ubiquitin-protein ligase activity; regulation of endopeptidase activity; anti-apoptosis; enzyme inhibitor activity; regulation of sequence-specific DNA binding transcription factor activity; regulation of protein serine/threonine kinase activity; kinase binding; negative regulation of cell cycle; blood vessel development; vasculature development; regulation of catabolic process; regulation of cell cycle; microtubule cytoskeleton]	tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCa, tscapeCRCa
u	TNFRSF12A	16:3068446-3072384 16p13.3	tumor necrosis factor receptor superfamily, member 12A [Source:HGNC Symbol;Acc:18152], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[substrate-dependent cell migration, cell attachment to substrate; positive regulation of axon extension; positive regulation of axonogenesis; regulation of cell growth; cell surface; blood vessel development; vasculature development]	snp3dGlioma, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	TNFRSF1A	12:6437923-6451280 12p13.31	tumor necrosis factor receptor superfamily, member 1A [Source:HGNC Symbol;Acc:11916], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[positive regulation of tyrosine phosphorylation of Stat1 protein; cellular response to estradiol stimulus; positive regulation of protein import into nucleus, translocation; tumor necrosis factor receptor activity; flavonoid metabolic process; tyrosine phosphorylation of Stat1 protein; negative regulation of interleukin-6 production; prostaglandin metabolic process; positive regulation of tumor necrosis factor production; tumor necrosis factor-mediated signaling pathway; diterpenoid metabolic process; protease binding; regulation of tyrosine phosphorylation of STAT protein; cellular response to mechanical stimulus; tetrapyrrole metabolic process; tumor necrosis factor production; regulation of tumor necrosis factor production; cellular response to tumor necrosis factor; positive regulation of inflammatory response; response to amino acid stimulus; positive regulation of angiogenesis; secondary metabolic process; response to tumor necrosis factor; response to alkaloid; response to estradiol stimulus; induction of apoptosis by extracellular signals; cellular response to abiotic stimulus; regulation of peptidyl-tyrosine phosphorylation; response to mechanical stimulus; positive regulation of I-kappaB kinase/NF-kappaB cascade; defense response to bacterium; regulation of inflammatory response; regulation of I-kappaB kinase/NF-kappaB cascade; membrane raft; response to lipopolysaccharide; I-kappaB kinase/NF-kappaB cascade; response to hypoxia; response to oxygen levels; fatty acid metabolic process; monocarboxylic acid metabolic process; nucleocytoplasmic transport; cell surface; blood vessel development; vasculature development; neuron projection; response to hormone stimulus; extracellular space]	snp3dDiabetes, snp3dObesity, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianCGHa, tcgaOvarianMethyl
u	TNKS1BP1	11:57067112-57092426 11q12.1	tankyrase 1 binding protein 1, 182kDa [Source:HGNC Symbol;Acc:19081], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[nuclear telomeric heterochromatin; ankyrin binding; telomere maintenance via telomerase; cytoskeletal protein binding]	tcgaOvarianMethyl

Continued on next page...

S	name	locus	description	studies
u	TOR1AIP2	1:179809102-179846934 1q25.2	torsin A interacting protein 2 [Source:HGNC Symbol;Acc:24055], type=ambiguous_orf,protein_coding, GO=[endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	TP53I3	2:24300303-24308731 2p23.3	tumor protein p53 inducible protein 3 [Source:HGNC Symbol;Acc:19373], type=processed_transcript,protein_coding, GO=[NADPH:quinone reductase activity; NADPH binding; quinone binding; induction of apoptosis by oxidative stress; NADP metabolic process; protein homodimerization activity]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	TP53INP2	20:33292094-33301243 20q11.22	tumor protein p53 inducible nuclear protein 2 [Source:HGNC Symbol;Acc:16104], type=protein_coding	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	TPD52L1	6:125440195-125585553 6q22.31	tumor protein D52-like 1 [Source:HGNC Symbol;Acc:12006], type=processed_transcript,protein_coding,retained_intron, GO=[caspase activator activity; DNA fragmentation involved in apoptotic nuclear change; apoptotic nuclear change; caspase regulator activity; positive regulation of JNK cascade; regulation of cysteine-type endopeptidase activity; positive regulation of MAP kinase activity; positive regulation of MAPKKK cascade; positive regulation of protein serine/threonine kinase activity; regulation of endopeptidase activity; protein heterodimerization activity; regulation of protein serine/threonine kinase activity; perinuclear region of cytoplasm; MAPKKK cascade; protein homodimerization activity]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u*	TPM1	15:63334831-63364114 15q22.2	tropomyosin 1 (alpha) [Source:HGNC Symbol;Acc:12010], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[positive regulation of heart rate by epinephrine; muscle thin filament tropomyosin; bleb; ruffle organization; positive regulation of ATPase activity; filamentous actin; positive regulation of stress fiber assembly; sarcomere organization; regulation of ATPase activity; ventricular cardiac muscle tissue morphogenesis; muscle filament sliding; structural constituent of muscle; stress fiber; ruffle membrane; actin filament bundle; actomyosin structure organization; actin filament; actin filament-based movement; cellular response to reactive oxygen species; structural constituent of cytoskeleton; negative regulation of cell migration; response to reactive oxygen species; regulation of actin filament-based process; actin filament organization; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; actin binding; regulation of cell motility; regulation of cellular component movement; actin filament-based process; regulation of cellular catabolic process; regulation of catabolic process; cytoskeletal protein binding]	tcgaBreastMethyl, tcgaGliomaGE
u*	TPM2	9:35681989-35691017 9p13.3	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:12011], type=processed_transcript,protein_coding, GO=[muscle thin filament tropomyosin; regulation of ATPase activity; muscle filament sliding; structural constituent of muscle; actin filament-based movement; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; actin binding; actin filament-based process; regulation of cellular catabolic process; regulation of catabolic process; cytoskeletal protein binding]	tcgaBreastGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
d	TRIM25	17:54965270-54991399 17q22	tripartite motif containing 25 [Source:HGNC Symbol;Acc:12932], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[negative regulation of type I interferon production; ubiquitin-protein ligase activity]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl, tscapeBCa
u	TRIM29	11:119981983-120056237 11q23.3	tripartite motif containing 29 [Source:HGNC Symbol;Acc:17274], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeBCd
u	TRIM48	11:55029658-55038595 11q11	tripartite motif containing 48 [Source:HGNC Symbol;Acc:19021], type=protein_coding	tcgaColonGE
u	TRNP1	1:27320198-27327147 1p36.11	TMF1-regulated nuclear protein 1 [Source:HGNC Symbol;Acc:34348], type=protein_coding	tcgaBreastGE, tcgaColonGE
d	TROAP	12:49717019-49725514 12q13.12	trophinin associated protein (tastin) [Source:HGNC Symbol;Acc:12327], type=nonsense_mediated_decay,protein_coding,retained_intron	tcgaGliomaGE, tcgaOvarianMethyl
u*	TSC2	16:2097466-2138716 16p13.3	tuberous sclerosis 2 [Source:HGNC Symbol;Acc:12363], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[TSC1-TSC2 complex; negative regulation of cell size; negative regulation of phosphatidylinositol 3-kinase cascade; 14-3-3 protein binding; negative regulation of TOR signaling cascade; negative regulation of protein kinase B signaling cascade; regulation of insulin receptor signaling pathway; insulin-like growth factor receptor signaling pathway; regulation of TOR signaling cascade; positive chemotaxis; acute-phase response; regulation of phosphatidylinositol 3-kinase cascade; caveola; negative regulation of MAP kinase activity; neural tube closure; growth cone; phosphatidylinositol-mediated signaling; negative regulation of protein serine/threonine kinase activity; phosphatase binding; fibroblast growth factor receptor signaling pathway; negative regulation of intracellular protein kinase cascade; epidermal growth factor receptor signaling pathway; negative regulation of kinase activity; insulin receptor signaling pathway; protein homooligomerization; membrane raft; cellular response to insulin stimulus; response to hypoxia; epithelial cell proliferation; nerve growth factor receptor signaling pathway; response to oxygen levels; GTPase activator activity; response to insulin stimulus; microsome; neuronal cell body; protein heterodimerization activity; regulation of GTPase activity; regulation of nucleotide catabolic process; regulation of purine nucleotide catabolic process; regulation of protein serine/threonine kinase activity; perinuclear region of cytoplasm; nucleocytoplasmic transport; negative regulation of cell cycle; regulation of cellular catabolic process; protein homodimerization activity; GTP catabolic process; regulation of catabolic process; neuron projection; small GTPase mediated signal transduction; regulation of cell cycle; response to hormone stimulus]	cosmicMetastasis, cosmicPrimary, tscapeHCCd
u*	TSC22D3	X:106956451-107020572 Xq22.3	TSC22 domain family, member 3 [Source:HGNC Symbol;Acc:3051], type=protein_coding, GO=[MyoD binding; negative regulation of skeletal muscle tissue development; response to osmotic stress; anti-apoptosis; negative regulation of transcription from RNA polymerase II promoter]	tcgaOvarianMethyl
u	TSPYL2	X:53111549-53117722 Xp11.22	TSPY-like 2 [Source:HGNC Symbol;Acc:24358], type=protein_coding,retained_intron, GO=[activation of signaling protein activity involved in unfolded protein response; rDNA binding; negative regulation of DNA replication; regulation of DNA replication; negative regulation of cell growth; nucleosome assembly; regulation of cell growth; negative regulation of cell cycle; nucleolus; regulation of cell cycle; microtubule cytoskeleton]	tcgaBreastGE, tcgaBreastMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	TTC21A	3:39149152-39180394 3p22.2	tetratricopeptide repeat domain 21A [Source:HGNC Symbol;Acc:30761], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron	
u	TUBB2A	6:3153903-3157809 6p25.2	tubulin, beta 2A class IIa [Source:HGNC Symbol;Acc:12412], type=processed_transcript,protein_coding, GO=['de novo' posttranslational protein folding; GTPase activity; microtubule; GTP binding; GTP catabolic process; microtubule cytoskeleton]	snp3dLungC, tcgaBreastGE, tcgaColonGE, tcgaColonMethyl, tscapeOvariana, tscapeSCLCd
u	TXNDC11	16:11772936-11836734 16p13.13	thioredoxin domain containing 11 [Source:HGNC Symbol;Acc:28030], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[cell redox homeostasis; endoplasmic reticulum membrane]	tcgaBreastGE, tcgaColonGE
u	UBE2Q2P2	15:82647360-82712277 15q25.2	ubiquitin-conjugating enzyme E2Q family member 2 pseudogene 2 [Source:HGNC Symbol;Acc:37440], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	
u	USP38	4:144106070-144144983 4q31.21	ubiquitin specific peptidase 38 [Source:HGNC Symbol;Acc:20067], type=nonsense_mediated_decay,protein_coding, GO=[ubiquitin thiolesterase activity]	tcgaBreastGE, tcgaGliomaGE, tcgaOvarianMethyl
d	VASN	16:4421849-4433529 16p13.3	vasorin [Source:HGNC Symbol;Acc:18517], type=protein_coding	tcgaBreastGESurv, tscapeHCCd, tscapeOvariand
u*	VCL	10:75757872-75879918 10q22.2	vinculin [Source:HGNC Symbol;Acc:12665], type=processed_transcript,protein_coding, GO=[beta-dystroglycan binding; adherens junction assembly; alpha-catenin binding; costamere; fascia adherens; epithelial cell-cell adhesion; cadherin binding; protein localization at cell surface; lamellipodium assembly; apical junction assembly; stress fiber; Rho GTPase binding; cell-cell adherens junction; actin filament bundle; beta-catenin binding; actin filament; platelet degranulation; negative regulation of cell migration; focal adhesion; cell-matrix adhesion; platelet activation; regulation of cell motility; regulation of cellular component movement]	tcgaColonGE, tcgaColonMethyl, tcgaGliomaCGHd, tcgaGliomaGE, tcgaOvarianMethyl, tscapeProstatea
u	VILL	3:38029550-38048679 3p22.2	villin-like [Source:HGNC Symbol;Acc:30906], type=nonsense_mediated_decay,protein_coding,retained_intron, GO=[actin filament capping; actin filament depolymerization; negative regulation of protein complex disassembly; protein depolymerization; structural constituent of cytoskeleton; regulation of actin filament polymerization; actin filament polymerization; actin polymerization or depolymerization; regulation of actin filament-based process; actin filament organization; actin binding; actin filament-based process; cytoskeletal protein binding]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonGESurv, tcgaColonMethyl
u	WDFY2	13:52158644-52334135 13q14.3	WD repeat and FYVE domain containing 2 [Source:HGNC Symbol;Acc:20482], type=processed_transcript,protein_coding	tcgaBreastMethyl, tcgaOvarianMethyl, tscapeBCd, tscapeGliomad, tscapeHCCd, tscapeNSCLCd, tscapeProstated, tscapeSCLCd

Continued on next page...

S	name	locus	description	studies
d*	WDR6	3:49044495-49053386 3p21.31	WD repeat domain 6 [Source:HGNC Symbol;Acc:12758], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[insulin receptor substrate binding; signalosome; soluble fraction; negative regulation of cell cycle; regulation of cell cycle]	tcgaGliomaGE, tcgaOvarianMethyl, tscapeOvariand
u	WDR60	7:158649269-158749438 7q36.3	WD repeat domain 60 [Source:HGNC Symbol;Acc:21862], type=nonsense_mediated_decay,protein_coding,retained_intron	tscapeNSCLCd, tscapeOvariana, tscapeOvariand
d	XXyac-YRM2039.2	9:14511-29739 9p24.3	[undefined], type=pseudogene,unprocessed_pseudogene	
u	ZBTB25	14:64915824-64971931 14q23.3	zinc finger and BTB domain containing 25 [Source:HGNC Symbol;Acc:13112], type=protein_coding	tcgaBreastGE, tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaOvarianMethyl
u	ZCCHC11	1:52873954-53019159 1p32.3	zinc finger, CCHC domain containing 11 [Source:HGNC Symbol;Acc:28981], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[RNA uridylyltransferase activity; miRNA catabolic process; miRNA metabolic process; pre-miRNA processing; regulation of lipopolysaccharide-mediated signaling pathway; negative regulation of NF-kappaB transcription factor activity; stem cell maintenance; stem cell differentiation; response to lipopolysaccharide; regulation of sequence-specific DNA binding transcription factor activity; nucleolus]	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaOvarianMethyl
u	ZDHHC8P1	22:23732793-23744913 22q11.23	zinc finger, DHHC-type containing 8 pseudogene 1 [Source:HGNC Symbol;Acc:26461], type=processed_transcript,pseudogene,transcribed_unprocessed_pseudogene	
u*	ZFHX3	16:72816784-73093597 16q22.2, 16q22.3	zinc finger homeobox 3 [Source:HGNC Symbol;Acc:777], type=protein_coding,retained_intron, GO=[positive regulation of myoblast differentiation; negative regulation of myoblast differentiation; negative regulation of muscle cell differentiation; myoblast differentiation; sequence-specific distal enhancer binding RNA polymerase II transcription factor activity; sequence-specific DNA binding RNA polymerase II transcription factor activity; transcription factor complex; negative regulation of transcription from RNA polymerase II promoter]	cosmicMetastasis, cosmicPrimary, tscapeOvariand
u	ZFP36	19:39897487-39900045 19q13.2	zinc finger protein 36, C3H type, homolog (mouse) [Source:HGNC Symbol;Acc:12862], type=protein_coding, GO=[regulation of nuclear-transcribed mRNA poly(A) tail shortening; positive regulation of nuclear-transcribed mRNA poly(A) tail shortening; RNA destabilization; 3'-UTR-mediated mRNA stabilization; 14-3-3 protein binding; C-C chemokine binding; AU-rich element binding; stress granule; single-stranded RNA binding; negative regulation of inflammatory response; tumor necrosis factor production; regulation of tumor necrosis factor production; mRNA binding; regulation of inflammatory response; protein kinase binding; kinase binding; negative regulation of transcription from RNA polymerase II promoter; regulation of cellular catabolic process; regulation of catabolic process]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl, tscapeNSCLCa, tscapeOvariana
u	ZNF185	X:152082986-152142025 Xq28	zinc finger protein 185 (LIM domain) [Source:HGNC Symbol;Acc:12976], type=protein_coding, GO=[focal adhesion]	tcgaColonMethyl, tcgaGliomaGE
u	ZNF189	9:104161155-104172942 9q31.1	zinc finger protein 189 [Source:HGNC Symbol;Acc:12980], type=protein_coding, GO=[negative regulation of transcription from RNA polymerase II promoter]	tcgaBreastGE
u*	ZNF622	5:16451628-16465901 5p15.1	zinc finger protein 622 [Source:HGNC Symbol;Acc:30958], type=protein_coding, GO=[induction of apoptosis by oxidative stress; positive regulation of JNK cascade; positive regulation of MAPKKK cascade; MAPKKK cascade; nucleolus]	tcgaBreastGE, tcgaColonMethyl, tcgaOvarianMethyl
d	ZNF664	12:124456392-124499974 12q24.31	zinc finger protein 664 [Source:HGNC Symbol;Acc:25406], type=processed_transcript,protein_coding,retained_intron	tcgaBreastGE, tcgaBreastMethyl, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl
u	ZYX	7:143078173-143088204 7q34	zyxin [Source:HGNC Symbol;Acc:13200], type=nonsense_mediated_decay,processed_transcript,protein_coding,retained_intron, GO=[stress fiber; cell-cell adherens junction; actin filament bundle; focal adhesion]	tcgaBreastMethyl, tcgaColonGE, tcgaColonMethyl, tcgaGliomaGE, tcgaOvarianMethyl, tscapeMelanomaa

14.2.1 GO enrichment of all candidates

Table 38: Enriched Gene Ontology terms [1] (FDR corrected $p \leq 0.05$). Ratio is the proportion of the annotated genes among the whole gene set. List is sorted based on the FDR corrected p-values. Green and blue borders are referring to up and down regulated genes, respectively.

Ratio	Type	Description	Genes
0.019	BP	activation of signaling protein activity involved in unfolded protein response	ASNS, DNAJC3, EDEM1, SHC1, SSR1, TSPYL2
0.109	BP	response to hormone stimulus	ABCC8, ANG, AP3S1, ARG1, ARG2, ASIP, ASNS, BTG1, CITED1, CRYAB, CST3, CTGF, DUSP1, FADS1, FOS, FOXO1, FOXO3, GHR, GPER, HADH, HSD11B2, JAK2, KLF9, NPC1, PGF, PRKAB2, SCAP, SHC1, SOCS1, SRD5A1, STAT3, STC2, TNFRSF1A, TSC2
0.054	BP	response to oxygen levels	ANG, ARG2, CAPN2, CRYAB, CST3, CTGF, DDIT4, HSD11B2, PDLIM1, PGF, PRKCE, SCAP, SCNN1G, SHC1, STC2, TNFRSF1A, TSC2
0.013	BP	JAK-STAT cascade involved in growth hormone signaling pathway	GHR, JAK2, SOCS1, STAT3
0.051	BP	response to hypoxia	ANG, ARG2, CAPN2, CRYAB, CST3, DDIT4, HSD11B2, PDLIM1, PGF, PRKCE, SCAP, SCNN1G, SHC1, STC2, TNFRSF1A, TSC2
0.015	MF	pancreatic ribonuclease activity	ANG, RNASE12, RNASE12, RNASE4, RNASE4
0.010	BP	regulation of nucleotide-binding oligomerization domain containing signaling pathway	BIRC2, BIRC3, TNFAIP3
0.035	BP	response to reactive oxygen species	ARG1, CRYAB, CST3, DUSP1, FOS, JUN, NET1, PRDX6, RHOB, SHC1, TPM1
0.020	CC	actin filament bundle	CNN2, CRYAB, FERMT2, SEPT11, TPM1, VCL, ZYX
0.029	BP	response to hydrogen peroxide	ARG1, CRYAB, CST3, DUSP1, JUN, NET1, PRDX6, RHOB, SHC1
0.012	MF	14-3-3 protein binding	DDIT4, PRKCE, TSC2, ZFP36
0.026	BP	response to amino acid stimulus	ARG1, ARG2, ASNS, CEBPB, COL6A1, CTGF, SOCS1, TNFRSF1A
0.006	BP	TRIF-dependent toll-like receptor signaling pathway	FOS, JUN
0.048	BP	response to insulin stimulus	ABCC8, AP3S1, CITED1, FADS1, FOXO1, FOXO3, GHR, HADH, HSD11B2, PRKAB2, SCAP, SHC1, SOCS1, SRD5A1, TSC2

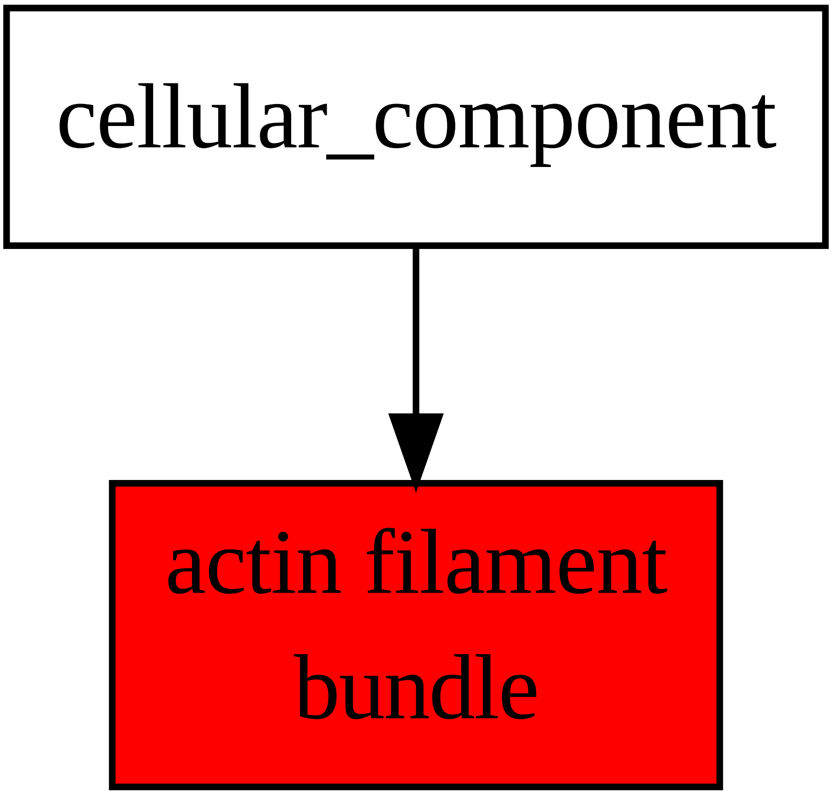


Figure 63: Relationships between the enriched *cellular component* Gene Ontology terms that were listed in Table 38. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

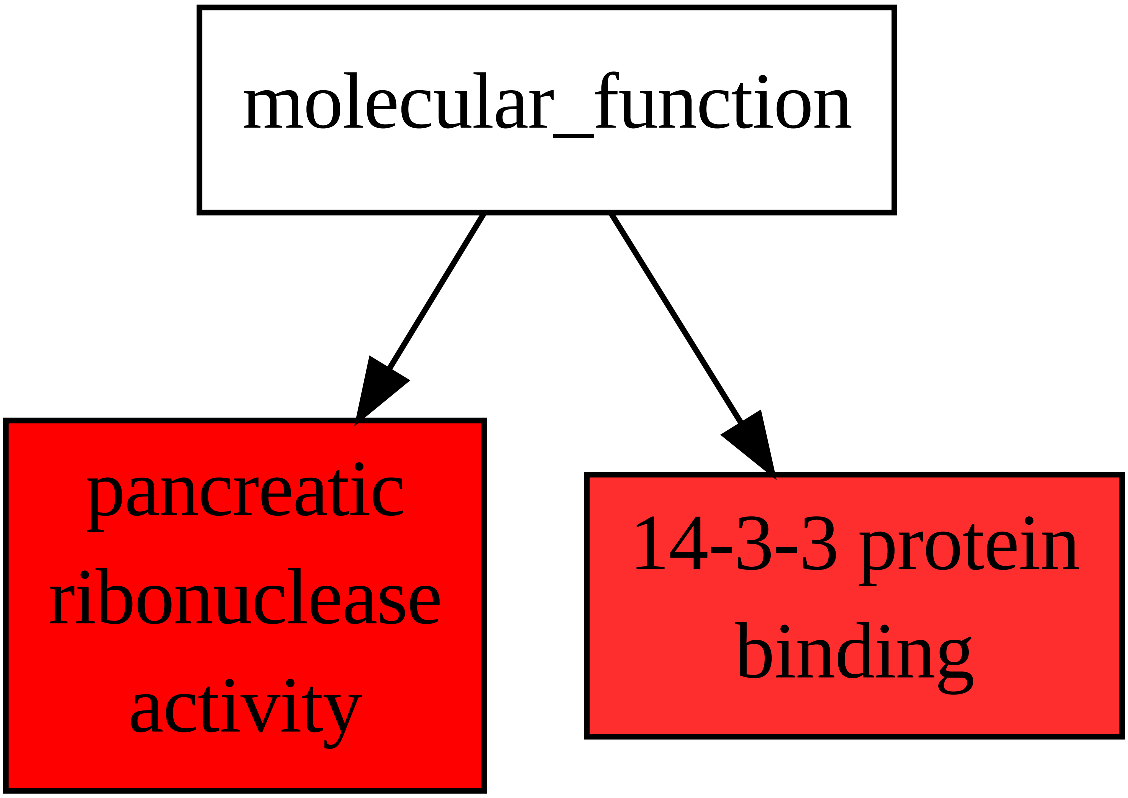


Figure 64: Relationships between the enriched *molecular function* Gene Ontology terms that were listed in Table 38. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

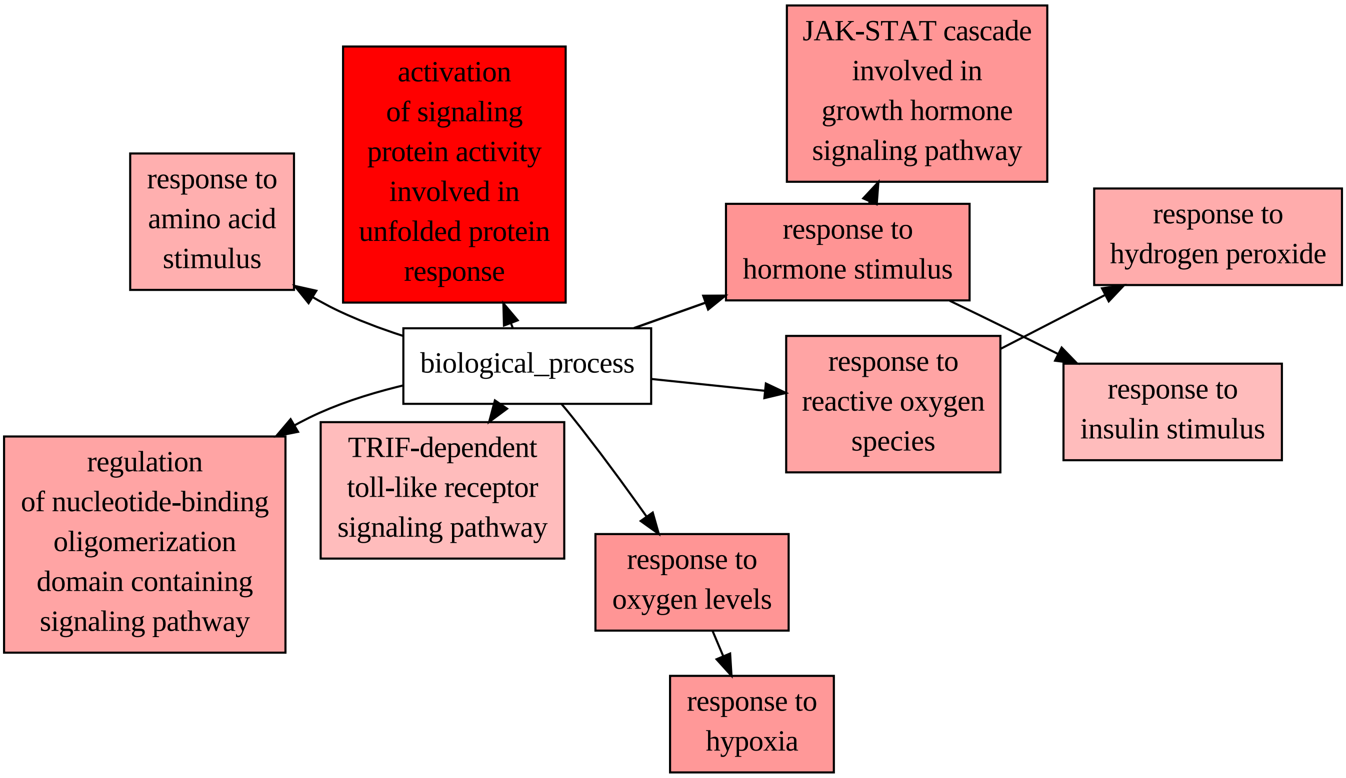


Figure 65: Relationships between the enriched *biological process* Gene Ontology terms that were listed in Table 38. The darkness of the red reflects the significance of the enrichment and the thicknesses of the edges are propotional to the numbers of genes sharing the following annotation.

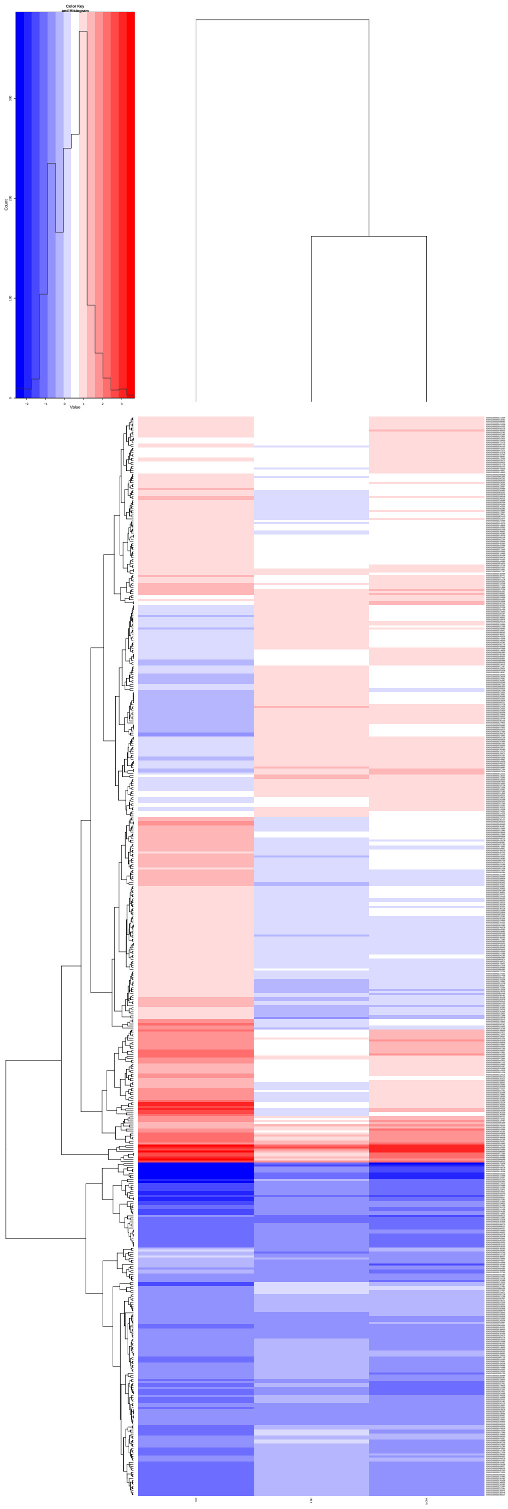


Figure 66: DEGs DHT, CPA, and RU486

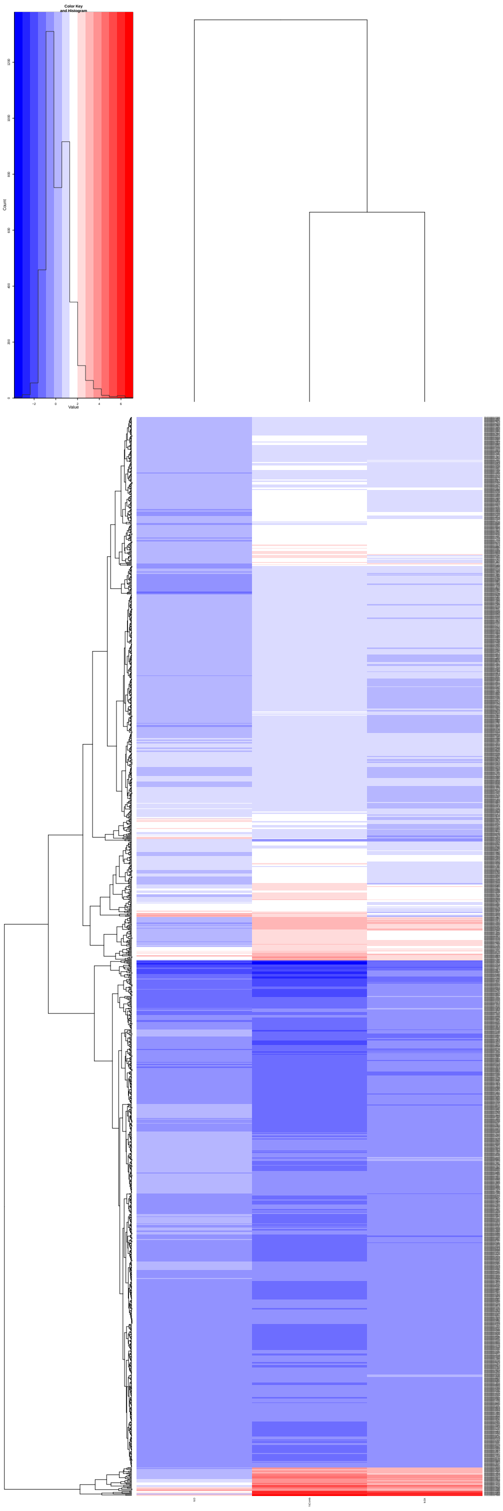


Figure 67: DEGs DHT DEX

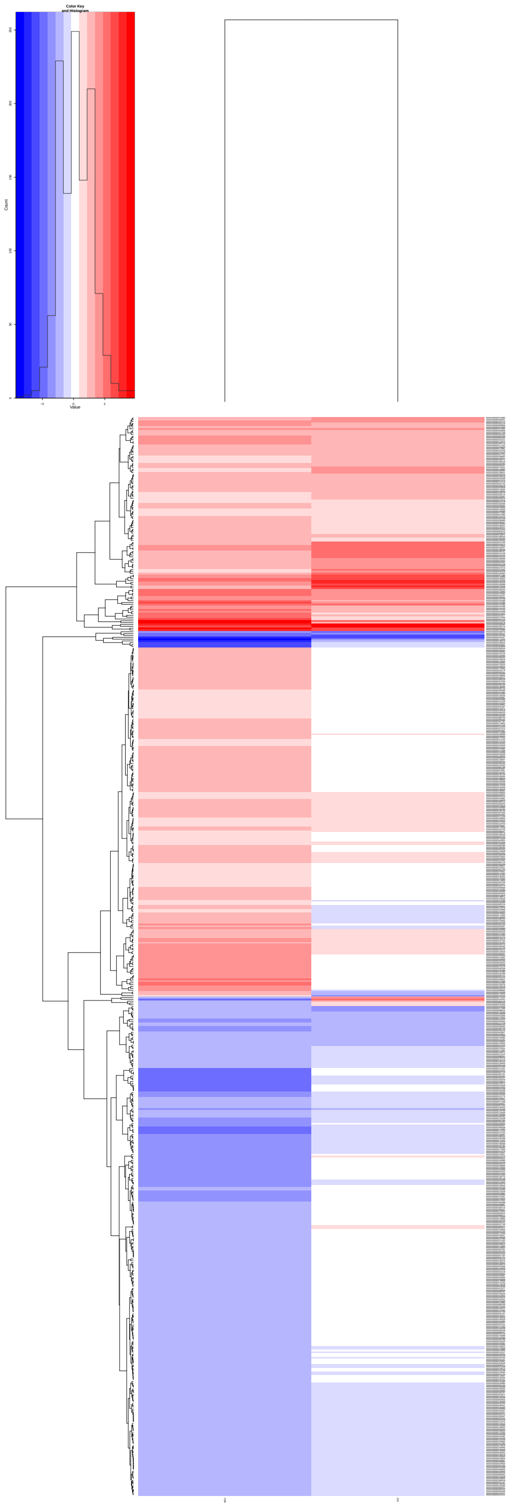


Figure 68: DHT VCaP and LNCap

15 ChIP-seq peaks

15.1 AR DHT overlaps

Chromosome specific statistics are shown in Table 39. A histogram of sequence lengths is shown in Figure 69.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	596	12	464	975	276651	0.00111
10	234	192	431	937	100927	0.000745
11	286	51	451	1184	129014	0.000956
12	224	3	425	933	95181	0.000711
13	152	197	492	1197	74796	0.000649
14	184	51	450	920	82754	0.000771
15	205	13	466	1065	95460	0.000931
16	156	51	424	1042	66155	0.000732
17	203	144	437	918	88640	0.001092
18	118	200	474	1125	55975	0.000717
19	69	202	410	947	28315	0.000479
2	404	119	445	1046	179618	0.000739
20	144	239	449	1609	64616	0.001025
21	72	196	464	768	33389	0.000694
22	59	176	396	640	23392	0.000456
3	440	122	496	1302	218250	0.001102
4	270	198	433	1056	116915	0.000612
5	362	5	456	1173	164925	0.000912
6	341	69	424	918	144422	0.000844
7	309	204	454	1124	140276	0.000881
8	303	70	460	934	139295	0.000952
9	212	223	442	854	93704	0.000664
X	104	57	394	812	40987	0.000264
Y	4	199	283	345	1131	1.9e-05
all 24	5451	3	450	1609	2454788	0.000793

Table 39: Chromosome specific distribution of the regions. The last line represents the overall statistics.

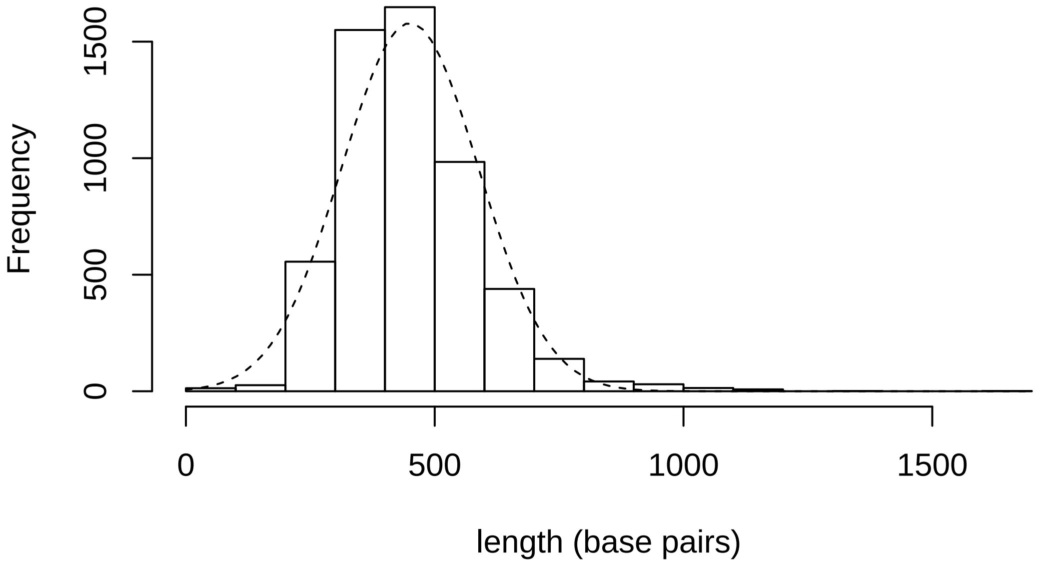
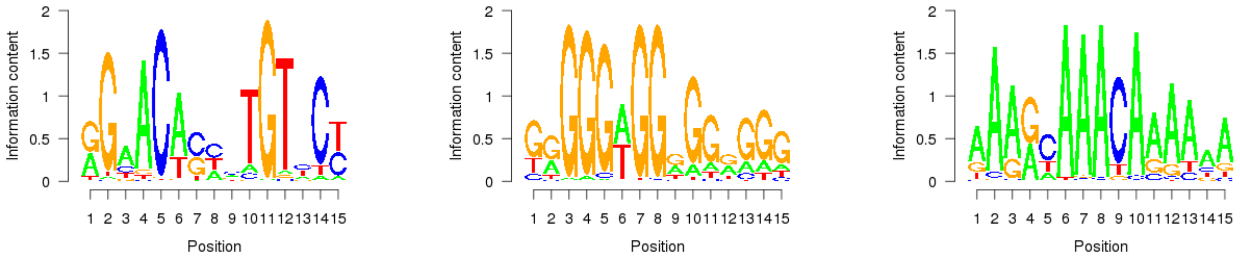


Figure 69: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTrrO-gCount** component.

property	value
genes	11937



(a) ARDHTrrO-deNovo-meme1: width=15, sites=221, llr=2285, E=4.3e-119 (b) ARDHTrrO-deNovo-meme2: width=15, sites=79, llr=934, E=3.8e-24 (c) ARDHTrrO-deNovo-meme3: width=15, sites=67, llr=787, E=9.8e-08

Figure 70: De novo motifs for the filtered AR DHT overlaps sequences.

Table 40: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	12.1339	0.1154	0.0095	575	94	30.25E-178	0.05192
FOXA1	2.7416	1.0367	0.3781	3577	3037	0.00E00	0.75933
FOXA1pAR	2.7287	0.2116	0.0775	1048	700	4.385E-136	0.13971
FOXF2	2.5973	0.3144	0.1210	1462	1123	23.37E-176	0.20372
TLX1::NFIC	2.4242	0.0187	0.0077	81	61	3.884E-08	0.01629
Foxa2	2.4154	0.8983	0.3719	3258	2641	0.00E00	0.89290
RXRA::VDR	1.9286	0.0092	0.0047	50	48	10.97E-04	0.00625
Tal1::Gata1	1.8703	0.0644	0.0344	335	344	27.45E-18	0.04558
ESR2	1.8151	0.0235	0.0129	111	113	3.617E-06	0.02121
FOXD1	1.7899	1.3797	0.7708	3965	5056	0.00E00	1.27732
ARMotifTH	1.7053	0.0729	0.0427	385	420	33.33E-18	0.05426
ARMotifT	1.6978	0.6996	0.4120	2692	3297	1.745E-242	0.57100
ARMotifTT	1.6774	0.0138	0.0082	75	82	7.988E-04	0.01016
Foxq1	1.6541	0.6535	0.3951	2529	3005	4.832E-224	0.63497
Stat3	1.6350	0.2421	0.1480	977	1177	2.953E-42	0.25403
STAT1	1.6209	0.0523	0.0322	224	270	22.79E-08	0.05389
AR	1.6146	0.0688	0.0426	356	414	34.99E-14	0.05409
GRMotifTH	1.6040	0.3760	0.2344	1652	2066	3.371E-90	0.31828
GABPA	1.5045	0.0923	0.0613	475	584	24.56E-16	0.07646
NR3C1	1.4972	0.4014	0.2680	1703	2321	27.17E-78	0.34691
Esrrb	1.4005	0.1274	0.0909	648	862	28.15E-18	0.10729
Gata1	1.3938	0.8275	0.5937	2933	4313	13.4E-216	0.78956
ELK4	1.3924	0.0279	0.0200	143	196	32.59E-04	0.02456
GRMotifT	1.3433	2.5673	1.9111	4961	8418	0.00E00	2.73905
MIZF	1.3138	0.0305	0.0232	162	227	29.91E-04	0.02699
FOXI1	1.3132	1.0398	0.7918	3256	4612	43.22E-298	1.59430
PPARG::RXRA	1.3018	0.0244	0.0187	126	187	3.679E-02	0.02183
GR	1.2932	0.3078	0.2380	1428	2054	41.49E-48	0.28284
RXR::RAR_DR5	1.2877	0.0314	0.0244	169	240	34.85E-04	0.02738
GRMotifTT	1.2803	0.0272	0.0212	144	213	2.161E-02	0.02351
Evi1	1.2607	0.0451	0.0358	236	341	6.531E-04	0.04306
ARMotifH	1.2587	9.0578	7.1962	5442	10068	0.00E00	16.63353
ARMotifHH	1.2493	0.4102	0.3283	1746	2618	2.602E-62	0.42277
NFIC	1.2489	2.8835	2.3089	4913	8611	0.00E00	3.86924
FOXO3	1.2241	1.9356	1.5813	4422	7413	0.00E00	2.50227
SP1	0.8240	1.0837	1.3152	2388	5012	15.36E-46	4.86185
MZF1_5-13	0.8201	1.2395	1.5113	3617	7325	5.436E-218	2.05672
Prrx2	0.7990	2.1784	2.7264	4326	8441	0.00E00	5.00259
CREB1	0.7777	0.6983	0.8979	2568	5413	2.073E-58	1.11064
FOXL1	0.7681	6.4465	8.3931	5162	9521	0.00E00	68.19580
Foxd3	0.7503	2.0802	2.7725	4026	7265	0.00E00	12.23549
Zfx	0.6844	0.1255	0.1834	569	1553	16.87E-08	0.20431
Ddit3::Cebpa	0.5330	0.2329	0.4370	1100	3114	95.64E-08	0.48703

15.2 AR DHT overlaps (up)

Chromosome specific statistics are shown in Table 41. A histogram of sequence lengths is shown in Figure 71.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	73	249	487	789	35571	0.000143
10	14	317	475	706	6647	4.9e-05
11	37	51	479	922	17709	0.000131
12	12	356	446	668	5355	4e-05
13	13	257	484	1197	6297	5.5e-05
14	7	276	439	551	3072	2.9e-05
15	19	263	491	754	9336	9.1e-05
16	11	263	476	1042	5233	5.8e-05
17	14	323	496	771	6946	8.6e-05
18	14	258	490	923	6857	8.8e-05
19	5	267	565	779	2825	4.8e-05
2	45	237	476	952	21420	8.8e-05
20	15	296	474	685	7108	0.000113
21	12	212	439	595	5264	0.000109
3	25	122	469	976	11716	5.9e-05
4	49	290	465	954	22789	0.000119
5	40	256	460	841	18396	0.000102
6	47	268	455	755	21396	0.000125
7	26	261	436	854	11327	7.1e-05
8	28	133	446	727	12482	8.5e-05
9	3	323	444	523	1331	9e-06
X	1	413	413	413	413	3e-06
all 22	510	51	470	1197	239490	7.7e-05

Table 41: Chromosome specific distribution of the regions. The last line represents the overall statistics.

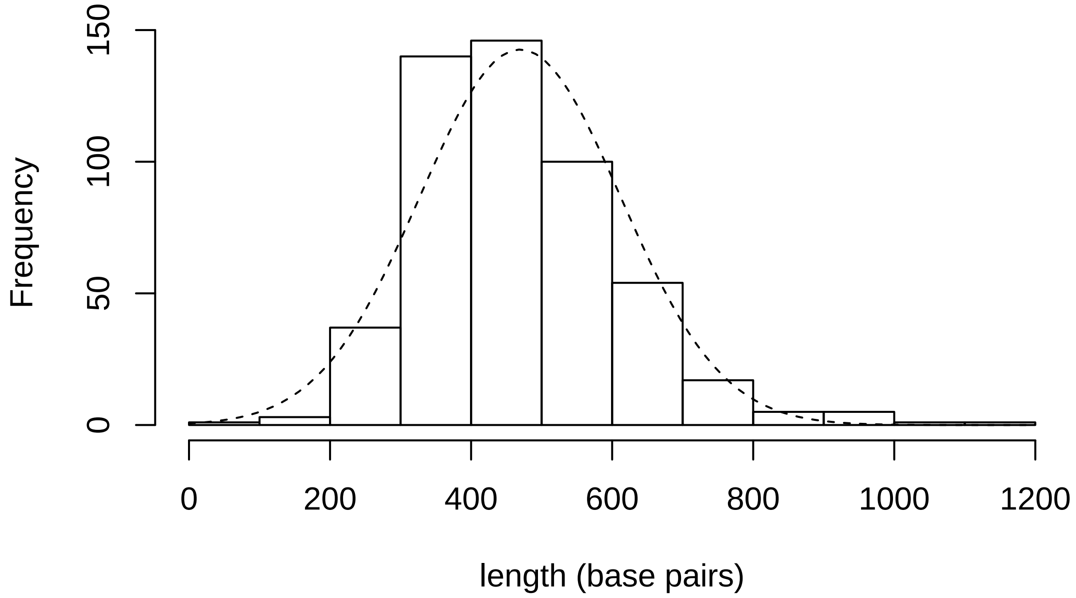
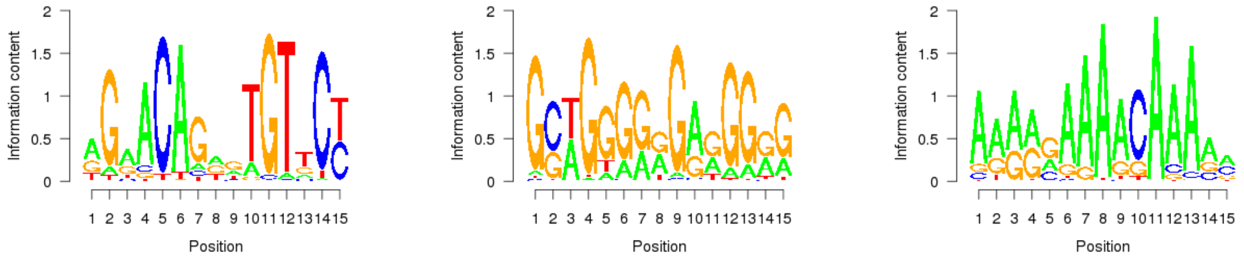


Figure 71: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTrrOu-gCount** component.

property	value
genes	195



(a) ARDHTrrOu-deNovo-meme1: width=15, sites=124, llr=1346, E=2.9e-40

(b) ARDHTrrOu-deNovo-meme2: width=15, sites=56, llr=682, E=4.2e-09

(c) ARDHTrrOu-deNovo-meme3: width=15, sites=87, llr=946, E=0.53

Figure 72: De novo motifs for the filtered AR DHT overlaps (up) sequences.

Table 42: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	11.3311	0.1294	0.0114	59	11	54.89E-20	0.06029
TLX1::NFIC	4.8922	0.0255	0.0052	8	3	1.816E-02	0.02153
FOXA1pAR	2.4409	0.1667	0.0683	82	58	45.51E-12	0.10810
FOXA1	2.4390	1.0216	0.4188	321	316	1.995E-52	0.73133
Foxa2	2.3548	0.9157	0.3888	303	270	6.808E-52	0.93757
FOXF2	2.3331	0.3137	0.1344	127	121	2.253E-12	0.22701
Esrrb	1.8955	0.1412	0.0745	65	65	28.0E-06	0.10702
NR3C1	1.8233	0.4922	0.2699	188	218	5.153E-16	0.39601
FOXD1	1.7521	1.4078	0.8035	369	503	3.501E-50	1.28034
GABPA	1.7231	0.0980	0.0569	49	51	9.085E-04	0.07286
GRMotifTH	1.6914	0.4216	0.2492	174	203	5.874E-14	0.34229
ARMotifT	1.5913	0.7373	0.4633	255	337	1.031E-22	0.65468
Pax5	1.5717	0.0667	0.0424	34	41	3.736E-02	0.04823
Foxq1	1.5574	0.6314	0.4054	234	296	1.567E-20	0.59542
Stat3	1.5090	0.2294	0.1520	91	119	2.031E-04	0.23497
Egr1	1.4481	0.1078	0.0745	50	65	1.817E-02	0.09762
GRMotifT	1.4230	2.8725	2.0186	475	814	2.124E-80	2.92809
NFIC	1.3252	3.1137	2.3495	478	827	24.76E-82	3.95410
NHLH1	1.3197	0.1392	0.1055	46	63	4.713E-02	0.20646
ARMotifH	1.3114	9.9569	7.5926	509	961	54.28E-94	18.79878
RORA_1	1.3091	0.2843	0.2172	130	183	5.781E-06	0.25317
GRMotifHH	1.2365	0.2941	0.2378	122	183	1.343E-04	0.30910
FOXI1	1.2250	1.0059	0.8211	317	455	1.559E-32	1.63986
FEV	1.2236	0.7706	0.6298	266	429	12.35E-18	0.77794
ARMotifHH	1.2177	0.4471	0.3671	178	259	24.7E-10	0.54667
EBF1	1.2177	0.7216	0.5926	221	346	3.073E-12	1.15954
NFE2L2	1.2065	0.1373	0.1138	68	104	3.788E-02	0.11928
Gata1	1.2002	0.7745	0.6453	265	434	57.54E-18	0.79538
Myf	1.2002	0.2706	0.2254	96	161	2.313E-02	0.42425
Pdx1	0.8083	2.4392	3.0176	419	818	20.05E-48	6.08266
Prrx2	0.7617	2.1235	2.7880	397	801	3.753E-38	5.23048
CREB1	0.7614	0.7000	0.9193	246	539	82.58E-08	1.07376
FOXL1	0.7307	6.3863	8.7404	482	902	3.607E-78	110.62686
Foxd3	0.7305	2.0647	2.8263	381	700	5.873E-38	12.18112

15.3 AR DHT overlaps (down)

Chromosome specific statistics are shown in Table 43. A histogram of sequence lengths is shown in Figure 73.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	13	328	506	858	6577	2.6e-05
2	10	279	396	497	3964	1.6e-05
3	24	232	501	814	12033	6.1e-05
4	4	259	417	538	1667	9e-06
5	5	349	438	536	2188	1.2e-05
6	8	326	416	561	3328	1.9e-05
7	14	287	502	764	7027	4.4e-05
8	10	296	416	555	4159	2.8e-05
9	3	270	304	339	912	6e-06
10	5	322	413	488	2067	1.5e-05
11	10	250	480	838	4805	3.6e-05
12	8	289	414	599	3315	2.5e-05
14	8	232	508	891	4066	3.8e-05
15	1	449	449	449	449	4e-06
16	7	278	388	529	2717	3e-05
17	1	290	290	290	290	4e-06
19	1	362	362	362	362	6e-06
20	1	693	693	693	693	1.1e-05
all 18	133	232	456	891	60619	2e-05

Table 43: Chromosome specific distribution of the regions. The last line represents the overall statistics.

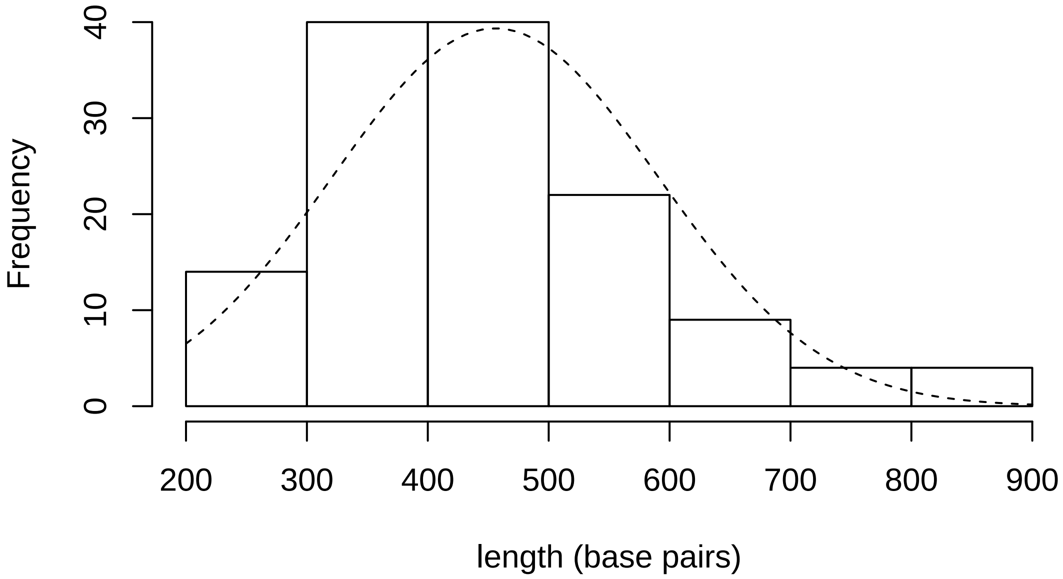
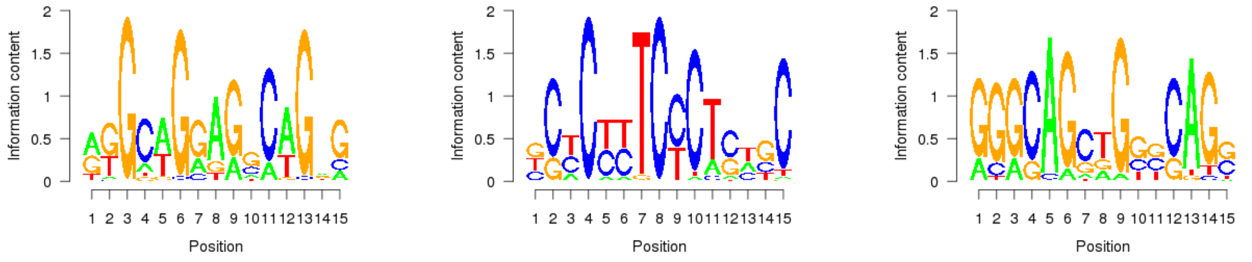


Figure 73: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTrrOd-gCount** component.

property	value
genes	73



(a) ARDHTrrOd-deNovo-meme1: width=15, sites=44, llr=470, E=0.21 (b) ARDHTrrOd-deNovo-meme2: width=15, sites=32, llr=370, E=12 (c) ARDHTrrOd-deNovo-meme3: width=15, sites=23, llr=283, E=10000

Figure 74: De novo motifs for the filtered AR DHT overlaps (down) sequences.

Table 44: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	1955.8872	0.0977	0.0000	11	0	13.35E-06	0.04259
FOXA1	1.9814	0.9098	0.4591	83	88	10.4E-14	0.66976
Foxa2	1.9766	0.6692	0.3385	70	74	3.77E-10	0.48477
FOXA1pAR	1.9318	0.1654	0.0856	20	19	1.427E-02	0.12606
FOXF2	1.7481	0.2857	0.1634	33	36	18.73E-04	0.23031
ARMotifHH	1.7049	0.4511	0.2646	44	55	5.327E-04	0.42157
INSM1	1.5853	0.2406	0.1518	28	30	54.87E-04	0.25726
Gata1	1.4063	0.9248	0.6576	78	116	3.669E-08	0.90328
GRMotifTH	1.4002	0.3759	0.2685	43	62	45.66E-04	0.29483
ARMotifT	1.3972	0.7068	0.5058	62	98	1.066E-04	0.66155
NFIC	1.3745	3.0752	2.2374	119	218	97.0E-20	4.02389
Zfx	1.3667	0.2180	0.1595	26	32	2.80E-02	0.22991
RUNX1	1.3655	0.3985	0.2918	41	67	2.792E-02	0.35473
TFAP2A	1.3502	2.1278	1.5759	91	148	2.634E-10	6.81825
FOXD1	1.3263	1.1353	0.8560	91	136	20.2E-12	1.11587
Myb	1.2918	0.9098	0.7043	79	125	10.7E-08	0.88469
HIF1A::ARNT	1.2524	0.5263	0.4202	43	63	55.58E-04	0.97367
ARMotifH	1.2475	9.3008	7.4553	133	257	23.77E-26	16.71005
Foxq1	1.2349	0.6391	0.5175	56	91	10.13E-04	0.75101
FOXI1	1.2325	0.8872	0.7198	74	111	31.74E-08	1.19175
GRMotifH	1.2114	6.4436	5.3191	131	253	3.726E-24	9.05269
ARID3A	0.8243	3.4286	4.1595	114	229	46.5E-16	10.38010
Nobox	0.8169	1.3985	1.7121	90	177	9.537E-08	2.92851
YY1	0.8148	3.6842	4.5214	130	252	16.68E-24	7.03418
Nkx2-5	0.8143	5.7669	7.0817	129	249	52.41E-24	20.09914
MZF1_5-13	0.8139	1.2857	1.5798	90	184	25.79E-08	1.95716
Sox5	0.8062	1.8571	2.3035	99	208	27.56E-10	3.29582
Prrx2	0.7802	2.0977	2.6887	97	212	2.872E-08	4.79547
Pdx1	0.7578	2.2556	2.9767	102	213	3.043E-10	5.42604
Foxd3	0.7208	1.7669	2.4514	92	168	40.68E-10	10.20173
FOXL1	0.6673	5.7669	8.6420	123	241	15.14E-20	58.66664

15.4 AR DHT overlaps (stable)

Chromosome specific statistics are shown in Table 45. A histogram of sequence lengths is shown in Figure 75.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	390	12	459	975	179179	0.000719
10	127	192	426	937	54041	0.000399
11	171	220	442	1046	75551	0.00056
12	135	3	411	933	55419	0.000414
13	57	280	490	1081	27939	0.000243
14	126	101	447	920	56359	0.000525
15	83	238	457	804	37922	0.00037
16	92	202	421	784	38772	0.000429
17	137	201	436	918	59684	0.000735
18	62	200	429	914	26603	0.000341
19	50	202	407	947	20344	0.000344
2	232	130	436	952	101178	0.000416
20	93	239	451	1609	41909	0.000665
21	30	196	448	704	13451	0.000279
22	36	208	397	640	14306	0.000279
3	281	122	506	1302	142177	0.000718
4	130	223	438	1056	56879	0.000298
5	191	12	454	1152	86681	0.000479
6	189	69	417	778	78891	0.000461
7	165	6	436	903	71895	0.000452
8	135	70	457	800	61651	0.000421
9	108	252	430	769	46395	0.000329
X	44	214	392	579	17268	0.000111
Y	3	275	311	345	932	1.6e-05
all 24	3067	3	445	1609	1365426	0.000441

Table 45: Chromosome specific distribution of the regions. The last line represents the overall statistics.

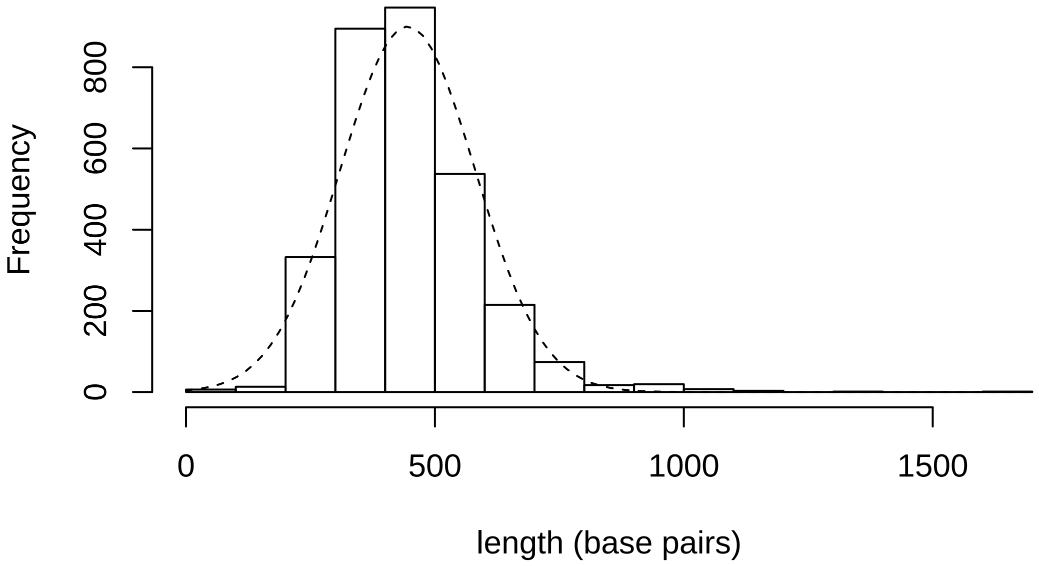
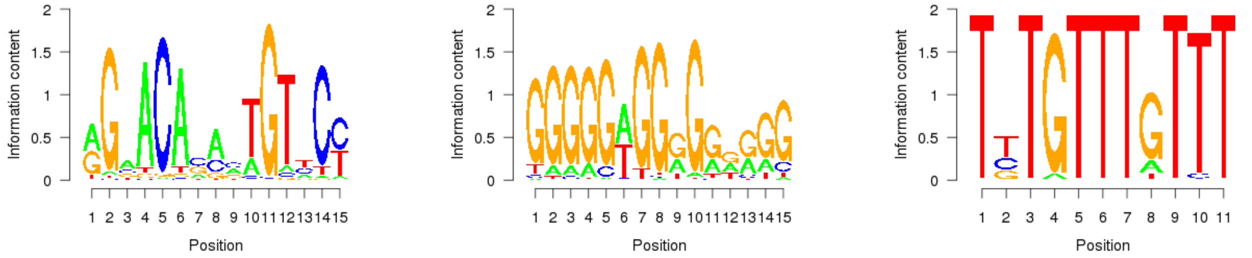


Figure 75: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTrrOs-gCount** component.

property	value
genes	2745



(a) ARDHTrrOs-deNovo-meme1: width=15, sites=211, llr=2123, E=4.8e-84

(b) ARDHTrrOs-deNovo-meme2: width=15, sites=68, llr=821, E=1.3e-18

(c) ARDHTrrOs-deNovo-meme3: width=11, sites=28, llr=359, E=1300

Figure 76: De novo motifs for the filtered AR DHT overlaps (stable) sequences.

Table 46: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	13.0460	0.1077	0.0082	301	46	17.99E-96	0.04810
FOXA1pAR	3.0760	0.2101	0.0683	587	344	10.85E-90	0.13117
FOXA1	2.7990	1.0392	0.3712	1999	1719	0.00E00	0.72083
FOXF2	2.7222	0.3171	0.1165	831	620	20.48E-106	0.19923
TLX1::NFIC	2.6972	0.0189	0.0070	47	31	3.573E-06	0.01557
Foxa2	2.5594	0.8845	0.3456	1806	1487	68.24E-318	0.69619
ARMotifTT	2.4062	0.0144	0.0059	44	34	88.28E-06	0.00879
RXRA::VDR	2.1788	0.0088	0.0040	27	23	66.4E-04	0.00566
ESR2	1.9827	0.0219	0.0110	60	57	2.061E-04	0.01775
STAT1	1.9120	0.0555	0.0290	128	143	7.186E-06	0.05314
ARMotifTH	1.9035	0.0685	0.0360	207	203	1.047E-12	0.04645
FOXD1	1.7885	1.3501	0.7548	2206	2853	26.15E-302	1.18013
Tal1::Gata1	1.7334	0.0633	0.0365	184	207	3.991E-08	0.04647
Stat3	1.6996	0.2467	0.1451	551	658	20.26E-26	0.25123
ARMotifT	1.6695	0.6626	0.3969	1471	1817	1.878E-128	0.53612
E2F1	1.6674	0.0192	0.0115	58	64	34.16E-04	0.01470
Foxq1	1.6609	0.6372	0.3836	1374	1670	68.24E-116	0.59892
PPARG::RXRA	1.6281	0.0268	0.0164	78	92	21.35E-04	0.02121
GRMotifTT	1.6128	0.0290	0.0180	87	103	11.73E-04	0.02182
GRMotifTH	1.6052	0.3641	0.2268	903	1137	1.058E-48	0.30322
NR3C1	1.5955	0.3853	0.2415	920	1186	12.82E-48	0.33196
GABPA	1.5007	0.0933	0.0622	265	333	1.199E-08	0.07884
AR	1.4317	0.0568	0.0396	168	222	1.374E-04	0.04604
ELK4	1.4040	0.0326	0.0232	91	128	2.803E-02	0.02944
Evi1	1.3940	0.0499	0.0358	148	193	2.826E-04	0.04316
FOXI1	1.3890	1.0199	0.7342	1800	2541	50.2E-164	1.23674
Gata1	1.3509	0.8108	0.6001	1602	2468	61.69E-106	0.78707
GRMotifT	1.3460	2.5207	1.8727	2800	4726	0.00E00	2.63286
ARMotifHH	1.3061	0.4108	0.3145	980	1440	3.039E-38	0.40598
Esrrb	1.2950	0.1223	0.0945	347	509	88.39E-08	0.10745
RXR::RAR_DR5	1.2919	0.0300	0.0232	91	128	2.803E-02	0.02699
ARMotifH	1.2583	8.9798	7.1364	3062	5684	0.00E00	15.86004
NFIC	1.2557	2.8910	2.3023	2759	4852	0.00E00	3.83705
FOXO3	1.2491	1.9214	1.5382	2462	4134	10.14E-302	2.35703
Pdx1	0.8275	2.3693	2.8633	2488	4885	1.028E-258	5.65612
MZF1_5-13	0.8204	1.2395	1.5109	2024	4152	24.72E-120	1.97570
IRF1	0.8157	0.2153	0.2640	579	1192	4.796E-02	0.30752
HLF	0.8143	0.4251	0.5221	936	2063	23.38E-06	0.67715
SP1	0.8118	1.0962	1.3504	1336	2827	20.15E-26	5.29829
CREB1	0.8050	0.7002	0.8697	1455	3055	17.88E-36	1.05013
Prrx2	0.7871	2.1259	2.7011	2389	4793	59.14E-220	4.99306
FOXL1	0.7809	6.2744	8.0344	2896	5383	0.00E00	61.05095
Foxd3	0.7753	2.0512	2.6457	2239	4017	28.82E-208	11.91659
Zfx	0.7059	0.1285	0.1821	333	847	53.75E-04	0.21751
Ddit3::Cebpa	0.5292	0.2277	0.4304	610	1713	5.03E-04	0.47879
SRF	0.5184	0.0101	0.0196	26	94	39.86E-04	0.02123

15.5 AR CPA overlaps

Chromosome specific statistics are shown in Table 47. A histogram of sequence lengths is shown in Figure 77.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	185	21	206	581	38135	0.000153
10	62	40	184	434	11420	8.4e-05
11	75	35	219	589	16431	0.000122
12	69	46	199	705	13725	0.000103
13	47	51	236	722	11094	9.6e-05
14	51	4	187	432	9526	8.9e-05
15	62	37	217	427	13440	0.000131
16	67	36	175	392	11740	0.00013
17	105	21	200	586	21043	0.000259
18	39	25	183	440	7153	9.2e-05
19	50	33	153	364	7631	0.000129
2	116	27	215	654	24899	0.000102
20	56	33	203	502	11373	0.00018
21	24	42	170	377	4071	8.5e-05
22	19	45	168	272	3195	6.2e-05
3	128	10	217	447	27721	0.00014
4	56	1	185	557	10368	5.4e-05
5	104	5	210	468	21839	0.000121
6	82	44	192	515	15727	9.2e-05
7	83	46	191	375	15874	1e-04
8	99	29	210	417	20744	0.000142
9	64	21	200	395	12784	9.1e-05
X	24	49	160	384	3831	2.5e-05
Y	4	114	186	283	745	1.3e-05
all 24	1671	1	200	722	334509	0.000108

Table 47: Chromosome specific distribution of the regions. The last line represents the overall statistics.

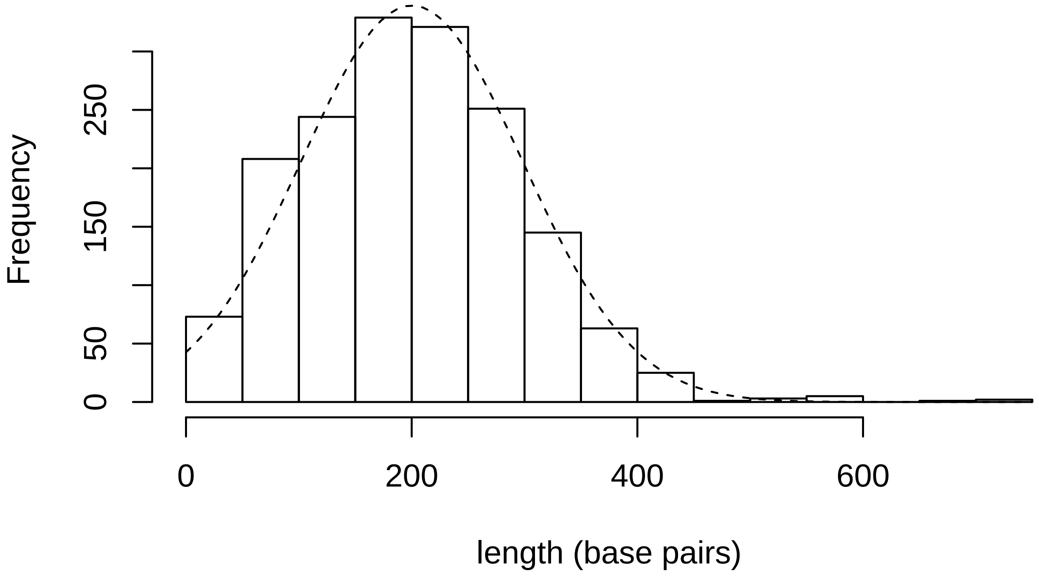
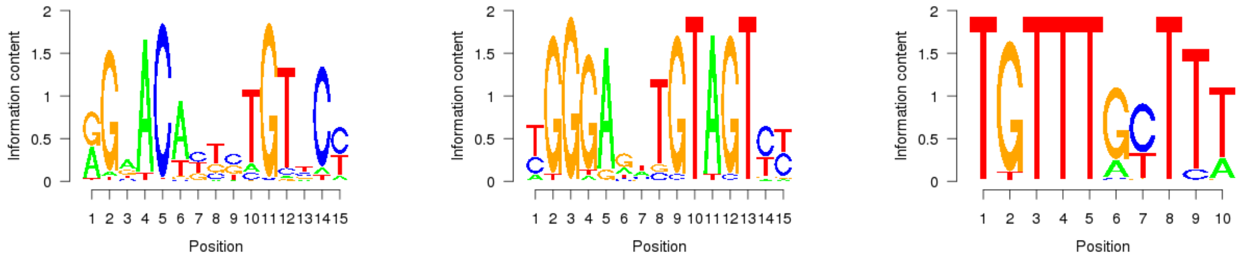


Figure 77: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPArrO-gCount** component.

property	value
genes	5628



(a) ARCPArrO-deNovo-meme1: width=15, sites=218, llr=2249, E=7.8e-204

(b) ARCPArrO-deNovo-meme2: width=15, sites=26, llr=357, E=1.5e-05

(c) ARCPArrO-deNovo-meme3: width=10, sites=37, llr=423, E=0.7

Figure 78: De novo motifs for the filtered AR CPA overlaps sequences.

Table 48: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	45.3297	0.0168	0.0003	13	1	19.04E-06	0.02572
Ar	40.6993	0.1722	0.0042	256	12	12.06E-102	0.07312
RREB1	26.8277	0.5363	0.0199	124	38	10.16E-30	3.42003
TLX1::NFIC	7.9029	0.0156	0.0019	19	5	13.56E-06	0.01001
E2F1	4.8582	0.0252	0.0051	40	16	1.607E-08	0.01284
PLAG1	4.1633	0.0390	0.0093	50	26	1.97E-08	0.02809
ELK4	3.7132	0.0300	0.0080	46	25	16.44E-08	0.01755
ESR2	3.7021	0.0180	0.0048	29	14	13.44E-06	0.01017
ARMotifTT	3.6707	0.0084	0.0023	14	7	45.56E-04	0.00438
SP1	3.5635	2.0564	0.5770	642	878	45.91E-38	13.98416
MIZF	3.4809	0.0270	0.0077	45	23	8.514E-08	0.01466
Foxa2	2.8928	0.4253	0.1470	562	390	74.48E-86	0.30059
FOXA1	2.8814	0.4811	0.1669	612	456	1.098E-88	0.32537
STAT1	2.8619	0.0360	0.0125	47	34	14.29E-06	0.02784
NR3C1	2.6880	0.2819	0.1049	386	295	13.83E-46	0.19588
FOXF2	2.5305	0.1344	0.0531	199	156	6.00E-20	0.08991
Stat3	2.4783	0.1404	0.0566	173	147	46.54E-16	0.12080
GABPA	2.4524	0.0624	0.0254	100	77	4.362E-10	0.03937
Klf4	2.2215	0.2016	0.0907	261	244	2.327E-20	0.18723
Egr1	2.1935	0.0798	0.0363	119	111	1.16E-08	0.05640
FOXA1pAR	2.1298	0.0720	0.0338	111	101	1.787E-08	0.05035
ARMotifT	2.1052	0.3887	0.1846	520	510	5.948E-48	0.28049
GRMotifTH	1.9944	0.2028	0.1016	285	293	66.19E-20	0.15632
Tal1::Gata1	1.9860	0.0288	0.0145	47	45	11.5E-04	0.01952
MZF1_1-4	1.9079	3.4379	1.8019	1323	2126	73.81E-168	15.10636
ARMotifHH	1.8020	0.2412	0.1338	334	359	28.94E-22	0.20354
FOXD1	1.7501	0.5945	0.3397	689	808	28.6E-58	0.54485
TFAP2A	1.7260	1.2891	0.7469	842	1158	18.38E-66	2.75466
Esrrb	1.6457	0.0678	0.0412	107	121	35.56E-06	0.05421
HIF1A::ARNT	1.6456	0.2747	0.1669	329	411	1.269E-14	0.29930
Arnt	1.5933	0.1128	0.0708	132	145	85.56E-08	0.14935
GRMotifT	1.5709	1.3521	0.8607	1114	1680	3.888E-112	1.38074
ARMotifH	1.5708	5.0378	3.2071	1561	2716	7.001E-256	8.77987
EBF1	1.5022	0.4049	0.2695	457	613	1.813E-20	0.46779
NFIC	1.4929	1.5381	1.0302	1157	1800	60.85E-120	1.81767
Pax5	1.4755	0.0342	0.0232	54	70	3.782E-02	0.02838
ARMotifTH	1.4728	0.0294	0.0199	49	60	2.592E-02	0.02354
Foxq1	1.4508	0.2627	0.1811	374	455	65.5E-20	0.26748
Mycn	1.4132	0.0714	0.0505	91	118	39.69E-04	0.08587
GRMotifHH	1.3901	0.1230	0.0885	184	245	10.69E-06	0.11346
NHLH1	1.3659	0.0756	0.0553	81	115	3.514E-02	0.10584
Myb	1.3389	0.4229	0.3159	537	806	1.933E-20	0.40945
Gata1	1.3130	0.3353	0.2554	453	649	81.39E-18	0.32161
ELK1	1.3060	0.4667	0.3573	573	880	6.028E-22	0.47369
FEV	1.3004	0.3233	0.2486	446	648	11.1E-16	0.30316
Myc	1.2647	0.0822	0.0650	108	158	1.88E-02	0.10114
Myf	1.2507	0.1332	0.1065	183	254	61.63E-06	0.18115
Hand1::Tcfe2a	1.2472	0.5837	0.4680	682	1114	14.09E-28	0.58213
GRMotifH	1.2416	3.0000	2.4162	1399	2546	3.468E-172	4.85764
Arnt::Ahr	1.2300	0.7564	0.6150	716	1087	41.76E-38	2.01989
TAL1::TCF3	1.2296	0.1080	0.0878	136	210	1.922E-02	0.13613
Mafb	1.2124	1.0330	0.8520	924	1548	60.3E-58	1.39239
FOXI1	1.2095	0.3929	0.3249	477	741	1.75E-14	0.49101
Sox5	0.8333	0.7708	0.9251	764	1584	2.16E-18	1.41148
YY1	0.8031	1.4925	1.8585	1124	2376	2.013E-66	3.02570
Fos	0.7954	0.5723	0.7195	641	1405	6.584E-08	0.89989
HLF	0.7499	0.1626	0.2168	217	559	3.641E-02	0.24210
HOXA5	0.7333	2.1626	2.9492	1217	2570	3.597E-88	6.27484
Nobox	0.7324	0.5369	0.7330	556	1274	13.2E-04	1.17375
Foxd3	0.6973	0.8038	1.1528	659	1366	29.98E-12	4.82710
Nkx2-5	0.6906	1.9970	2.8916	1129	2438	86.64E-66	7.21046
IRF1	0.6818	0.0750	0.1100	109	293	1.201E-02	0.12929
ARID3A	0.6587	1.1458	1.7395	886	2010	32.2E-24	3.58849
NFIL3	0.6362	0.0534	0.0839	74	217	37.08E-04	0.09892
Pdx1	0.6021	0.7600	1.2625	710	1828	60.84E-06	2.08079
PBX1	0.5933	0.0330	0.0556	54	148	3.50E-02	0.06683
FOXL1	0.5359	1.9400	3.6201	1042	2381	1.493E-42	21.07970
Ddit3::Cebpa	0.4984	0.0888	0.1782	135	457	66.11E-08	0.17986
Lhx3	0.4816	0.0762	0.1583	99	339	4.018E-06	0.24016
MEF2A	0.4684	0.0714	0.1525	104	381	9.709E-08	0.16448

15.6 AR CPA overlaps (up)

Chromosome specific statistics are shown in Table 49. A histogram of sequence lengths is shown in Figure 79.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	10	156	258	379	2580	1e-05
2	11	58	242	403	2664	1.1e-05
3	10	43	211	364	2107	1.1e-05
4	10	113	192	326	1925	1e-05
5	5	209	295	340	1474	8e-06
6	12	119	217	325	2607	1.5e-05
7	2	168	241	314	482	3e-06
8	10	126	239	368	2388	1.6e-05
9	2	160	172	183	343	2e-06
10	11	39	172	381	1892	1.4e-05
11	7	184	334	589	2336	1.7e-05
12	4	232	261	283	1045	8e-06
13	4	51	147	189	587	5e-06
14	2	189	210	230	419	4e-06
15	6	51	214	381	1281	1.2e-05
16	1	217	217	217	217	2e-06
17	5	150	283	421	1416	1.7e-05
18	1	306	306	306	306	4e-06
19	4	127	207	364	829	1.4e-05
20	3	206	290	335	870	1.4e-05
21	6	42	199	281	1196	2.5e-05
all 21	126	39	230	589	28964	9e-06

Table 49: Chromosome specific distribution of the regions. The last line represents the overall statistics.

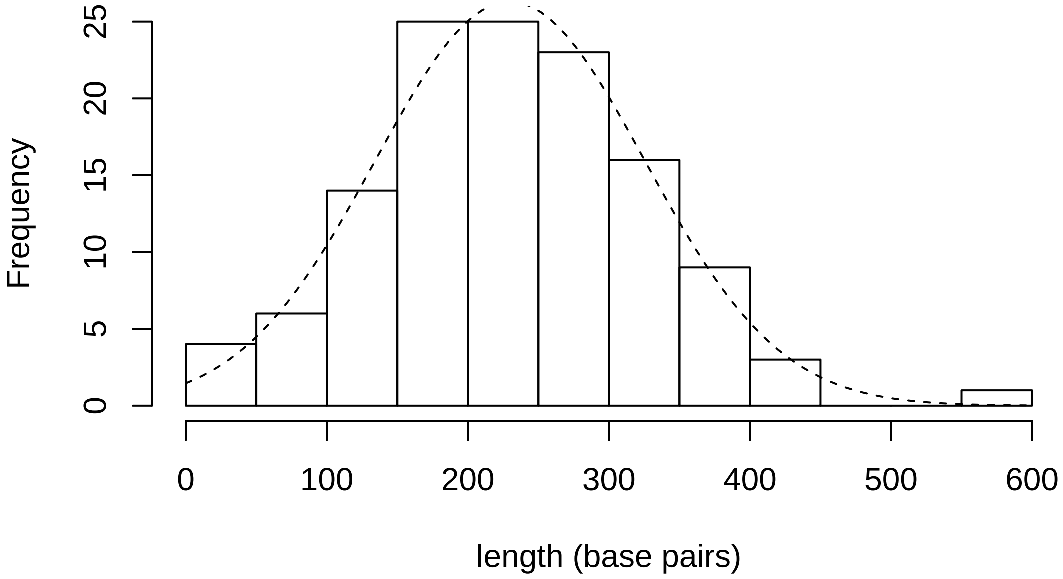
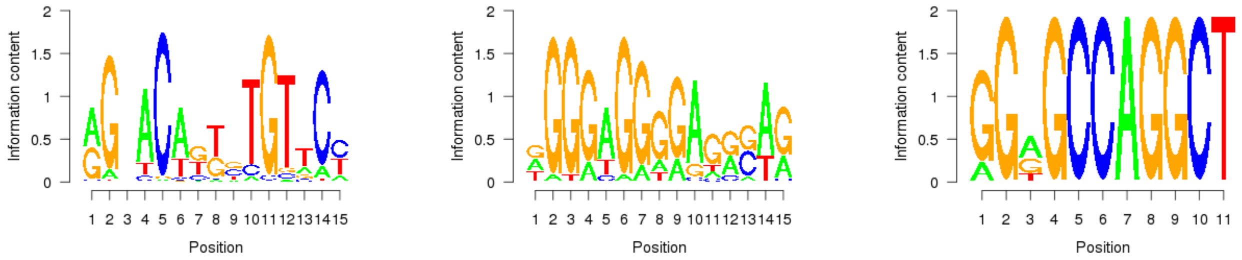


Figure 79: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPArrOu-gCount** component.

property	value
genes	81



(a) ARCPArrOu-deNovo-meme1: width=15, sites=82, llr=797, E=6.8e-58 (b) ARCPArrOu-deNovo-meme2: width=15, sites=24, llr=282, E=16 (c) ARCPArrOu-deNovo-meme3: width=11, sites=6, llr=85, E=3e+06

Figure 80: De novo motifs for the filtered AR CPA overlaps (up) sequences.

Table 50: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	68.7919	0.2937	0.0042	32	1	1.321E-14	0.12713
GABPA	5.0001	0.0635	0.0127	8	2	63.32E-04	0.03499
Foxa2	3.7102	0.5794	0.1561	53	31	13.66E-12	0.39411
FOXA1	3.2364	0.5873	0.1814	58	38	5.526E-12	0.35163
ARMotifT	3.1344	0.5952	0.1899	55	40	3.434E-10	0.43738
SP1	3.0750	1.6349	0.5316	54	72	74.25E-06	6.42639
Stat3	2.6630	0.1349	0.0506	13	11	4.875E-02	0.10686
FOXF2	2.5514	0.1508	0.0591	17	13	93.39E-04	0.09945
GRMotifTH	2.5270	0.3413	0.1350	30	28	9.984E-04	0.26935
NR3C1	2.5228	0.4365	0.1730	44	37	1.455E-06	0.28898
GRMotifHH	2.2223	0.2063	0.0928	22	20	74.95E-04	0.15374
ARMotifHH	2.0516	0.2857	0.1392	30	31	28.47E-04	0.20963
GRMotifT	2.0369	1.7619	0.8650	99	134	3.727E-16	1.50474
Foxq1	2.0183	0.3492	0.1730	38	35	61.55E-06	0.25165
TFAP2A	1.8492	1.3889	0.7511	63	94	22.84E-06	3.26996
ARMotifH	1.8100	6.0714	3.3544	123	212	10.57E-24	9.63499
FOXD1	1.7099	0.7143	0.4177	59	82	26.55E-06	0.55965
NFIC	1.6735	1.8571	1.1097	93	142	2.908E-12	2.48214
FEV	1.5489	0.4444	0.2869	47	57	1.604E-04	0.34155
MZF1_1-4	1.4875	2.8810	1.9367	97	175	24.2E-12	8.60390
Cebpa	1.4269	0.5238	0.3671	47	66	13.58E-04	0.50970
GRMotifH	1.3643	3.7302	2.7342	116	204	15.22E-20	5.20078
FOXO3	1.3480	1.0238	0.7595	82	117	7.193E-10	1.02753
FOXI1	1.3331	0.5794	0.4346	53	69	69.58E-06	0.65378
SPI1	1.3204	1.1032	0.8354	78	127	20.64E-08	1.09983
NR4A2	1.3081	1.0873	0.8312	75	119	49.58E-08	1.28366
Spz1	1.2539	0.3968	0.3165	42	63	1.009E-02	0.37004
Sox5	0.8139	0.9444	1.1603	70	145	7.711E-04	1.57003
HOXA5	0.7641	2.7857	3.6456	100	215	4.447E-10	7.44824
YY1	0.7311	1.5238	2.0844	90	186	11.01E-08	2.84970
Nkx2-5	0.7192	2.4762	3.4430	98	206	10.03E-10	8.06301
Arnt::Ahr	0.6617	0.7063	1.0675	59	112	44.39E-04	5.02703
ARID3A	0.6094	1.2857	2.1097	81	178	39.8E-06	3.74783
FOXL1	0.5183	2.2698	4.3797	92	200	12.09E-08	22.11289
MEF2A	0.3257	0.0714	0.2194	7	39	1.946E-02	0.24516

15.7 AR CPA overlaps (down)

Chromosome specific statistics are shown in Table 51. A histogram of sequence lengths is shown in Figure 81.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	2	163	204	246	409	2e-06
2	4	132	227	343	908	4e-06
3	4	63	226	447	906	5e-06
5	3	66	189	289	568	3e-06
7	3	169	205	275	616	4e-06
8	2	166	206	247	413	3e-06
10	3	60	128	208	383	3e-06
11	2	135	188	242	377	3e-06
12	1	186	186	186	186	1e-06
16	1	128	128	128	128	1e-06
19	1	48	48	48	48	1e-06
all 11	26	48	190	447	4942	2e-06

Table 51: Chromosome specific distribution of the regions. The last line represents the overall statistics.

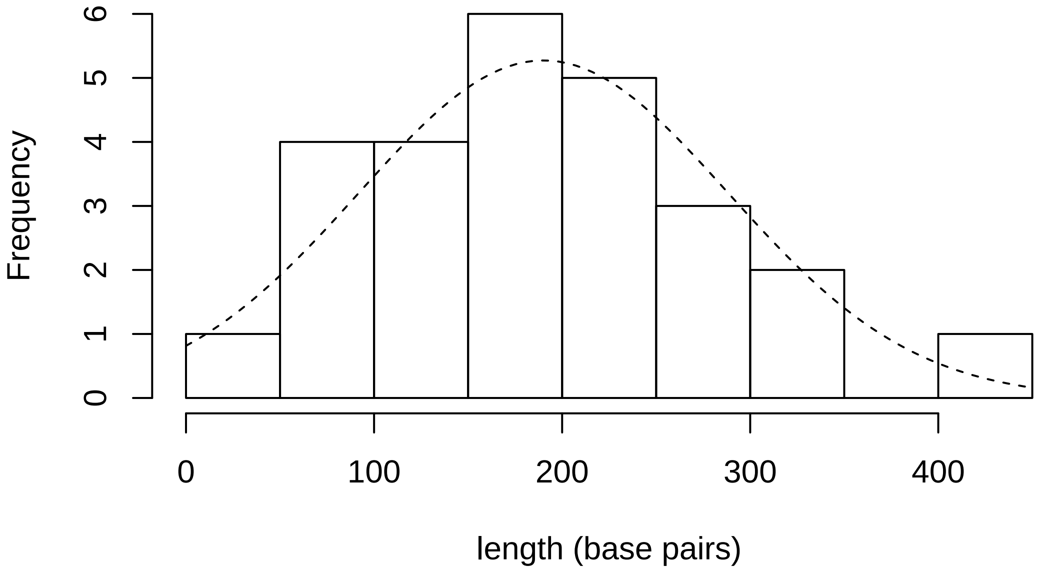
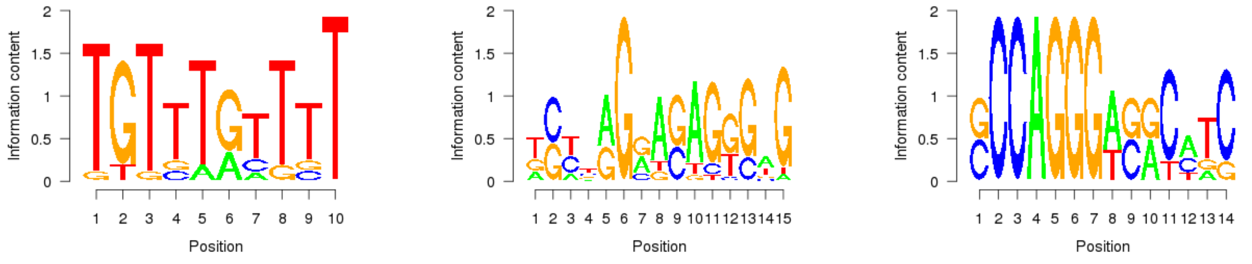


Figure 81: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPArrOd-gCount** component.

property	value
genes	23



(a) ARCPArrOd-deNovo-meme1: width=10, sites=16, llr=145, E=3.2 (b) ARCPArrOd-deNovo-meme2: width=15, sites=18, llr=176, E=0.77 (c) ARCPArrOd-deNovo-meme3: width=14, sites=6, llr=85, E=39000

Figure 82: De novo motifs for the filtered AR CPA overlaps (down) sequences.

Table 52: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Stat3	3847.1538	0.1923	0.0000	4	0	2.099E-02	0.08895
SP1	10.4059	3.5385	0.3400	12	13	2.951E-02	23.95561
INSM1	9.5939	0.1923	0.0200	5	1	2.614E-02	0.07368
FOXA1	3.4181	0.6154	0.1800	13	7	5.602E-04	0.35702
Foxq1	3.2033	0.1923	0.0600	5	1	2.614E-02	0.17544
FEV	3.0759	0.3077	0.1000	8	5	3.098E-02	0.14368
MZF1_1-4	3.0031	4.3846	1.4600	25	31	88.41E-08	18.65175
Foxa2	2.6437	0.4231	0.1600	10	8	2.384E-02	0.21667
ELF5	2.2434	0.8077	0.3600	15	14	23.14E-04	0.54649
SPI1	2.2114	0.8846	0.4000	15	16	49.33E-04	0.59561
NR4A2	2.1033	1.3462	0.6400	19	22	4.07E-04	1.27912
Mafb	2.0395	1.3462	0.6600	18	23	17.99E-04	1.18877
NFATC2	2.0031	0.9615	0.4800	14	19	3.08E-02	0.73877
GRMotifT	1.7823	1.4615	0.8200	16	25	2.191E-02	1.79842
ARMotifH	1.7295	5.1538	2.9800	25	43	15.41E-06	9.02930
NFIC	1.6968	1.7308	1.0200	20	29	8.421E-04	1.90316
MZF1_5-13	1.6153	0.8077	0.5000	13	16	3.194E-02	0.98877
ETS1	1.5734	3.4615	2.2000	22	40	6.891E-04	4.95579
TFAP2A	1.4423	0.6923	0.4800	13	12	80.66E-04	1.07719
SPIB	1.4151	1.5000	1.0600	16	28	3.915E-02	2.16842
Nkx2-5	0.8001	2.1923	2.7400	19	43	2.782E-02	6.33053
En1	0.6845	1.6154	2.3600	19	37	1.207E-02	3.72211
HOXA5	0.6553	1.7692	2.7000	19	43	2.782E-02	4.95912

15.8 AR CPA overlaps (stable)

Chromosome specific statistics are shown in Table 53. A histogram of sequence lengths is shown in Figure 83.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	123	36	202	581	24869	1e-04
10	40	45	178	434	7133	5.3e-05
11	42	35	217	400	9115	6.8e-05
12	37	51	192	361	7105	5.3e-05
13	20	52	262	722	5247	4.6e-05
14	38	8	180	432	6834	6.4e-05
15	28	48	211	390	5911	5.8e-05
16	45	37	178	389	8028	8.9e-05
17	78	30	209	586	16283	0.000201
18	22	25	182	339	3994	5.1e-05
19	38	33	150	364	5712	9.7e-05
2	78	27	208	654	16217	6.7e-05
20	34	42	188	502	6400	0.000102
21	24	42	222	967	5340	0.000111
22	16	80	173	258	2762	5.4e-05
3	74	41	218	447	16158	8.2e-05
4	28	1	170	557	4764	2.5e-05
5	62	5	210	401	13011	7.2e-05
6	59	46	181	338	10651	6.2e-05
7	48	46	187	375	8984	5.6e-05
8	48	29	213	382	10218	7e-05
9	30	21	172	379	5163	3.7e-05
X	14	49	183	384	2559	1.6e-05
Y	1	180	180	180	180	3e-06
all 24	1027	1	197	967	202638	6.5e-05

Table 53: Chromosome specific distribution of the regions. The last line represents the overall statistics.

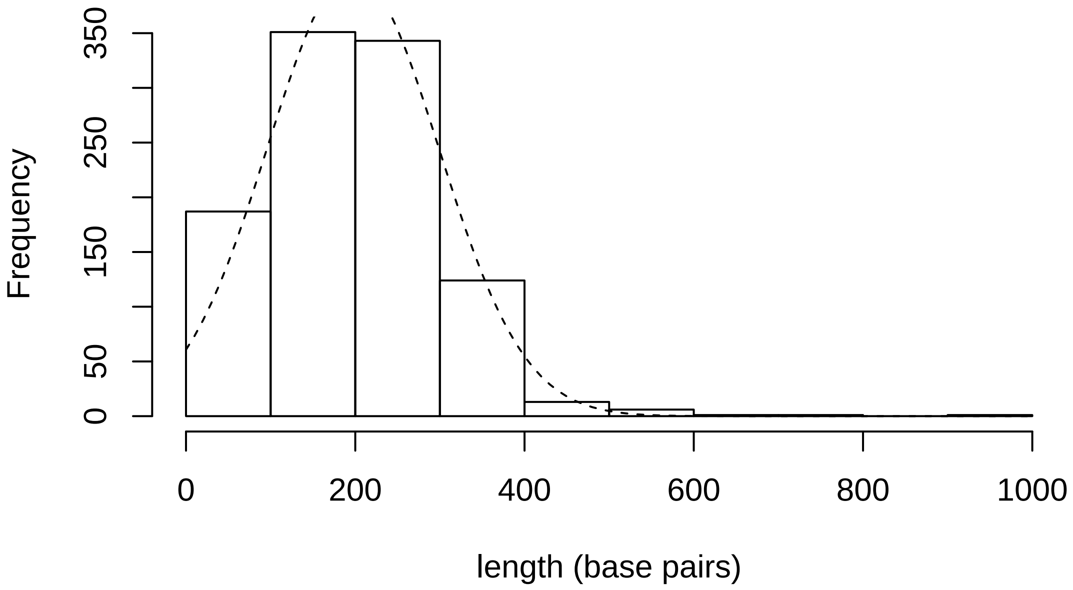
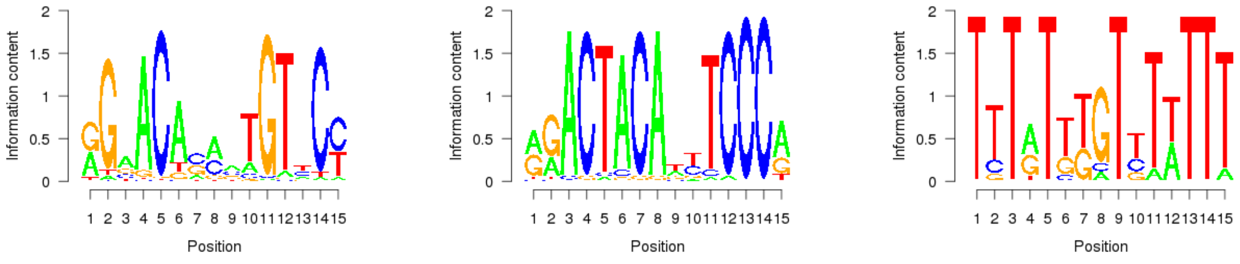


Figure 83: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPArrOs-gCount** component.

property	value
genes	1418



(a) ARCPArrOs-deNovo-meme1: width=15, sites=226, llr=2261, E=1.4e-189 (b) ARCPArrOs-deNovo-meme2: width=15, sites=37, llr=523, E=2.1e-34 (c) ARCPArrOs-deNovo-meme3: width=15, sites=11, llr=164, E=2e+08

Figure 84: De novo motifs for the filtered AR CPA overlaps (stable) sequences.

Table 54: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	176.7812	0.0088	0.0000	7	0	12.03E-04	0.00439
E2F1	41.3219	0.0234	0.0005	22	1	26.81E-10	0.00975
RREB1	27.1960	0.6357	0.0233	83	29	41.43E-20	4.76286
Ar	24.3163	0.1650	0.0067	152	13	40.22E-58	0.07005
PLAG1	6.8601	0.0430	0.0062	34	10	51.34E-10	0.02742
TLX1::NFIC	5.5633	0.0146	0.0026	12	4	16.91E-04	0.00944
SP1	3.9598	2.3506	0.5936	439	531	41.28E-38	17.93885
ELK4	3.6418	0.0322	0.0088	32	17	9.572E-06	0.01733
STAT1	3.5446	0.0332	0.0093	26	17	5.607E-04	0.02340
Egr1	3.5320	0.1045	0.0295	94	53	92.6E-16	0.06534
Stat3	2.8442	0.1357	0.0477	105	81	24.27E-12	0.10601
MIZF	2.8169	0.0293	0.0104	30	20	2.284E-04	0.01665
FOXA1	2.7306	0.4375	0.1602	340	266	8.651E-46	0.30926
Foxa2	2.4485	0.3809	0.1555	310	250	1.016E-38	0.28820
GRMotifTT	2.3854	0.0137	0.0057	14	11	3.997E-02	0.00840
Tal1::Gata1	2.2711	0.0283	0.0124	28	24	46.36E-04	0.01831
GABPA	2.2304	0.0625	0.0280	63	50	1.244E-06	0.04176
ESR2	2.2296	0.0186	0.0083	18	13	98.43E-04	0.01443
Klf4	2.1484	0.2295	0.1068	187	174	3.873E-16	0.20906
TFAP2A	2.0950	1.5010	0.7164	546	690	12.2E-54	4.21599
MZF1_1-4	2.0883	3.7793	1.8097	808	1323	1.183E-100	18.73580
NR3C1	2.0863	0.2510	0.1203	209	204	43.14E-18	0.19987
Pax5	2.0793	0.0410	0.0197	39	38	31.42E-04	0.02840
FOXA1pAR	1.9932	0.0703	0.0353	68	59	3.231E-06	0.05669
FOXF2	1.9491	0.1152	0.0591	102	109	2.892E-06	0.08800
ARMotifT	1.9424	0.3545	0.1825	294	306	1.597E-24	0.26757
Arnt	1.8514	0.1143	0.0617	76	77	30.02E-06	0.15689
HIF1A::ARNT	1.8096	0.3105	0.1716	223	253	6.057E-14	0.36123
ARMotifHH	1.7893	0.2412	0.1348	206	220	3.564E-14	0.21137
Esrrb	1.7572	0.0684	0.0389	66	73	7.034E-04	0.05145
NHLH1	1.7022	0.0645	0.0378	43	49	1.301E-02	0.07807
GRMotifTH	1.6742	0.1875	0.1120	164	196	2.836E-08	0.15977
ARMotifH	1.6400	5.0713	3.0923	956	1674	44.96E-158	8.90893
EBF1	1.6325	0.4189	0.2566	293	366	44.07E-18	0.46642
Myf	1.6322	0.1270	0.0778	106	142	9.69E-04	0.11431
Mycn	1.6026	0.0781	0.0487	58	71	86.05E-04	0.09544
FOXD1	1.5994	0.5439	0.3401	390	507	5.593E-26	0.51380
NFIC	1.5598	1.5283	0.9798	708	1067	24.25E-78	1.81323
GRMotifT	1.5265	1.2852	0.8419	669	1008	97.69E-68	1.34111
ELK1	1.4661	0.4834	0.3297	361	499	10.9E-20	0.48368
Foxq1	1.4581	0.2275	0.1560	201	255	25.35E-10	0.21322
Arnt::Ahr	1.4236	0.8398	0.5899	452	658	7.386E-28	1.79409
Myb	1.3499	0.4248	0.3147	326	507	6.019E-12	0.39916
GR	1.3410	0.1279	0.0954	122	167	4.572E-04	0.11497
GRMotifHH	1.3250	0.1182	0.0892	109	154	27.72E-04	0.11041
Mafb	1.3221	1.0527	0.7963	580	926	4.092E-42	1.37672
FEV	1.2833	0.3193	0.2488	270	416	1.401E-08	0.28742
GRMotifH	1.2024	2.8418	2.3634	842	1565	1.236E-98	4.69028
GATA3	0.8137	2.2031	2.7076	741	1608	9.866E-52	5.33574
YY1	0.7901	1.4688	1.8590	678	1466	5.193E-38	2.83690
GATA2	0.7895	4.3447	5.5029	879	1832	6.122E-100	14.35458
SRY	0.7569	1.2422	1.6413	580	1292	2.388E-20	3.03598
Sox5	0.7260	0.6699	0.9228	428	1004	17.1E-06	1.35389
Fos	0.7010	0.5029	0.7175	366	894	1.925E-02	0.79871
HOXA5	0.6948	2.0469	2.9461	719	1615	10.97E-44	6.24967
HLF	0.6368	0.1416	0.2224	112	329	55.69E-04	0.26437
Foxd3	0.6285	0.7441	1.1840	371	865	23.27E-04	4.93024
Nkx2-5	0.6260	1.8232	2.9124	660	1524	4.824E-30	7.50633
ARID3A	0.5803	1.0430	1.7973	500	1269	29.47E-08	3.83214
IRF1	0.5519	0.0684	0.1239	61	199	14.98E-04	0.13505
NFIL3	0.5355	0.0508	0.0949	45	147	45.21E-04	0.10918
FOXL1	0.4955	1.6953	3.4215	589	1471	14.51E-16	17.19389
MEF2A	0.4727	0.0723	0.1529	63	227	81.62E-06	0.17984
Ddit3::Cebpa	0.4397	0.0820	0.1866	78	285	13.75E-06	0.19080
Lhx3	0.4047	0.0654	0.1617	54	204	51.16E-06	0.25757

15.9 AR RU486 overlaps

Chromosome specific statistics are shown in Table 55. A histogram of sequence lengths is shown in Figure 85.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	71	26	174	464	12326	4.9e-05
10	24	38	127	340	3040	2.2e-05
11	34	32	171	515	5820	4.3e-05
12	28	37	119	256	3320	2.5e-05
13	23	38	185	346	4263	3.7e-05
14	20	38	124	275	2484	2.3e-05
15	19	36	165	288	3141	3.1e-05
16	30	37	118	281	3534	3.9e-05
17	41	23	148	566	6064	7.5e-05
18	12	50	149	304	1790	2.3e-05
19	17	21	103	288	1746	3e-05
2	63	14	144	415	9085	3.7e-05
20	19	37	169	509	3220	5.1e-05
21	7	39	72	207	506	1.1e-05
22	5	69	122	180	608	1.2e-05
3	51	33	172	349	8770	4.4e-05
4	23	33	146	326	3366	1.8e-05
5	33	33	159	295	5262	2.9e-05
6	18	4	120	268	2166	1.3e-05
7	29	15	107	286	3101	1.9e-05
8	34	29	140	300	4752	3.2e-05
9	22	8	123	248	2703	1.9e-05
X	9	34	74	173	664	4e-06
Y	14	9	91	288	1279	2.2e-05
all 24	646	4	144	566	93010	3e-05

Table 55: Chromosome specific distribution of the regions. The last line represents the overall statistics.

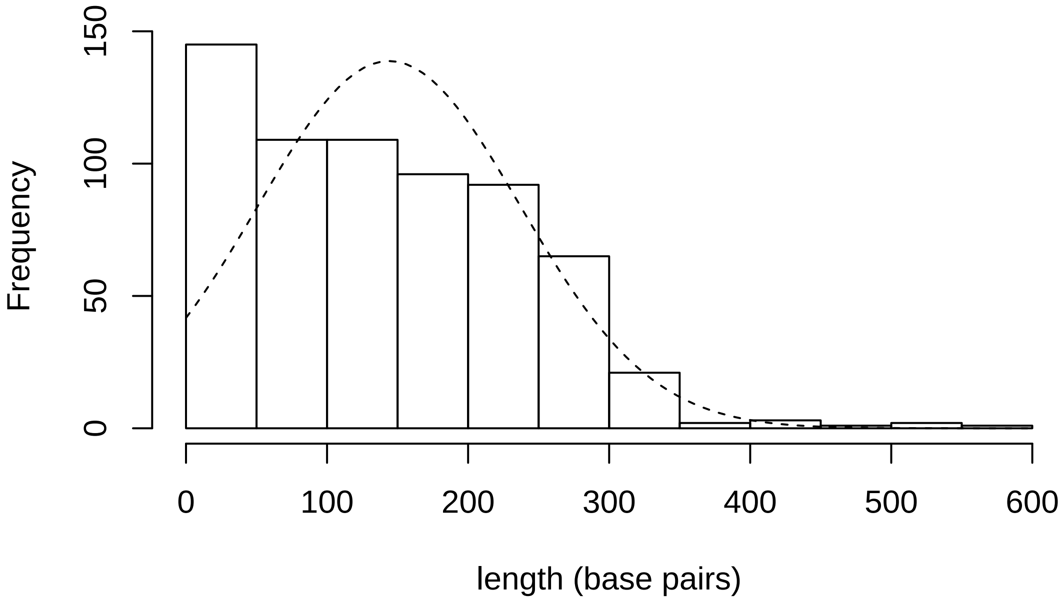
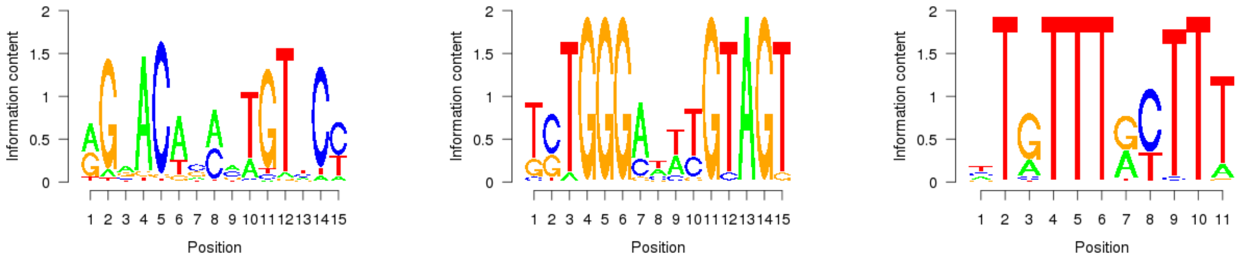


Figure 85: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARRU486rrO-gCount** component.

property	value
genes	2387



(a) ARRU486rrO-deNovo-meme1: width=15, sites=181, llr=1732, E=1.9e-118

(b) ARRU486rrO-deNovo-meme2: width=15, sites=18, llr=268, E=6.3e-06

(c) ARRU486rrO-deNovo-meme3: width=11, sites=43, llr=471, E=0.0069

Figure 86: De novo motifs for the filtered AR RU486 overlaps sequences.

Table 56: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	746.3416	0.0373	0.0000	10	0	68.4E-06	0.06195
RREB1	74.9756	1.0730	0.0143	108	12	1.031E-38	3.46974
Ar	36.0339	0.1227	0.0034	73	4	1.023E-28	0.05082
PLAG1	10.7007	0.0543	0.0050	27	6	3.552E-08	0.03056
E2F1	10.3038	0.0264	0.0025	17	3	7.615E-06	0.01078
ARMotifTT	8.7904	0.0078	0.0008	5	1	3.999E-02	0.00326
SP1	7.6880	3.4767	0.4522	271	278	91.5E-30	19.99165
ESR2	6.0691	0.0155	0.0025	10	3	38.92E-04	0.00703
MZF1_1-4	3.4621	4.6211	1.3347	469	685	44.23E-58	21.31374
FOXF2	3.2922	0.1134	0.0344	67	40	4.328E-10	0.06699
MIZF	2.8669	0.0217	0.0076	14	9	1.601E-02	0.01238
Klf4	2.7752	0.2143	0.0772	104	79	5.08E-12	0.17939
Foxa2	2.7614	0.3012	0.1091	155	100	28.37E-24	0.27838
FOXA1	2.7027	0.3447	0.1275	175	139	29.01E-22	0.23750
NR3C1	2.6401	0.1972	0.0747	108	77	13.36E-14	0.14419
Stat3	2.6045	0.1071	0.0411	53	44	22.95E-06	0.08415
STAT1	2.5056	0.0295	0.0117	15	12	3.833E-02	0.02529
NFKB1	2.2175	0.0373	0.0168	20	16	1.361E-02	0.03648
Pax5	2.2163	0.0280	0.0126	17	15	4.452E-02	0.01875
GRMotifTH	2.2001	0.1366	0.0621	81	71	18.39E-08	0.09139
Egr1	2.1731	0.0730	0.0336	42	40	14.97E-04	0.05170
Arnt	2.1077	0.0761	0.0361	35	30	13.52E-04	0.08686
ARMotifT	2.0506	0.2547	0.1242	132	139	17.72E-10	0.19127
HIF1A::ARNT	1.9541	0.2050	0.1049	96	99	93.88E-08	0.21963
Myf	1.9396	0.1009	0.0520	53	47	73.65E-06	0.11238
ARMotifHH	1.9093	0.2019	0.1057	109	111	5.43E-08	0.16474
TFAP2A	1.8538	0.9720	0.5243	279	353	9.606E-22	2.05264
FOXD1	1.7476	0.4208	0.2408	191	236	11.94E-12	0.40131
ARMotifH	1.6246	3.6009	2.2164	533	893	5.092E-70	7.09321
GRMotifT	1.5553	0.9068	0.5831	322	495	1.421E-20	0.93407
NFIC	1.5380	1.0916	0.7097	332	522	34.12E-22	1.41697
Foxq1	1.4854	0.1894	0.1275	100	120	37.59E-06	0.21423
Myb	1.4806	0.3230	0.2181	162	231	2.28E-06	0.28267
Gata1	1.4076	0.2516	0.1787	135	180	8.333E-06	0.23564
GR	1.3333	0.1040	0.0780	61	85	3.509E-02	0.09594
FEV	1.3047	0.2003	0.1535	113	162	9.153E-04	0.18909
Mafb	1.2651	0.7780	0.6149	283	461	21.95E-14	1.05428
ELK1	1.2586	0.3168	0.2517	163	245	15.03E-06	0.32133
NR4A2	1.2514	0.6320	0.5050	264	420	4.47E-12	0.73051
GRMotifH	1.2033	2.0140	1.6737	432	823	61.9E-32	3.76858
GATA3	0.8231	1.6599	2.0168	395	855	5.71E-18	4.81386
SRY	0.8095	0.9379	1.1586	291	635	3.249E-06	2.21085
GATA2	0.7865	3.1413	3.9941	469	1053	58.69E-32	11.40447
Foxd3	0.7855	0.7407	0.9430	198	422	3.087E-02	4.22503
YY1	0.6982	0.9876	1.4144	316	761	7.948E-06	3.16041
HOXA5	0.6683	1.4022	2.0982	354	845	26.09E-10	4.71874
Nkx2-5	0.6212	1.2981	2.0898	335	799	15.16E-08	5.30473
ARID3A	0.5992	0.7516	1.2542	255	626	2.14E-02	2.61464
MEF2A	0.4801	0.0652	0.1359	35	124	31.87E-04	0.16857
Prrx2	0.4628	0.4130	0.8926	169	565	61.98E-04	1.40738
FOXL1	0.4208	1.2112	2.8784	304	783	8.533E-04	30.65219
Ddit3::Cebpa	0.4199	0.0606	0.1443	38	140	10.72E-04	0.14210
Lhx3	0.4102	0.0512	0.1250	24	104	4.759E-04	0.16456
NFIL3	0.4000	0.0295	0.0738	14	68	15.88E-04	0.09960

15.10 AR RU486 overlaps (up)

Chromosome specific statistics are shown in Table 57. A histogram of sequence lengths is shown in Figure 87.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	1	190	190	190	190	1e-06
2	4	122	172	190	689	3e-06
3	1	180	180	180	180	1e-06
4	1	164	164	164	164	1e-06
5	4	170	205	273	819	5e-06
6	1	180	180	180	180	1e-06
7	2	15	56	98	113	1e-06
8	3	71	136	219	409	3e-06
12	1	113	113	113	113	1e-06
17	2	124	212	301	425	5e-06
19	3	21	91	172	274	5e-06
20	2	169	201	233	402	6e-06
21	1	207	207	207	207	4e-06
all 13	26	15	160	301	4165	1e-06

Table 57: Chromosome specific distribution of the regions. The last line represents the overall statistics.

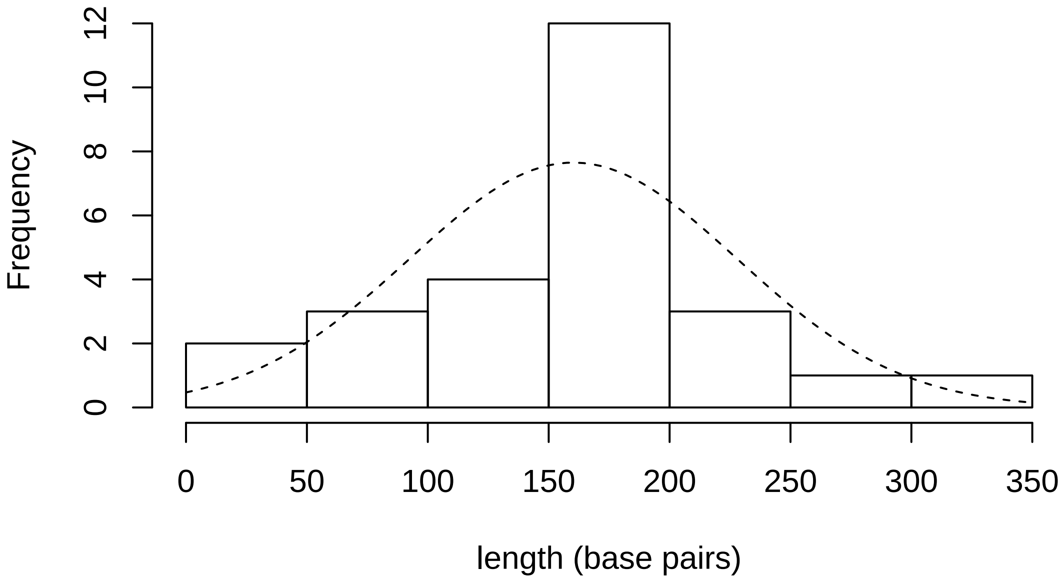
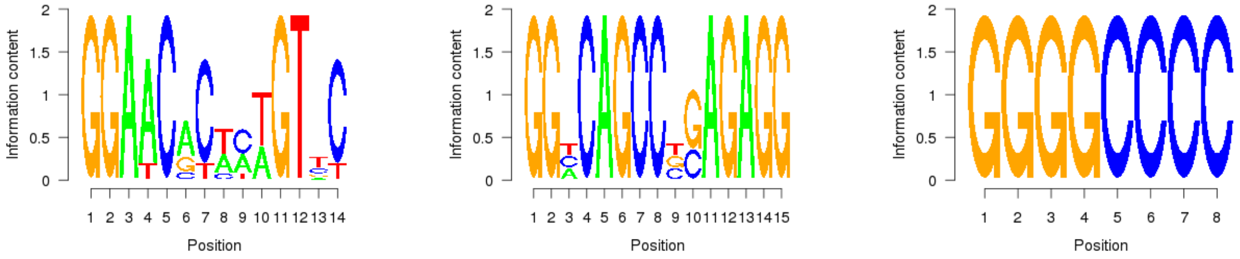


Figure 87: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARRU486rrOu-gCount** component.

property	value
genes	22



(a) ARRU486rrOu-deNovo-meme1: width=14, sites=8, llr=109, E=12

(b) ARRU486rrOu-deNovo-meme2: width=15, sites=3, llr=55, E=46000

(c) ARRU486rrOu-deNovo-meme3: width=8, sites=2, llr=23, E=270000

Figure 88: De novo motifs for the filtered AR RU486 overlaps (up) sequences.

Table 58: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	3847.1538	0.1923	0.0000	4	0	2.41E-02	0.09126
GRMotifHH	3077.9231	0.1538	0.0000	4	0	2.41E-02	0.05183
HIF1A::ARNT	3077.9231	0.1538	0.0000	4	0	2.41E-02	0.05183
FOXA1	8.6093	0.5385	0.0625	13	2	7.597E-06	0.23417
Foxa2	3.3220	0.3462	0.1042	9	3	31.25E-04	0.23769
Foxq1	2.0766	0.3462	0.1667	9	7	4.432E-02	0.20678
GRMotifT	1.8461	1.2692	0.6875	16	25	2.822E-02	1.16623
Mafb	1.8461	0.8846	0.4792	15	13	21.1E-04	1.25213
ARMotifH	1.8015	4.6538	2.5833	25	43	23.17E-06	7.01166
NFIC	1.8011	1.5385	0.8542	18	25	42.37E-04	1.78545
SOX10	1.2908	3.3077	2.5625	24	40	61.99E-06	3.48926
GRMotifH	1.2513	2.3462	1.8750	23	39	2.169E-04	2.45039
SPI1	1.2095	0.7308	0.6042	14	17	2.301E-02	0.80637
En1	0.6413	1.2692	1.9792	18	38	4.398E-02	2.17253

15.11 AR RU486 overlaps (down)

Chromosome specific statistics are shown in Table 59. A histogram of sequence lengths is shown in Figure 89.

		length				
chromosome	frequency	min	mean	max	total	coverage
3	1	79	79	79	79	0
7	1	217	217	217	217	1e-06
10	1	50	50	50	50	0
11	1	177	177	177	177	1e-06
all 4	4	50	131	217	523	0

Table 59: Chromosome specific distribution of the regions. The last line represents the overall statistics.

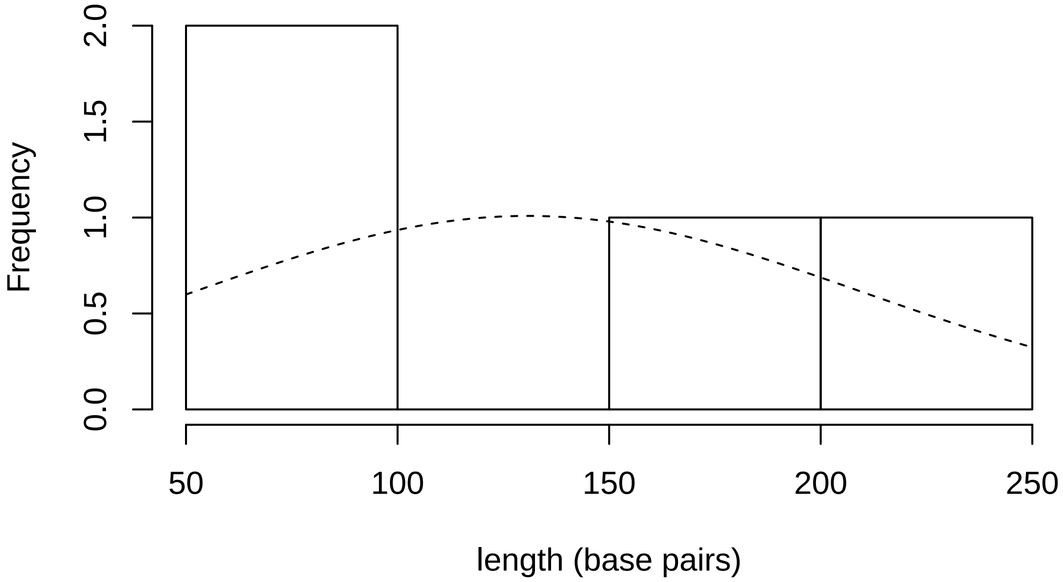
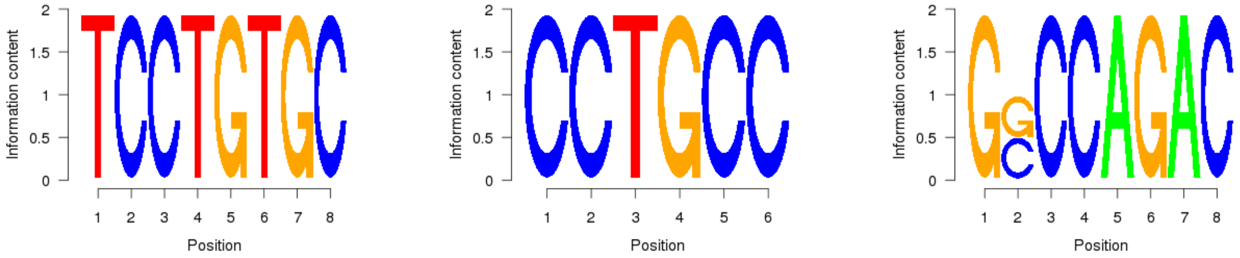


Figure 89: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARRU486rrOd-gCount** component.

property	**value**
genes	5



(a) ARRU486rrOd-deNovo-meme1: width=8, sites=2, llr=22, E=2900 (b) ARRU486rrOd-deNovo-meme2: width=6, sites=2, llr=17, E=2900 (c) ARRU486rrOd-deNovo-meme3: width=8, sites=2, llr=21, E=3700

Figure 90: De novo motifs for the filtered AR RU486 overlaps (down) sequences.

Table 60: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var

15.12 AR RU486 overlaps (stable)

Chromosome specific statistics are shown in Table 61. A histogram of sequence lengths is shown in Figure 91.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	52	26	174	576	9053	3.6e-05
10	13	38	126	340	1634	1.2e-05
11	18	52	145	239	2603	1.9e-05
12	19	39	123	256	2338	1.7e-05
13	11	40	150	287	1647	1.4e-05
14	18	38	135	295	2434	2.3e-05
15	10	36	137	297	1372	1.3e-05
16	25	41	109	281	2717	3e-05
17	39	23	138	566	5398	6.6e-05
18	9	61	132	246	1188	1.5e-05
19	13	21	90	284	1174	2e-05
2	47	14	143	415	6700	2.8e-05
20	9	44	122	219	1099	1.7e-05
21	4	39	49	70	196	4e-06
22	1	180	180	180	180	4e-06
3	39	34	184	349	7177	3.6e-05
4	12	33	156	326	1875	1e-05
5	17	33	210	1127	3572	2e-05
6	12	34	113	268	1355	8e-06
7	20	15	100	286	1999	1.3e-05
8	21	36	132	300	2778	1.9e-05
9	13	42	120	248	1563	1.1e-05
X	9	34	60	173	539	3e-06
Y	6	39	120	288	723	1.2e-05
all 24	437	14	140	1127	61314	2e-05

Table 61: Chromosome specific distribution of the regions. The last line represents the overall statistics.

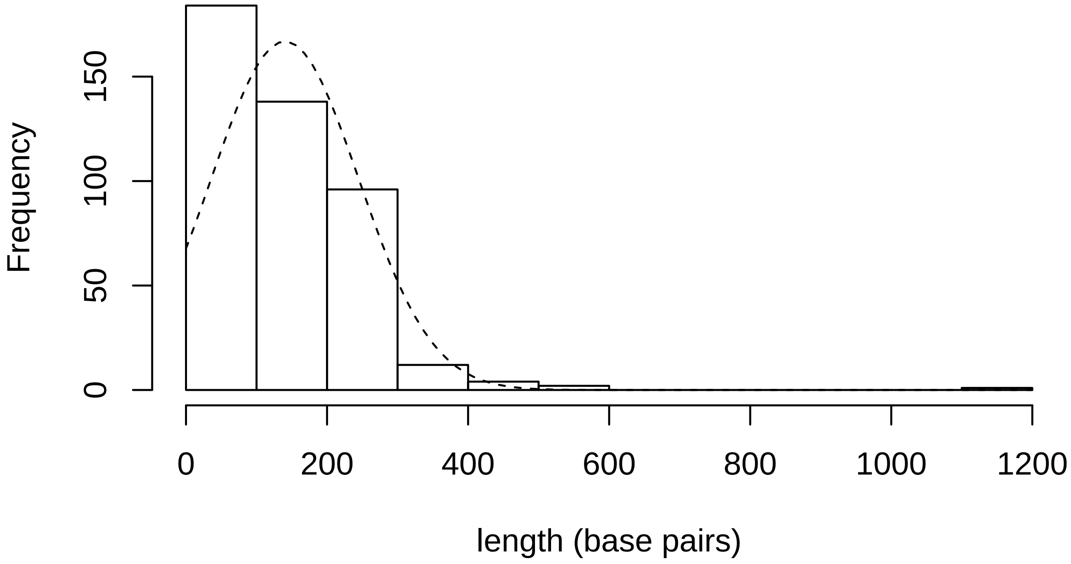
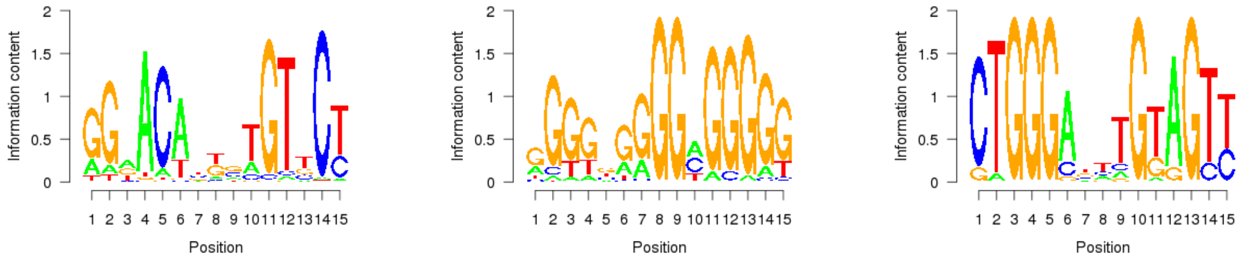


Figure 91: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARRU486rrOs-gCount** component.

property	value
genes	605



(a) ARRU486rrOs-deNovo-meme1: width=15, sites=145, llr=1387, E=1.4e-75 (b) ARRU486rrOs-deNovo-meme2: width=15, sites=29, llr=349, E=38000 (c) ARRU486rrOs-deNovo-meme3: width=15, sites=19, llr=267, E=0.13

Figure 92: De novo motifs for the filtered AR RU486 overlaps (stable) sequences.

Table 62: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
ESR2	458.6659	0.0229	0.0000	10	0	57.34E-06	0.00788
Pax4	412.8993	0.0206	0.0000	6	0	32.86E-04	0.01186
ARMotifTT	184.0664	0.0092	0.0000	4	0	2.622E-02	0.00317
RREB1	110.5509	1.0801	0.0097	80	7	60.44E-32	3.06683
Ar	79.6294	0.1007	0.0012	39	1	88.5E-18	0.04241
PLAG1	17.5508	0.0435	0.0024	16	2	3.764E-06	0.02117
GRMotifTT	14.5104	0.0183	0.0012	8	1	20.71E-04	0.00710
E2F1	9.2468	0.0229	0.0024	10	2	11.21E-04	0.00944
SP1	7.8712	3.6156	0.4593	198	191	30.87E-26	17.77707
MZF1_1-4	3.5797	4.7368	1.3232	322	464	4.505E-42	20.17866
NFKB1	3.4443	0.0503	0.0146	18	9	7.852E-04	0.04216
Egr1	3.4196	0.0915	0.0267	35	22	16.47E-06	0.05635
FOXA1pAR	2.9537	0.0503	0.0170	21	14	21.62E-04	0.02937
Klf4	2.9502	0.2403	0.0814	80	56	40.36E-12	0.18945
GABPA	2.7329	0.0366	0.0134	16	10	62.66E-04	0.02257
GRMotifTH	2.7184	0.1190	0.0437	48	34	1.761E-06	0.07455
FOXF2	2.4197	0.1030	0.0425	41	35	2.04E-04	0.06586
FOXA1	2.3536	0.2860	0.1215	102	88	25.04E-12	0.20875
Foxa2	2.3430	0.2563	0.1094	95	75	10.62E-12	0.21097
NR3C1	2.3380	0.1762	0.0753	65	59	2.68E-06	0.12523
ARMotifT	2.1757	0.2380	0.1094	85	84	21.06E-08	0.17167
TFAP2A	2.1107	0.9977	0.4727	192	205	60.54E-22	2.09597
ARMotifHH	2.0035	0.1899	0.0948	71	66	1.14E-06	0.15125
GR	1.8102	0.1144	0.0632	44	50	58.32E-04	0.08717
HIF1A::ARNT	1.6698	0.2151	0.1288	66	81	10.32E-04	0.26073
ARMotifH	1.5876	3.4531	2.1750	353	606	1.804E-44	7.66432
GRMotifT	1.5680	0.8535	0.5443	205	311	26.93E-14	0.93252
EBF1	1.5672	0.2952	0.1883	82	122	55.81E-04	0.37807
NFIC	1.5612	1.0206	0.6537	217	347	12.13E-14	1.32132
Stat3	1.5061	0.0732	0.0486	28	31	3.398E-02	0.07616
FOXD1	1.4459	0.3707	0.2564	120	174	21.4E-06	0.36742
Mafb	1.4451	0.7849	0.5431	193	299	35.15E-12	1.03946
Arnt::Ahr	1.4421	0.5835	0.4046	138	197	48.95E-08	1.48658
Myb	1.4377	0.3249	0.2260	109	150	26.94E-06	0.32138
Gata1	1.4051	0.2220	0.1580	84	112	4.842E-04	0.20024
ELK1	1.3045	0.3249	0.2491	115	162	20.17E-06	0.32203
MZF1_5-13	1.2258	0.5675	0.4629	173	258	11.44E-10	0.75536
ZNF354C	1.2064	1.1625	0.9635	246	431	12.65E-16	2.40958
GATA3	0.8054	1.5492	1.9235	247	586	5.787E-08	4.79932
AP1	0.7857	0.7437	0.9465	190	426	5.736E-04	1.49062
GATA2	0.7840	3.0435	3.8821	307	708	1.33E-18	14.19420
YY1	0.7127	0.9863	1.3840	203	518	45.49E-04	2.86714
SRY	0.6954	0.7849	1.1288	178	434	2.33E-02	2.31127
HOXA5	0.6531	1.2998	1.9903	231	572	16.79E-06	4.69877
Nobox	0.6324	0.3181	0.5030	81	251	4.664E-02	0.76910
Cebpa	0.6109	0.1922	0.3147	60	187	3.195E-02	0.40955
Nkx2-5	0.5740	1.1648	2.0292	207	552	90.46E-04	5.84330
Prrx2	0.4817	0.3822	0.7934	101	363	37.04E-04	1.30449
FOXL1	0.4590	1.1785	2.5674	196	529	3.913E-02	12.19439
Ddit3::Cebpa	0.4413	0.0595	0.1349	25	97	51.03E-04	0.12558
Lhx3	0.4389	0.0389	0.0887	12	52	1.65E-02	0.12198

15.13 AR DHT vs AR CPA overlaps

Chromosome specific statistics are shown in Table 63. A histogram of sequence lengths is shown in Figure 93.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	144	21	229	539	32987	0.000132
10	49	45	209	434	10261	7.6e-05
11	61	35	238	589	14488	0.000107
12	49	100	237	705	11634	8.7e-05
13	33	57	275	722	9066	7.9e-05
14	37	4	217	432	8040	7.5e-05
15	54	37	228	427	12296	0.00012
16	44	37	207	392	9095	0.000101
17	80	21	211	421	16848	0.000207
18	28	25	208	431	5828	7.5e-05
19	26	90	209	364	5425	9.2e-05
2	88	61	235	442	20674	8.5e-05
20	49	33	215	502	10523	0.000167
21	17	42	196	377	3326	6.9e-05
22	14	95	187	258	2620	5.1e-05
3	110	10	233	447	25661	0.00013
4	43	1	210	557	9015	4.7e-05
5	89	5	223	468	19871	0.00011
6	68	44	210	515	14285	8.3e-05
7	64	55	221	375	14156	8.9e-05
8	86	29	222	417	19099	0.00013
9	51	88	227	395	11562	8.2e-05
X	20	56	175	384	3495	2.3e-05
all 23	1304	1	223	722	290255	9.4e-05

Table 63: Chromosome specific distribution of the regions. The last line represents the overall statistics.

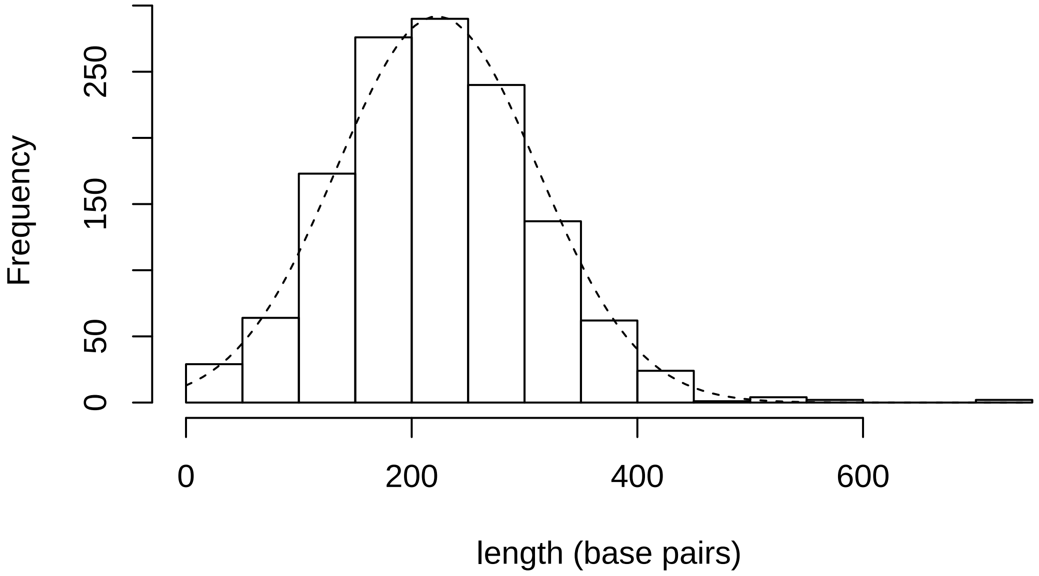
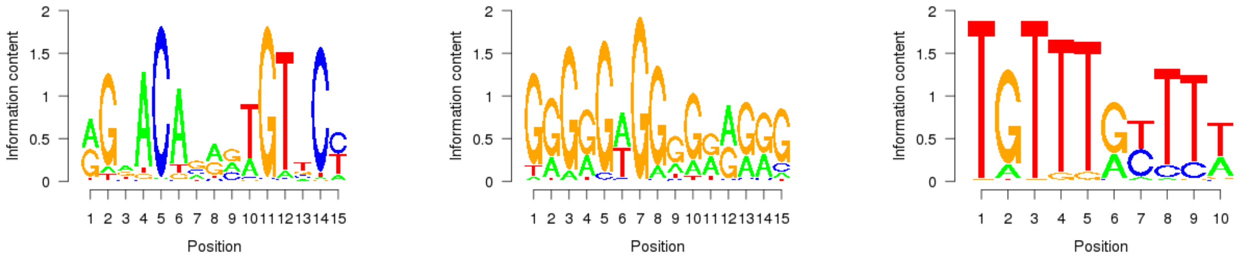


Figure 93: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrO-gCount** component.

property	value
genes	4117



(a) ARDHTvsARCPArrO-deNovo-meme1: width=15, sites=275, llr=2732, E=3.3e-244

(b) ARDHTvsARCPArrO-deNovo-meme2: width=15, sites=58, llr=674, E=3.6e-13

(c) ARDHTvsARCPArrO-deNovo-meme3: width=10, sites=143, llr=1325, E=2.2e-20

Figure 94: De novo motifs for the filtered AR DHT vs AR CPA overlaps sequences.

Table 64: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	48.3586	0.2015	0.0041	235	10	24.25E-96	0.08322
TLX1::NFIC	4.0716	0.0169	0.0041	16	7	9.991E-04	0.01334
MIZF	3.1891	0.0277	0.0086	36	21	10.21E-06	0.01506
FOXA1	3.1519	0.5908	0.1874	582	395	47.92E-104	0.37343
ESR2	2.9956	0.0223	0.0074	28	17	1.823E-04	0.01352
Foxa2	2.9009	0.5138	0.1771	529	356	4.729E-90	0.34736
NR3C1	2.6992	0.3369	0.1248	360	286	27.64E-44	0.21833
FOXF2	2.5046	0.1662	0.0663	191	149	3.58E-20	0.11507
GRMotifTH	2.3488	0.2438	0.1038	266	243	14.99E-24	0.16908
ARMotifT	2.3305	0.4723	0.2026	488	419	80.69E-62	0.33053
FOXA1pAR	2.2004	0.0862	0.0391	104	85	7.823E-10	0.06426
ELK4	2.1609	0.0223	0.0103	27	22	40.46E-04	0.01911
Tal1::Gata1	2.1514	0.0346	0.0161	44	39	5.232E-04	0.02257
Stat3	2.0674	0.1508	0.0729	146	145	6.69E-10	0.13944
STAT1	1.9923	0.0362	0.0181	35	34	64.74E-04	0.03563
GABPA	1.8925	0.0554	0.0292	71	67	21.93E-06	0.04119
FOXD1	1.7716	0.7238	0.4086	650	772	5.653E-64	0.59692
Egr1	1.7462	0.0669	0.0383	78	87	3.536E-04	0.05509
GRMotifT	1.7326	1.6092	0.9287	1007	1398	15.01E-144	1.46236
ARMotifTH	1.7195	0.0362	0.0210	47	50	44.93E-04	0.02614
Tcfcp2l1	1.7106	0.0423	0.0247	49	56	96.0E-04	0.03527
ARMotifHH	1.6860	0.2715	0.1610	292	341	1.229E-16	0.22740
GRMotifHH	1.6234	0.1485	0.0914	172	197	1.022E-08	0.12579
ARMotifH	1.6224	5.6677	3.4934	1277	2233	92.82E-234	8.61604
Esrrb	1.5584	0.0777	0.0498	97	117	3.30E-04	0.06031
Foxq1	1.5246	0.3146	0.2063	349	398	70.79E-24	0.30638
NFIC	1.5241	1.7469	1.1462	997	1481	8.953E-130	2.02156
Gata1	1.4817	0.4046	0.2731	425	549	2.375E-24	0.34875
NHLH1	1.4596	0.0854	0.0585	70	91	1.251E-02	0.11587
GR	1.3798	0.1654	0.1199	199	262	33.32E-08	0.14417
GRMotifH	1.3312	3.5138	2.6396	1209	2110	24.51E-196	4.78978
EBF1	1.3309	0.4254	0.3196	374	558	25.73E-14	0.54178
Myb	1.2952	0.4438	0.3427	440	673	38.54E-18	0.42728
TFAP2A	1.2877	1.1238	0.8727	638	985	93.93E-40	2.64237
Myc	1.2818	0.0892	0.0696	92	133	2.211E-02	0.10819
Hand1::Tcfe2a	1.2484	0.6715	0.5379	597	956	1.871E-30	0.68725
ELK1	1.2484	0.4854	0.3888	467	730	2.493E-18	0.49090
Myf	1.2471	0.1546	0.1240	166	241	3.319E-04	0.18095
SOX10	1.2433	4.6215	3.7171	1240	2253	59.32E-206	7.35151
FEV	1.2213	0.3562	0.2916	380	598	11.49E-12	0.33195
FOXI1	1.2175	0.4754	0.3904	450	646	34.43E-22	0.61073
NR4A2	1.2058	1.0215	0.8472	791	1281	18.53E-62	1.10154
Fos	0.8254	0.6823	0.8266	588	1275	5.353E-12	0.94913
MZF1_5-13	0.8127	0.6346	0.7809	564	1192	18.63E-12	0.97961
YY1	0.8024	1.6831	2.0976	981	1999	3.771E-82	2.89745
Nobox	0.7787	0.6585	0.8456	522	1101	62.85E-10	1.31878
HOXA5	0.7772	2.5869	3.3287	1090	2124	1.634E-124	6.54111
Nkx2-5	0.7286	2.4046	3.3002	1014	2024	1.123E-94	7.73986
ARID3A	0.7091	1.3977	1.9712	824	1649	39.97E-48	4.05630
NFIL3	0.6524	0.0677	0.1038	73	196	3.606E-02	0.13925
Pdx1	0.6479	0.9300	1.4353	662	1583	46.7E-14	2.18291
Foxd3	0.5812	0.7638	1.3143	581	1220	58.17E-14	4.21525
Prrx2	0.5784	0.7923	1.3699	587	1548	83.51E-06	1.99791
FOXL1	0.5704	2.3462	4.1129	959	1957	7.643E-76	22.52481
Lhx3	0.5151	0.0969	0.1882	98	302	5.796E-04	0.29027
Ddit3::Cebpa	0.4901	0.1023	0.2088	120	423	87.29E-08	0.20503
MEF2A	0.4639	0.0831	0.1792	94	315	35.83E-06	0.22750

15.14 AR DHT vs AR CPA overlaps (up)

Chromosome specific statistics are shown in Table 65. A histogram of sequence lengths is shown in Figure 95.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	26	90	246	447	6397	2.6e-05
10	4	170	256	381	1024	8e-06
11	12	172	317	589	3806	2.8e-05
12	3	232	280	324	839	6e-06
13	4	171	257	432	1029	9e-06
14	1	411	411	411	411	4e-06
15	8	51	220	381	1763	1.7e-05
16	1	304	304	304	304	3e-06
17	5	152	275	421	1377	1.7e-05
18	1	223	223	223	223	3e-06
19	4	127	207	364	829	1.4e-05
2	16	118	256	403	4089	1.7e-05
20	5	195	266	335	1330	2.1e-05
21	4	42	167	281	667	1.4e-05
3	8	15	227	364	1816	9e-06
4	10	113	181	326	1807	9e-06
5	16	64	264	366	4228	2.3e-05
6	16	116	211	325	3381	2e-05
7	4	168	237	291	947	6e-06
8	7	180	244	329	1706	1.2e-05
9	1	129	129	129	129	1e-06
X	1	56	56	56	56	0
all 22	157	15	243	589	38158	1.2e-05

Table 65: Chromosome specific distribution of the regions. The last line represents the overall statistics.

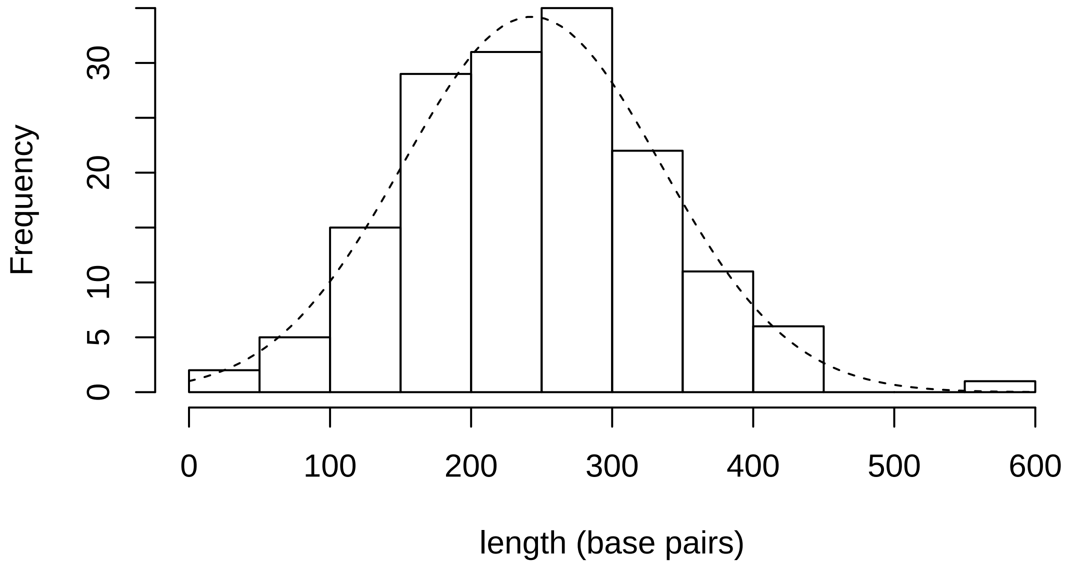
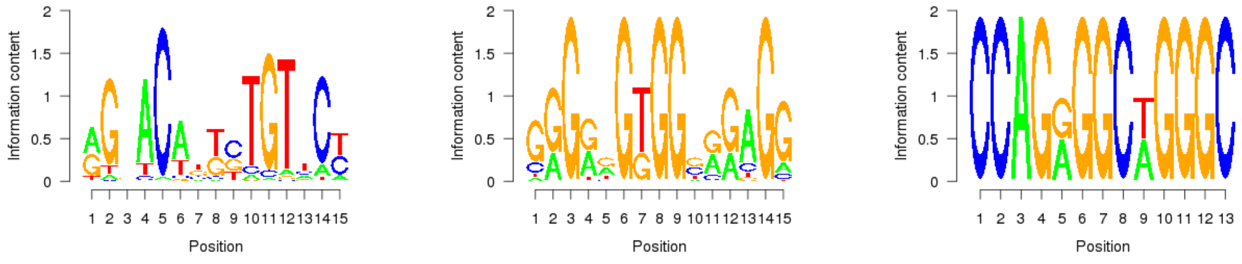


Figure 95: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the seqeuce lengths.

The following table shows the properties of **ARDHTvsARCPArrOu-gCount** component.

property	value
genes	113



(a) ARDHTvsARCPArrOu-deNovo-meme1: width=15, sites=106, llr=977, E=1.6e-62

(b) ARDHTvsARCPArrOu-deNovo-meme2: width=15, sites=17, llr=219, E=21000

(c) ARDHTvsARCPArrOu-deNovo-meme3: width=13, sites=2, llr=35, E=5.1e+07

Figure 96: De novo motifs for the filtered AR DHT vs AR CPA overlaps (up) sequences.

Table 66: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	4969.1529	0.2484	0.0000	33	0	20.83E-16	0.11097
NR3C1	3.7059	0.4586	0.1237	56	33	35.09E-12	0.28180
Foxa2	3.2430	0.6242	0.1924	72	48	4.184E-14	0.41848
FOXA1	3.1852	0.7006	0.2199	84	56	10.73E-18	0.41257
FOXF2	3.1259	0.1720	0.0550	25	15	1.327E-04	0.10039
FOXA1pAR	2.7777	0.0955	0.0344	15	9	57.43E-04	0.05728
MAX	2.5352	0.1656	0.0653	21	14	14.0E-04	0.13978
ARMotifT	2.3938	0.5924	0.2474	69	61	4.093E-10	0.43452
Foxq1	2.1621	0.3567	0.1649	47	43	9.328E-06	0.25024
GRMotifTH	1.9715	0.3185	0.1615	40	44	11.02E-04	0.22818
ARMotifHH	1.9374	0.2930	0.1512	39	39	4.153E-04	0.22353
Stat3	1.9371	0.1465	0.0756	19	17	1.99E-02	0.13530
GRMotifT	1.9264	2.0191	1.0481	138	192	26.18E-26	1.54009
USF1	1.8533	0.4076	0.2199	36	38	17.46E-04	0.52669
GRMotifHH	1.8057	0.2420	0.1340	32	35	62.91E-04	0.19187
GR	1.7869	0.1720	0.0962	25	26	1.658E-02	0.12583
ARMotifH	1.7723	6.6752	3.7663	155	270	11.64E-30	9.64078
FOXD1	1.6431	0.7962	0.4845	79	104	11.51E-08	0.73392
TFAP2A	1.5830	1.2675	0.8007	76	110	3.717E-06	3.27389
NFIC	1.5547	1.9554	1.2577	120	184	5.342E-16	2.53691
FOXI1	1.4827	0.5350	0.3608	60	78	73.11E-06	0.52632
GRMotifH	1.3662	4.0000	2.9278	149	259	2.839E-26	5.30809
FEV	1.3035	0.4076	0.3127	56	74	2.952E-04	0.34759
Myb	1.2939	0.4713	0.3643	54	85	65.8E-04	0.48698
NR4A2	1.2751	1.1656	0.9141	103	162	1.478E-10	1.23266
Sox17	1.2637	0.8599	0.6804	82	140	19.24E-06	0.85342
ELK1	1.2472	0.4586	0.3677	55	86	49.42E-04	0.42837
Gata1	1.2429	0.3631	0.2921	52	71	13.19E-04	0.30647
SOX10	1.2357	5.3248	4.3093	152	281	1.178E-26	8.67959
Arnt::Ahr	1.2048	0.9108	0.7560	84	124	26.91E-08	2.07802
ELF5	1.2009	1.1019	0.9175	103	156	42.8E-12	1.19431
GATA2	0.8302	5.6115	6.7595	152	284	1.953E-26	14.61937
HOXA5	0.8029	2.9936	3.7285	129	263	2.456E-14	7.89625
Sox5	0.7928	0.9236	1.1649	83	177	12.99E-04	1.58637
Foxd3	0.7362	0.8981	1.2199	74	139	13.47E-04	3.67530
ARID3A	0.7230	1.5032	2.0790	109	203	10.68E-10	3.84395
Nkx2-5	0.7122	2.5159	3.5326	126	254	17.78E-14	7.82342
Pdx1	0.7050	1.1338	1.6082	90	205	6.318E-04	2.65434
YY1	0.6708	1.5605	2.3265	118	248	2.212E-10	2.91385
Prrx2	0.6501	0.9427	1.4502	80	195	2.189E-02	2.28809
Fos	0.6404	0.6624	1.0344	77	178	1.855E-02	1.06683
FOXL1	0.5798	2.5541	4.4055	120	245	22.29E-12	21.62971

15.15 AR DHT vs AR CPA overlaps (down)

Chromosome specific statistics are shown in Table 67. A histogram of sequence lengths is shown in Figure 97.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	4	105	234	345	938	4e-06
2	1	132	132	132	132	1e-06
3	2	78	262	447	525	3e-06
5	1	271	271	271	271	1e-06
6	1	201	201	201	201	1e-06
7	3	169	225	275	676	4e-06
8	1	247	247	247	247	2e-06
11	3	157	235	307	706	5e-06
12	1	186	186	186	186	1e-06
16	3	141	209	271	627	7e-06
all 10	20	78	225	447	4509	1e-06

Table 67: Chromosome specific distribution of the regions. The last line represents the overall statistics.

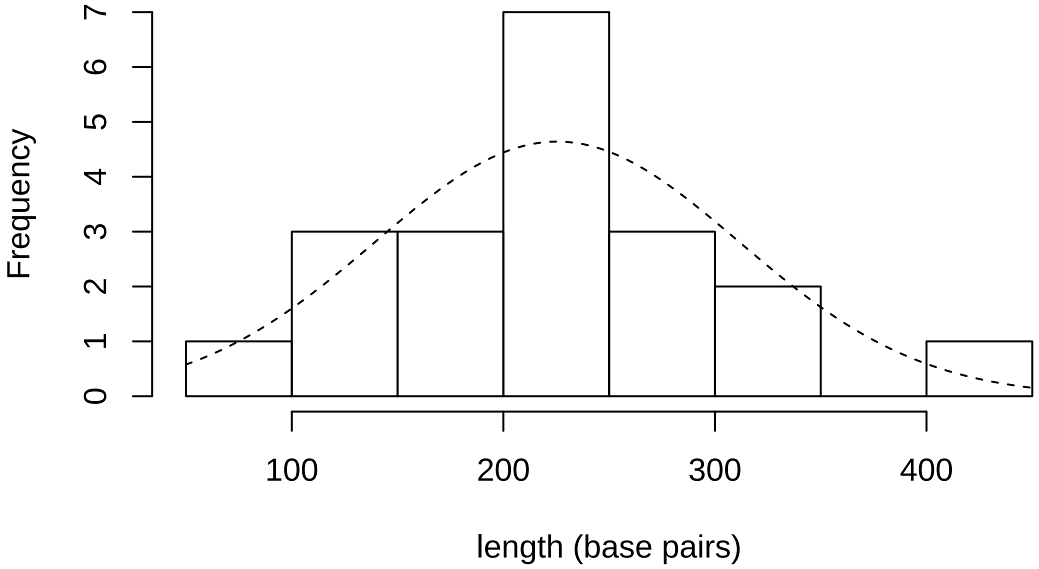
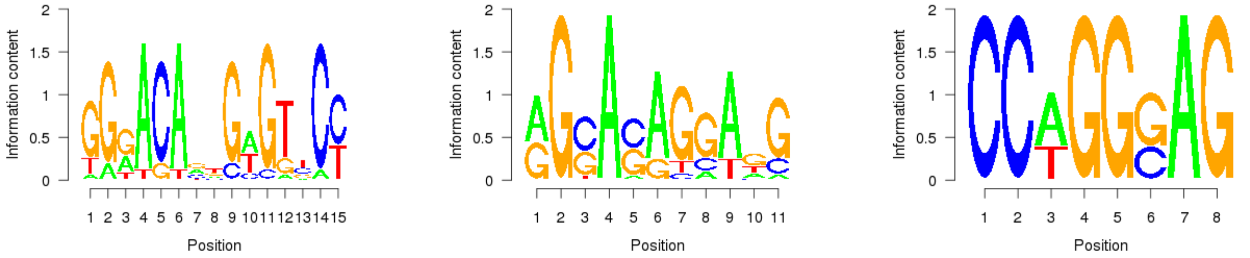


Figure 97: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrOd-gCount** component.

property	value
genes	21



(a) ARDHTvsARCPArrOd-deNovo-meme1: width=15, sites=15, llr=161, E=0.0039

(b) ARDHTvsARCPArrOd-deNovo-meme2: width=11, sites=16, llr=137, E=6200

(c) ARDHTvsARCPArrOd-deNovo-meme3: width=8, sites=8, llr=78, E=160000

Figure 98: De novo motifs for the filtered AR DHT vs AR CPA overlaps (down) sequences.

Table 68: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	4001.0000	0.2000	0.0000	4	0	1.90E-02	0.06429
ARMotifT	2.9244	0.4500	0.1538	8	6	3.69E-02	0.22735
NR4A2	2.3249	1.5500	0.6667	16	20	9.073E-04	1.17124
NFIC	2.0614	1.8500	0.8974	17	23	5.214E-04	1.51958
ARMotifH	1.7989	6.5500	3.6410	20	38	1.134E-04	7.51373
MZF1_1-4	1.7927	2.8500	1.5897	20	26	8.494E-06	3.12040
ZNF354C	1.4936	1.8000	1.2051	17	25	8.677E-04	2.21099
TFAP2A	1.4230	1.3500	0.9487	10	11	4.331E-02	7.42373
GRMotifT	1.4058	1.5500	1.1026	16	27	49.89E-04	1.50321
SPIB	1.2787	2.0000	1.5641	17	34	50.21E-04	1.96727
GRMotifH	1.2447	3.0000	2.4103	19	35	3.523E-04	4.03507
BRCA1	0.7959	1.0000	1.2564	15	25	1.07E-02	1.41905
HOXA5	0.5014	1.8000	3.5897	16	36	2.135E-02	6.05143

15.16 AR DHT vs AR CPA overlaps (stable)

Chromosome specific statistics are shown in Table 69. A histogram of sequence lengths is shown in Figure 99.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	90	49	232	539	20875	8.4e-05
10	29	45	203	380	5878	4.3e-05
11	25	35	228	421	5703	4.2e-05
12	23	100	226	361	5202	3.9e-05
13	8	145	316	722	2526	2.2e-05
14	24	4	214	432	5132	4.8e-05
15	19	111	228	381	4338	4.2e-05
16	24	37	194	389	4657	5.2e-05
17	57	21	210	403	11976	0.000147
18	10	25	195	315	1947	2.5e-05
19	21	104	219	364	4589	7.8e-05
2	45	105	241	442	10853	4.5e-05
20	37	42	215	502	7968	0.000126
21	4	131	200	297	801	1.7e-05
22	7	112	203	256	1421	2.8e-05
3	56	15	246	447	13790	7e-05
4	20	1	230	557	4601	2.4e-05
5	43	53	220	366	9474	5.2e-05
6	39	44	207	340	8057	4.7e-05
7	31	90	223	348	6917	4.3e-05
8	29	50	220	382	6380	4.4e-05
9	20	88	211	395	4228	3e-05
X	9	125	189	279	1698	1.1e-05
all 23	670	1	222	722	149011	4.8e-05

Table 69: Chromosome specific distribution of the regions. The last line represents the overall statistics.

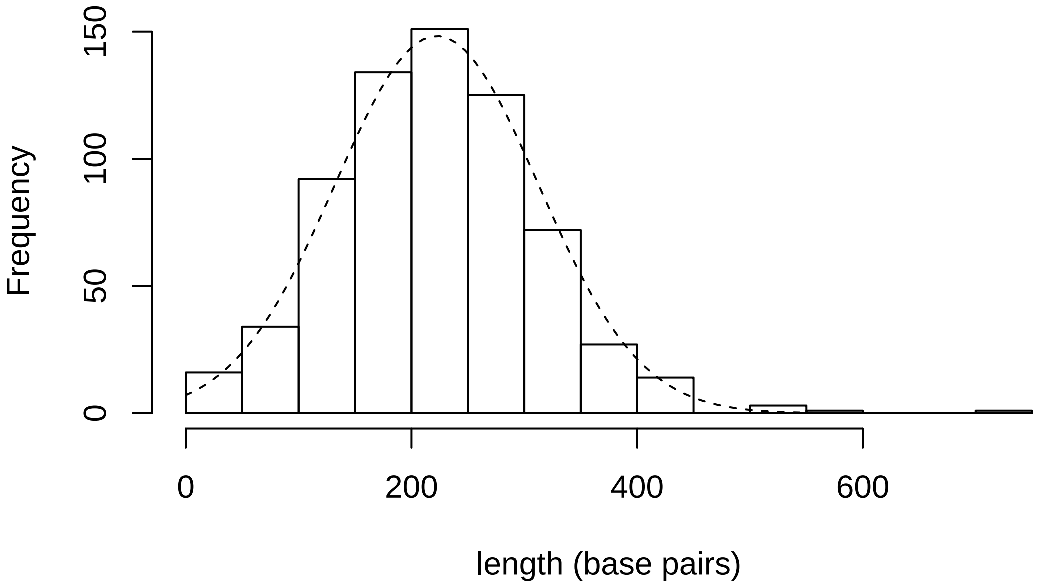
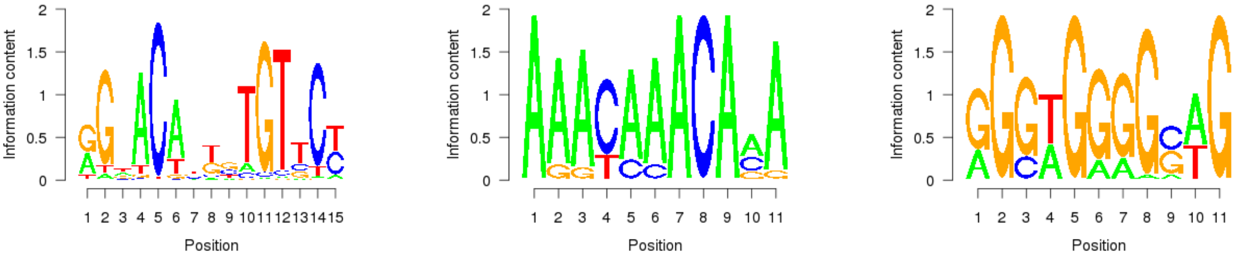


Figure 99: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrOs-gCount** component.

property	value
genes	914



(a) ARDHTvsARCPArrOs-deNovo-meme1: width=15, sites=273, llr=2606, E=2.5e-206

(b) ARDHTvsARCPArrOs-deNovo-meme2: width=11, sites=34, llr=400, E=1.5

(c) ARDHTvsARCPArrOs-deNovo-meme3: width=11, sites=41, llr=450, E=8200000

Figure 100: De novo motifs for the filtered AR DHT vs AR CPA overlaps (stable) sequences.

Table 70: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	46.9437	0.1874	0.0039	112	4	32.46E-48	0.07821
TLX1::NFIC	13.8505	0.0225	0.0016	11	2	4.19E-04	0.01285
E2F1	3.4593	0.0165	0.0047	11	6	1.688E-02	0.00871
GRMotifTT	3.3916	0.0135	0.0039	9	5	3.735E-02	0.00719
RORA_2	3.3916	0.0135	0.0039	9	5	3.735E-02	0.00719
FOXA1	2.8820	0.5592	0.1940	285	216	4.959E-46	0.35108
STAT1	2.7510	0.0435	0.0158	19	17	2.79E-02	0.03814
Foxa2	2.6772	0.4963	0.1853	263	199	68.15E-42	0.33632
NR3C1	2.6758	0.3208	0.1199	176	143	15.8E-22	0.21136
FOXF2	2.5412	0.1664	0.0655	98	80	1.23E-10	0.10680
Stat3	2.5412	0.1664	0.0655	79	70	17.08E-08	0.14196
ESR2	2.4788	0.0255	0.0103	17	7	3.55E-04	0.02251
RXR::RAR_DR5	2.4621	0.0195	0.0079	13	10	4.153E-02	0.01175
Egr1	2.3163	0.0750	0.0323	44	38	1.682E-04	0.05415
Tcfcp2l1	1.9668	0.0435	0.0221	25	25	2.363E-02	0.03584
GABPA	1.9508	0.0570	0.0292	37	36	29.44E-04	0.03934
ARMotifHH	1.9317	0.2804	0.1451	158	159	13.91E-14	0.21710
ARMotifT	1.9075	0.4333	0.2271	234	249	6.208E-22	0.31693
ARMotifTH	1.8986	0.0345	0.0181	23	22	2.266E-02	0.02425
GRMotifTH	1.8538	0.2369	0.1278	135	148	18.08E-10	0.18774
FOXA1pAR	1.7945	0.0765	0.0426	49	47	3.364E-04	0.06169
FOXD1	1.7292	0.6642	0.3841	320	375	1.26E-32	0.56206
Esrrb	1.6956	0.0870	0.0513	56	63	15.68E-04	0.06369
ARMotifH	1.6264	5.6912	3.4992	658	1153	11.99E-124	8.48779
NFIC	1.6140	1.8126	1.1230	520	772	3.815E-72	2.00942
EBF1	1.5859	0.4528	0.2855	203	276	68.75E-12	0.49232
GRMotifT	1.5736	1.5637	0.9937	511	773	19.81E-68	1.46640
Myf	1.5624	0.1454	0.0931	82	91	32.92E-06	0.15156
NHLH1	1.5573	0.0885	0.0568	36	44	3.928E-02	0.12313
TFAP2A	1.4900	1.2339	0.8281	343	506	5.716E-26	2.63910
Foxq1	1.4776	0.2774	0.1877	159	201	90.37E-10	0.25053
Arnt	1.4301	0.1184	0.0828	55	62	18.36E-04	0.17296
SP1	1.4182	0.8411	0.5931	229	381	3.735E-08	2.23581
Gata1	1.4123	0.3943	0.2792	208	295	2.733E-10	0.35277
GR	1.3921	0.1559	0.1120	98	137	11.95E-04	0.12240
Myb	1.3559	0.4513	0.3328	227	354	14.88E-10	0.41306
Klf4	1.3265	0.1454	0.1096	88	121	21.37E-04	0.14334
HIF1A::ARNT	1.3120	0.2639	0.2011	128	186	1.528E-04	0.40693
GRMotifH	1.2960	3.4138	2.6341	618	1128	9.267E-98	4.50141
GRMotifHH	1.2722	0.1274	0.1002	78	111	96.67E-04	0.12243
Mafb	1.2589	1.1874	0.9432	417	691	1.473E-34	1.44237
FEV	1.2563	0.3418	0.2721	182	299	20.29E-06	0.31816
Hand1::Tcfe2a	1.2559	0.6567	0.5229	302	499	21.84E-16	0.64247
ELK1	1.2393	0.4858	0.3920	237	403	3.054E-08	0.48121
FOXI1	1.2178	0.4543	0.3730	224	335	2.351E-10	0.55884
SRY	0.8306	1.5052	1.8123	459	903	1.42E-34	3.14854
Fos	0.8153	0.6822	0.8368	296	677	12.7E-06	0.98773
CREB1	0.8072	0.3673	0.4550	195	416	2.734E-02	0.53093
YY1	0.8034	1.7226	2.1443	505	1019	27.37E-46	4.13444
Sox5	0.7984	0.8261	1.0347	344	706	76.65E-14	1.46604
Nobox	0.7414	0.5952	0.8028	243	548	35.36E-04	1.37035
HOXA5	0.7271	2.4738	3.4022	555	1128	18.01E-62	6.53254
Nkx2-5	0.7035	2.2624	3.2161	495	1040	6.235E-40	7.70395
ARID3A	0.6687	1.2879	1.9259	399	861	2.487E-18	4.01845
Pdx1	0.6128	0.8516	1.3896	317	797	54.56E-06	2.27837
MEF2A	0.5791	0.0900	0.1554	52	151	4.935E-02	0.18349
Prrx2	0.5596	0.7361	1.3155	290	789	2.119E-02	2.03313
FOXL1	0.5099	2.0840	4.0868	460	1032	9.83E-28	23.21870
Lhx3	0.5089	0.0855	0.1680	46	150	91.47E-04	0.23388
Foxd3	0.4872	0.7046	1.4464	286	640	18.86E-06	6.59702
Ddit3::Cebpa	0.4195	0.0900	0.2145	53	215	28.68E-06	0.21977

15.17 AR DHT vs AR CPA unique for ARDHTrrO

Chromosome specific statistics are shown in Table 71. A histogram of sequence lengths is shown in Figure 101.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	440	12	445	920	195802	0.000786
10	183	192	421	931	77039	0.000568
11	222	51	438	1046	97345	0.000721
12	174	3	405	883	70522	0.000527
13	116	197	471	1068	54585	0.000474
14	147	51	436	920	64158	0.000598
15	148	13	445	821	65888	0.000643
16	105	51	418	1042	43907	0.000486
17	126	144	416	673	52388	0.000645
18	89	200	451	923	40170	0.000514
19	45	202	360	616	16212	0.000274
2	304	119	426	1046	129498	0.000532
20	98	239	414	776	40568	0.000644
21	56	196	442	768	24734	0.000514
22	44	176	391	640	17187	0.000335
3	322	122	473	1117	152151	0.000768
4	222	198	422	954	93740	0.00049
5	261	5	438	1173	114270	0.000632
6	270	69	411	918	111006	0.000649
7	241	204	444	1124	107073	0.000673
8	210	70	450	934	94422	0.000645
9	159	223	428	854	68021	0.000482
X	84	57	378	647	31723	0.000204
Y	4	199	283	345	1131	1.9e-05
all 24	4070	3	433	1173	1763540	0.00057

Table 71: Chromosome specific distribution of the regions. The last line represents the overall statistics.

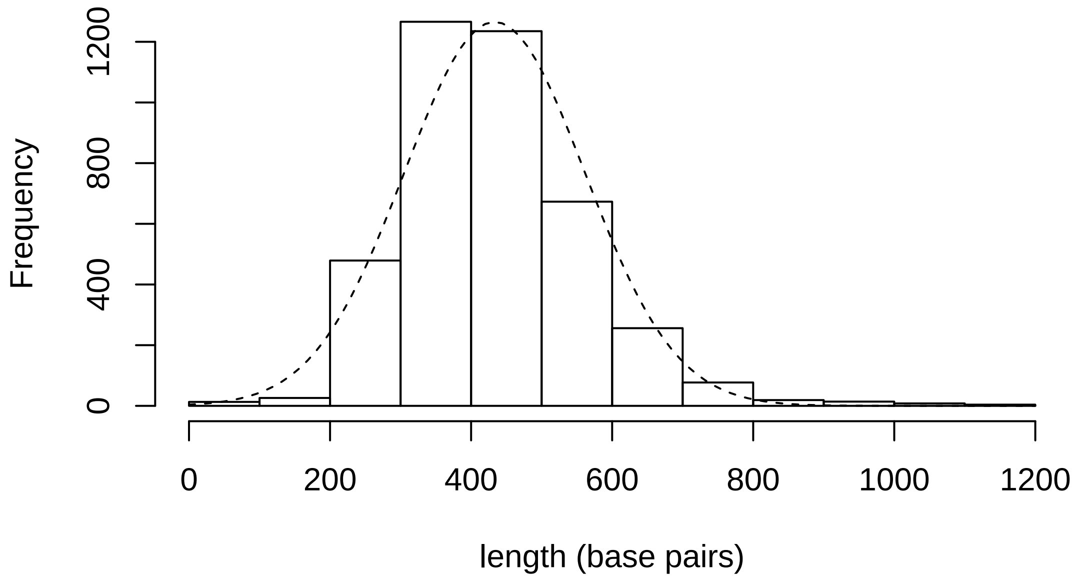
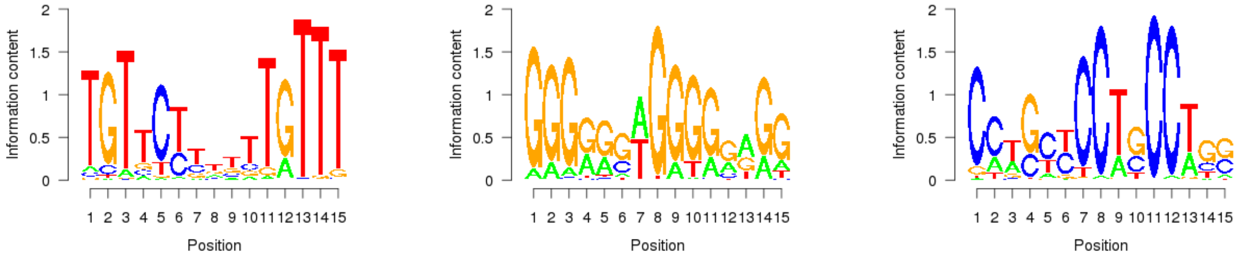


Figure 101: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU1-gCount** component.

property	**value**
genes	9837



(a) ARDHTvsARCPArrU1-deNovo-meme1: width=15, sites=151, llr=1603, E=9.3e-59 (b) ARDHTvsARCPArrU1-deNovo-meme2: width=15, sites=54, llr=656, E=5e-08 (c) ARDHTvsARCPArrU1-deNovo-meme3: width=15, sites=55, llr=640, E=27000

Figure 102: De novo motifs for the filtered AR DHT vs AR CPA unique for ARDHTrrO sequences.

Table 72: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	12.4044	0.0801	0.0064	306	46	62.52E-98	0.03494
FOXA1pAR	3.1615	0.2335	0.0738	867	495	13.96E-140	0.14627
FOXA1	2.8594	1.0482	0.3665	2713	2186	0.00E00	0.72831
TLX1::NFIC	2.7636	0.0175	0.0063	57	38	32.45E-08	0.01416
Foxa2	2.6044	0.9118	0.3500	2467	1963	0.00E00	0.73303
FOXF2	2.5370	0.3196	0.1259	1117	890	24.43E-132	0.20425
Tal1::Gata1	1.9661	0.0647	0.0329	251	240	5.387E-16	0.04608
ARMotifTH	1.8767	0.0745	0.0397	291	299	6.44E-16	0.05216
FOXD1	1.8476	1.3872	0.7508	2997	3754	0.00E00	1.20381
RXRA::VDR	1.8170	0.0086	0.0047	35	36	1.322E-02	0.00603
Foxq1	1.7020	0.6691	0.3931	1922	2274	3.309E-178	0.59126
ARMotifT	1.6869	0.6802	0.4032	1963	2449	97.16E-172	0.55585
AR	1.6558	0.0718	0.0433	275	317	38.08E-12	0.05586
Stat3	1.6547	0.2281	0.1378	702	813	1.829E-34	0.24772
GRMotifTH	1.6072	0.3594	0.2236	1201	1507	9.441E-66	0.28803
GABPA	1.5220	0.0853	0.0560	329	400	13.97E-12	0.07105
ARMotifTT	1.5100	0.0143	0.0094	58	71	1.595E-02	0.01115
PPARG::RXRA	1.4503	0.0226	0.0156	85	115	1.859E-02	0.01992
MIZF	1.4433	0.0270	0.0187	107	140	33.18E-04	0.02217
NR3C1	1.4186	0.3631	0.2559	1177	1657	32.22E-48	0.32769
ESR2	1.4115	0.0187	0.0132	67	88	2.653E-02	0.01882
Gata1	1.4042	0.8265	0.5886	2207	3225	12.17E-170	0.77529
Evi1	1.4000	0.0447	0.0319	177	237	1.792E-04	0.03712
RXR::RAR_DR5	1.3777	0.0312	0.0226	125	167	22.57E-04	0.02685
FOXI1	1.3774	1.0543	0.7654	2488	3442	8.527E-248	1.30960
STAT1	1.3480	0.0457	0.0339	150	196	3.247E-04	0.05844
GRMotifT	1.3433	2.4496	1.8235	3667	6262	0.00E00	2.49148
GR	1.3209	0.3056	0.2313	1055	1501	30.86E-38	0.28260
ELK4	1.3176	0.0243	0.0185	93	134	4.054E-02	0.02247
Arnt	1.3074	0.1792	0.1371	510	689	5.985E-14	0.25940
GRMotifTT	1.2786	0.0268	0.0209	105	156	4.796E-02	0.02382
Esrrb	1.2553	0.1146	0.0912	440	664	28.48E-08	0.10024
ARMotifH	1.2361	8.5098	6.8841	4061	7554	0.00E00	14.31218
NFIC	1.2311	2.7026	2.1952	3632	6347	0.00E00	3.49935
ARMotifHH	1.2261	0.3778	0.3082	1221	1863	5.621E-40	0.38645
FOXO3	1.2193	1.9275	1.5808	3312	5606	0.00E00	2.31970
GRMotifHH	1.2046	0.2340	0.1943	816	1235	82.45E-20	0.24151
Foxd3	0.8263	2.1246	2.5714	3051	5405	14.64E-306	10.48253
Prrx2	0.8171	2.1905	2.6808	3269	6374	0.00E00	4.87660
FOXL1	0.8117	6.5821	8.1087	3881	7170	0.00E00	52.75903
CREB1	0.7912	0.6590	0.8330	1843	3897	39.46E-40	1.01138
MZF1_5-13	0.7868	1.1190	1.4222	2576	5390	2.059E-132	1.81035
Lhx3	0.7835	0.2795	0.3567	804	1709	4.569E-02	0.59764
SP1	0.7360	0.8891	1.2080	1632	3584	48.25E-22	4.03480
Klf4	0.6940	0.1438	0.2072	494	1273	10.71E-04	0.24214
PLAG1	0.6177	0.0108	0.0175	44	129	1.585E-02	0.01583
Zfx	0.6167	0.1023	0.1659	354	1060	61.27E-10	0.18051
Ddit3::Cebpa	0.5528	0.2252	0.4074	800	2246	78.68E-06	0.44405
RREB1	0.4952	0.0253	0.0512	80	226	36.16E-04	0.23041

15.18 AR DHT vs AR CPA unique for ARDHTrrO (up)

Chromosome specific statistics are shown in Table 73. A histogram of sequence lengths is shown in Figure 103.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	46	249	458	756	21072	8.5e-05
2	28	237	415	693	11633	4.8e-05
3	18	122	446	583	8034	4.1e-05
4	37	290	454	954	16796	8.8e-05
5	22	304	424	736	9327	5.2e-05
6	31	272	456	755	14135	8.3e-05
7	15	288	468	854	7025	4.4e-05
8	21	133	427	727	8969	6.1e-05
9	2	323	404	485	808	6e-06
10	6	317	414	581	2485	1.8e-05
11	25	51	445	800	11117	8.2e-05
12	9	356	416	566	3743	2.8e-05
13	9	281	436	524	3921	3.4e-05
14	4	276	415	544	1659	1.5e-05
15	9	263	430	653	3870	3.8e-05
16	10	263	485	1042	4848	5.4e-05
17	9	323	427	546	3841	4.7e-05
18	13	258	488	923	6345	8.1e-05
19	2	267	442	616	883	1.5e-05
20	10	296	419	685	4189	6.6e-05
21	7	212	423	537	2963	6.2e-05
all 21	333	51	443	1042	147663	4.8e-05

Table 73: Chromosome specific distribution of the regions. The last line represents the overall statistics.

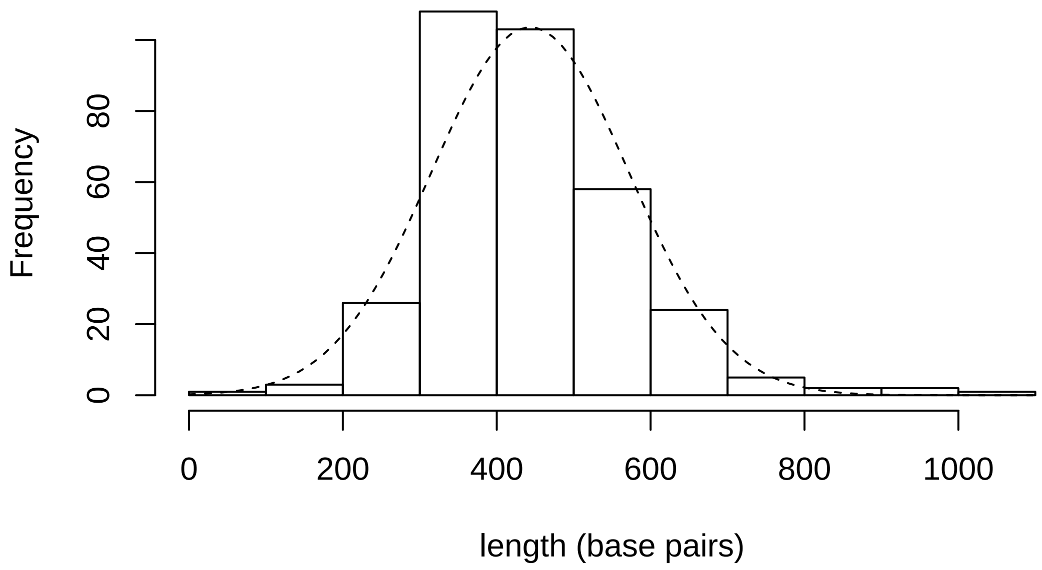
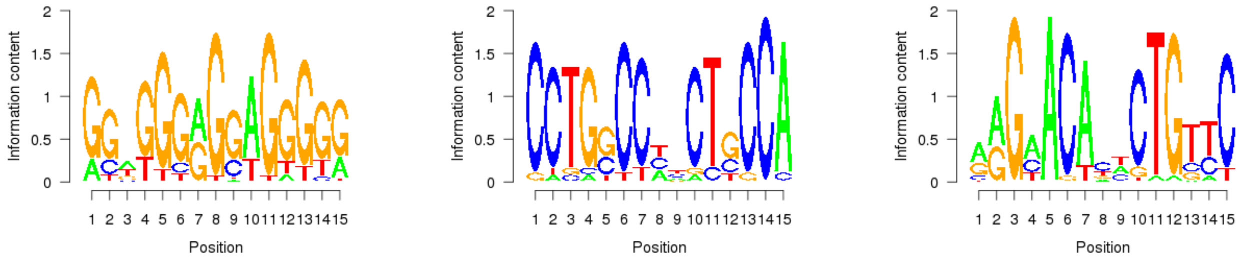


Figure 103: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU1u-gCount** component.

property	value
genes	163



(a) ARDHTvsARCPArrU1u-deNovo-meme1: width=15, sites=34, llr=446, E=5.2e-09

(b) ARDHTvsARCPArrU1u-deNovo-meme2: width=15, sites=18, llr=254, E=200

(c) ARDHTvsARCPArrU1u-deNovo-meme3: width=15, sites=32, llr=396, E=13000

Figure 104: De novo motifs for the filtered AR DHT vs AR CPA unique for ARDHTrrO (up) sequences.

Table 74: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	4.9194	0.0631	0.0128	20	8	69.29E-06	0.03144
FOXF2	2.8426	0.3634	0.1278	93	71	65.82E-14	0.25769
Foxa2	2.7884	0.9399	0.3371	194	152	60.67E-38	0.83266
FOXA1	2.7787	1.0210	0.3674	206	172	83.95E-40	0.79667
RXR::RAR_DR5	2.5991	0.0541	0.0208	17	13	1.503E-02	0.03340
Esrrb	2.0045	0.1441	0.0719	43	43	8.604E-04	0.10228
FOXA1pAR	1.9477	0.1712	0.0879	54	45	3.381E-06	0.14083
FOXD1	1.9353	1.4655	0.7572	249	318	3.918E-38	1.24947
Foxq1	1.8974	0.6456	0.3403	158	162	16.15E-20	0.58349
ARMotifT	1.8001	0.6787	0.3770	157	188	13.35E-16	0.56099
AR	1.7971	0.0661	0.0367	22	22	3.249E-02	0.04686
GRMotifTH	1.6679	0.3784	0.2268	104	126	11.56E-08	0.30178
Stat3	1.5806	0.2222	0.1406	59	73	15.18E-04	0.20943
NR3C1	1.4754	0.4054	0.2748	107	152	7.774E-06	0.33478
GRMotifT	1.4295	2.6216	1.8339	301	522	21.14E-48	2.66799
GR	1.3683	0.3213	0.2348	88	127	3.664E-04	0.28468
FOXO3	1.3512	2.0571	1.5224	280	448	28.37E-42	2.40944
Gata1	1.3495	0.7718	0.5719	169	264	10.66E-12	0.71671
NFIC	1.3018	2.8468	2.1869	309	508	8.962E-54	3.42066
FEV	1.3006	0.7417	0.5703	164	259	1.038E-10	0.71982
ARMotifH	1.2879	9.0691	7.0415	332	620	49.27E-62	15.23374
FOXI1	1.2595	1.0060	0.7987	206	292	15.41E-22	1.39662
ELF5	1.2209	2.0811	1.7045	281	478	32.09E-40	2.47178
Hand1::Tcfe2a	1.2187	1.3063	1.0719	237	392	63.71E-26	1.40132
Spz1	0.8220	0.6066	0.7380	151	320	2.315E-04	0.75183
Prrx2	0.8042	2.1712	2.6997	257	529	9.892E-24	5.26461
SP1	0.7847	1.0931	1.3930	149	316	3.395E-04	5.10751
MZF1_5-13	0.7535	1.1772	1.5623	231	463	16.46E-18	1.99881
CREB1	0.7533	0.6727	0.8930	150	326	5.664E-04	1.09990
FOXL1	0.7342	6.5435	8.9121	313	585	3.06E-50	89.08590
Foxd3	0.7326	2.0270	2.7668	250	461	34.74E-26	10.40256

15.19 AR DHT vs AR CPA unique for ARDHTrrO (down)

Chromosome specific statistics are shown in Table 75. A histogram of sequence lengths is shown in Figure 105.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	9	328	501	858	4508	1.8e-05
2	7	279	396	497	2769	1.1e-05
3	19	358	504	714	9571	4.8e-05
4	2	395	435	475	870	5e-06
5	4	349	413	468	1652	9e-06
6	7	326	409	561	2861	1.7e-05
7	9	287	480	654	4323	2.7e-05
8	8	296	423	555	3384	2.3e-05
9	3	270	304	339	912	6e-06
10	5	322	413	488	2067	1.5e-05
11	7	250	470	717	3288	2.4e-05
12	5	289	428	599	2142	1.6e-05
14	7	232	520	891	3637	3.4e-05
15	1	449	449	449	449	4e-06
16	4	287	408	529	1632	1.8e-05
17	1	290	290	290	290	4e-06
19	1	362	362	362	362	6e-06
20	1	693	693	693	693	1.1e-05
all 18	100	232	454	891	45410	1.5e-05

Table 75: Chromosome specific distribution of the regions. The last line represents the overall statistics.

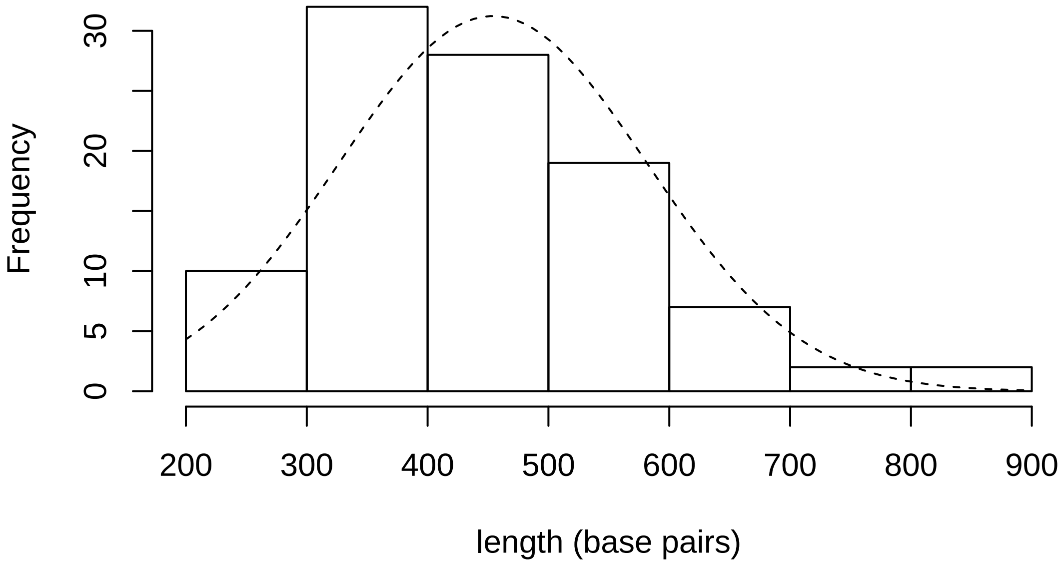
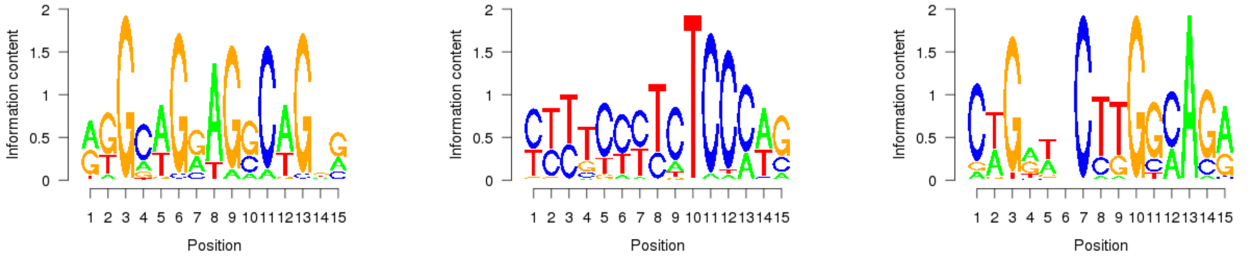


Figure 105: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU1d-gCount** component.

property	value
genes	63



(a) ARDHTvsARCPArrU1d-deNovo-meme1: width=15, sites=28, llr=325, E=0.19

(b) ARDHTvsARCPArrU1d-deNovo-meme2: width=15, sites=29, llr=329, E=1800

(c) ARDHTvsARCPArrU1d-deNovo-meme3: width=15, sites=23, llr=268, E=2100000

Figure 106: De novo motifs for the filtered AR DHT vs AR CPA unique for ARDHTrrO (down) sequences.

Table 76: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Zfp423	16.9485	0.0900	0.0053	5	1	3.419E-02	0.06801
T	9.4200	0.0500	0.0053	5	1	3.419E-02	0.02033
FOXF2	2.7435	0.2600	0.0947	23	18	9.968E-04	0.14991
FOXA1	2.5424	0.9100	0.3579	62	59	24.88E-12	0.56687
GABPA	2.2788	0.1200	0.0526	12	9	3.177E-02	0.07727
Foxa2	1.8173	0.6600	0.3632	51	49	4.142E-08	0.61645
ARMotifT	1.7249	0.6900	0.4000	46	61	1.147E-04	0.58304
Gata1	1.6336	0.9200	0.5632	61	83	14.67E-08	0.69358
FOXD1	1.6164	1.1400	0.7053	70	82	9.529E-12	1.07238
GRMotifTH	1.5436	0.3900	0.2526	34	42	25.23E-04	0.30069
Foxq1	1.5392	0.6400	0.4158	42	63	23.86E-04	0.54840
RORA_1	1.4499	0.2900	0.2000	28	37	2.188E-02	0.19211
TFAP2A	1.3861	2.0500	1.4789	64	111	3.803E-06	4.81499
USF1	1.3722	0.6500	0.4737	33	50	2.502E-02	1.02476
GRMotifT	1.3427	2.5300	1.8842	92	157	2.867E-16	2.58715
Nr2e3	1.2581	0.4900	0.3895	29	41	3.115E-02	0.73644
NR4A2	1.2491	2.1300	1.7053	88	153	4.277E-14	2.14749
FEV	1.2318	0.5900	0.4789	45	74	31.2E-04	0.50662
ARMotifH	1.2232	9.0000	7.3579	100	187	16.06E-20	16.20876
Arnt::Ahr	1.2214	1.6200	1.3263	70	120	9.246E-08	3.78194
ELK1	1.2165	0.8900	0.7316	56	95	1.065E-04	0.88839
GRMotifH	1.2103	6.5800	5.4368	98	185	3.413E-18	9.73260
YY1	0.8273	3.6400	4.4000	98	187	4.758E-18	6.05703
Nkx3-2	0.8255	1.8900	2.2895	85	165	17.57E-12	2.56514
Nkx2-5	0.8167	5.7900	7.0895	98	185	3.413E-18	23.10970
Sox5	0.8039	1.7600	2.1895	73	156	1.545E-06	3.26472
ARID3A	0.7925	3.3700	4.2526	88	164	30.85E-14	13.37102
SP1	0.7738	1.2300	1.5895	54	94	3.518E-04	8.13895
Nobox	0.7677	1.3900	1.8105	69	127	78.06E-08	3.56593
Pdx1	0.7562	2.3600	3.1211	80	165	56.81E-10	7.70659
Prrx2	0.6965	2.1700	3.1158	79	160	79.82E-10	6.76183
MZF1_5-13	0.6866	1.1600	1.6895	64	153	9.668E-04	2.09165
FOXL1	0.5751	5.5000	9.5632	95	180	1.832E-16	126.19164
Foxd3	0.5703	1.8100	3.1737	70	131	60.92E-08	13.97404

15.20 AR DHT vs AR CPA unique for ARDHTrrO (stable)

Chromosome specific statistics are shown in Table 77. A histogram of sequence lengths is shown in Figure 107.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	265	12	438	920	115975	0.000465
10	78	192	410	654	31997	0.000236
11	134	220	436	1046	58366	0.000432
12	94	3	395	757	37099	0.000277
13	39	280	472	1050	18422	0.00016
14	83	101	427	920	35466	0.00033
15	61	238	442	748	26958	0.000263
16	65	202	420	784	27280	0.000302
17	81	201	417	656	33798	0.000416
18	44	200	415	914	18262	0.000234
19	31	202	356	616	11027	0.000186
2	155	130	413	731	64010	0.000263
20	56	239	403	776	22576	0.000358
21	22	196	443	651	9740	0.000202
22	28	208	402	640	11268	0.00022
3	163	122	476	1117	77530	0.000392
4	90	223	427	689	38415	0.000201
5	118	12	429	1152	50586	0.00028
6	136	69	403	778	54830	0.00032
7	118	214	433	903	51040	0.000321
8	80	70	457	760	36533	0.00025
9	79	252	421	736	33271	0.000236
X	28	214	379	579	10619	6.8e-05
Y	3	275	311	345	932	1.6e-05
all 24	2051	3	427	1152	876000	0.000283

Table 77: Chromosome specific distribution of the regions. The last line represents the overall statistics.

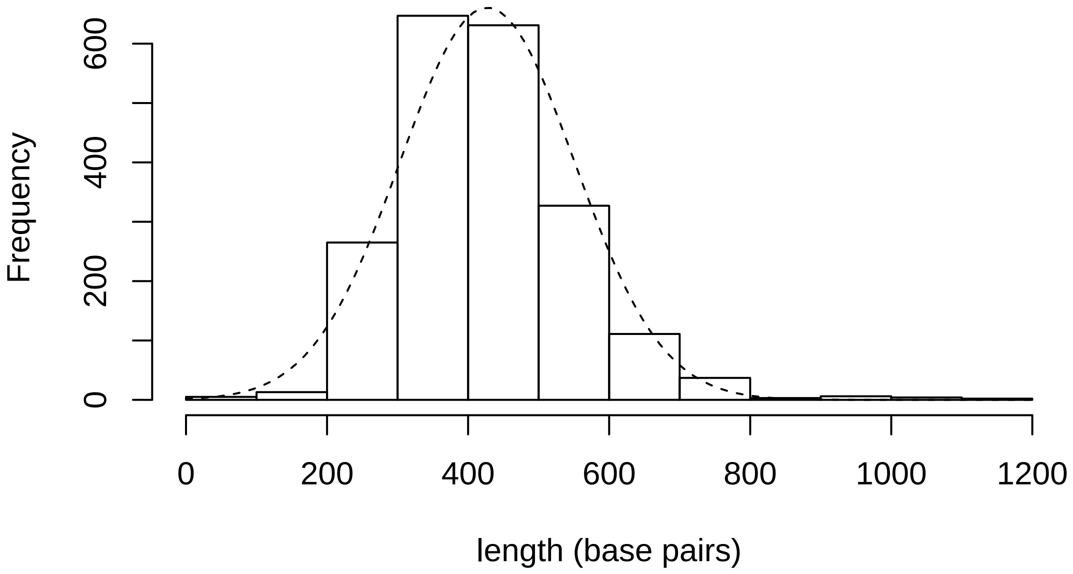
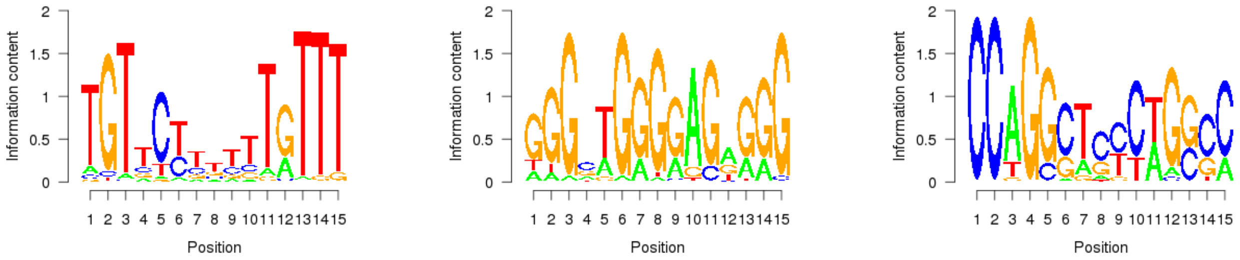


Figure 107: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU1s-gCount** component.

property	value
genes	2089



(a) ARDHTvsARCPArrU1s-deNovo-meme1: width=15, sites=163, llr=1683, E=4e-61 (b) ARDHTvsARCPArrU1s-deNovo-meme2: width=15, sites=33, llr=434, E=0.007 (c) ARDHTvsARCPArrU1s-deNovo-meme3: width=15, sites=26, llr=353, E=1800

Figure 108: De novo motifs for the filtered AR DHT vs AR CPA unique for ARDHTrrO (stable) sequences.

Table 78: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	9.6697	0.0785	0.0081	150	30	10.5E-44	0.03563
TLX1::NFIC	3.1011	0.0171	0.0055	29	17	97.8E-06	0.01282
FOXA1	2.9392	1.0546	0.3588	1361	1112	8.716E-268	0.72734
FOXA1pAR	2.9071	0.2341	0.0805	437	269	15.76E-66	0.15751
FOXF2	2.5863	0.3249	0.1256	575	436	38.04E-74	0.20930
Foxa2	2.5494	0.8941	0.3507	1222	970	40.97E-226	0.79508
ARMotifTT	2.5129	0.0132	0.0052	27	20	17.15E-04	0.00792
RXRA::VDR	2.3244	0.0098	0.0042	20	16	1.397E-02	0.00608
Tal1::Gata1	2.2784	0.0654	0.0287	128	109	82.75E-12	0.04211
Evi1	2.0230	0.0517	0.0255	104	95	8.10E-08	0.03515
ARMotifTH	1.8191	0.0683	0.0375	137	138	2.20E-08	0.04931
FOXD1	1.7988	1.3527	0.7520	1492	1907	48.6E-212	1.17209
Stat3	1.7598	0.2298	0.1305	355	391	2.769E-20	0.23162
STAT1	1.7506	0.0498	0.0284	83	93	3.505E-04	0.04679
PPARG::RXRA	1.7359	0.0254	0.0146	48	56	1.548E-02	0.01971
ELK4	1.7098	0.0312	0.0182	58	66	46.84E-04	0.02598
Foxq1	1.7065	0.6537	0.3830	936	1087	84.54E-88	0.60896
AR	1.6741	0.0580	0.0347	114	131	35.2E-06	0.04335
ARMotifT	1.6726	0.6420	0.3838	953	1190	7.055E-80	0.52691
GRMotifTH	1.6582	0.3556	0.2144	596	720	11.16E-36	0.28723
GABPA	1.6274	0.0878	0.0539	169	200	49.35E-08	0.06753
GRMotifTT	1.4518	0.0254	0.0175	50	65	4.981E-02	0.02116
NR3C1	1.4095	0.3507	0.2488	578	820	1.067E-22	0.31223
Gata1	1.4047	0.8166	0.5813	1090	1605	1.235E-80	0.77003
FOXI1	1.3427	1.0244	0.7629	1221	1713	64.47E-116	1.38040
GRMotifT	1.3371	2.4088	1.8015	1846	3103	16.2E-288	2.51045
ARMotifHH	1.2833	0.3795	0.2957	619	906	11.09E-24	0.37463
ARMotifH	1.2705	8.4605	6.6592	2047	3790	0.00E00	14.01176
Esrrb	1.2670	0.1083	0.0855	208	305	2.224E-04	0.09795
Pax5	1.2516	0.0541	0.0433	110	159	1.586E-02	0.04756
NFIC	1.2482	2.7146	2.1748	1825	3198	1.002E-266	3.50316
GR	1.2438	0.2829	0.2275	494	741	2.624E-14	0.27424
HNF1B	1.2394	0.0937	0.0756	170	273	2.073E-02	0.08944
FOXO3	1.2288	1.8941	1.5414	1641	2754	57.73E-202	2.32532
Myb	1.2073	0.8220	0.6808	1129	1835	27.24E-74	0.81241
TAL1::TCF3	1.2057	0.2541	0.2108	374	604	1.382E-06	0.31622
CREB1	0.8291	0.6727	0.8114	941	1984	20.64E-22	0.92857
Foxd3	0.8282	2.0693	2.4984	1504	2683	1.115E-142	10.09679
HLF	0.8264	0.4098	0.4958	606	1345	20.1E-04	0.60729
Prrx2	0.8195	2.0976	2.5597	1614	3153	3.746E-158	4.56628
FOXL1	0.7880	6.2893	7.9815	1948	3565	50.68E-318	65.62897
MZF1_5-13	0.7761	1.1039	1.4224	1272	2679	12.74E-62	1.94441
SP1	0.7075	0.9161	1.2949	825	1875	16.66E-10	4.62638
PBX1	0.6947	0.0785	0.1131	153	391	2.109E-02	0.10954
Zfx	0.6213	0.1063	0.1712	185	545	70.13E-06	0.18600
RREB1	0.5987	0.0263	0.0440	44	127	2.411E-02	0.06464
Ddit3::Cebpa	0.5367	0.2176	0.4054	393	1102	39.78E-04	0.44901
Pax6	0.4191	0.0039	0.0094	8	34	4.934E-02	0.00810

15.21 AR DHT vs AR CPA unique for ARCPArrO

Chromosome specific statistics are shown in Table 79. A histogram of sequence lengths is shown in Figure 109.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	40	36	125	309	4986	2e-05
10	13	40	86	265	1114	8e-06
11	14	47	135	284	1892	1.4e-05
12	20	46	104	233	2089	1.6e-05
13	12	52	156	301	1867	1.6e-05
14	14	47	106	230	1481	1.4e-05
15	8	48	135	221	1079	1.1e-05
16	22	36	115	324	2535	2.8e-05
17	25	30	164	586	4108	5.1e-05
18	11	43	116	216	1279	1.6e-05
19	24	33	90	183	2162	3.7e-05
2	28	27	148	654	4148	1.7e-05
20	7	52	107	266	751	1.2e-05
21	7	46	106	236	745	1.5e-05
22	5	45	115	272	575	1.1e-05
3	17	42	110	219	1876	9e-06
4	12	52	92	151	1098	6e-06
5	13	48	121	297	1578	9e-06
6	13	46	92	254	1199	7e-06
7	19	46	88	233	1673	1.1e-05
8	11	49	137	337	1508	1e-05
9	13	21	92	226	1200	8e-06
X	4	49	76	132	304	2e-06
Y	4	114	186	283	745	1.3e-05
all 24	356	21	118	654	41992	1.4e-05

Table 79: Chromosome specific distribution of the regions. The last line represents the overall statistics.

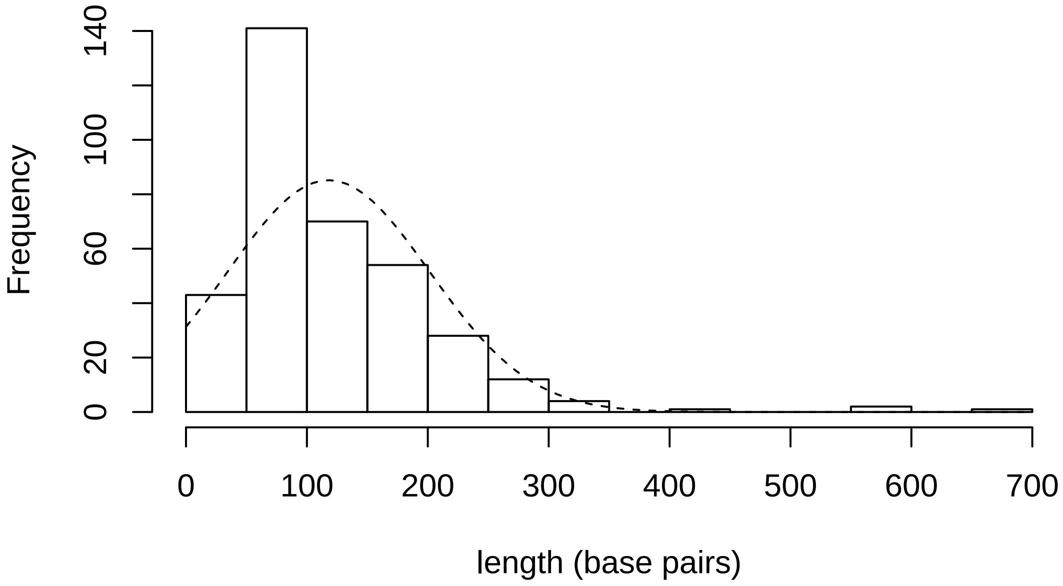
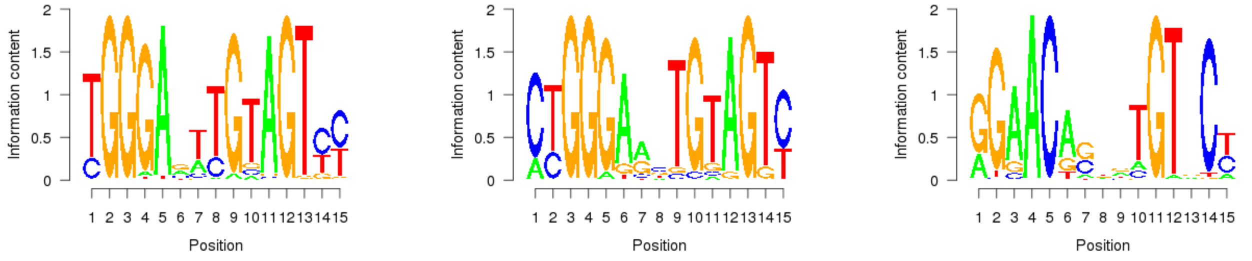


Figure 109: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU2-gCount** component.

property	value
genes	1801



(a) ARDHTvsARCPArrU2-deNovo-meme1: width=15, sites=56, llr=806, E=5.2e-104

(b) ARDHTvsARCPArrU2-deNovo-meme2: width=15, sites=21, llr=298, E=2.3e-10

(c) ARDHTvsARCPArrU2-deNovo-meme3: width=15, sites=43, llr=486, E=1.5e-11

Figure 110: De novo motifs for the filtered AR DHT vs AR CPA unique for ARCPArrO sequences.

Table 80: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	1517.8539	0.0758	0.0000	12	0	7.882E-06	0.11758
RREB1	201.3461	2.4213	0.0120	108	4	22.75E-48	15.09955
Ar	41.7948	0.0646	0.0015	19	1	4.257E-08	0.03073
E2F1	41.7948	0.0646	0.0015	22	1	21.65E-10	0.02487
PLAG1	29.7029	0.1348	0.0045	34	3	34.86E-14	0.07865
SP1	15.6031	6.8680	0.4401	234	145	7.579E-58	53.49825
ELK4	12.3826	0.0562	0.0045	18	3	2.189E-06	0.02589
MIZF	8.3216	0.0253	0.0030	9	2	28.59E-04	0.01064
MZF1_1-4	7.2319	8.0225	1.1093	312	340	3.849E-68	50.50424
Klf4	6.0950	0.4747	0.0778	112	46	43.88E-28	0.36100
STAT1	4.8529	0.0365	0.0075	12	3	5.742E-04	0.02315
Egr1	4.6842	0.1264	0.0269	40	16	39.44E-10	0.07344
TFAP2A	4.5947	1.8848	0.4102	197	166	12.37E-34	3.40851
NFKB1	4.2085	0.0506	0.0120	13	7	78.9E-04	0.04237
GABPA	4.0137	0.0843	0.0210	27	14	29.74E-06	0.04703
HIF1A::ARNT	3.4015	0.3820	0.1123	85	62	6.814E-12	0.36121
Pax5	3.1826	0.0478	0.0150	17	9	16.26E-04	0.02765
Stat3	3.0673	0.1011	0.0329	26	18	6.742E-04	0.08281
Arnt	2.6876	0.1208	0.0449	27	23	36.6E-04	0.15229
Mycn	2.3433	0.0702	0.0299	19	15	1.184E-02	0.06552
Myb	2.2439	0.3427	0.1527	92	91	97.13E-10	0.27273
MZF1_5-13	2.1143	0.8483	0.4012	182	194	1.593E-22	0.91761
EBF1	1.9944	0.3315	0.1662	80	84	1.195E-06	0.35365
ELK1	1.9437	0.4045	0.2081	104	120	5.377E-08	0.35072
Arnt::Ahr	1.8532	0.6770	0.3653	122	152	70.97E-10	1.81553
INSM1	1.7545	0.0815	0.0464	27	29	2.803E-02	0.06303
Zfx	1.6882	0.1011	0.0599	30	36	4.84E-02	0.09224
ZNF354C	1.6279	1.2697	0.7799	205	309	12.24E-18	1.86164
FEV	1.5489	0.1994	0.1287	62	78	16.45E-04	0.16513
Mafb	1.5275	0.7135	0.4671	141	208	3.181E-08	0.93172
ARMotifHH	1.4945	0.1320	0.0883	41	51	2.011E-02	0.12222
ARMotifH	1.4632	2.7753	1.8967	275	487	1.116E-30	5.65509
NFIC	1.2093	0.7893	0.6527	154	270	1.022E-06	1.32254
GRMotifH	0.7842	1.1517	1.4686	182	456	5.756E-04	2.48824
En1	0.7492	0.8961	1.1961	175	398	1.067E-04	1.92900
SOX10	0.7356	1.4635	1.9895	216	498	40.04E-10	4.15808
FOXC1	0.6697	1.1489	1.7156	175	476	1.435E-02	3.34276
GATA2	0.5452	1.7500	3.2096	212	574	12.05E-06	8.62772
FOXO3	0.5154	0.2191	0.4251	60	196	2.805E-02	0.51811
Sox17	0.5068	0.1798	0.3548	55	189	1.127E-02	0.34264
FOXI1	0.4655	0.0871	0.1871	24	103	15.52E-04	0.19182
Fos	0.4347	0.1770	0.4072	50	194	10.5E-04	0.46863
HLF	0.4291	0.0674	0.1572	18	86	10.45E-04	0.16300
SOX9	0.4291	0.0674	0.1572	22	95	20.13E-04	0.13367
RORA_1	0.3956	0.0225	0.0569	7	37	1.785E-02	0.04686
Ddit3::Cebpa	0.3912	0.0421	0.1078	15	66	69.82E-04	0.08955
IRF1	0.3869	0.0197	0.0509	4	30	1.004E-02	0.05802
Cebpa	0.3826	0.0899	0.2350	25	131	25.5E-06	0.22885
Gfi	0.3799	0.0955	0.2515	29	143	37.96E-06	0.22107
Sox5	0.3552	0.1882	0.5299	50	220	46.37E-06	0.69786
SRY	0.3433	0.3315	0.9656	78	337	56.7E-06	1.42177
Nkx2-5	0.2866	0.4972	1.7350	108	439	19.45E-04	3.96182
MEF2A	0.2723	0.0281	0.1033	10	57	19.09E-04	0.10450
FOXL1	0.2360	0.4747	2.0120	78	392	24.75E-08	8.31426
Nobox	0.2192	0.0899	0.4102	30	179	17.3E-08	0.51276
ARID3A	0.2167	0.2247	1.0374	57	319	63.76E-10	1.82940
Pdx1	0.2036	0.1404	0.6901	45	260	1.05E-08	0.97556
NKX3-1	0.1854	0.0421	0.2275	12	116	2.679E-08	0.25588
Prrx2	0.1844	0.1264	0.6856	32	265	23.57E-14	0.94616
NFIL3	0.0406	0.0028	0.0704	1	38	63.36E-06	0.06232
Lhx3	0.0367	0.0028	0.0778	1	40	37.2E-06	0.07650

15.22 AR DHT vs AR CPA unique for ARCPArrO (up)

Chromosome specific statistics are shown in Table 81. A histogram of sequence lengths is shown in Figure 111.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	3	131	201	240	602	2e-06
2	1	58	58	58	58	0
3	3	62	162	219	487	2e-06
6	1	254	254	254	254	1e-06
7	2	51	58	65	116	1e-06
8	1	49	49	49	49	0
11	1	54	54	54	54	0
12	1	100	100	100	100	1e-06
13	2	51	80	110	161	1e-06
14	1	230	230	230	230	2e-06
17	1	150	150	150	150	2e-06
all 11	17	49	133	254	2261	1e-06

Table 81: Chromosome specific distribution of the regions. The last line represents the overall statistics.

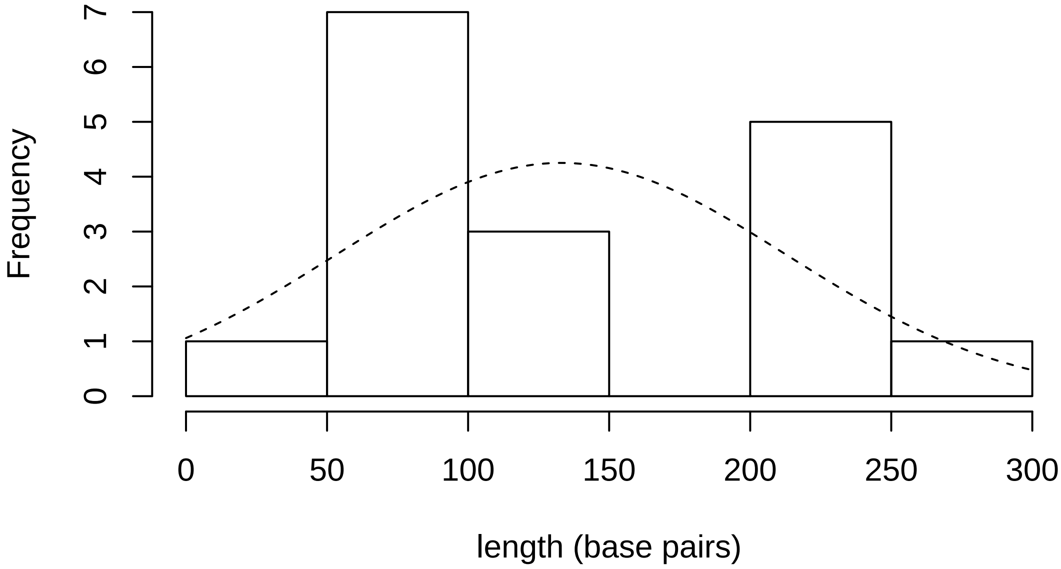
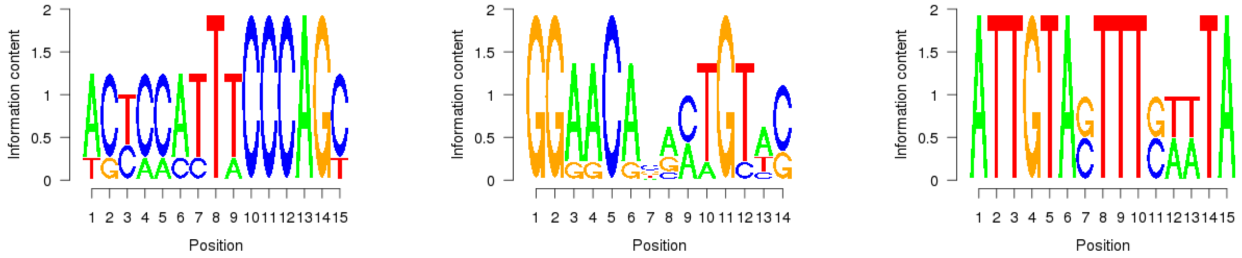


Figure 111: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU2u-gCount** component.

property	value
genes	20



(a) ARDHTvsARCPArrU2u-deNovo-meme1: width=15, sites=5, llr=80, E=540 (b) ARDHTvsARCPArrU2u-deNovo-meme2: width=14, sites=7, llr=91, E=4600 (c) ARDHTvsARCPArrU2u-deNovo-meme3: width=15, sites=2, llr=40, E=67000

Figure 112: De novo motifs for the filtered AR DHT vs AR CPA unique for ARCPArrO (up) sequences.

Table 82: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
RREB1	43530.4118	2.1765	0.0000	6	0	14.79E-04	6.27796
Ar	5883.3529	0.2941	0.0000	4	0	1.853E-02	0.13265
SP1	79.5450	7.2353	0.0909	11	3	60.41E-06	37.68327
TFAP2A	19.4042	2.3529	0.1212	11	3	60.41E-06	4.92408
MZF1_1-4	7.2922	8.1765	1.1212	15	17	3.353E-04	33.60163
EBF1	5.8196	0.3529	0.0606	6	2	1.81E-02	0.13714
Klf4	5.3364	0.6471	0.1212	6	3	4.054E-02	0.54082
FEV	4.3663	0.5294	0.1212	7	3	1.327E-02	0.31878
ARMotifH	1.4753	3.3529	2.2727	14	28	1.68E-02	5.13306

15.23 AR DHT vs AR CPA unique for ARCPArrO (down)

Chromosome specific statistics are shown in Table 83. A histogram of sequence lengths is shown in Figure 113.

		length				
chromosome	frequency	min	mean	max	total	coverage
12	1	46	46	46	46	0
16	2	128	140	151	279	3e-06
17	2	55	67	79	134	2e-06
19	2	48	73	98	146	2e-06
all 4	7	46	86	151	605	0

Table 83: Chromosome specific distribution of the regions. The last line represents the overall statistics.

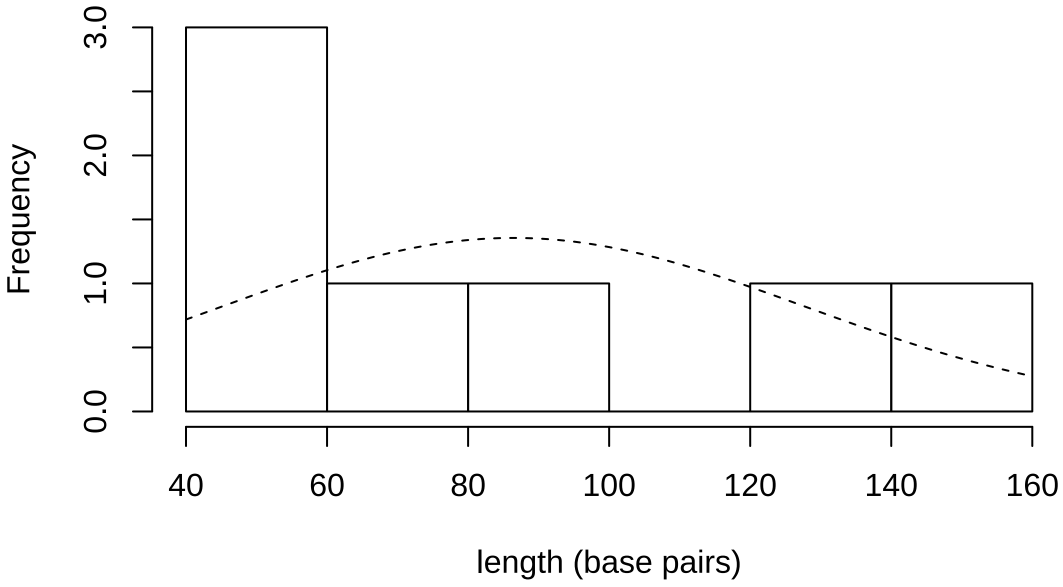
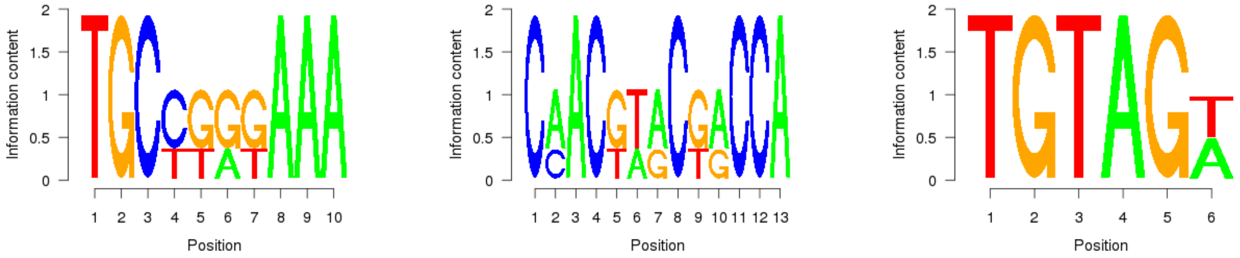


Figure 113: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU2d-gCount** component.

property	value
genes	10



(a) ARDHTvsARCPArrU2d-deNovo-meme1: width=10, sites=3, llr=36, E=800

(b) ARDHTvsARCPArrU2d-deNovo-meme2: width=13, sites=3, llr=43, E=1300

(c) ARDHTvsARCPArrU2d-deNovo-meme3: width=6, sites=2, llr=17, E=4100

Figure 114: De novo motifs for the filtered AR DHT vs AR CPA unique for ARCPArrO (down) sequences.

Table 84: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
SP1	148572.4286	7.4286	0.0000	5	0	29.08E-04	35.20000
HIF1A::ARNT	17143.8571	0.8571	0.0000	4	0	1.385E-02	0.43158
MZF1_1-4	12.9991	9.0000	0.6923	7	6	79.82E-04	41.09474

15.24 AR DHT vs AR CPA unique for ARCPArrO (stable)

Chromosome specific statistics are shown in Table 85. A histogram of sequence lengths is shown in Figure 115.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	37	36	126	309	4650	1.9e-05
10	5	40	53	60	264	2e-06
11	8	54	141	213	1131	8e-06
12	16	46	98	166	1567	1.2e-05
13	3	227	251	297	754	7e-06
14	10	47	101	219	1013	9e-06
15	8	48	135	221	1079	1.1e-05
16	11	44	127	246	1393	1.5e-05
17	21	30	161	586	3385	4.2e-05
18	5	53	126	216	628	8e-06
19	20	33	96	183	1914	3.2e-05
2	17	27	175	654	2978	1.2e-05
20	5	52	76	127	381	6e-06
21	6	46	99	236	593	1.2e-05
22	2	80	87	94	174	3e-06
3	12	42	123	219	1476	7e-06
4	4	53	84	151	335	2e-06
5	7	54	143	291	1001	6e-06
6	9	46	71	153	641	4e-06
7	13	46	94	233	1218	8e-06
8	9	47	138	337	1240	8e-06
9	8	21	102	226	816	6e-06
X	3	49	57	63	172	1e-06
all 23	239	21	121	654	28803	9e-06

Table 85: Chromosome specific distribution of the regions. The last line represents the overall statistics.

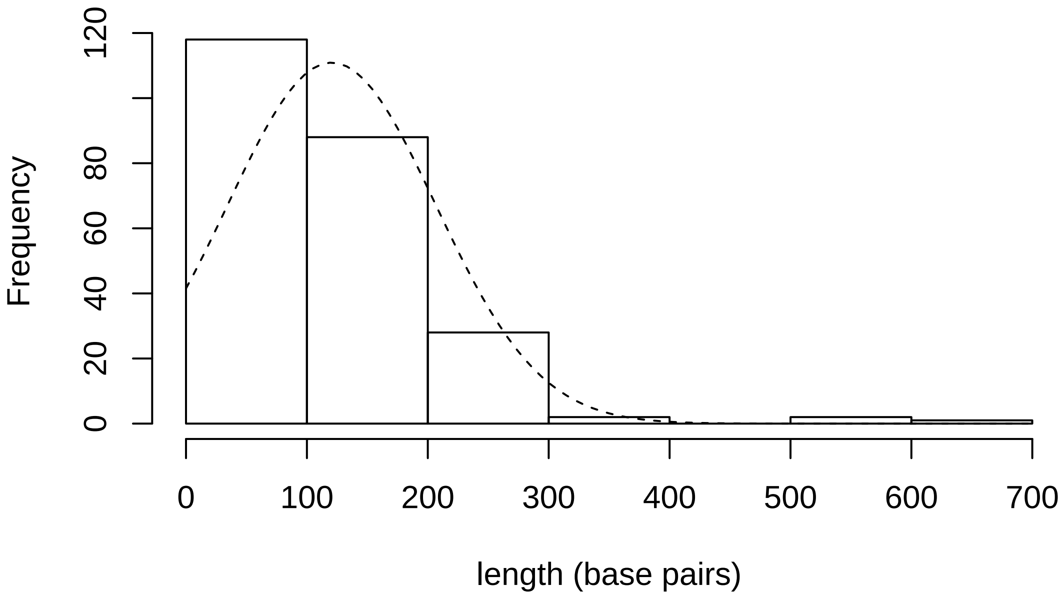
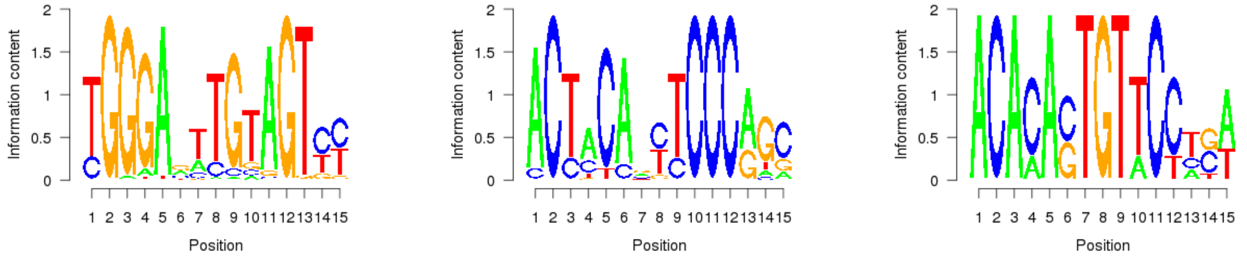


Figure 115: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARCPArrU2s-gCount** component.

property	value
genes	460



(a) ARDHTvsARCPArrU2s-deNovo-meme1: width=15, sites=50, llr=694, E=2.8e-86
(b) ARDHTvsARCPArrU2s-deNovo-meme2: width=15, sites=25, llr=325, E=4.9e-11
(c) ARDHTvsARCPArrU2s-deNovo-meme3: width=15, sites=9, llr=147, E=80

Figure 116: De novo motifs for the filtered AR DHT vs AR CPA unique for ARCPArrO (stable) sequences.

Table 86: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
PLAG1	2260.4142	0.1130	0.0000	20	0	27.01E-10	0.05855
E2F1	1088.8661	0.0544	0.0000	12	0	8.263E-06	0.02163
Pax4	1005.1841	0.0502	0.0000	7	0	12.53E-04	0.04075
RREB1	410.6578	1.8703	0.0045	64	2	4.023E-28	6.04081
ELK4	30.9174	0.0711	0.0023	15	1	2.276E-06	0.03156
Ar	21.8305	0.0502	0.0023	10	1	3.108E-04	0.02456
MIZF	16.3783	0.0377	0.0023	9	1	8.238E-04	0.01445
SP1	12.3867	5.8033	0.4685	152	86	50.48E-40	30.51352
Klf4	9.9869	0.4728	0.0473	75	21	2.484E-22	0.35441
Egr1	9.8751	0.1339	0.0135	30	6	9.417E-10	0.05848
GABPA	8.3327	0.1130	0.0135	24	6	28.14E-08	0.05485
HIF1A::ARNT	6.4985	0.4979	0.0766	72	32	1.449E-16	0.41455
MZF1_1-4	6.3420	6.9707	1.0991	208	222	11.42E-46	29.04231
Arnt	6.2382	0.1548	0.0248	22	6	1.769E-06	0.18860
TFAP2A	4.8044	2.0669	0.4302	144	121	2.288E-26	3.63636
Mycn	3.7100	0.0921	0.0248	16	9	32.67E-04	0.07244
STAT1	3.3336	0.0377	0.0113	8	4	4.203E-02	0.02597
Stat3	2.9480	0.1130	0.0383	20	15	60.14E-04	0.08969
Myc	2.9378	0.0795	0.0270	14	10	2.244E-02	0.06685
Pax5	2.9132	0.0460	0.0158	11	6	1.755E-02	0.02863
EBF1	2.8500	0.3724	0.1306	62	51	6.965E-08	0.31285
Arnt::Ahr	2.4492	0.7448	0.3041	89	95	49.81E-10	1.03161
ELK1	2.3050	0.4310	0.1869	74	68	1.481E-08	0.36854
Zfx	2.1219	0.1004	0.0473	21	20	2.581E-02	0.07337
MZF1_5-13	2.0976	0.8410	0.4009	125	118	2.456E-18	0.98635
Myb	1.9460	0.3682	0.1892	63	76	1.54E-04	0.30599
FEV	1.6478	0.2301	0.1396	48	52	5.793E-04	0.19202
Mafb	1.6472	0.7531	0.4572	102	155	2.877E-06	0.78626
ARMotifH	1.5395	2.8745	1.8671	193	312	4.184E-26	5.26548
ZNF354C	1.5144	1.2552	0.8288	134	211	1.491E-10	1.81623
NFIC	1.3642	0.7866	0.5766	107	162	61.23E-08	1.06945
SPIB	0.8140	0.7113	0.8739	100	219	1.812E-02	1.48992
GRMotifH	0.7898	1.1883	1.5045	129	283	61.96E-06	2.97809
En1	0.7869	0.9623	1.2230	124	270	1.791E-04	2.22895
FOXC1	0.6894	1.2343	1.7905	122	301	48.48E-04	4.18251
SOX10	0.6581	1.4644	2.2252	142	336	13.38E-06	6.03057
FOXD1	0.5594	0.1172	0.2095	21	78	2.595E-02	0.22810
GATA2	0.5527	1.8410	3.3311	144	382	1.839E-04	10.35082
FOXO3	0.5365	0.2259	0.4212	40	135	4.625E-02	0.51607
Gata1	0.5091	0.0837	0.1644	17	62	4.555E-02	0.16765
FOXI1	0.4646	0.1004	0.2162	17	66	2.485E-02	0.37671
SOX9	0.4513	0.0711	0.1577	15	58	3.387E-02	0.15237
Gfi	0.4112	0.1130	0.2748	22	102	11.8E-04	0.24999
Cebpa	0.3997	0.0837	0.2095	15	76	15.52E-04	0.21746
Sox5	0.3964	0.2008	0.5068	35	134	81.37E-04	0.81507
IRF1	0.3721	0.0209	0.0563	2	23	1.028E-02	0.06845
SRY	0.3414	0.3222	0.9437	51	211	20.8E-04	1.83255
Ddit3::Cebpa	0.2755	0.0335	0.1216	8	44	84.59E-04	0.11785
Nobox	0.2539	0.1046	0.4122	22	116	1.238E-04	0.49070
FOXL1	0.2379	0.4603	1.9347	54	267	33.15E-06	7.61912
NKX3-1	0.2277	0.0502	0.2207	9	78	12.16E-06	0.22329
ARID3A	0.2251	0.1967	0.8739	36	184	24.73E-06	1.84157
Pdx1	0.2091	0.1506	0.7207	33	178	9.173E-06	1.00065
Prrx2	0.1689	0.1130	0.6689	20	171	16.6E-10	0.86261
NFIL3	0.0013	0.0000	0.0383	0	16	80.44E-04	0.02724
Lhx3	0.0008	0.0000	0.0631	0	21	19.25E-04	0.06577

15.25 AR DHT vs AR RU486 overlaps

Chromosome specific statistics are shown in Table 87. A histogram of sequence lengths is shown in Figure 117.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	55	26	207	464	11375	4.6e-05
10	12	84	204	340	2452	1.8e-05
11	25	78	202	515	5052	3.7e-05
12	20	65	146	256	2916	2.2e-05
13	15	72	235	346	3522	3.1e-05
14	11	85	183	275	2017	1.9e-05
15	15	116	198	288	2974	2.9e-05
16	11	97	164	281	1801	2e-05
17	24	23	157	307	3771	4.6e-05
18	9	97	174	304	1563	2e-05
19	9	21	155	288	1394	2.4e-05
2	27	74	198	366	5356	2.2e-05
20	14	87	210	509	2941	4.7e-05
21	3	42	103	207	310	6e-06
22	5	69	122	180	608	1.2e-05
3	42	50	198	349	8327	4.2e-05
4	16	77	192	326	3066	1.6e-05
5	28	59	178	295	4980	2.8e-05
6	13	4	143	268	1863	1.1e-05
7	16	15	155	286	2483	1.6e-05
8	30	29	147	300	4404	3e-05
9	16	8	141	248	2251	1.6e-05
X	2	141	157	173	314	2e-06
all 23	418	4	181	515	75740	2.4e-05

Table 87: Chromosome specific distribution of the regions. The last line represents the overall statistics.

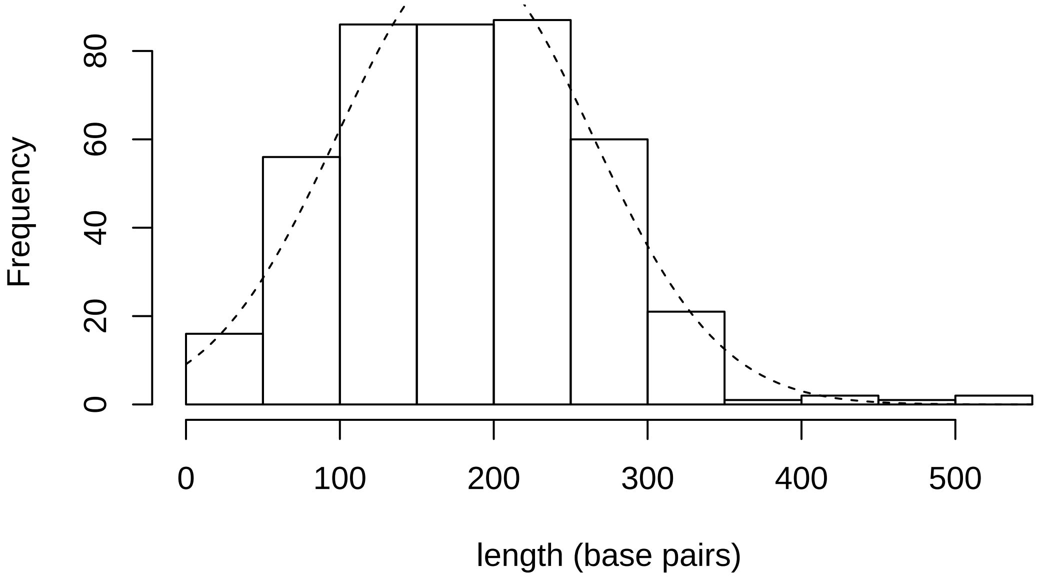
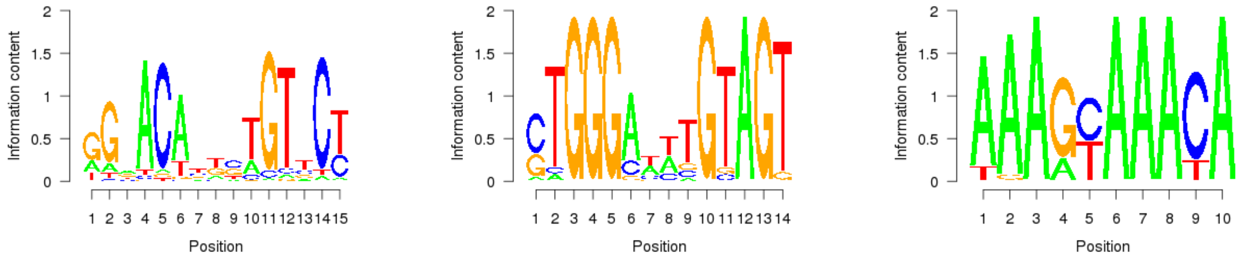


Figure 117: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrO-gCount** component.

property	value
genes	1595



(a) ARDHTvsARRU486rrO-deNovo-meme1: width=15, sites=278, llr=2392, E=8.6e-179

(b) ARDHTvsARRU486rrO-deNovo-meme2: width=14, sites=18, llr=248, E=9.3

(c) ARDHTvsARRU486rrO-deNovo-meme3: width=10, sites=28, llr=321, E=780

Figure 118: De novo motifs for the filtered AR DHT vs AR RU486 overlaps sequences.

Table 88: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	71.9339	0.1899	0.0026	73	2	53.12E-32	0.07538
ESR2	9.1221	0.0240	0.0026	10	2	12.47E-04	0.01001
FOXF2	3.9979	0.1659	0.0415	63	32	11.56E-12	0.08965
Stat3	3.7082	0.1490	0.0402	46	26	9.691E-08	0.11097
STAT1	3.7000	0.0433	0.0117	14	8	82.39E-04	0.03065
Foxa2	3.6714	0.4519	0.1231	150	81	2.851E-30	0.29620
FOXA1	3.5642	0.5264	0.1477	172	104	33.61E-34	0.31311
GRMotifTT	3.3225	0.0216	0.0065	9	5	4.124E-02	0.01166
Egr1	3.1265	0.0649	0.0207	25	14	1.665E-04	0.04165
MIZF	2.9057	0.0264	0.0091	11	7	3.479E-02	0.01493
ARMotifHH	2.7707	0.2764	0.0997	95	68	49.21E-14	0.18784
Mycn	2.7313	0.0673	0.0246	20	15	76.34E-04	0.05825
GABPA	2.6238	0.0409	0.0155	17	12	1.088E-02	0.02383
ARMotifT	2.4947	0.3846	0.1541	129	104	1.209E-16	0.27252
GRMotifTH	2.4454	0.2091	0.0855	80	64	26.35E-10	0.12746
FOXA1pAR	2.4389	0.0601	0.0246	23	19	80.05E-04	0.03907
NR3C1	2.3826	0.2933	0.1231	103	92	81.77E-12	0.19323
FOXD1	1.9914	0.6346	0.3187	185	202	28.46E-20	0.51648
Foxq1	1.8555	0.2861	0.1541	97	106	31.78E-08	0.22942
Esrrb	1.7929	0.0697	0.0389	28	29	2.186E-02	0.05061
NR2F1	1.7803	0.0577	0.0324	23	23	3.398E-02	0.04463
GRMotifT	1.7270	1.3221	0.7655	298	394	2.296E-40	1.13997
HIF1A::ARNT	1.7114	0.2284	0.1334	71	82	1.811E-04	0.24347
ARMotifH	1.7052	4.8462	2.8420	404	673	39.68E-76	7.33170
TFAP2A	1.7020	1.0913	0.6412	205	268	8.594E-18	2.29732
Arnt	1.6394	0.0913	0.0557	29	28	1.006E-02	0.10908
NFIC	1.6241	1.5000	0.9236	284	430	2.42E-30	1.63464
Gata1	1.5276	0.3582	0.2345	125	150	1.196E-08	0.31031
GRMotifHH	1.5181	0.1298	0.0855	44	57	3.186E-02	0.12458
Myf	1.3983	0.1250	0.0894	45	56	1.828E-02	0.15727
GR	1.3916	0.1442	0.1036	56	73	1.052E-02	0.12426
ELK1	1.3255	0.4087	0.3083	135	191	59.5E-08	0.39080
GRMotifH	1.3249	2.8438	2.1464	375	630	31.13E-60	3.84227
Arnt::Ahr	1.3138	0.5769	0.4391	148	240	6.395E-06	0.80607
Mafb	1.2840	0.9880	0.7694	229	371	8.332E-16	1.17676
SP1	1.2800	0.5986	0.4676	110	193	97.88E-04	1.71085
NR4A2	1.2771	0.8702	0.6813	230	350	7.892E-18	0.88647
FOXI1	1.2656	0.3918	0.3096	118	176	68.64E-06	0.46838
Myb	1.2106	0.4014	0.3316	126	209	4.192E-04	0.40134
Hand1::Tcfe2a	1.2062	0.5625	0.4663	166	271	22.45E-08	0.60741
YY1	0.7344	1.3005	1.7707	270	580	62.37E-16	2.60458
HOXA5	0.7075	1.9760	2.7927	309	631	14.93E-26	5.44140
ARID3A	0.6895	1.0913	1.5829	238	488	62.0E-12	2.83870
Nkx2-5	0.6815	1.8582	2.7267	292	618	5.535E-20	6.31161
Foxd3	0.6427	0.6418	0.9987	157	320	20.24E-04	3.49373
Ddit3::Cebpa	0.5173	0.0817	0.1580	33	108	2.464E-02	0.14281
FOXL1	0.5117	1.7188	3.3588	269	590	3.763E-14	13.19194
Lhx3	0.4678	0.0769	0.1645	23	89	61.23E-04	0.21712

15.26 AR DHT vs AR RU486 overlaps (up)

Chromosome specific statistics are shown in Table 89. A histogram of sequence lengths is shown in Figure 119.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	11	100	231	430	2542	1e-05
2	5	122	168	190	842	3e-06
3	4	98	188	318	750	4e-06
4	1	164	164	164	164	1e-06
5	11	107	197	273	2165	1.2e-05
6	1	180	180	180	180	1e-06
8	2	168	172	175	343	2e-06
10	2	213	232	251	464	3e-06
11	6	187	302	515	1814	1.3e-05
12	2	113	160	206	319	2e-06
13	1	346	346	346	346	3e-06
14	1	222	222	222	222	2e-06
15	1	132	132	132	132	1e-06
17	2	105	189	273	378	5e-06
19	3	21	91	172	274	5e-06
20	2	169	201	233	402	6e-06
21	1	207	207	207	207	4e-06
all 17	56	21	206	515	11544	4e-06

Table 89: Chromosome specific distribution of the regions. The last line represents the overall statistics.

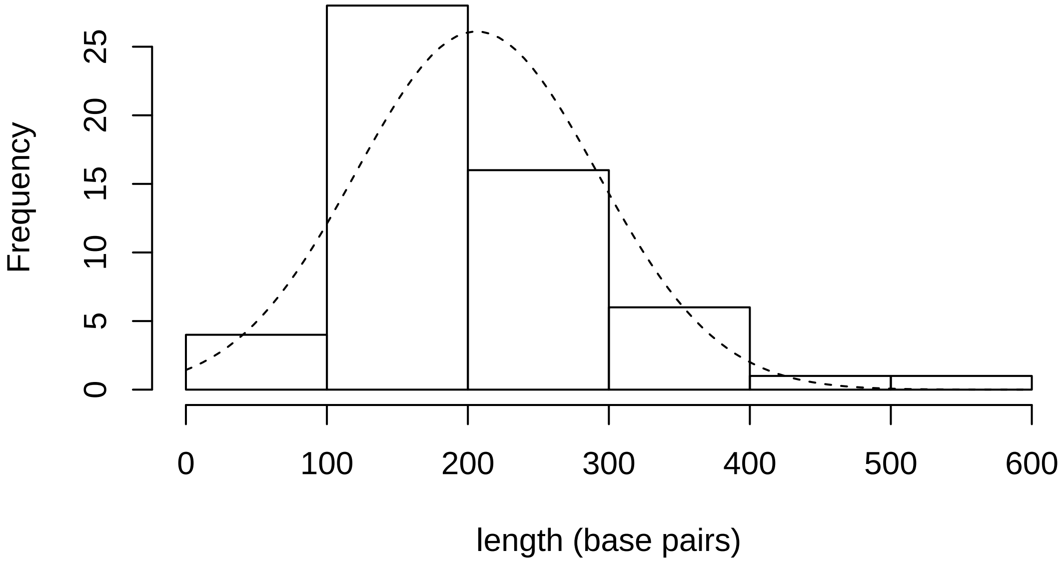
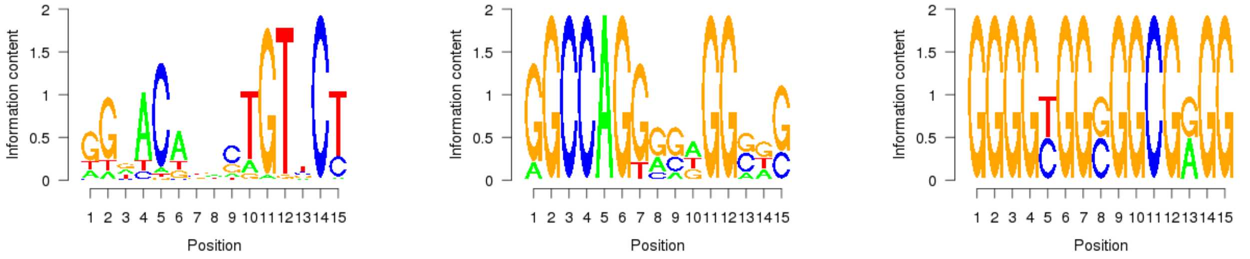


Figure 119: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrOu-gCount** component.

property	value
genes	52



(a) ARDHTvsARRU486rrOu-deNovo-meme1: width=15, sites=43, llr=395, E=2.2e-19

(b) ARDHTvsARRU486rrOu-deNovo-meme2: width=15, sites=7, llr=103, E=530000

(c) ARDHTvsARRU486rrOu-deNovo-meme3: width=15, sites=2, llr=39, E=4200000

Figure 120: De novo motifs for the filtered AR DHT vs AR RU486 overlaps (up) sequences.

Table 90: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	5001.0000	0.2500	0.0000	11	0	9.019E-06	0.12764
FOXA1	6.9396	0.6429	0.0926	31	10	36.76E-12	0.27667
Stat3	5.1354	0.1429	0.0278	7	2	1.204E-02	0.08750
Foxa2	3.8560	0.5000	0.1296	22	11	5.838E-06	0.32665
FOXF2	2.8912	0.1607	0.0556	9	6	4.061E-02	0.08361
FOXD1	2.7640	0.7679	0.2778	27	24	49.88E-06	0.64114
NR3C1	2.2496	0.3750	0.1667	18	13	10.72E-04	0.30507
ARMotifT	2.0890	0.4643	0.2222	19	20	93.42E-04	0.43409
Foxq1	2.0201	0.3929	0.1944	19	17	30.2E-04	0.29280
ARMotifH	1.7893	5.9643	3.3333	56	100	6.806E-12	8.85396
NFIC	1.7372	2.1071	1.2130	44	66	27.23E-08	2.69291
GRMotifT	1.7060	1.6429	0.9630	46	67	2.683E-08	1.51998
BRCA1	1.5979	1.0357	0.6481	35	51	1.24E-04	0.83495
TFAP2A	1.5309	1.3750	0.8981	27	44	1.491E-02	4.91650
Gata1	1.4930	0.4286	0.2870	22	25	52.49E-04	0.33469
FEV	1.4834	0.3571	0.2407	19	24	3.069E-02	0.23986
ELF5	1.4396	0.9464	0.6574	34	48	1.524E-04	0.97082
FOXO3	1.4104	0.8750	0.6204	33	50	5.80E-04	0.69909
GRMotifH	1.3852	3.2321	2.3333	55	88	3.668E-12	4.17040
Mafb	1.3520	1.2143	0.8981	36	58	2.27E-04	1.31898
SPI1	1.3038	0.8571	0.6574	29	51	1.376E-02	0.85063
ARID3A	0.7100	1.3214	1.8611	40	72	74.92E-06	4.14645
Nkx2-5	0.6678	1.9107	2.8611	42	84	73.73E-06	6.99865
HOXA5	0.6602	2.0357	3.0833	37	90	1.008E-02	6.82609
YY1	0.6555	1.2321	1.8796	38	86	31.75E-04	2.37348
FOXL1	0.5877	1.9643	3.3426	39	85	12.75E-04	12.57859

15.27 AR DHT vs AR RU486 overlaps (down)

Chromosome specific statistics are shown in Table 91. A histogram of sequence lengths is shown in Figure 121.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	2	254	280	307	561	2e-06
3	1	261	261	261	261	1e-06
7	1	217	217	217	217	1e-06
11	2	177	209	241	418	3e-06
16	1	132	132	132	132	1e-06
all 5	7	132	227	307	1589	1e-06

Table 91: Chromosome specific distribution of the regions. The last line represents the overall statistics.

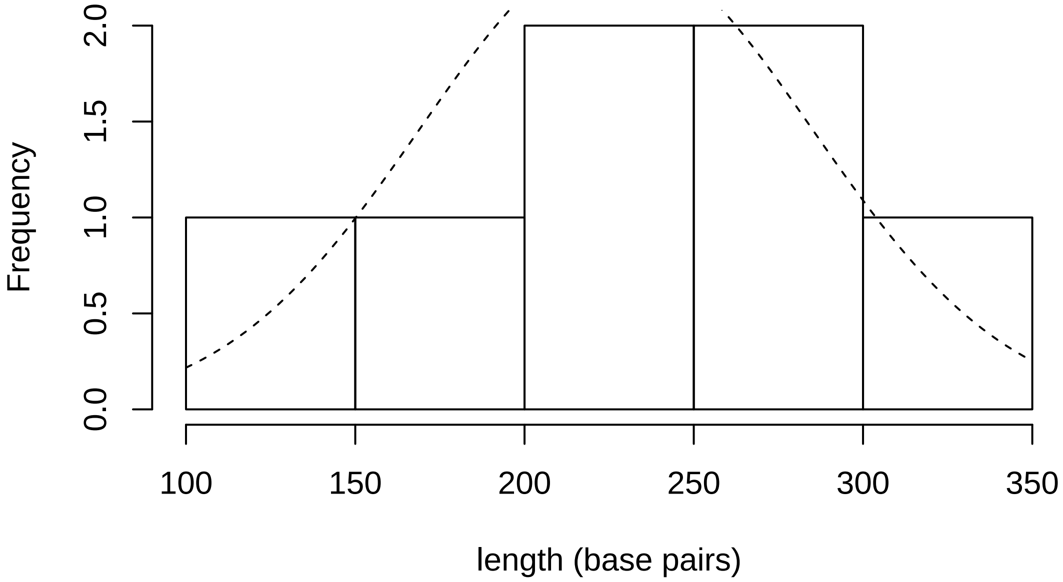
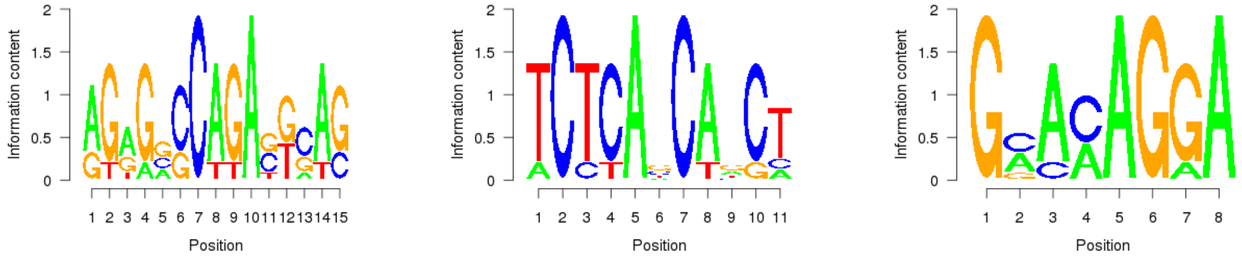


Figure 121: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrOd-gCount** component.

property	**value**
genes	10



(a) ARDHTvsARRU486rrOd-deNovo-meme1: width=15, sites=7, llr=87, E=870

(b) ARDHTvsARRU486rrOd-deNovo-meme2: width=11, sites=7, llr=69, E=6600

(c) ARDHTvsARRU486rrOd-deNovo-meme3: width=8, sites=7, llr=60, E=21000

Figure 122: De novo motifs for the filtered AR DHT vs AR RU486 overlaps (down) sequences.

Table 92: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
BRCA1	2.9998	1.2857	0.4286	6	6	3.475E-02	0.61429
ELF5	1.9999	0.8571	0.4286	5	3	3.901E-02	0.65714
ARMotifH	1.5385	5.7143	3.7143	7	13	4.006E-02	5.34762
GATA2	0.7423	5.1429	6.9286	7	14	4.726E-02	11.03333

15.28 AR DHT vs AR RU486 overlaps (stable)

Chromosome specific statistics are shown in Table 93. A histogram of sequence lengths is shown in Figure 123.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	37	26	202	464	7464	3e-05
10	6	86	194	259	1161	9e-06
11	10	78	175	285	1747	1.3e-05
12	13	65	137	223	1782	1.3e-05
13	5	106	205	287	1026	9e-06
14	10	85	189	275	1888	1.8e-05
15	4	140	207	288	829	8e-06
16	5	97	151	281	755	8e-06
17	19	33	155	301	2937	3.6e-05
18	3	162	166	173	498	6e-06
19	9	21	155	288	1394	2.4e-05
2	13	74	198	366	2574	1.1e-05
20	11	87	211	509	2323	3.7e-05
22	3	109	138	180	415	8e-06
3	20	78	230	349	4595	2.3e-05
4	11	77	197	326	2168	1.1e-05
5	13	59	181	267	2353	1.3e-05
6	6	92	174	268	1043	6e-06
7	11	15	134	286	1479	9e-06
8	12	53	122	238	1467	1e-05
9	8	64	141	221	1130	8e-06
X	1	173	173	173	173	1e-06
all 22	230	15	179	509	41201	1.3e-05

Table 93: Chromosome specific distribution of the regions. The last line represents the overall statistics.

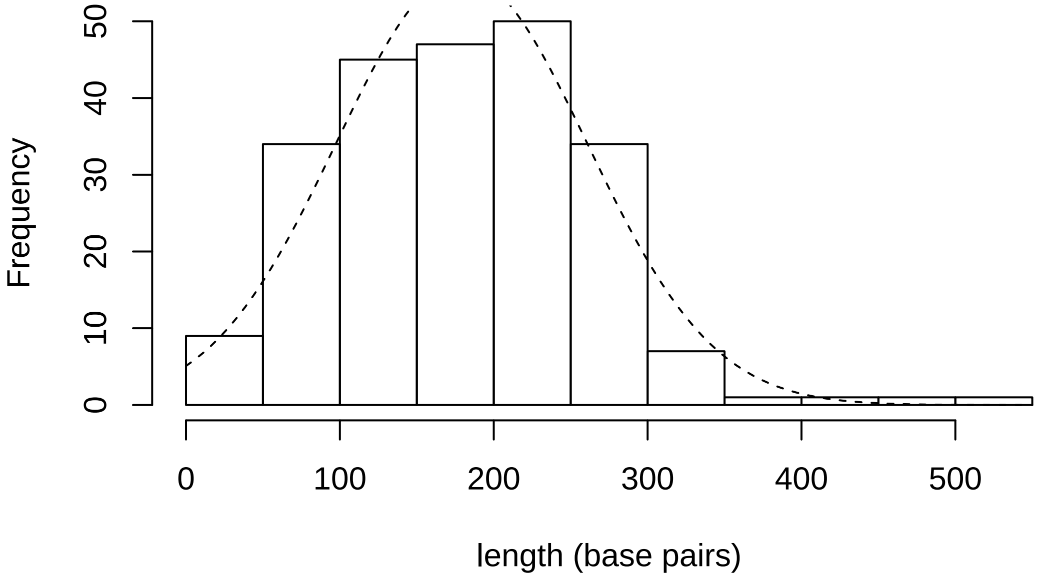
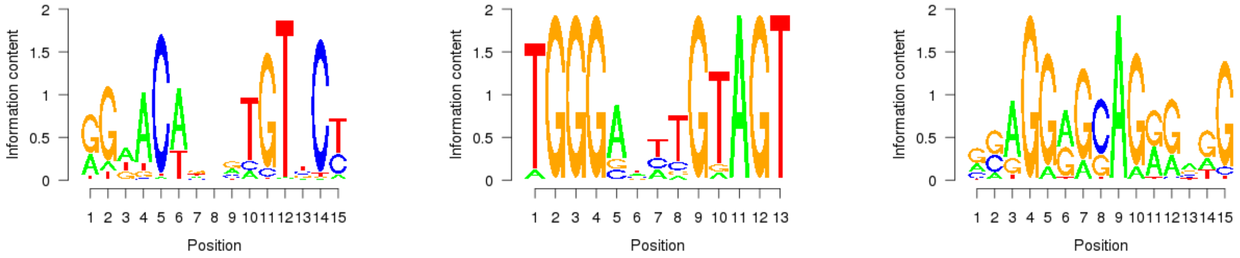


Figure 123: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrOs-gCount** component.

property	value
genes	376



(a) ARDHTvsARRU486rrOs-deNovo-meme1: width=15, sites=125, llr=1174, E=8.2e-83

(b) ARDHTvsARRU486rrOs-deNovo-meme2: width=13, sites=15, llr=199, E=180

(c) ARDHTvsARRU486rrOs-deNovo-meme3: width=15, sites=30, llr=336, E=1e+06

Figure 124: De novo motifs for the filtered AR DHT vs AR RU486 overlaps (stable) sequences.

Table 94: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
ELK4	522.7391	0.0261	0.0000	6	0	33.04E-04	0.00901
Ar	34.3085	0.1609	0.0046	35	2	1.355E-14	0.06167
NR3C1	3.6926	0.3000	0.0812	58	33	64.81E-12	0.17824
Foxa2	3.0895	0.4087	0.1323	77	51	21.99E-14	0.24925
FOXA1	2.6088	0.4783	0.1833	85	69	2.123E-12	0.32267
ARMotifT	2.4386	0.3565	0.1462	65	53	1.119E-08	0.25938
GRMotifTH	2.4084	0.1957	0.0812	44	33	3.896E-06	0.11563
ARMotifHH	2.1460	0.2739	0.1276	52	43	1.488E-06	0.22263
GR	2.1315	0.1435	0.0673	30	26	14.89E-04	0.10634
FOXF2	2.1149	0.1522	0.0719	33	30	12.22E-04	0.09911
Stat3	1.9835	0.1565	0.0789	26	27	1.834E-02	0.14937
TFAP2A	1.9322	1.2957	0.6705	123	160	1.582E-12	2.56927
FOXD1	1.8028	0.5522	0.3063	95	113	66.26E-10	0.43260
GRMotifT	1.7143	1.2609	0.7355	158	211	80.31E-22	1.12362
Myb	1.6555	0.3957	0.2390	65	86	3.795E-04	0.37737
ARMotifH	1.5822	4.6696	2.9513	223	373	3.548E-42	6.83281
NFIC	1.5631	1.4652	0.9374	153	230	1.096E-16	1.70654
Gata1	1.4696	0.3478	0.2367	66	85	1.853E-04	0.30892
USF1	1.3741	0.1913	0.1392	32	39	2.94E-02	0.25703
Mafb	1.3703	1.0174	0.7425	132	204	27.98E-12	1.06618
Myf	1.3508	0.1348	0.0998	28	32	2.953E-02	0.15108
Hand1::Tcfe2a	1.3428	0.5826	0.4339	98	149	3.629E-06	0.54108
Foxq1	1.2992	0.2261	0.1740	44	60	1.888E-02	0.24939
EBF1	1.2934	0.3391	0.2622	57	89	1.901E-02	0.37850
FEV	1.2895	0.2783	0.2158	58	75	9.88E-04	0.26623
ELK1	1.2776	0.3913	0.3063	71	114	40.17E-04	0.35370
SP1	1.2519	0.6913	0.5522	67	121	3.959E-02	2.07964
SPIB	0.8170	1.0957	1.3411	137	271	4.146E-08	3.59665
YY1	0.8053	1.3565	1.6845	155	314	35.35E-12	3.11815
NFATC2	0.7754	0.5739	0.7401	99	205	41.94E-04	0.85649
Sox5	0.7706	0.6043	0.7842	96	198	64.25E-04	1.01633
HOXA5	0.7660	1.9870	2.5940	177	348	13.89E-18	4.99722
Nkx2-5	0.6852	1.7391	2.5383	156	319	31.57E-12	5.86855
ARID3A	0.6383	0.9478	1.4849	119	266	3.916E-04	2.52468
TBP	0.5146	0.0609	0.1183	11	49	2.212E-02	0.10698
FOXL1	0.4486	1.3739	3.0626	131	325	2.679E-04	10.54672
Lhx3	0.3990	0.0435	0.1090	8	36	4.617E-02	0.12437
NFIL3	0.3979	0.0304	0.0766	5	27	4.608E-02	0.08421
Ddit3::Cebpa	0.3605	0.0652	0.1810	14	60	1.651E-02	0.19078

15.29 AR DHT vs AR RU486 unique for ARDHTrrO

Chromosome specific statistics are shown in Table 95. A histogram of sequence lengths is shown in Figure 125.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	538	12	454	920	244312	0.00098
10	222	192	424	931	94226	0.000695
11	261	51	441	1046	115011	0.000852
12	204	3	418	933	85244	0.000637
13	137	197	480	1081	65758	0.000571
14	174	51	445	920	77479	0.000722
15	187	13	457	821	85430	0.000833
16	142	51	420	1042	59690	0.000661
17	180	144	423	771	76160	0.000938
18	109	200	463	1125	50471	0.000646
19	62	202	387	746	23982	0.000406
2	370	119	435	1046	161102	0.000662
20	132	239	429	778	56607	0.000898
21	69	196	459	768	31696	0.000659
22	53	176	396	640	21003	0.000409
3	394	122	481	1117	189353	0.000956
4	254	198	428	954	108766	0.000569
5	333	5	453	1173	150831	0.000834
6	326	69	419	918	136579	0.000798
7	287	204	444	1124	127518	0.000801
8	271	70	452	934	122536	0.000837
9	197	223	441	854	86808	0.000615
X	102	57	391	647	39871	0.000257
Y	4	199	283	345	1131	1.9e-05
all 24	5008	3	442	1173	2211564	0.000714

Table 95: Chromosome specific distribution of the regions. The last line represents the overall statistics.

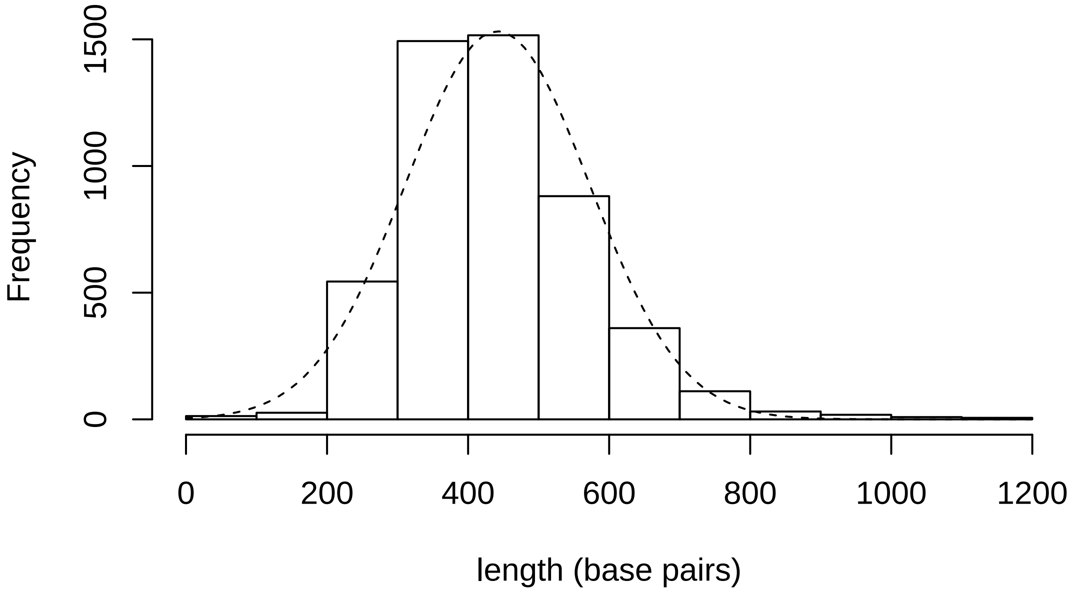
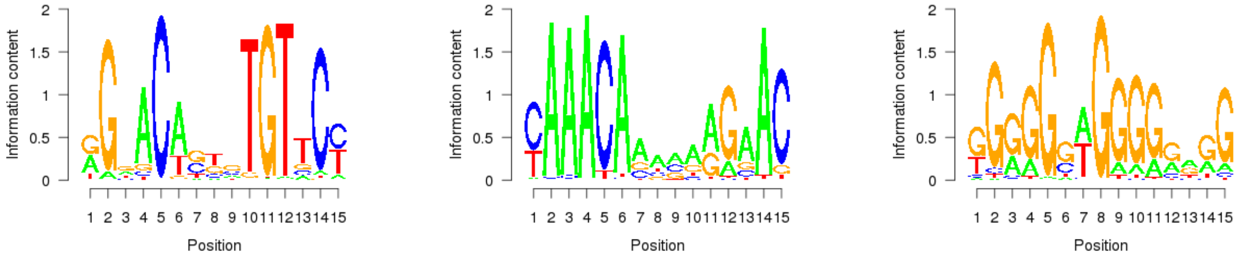


Figure 125: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU1-gCount** component.

property	value
genes	11274



(a) ARDHTvsARRU486rrU1-deNovo-meme1: width=15, sites=155, llr=1675, E=3e-76

(b) ARDHTvsARRU486rrU1-deNovo-meme2: width=15, sites=89, llr=1051, E=5.6e-42

(c) ARDHTvsARRU486rrU1-deNovo-meme3: width=15, sites=88, llr=985, E=5.9e-16

Figure 126: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARDHTrrO sequences.

Table 96: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	13.2233	0.1077	0.0081	492	74	1.79E-156	0.04799
FOXA1pAR	2.8545	0.2187	0.0766	995	629	70.65E-142	0.14684
FOXA1	2.7783	1.0402	0.3743	3299	2821	0.00E00	0.71490
Foxa2	2.5983	0.8977	0.3455	3005	2349	0.00E00	0.75291
FOXF2	2.5822	0.3164	0.1225	1351	1045	25.26E-164	0.20669
TLX1::NFIC	2.5253	0.0192	0.0076	77	58	6.532E-08	0.01592
ARMotifTT	2.1247	0.0132	0.0062	66	58	19.26E-06	0.00854
Tal1::Gata1	1.9100	0.0633	0.0331	303	306	99.68E-18	0.04437
CTCF	1.8607	0.0056	0.0030	28	28	2.339E-02	0.00388
ARMotifTH	1.8103	0.0737	0.0407	357	369	74.35E-20	0.05404
FOXD1	1.8052	1.3783	0.7635	3660	4643	0.00E00	1.22058
AR	1.7787	0.0707	0.0397	336	358	2.199E-16	0.05255
ESR2	1.7775	0.0226	0.0127	96	108	2.001E-04	0.02003
ARMotifT	1.7254	0.6956	0.4031	2458	2949	76.46E-232	0.57837
Foxq1	1.7029	0.6578	0.3863	2338	2706	75.66E-222	0.59970
Stat3	1.6887	0.2319	0.1373	871	1033	7.964E-40	0.23214
GRMotifTH	1.5968	0.3692	0.2312	1500	1891	18.57E-82	0.30616
GRMotifTT	1.5316	0.0260	0.0169	126	156	3.136E-04	0.02065
RXR::RAR_DR5	1.4915	0.0320	0.0214	158	199	77.01E-06	0.02501
STAT1	1.4863	0.0497	0.0335	196	256	35.64E-06	0.05399
NR3C1	1.4810	0.3889	0.2626	1528	2105	13.04E-68	0.34016
GABPA	1.4378	0.0881	0.0613	421	531	71.06E-14	0.07534
Gata1	1.4091	0.8208	0.5825	2687	3972	3.304E-198	0.76657
ELK4	1.3974	0.0264	0.0189	124	168	40.2E-04	0.02379
PPARG::RXRA	1.3843	0.0232	0.0167	109	152	1.41E-02	0.02055
FOXI1	1.3583	1.0374	0.7637	3003	4200	42.81E-286	1.34661
GRMotifT	1.3508	2.5258	1.8698	4547	7715	0.00E00	2.63479
GR	1.3309	0.3058	0.2298	1298	1802	1.105E-48	0.28634
Esrrb	1.2576	0.1209	0.0961	568	832	1.566E-10	0.10917
ARMotifHH	1.2564	0.3955	0.3148	1558	2320	1.669E-56	0.41238
ARMotifH	1.2484	8.8238	7.0680	4999	9317	0.00E00	15.45503
Evi1	1.2460	0.0447	0.0359	216	326	39.89E-04	0.04038
NFIC	1.2426	2.8106	2.2620	4504	7899	0.00E00	3.66469
FOXO3	1.2260	1.9281	1.5727	4066	6848	0.00E00	2.32473
TAL1::TCF3	1.2116	0.2583	0.2132	911	1461	1.015E-14	0.33089
FEV	1.2027	0.6714	0.5582	2423	3846	88.48E-134	0.65656
NHLH1	1.2010	0.1338	0.1114	414	643	30.6E-06	0.21966
Prrx2	0.8111	2.1748	2.6813	3984	7843	0.00E00	4.74610
MZF1_5-13	0.8101	1.1954	1.4757	3285	6690	9.023E-194	1.98531
Foxd3	0.7959	2.0721	2.6035	3710	6677	0.00E00	10.36792
SP1	0.7802	1.0018	1.2840	2122	4505	1.191E-36	5.19287
FOXL1	0.7787	6.4666	8.3048	4754	8781	0.00E00	66.57672
NF-kappaB	0.7716	0.1796	0.2328	669	1637	1.392E-02	0.31859
CREB1	0.7522	0.6736	0.8955	2295	5099	96.87E-42	1.06253
Klf4	0.7467	0.1640	0.2197	675	1649	1.608E-02	0.29013
Zfx	0.6285	0.1137	0.1809	476	1400	4.238E-10	0.19761
Ddit3::Cebpa	0.5272	0.2281	0.4327	988	2881	9.314E-08	0.47154

15.30 AR DHT vs AR RU486 unique for ARDHTrrO (up)

Chromosome specific statistics are shown in Table 97. A histogram of sequence lengths is shown in Figure 127.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	61	249	482	782	29383	0.000118
10	8	317	432	581	3458	2.6e-05
11	31	51	451	800	13993	0.000104
12	10	356	419	566	4194	3.1e-05
13	12	257	425	599	5100	4.4e-05
14	4	276	415	544	1659	1.5e-05
15	16	263	476	672	7622	7.4e-05
16	11	263	476	1042	5233	5.8e-05
17	12	323	486	771	5838	7.2e-05
18	14	258	490	923	6857	8.8e-05
19	3	267	497	616	1491	2.5e-05
2	39	237	455	833	17731	7.3e-05
20	13	296	467	685	6072	9.6e-05
21	10	212	412	537	4120	8.6e-05
3	21	122	438	583	9206	4.6e-05
4	46	290	467	954	21468	0.000112
5	26	304	438	736	11397	6.3e-05
6	46	268	451	755	20766	0.000121
7	19	288	465	854	8840	5.6e-05
8	26	133	446	727	11593	7.9e-05
9	3	323	444	523	1331	9e-06
X	1	413	413	413	413	3e-06
all 22	432	51	458	1042	197765	6.4e-05

Table 97: Chromosome specific distribution of the regions. The last line represents the overall statistics.

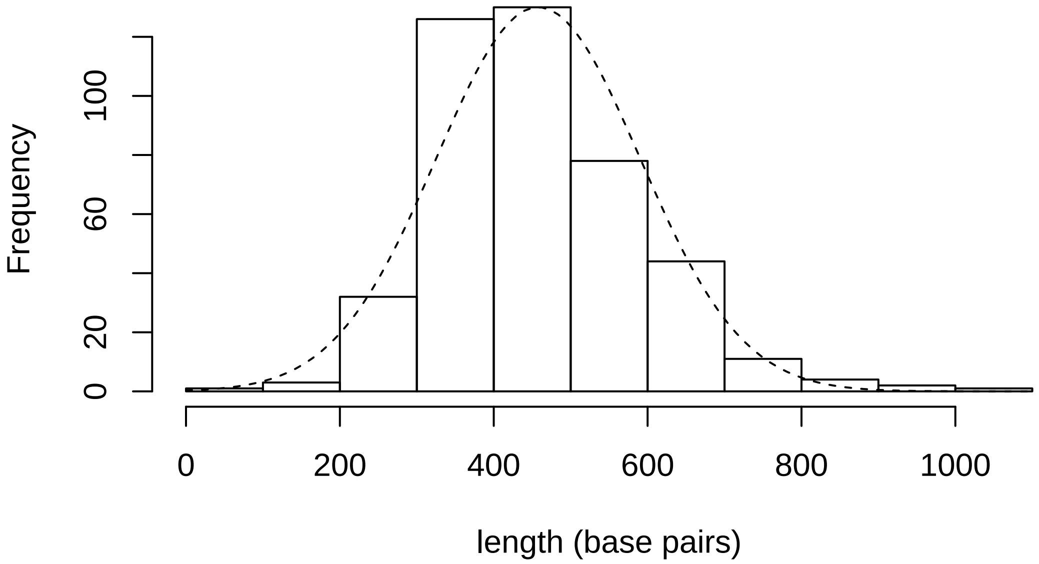
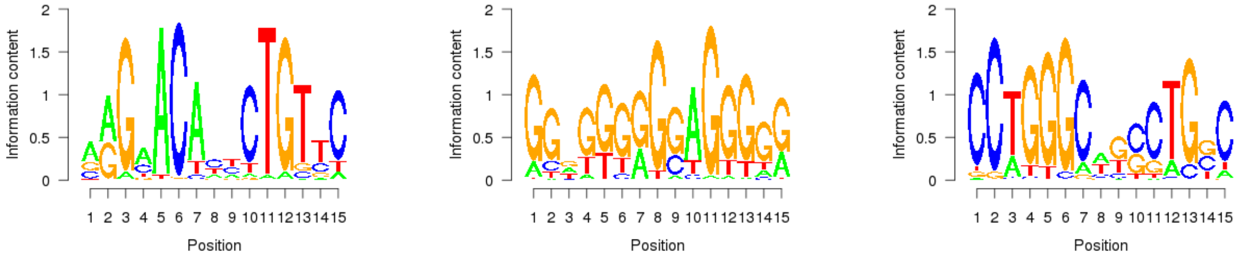


Figure 127: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU1u-gCount** component.

property	value
genes	180



(a) ARDHTvsARRU486rrU1u-deNovo-meme1: width=15, sites=84, llr=953, E=2.4e-25 (b) ARDHTvsARRU486rrU1u-deNovo-meme2: width=15, sites=55, llr=664, E=1.6e-10 (c) ARDHTvsARRU486rrU1u-deNovo-meme3: width=15, sites=42, llr=519, E=0.026

Figure 128: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARDHTrrO (up) sequences.

Table 98: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	22.1671	0.1088	0.0049	43	4	1.475E-16	0.04540
FOXA1	2.6077	1.0394	0.3985	273	244	11.37E-50	0.77507
Foxa2	2.5526	0.9306	0.3645	258	222	2.136E-46	0.75704
FOXF2	2.5455	0.3310	0.1300	111	95	47.17E-14	0.24577
FOXA1pAR	2.4296	0.1713	0.0705	71	51	11.14E-10	0.11174
GABPA	2.4229	0.0972	0.0401	41	32	44.61E-06	0.05942
RXR::RAR_DR5	2.3778	0.0463	0.0194	19	16	1.686E-02	0.02948
ARMotifT	1.8574	0.7222	0.3888	212	256	10.98E-22	0.58192
AR	1.8445	0.0718	0.0389	31	30	55.2E-04	0.05091
FOXD1	1.7802	1.4190	0.7971	316	418	12.09E-46	1.30769
GRMotifTH	1.6859	0.4097	0.2430	145	177	65.21E-12	0.31559
Foxq1	1.6838	0.6343	0.3767	197	237	54.36E-20	0.56000
Pax5	1.6414	0.0579	0.0352	25	28	4.823E-02	0.04280
NR3C1	1.6351	0.4769	0.2916	153	203	3.445E-10	0.40471
GRMotifT	1.4435	2.7801	1.9259	398	690	9.794E-66	2.88780
GRMotifHH	1.4435	0.2824	0.1956	101	141	89.58E-06	0.26570
Stat3	1.4403	0.2153	0.1495	75	99	9.412E-04	0.21916
ARMotifH	1.3263	9.6157	7.2503	431	815	38.88E-80	16.01896
GR	1.3115	0.3171	0.2418	114	173	1.256E-04	0.28712
FOXO3	1.3008	2.0231	1.5553	361	598	32.14E-52	2.36126
ARMotifHH	1.2770	0.4236	0.3317	144	217	58.43E-08	0.43566
FOXI1	1.2740	0.9861	0.7740	265	377	17.71E-28	1.19348
FEV	1.2597	0.7500	0.5954	220	347	44.65E-16	0.73368
NFIC	1.2565	2.9954	2.3840	402	698	10.29E-68	3.96536
Myb	1.2348	0.8912	0.7217	248	413	2.798E-18	0.87345
Gata1	1.2338	0.7616	0.6173	220	353	1.345E-14	0.80126
GRMotifH	1.2070	6.7037	5.5541	426	813	13.83E-76	10.21518
Hand1::Tcfe2a	1.2015	1.3519	1.1252	308	545	6.605E-30	1.39489
Pdx1	0.8123	2.4745	3.0462	358	719	1.853E-40	6.11686
Foxd3	0.7536	2.0162	2.6756	323	604	6.229E-32	9.60641
FOXL1	0.7479	6.4560	8.6318	407	777	59.36E-66	51.22949
Prrx2	0.7419	2.1690	2.9235	338	704	5.978E-32	5.60933
CREB1	0.7270	0.6713	0.9235	198	457	2.254E-04	1.08893

15.31 AR DHT vs AR RU486 unique for ARDHTrrO (down)

Chromosome specific statistics are shown in Table 99. A histogram of sequence lengths is shown in Figure 129.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	11	328	489	858	5376	2.2e-05
2	8	279	386	497	3090	1.3e-05
3	20	358	499	714	9979	5e-05
4	2	395	435	475	870	5e-06
5	5	349	438	536	2188	1.2e-05
6	8	326	416	561	3328	1.9e-05
7	11	287	497	764	5470	3.4e-05
8	9	296	412	555	3708	2.5e-05
9	3	270	304	339	912	6e-06
10	5	322	413	488	2067	1.5e-05
11	8	250	443	717	3542	2.6e-05
12	6	289	413	599	2480	1.9e-05
14	7	232	520	891	3637	3.4e-05
15	1	449	449	449	449	4e-06
16	6	278	374	529	2243	2.5e-05
17	1	290	290	290	290	4e-06
19	1	362	362	362	362	6e-06
20	1	693	693	693	693	1.1e-05
all 18	113	232	449	891	50684	1.6e-05

Table 99: Chromosome specific distribution of the regions. The last line represents the overall statistics.

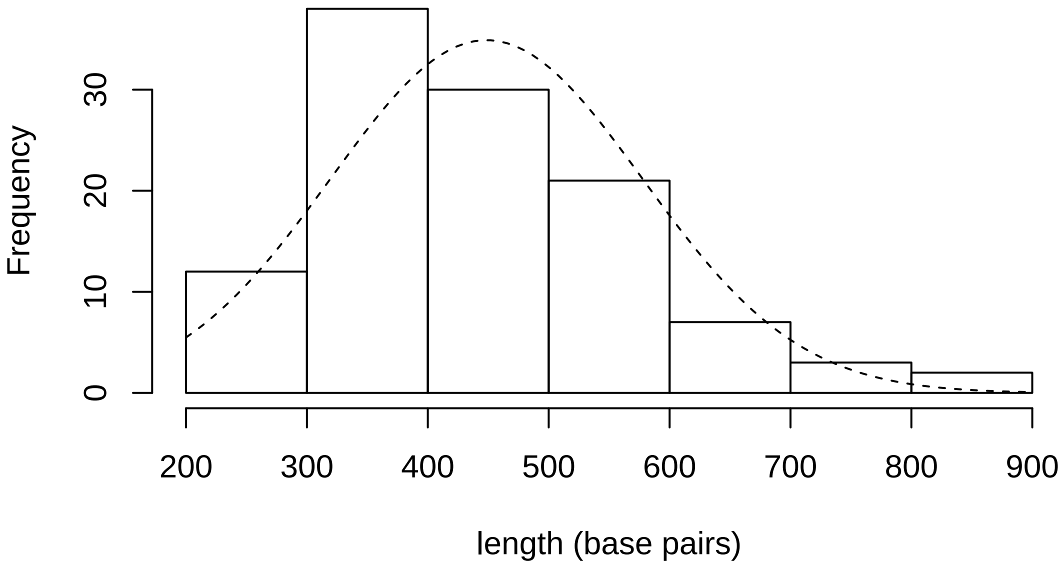
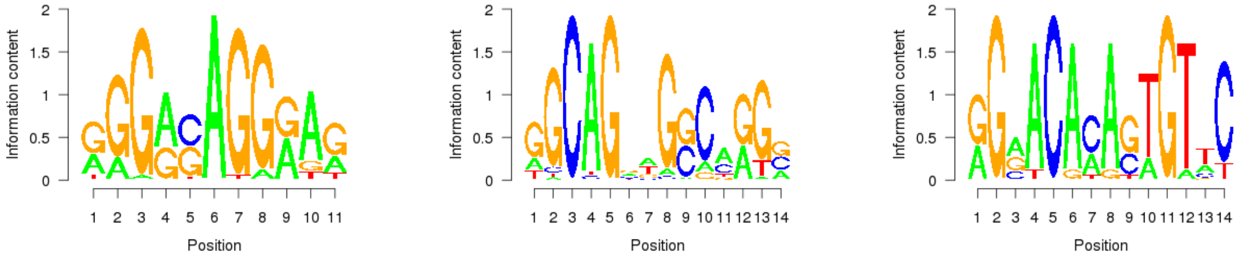


Figure 129: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU1d-gCount** component.

property	value
genes	66



(a) ARDHTvsARRU486rrU1d-deNovo-meme1: width=11, sites=44, llr=435, E=0.3 (b) ARDHTvsARRU486rrU1d-deNovo-meme2: width=14, sites=38, llr=405, E=1.3 (c) ARDHTvsARRU486rrU1d-deNovo-meme3: width=14, sites=15, llr=195, E=1e+06

Figure 130: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARDHTrrO (down) sequences.

Table 100: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
ESR2	885.9558	0.0442	0.0000	4	0	2.754E-02	0.02163
T	885.9558	0.0442	0.0000	5	0	97.16E-04	0.01538
Ar	16.4061	0.0796	0.0048	8	1	21.01E-04	0.03653
FOXA1	2.0631	0.9027	0.4375	69	71	57.83E-12	0.65925
ARMotifT	1.8406	0.6726	0.3654	52	64	20.69E-06	0.53758
Foxa2	1.8164	0.6637	0.3654	58	53	34.91E-10	0.63740
GRMotifTH	1.7150	0.3628	0.2115	36	40	11.13E-04	0.26404
GRMotifHH	1.6564	0.2389	0.1442	22	25	3.961E-02	0.20900
HIF1A::ARNT	1.6005	0.5310	0.3317	36	51	1.567E-02	0.67237
Myb	1.4955	0.9204	0.6154	69	95	6.571E-08	0.75726
ARMotifHH	1.4781	0.4690	0.3173	39	46	9.513E-04	0.53401
Gata1	1.4411	0.8938	0.6202	66	92	42.45E-08	0.75376
NR4A2	1.3848	2.1504	1.5529	100	160	1.121E-16	2.18752
GRMotifT	1.3460	2.5044	1.8606	105	167	29.7E-20	2.66737
Arnt::Ahr	1.3428	1.5752	1.1731	77	126	3.706E-08	3.90382
ARMotifH	1.3317	9.1681	6.8846	113	207	11.96E-22	15.86515
NFIC	1.3271	3.1327	2.3606	102	178	2.205E-16	4.70195
TBP	1.3204	0.2920	0.2212	29	37	2.454E-02	0.29237
Foxq1	1.3120	0.5929	0.4519	45	67	33.91E-04	0.69453
GRMotifH	1.2624	6.3363	5.0192	111	203	1.793E-20	9.43174
En1	0.8325	4.3628	5.2404	112	202	28.07E-22	6.74529
YY1	0.8261	3.5664	4.3173	111	206	2.979E-20	6.20656
Sox5	0.8254	1.7699	2.1442	79	163	2.271E-06	3.48734
MZF1_5-13	0.8194	1.2212	1.4904	75	145	4.658E-06	2.33986
Prrx2	0.7985	2.0885	2.6154	85	174	5.315E-08	4.93960
ARID3A	0.7910	3.3540	4.2404	96	187	2.737E-12	10.40423
Pdx1	0.7546	2.2566	2.9904	86	185	8.968E-08	5.68425
Nobox	0.7443	1.3097	1.7596	73	154	65.93E-06	2.45925
FOXL1	0.6934	5.3805	7.7596	103	191	5.222E-16	36.42204
Foxd3	0.5952	1.7168	2.8846	75	147	6.176E-06	11.46883

15.32 AR DHT vs AR RU486 unique for ARDHTrrO (stable)

Chromosome specific statistics are shown in Table 101. A histogram of sequence lengths is shown in Figure 131.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	317	12	448	920	141877	0.000569
10	100	192	416	654	41600	0.000307
11	150	220	438	1046	65695	0.000487
12	105	3	406	933	42641	0.000319
13	42	280	495	1081	20810	0.000181
14	97	101	438	920	42464	0.000396
15	76	238	454	804	34477	0.000336
16	83	202	421	784	34915	0.000386
17	116	201	421	771	48847	0.000602
18	51	200	427	914	21763	0.000279
19	43	202	372	746	16011	0.000271
2	187	130	427	833	79768	0.000328
20	80	239	421	778	33671	0.000534
21	26	196	458	704	11907	0.000247
22	32	208	399	640	12778	0.000249
3	197	122	484	1117	95306	0.000481
4	100	223	429	689	42888	0.000224
5	147	12	445	1152	65426	0.000362
6	169	69	415	778	70193	0.00041
7	138	214	436	903	60219	0.000378
8	98	70	452	760	44257	0.000302
9	92	252	428	769	39400	0.000279
X	36	214	392	579	14097	9.1e-05
Y	3	275	311	345	932	1.6e-05
all 24	2485	3	435	1152	1081942	0.000349

Table 101: Chromosome specific distribution of the regions. The last line represents the overall statistics.

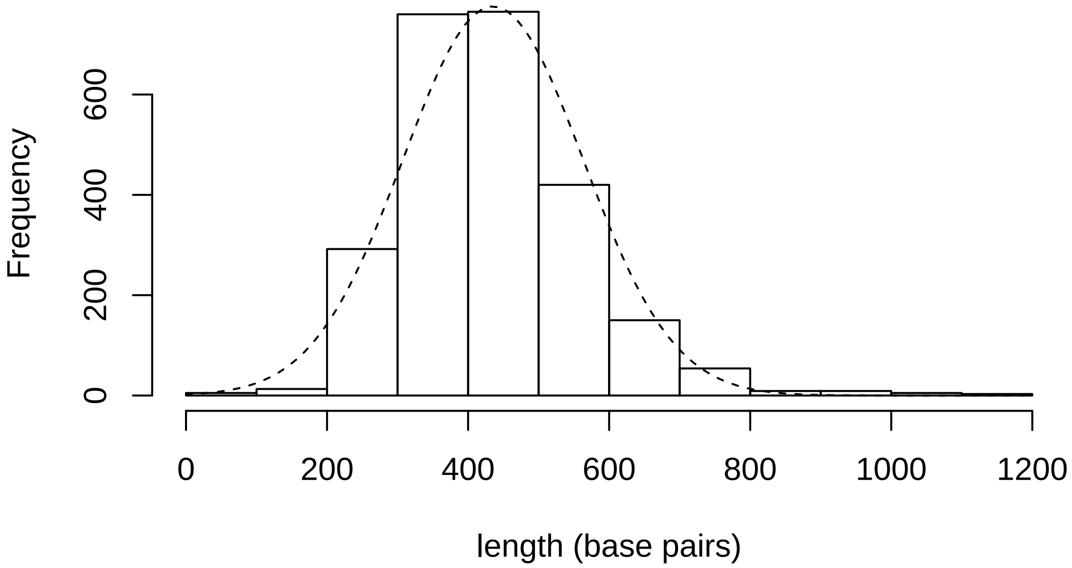
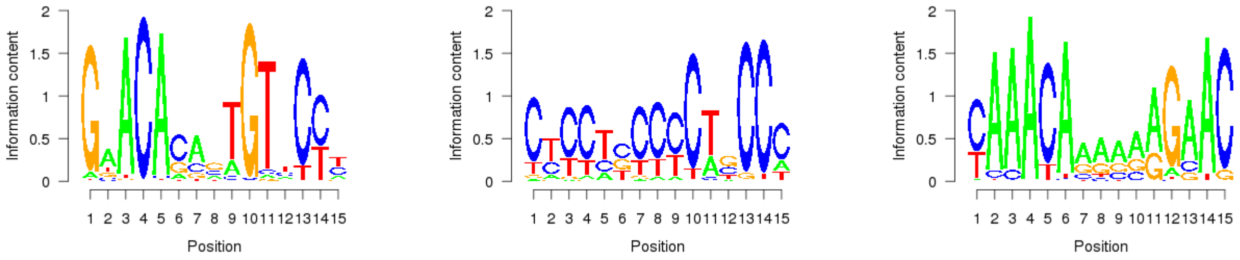


Figure 131: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU1s-gCount** component.

property	value
genes	2400



(a) ARDHTvsARRU486rrU1s-deNovo-meme1: width=15, sites=106, llr=1190, E=6.9e-40 (b) ARDHTvsARRU486rrU1s-deNovo-meme2: width=15, sites=143, llr=1443, E=1.5e-15 (c) ARDHTvsARRU486rrU1s-deNovo-meme3: width=15, sites=67, llr=825, E=8.3e-28

Figure 132: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARDHTrrO (stable) sequences.

Table 102: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	11.4929	0.1039	0.0090	233	41	20.78E-72	0.04772
TLX1::NFIC	4.3239	0.0205	0.0047	42	17	71.33E-10	0.01401
FOXA1	2.8814	1.0358	0.3595	1626	1349	40.07E-314	0.71752
FOXF2	2.7211	0.3217	0.1182	682	506	82.73E-90	0.20491
FOXA1pAR	2.7027	0.2142	0.0792	485	320	3.254E-66	0.14513
Foxa2	2.5345	0.8780	0.3464	1462	1199	7.461E-260	0.73831
Tal1::Gata1	2.5308	0.0640	0.0253	152	117	57.14E-16	0.03946
ARMotifTH	1.9455	0.0709	0.0364	173	162	3.867E-12	0.04994
FOXD1	1.8436	1.3305	0.7217	1783	2274	56.31E-250	1.14271
ESR2	1.8412	0.0209	0.0113	46	49	56.23E-04	0.01754
GRMotifTH	1.7187	0.3684	0.2143	735	876	5.095E-46	0.30150
ARMotifT	1.7091	0.6590	0.3856	1181	1416	72.53E-110	0.54376
ELK4	1.7076	0.0322	0.0188	72	84	21.86E-04	0.02713
Stat3	1.6919	0.2387	0.1411	439	519	25.93E-22	0.24419
Foxq1	1.6660	0.6320	0.3794	1104	1299	2.932E-98	0.61546
PPARG::RXRA	1.6465	0.0258	0.0156	60	73	1.103E-02	0.02018
Evi1	1.5388	0.0491	0.0319	118	134	18.92E-06	0.04791
STAT1	1.5215	0.0548	0.0360	104	138	36.46E-04	0.06082
NR3C1	1.5211	0.3716	0.2443	726	982	16.33E-34	0.32326
GABPA	1.5105	0.0922	0.0610	214	270	27.57E-08	0.07535
AR	1.5037	0.0596	0.0396	143	180	68.28E-06	0.04718
Gata1	1.4033	0.8027	0.5720	1294	1935	67.28E-92	0.75638
GRMotifT	1.3837	2.4827	1.7943	2256	3788	0.00E00	2.55187
FOXI1	1.3530	0.9988	0.7382	1446	2061	29.42E-130	1.30975
RXR::RAR_DR5	1.3475	0.0306	0.0227	75	103	2.984E-02	0.02591
ARMotifHH	1.3022	0.4026	0.3091	788	1146	2.516E-32	0.39211
ARMotifH	1.2878	8.7983	6.8322	2481	4634	0.00E00	14.74912
NFIC	1.2519	2.8281	2.2590	2234	3942	0.00E00	3.68539
GR	1.2417	0.2818	0.2269	598	904	77.59E-18	0.26853
TEAD1	1.2300	0.0845	0.0687	200	309	33.5E-04	0.07570
GRMotifHH	1.2294	0.2456	0.1997	510	791	17.82E-12	0.24661
FOXO3	1.2213	1.8873	1.5453	1982	3326	2.797E-242	2.53596
TAL1::TCF3	1.2050	0.2528	0.2098	456	704	12.18E-10	0.32522
SP1	0.8317	1.0552	1.2687	1075	2300	5.148E-20	4.08208
Pdx1	0.8233	2.3120	2.8082	1997	3954	52.77E-204	5.36547
CREB1	0.7888	0.6824	0.8651	1149	2456	17.63E-26	1.02622
Prrx2	0.7846	2.0737	2.6429	1926	3876	11.77E-176	4.78492
NF-kappaB	0.7550	0.1779	0.2357	328	833	2.567E-02	0.31818
FOXL1	0.7536	6.1220	8.1240	2344	4356	0.00E00	68.75295
Foxd3	0.7385	1.9807	2.6819	1785	3293	33.03E-156	11.27476
Zfx	0.6580	0.1220	0.1854	254	703	3.675E-04	0.21023
Ddit3::Cebpa	0.5105	0.2214	0.4337	483	1400	2.774E-04	0.48233

15.33 AR DHT vs AR RU486 unique for ARRU486rrO

Chromosome specific statistics are shown in Table 103. A histogram of sequence lengths is shown in Figure 133.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	16	35	58	158	921	4e-06
10	12	38	49	72	588	4e-06
11	9	32	85	181	768	6e-06
12	8	37	48	86	388	3e-06
13	8	38	93	252	741	6e-06
14	9	38	52	127	467	4e-06
15	4	36	42	55	167	2e-06
16	19	37	91	220	1733	1.9e-05
17	17	25	135	566	2293	2.8e-05
18	3	50	76	102	227	3e-06
19	8	37	44	62	352	6e-06
2	36	14	104	415	3729	1.5e-05
20	5	37	56	102	279	4e-06
21	4	39	49	70	196	4e-06
3	9	33	49	90	443	2e-06
4	7	33	43	60	300	2e-06
5	5	33	56	90	282	2e-06
6	5	34	61	156	303	2e-06
7	13	32	48	103	618	4e-06
8	4	43	87	141	348	2e-06
9	6	42	75	181	452	3e-06
X	7	34	50	69	350	2e-06
Y	14	9	91	288	1279	2.2e-05
all 23	228	9	76	566	17224	6e-06

Table 103: Chromosome specific distribution of the regions. The last line represents the overall statistics.

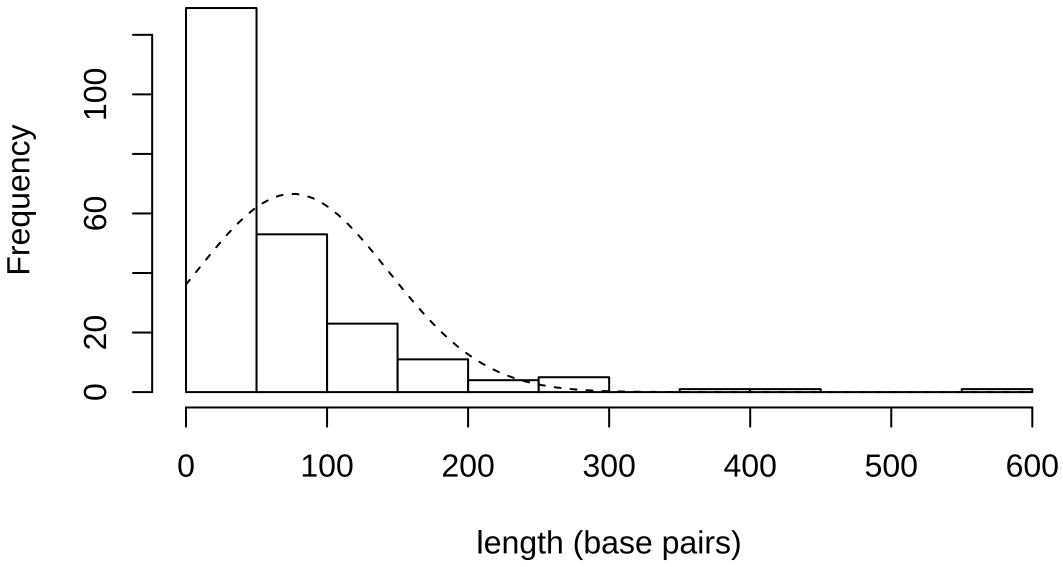
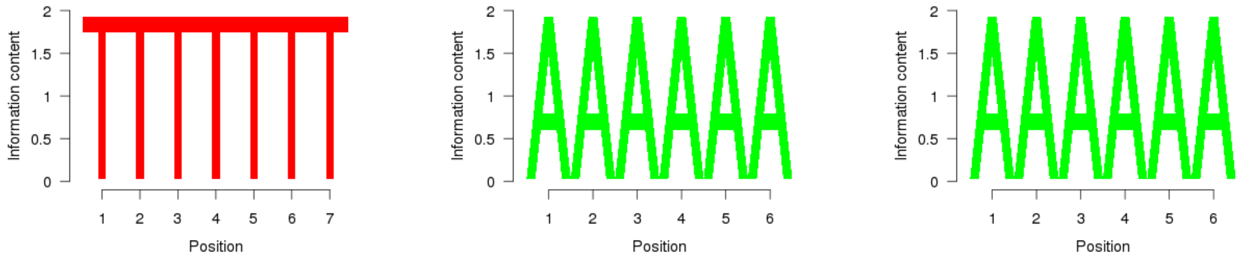


Figure 133: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU2-gCount** component.

property	value
genes	853



(a) ARDHTvsARRU486rrU2-deNovo-meme1: width=7, sites=2, llr=21, E=2.9e+07
(b) ARDHTvsARRU486rrU2-deNovo-meme2: width=6, sites=2, llr=18, E=4.8e+07
(c) ARDHTvsARRU486rrU2-deNovo-meme3: width=6, sites=2, llr=18, E=4.8e+07

Figure 134: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARRU486rrO sequences.

Table 104: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	2106.2632	0.1053	0.0000	10	0	77.59E-06	0.17700
RREB1	112.3194	3.0044	0.0267	104	5	2.928E-46	9.20047
SP1	40.3950	8.7281	0.2160	161	53	5.329E-56	48.59702
PLAG1	28.6277	0.1404	0.0049	24	2	23.93E-10	0.07542
MZF1_1-4	14.5773	9.9430	0.6820	185	155	29.87E-44	50.86037
Klf4	11.5504	0.4211	0.0364	65	14	1.327E-20	0.26878
Egr1	8.9939	0.0877	0.0097	17	4	26.03E-06	0.04867
E2F1	8.9532	0.0439	0.0049	10	2	14.24E-04	0.01843
NFKB1	4.6831	0.0570	0.0121	12	4	20.07E-04	0.03364
INSM1	3.9632	0.0482	0.0121	11	5	1.031E-02	0.02441
MZF1_5-13	2.8761	0.6842	0.2379	110	78	10.74E-20	0.49952
TFAP2A	2.7502	0.7544	0.2743	74	77	53.85E-08	1.19262
REL	1.9310	0.1360	0.0704	28	24	33.47E-04	0.11013
ZNF354C	1.8764	0.9474	0.5049	99	142	1.50E-06	1.42269
Arnt::Ahr	1.5810	0.4912	0.3107	51	75	2.973E-02	1.68388
Myb	1.4816	0.1798	0.1214	36	44	2.578E-02	0.15659
Mafb	1.4520	0.3947	0.2718	54	84	4.08E-02	0.49803
ETS1	0.8303	0.8947	1.0777	109	225	11.8E-04	2.28153
GATA3	0.5992	0.5482	0.9150	57	210	1.853E-02	1.72495
GRMotifH	0.5818	0.4956	0.8519	57	199	4.195E-02	1.53302
YY1	0.5800	0.4167	0.7184	46	162	2.405E-02	1.56201
En1	0.5457	0.4079	0.7476	54	186	4.403E-02	1.13263
GRMotifT	0.5390	0.1491	0.2767	24	90	1.456E-02	0.30012
Cebpa	0.5062	0.0614	0.1214	10	41	4.253E-02	0.13709
AP1	0.4972	0.2281	0.4587	36	125	2.595E-02	0.70461
Gfi	0.4290	0.0614	0.1432	12	56	78.34E-04	0.11686
HOXA5	0.3339	0.3509	1.0510	45	209	1.226E-04	1.94022
Sox17	0.3245	0.0614	0.1893	12	68	7.53E-04	0.16397
SRY	0.3163	0.1535	0.4854	24	116	2.998E-04	0.82114
Nkx2-5	0.3161	0.2632	0.8325	43	177	16.51E-04	1.34466
Prrx2	0.3103	0.1009	0.3252	19	95	4.754E-04	0.37635
Fos	0.3061	0.0921	0.3010	15	91	68.35E-06	0.39147
FOXI1	0.3015	0.0351	0.1165	6	35	1.228E-02	0.18638
Pdx1	0.3013	0.1009	0.3350	20	102	2.655E-04	0.36385
FOXD1	0.2878	0.0307	0.1068	6	40	38.98E-04	0.09223
ARMotifT	0.2587	0.0175	0.0680	3	24	1.694E-02	0.06635
SOX9	0.2586	0.0219	0.0850	4	30	86.24E-04	0.08059
Foxq1	0.2364	0.0132	0.0558	3	20	4.723E-02	0.05156
ARID3A	0.2289	0.1272	0.5558	17	132	11.68E-08	0.88575
Sox5	0.2201	0.0614	0.2791	11	90	3.544E-06	0.28638
FOXL1	0.2173	0.2763	1.2718	35	182	12.79E-06	7.49704
FOXA1	0.2091	0.0132	0.0631	3	24	1.694E-02	0.05272
NKX3-1	0.1974	0.0263	0.1335	4	44	2.606E-04	0.21782
Nobox	0.1956	0.0351	0.1796	7	56	2.172E-04	0.18700
Nr2e3	0.1453	0.0088	0.0607	1	18	1.288E-02	0.07490

15.34 AR DHT vs AR RU486 unique for ARRU486rrO (up)

Chromosome specific statistics are shown in Table 105. A histogram of sequence lengths is shown in Figure 135.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	2	40	82	125	165	1e-06
2	1	52	52	52	52	0
3	1	45	45	45	45	0
7	1	48	48	48	48	0
all 4	5	40	62	125	310	0

Table 105: Chromosome specific distribution of the regions. The last line represents the overall statistics.

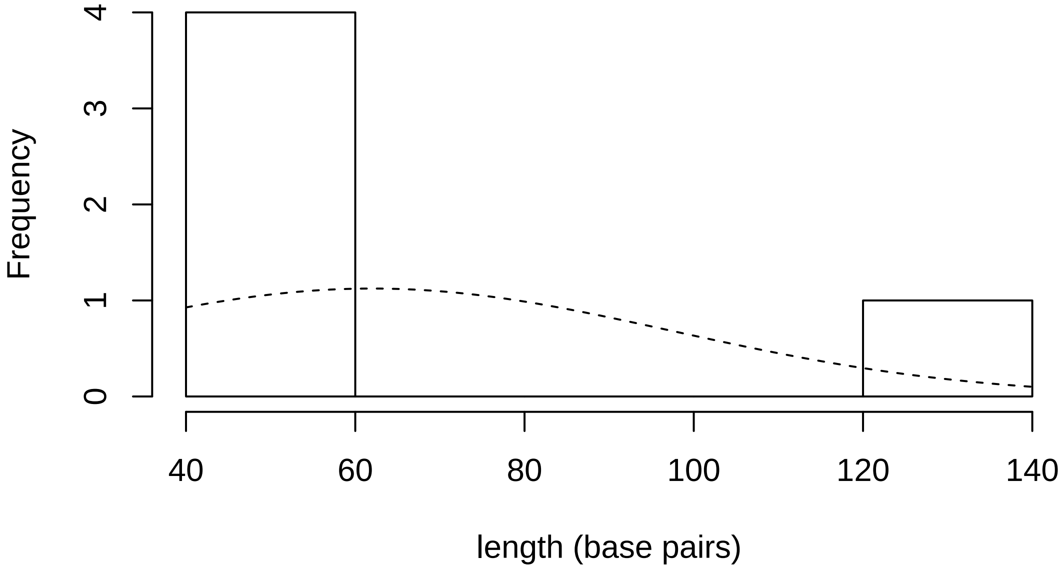
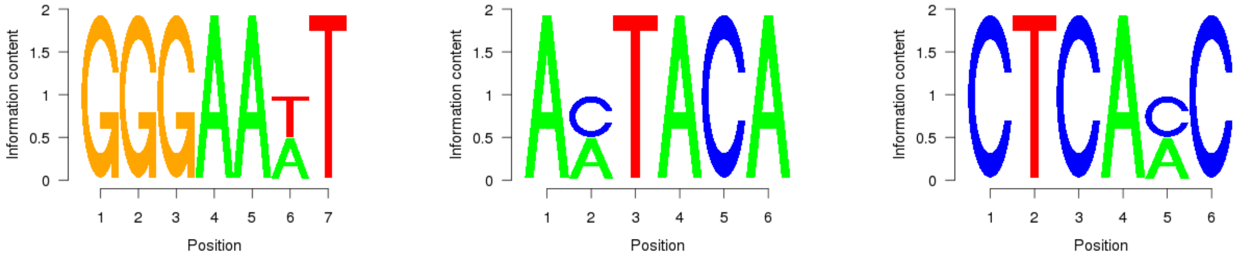


Figure 135: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU2u-gCount** component.

property	value
genes	6



(a) ARDHTvsARRU486rrU2u-deNovo-meme1: width=7, sites=2, llr=18, E=5900

(b) ARDHTvsARRU486rrU2u-deNovo-meme2: width=6, sites=2, llr=16, E=5800

(c) ARDHTvsARRU486rrU2u-deNovo-meme3: width=6, sites=2, llr=15, E=17000

Figure 136: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARRU486rrO (up) sequences.

Table 106: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
RREB1	76001.0000	3.8000	0.0000	3	0	3.998E-02	10.06667

15.35 AR DHT vs AR RU486 unique for ARRU486rrO (down)

Chromosome specific statistics are shown in Table 107. A histogram of sequence lengths is shown in Figure 137.

		length				
chromosome	frequency	min	mean	max	total	coverage
12	1	40	40	40	40	0
15	1	36	36	36	36	0
16	1	41	41	41	41	0
17	1	44	44	44	44	1e-06
19	1	37	37	37	37	1e-06
20	1	102	102	102	102	2e-06
all 6	6	36	50	102	300	0

Table 107: Chromosome specific distribution of the regions. The last line represents the overall statistics.

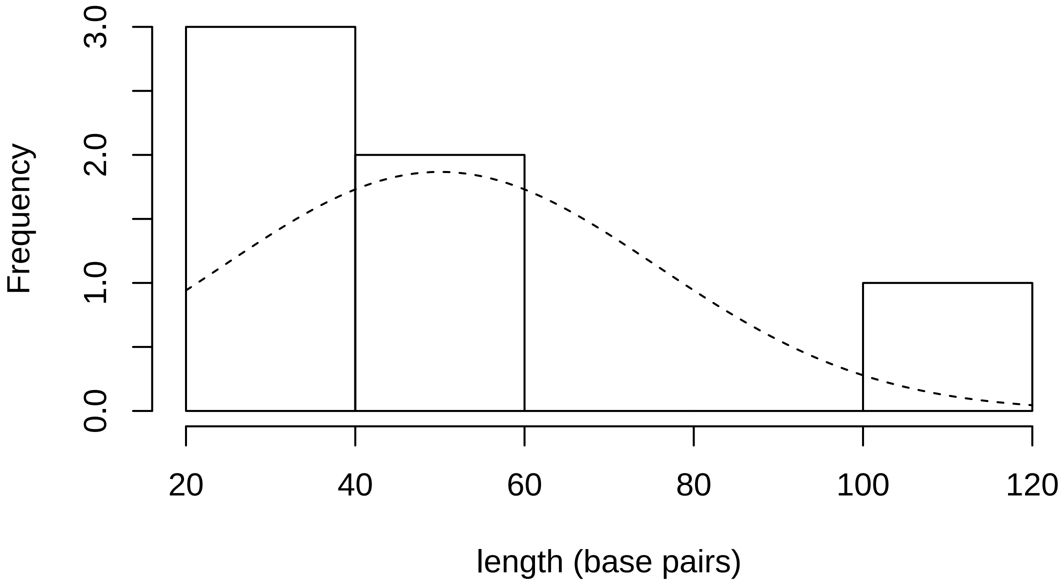
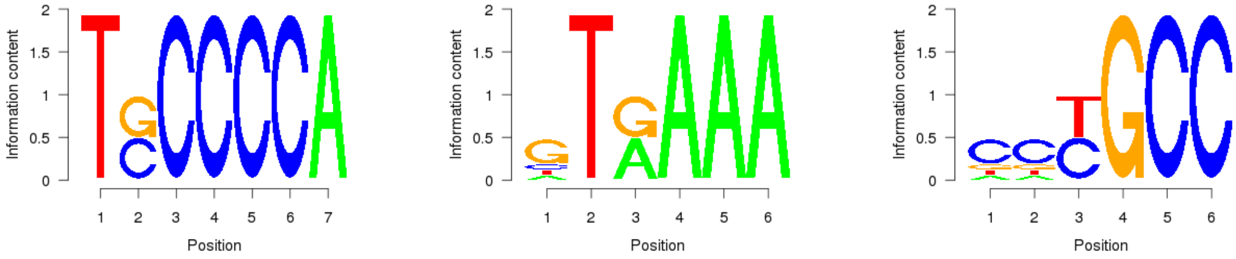


Figure 137: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU2d-gCount** component.

property	value
genes	6



(a) ARDHTvsARRU486rrU2d-deNovo-meme1: width=7, sites=2, llr=18, E=5500 (b) ARDHTvsARRU486rrU2d-deNovo-meme2: width=6, sites=2, llr=14, E=5000 (c) ARDHTvsARRU486rrU2d-deNovo-meme3: width=6, sites=2, llr=11, E=31000

Figure 138: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARRU486rrO (down) sequences.

Table 108: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
SP1	250001.0000	12.5000	0.0000	6	0	2.054E-04	47.91176
RREB1	90001.0000	4.5000	0.0000	4	0	91.66E-04	9.44118
PLAG1	10001.0000	0.5000	0.0000	3	0	4.417E-02	0.14706
MZF1_1-4	163.9023	13.6667	0.0833	6	1	7.636E-04	56.48693

15.36 AR DHT vs AR RU486 unique for ARRU486rrO (stable)

Chromosome specific statistics are shown in Table 109. A histogram of sequence lengths is shown in Figure 139.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	12	35	61	158	728	3e-06
10	5	38	44	50	219	2e-06
11	6	32	104	181	627	5e-06
12	5	39	52	86	259	2e-06
13	2	139	142	146	285	2e-06
14	5	40	44	48	222	2e-06
15	2	36	38	40	76	1e-06
16	4	41	62	86	248	3e-06
17	15	25	132	566	1973	2.4e-05
19	7	37	45	62	315	5e-06
2	26	14	120	415	3133	1.3e-05
20	4	37	57	102	228	4e-06
21	4	39	49	70	196	4e-06
3	4	34	63	90	252	1e-06
4	4	33	40	45	162	1e-06
5	3	33	56	90	169	1e-06
6	4	34	37	40	147	1e-06
7	6	32	46	59	273	2e-06
8	3	43	101	141	303	2e-06
9	3	42	61	96	182	1e-06
X	5	34	51	69	256	2e-06
Y	1	39	39	39	39	1e-06
all 22	130	14	79	566	10292	3e-06

Table 109: Chromosome specific distribution of the regions. The last line represents the overall statistics.

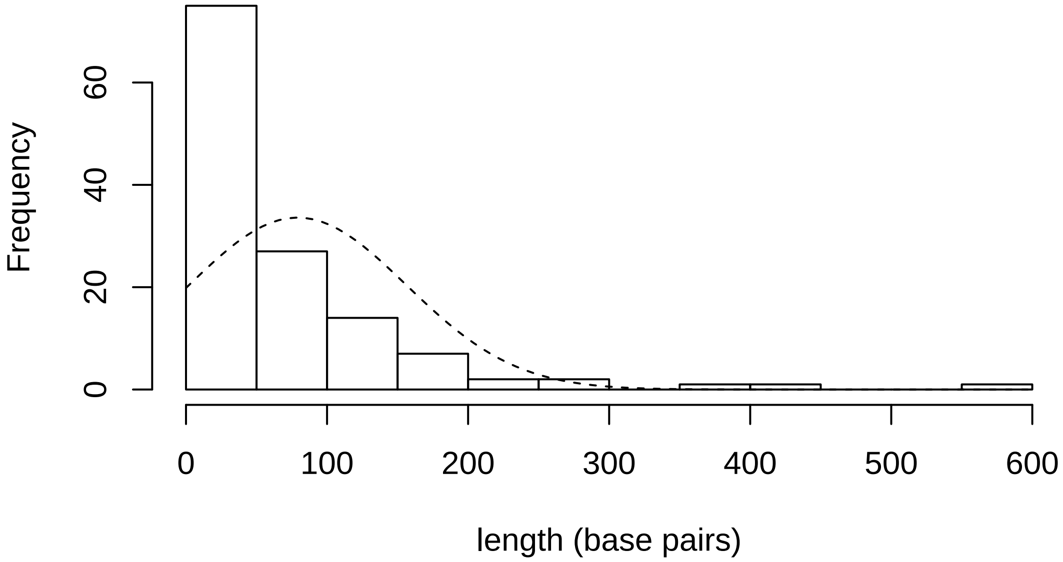
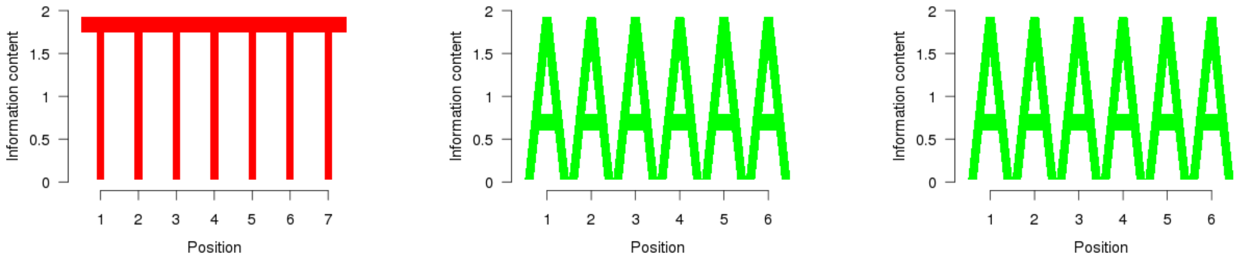


Figure 139: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARDHTvsARRU486rrU2s-gCount** component.

property	value
genes	201



(a) ARDHTvsARRU486rrU2s-deNovo-meme1: width=7, sites=2, llr=21, E=1.3e+07

(b) ARDHTvsARRU486rrU2s-deNovo-meme2: width=6, sites=2, llr=18, E=2.1e+07

(c) ARDHTvsARRU486rrU2s-deNovo-meme3: width=6, sites=2, llr=18, E=2.1e+07

Figure 140: De novo motifs for the filtered AR DHT vs AR RU486 unique for ARRU486rrO (stable) sequences.

Table 110: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	1847.1538	0.0923	0.0000	6	0	31.01E-04	0.07919
E2F1	616.3846	0.0308	0.0000	4	0	2.56E-02	0.01058
RREB1	226.4895	2.7846	0.0122	58	2	11.12E-28	7.77469
SP1	43.1748	8.2846	0.1918	93	30	1.29E-34	39.13101
PLAG1	24.2156	0.1000	0.0041	11	1	89.34E-06	0.04673
Klf4	20.6825	0.4231	0.0204	38	5	73.15E-16	0.25775
Egr1	14.9066	0.0615	0.0041	8	1	18.52E-04	0.02349
MZF1_1-4	13.6516	9.5846	0.7020	110	98	18.05E-28	43.47612
NFKB1	13.0448	0.0538	0.0041	6	1	1.349E-02	0.02628
INSM1	5.6255	0.0462	0.0082	6	2	3.929E-02	0.02093
Zfx	4.7002	0.0769	0.0163	9	4	1.629E-02	0.04138
MZF1_5-13	3.1056	0.6846	0.2204	64	42	14.19E-14	0.49858
HIF1A::ARNT	2.7810	0.2385	0.0857	20	18	1.194E-02	0.25345
TFAP2A	2.5656	0.8692	0.3388	46	45	8.96E-06	1.61914
Arnt::Ahr	2.4578	0.4615	0.1878	28	33	1.627E-02	0.66320
REL	1.8022	0.1692	0.0939	21	19	95.84E-04	0.13262
Mafb	1.7252	0.5000	0.2898	38	54	1.379E-02	0.56331
ZNF354C	1.3874	0.9231	0.6653	56	88	7.617E-04	1.65623
ETS1	0.7651	0.9462	1.2367	63	148	3.815E-02	2.71140
YY1	0.5923	0.4231	0.7143	27	111	3.241E-02	1.02923
GRMotifH	0.5469	0.5000	0.9143	29	119	3.51E-02	2.00609
GATA3	0.5374	0.5308	0.9878	28	133	55.13E-04	1.83711
FOXO3	0.3881	0.1077	0.2776	10	47	2.944E-02	0.37452
GRMotifT	0.3642	0.1308	0.3592	12	67	34.44E-04	0.39465
HOXA5	0.3433	0.3769	1.0980	26	133	18.64E-04	2.18272
NKX3-1	0.3429	0.0462	0.1347	4	26	3.408E-02	0.15760
FOXL1	0.3414	0.3692	1.0816	24	107	1.246E-02	3.68382
FOXI1	0.2947	0.0385	0.1306	3	28	93.4E-04	0.12125
SRY	0.2860	0.1692	0.5918	14	85	6.837E-04	0.96960
Nkx2-5	0.2471	0.2692	1.0898	24	116	44.11E-04	1.97002
SOX9	0.2462	0.0231	0.0939	2	18	4.466E-02	0.09678
FOXA1	0.1989	0.0154	0.0776	2	19	3.464E-02	0.05301
Prrx2	0.1945	0.1000	0.5143	11	79	2.021E-04	0.64566
Sox5	0.1934	0.0615	0.3184	8	51	37.89E-04	0.40716
ARID3A	0.1908	0.1308	0.6857	11	88	39.45E-06	0.98324
Pdx1	0.1664	0.0923	0.5551	12	83	2.178E-04	0.72083
Nr2e3	0.1350	0.0154	0.1143	1	19	1.281E-02	0.14866
FOXD1	0.1259	0.0231	0.1837	2	41	1.445E-04	0.13865
Nobox	0.0993	0.0308	0.3102	4	49	1.825E-04	0.39287
Lhx3	0.0009	0.0000	0.0531	0	11	3.806E-02	0.04425

15.37 AR CPA vs AR RU486 overlaps

Chromosome specific statistics are shown in Table 111. A histogram of sequence lengths is shown in Figure 141.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	61	26	178	464	10867	4.4e-05
10	20	38	136	340	2721	2e-05
11	30	39	175	515	5261	3.9e-05
12	25	37	117	256	2934	2.2e-05
13	21	23	186	346	3908	3.4e-05
14	18	40	127	275	2290	2.1e-05
15	16	40	188	288	3014	2.9e-05
16	21	37	129	281	2707	3e-05
17	34	23	159	566	5396	6.6e-05
18	10	49	156	304	1558	2e-05
19	17	21	99	288	1679	2.8e-05
2	45	29	157	415	7070	2.9e-05
20	16	44	185	496	2955	4.7e-05
21	7	39	71	207	499	1e-05
22	5	69	116	153	581	1.1e-05
3	46	37	180	349	8290	4.2e-05
4	20	15	155	322	3092	1.6e-05
5	31	33	162	295	5007	2.8e-05
6	18	4	118	268	2123	1.2e-05
7	23	15	118	286	2723	1.7e-05
8	33	5	136	300	4479	3.1e-05
9	17	8	130	248	2209	1.6e-05
X	5	34	89	173	443	3e-06
Y	4	69	148	276	592	1e-05
all 24	543	4	152	566	82398	2.7e-05

Table 111: Chromosome specific distribution of the regions. The last line represents the overall statistics.

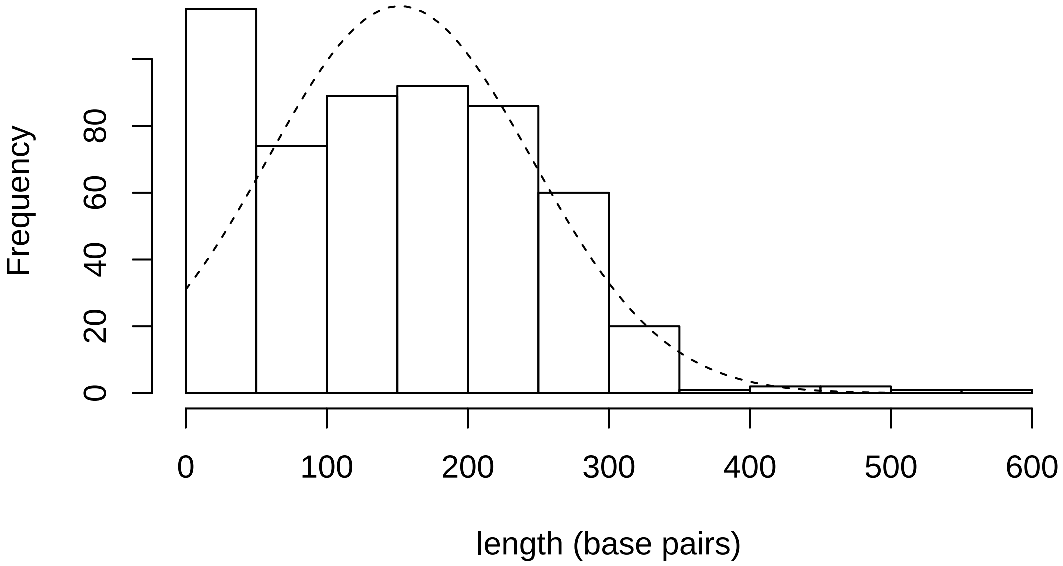
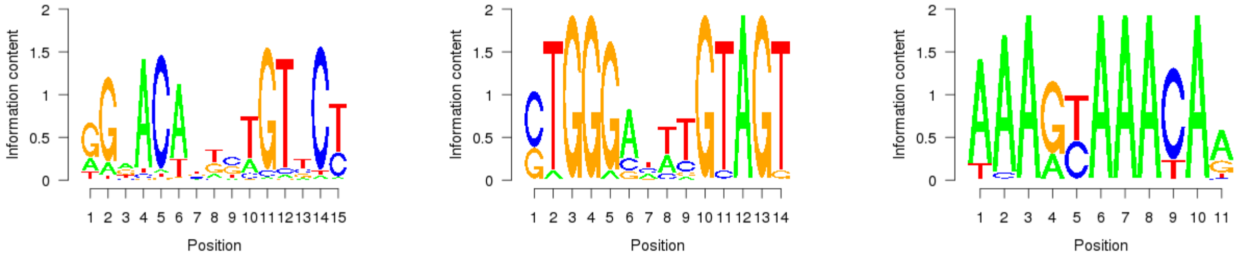


Figure 141: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrO-gCount** component.

property	value
genes	2088



(a) ARCPAvsARRU486rrO-deNovo-meme1: width=15, sites=220, llr=2051, E=1.7e-151 (b) ARCPAvsARRU486rrO-deNovo-meme2: width=14, sites=17, llr=238, E=29 (c) ARCPAvsARRU486rrO-deNovo-meme3: width=11, sites=24, llr=284, E=310000

Figure 142: De novo motifs for the filtered AR CPA vs AR RU486 overlaps sequences.

Table 112: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Pax4	815.8148	0.0407	0.0000	9	0	1.686E-04	0.07086
ARMotifTT	186.1852	0.0093	0.0000	5	0	95.56E-04	0.00322
RREB1	89.3176	1.0667	0.0119	80	12	46.96E-28	3.61550
Ar	46.5695	0.1407	0.0030	70	3	1.245E-28	0.05747
GRMotifTT	16.0570	0.0167	0.0010	9	1	8.377E-04	0.00642
SP1	6.4918	3.2944	0.5074	217	244	5.837E-20	20.40605
PLAG1	5.3446	0.0426	0.0079	18	8	4.238E-04	0.02609
E2F1	5.0869	0.0204	0.0040	11	4	39.91E-04	0.00960
ESR2	3.7097	0.0185	0.0050	10	4	90.22E-04	0.01089
Tal1::Gata1	3.4054	0.0204	0.0059	11	6	1.855E-02	0.01086
FOXA1	3.2534	0.3870	0.1189	167	112	2.394E-26	0.24362
Foxa2	3.2329	0.3333	0.1031	146	89	1.986E-24	0.23381
FOXF2	3.0509	0.1241	0.0406	61	41	2.289E-08	0.07395
MZF1_1-4	3.0388	4.4815	1.4747	397	594	1.381E-48	21.74318
ARMotifT	2.4696	0.2889	0.1169	125	104	4.579E-14	0.21029
ARMotifHH	2.3846	0.2222	0.0932	99	80	43.76E-12	0.16953
Egr1	2.3335	0.0741	0.0317	35	30	10.51E-04	0.05469
NR3C1	2.2603	0.2241	0.0991	102	90	4.124E-10	0.16762
Klf4	2.2323	0.1815	0.0813	78	72	55.43E-08	0.15574
GRMotifHH	2.0543	0.1019	0.0496	45	42	4.894E-04	0.08778
Stat3	1.9695	0.1074	0.0545	45	47	24.03E-04	0.09610
GRMotifTH	1.9625	0.1537	0.0783	76	77	8.485E-06	0.10533
FOXD1	1.9143	0.4630	0.2418	179	198	62.47E-16	0.40986
TFAP2A	1.8754	1.0019	0.5342	237	279	10.13E-22	2.29522
GRMotifT	1.7509	1.0204	0.5828	299	419	1.733E-26	0.97512
ARMotifH	1.6920	3.9241	2.3191	461	793	9.453E-64	7.05632
HIF1A::ARNT	1.6154	0.2130	0.1318	84	108	6.098E-04	0.24567
Foxq1	1.5523	0.2093	0.1348	93	110	23.89E-06	0.22156
NFIC	1.5236	1.1944	0.7839	304	467	10.55E-24	1.55863
GR	1.4894	0.1093	0.0733	55	70	1.143E-02	0.08888
Gata1	1.4083	0.2778	0.1972	125	168	7.837E-06	0.25734
EBF1	1.3990	0.2870	0.2052	111	162	5.453E-04	0.32519
Myb	1.3044	0.3426	0.2626	144	215	16.21E-06	0.34061
BRCA1	1.2413	0.7111	0.5728	241	404	22.84E-12	0.79364
Arnt::Ahr	1.2235	0.5444	0.4450	171	275	4.44E-06	1.37507
GRMotifH	1.2114	2.2056	1.8206	387	725	15.15E-34	3.82741
Mafb	1.2049	0.8037	0.6670	246	415	9.162E-12	1.17176
SOX10	1.2025	2.9593	2.4609	417	812	2.979E-40	6.02015
GATA2	0.8199	3.3926	4.1378	404	891	3.196E-30	11.88497
YY1	0.7591	1.0630	1.4004	285	640	1.583E-08	2.51689
HOXA5	0.6844	1.4963	2.1863	315	747	1.681E-10	4.72445
Nkx2-5	0.6816	1.4111	2.0704	295	694	2.023E-08	5.26202
ARID3A	0.6271	0.8241	1.3142	240	546	1.406E-04	2.68487
HLF	0.6165	0.1185	0.1923	51	157	2.255E-02	0.22935
FOXL1	0.4859	1.3222	2.7215	273	659	7.913E-06	23.09393
Lhx3	0.4762	0.0500	0.1051	20	81	46.71E-04	0.13280
Ddit3::Cebpa	0.4607	0.0648	0.1407	34	114	1.265E-02	0.14391
NFIL3	0.3644	0.0278	0.0763	11	60	15.29E-04	0.08562

15.38 AR CPA vs AR RU486 overlaps (up)

Chromosome specific statistics are shown in Table 113. A histogram of sequence lengths is shown in Figure 143.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	11	100	229	430	2517	1e-05
2	6	52	149	190	894	4e-06
3	5	45	151	279	756	4e-06
4	1	164	164	164	164	1e-06
5	11	84	191	273	2100	1.2e-05
6	1	137	137	137	137	1e-06
7	1	48	48	48	48	0
8	2	165	166	168	333	2e-06
10	2	213	232	251	464	3e-06
11	6	187	298	515	1790	1.3e-05
12	2	113	160	206	319	2e-06
13	1	346	346	346	346	3e-06
14	1	222	222	222	222	2e-06
15	1	132	132	132	132	1e-06
17	2	105	189	273	378	5e-06
19	4	21	67	146	269	5e-06
20	2	169	201	233	402	6e-06
21	1	207	207	207	207	4e-06
all 18	60	21	191	515	11478	4e-06

Table 113: Chromosome specific distribution of the regions. The last line represents the overall statistics.

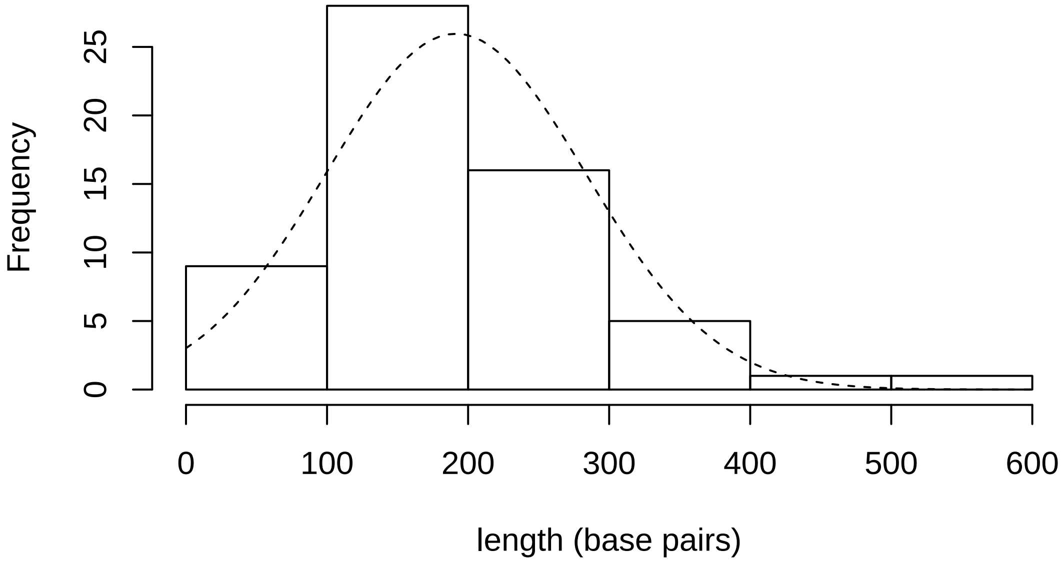
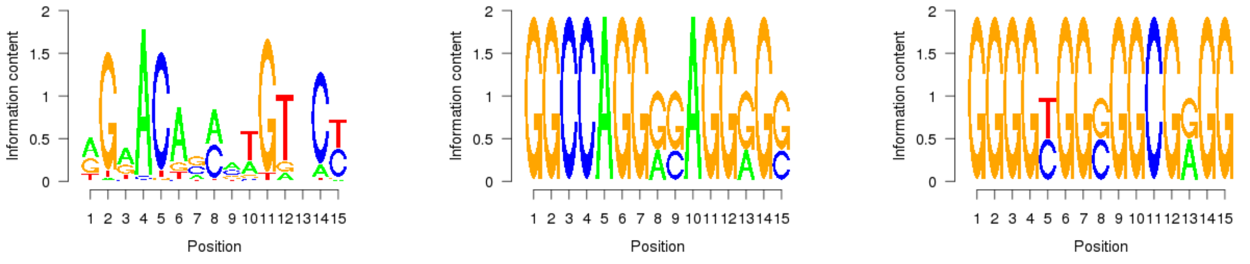


Figure 143: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrOu-gCount** component.

property	value
genes	54



(a) ARCPAvsARRU486rrOu-deNovo-meme1: width=15, sites=42, llr=393, E=2.6e-18 (b) ARCPAvsARRU486rrOu-deNovo-meme2: width=15, sites=3, llr=56, E=1400000 (c) ARCPAvsARRU486rrOu-deNovo-meme3: width=15, sites=2, llr=39, E=4200000

Figure 144: De novo motifs for the filtered AR CPA vs AR RU486 overlaps (up) sequences.

Table 114: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	26.9164	0.2333	0.0086	11	1	48.5E-06	0.12412
Stat3	5.1475	0.1333	0.0259	7	3	2.998E-02	0.07036
NR3C1	4.5088	0.3500	0.0776	18	9	1.005E-04	0.18792
GRMotifTH	4.5077	0.2333	0.0517	10	6	1.863E-02	0.14701
USF1	3.1221	0.3500	0.1121	13	9	92.4E-04	0.32818
Foxa2	3.0068	0.4667	0.1552	22	16	1.69E-04	0.30844
FOXA1	2.8995	0.6000	0.2069	31	22	45.77E-08	0.31740
ARMotifT	2.7920	0.4333	0.1552	19	18	52.69E-04	0.31429
Foxq1	2.6577	0.3667	0.1379	19	16	22.9E-04	0.21597
FOXD1	2.0782	0.7167	0.3448	27	32	12.87E-04	0.59347
TFAP2A	2.0675	1.2833	0.6207	29	34	4.653E-04	3.57062
GRMotifT	1.9125	1.5333	0.8017	46	59	1.86E-08	1.42023
NFIC	1.8841	1.9167	1.0172	43	67	4.549E-06	2.51737
ARMotifH	1.8293	5.5667	3.0431	58	102	12.48E-12	9.21919
Gata1	1.7260	0.4167	0.2414	22	23	34.0E-04	0.32594
ELK1	1.6915	0.3500	0.2069	17	20	4.047E-02	0.30568
MZF1_1-4	1.5003	2.4833	1.6552	44	80	20.23E-06	9.29321
Sox17	1.3979	0.7833	0.5603	26	44	3.725E-02	0.95273
Mafb	1.3963	1.0833	0.7759	36	56	3.33E-04	1.16854
BRCA1	1.3203	0.9333	0.7069	34	49	3.831E-04	1.09597
GRMotifH	1.2938	2.9333	2.2672	54	90	6.088E-10	4.49140
ZNF354C	1.2794	1.5000	1.1724	42	65	8.363E-06	1.99883
Arnt::Ahr	1.2173	0.5667	0.4655	26	36	76.86E-04	0.66286
SRY	0.8003	1.4833	1.8534	40	85	15.25E-04	3.51377
Pax2	0.7915	1.0167	1.2845	36	81	1.537E-02	1.36818
En1	0.7882	1.7667	2.2414	45	94	67.01E-06	3.22792
ARID3A	0.7250	1.2500	1.7241	40	78	5.743E-04	3.69893
YY1	0.6984	1.1500	1.6466	38	83	51.86E-04	2.02234
Nkx2-5	0.5945	1.7833	3.0000	42	88	4.452E-04	7.99269
HOXA5	0.5734	1.8833	3.2845	37	95	3.322E-02	7.93961
FOXL1	0.4758	1.8333	3.8534	38	92	1.383E-02	22.80127

15.39 AR CPA vs AR RU486 overlaps (down)

Chromosome specific statistics are shown in Table 115. A histogram of sequence lengths is shown in Figure 145.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	2	241	274	307	548	2e-06
3	1	261	261	261	261	1e-06
7	1	217	217	217	217	1e-06
11	2	177	209	241	418	3e-06
12	1	37	37	37	37	0
16	1	127	127	127	127	1e-06
17	1	44	44	44	44	1e-06
19	1	37	37	37	37	1e-06
all 8	10	37	169	307	1689	1e-06

Table 115: Chromosome specific distribution of the regions. The last line represents the overall statistics.

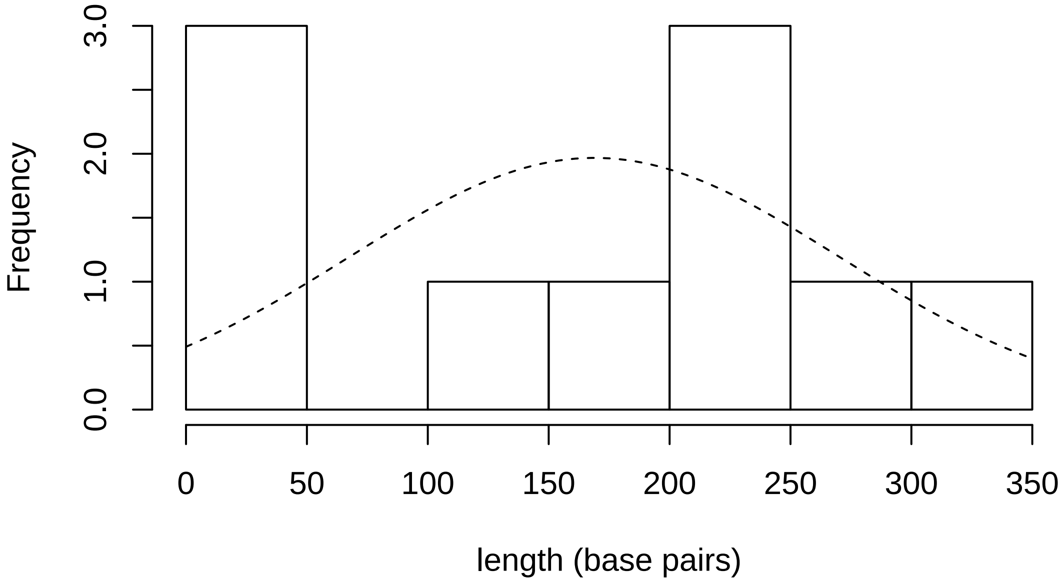
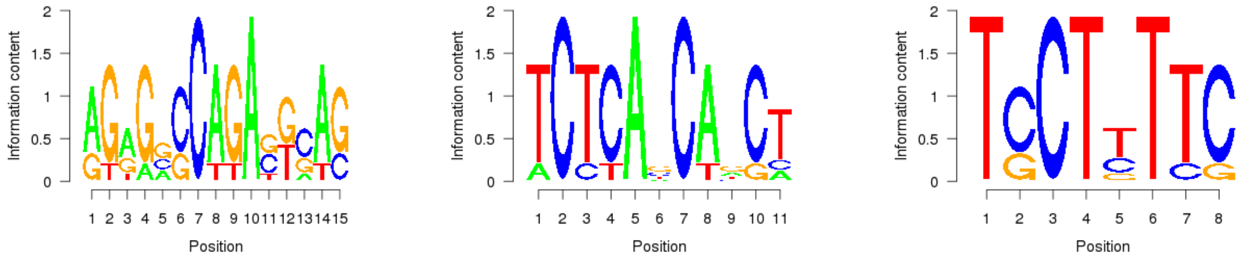


Figure 145: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrOd-gCount** component.

property	value
genes	13



(a) ARCPAvsARRU486rrOd-deNovo-meme1: width=15, sites=7, llr=87, E=530

(b) ARCPAvsARRU486rrOd-deNovo-meme2: width=11, sites=7, llr=69, E=5300

(c) ARCPAvsARRU486rrOd-deNovo-meme3: width=8, sites=7, llr=61, E=4400

Figure 146: De novo motifs for the filtered AR CPA vs AR RU486 overlaps (down) sequences.

Table 116: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
MZF1_1-4	5.7862	6.7000	1.1579	10	13	34.02E-04	26.49507

15.40 AR CPA vs AR RU486 overlaps (stable)

Chromosome specific statistics are shown in Table 117. A histogram of sequence lengths is shown in Figure 147.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	42	26	169	464	7106	2.9e-05
10	10	38	134	259	1338	1e-05
11	12	48	161	266	1928	1.4e-05
12	16	37	107	214	1711	1.3e-05
13	6	59	176	287	1059	9e-06
14	14	40	146	275	2041	1.9e-05
15	5	40	174	288	869	8e-06
16	7	41	120	281	841	9e-06
17	27	33	157	566	4242	5.2e-05
18	3	130	155	173	465	6e-06
19	16	21	103	288	1642	2.8e-05
2	22	29	178	415	3908	1.6e-05
20	13	44	181	496	2347	3.7e-05
21	4	39	47	66	189	4e-06
22	3	109	129	153	388	8e-06
3	22	49	212	349	4673	2.4e-05
4	13	15	162	322	2108	1.1e-05
5	15	46	160	267	2407	1.3e-05
6	10	34	119	268	1190	7e-06
7	14	15	111	286	1559	1e-05
8	15	5	112	238	1677	1.1e-05
9	9	42	123	221	1105	8e-06
X	4	34	76	173	302	2e-06
all 23	302	5	149	566	45095	1.5e-05

Table 117: Chromosome specific distribution of the regions. The last line represents the overall statistics.

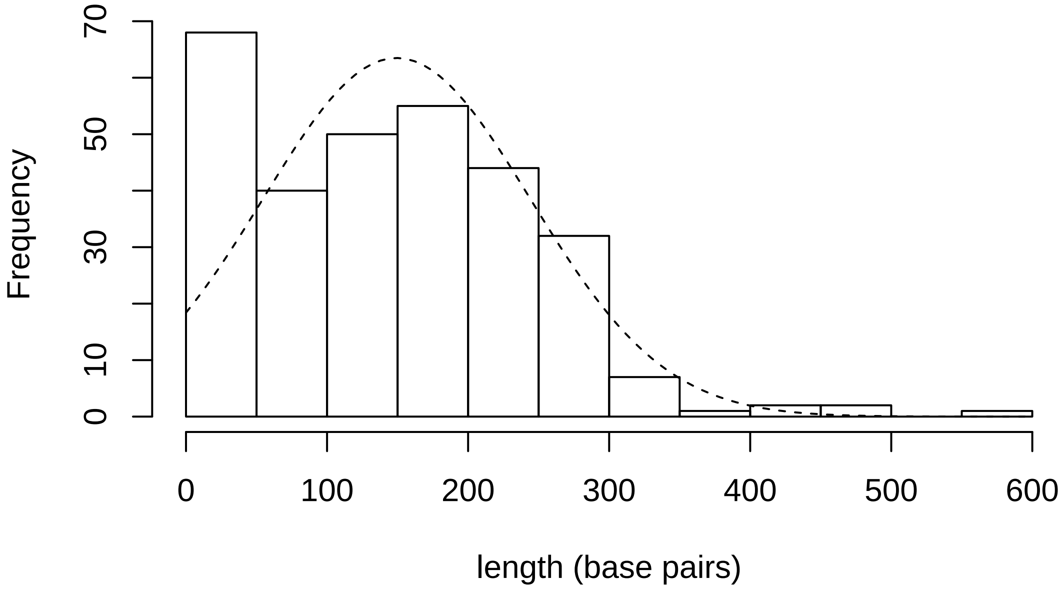
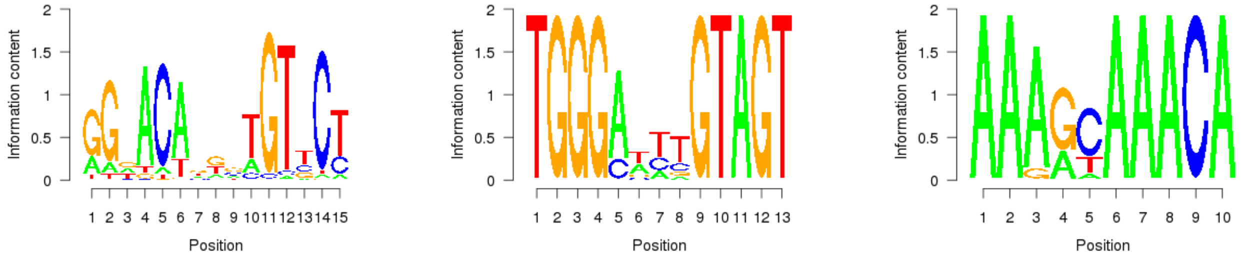


Figure 147: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrOs-gCount** component.

property	value
genes	495



(a) ARCPAvsARRU486rrOs-deNovo-meme1: width=15, sites=121, llr=1138, E=1.3e-62 (b) ARCPAvsARRU486rrOs-deNovo-meme2: width=13, sites=11, llr=158, E=68000 (c) ARCPAvsARRU486rrOs-deNovo-meme3: width=10, sites=13, llr=159, E=1.8e+07

Figure 148: De novo motifs for the filtered AR CPA vs AR RU486 overlaps (stable) sequences.

Table 118: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	2326.5814	0.1163	0.0000	33	0	45.62E-16	0.04345
Pax4	665.4518	0.0332	0.0000	5	0	92.81E-04	0.02992
RREB1	197.1233	1.0565	0.0053	47	3	41.06E-20	3.37112
PLAG1	18.2825	0.0332	0.0018	8	1	20.73E-04	0.01718
MIZF	12.8060	0.0233	0.0018	7	1	54.79E-04	0.00916
E2F1	10.9805	0.0199	0.0018	6	1	1.44E-02	0.00803
ESR2	10.9805	0.0199	0.0018	6	1	1.44E-02	0.00803
SP1	8.3789	3.3223	0.3965	131	128	2.636E-16	16.87168
Tal1::Gata1	5.5667	0.0199	0.0035	6	2	4.193E-02	0.00916
FOXF2	3.4375	0.1096	0.0319	31	17	9.556E-06	0.06242
MZF1_1-4	3.3737	4.5083	1.3363	221	320	75.25E-30	19.09741
Egr1	3.3472	0.0831	0.0248	23	14	4.911E-04	0.04768
Foxa2	3.1754	0.2924	0.0920	75	48	2.372E-12	0.17499
NR3C1	3.0660	0.2226	0.0726	56	38	2.199E-08	0.14628
Tcfcp2l1	2.9977	0.0532	0.0177	13	8	1.433E-02	0.04303
NHLH1	2.8961	0.0565	0.0195	12	8	2.812E-02	0.04982
Klf4	2.5586	0.1993	0.0779	48	40	13.6E-06	0.15435
FOXA1	2.5522	0.3389	0.1327	82	70	6.042E-10	0.22523
Stat3	2.1540	0.1030	0.0478	24	23	1.627E-02	0.09031
Zfx	2.0771	0.1030	0.0496	26	27	2.216E-02	0.07975
ARMotifT	2.0542	0.2691	0.1310	64	67	18.59E-06	0.20723
TFAP2A	2.0173	1.1462	0.5681	139	166	10.39E-14	2.47146
ARMotifHH	1.9382	0.2093	0.1080	52	55	2.901E-04	0.16444
HIF1A::ARNT	1.9336	0.2259	0.1168	45	54	60.33E-04	0.25811
GR	1.8763	0.1096	0.0584	30	29	58.95E-04	0.08898
GRMotifTH	1.7568	0.1462	0.0832	43	42	5.277E-04	0.11033
EBF1	1.6603	0.3056	0.1841	65	87	16.97E-04	0.31172
GRMotifT	1.6208	0.9668	0.5965	157	226	49.07E-14	1.02034
Myf	1.5398	0.1063	0.0690	28	33	4.676E-02	0.11003
ARMotifH	1.5202	3.7641	2.4761	261	432	15.54E-40	7.21731
FOXD1	1.4859	0.3787	0.2549	89	113	6.26E-06	0.35507
ELK1	1.4581	0.3123	0.2142	75	103	5.743E-04	0.28627
FEV	1.4472	0.2126	0.1469	58	74	21.77E-04	0.18271
NFIC	1.4129	1.1429	0.8088	163	263	10.95E-12	1.52846
Mafb	1.3191	0.8405	0.6372	143	235	2.452E-08	0.98392
Myb	1.2513	0.3389	0.2708	76	129	2.139E-02	0.34672
Gata1	1.2361	0.2691	0.2177	66	101	1.30E-02	0.27970
NR4A2	1.2167	0.6611	0.5434	133	210	9.998E-08	0.75878
ZNF354C	1.2081	1.2359	1.0230	186	304	7.772E-16	1.83798
SPIB	0.8321	0.8704	1.0460	145	310	1.194E-04	1.57087
YY1	0.8266	1.1163	1.3504	163	363	6.347E-06	2.07435
SRY	0.8263	0.8804	1.0655	139	289	1.826E-04	1.93410
Foxd3	0.7787	0.6312	0.8106	95	184	2.487E-02	3.31228
AP1	0.7455	0.8405	1.1274	139	336	77.55E-04	1.53680
HOXA5	0.6949	1.5116	2.1752	182	419	7.633E-08	4.73912
Nkx2-5	0.6071	1.3023	2.1451	156	391	10.82E-04	5.55963
ARID3A	0.5834	0.7176	1.2301	121	279	3.069E-02	2.67129
Prrx2	0.4176	0.3754	0.8991	74	268	1.707E-02	1.34762
TBP	0.4061	0.0532	0.1310	13	54	2.278E-02	0.18341
Lhx3	0.3416	0.0332	0.0973	8	41	1.548E-02	0.13424
NFIL3	0.3374	0.0233	0.0690	5	30	2.234E-02	0.07579
Ddit3::Cebpa	0.3239	0.0498	0.1540	14	74	10.28E-04	0.13871

15.41 AR CPA vs AR RU486 unique for ARCPArrO

Chromosome specific statistics are shown in Table 119. A histogram of sequence lengths is shown in Figure 149.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	121	21	179	433	21715	8.7e-05
10	41	40	174	323	7141	5.3e-05
11	46	35	195	421	8948	6.6e-05
12	43	51	187	388	8060	6e-05
13	26	51	203	318	5282	4.6e-05
14	34	4	175	353	5966	5.6e-05
15	45	37	194	381	8708	8.5e-05
16	46	36	166	392	7634	8.4e-05
17	72	21	173	318	12422	0.000153
18	29	25	157	339	4552	5.8e-05
19	34	33	138	312	4689	7.9e-05
2	68	27	204	389	13874	5.7e-05
20	39	33	184	310	7179	0.000114
21	17	42	179	377	3047	6.3e-05
22	14	45	155	272	2167	4.2e-05
3	78	10	184	382	14376	7.3e-05
4	36	1	157	326	5648	3e-05
5	73	5	187	410	13634	7.5e-05
6	64	44	182	314	11647	6.8e-05
7	60	46	185	312	11114	7e-05
8	64	34	194	395	12418	8.5e-05
9	48	21	192	395	9238	6.5e-05
X	19	56	162	279	3074	2e-05
all 23	1117	1	181	433	202533	6.5e-05

Table 119: Chromosome specific distribution of the regions. The last line represents the overall statistics.

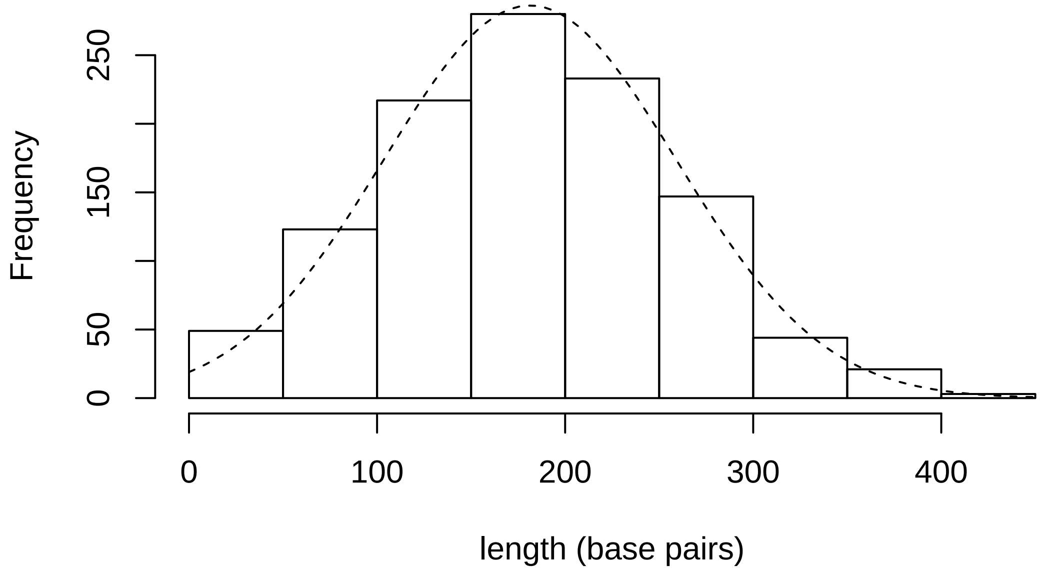
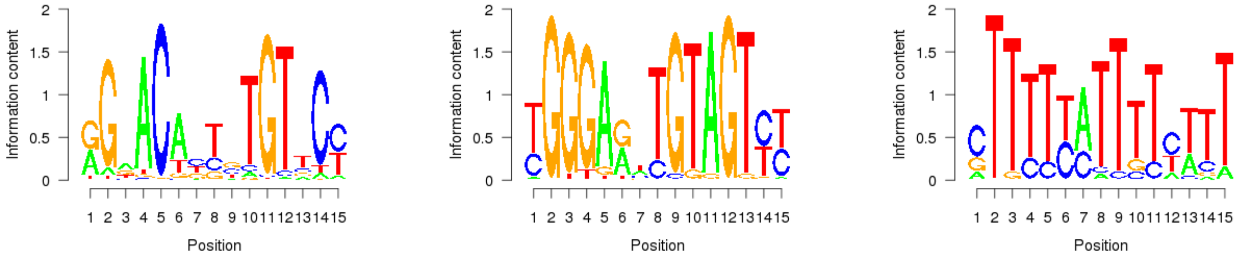


Figure 149: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU1-gCount** component.

property	value
genes	3994



(a) ARCPAvsARRU486rrU1-deNovo-meme1: width=15, sites=230, llr=2312, E=1.1e-218 (b) ARCPAvsARRU486rrU1-deNovo-meme2: width=15, sites=30, llr=431, E=4.3e-25 (c) ARCPAvsARRU486rrU1-deNovo-meme3: width=15, sites=20, llr=257, E=1.1e+08

Figure 150: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARCPArrO sequences.

Table 120: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	52.9526	0.1815	0.0034	177	7	11.27E-72	0.07767
RREB1	12.3928	0.1860	0.0150	40	20	32.4E-08	0.62946
TLX1::NFIC	5.5071	0.0162	0.0029	13	4	8.073E-04	0.01188
PLAG1	4.8912	0.0332	0.0068	27	13	26.5E-06	0.02393
STAT1	4.3247	0.0377	0.0087	32	16	6.107E-06	0.02603
ELK4	3.7077	0.0323	0.0087	32	18	23.54E-06	0.01981
ESR2	3.6923	0.0162	0.0043	17	7	4.719E-04	0.01029
E2F1	2.8418	0.0207	0.0072	22	15	27.3E-04	0.01242
FOXA1	2.7919	0.4582	0.1641	400	302	70.39E-58	0.29810
Foxa2	2.7888	0.4079	0.1462	369	253	2.071E-56	0.29682
NR3C1	2.7379	0.2749	0.1004	253	193	3.584E-30	0.18186
FOXF2	2.4500	0.1195	0.0487	120	95	4.054E-12	0.08066
FOXA1pAR	2.3617	0.0719	0.0304	77	61	8.878E-08	0.04604
ARMotifT	2.3117	0.3827	0.1655	344	309	1.632E-36	0.26612
GABPA	2.2381	0.0638	0.0285	67	57	3.93E-06	0.04293
MIZF	2.2103	0.0225	0.0101	25	21	77.88E-04	0.01424
SP1	2.1526	1.2093	0.5618	362	550	7.871E-14	5.60802
Stat3	2.0723	0.1321	0.0637	106	111	1.705E-06	0.12266
Tal1::Gata1	2.0644	0.0270	0.0130	30	27	61.83E-04	0.01758
GRMotifTH	2.0321	0.1923	0.0946	181	183	1.21E-12	0.14862
Klf4	1.9832	0.1752	0.0883	150	155	10.64E-10	0.17058
Egr1	1.8604	0.0638	0.0343	66	67	1.925E-04	0.05266
FOXD1	1.8527	0.5678	0.3065	454	502	15.75E-42	0.48147
AR	1.7560	0.0305	0.0174	34	35	1.354E-02	0.02213
GRMotifT	1.7077	1.2866	0.7534	744	1036	9.004E-84	1.22564
ARMotifTH	1.7000	0.0288	0.0169	32	35	3.036E-02	0.02060
ARMotifHH	1.6568	0.2183	0.1318	206	240	51.81E-12	0.18229
ARMotifH	1.6421	4.7179	2.8731	1061	1802	83.14E-186	6.93255
EBF1	1.5993	0.3836	0.2399	298	370	2.82E-16	0.43026
Esrrb	1.5949	0.0593	0.0372	62	74	54.24E-04	0.04792
Arnt	1.5728	0.1078	0.0685	87	97	1.12E-04	0.13268
Foxq1	1.5616	0.2480	0.1588	240	271	1.529E-14	0.24312
TFAP2A	1.5601	1.1438	0.7331	535	793	2.967E-34	2.32616
NFIC	1.5428	1.4133	0.9160	774	1127	18.61E-88	1.57045
HIF1A::ARNT	1.4902	0.2525	0.1694	202	273	27.38E-08	0.30546
GR	1.4532	0.1312	0.0903	135	174	46.4E-06	0.10998
MZF1_1-4	1.4003	2.3810	1.7003	840	1423	1.97E-90	6.32312
ELK1	1.3954	0.4250	0.3045	357	533	4.053E-14	0.38798
GRMotifHH	1.3821	0.1114	0.0806	115	146	1.911E-04	0.10314
FEV	1.3747	0.3019	0.2196	280	401	3.605E-10	0.26462
GRMotifH	1.3292	2.8733	2.1617	957	1674	7.87E-130	3.97257
Myc	1.3130	0.0818	0.0623	74	102	2.281E-02	0.09887
TAL1::TCF3	1.2963	0.1051	0.0811	88	132	4.323E-02	0.12421
Mycn	1.2642	0.0647	0.0512	60	81	3.755E-02	0.08167
Myf	1.2577	0.1123	0.0893	107	146	23.23E-04	0.14253
Arnt::Ahr	1.2453	0.6990	0.5613	460	681	1.922E-24	1.82981
Myb	1.2451	0.3684	0.2958	325	496	48.91E-12	0.37073
Hand1::Tcfe2a	1.2272	0.5319	0.4334	437	698	4.152E-18	0.54364
FOXO3	1.2079	0.7421	0.6144	523	860	5.854E-26	0.89375
YY1	0.8073	1.3684	1.6950	739	1558	1.403E-42	2.42570
Nobox	0.7579	0.4825	0.6366	349	783	1.533E-02	0.96999
HOXA5	0.7360	2.0216	2.7466	820	1718	6.486E-62	5.16021
Nkx2-5	0.6901	1.8086	2.6207	741	1597	34.95E-42	7.12485
ARID3A	0.6784	1.0431	1.5376	568	1290	14.02E-14	3.31221
Pdx1	0.6363	0.7125	1.1197	462	1194	36.63E-04	1.71997
Foxd3	0.5946	0.6110	1.0275	404	848	10.12E-06	3.86043
IRF1	0.5841	0.0620	0.1062	65	176	4.21E-02	0.12148
FOXL1	0.5655	1.7916	3.1680	690	1535	10.17E-30	18.20757
NFIL3	0.5295	0.0521	0.0985	50	146	1.929E-02	0.16660
Lhx3	0.5135	0.0746	0.1453	65	202	25.36E-04	0.23295
Ddit3::Cebpa	0.4682	0.0809	0.1728	78	294	1.89E-06	0.17493
MEF2A	0.3801	0.0539	0.1419	56	212	21.81E-06	0.18111

15.42 AR CPA vs AR RU486 unique for ARCPArrO (up)

Chromosome specific statistics are shown in Table 121. A histogram of sequence lengths is shown in Figure 151.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	18	90	211	299	3795	1.5e-05
10	2	170	176	183	353	3e-06
11	7	54	209	421	1466	1.1e-05
12	2	100	192	283	383	3e-06
13	5	51	152	250	758	7e-06
14	1	230	230	230	230	2e-06
15	7	51	214	381	1500	1.5e-05
16	1	304	304	304	304	3e-06
17	4	150	207	265	827	1e-05
18	1	223	223	223	223	3e-06
19	1	165	165	165	165	3e-06
2	11	118	240	389	2635	1.1e-05
20	3	195	222	265	666	1.1e-05
21	3	42	129	223	386	8e-06
3	6	15	158	231	947	5e-06
4	9	113	178	326	1600	8e-06
5	5	64	181	275	905	5e-06
6	16	116	208	314	3323	1.9e-05
7	5	51	204	312	1019	6e-06
8	6	49	205	329	1228	8e-06
9	1	129	129	129	129	1e-06
X	1	56	56	56	56	0
all 22	115	15	199	421	22898	7e-06

Table 121: Chromosome specific distribution of the regions. The last line represents the overall statistics.

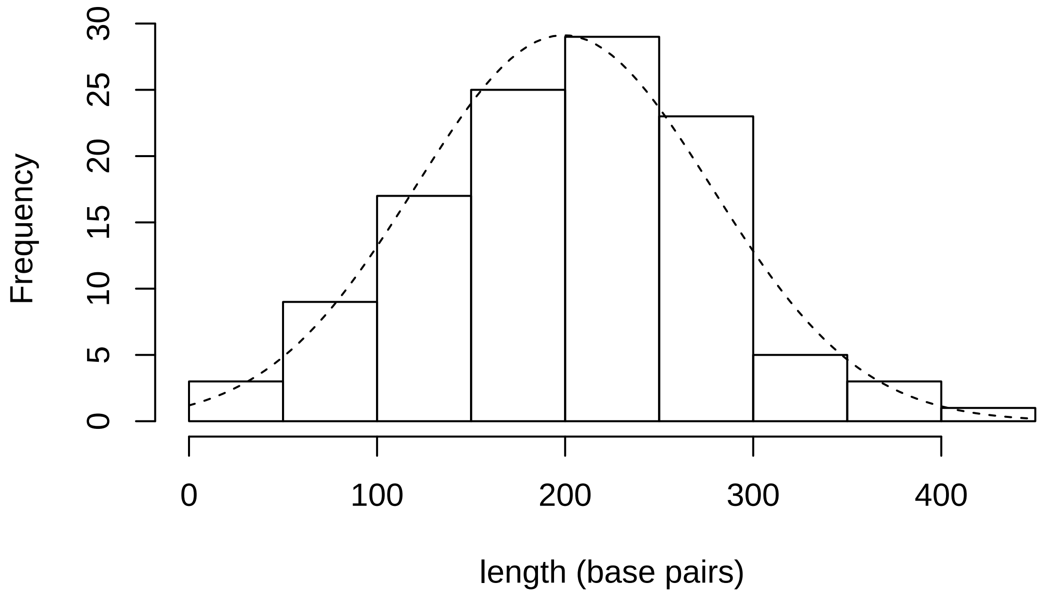
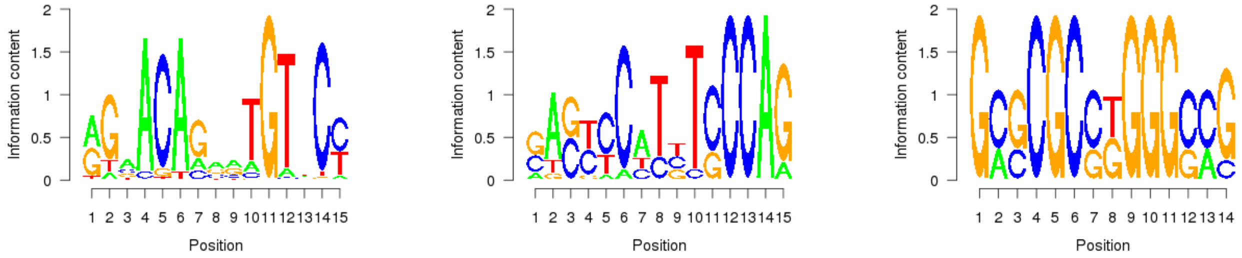


Figure 151: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU1u-gCount** component.

property	value
genes	98



(a) ARCPAvsARRU486rrU1u-deNovo-meme1: width=15, sites=59, llr=616, E=9.7e-46

(b) ARCPAvsARRU486rrU1u-deNovo-meme2: width=15, sites=14, llr=180, E=130000

(c) ARCPAvsARRU486rrU1u-deNovo-meme3: width=14, sites=6, llr=96, E=130000

Figure 152: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARCPArrO (up) sequences.

Table 122: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	27.5117	0.2609	0.0094	26	2	74.8E-12	0.11309
AR	4.2898	0.0609	0.0142	7	3	4.215E-02	0.02974
Foxa2	3.9402	0.5391	0.1368	49	24	5.654E-12	0.33643
FOXA1	3.5808	0.5913	0.1651	52	33	91.54E-12	0.33300
NR3C1	3.2252	0.4261	0.1321	36	23	96.6E-08	0.30941
FOXA1pAR	2.8940	0.0957	0.0330	11	7	2.822E-02	0.05218
FOXF2	2.8472	0.1478	0.0519	15	11	1.486E-02	0.09081
ARMotifHH	2.2684	0.2783	0.1226	29	25	6.171E-04	0.17703
GRMotifTH	2.2684	0.2783	0.1226	27	25	23.17E-04	0.18317
ARMotifT	2.1818	0.5043	0.2311	43	43	27.42E-06	0.36806
FOXD1	1.7742	0.6696	0.3774	53	65	15.27E-06	0.56939
TFAP2A	1.7583	1.0783	0.6132	50	67	1.97E-04	2.38866
GRMotifT	1.6820	1.7217	1.0236	92	135	4.993E-14	1.45496
NFIC	1.6009	1.4348	0.8962	79	107	1.354E-10	1.75338
Arnt::Ahr	1.5920	0.8261	0.5189	56	73	13.51E-06	1.08737
Foxq1	1.5873	0.2696	0.1698	26	31	2.613E-02	0.23090
ARMotifH	1.5422	5.5652	3.6085	111	201	7.253E-20	7.22155
Cebpa	1.5132	0.4783	0.3160	36	55	3.383E-02	0.45547
GRMotifH	1.4421	3.5304	2.4481	103	178	1.947E-16	5.06874
FOXO3	1.3698	0.9304	0.6792	67	102	2.263E-06	0.89060
FEV	1.3496	0.3565	0.2642	37	45	25.46E-04	0.31358
Myb	1.3407	0.4174	0.3113	36	55	3.383E-02	0.39956
SOX10	1.2844	4.4348	3.4528	105	202	7.294E-16	6.35178
ELK1	1.2641	0.4174	0.3302	38	59	2.733E-02	0.37245
MZF1_1-4	1.2438	2.1826	1.7547	85	146	12.29E-10	6.06767
BRCA1	1.2399	0.9826	0.7925	67	110	10.41E-06	0.97402
SPI1	1.2369	0.9043	0.7311	64	97	8.05E-06	0.98730
Sox17	1.2140	0.7043	0.5802	53	95	53.06E-04	0.64642
Nkx3-2	0.8044	0.8348	1.0377	61	119	18.83E-04	1.24733
Pax2	0.7970	1.0000	1.2547	67	139	7.022E-04	1.50025
Pdx1	0.7788	0.9478	1.2170	59	138	3.34E-02	1.61076
Nkx2-5	0.7767	2.1652	2.7877	84	173	21.51E-08	5.66933
GATA2	0.7607	4.2087	5.5330	106	203	2.06E-16	11.69485
GATA3	0.7279	1.9913	2.7358	86	185	17.35E-08	4.94948
ZNF354C	0.7202	1.1652	1.6179	75	145	7.059E-06	2.60489
ARID3A	0.7023	1.1826	1.6840	67	152	27.95E-04	2.52678
FOXL1	0.6334	2.2348	3.5283	79	169	7.871E-06	10.66944
YY1	0.5916	1.2000	2.0283	73	171	5.899E-04	2.91222

15.43 AR CPA vs AR RU486 unique for ARCPArrO (down)

Chromosome specific statistics are shown in Table 123. A histogram of sequence lengths is shown in Figure 153.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	2	105	176	246	351	1e-06
2	1	132	132	132	132	1e-06
3	1	78	78	78	78	0
5	1	271	271	271	271	1e-06
6	1	201	201	201	201	1e-06
7	2	169	200	232	401	3e-06
8	1	247	247	247	247	2e-06
11	1	157	157	157	157	1e-06
12	1	186	186	186	186	1e-06
16	4	128	159	215	635	7e-06
17	1	79	79	79	79	1e-06
19	1	98	98	98	98	2e-06
all 12	17	78	167	271	2836	1e-06

Table 123: Chromosome specific distribution of the regions. The last line represents the overall statistics.

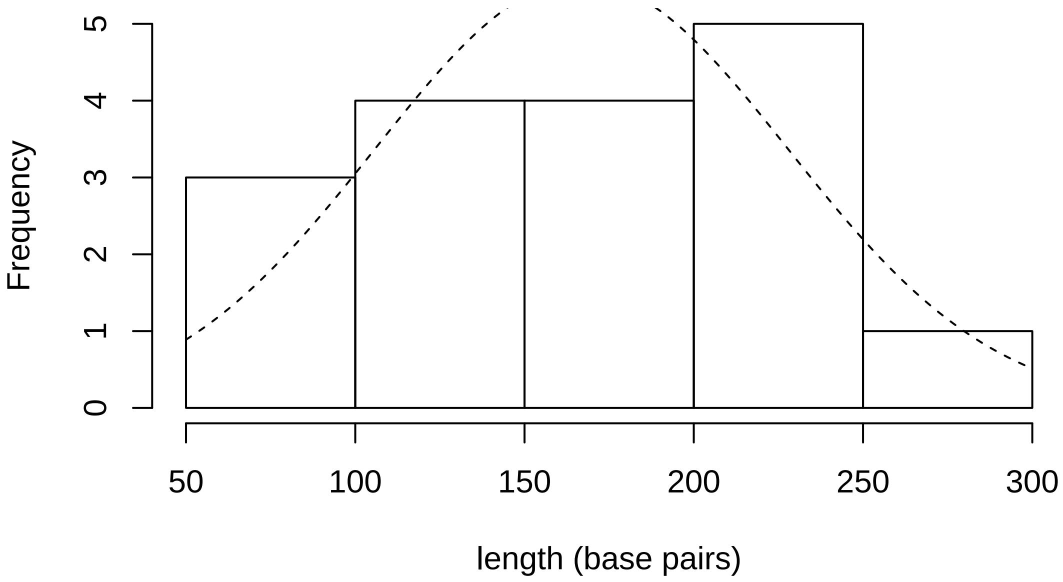
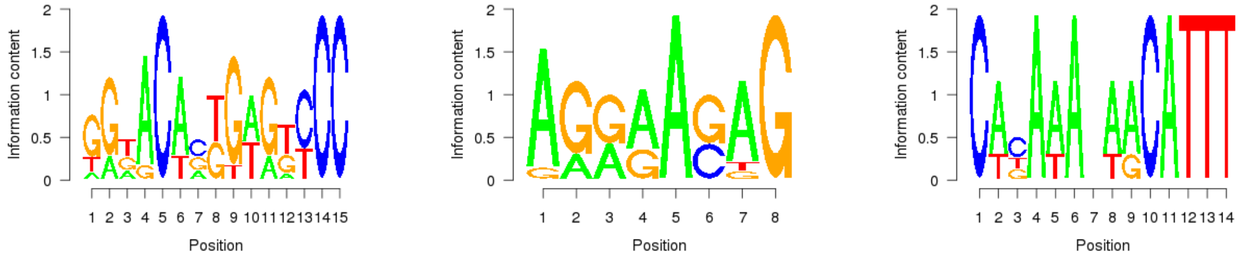


Figure 153: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU1d-gCount** component.

property	value
genes	19



(a) ARCPAvsARRU486rrU1d-deNovo-meme1: width=15, sites=9, llr=112, E=7.9 (b) ARCPAvsARRU486rrU1d-deNovo-meme2: width=8, sites=12, llr=93, E=1600 (c) ARCPAvsARRU486rrU1d-deNovo-meme3: width=14, sites=4, llr=62, E=2200

Figure 154: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARCPArrO (down) sequences.

Table 124: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
HIF1A::ARNT	4.8514	0.5882	0.1212	6	3	4.054E-02	0.40980
FOXO3	3.3966	0.8235	0.2424	9	5	51.89E-04	0.65959
ARMotifH	2.1176	5.6471	2.6667	17	31	3.592E-04	6.58939
NR4A2	1.6035	1.1176	0.6970	12	15	1.102E-02	0.95347
NFIC	1.5882	1.5882	1.0000	14	19	26.72E-04	1.87755
MZF1_1-4	1.5457	2.5294	1.6364	17	27	1.649E-04	2.13918
ETS1	1.3718	3.1176	2.2727	15	30	65.23E-04	4.12898
Mafb	1.3172	1.1176	0.8485	12	18	2.406E-02	1.15959
BRCA1	1.2017	0.7647	0.6364	12	17	1.893E-02	0.42612
En1	0.7886	1.5294	1.9394	15	27	39.22E-04	2.16327

15.44 AR CPA vs AR RU486 unique for ARCPArrO (stable)

Chromosome specific statistics are shown in Table 125. A histogram of sequence lengths is shown in Figure 155.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	85	36	178	433	15115	6.1e-05
10	24	40	173	302	4158	3.1e-05
11	22	35	185	421	4070	3e-05
12	24	51	161	361	3868	2.9e-05
13	5	145	247	312	1234	1.1e-05
14	21	4	143	253	3004	2.8e-05
15	22	48	194	381	4259	4.2e-05
16	28	37	161	389	4505	5e-05
17	52	21	171	318	8903	0.00011
18	12	25	147	305	1767	2.3e-05
19	26	33	140	297	3653	6.2e-05
2	40	27	201	365	8027	3.3e-05
20	29	42	184	310	5338	8.5e-05
21	6	93	188	297	1130	2.3e-05
22	6	80	154	245	921	1.8e-05
3	46	15	184	382	8481	4.3e-05
4	12	1	158	258	1901	1e-05
5	36	53	192	358	6909	3.8e-05
6	38	44	177	295	6725	3.9e-05
7	31	46	176	312	5462	3.4e-05
8	24	47	176	329	4217	2.9e-05
9	20	21	178	395	3568	2.5e-05
X	8	125	189	279	1509	1e-05
all 23	617	1	176	433	108724	3.5e-05

Table 125: Chromosome specific distribution of the regions. The last line represents the overall statistics.

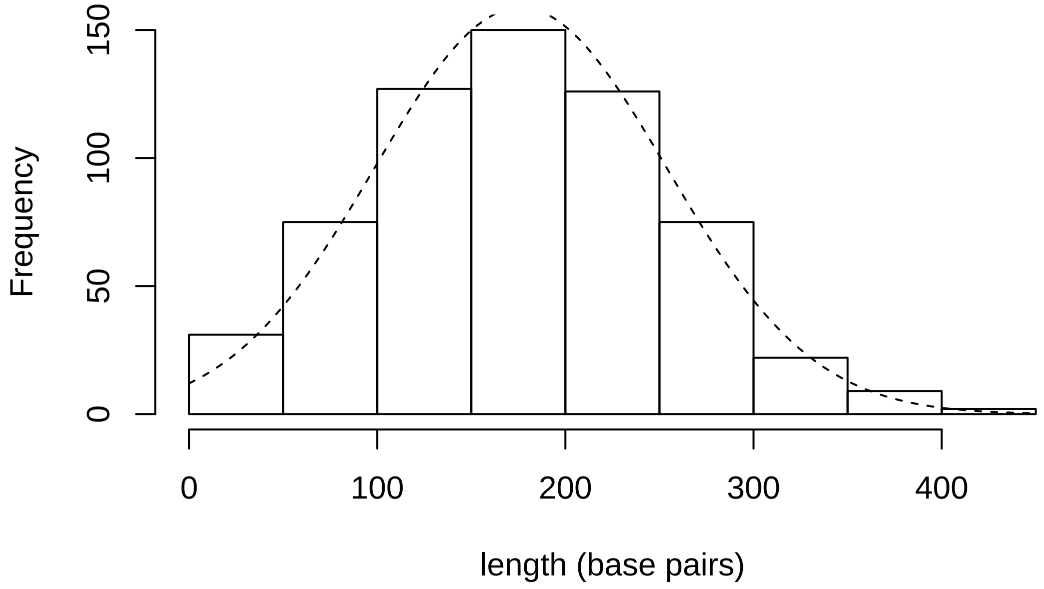
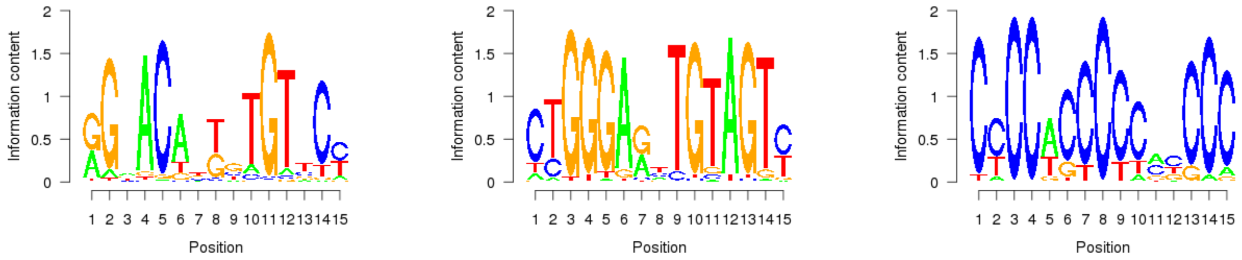


Figure 155: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU1s-gCount** component.

property	value
genes	909



(a) ARCPAvsARRU486rrU1s-deNovo-meme1: width=15, sites=227, llr=2132, E=3.7e-145
(b) ARCPAvsARRU486rrU1s-deNovo-meme2: width=15, sites=45, llr=609, E=7.9e-42
(c) ARCPAvsARRU486rrU1s-deNovo-meme3: width=15, sites=24, llr=321, E=3.2

Figure 156: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARCPArrO (stable) sequences.

Table 126: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	60.3537	0.1612	0.0026	86	3	17.11E-36	0.07062
TLX1::NFIC	21.2027	0.0195	0.0009	9	1	8.60E-04	0.01076
RREB1	20.2258	0.1954	0.0096	23	10	46.1E-06	0.65864
ELK4	6.0195	0.0423	0.0070	22	8	18.66E-06	0.02467
E2F1	5.9841	0.0212	0.0035	12	4	17.92E-04	0.01072
STAT1	5.0603	0.0489	0.0096	21	9	97.63E-06	0.03531
PLAG1	3.4044	0.0358	0.0105	17	12	1.13E-02	0.02467
GABPA	3.1896	0.0782	0.0245	44	28	2.051E-06	0.04594
MIZF	2.9698	0.0261	0.0087	16	10	72.5E-04	0.01458
FOXA1	2.7679	0.4283	0.1547	205	155	75.07E-30	0.29133
SP1	2.5727	1.3404	0.5210	220	288	7.06E-14	6.44373
Foxa2	2.5334	0.3876	0.1530	190	150	1.116E-24	0.28001
HIF1A::ARNT	2.5186	0.3127	0.1241	130	123	13.67E-12	0.28261
NR3C1	2.5127	0.2329	0.0927	122	100	24.87E-14	0.15466
FOXF2	2.5053	0.1205	0.0481	65	51	35.21E-08	0.08283
Stat3	2.4374	0.1450	0.0594	61	54	11.68E-06	0.13374
Klf4	2.4311	0.2020	0.0830	94	88	4.693E-08	0.17400
Egr1	2.3933	0.0733	0.0306	42	33	87.15E-06	0.04915
ESR2	2.3196	0.0163	0.0070	10	6	3.823E-02	0.01242
Esrrb	2.3144	0.0749	0.0323	42	37	4.455E-04	0.05070
FOXA1pAR	2.2815	0.0619	0.0271	37	27	1.036E-04	0.04456
Arnt	2.1125	0.1238	0.0586	53	50	1.741E-04	0.12599
TFAP2A	2.1019	1.3046	0.6206	320	417	33.88E-30	2.30523
ARMotifT	2.0542	0.3322	0.1617	171	167	7.764E-16	0.23388
Mycn	1.9981	0.0717	0.0358	35	34	49.7E-04	0.06767
GRMotifTH	1.9881	0.1808	0.0909	93	96	1.073E-06	0.14838
EBF1	1.8266	0.4088	0.2238	178	182	14.5E-16	0.44894
ARMotifHH	1.7830	0.2182	0.1224	117	119	54.87E-10	0.17831
FOXD1	1.7525	0.5163	0.2946	230	279	21.68E-18	0.43865
NFIC	1.6801	1.4202	0.8453	430	593	24.95E-54	1.47027
GRMotifT	1.6702	1.1840	0.7089	395	540	7.901E-44	1.13402
ARMotifH	1.6510	4.6140	2.7946	586	995	38.61E-104	6.82009
Foxq1	1.5755	0.2231	0.1416	117	137	83.29E-08	0.20953
MZF1_1-4	1.5731	2.5261	1.6058	469	757	12.49E-56	6.54905
Arnt::Ahr	1.4684	0.7573	0.5157	261	371	2.569E-16	1.43306
Myb	1.4258	0.3876	0.2719	185	260	1.002E-08	0.35717
GR	1.3396	0.1042	0.0778	61	84	2.555E-02	0.08861
ELK1	1.3091	0.4349	0.3322	199	312	16.31E-08	0.41826
Mafb	1.3024	0.9609	0.7378	340	541	5.291E-24	1.06675
GRMotifH	1.2865	2.7541	2.1407	522	926	70.5E-70	3.86483
FEV	1.2628	0.2980	0.2360	149	229	88.37E-06	0.28473
Hand1::Tcfe2a	1.2449	0.4886	0.3925	223	366	2.342E-08	0.47006
INSM1	1.2345	0.0896	0.0726	52	70	3.681E-02	0.09287
GATA3	0.8179	1.9691	2.4073	445	941	1.721E-32	4.19769
YY1	0.7953	1.3404	1.6853	400	857	5.624E-22	2.37912
GATA2	0.7945	3.8322	4.8234	534	1086	3.552E-64	10.31109
SRY	0.7749	1.0912	1.4082	343	734	45.18E-14	2.33432
Sox5	0.7175	0.6140	0.8558	247	575	29.89E-04	1.12469
HOXA5	0.6964	1.7769	2.5516	429	940	65.06E-28	4.61991
HLF	0.6769	0.1450	0.2142	67	204	1.459E-02	0.24049
Nkx2-5	0.6432	1.6238	2.5245	381	852	62.8E-18	6.07829
ARID3A	0.5616	0.8974	1.5979	278	714	31.37E-04	3.38169
NFIL3	0.5406	0.0472	0.0874	25	81	3.586E-02	0.10104
Lhx3	0.5061	0.0668	0.1320	32	104	1.934E-02	0.18841
FOXL1	0.4584	1.5277	3.3330	345	877	3.361E-08	15.52158
MEF2A	0.4515	0.0635	0.1407	35	117	1.006E-02	0.17601
Ddit3::Cebpa	0.3728	0.0651	0.1748	34	164	3.706E-06	0.17600
PBX1	0.2469	0.0114	0.0463	7	48	12.06E-04	0.03981

15.45 AR CPA vs AR RU486 unique for ARRU486rrO

Chromosome specific statistics are shown in Table 127. A histogram of sequence lengths is shown in Figure 157.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	10	39	97	222	969	4e-06
10	4	41	50	72	198	1e-06
11	4	32	82	140	328	2e-06
12	3	37	85	133	256	2e-06
13	1	43	43	43	43	0
14	2	38	40	41	79	1e-06
15	3	36	42	55	127	1e-06
16	9	41	76	121	682	8e-06
17	7	25	78	230	543	7e-06
18	2	75	88	102	177	2e-06
19	1	62	62	62	62	1e-06
2	18	14	91	252	1638	7e-06
20	3	37	63	102	190	3e-06
3	5	33	49	90	244	1e-06
4	3	33	50	77	149	1e-06
5	2	33	56	80	113	1e-06
7	6	32	60	112	363	2e-06
8	2	29	36	43	72	0
9	5	43	91	181	455	3e-06
X	4	36	52	64	207	1e-06
Y	10	9	65	154	648	1.1e-05
all 21	104	9	73	252	7543	2e-06

Table 127: Chromosome specific distribution of the regions. The last line represents the overall statistics.

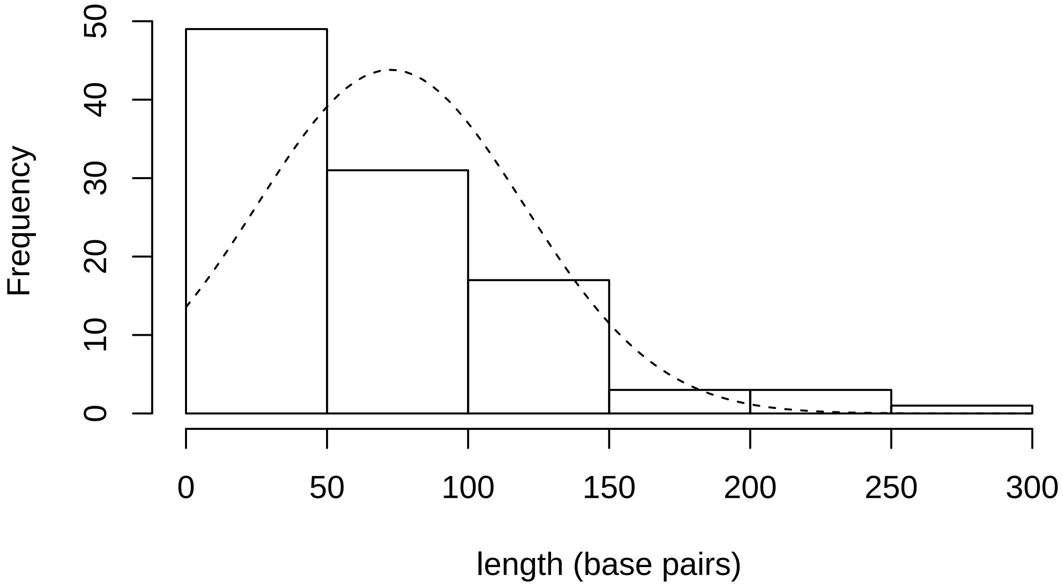
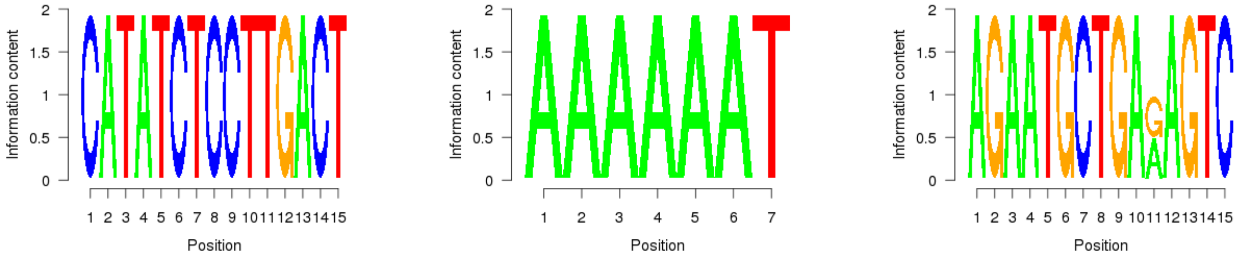


Figure 157: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU2-gCount** component.

property	value
genes	389



(a) ARCPAvsARRU486rrU2-deNovo-meme1: width=15, sites=2, llr=42, E=1300000

(b) ARCPAvsARRU486rrU2-deNovo-meme2: width=7, sites=2, llr=20, E=3300000

(c) ARCPAvsARRU486rrU2-deNovo-meme3: width=15, sites=2, llr=40, E=3700000

Figure 158: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARRU486rrO sequences.

Table 128: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
PLAG1	2308.6923	0.1154	0.0000	9	0	2.426E-04	0.06160
Myf	1924.0769	0.0962	0.0000	6	0	45.47E-04	0.06919
E2F1	962.5385	0.0481	0.0000	5	0	1.216E-02	0.01730
RREB1	196.6334	1.0962	0.0055	27	1	14.82E-12	2.66407
SP1	15.8383	4.2885	0.2707	50	24	3.983E-12	18.61008
Klf4	13.2048	0.3654	0.0276	24	5	8.963E-08	0.24828
Egr1	10.3576	0.0577	0.0055	6	1	1.875E-02	0.02404
MZF1_1-4	6.3206	5.0288	0.7956	65	83	8.627E-08	20.44361
MZF1_5-13	2.9528	0.5385	0.1823	45	30	2.819E-08	0.31411
TFAP2A	2.0734	0.5385	0.2597	32	32	17.48E-04	0.64710
ZNF354C	1.4503	0.7692	0.5304	42	65	1.374E-02	1.06096
SOX10	1.4385	1.5577	1.0829	55	105	58.74E-04	3.97994
YY1	0.5466	0.3654	0.6685	21	82	4.748E-02	0.93062
SRY	0.4602	0.2212	0.4807	14	62	1.901E-02	0.55473
HOXA5	0.4188	0.4327	1.0331	24	99	3.009E-02	1.54628
SOX9	0.2491	0.0192	0.0773	1	14	3.866E-02	0.06022
ARID3A	0.2487	0.1346	0.5414	9	60	9.185E-04	0.69713
Nobox	0.2354	0.0481	0.2044	5	30	2.097E-02	0.19652

15.46 AR CPA vs AR RU486 unique for ARRU486rrO (up)

Chromosome specific statistics are shown in Table 129. A histogram of sequence lengths is shown in Figure 159.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	2	40	82	125	165	1e-06
all 1	2	40	82	125	165	0

Table 129: Chromosome specific distribution of the regions. The last line represents the overall statistics.

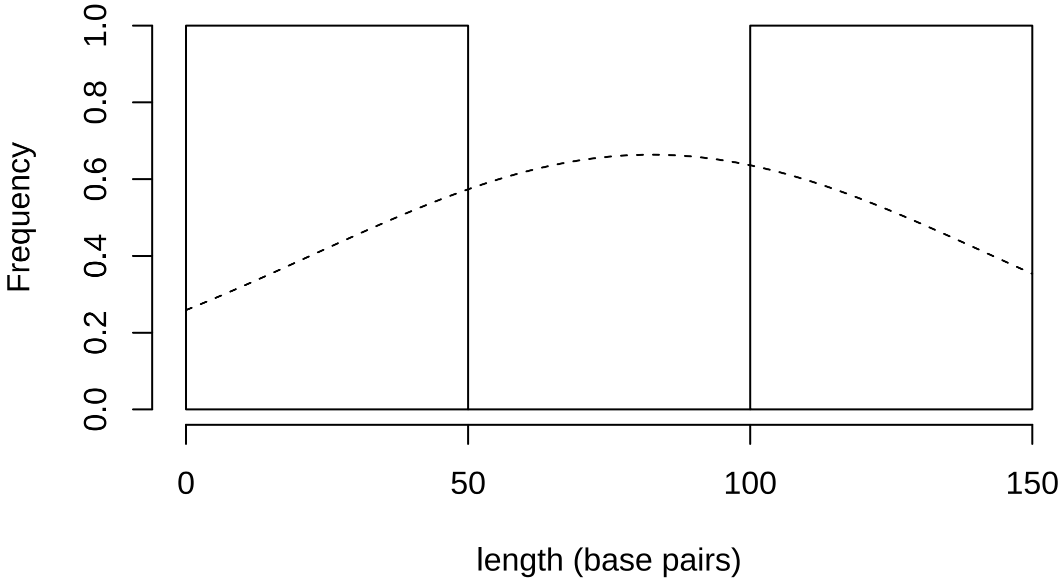
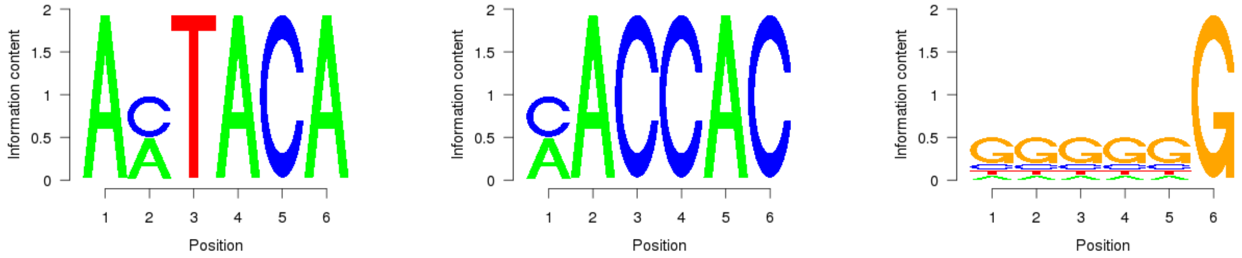


Figure 159: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU2u-gCount** component.

property	value
genes	2



(a) ARCPAvsARRU486rrU2u-deNovo-meme1: width=6, sites=2, llr=16, E=650 (b) ARCPAvsARRU486rrU2u-deNovo-meme2: width=6, sites=2, llr=15, E=2000 (c) ARCPAvsARRU486rrU2u-deNovo-meme3: width=6, sites=2, llr=5, E=17000

Figure 160: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARRU486rrO (up) sequences.

Table 130: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var

15.47 AR CPA vs AR RU486 unique for ARRU486rrO (down)

Chromosome specific statistics are shown in Table 131. A histogram of sequence lengths is shown in Figure 161.

		length				
chromosome	frequency	min	mean	max	total	coverage
15	1	36	36	36	36	0
16	1	41	41	41	41	0
20	1	102	102	102	102	2e-06
all 3	3	36	60	102	179	0

Table 131: Chromosome specific distribution of the regions. The last line represents the overall statistics.

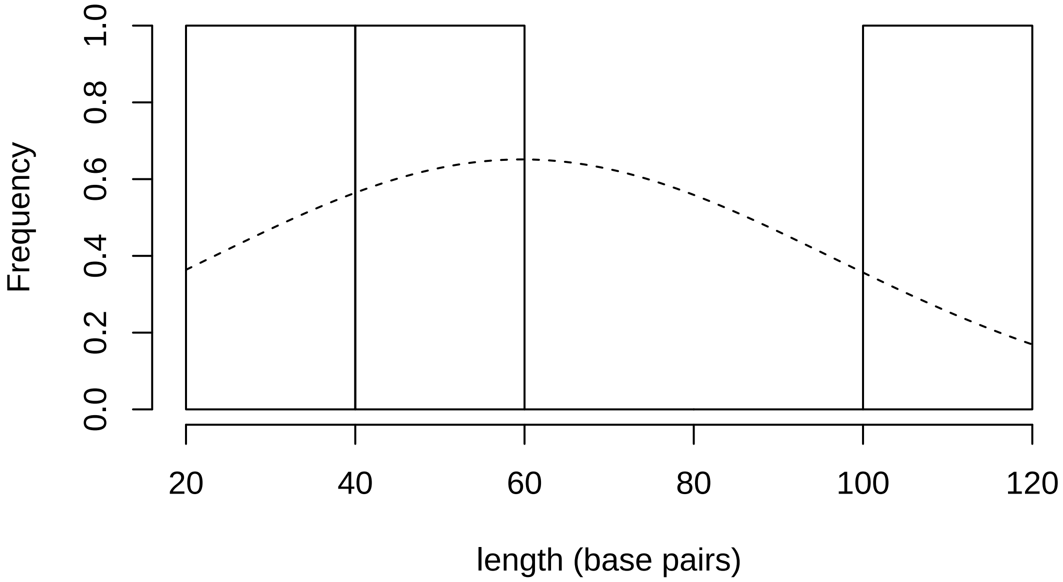
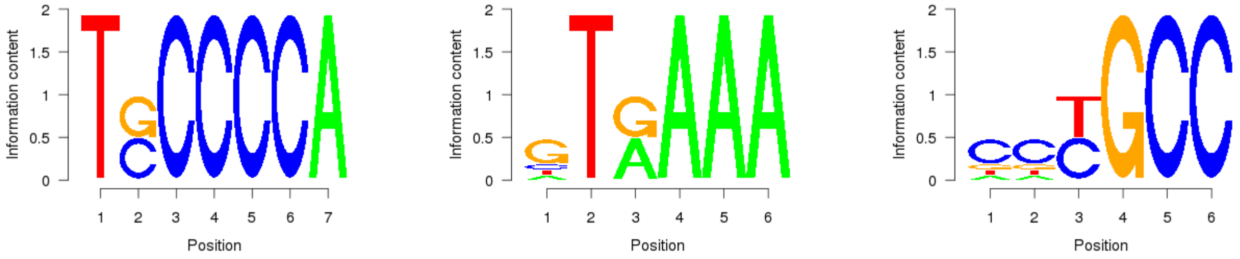


Figure 161: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU2d-gCount** component.

property	value
genes	3



(a) ARCPAvsARRU486rrU2d-deNovo-meme1: width=7, sites=2, llr=18, E=5500

(b) ARCPAvsARRU486rrU2d-deNovo-meme2: width=6, sites=2, llr=14, E=5000

(c) ARCPAvsARRU486rrU2d-deNovo-meme3: width=6, sites=2, llr=11, E=31000

Figure 162: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARRU486rrO (down) sequences.

Table 132: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
SP1	186667.6667	9.3333	0.0000	3	0	2.445E-02	35.36111

15.48 AR CPA vs AR RU486 unique for ARRU486rrO (stable)

Chromosome specific statistics are shown in Table 133. A histogram of sequence lengths is shown in Figure 163.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	7	39	103	222	721	3e-06
10	1	42	42	42	42	0
11	4	32	82	140	328	2e-06
12	2	86	110	133	219	2e-06
13	1	139	139	139	139	1e-06
14	1	41	41	41	41	0
15	1	36	36	36	36	0
16	2	41	64	86	127	1e-06
17	7	25	78	230	543	7e-06
19	1	62	62	62	62	1e-06
2	17	14	94	252	1592	7e-06
20	2	37	70	102	139	2e-06
3	2	34	62	90	124	1e-06
4	2	33	55	77	110	1e-06
5	1	33	33	33	33	0
7	3	32	62	112	186	1e-06
8	1	43	43	43	43	0
9	2	72	84	96	168	1e-06
X	2	49	56	64	113	1e-06
Y	1	39	39	39	39	1e-06
all 20	60	14	80	252	4805	2e-06

Table 133: Chromosome specific distribution of the regions. The last line represents the overall statistics.

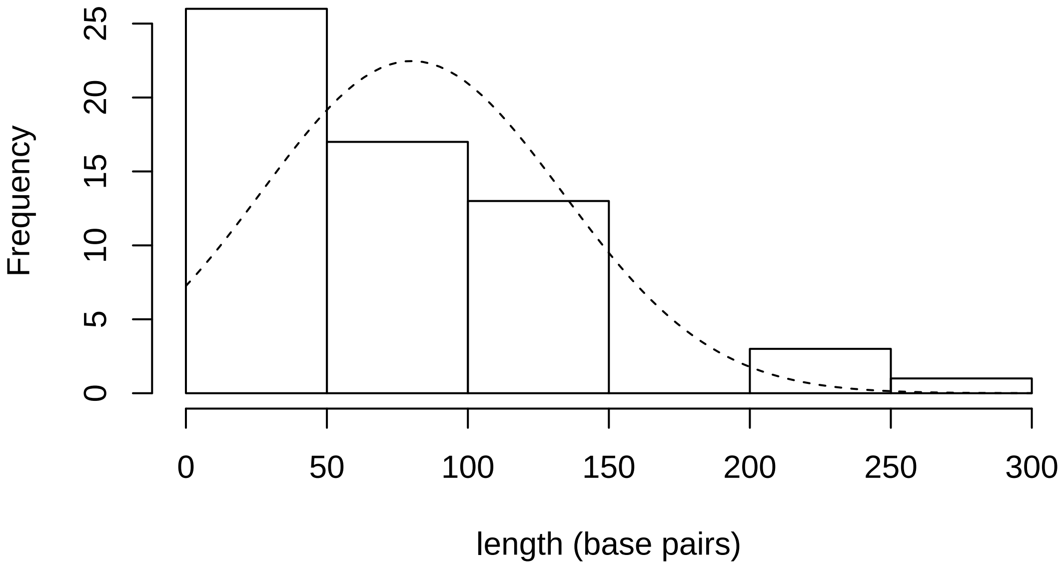
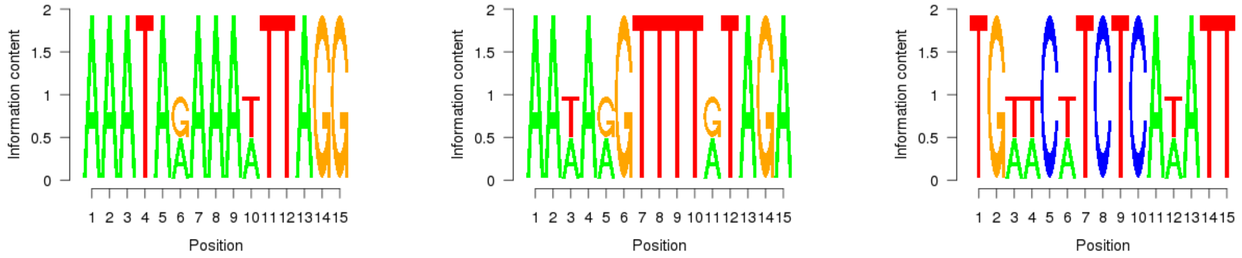


Figure 163: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARCPAvsARRU486rrU2s-gCount** component.

property	value
genes	82



(a) ARCPAvsARRU486rrU2s-deNovo-meme1: width=15, sites=2, llr=40, E=550000
(b) ARCPAvsARRU486rrU2s-deNovo-meme2: width=15, sites=2, llr=38, E=1500000
(c) ARCPAvsARRU486rrU2s-deNovo-meme3: width=15, sites=2, llr=37, E=2500000

Figure 164: De novo motifs for the filtered AR CPA vs AR RU486 unique for ARRU486rrO (stable) sequences.

Table 134: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
RREB1	15667.6667	0.7833	0.0000	14	0	46.26E-08	1.26408
SP1	13.7869	3.8167	0.2768	28	20	6.968E-06	15.31565
Klf4	11.1810	0.3000	0.0268	12	2	91.34E-06	0.20138
Myf	9.3101	0.1667	0.0179	6	2	3.683E-02	0.12376
MZF1_1-4	6.4753	4.6833	0.7232	41	53	2.387E-06	18.21121
REL	4.0416	0.2167	0.0536	11	4	21.58E-04	0.14562
TFAP2A	3.2102	0.7167	0.2232	23	20	7.128E-04	0.69659
MZF1_5-13	2.2254	0.5167	0.2321	25	24	6.733E-04	0.31644
Mafb	1.9248	0.5500	0.2857	19	24	4.565E-02	0.58735
ARID3A	0.2435	0.1500	0.6161	6	39	1.899E-02	0.91595

15.49 GR DEX overlaps

Chromosome specific statistics are shown in Table 135. A histogram of sequence lengths is shown in Figure 165.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	1695	1	317	1031	537004	0.002154
10	735	20	292	949	214268	0.001581
11	724	16	292	1118	211729	0.001568
12	646	2	292	989	188734	0.00141
13	528	1	328	1787	173328	0.001505
14	566	2	306	1050	172917	0.001611
15	574	18	298	1107	171253	0.00167
16	467	3	295	1638	137998	0.001527
17	605	30	285	978	172159	0.00212
18	364	3	319	1991	115965	0.001485
19	203	64	262	973	53261	0.000901
2	1237	14	297	1946	367799	0.001512
20	421	21	282	1249	118913	0.001887
21	218	31	293	1440	63910	0.001328
22	213	5	263	845	55962	0.001091
3	1273	0	324	969	412699	0.002084
4	793	0	282	2287	223705	0.00117
5	1200	16	307	941	368537	0.002037
6	859	6	289	1818	247825	0.001448
7	958	0	299	1103	286103	0.001798
8	886	1	303	1006	268617	0.001835
9	710	5	287	1246	203637	0.001442
X	382	43	252	1178	96148	0.000619
Y	50	109	253	408	12672	0.000213
all 24	16307	0	299	2287	4875143	0.001575

Table 135: Chromosome specific distribution of the regions. The last line represents the overall statistics.

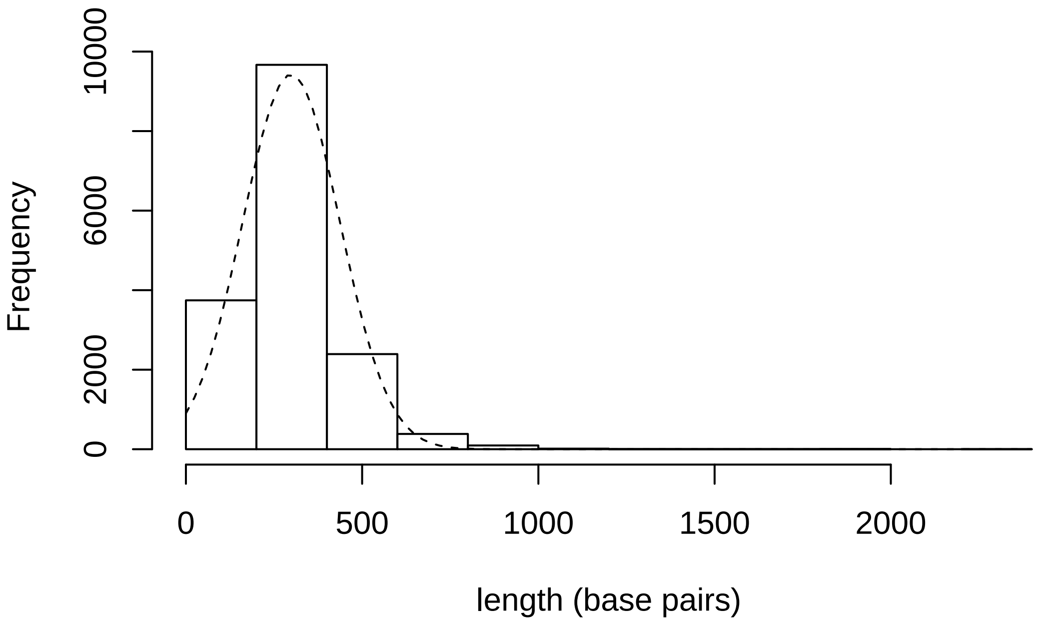
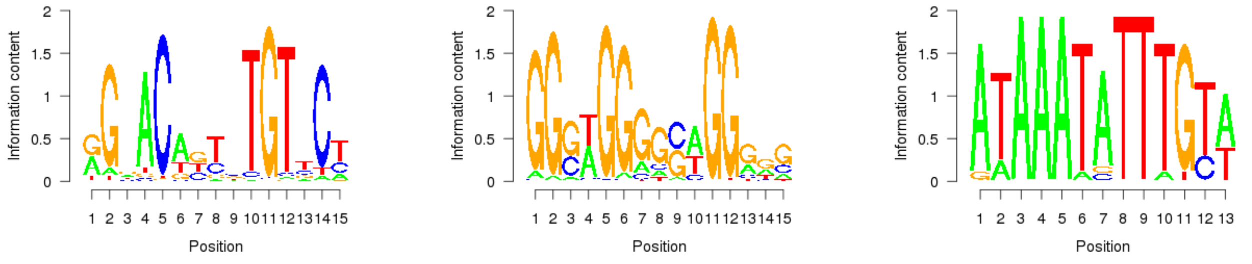


Figure 165: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRDEXrrO-gCount** component.

property	value
genes	21484



(a) GRDEXrrO-deNovo-meme1: width=15, sites=344, llr=3299, E=1.5e-220

(b) GRDEXrrO-deNovo-meme2: width=15, sites=73, llr=857, E=5.1e-12

(c) GRDEXrrO-deNovo-meme3: width=13, sites=16, llr=231, E=7.1e+07

Figure 166: De novo motifs for the filtered GR DEX overlaps sequences.

Table 136: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	21.9567	0.1410	0.0064	2031	184	0.00E00	0.06943
TLX1::NFIC	4.1919	0.0163	0.0038	213	93	23.66E-38	0.01137
ARMotifTH	2.9616	0.0829	0.0280	1165	828	16.86E-120	0.06584
ARMotifTT	2.6083	0.0135	0.0051	215	153	16.56E-22	0.00826
ARMotifT	2.4925	0.6688	0.2683	7502	6835	0.00E00	0.60704
FOXA1	2.4399	0.6168	0.2528	7131	6460	0.00E00	0.46245
GRMotifTH	2.4122	0.3642	0.1510	4615	4172	0.00E00	0.33279
GRMotifTT	2.2895	0.0332	0.0145	521	430	5.704E-40	0.02221
ESR2	2.2730	0.0194	0.0085	269	247	78.28E-18	0.01541
NR3C1	2.2673	0.3855	0.1700	4926	4611	0.00E00	0.29978
Foxa2	2.1973	0.5466	0.2487	6430	5679	0.00E00	0.53513
FOXF2	2.1855	0.1889	0.0864	2728	2456	2.206E-218	0.13169
AR	2.1245	0.0614	0.0289	950	854	25.64E-64	0.04323
CTCF	2.0094	0.0046	0.0023	75	68	13.72E-06	0.00312
ARMotifHH	1.9029	0.4028	0.2117	4906	5314	0.00E00	0.61475
Tal1::Gata1	1.8948	0.0420	0.0221	667	661	77.17E-36	0.02955
Stat3	1.7828	0.1644	0.0922	2042	2248	1.173E-96	0.16183
GR	1.7243	0.2682	0.1555	3704	4143	10.92E-216	0.26390
GRMotifT	1.7177	2.1284	1.2391	13736	20382	0.00E00	2.72954
GABPA	1.6980	0.0638	0.0375	975	1084	1.514E-38	0.05143
FOXD1	1.6938	0.8745	0.5163	8785	11375	0.00E00	0.82378
RXRA::VDR	1.6885	0.0072	0.0043	107	128	6.542E-04	0.00776
GRMotifHH	1.6578	0.2167	0.1307	2884	3441	10.24E-126	0.20769
STAT1	1.6322	0.0345	0.0211	435	518	29.31E-14	0.03644
PPARG::RXRA	1.6060	0.0163	0.0102	259	303	1.213E-08	0.01280
Evi1	1.5717	0.0323	0.0205	491	608	52.04E-14	0.02819
Foxq1	1.5655	0.4140	0.2645	5078	6322	2.67E-286	0.41294
ARMotifH	1.5157	7.1720	4.7319	16101	29091	0.00E00	17.13191
MIZF	1.4514	0.0227	0.0156	338	464	5.393E-06	0.02964
RORA_2	1.4189	0.0187	0.0131	296	398	7.619E-06	0.01527
Esrrb	1.4097	0.0875	0.0621	1336	1787	23.74E-30	0.07610
Tcfcp2l1	1.3920	0.0508	0.0365	744	1012	12.81E-14	0.04977
NHLH1	1.3803	0.0937	0.0679	988	1335	22.14E-20	0.13495
Gata1	1.3649	0.5390	0.3949	6343	9313	1.624E-302	0.52778
RXR::RAR_DR5	1.3562	0.0220	0.0162	355	483	1.616E-06	0.01861
ELK4	1.3560	0.0182	0.0134	286	393	36.2E-06	0.01608
GRMotifH	1.3531	4.8429	3.5792	15649	28232	0.00E00	9.37537
TAL1::TCF3	1.3529	0.1976	0.1460	2398	3292	2.905E-60	0.24741
FOXA1pAR	1.3084	0.0658	0.0503	977	1330	1.689E-18	0.07163
FEV	1.2955	0.4868	0.3757	6016	9067	94.46E-252	0.48802
NFIC	1.2708	1.9490	1.5337	12858	21416	0.00E00	2.92683
FOXI1	1.2691	0.6697	0.5277	6895	10275	0.00E00	0.95960
Arnt	1.2608	0.1352	0.1073	1492	2165	20.49E-24	0.21204
NR2F1	1.2575	0.0863	0.0686	1312	1968	2.028E-16	0.08225
TEAD1	1.2458	0.0617	0.0495	955	1452	4.758E-10	0.05577
Hand1::Tcfe2a	1.2339	0.8998	0.7292	9080	14872	0.00E00	1.00518
FOXO3	1.2228	1.2965	1.0603	10738	17827	0.00E00	1.71274
Myb	1.2210	0.5806	0.4755	6765	10933	79.9E-276	0.60742
ELK1	1.2145	0.6304	0.5191	7131	11502	8.029E-316	0.70745
Zfp423	0.8038	0.0305	0.0380	418	912	3.389E-02	0.05113
Pdx1	0.7989	1.5560	1.9476	10869	22268	0.00E00	3.81797
CREB1	0.7908	0.4678	0.5916	5655	12184	12.18E-48	0.72678
PBX1	0.7883	0.0597	0.0757	919	2074	15.03E-04	0.08523
Klf4	0.7874	0.1149	0.1460	1600	3695	6.52E-04	0.18269
MEF2A	0.7774	0.1892	0.2434	2324	5379	2.697E-02	0.37490
MZF1_5-13	0.7772	0.7619	0.9803	7865	17178	21.53E-168	1.49053
FOXL1	0.7739	4.3604	5.6345	13830	26532	0.00E00	44.12125
SP1	0.7687	0.6579	0.8560	4890	11213	6.484E-14	3.24441
Prrx2	0.7355	1.3553	1.8428	10079	21734	0.00E00	3.37742
NF-kappaB	0.7351	0.1106	0.1505	1332	3580	1.323E-16	0.22002
Lhx3	0.7307	0.1763	0.2413	2089	4835	67.86E-04	0.40431
Foxd3	0.7047	1.2736	1.8074	8869	17621	0.00E00	7.45799
IRF1	0.7001	0.1288	0.1840	1844	4586	1.883E-08	0.21477
PLAG1	0.6791	0.0071	0.0105	113	300	21.6E-04	0.01040
NFKB1	0.6608	0.0303	0.0459	395	1011	1.541E-06	0.06721
Zfx	0.6448	0.0776	0.1203	1028	3116	20.68E-30	0.15011
IRF2	0.6004	0.0033	0.0055	53	165	15.38E-04	0.00471
RREB1	0.5851	0.0167	0.0286	203	569	1.93E-06	0.08568
Ddit3::Cebpa	0.5080	0.1473	0.2901	2154	6667	6.348E-42	0.31142
EWSR1-FLI1	0.1729	0.0026	0.0155	27	100	18.7E-04	0.11555

15.50 GR DEX overlaps (up)

Chromosome specific statistics are shown in Table 137. A histogram of sequence lengths is shown in Figure 167.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	244	15	343	943	83667	0.000336
10	83	128	305	737	25348	0.000187
11	97	63	344	779	33342	0.000247
12	58	58	307	765	17826	0.000133
13	25	86	279	544	6978	6.1e-05
14	49	102	325	728	15912	0.000148
15	38	113	322	911	12238	0.000119
16	83	3	306	639	25417	0.000281
17	60	73	289	712	17368	0.000214
18	14	131	485	1991	6785	8.7e-05
19	15	101	317	703	4749	8e-05
2	137	98	332	879	45495	0.000187
20	65	105	310	811	20153	0.00032
21	6	31	440	1440	2637	5.5e-05
22	30	125	271	440	8139	0.000159
3	152	64	316	837	48046	0.000243
4	84	0	321	734	26983	0.000141
5	145	16	313	939	45443	0.000251
6	165	14	315	799	52006	0.000304
7	50	57	323	830	16167	0.000102
8	74	115	324	931	23994	0.000164
9	75	32	304	1246	22773	0.000161
X	49	102	279	667	13690	8.8e-05
all 23	1798	0	320	1991	575156	0.000186

Table 137: Chromosome specific distribution of the regions. The last line represents the overall statistics.

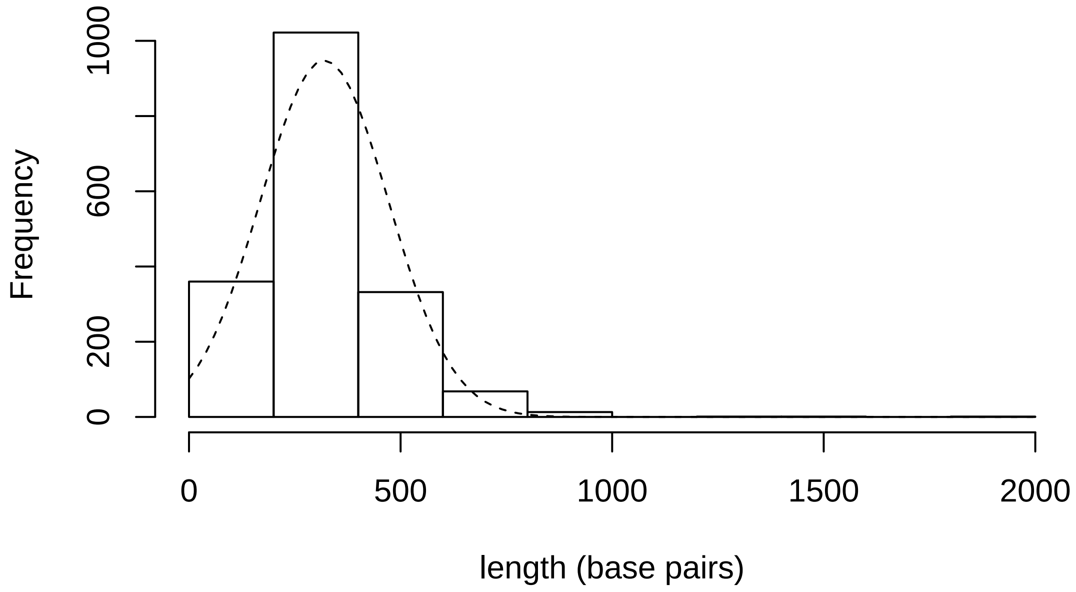
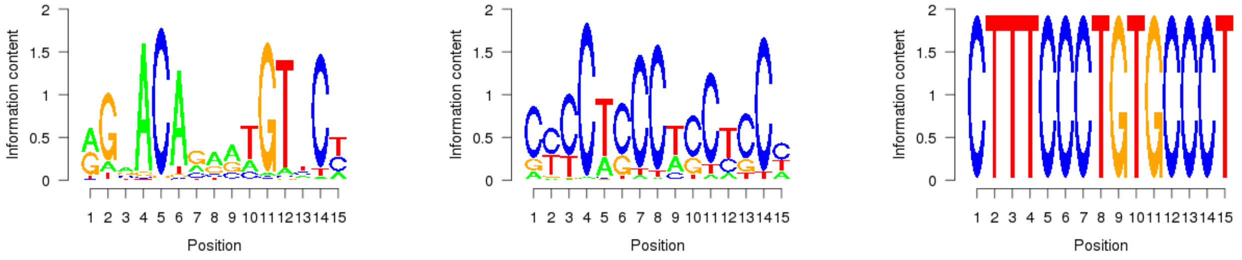


Figure 167: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRDEXrrOu-gCount** component.

property	value
genes	374



(a) GRDEXrrOu-deNovo-meme1: width=15, sites=341, llr=3199, E=1.4e-204 (b) GRDEXrrOu-deNovo-meme2: width=15, sites=87, llr=977, E=7.8e-14 (c) GRDEXrrOu-deNovo-meme3: width=15, sites=2, llr=42, E=2.6e+09

Figure 168: De novo motifs for the filtered GR DEX overlaps (up) sequences.

Table 138: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	29.2949	0.1665	0.0056	273	19	1.991E-104	0.06860
ESR2	4.4079	0.0329	0.0074	44	22	7.434E-08	0.02877
TLX1::NFIC	3.7294	0.0200	0.0053	28	14	25.09E-06	0.01499
ARMotifTT	3.0597	0.0128	0.0042	23	13	4.29E-04	0.00750
GRMotifTT	2.7199	0.0340	0.0125	59	41	33.41E-08	0.02070
GRMotifTH	2.6623	0.4059	0.1524	573	456	91.62E-74	0.30928
AR	2.5075	0.0663	0.0264	114	89	26.77E-12	0.04173
NR3C1	2.4683	0.4371	0.1770	617	517	6.581E-76	0.30703
ARMotifT	2.4636	0.6832	0.2773	832	768	1.959E-108	0.57084
ARMotifTH	2.4440	0.0718	0.0294	126	97	96.95E-14	0.04411
CTCF	2.4169	0.0072	0.0030	13	10	4.708E-02	0.00443
ARMotifHH	2.2481	0.4861	0.2162	612	577	11.23E-64	1.46495
GABPA	2.1716	0.0818	0.0377	138	119	12.17E-12	0.05796
PPARG::RXRA	2.0608	0.0245	0.0119	44	39	5.366E-04	0.01638
FOXA1	1.9061	0.5161	0.2708	691	759	30.51E-62	0.41744
Stat3	1.8345	0.1682	0.0916	233	255	88.71E-14	0.16040
GRMotifT	1.7540	2.3174	1.3212	1559	2318	6.749E-254	2.94314
ELK4	1.7249	0.0256	0.0148	44	48	88.66E-04	0.01978
GR	1.7106	0.2856	0.1670	420	481	29.96E-26	0.25082
Foxa2	1.6917	0.4465	0.2639	597	674	21.48E-46	0.49507
FOXF2	1.6192	0.1503	0.0928	253	288	73.26E-14	0.11752
Egr1	1.6176	0.0869	0.0537	134	165	35.99E-06	0.07916
ARMotifH	1.6033	8.0768	5.0377	1779	3234	9.73E-322	23.43710
NHLH1	1.5755	0.1164	0.0738	127	156	60.81E-06	0.16478
Mycn	1.5453	0.1063	0.0688	144	175	9.277E-06	0.12200
NR2F1	1.5311	0.1158	0.0756	192	243	56.56E-08	0.09280
GRMotifHH	1.5262	0.2300	0.1507	348	415	17.11E-18	0.22428
Arnt	1.5018	0.1581	0.1053	190	241	75.74E-08	0.19818
Tal1::Gata1	1.4286	0.0373	0.0261	66	84	1.311E-02	0.03103
Tcfcp2l1	1.4041	0.0562	0.0400	96	124	24.42E-04	0.04978
FOXD1	1.3959	0.7472	0.5353	872	1275	2.855E-58	0.78047
NFYA	1.3819	0.0451	0.0326	75	103	2.587E-02	0.04063
Myc	1.3734	0.1275	0.0928	176	247	1.529E-04	0.14925
Myf	1.3576	0.2210	0.1628	296	414	80.93E-10	0.33537
Pax5	1.3573	0.0451	0.0332	79	108	1.968E-02	0.03867
ELK1	1.3496	0.7261	0.5380	864	1313	88.47E-54	0.75030
GRMotifH	1.3229	5.0557	3.8218	1732	3141	63.82E-296	9.36840
NFIC	1.3162	2.1559	1.6379	1466	2452	2.352E-188	3.02142
Foxq1	1.2907	0.3614	0.2800	499	740	25.47E-18	0.39442
HIF1A::ARNT	1.2897	0.3335	0.2586	411	652	13.87E-10	0.52183
NR4A2	1.2655	1.5223	1.2028	1299	2180	39.24E-132	1.78226
TFAP2A	1.2651	1.4493	1.1456	1025	1656	4.872E-72	4.27288
Klf4	1.2469	0.1971	0.1581	276	429	21.16E-06	0.24826
Myb	1.2397	0.6169	0.4976	774	1252	39.16E-36	0.63443
EBF1	1.2334	0.5267	0.4270	629	982	6.802E-24	0.72352
FEV	1.2305	0.5084	0.4131	682	1086	40.48E-28	0.50301
MAX	1.2269	0.1659	0.1352	228	354	3.511E-04	0.29301
TEAD1	1.2147	0.0674	0.0555	116	181	4.606E-02	0.06031
Hand1::Tcfe2a	1.2122	0.9800	0.8084	1054	1778	9.137E-72	1.04238
HOXA5	0.8325	4.0067	4.8126	1631	3162	28.85E-228	12.94804
YY1	0.8278	2.5702	3.1047	1550	3013	97.09E-192	6.92414
Nobox	0.8257	0.9577	1.1598	879	1819	24.45E-26	2.18144
Nkx2-5	0.7767	3.6715	4.7272	1531	3032	33.36E-180	15.28181
ARID3A	0.7472	2.1665	2.8995	1306	2642	18.49E-102	8.08820
Pdx1	0.7169	1.4705	2.0513	1133	2516	17.88E-52	4.06907
PBX1	0.6801	0.0607	0.0893	101	258	4.43E-02	0.11873
Prrx2	0.6771	1.3012	1.9217	1085	2463	16.45E-42	3.55884
MEF2A	0.6324	0.1631	0.2580	232	635	43.14E-04	0.33623
Lhx3	0.6305	0.1514	0.2402	198	552	17.96E-04	0.34904
FOXL1	0.6252	3.7528	6.0030	1455	2966	24.84E-146	48.12379
Foxd3	0.5844	1.1487	1.9656	905	2033	17.78E-22	8.39237
Ddit3::Cebpa	0.5507	0.1631	0.2963	260	753	4.463E-04	0.32843
Pou5f1	0.4138	0.0039	0.0095	7	32	4.359E-02	0.00749

15.51 GR DEX overlaps (down)

Chromosome specific statistics are shown in Table 139. A histogram of sequence lengths is shown in Figure 169.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	31	10	283	662	8778	3.5e-05
10	5	127	281	426	1406	1e-05
11	3	283	331	411	994	7e-06
12	13	103	289	660	3757	2.8e-05
13	2	150	234	318	468	4e-06
14	33	92	365	700	12055	0.000112
15	5	228	292	386	1459	1.4e-05
16	21	130	324	1638	6801	7.5e-05
17	6	143	336	522	2013	2.5e-05
18	2	212	216	221	433	6e-06
19	11	154	289	433	3174	5.4e-05
2	23	132	309	584	7096	2.9e-05
22	2	179	248	316	495	1e-05
3	32	147	379	956	12142	6.1e-05
4	22	117	258	586	5672	3e-05
5	33	141	289	509	9538	5.3e-05
6	13	35	230	422	2985	1.7e-05
7	18	170	338	495	6084	3.8e-05
8	10	168	258	341	2578	1.8e-05
9	16	8	280	481	4485	3.2e-05
X	1	290	290	290	290	2e-06
all 21	302	8	307	1638	92703	3e-05

Table 139: Chromosome specific distribution of the regions. The last line represents the overall statistics.

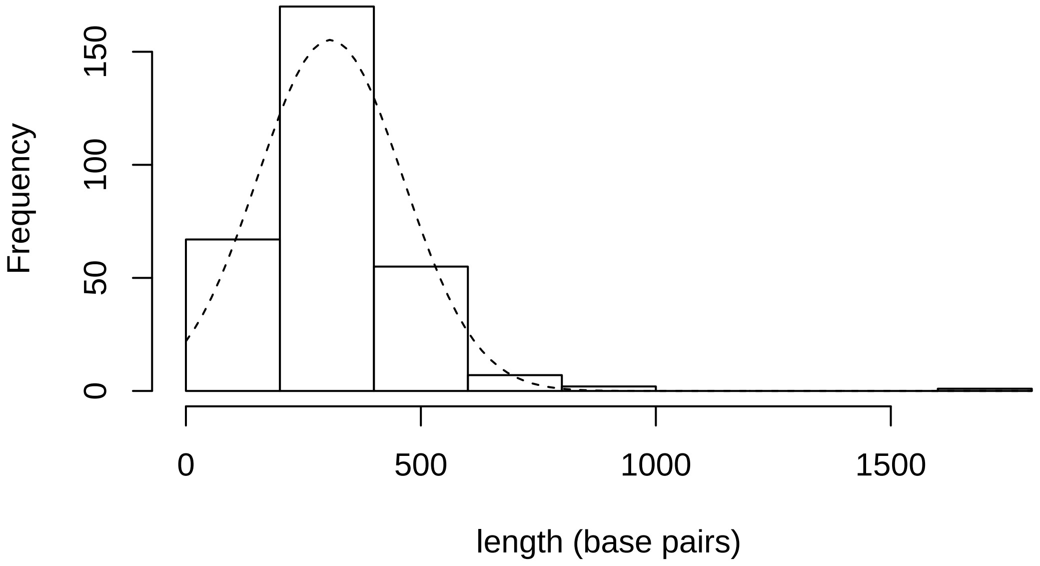
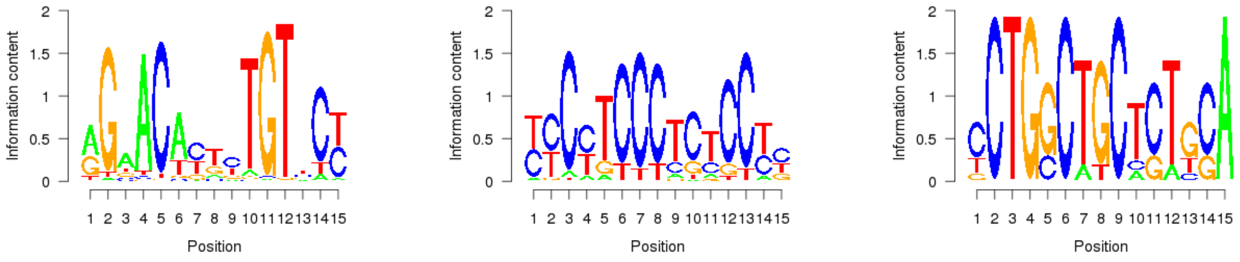


Figure 169: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRDEXrrOd-gCount** component.

property	value
genes	84



(a) GRDEXrrOd-deNovo-meme1: width=15, sites=87, llr=905, E=3.8e-29
(b) GRDEXrrOd-deNovo-meme2: width=15, sites=44, llr=492, E=19000
(c) GRDEXrrOd-deNovo-meme3: width=15, sites=8, llr=128, E=5.4e+07

Figure 170: De novo motifs for the filtered GR DEX overlaps (down) sequences.

Table 140: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	34.1366	0.1229	0.0036	36	2	80.81E-16	0.04547
Tal1::Gata1	3.2653	0.0465	0.0142	13	8	1.47E-02	0.02716
NR3C1	2.5000	0.4219	0.1687	93	84	80.61E-12	0.61525
GRMotifTH	2.4354	0.3721	0.1528	76	74	17.69E-08	0.65658
Foxa2	2.4020	0.4651	0.1936	113	92	4.08E-16	0.33052
ARMotifTH	2.3349	0.0498	0.0213	15	10	1.189E-02	0.03726
FOXA1	2.2917	0.5781	0.2522	123	118	52.19E-16	0.45241
ARMotifT	1.9133	0.5914	0.3091	129	138	5.174E-14	0.48504
Stat3	1.8310	0.1561	0.0853	37	37	24.45E-04	0.15128
Esrrb	1.7361	0.0864	0.0497	26	27	2.293E-02	0.06098
ARMotifHH	1.6624	0.3455	0.2078	83	96	2.462E-06	0.31341
GRMotifT	1.6148	2.1196	1.3126	250	374	2.131E-38	2.67254
MAX	1.5627	0.2027	0.1297	46	58	1.036E-02	0.20535
RORA_1	1.4728	0.2093	0.1421	58	71	11.88E-04	0.17999
ARMotifH	1.4379	6.9136	4.8082	298	538	35.93E-56	17.06199
Gata1	1.4172	0.5714	0.4032	124	177	3.82E-08	0.54083
FOXD1	1.4134	0.7708	0.5453	149	223	80.91E-12	0.77259
FOXF2	1.3853	0.1329	0.0959	38	49	3.45E-02	0.11561
NFIC	1.3788	2.0033	1.4529	252	387	2.886E-38	2.50743
ELK1	1.3387	0.7110	0.5311	149	216	19.34E-12	0.67950
Hand1::Tcfe2a	1.3126	0.9302	0.7087	171	265	6.345E-14	1.28782
USF1	1.3102	0.4585	0.3499	72	121	2.91E-02	0.65250
Foxq1	1.2874	0.3522	0.2735	86	128	5.542E-04	0.33576
EBF1	1.2744	0.4618	0.3623	97	154	3.837E-04	0.52008
GRMotifH	1.2689	4.6811	3.6892	284	528	4.389E-46	10.43216
Myb	1.2629	0.6146	0.4867	120	202	22.86E-06	1.04653
NR4A2	1.2554	1.4850	1.1829	210	346	21.09E-22	2.46957
FOXO3	1.2539	1.3987	1.1155	205	344	14.99E-20	1.72583
FEV	1.2418	0.5316	0.4281	119	188	4.204E-06	0.52478
Sox17	1.2286	1.0365	0.8437	181	300	2.369E-14	1.12878
AP1	1.2156	2.4485	2.0142	255	449	1.517E-34	4.29818
Pdx1	0.8278	1.6777	2.0266	199	421	2.189E-12	4.30384
Foxd3	0.7680	1.3123	1.7087	168	326	85.01E-10	6.91737
FOXL1	0.7507	4.2990	5.7265	261	498	3.267E-34	36.76782
Prrx2	0.7507	1.4053	1.8721	178	404	18.76E-08	3.69882

15.52 GR DEX overlaps (stable)

Chromosome specific statistics are shown in Table 141. A histogram of sequence lengths is shown in Figure 171.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	1039	2	311	1031	323262	0.001297
10	389	20	287	949	111698	0.000824
11	449	16	291	804	130680	0.000968
12	350	4	286	989	100178	0.000748
13	188	27	318	1787	59704	0.000518
14	271	2	295	848	79998	0.000745
15	292	18	297	1107	86815	0.000847
16	282	15	288	1638	81350	9e-04
17	351	32	280	978	98139	0.001209
18	116	49	302	1991	35047	0.000449
19	162	64	261	832	42303	0.000715
2	612	14	284	773	173884	0.000715
20	247	21	266	1249	65740	0.001043
21	104	31	281	838	29182	0.000606
22	154	106	267	845	41046	8e-04
3	601	3	303	895	182316	0.000921
4	406	0	287	2287	116561	0.00061
5	538	16	295	882	158544	0.000876
6	464	7	287	1181	133243	0.000779
7	494	19	299	1103	147871	0.000929
8	420	1	297	931	124913	0.000853
9	319	31	276	1246	87893	0.000622
X	180	43	251	1178	45267	0.000292
Y	34	109	267	408	9083	0.000153
all 24	8462	0	291	2287	2464717	0.000796

Table 141: Chromosome specific distribution of the regions. The last line represents the overall statistics.

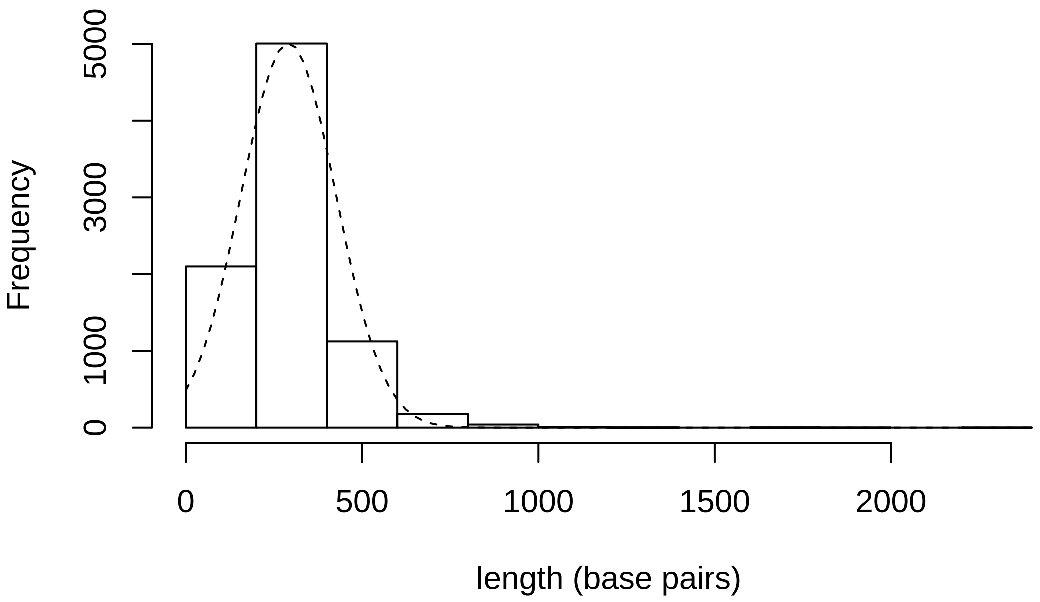
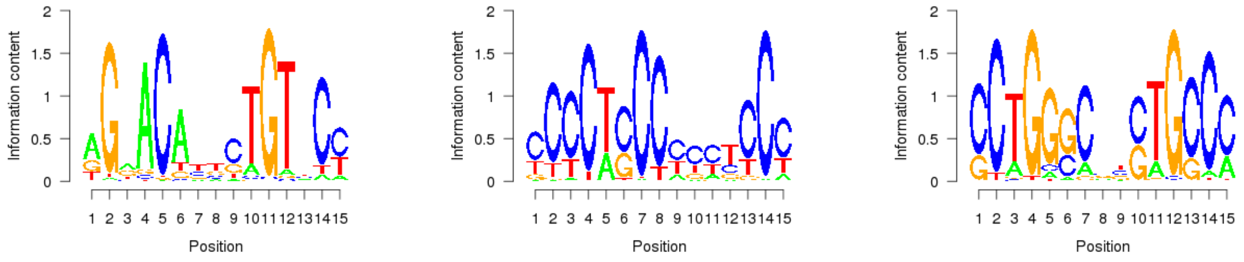


Figure 171: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRDEXrrOs-gCount** component.

property	value
genes	4452



(a) GRDEXrrOs-deNovo-meme1: width=15, sites=318, llr=3038, E=1e-194 (b) GRDEXrrOs-deNovo-meme2: width=15, sites=98, llr=1065, E=2.5e-12 (c) GRDEXrrOs-deNovo-meme3: width=15, sites=43, llr=528, E=45000

Figure 172: De novo motifs for the filtered GR DEX overlaps (stable) sequences.

Table 142: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	24.9888	0.1407	0.0056	1045	84	0.00E00	0.07521
TLX1::NFIC	3.7521	0.0175	0.0046	121	59	10.61E-20	0.01251
ARMotifTH	2.9487	0.0781	0.0264	584	408	8.258E-62	0.05694
ESR2	2.6671	0.0211	0.0079	153	118	6.864E-14	0.01504
FOXA1	2.4718	0.6011	0.2432	3660	3215	0.00E00	0.43913
GRMotifTH	2.4011	0.3540	0.1474	2365	2114	1.414E-232	0.30104
ARMotifT	2.3919	0.6366	0.2661	3814	3492	0.00E00	0.49753
NR3C1	2.3428	0.3812	0.1627	2554	2303	29.25E-258	0.28259
ARMotifTT	2.3423	0.0114	0.0048	94	75	1.867E-08	0.00730
Foxa2	2.3404	0.5331	0.2277	3315	2734	0.00E00	0.47837
GRMotifTT	2.3246	0.0315	0.0135	255	210	3.138E-20	0.02137
FOXF2	2.1127	0.1795	0.0849	1348	1246	12.27E-102	0.12730
RXRA::VDR	2.0383	0.0078	0.0038	55	60	45.37E-04	0.00980
ARMotifHH	2.0015	0.4116	0.2056	2578	2664	1.719E-208	0.72766
AR	1.9885	0.0565	0.0284	459	436	14.28E-28	0.03958
Tal1::Gata1	1.8870	0.0374	0.0198	311	303	18.61E-18	0.02641
GABPA	1.8741	0.0667	0.0356	530	540	26.5E-28	0.04991
PPARG::RXRA	1.7804	0.0182	0.0102	147	160	1.333E-06	0.01366
CTCF	1.7441	0.0057	0.0032	48	50	45.07E-04	0.00415
GR	1.7382	0.2609	0.1501	1848	2110	98.65E-102	0.29613
GRMotifT	1.7207	2.0996	1.2202	7110	10510	0.00E00	2.75291
FOXD1	1.6728	0.8326	0.4977	4397	5686	0.00E00	0.79931
Stat3	1.6438	0.1635	0.0994	1072	1262	85.31E-44	0.16444
GRMotifHH	1.6427	0.2185	0.1330	1507	1822	5.877E-64	0.20982
ELK4	1.5384	0.0196	0.0127	158	197	1.006E-04	0.01591
ARMotifH	1.5343	7.1101	4.6341	8356	15038	0.00E00	17.18444
RXR::RAR_DR5	1.5042	0.0238	0.0158	197	246	11.81E-06	0.01881
STAT1	1.4933	0.0353	0.0236	237	313	19.95E-06	0.03730
Foxq1	1.4754	0.3837	0.2600	2473	3234	14.9E-118	0.39458
RORA_2	1.4728	0.0179	0.0121	148	191	5.36E-04	0.01417
Esrrb	1.4613	0.0891	0.0609	709	914	98.13E-20	0.07418
E2F1	1.4223	0.0096	0.0067	79	105	2.363E-02	0.00791
GRMotifH	1.3536	4.7098	3.4794	8098	14451	0.00E00	8.44631
Tcfcp2l1	1.3529	0.0525	0.0388	398	566	1.892E-06	0.05136
MIZF	1.3528	0.0213	0.0157	175	244	20.65E-04	0.01810
Gata1	1.3337	0.5060	0.3794	3145	4700	22.33E-136	0.49669
TAL1::TCF3	1.3318	0.1843	0.1384	1187	1634	27.49E-30	0.21777
Evi1	1.3230	0.0306	0.0231	233	356	86.15E-04	0.03162
NFIC	1.3148	1.9585	1.4896	6691	10957	0.00E00	3.30935
Arnt	1.3129	0.1386	0.1056	791	1133	6.499E-14	0.20523
NHLH1	1.2992	0.0926	0.0713	500	745	1.665E-06	0.13364
NR2F1	1.2744	0.0875	0.0687	683	1028	59.04E-10	0.08050
TEAD1	1.2630	0.0608	0.0481	493	738	3.027E-06	0.05335
FEV	1.2613	0.4733	0.3753	3065	4670	38.05E-122	0.46923
Myc	1.2453	0.1048	0.0842	692	1034	18.13E-10	0.13950
FOXI1	1.2443	0.6316	0.5076	3426	5175	3.245E-160	0.90266
FOXA1pAR	1.2441	0.0626	0.0503	477	707	2.379E-06	0.06663
Mycn	1.2370	0.0836	0.0676	535	801	76.26E-08	0.11169
Hand1::Tcfe2a	1.2358	0.8886	0.7190	4679	7603	2.016E-298	1.05793
MYC::MAX	1.2318	0.0467	0.0379	316	479	9.669E-04	0.05666
FOXO3	1.2215	1.2387	1.0141	5466	9007	0.00E00	1.63736
ELK1	1.2163	0.6291	0.5173	3691	6017	2.805E-158	0.73082
NR4A2	1.2035	1.3501	1.1218	5932	9748	0.00E00	1.76921
CREB1	0.8073	0.4631	0.5737	2938	6063	98.37E-34	0.72954
MZF1_5-13	0.8067	0.7801	0.9670	4092	8804	80.06E-94	1.79175
Pdx1	0.7780	1.4376	1.8478	5444	11339	2.918E-288	3.56660
MEF2A	0.7655	0.1735	0.2267	1111	2660	49.3E-04	0.31199
FOXL1	0.7636	4.0939	5.3617	7015	13599	0.00E00	37.05582
NF-kappaB	0.7632	0.1137	0.1490	697	1839	2.337E-08	0.23079
NFKB1	0.7340	0.0336	0.0458	223	534	64.53E-04	0.06524
Prrx2	0.7137	1.2549	1.7583	5019	11130	1.982E-184	3.13558
IRF1	0.7103	0.1248	0.1757	945	2277	8.986E-04	0.20436
Lhx3	0.7014	0.1620	0.2309	1037	2443	1.023E-02	0.37439
Zfx	0.6960	0.0829	0.1192	565	1591	16.09E-12	0.15587
PBX1	0.6822	0.0523	0.0767	418	1057	21.29E-06	0.10307
Foxd3	0.6757	1.1961	1.7703	4437	8973	12.49E-152	7.48302
PLAG1	0.6233	0.0079	0.0127	65	184	54.84E-04	0.01276
RREB1	0.5982	0.0155	0.0259	97	272	9.898E-04	0.06969
Ddit3::Cebpa	0.4884	0.1392	0.2851	1054	3384	26.5E-28	0.30901
EWSR1-FLI1	0.0941	0.0025	0.0269	17	69	48.25E-04	0.21027

15.53 AR DHT vs GR DEX overlaps

Chromosome specific statistics are shown in Table 143. A histogram of sequence lengths is shown in Figure 173.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	367	15	369	862	135283	0.000543
10	155	20	320	886	49625	0.000366
11	169	25	346	1118	58421	0.000433
12	131	4	335	813	43909	0.000328
13	104	83	406	850	42195	0.000366
14	121	9	345	848	41760	0.000389
15	134	13	339	804	45370	0.000442
16	96	51	340	599	32628	0.000361
17	146	0	318	840	46370	0.000571
18	80	44	386	984	30848	0.000395
19	54	75	314	746	16953	0.000287
2	253	53	339	689	85819	0.000353
20	96	72	330	673	31719	0.000503
21	49	18	330	617	16182	0.000336
22	33	153	288	465	9503	0.000185
3	287	0	376	873	108049	0.000546
4	169	12	334	725	56521	0.000296
5	257	1	345	739	88673	0.00049
6	214	3	326	918	69776	0.000408
7	199	1	344	830	68420	0.00043
8	220	19	343	770	75416	0.000515
9	133	51	339	783	45093	0.000319
X	60	19	301	667	18063	0.000116
Y	1	248	248	248	248	4e-06
all 24	3528	0	345	1118	1216844	0.000393

Table 143: Chromosome specific distribution of the regions. The last line represents the overall statistics.

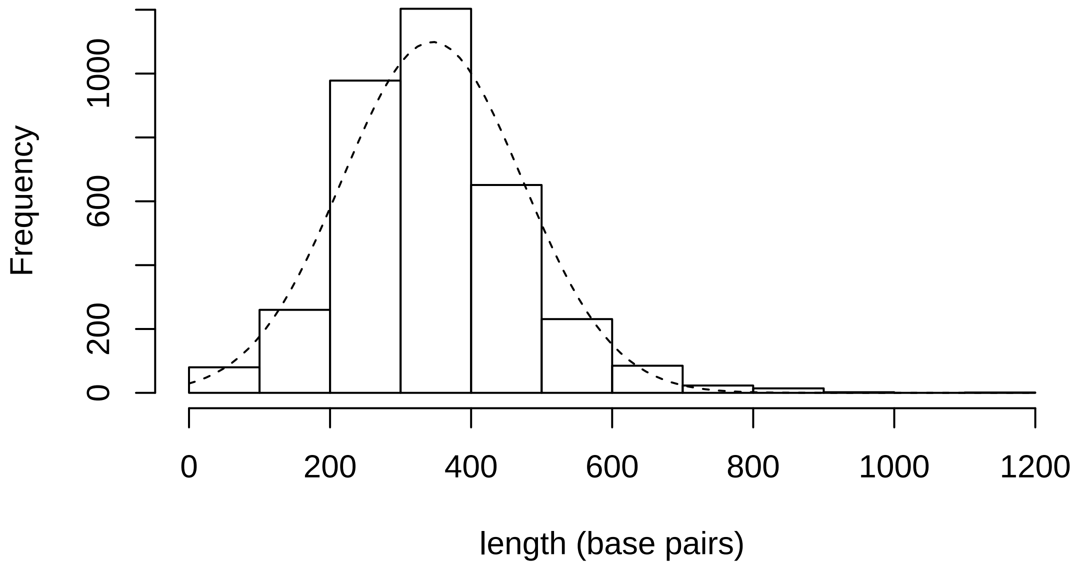
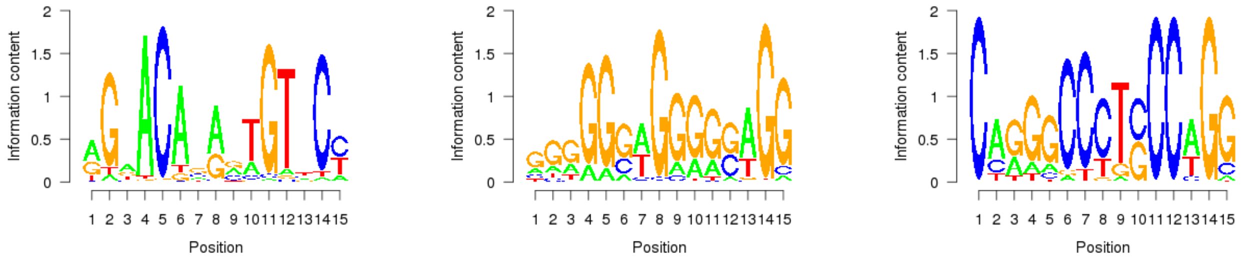


Figure 173: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrO-gCount** component.

property	value
genes	8350



(a) ARGRrrO-deNovo-meme1: width=15, sites=351, llr=3405, E=5.4e-281 (b) ARGRrrO-deNovo-meme2: width=15, sites=90, llr=1000, E=4e-17 (c) ARGRrrO-deNovo-meme3: width=15, sites=23, llr=322, E=3400

Figure 174: De novo motifs for the filtered AR DHT vs GR DEX overlaps sequences.

Table 144: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	24.5508	0.1574	0.0064	504	42	8.809E-186	0.06590
TLX1::NFIC	3.8413	0.0182	0.0047	52	24	12.11E-10	0.01305
FOXA1	2.9365	0.8653	0.2947	2035	1598	0.00E00	0.59682
Foxa2	2.6771	0.7491	0.2798	1843	1394	2.67E-322	0.61259
FOXF2	2.6570	0.2557	0.0962	786	589	16.19E-94	0.16326
Tal1::Gata1	2.2803	0.0557	0.0244	189	160	23.65E-16	0.03561
ARMotifTT	2.2591	0.0131	0.0058	46	37	1.058E-04	0.00843
ARMotifT	2.2268	0.6872	0.3086	1693	1680	32.14E-206	0.51286
ESR2	2.1565	0.0236	0.0109	71	61	4.637E-06	0.02299
ARMotifTH	2.1376	0.0690	0.0323	235	210	23.71E-18	0.04540
FOXA1pAR	2.1372	0.1224	0.0573	403	334	9.576E-36	0.09074
GRMotifTH	2.0685	0.3554	0.1718	1017	1021	6.543E-86	0.26531
AR	2.0535	0.0616	0.0300	209	198	10.71E-14	0.04091
NR3C1	1.9633	0.3980	0.2027	1100	1154	5.57E-90	0.30749
RXRA::VDR	1.9313	0.0082	0.0042	29	28	1.483E-02	0.00560
Stat3	1.8856	0.2000	0.1060	536	568	29.7E-32	0.18905
FOXD1	1.8790	1.1273	0.5999	2288	2769	63.28E-296	0.98239
Foxq1	1.7832	0.5290	0.2966	1390	1548	60.17E-122	0.46445
GRMotifTT	1.7123	0.0273	0.0159	94	103	1.012E-04	0.02026
GRMotifT	1.5873	2.2628	1.4255	3047	4805	0.00E00	2.28467
GABPA	1.5828	0.0724	0.0458	249	286	2.336E-10	0.05715
Gata1	1.5643	0.6960	0.4449	1682	2250	3.996E-128	0.61499
ARMotifHH	1.5454	0.3662	0.2369	1034	1279	2.689E-58	0.33664
GR	1.4966	0.2707	0.1809	824	1024	19.26E-40	0.23335
Esrrb	1.4500	0.1057	0.0729	351	455	1.596E-10	0.08726
STAT1	1.4449	0.0392	0.0271	107	146	80.47E-04	0.04378
GRMotifHH	1.4434	0.2185	0.1513	648	852	40.98E-24	0.20446
FOXI1	1.4238	0.8386	0.5890	1819	2478	10.44E-148	1.03630
ARMotifH	1.4172	7.6872	5.4240	3474	6399	0.00E00	13.80788
PPARG::RXRA	1.3956	0.0207	0.0148	69	95	4.697E-02	0.01819
RXR::RAR_DR5	1.3942	0.0264	0.0189	92	125	1.432E-02	0.02128
NHLH1	1.3858	0.1111	0.0801	244	339	19.8E-06	0.16012
Evi1	1.3613	0.0369	0.0271	125	177	88.08E-04	0.03118
NFIC	1.3505	2.3591	1.7469	2976	4966	0.00E00	3.04710
GRMotifH	1.2824	5.3062	4.1377	3420	6269	0.00E00	8.18701
TAL1::TCF3	1.2637	0.2108	0.1668	530	807	6.621E-10	0.27089
FEV	1.2461	0.5531	0.4439	1444	2263	1.668E-64	0.53685
FOXO3	1.2452	1.5267	1.2260	2599	4169	34.96E-288	1.88694
Hand1::Tcfe2a	1.2432	1.0426	0.8387	2169	3574	9.768E-166	1.06327
Arnt	1.2397	0.1474	0.1189	371	536	16.54E-08	0.19960
Myb	1.2372	0.6770	0.5472	1670	2678	30.11E-88	0.66067
NR2F1	1.2233	0.0997	0.0815	327	508	1.292E-04	0.09120
Pax5	1.2103	0.0435	0.0359	147	228	3.536E-02	0.04199
TEAD1	1.2035	0.0662	0.0550	223	353	86.78E-04	0.05958
YY1	0.8227	2.7043	3.2869	3152	6062	0.00E00	5.53173
Pdx1	0.7997	1.8295	2.2877	2578	5155	26.27E-206	4.42394
SP1	0.7918	0.7878	0.9950	1242	2700	8.586E-12	3.96303
MZF1_5-13	0.7850	0.8841	1.1262	1926	4047	10.97E-68	1.52620
NF-kappaB	0.7766	0.1369	0.1763	371	921	1.033E-02	0.22967
CREB1	0.7752	0.5179	0.6681	1343	2943	32.18E-16	0.76723
FOXL1	0.7609	4.9173	6.4628	3183	5911	0.00E00	44.54561
Foxd3	0.7590	1.5676	2.0653	2285	4207	34.0E-160	8.06951
Prrx2	0.7548	1.6122	2.1360	2442	5035	5.16E-162	3.87307
Zfx	0.6394	0.0852	0.1333	258	757	83.04E-08	0.14214
Ddit3::Cebpa	0.5111	0.1642	0.3213	515	1586	10.34E-10	0.34597

15.54 AR DHT vs GR DEX overlaps (up)

Chromosome specific statistics are shown in Table 145. A histogram of sequence lengths is shown in Figure 175.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	98	15	399	862	39056	0.000157
10	24	141	336	579	8065	6e-05
11	34	63	364	779	12388	9.2e-05
12	21	70	360	813	7570	5.7e-05
13	13	131	368	579	4779	4.1e-05
14	23	204	396	626	9111	8.5e-05
15	24	132	380	672	9123	8.9e-05
16	18	251	398	599	7168	7.9e-05
17	30	135	366	771	10973	0.000135
18	19	229	453	860	8615	0.00011
19	14	148	386	624	5402	9.1e-05
2	52	82	366	689	19010	7.8e-05
20	24	72	338	571	8107	0.000129
21	7	18	326	457	2284	4.7e-05
22	6	153	264	415	1585	3.1e-05
3	48	1	368	664	17642	8.9e-05
4	44	74	367	725	16139	8.4e-05
5	65	87	361	739	23446	0.00013
6	54	15	339	597	18317	0.000107
7	32	207	385	830	12313	7.7e-05
8	27	22	349	770	9415	6.4e-05
9	26	51	381	783	9903	7e-05
X	9	126	321	667	2886	1.9e-05
all 23	712	1	370	862	263297	8.5e-05

Table 145: Chromosome specific distribution of the regions. The last line represents the overall statistics.

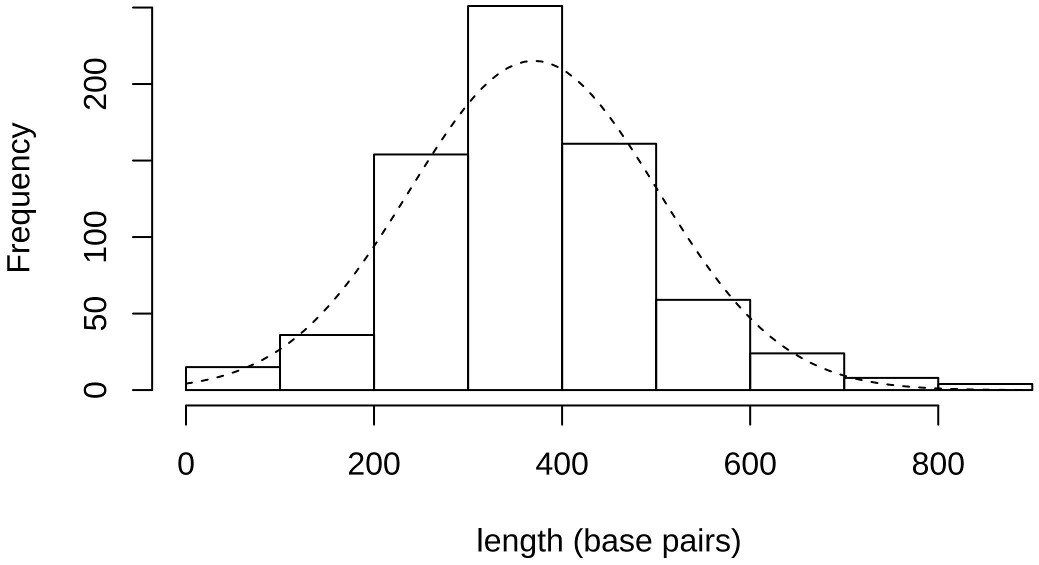
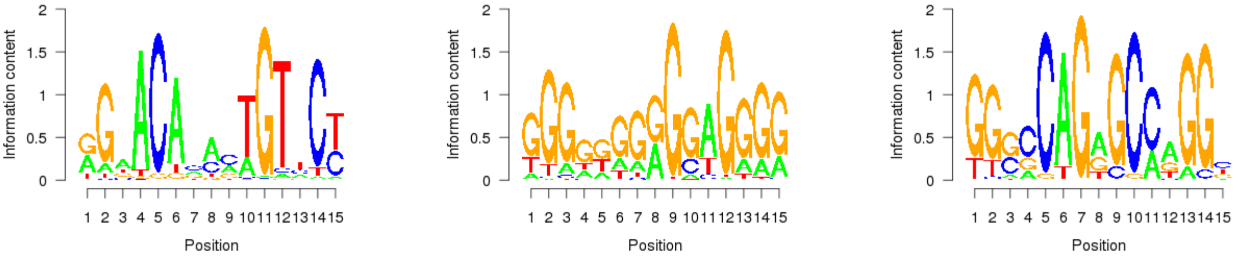


Figure 175: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrOu-gCount** component.

property	value
genes	389



(a) ARGRrrOu-deNovo-meme1: width=15, sites=281, llr=2755, E=1.3e-178 (b) ARGRrrOu-deNovo-meme2: width=15, sites=85, llr=972, E=2.3e-24 (c) ARGRrrOu-deNovo-meme3: width=15, sites=30, llr=390, E=1300

Figure 176: De novo motifs for the filtered AR DHT vs GR DEX overlaps (up) sequences.

Table 146: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	16.7521	0.1871	0.0111	117	15	14.16E-42	0.08420
CTCF	10.7278	0.0084	0.0007	6	1	1.40E-02	0.00339
ESR2	5.0293	0.0338	0.0067	22	8	14.83E-06	0.01868
TLX1::NFIC	3.2311	0.0169	0.0052	10	5	1.805E-02	0.01303
FOXA1	2.6978	0.8340	0.3091	396	328	1.015E-68	0.61040
Foxa2	2.5005	0.7286	0.2913	358	292	88.97E-60	0.65766
FOXF2	2.2701	0.2138	0.0941	128	118	9.542E-12	0.15698
ARMotifT	2.0682	0.7145	0.3454	355	371	12.77E-44	0.55438
NR3C1	2.0522	0.4838	0.2357	265	272	49.22E-28	0.35807
GABPA	1.9232	0.1013	0.0526	67	68	54.88E-06	0.07337
FOXA1pAR	1.8965	0.1041	0.0549	72	67	3.221E-06	0.08517
GRMotifTH	1.7993	0.3882	0.2157	220	249	39.91E-18	0.34431
Tcfcp2l1	1.7435	0.0802	0.0460	49	58	82.15E-04	0.06806
Stat3	1.7320	0.2068	0.1193	116	135	95.28E-08	0.19619
FOXD1	1.7101	1.0408	0.6086	437	574	24.49E-50	0.95586
ARMotifTH	1.7068	0.0759	0.0445	54	55	4.487E-04	0.06007
GRMotifT	1.5954	2.4824	1.5560	636	1002	2.922E-106	2.56638
Esrrb	1.5686	0.1210	0.0771	84	99	1.334E-04	0.09057
ARMotifHH	1.5473	0.4416	0.2854	239	299	3.229E-16	0.42536
Mycn	1.5309	0.1294	0.0845	69	84	15.51E-04	0.15707
Myc	1.5231	0.1547	0.1016	83	103	4.877E-04	0.18426
AR	1.4973	0.0633	0.0423	45	56	2.259E-02	0.04806
ARMotifH	1.4828	8.7229	5.8829	704	1302	9.947E-128	15.73259
NR2F1	1.4702	0.1308	0.0890	86	110	6.849E-04	0.11121
Arnt	1.4669	0.1871	0.1275	94	113	59.83E-06	0.25344
Myf	1.4648	0.2335	0.1594	124	169	53.4E-06	0.28875
Tal1::Gata1	1.4619	0.0520	0.0356	37	46	4.465E-02	0.04152
NFIC	1.4469	2.6568	1.8362	610	1048	1.916E-86	3.21740
Foxq1	1.4373	0.4923	0.3425	267	358	33.46E-18	0.48564
GRMotifHH	1.4269	0.2475	0.1735	146	196	1.88E-06	0.23720
GR	1.4193	0.2799	0.1972	173	227	1.031E-08	0.24383
NHLH1	1.4047	0.1364	0.0971	61	87	3.757E-02	0.18687
EBF1	1.3909	0.6259	0.4500	290	426	1.009E-16	0.75219
TAL1::TCF3	1.3774	0.2236	0.1623	117	165	3.11E-04	0.25092
NFE2L2	1.3659	0.1266	0.0927	83	120	1.043E-02	0.10615
Gata1	1.3618	0.6653	0.4885	335	495	1.69E-22	0.61969
Myb	1.3384	0.7679	0.5738	361	552	55.14E-26	0.76745
GRMotifH	1.2802	5.7707	4.5078	693	1299	5.911E-120	8.93223
Hand1::Tcfe2a	1.2707	1.1181	0.8799	455	757	97.06E-40	1.12241
TFAP2A	1.2339	1.6428	1.3314	450	711	96.92E-42	5.48484
MAX	1.2259	0.1772	0.1446	105	160	58.9E-04	0.19960
FEV	1.2138	0.6020	0.4959	311	503	10.09E-16	0.58709
SPI1	1.2073	1.7004	1.4085	558	966	14.56E-66	1.98972
NR4A2	1.2014	1.7482	1.4552	551	951	22.13E-64	2.02937
MZF1_5-13	0.8282	1.0253	1.2380	433	874	10.59E-24	1.60428
HOXA5	0.8268	4.7525	5.7480	672	1293	6.504E-106	13.28323
ARID3A	0.8220	2.7018	3.2869	585	1130	98.01E-68	7.88836
YY1	0.8091	2.8875	3.5686	643	1266	20.35E-90	5.79305
Nkx2-5	0.8077	4.4880	5.5567	642	1256	16.76E-90	16.00694
Pdx1	0.7693	1.8214	2.3677	516	1081	20.89E-40	4.37926
CREB1	0.7473	0.5584	0.7472	292	662	1.092E-04	0.83863
Prrx2	0.6904	1.5696	2.2735	492	1046	1.043E-32	4.01023
Foxd3	0.6488	1.4487	2.2328	444	876	77.85E-28	8.51241
FOXL1	0.6343	4.5359	7.1505	633	1241	34.24E-86	89.18904
Ddit3::Cebpa	0.4617	0.1660	0.3595	105	358	5.087E-04	0.38003

15.55 AR DHT vs GR DEX overlaps (down)

Chromosome specific statistics are shown in Table 147. A histogram of sequence lengths is shown in Figure 177.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	28	157	350	573	9801	3.9e-05
10	13	121	260	425	3377	2.5e-05
11	15	177	355	602	5323	3.9e-05
12	9	140	335	595	3015	2.3e-05
13	6	83	440	839	2640	2.3e-05
14	10	114	356	551	3557	3.3e-05
15	13	226	315	431	4089	4e-05
16	21	156	320	573	6729	7.4e-05
17	18	201	312	522	5622	6.9e-05
19	11	106	296	448	3258	5.5e-05
2	18	203	335	630	6032	2.5e-05
20	11	198	347	571	3814	6.1e-05
21	3	252	354	537	1061	2.2e-05
3	24	178	418	637	10025	5.1e-05
4	2	293	355	417	710	4e-06
5	11	246	353	432	3881	2.1e-05
6	5	206	343	472	1717	1e-05
7	14	64	288	460	4033	2.5e-05
8	18	31	306	507	5507	3.8e-05
9	5	106	288	396	1442	1e-05
X	1	235	235	235	235	2e-06
all 21	256	31	335	839	85868	2.8e-05

Table 147: Chromosome specific distribution of the regions. The last line represents the overall statistics.

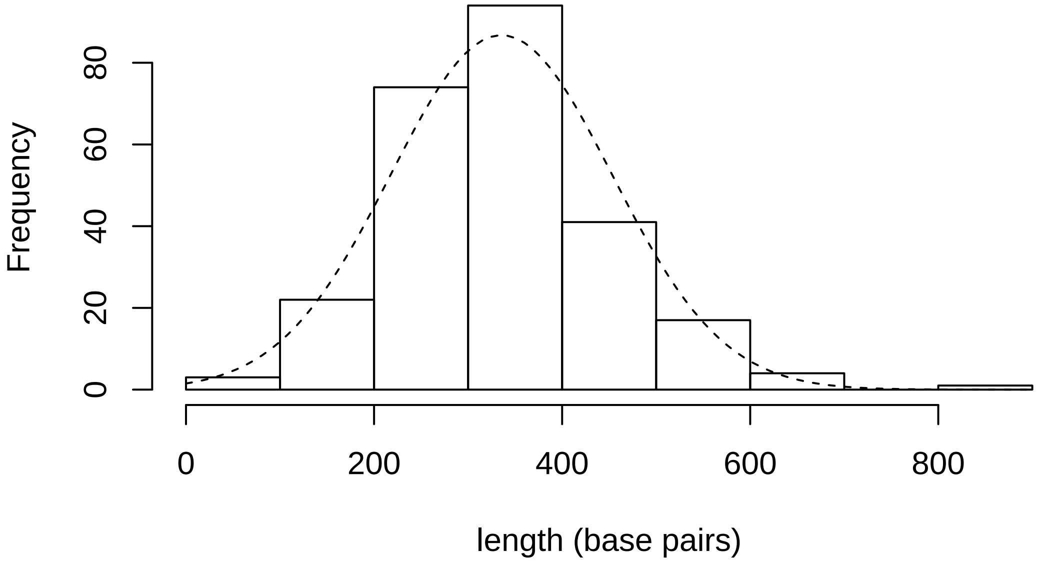
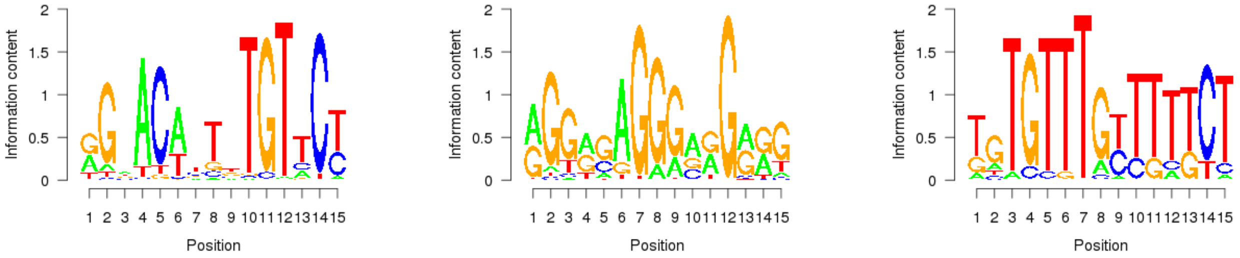


Figure 177: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrOd-gCount** component.

property	value
genes	173



(a) ARGRrrOd-deNovo-meme1: width=15, sites=87, llr=889, E=3.6e-26

(b) ARGRrrOd-deNovo-meme2: width=15, sites=61, llr=662, E=1.5e-09

(c) ARGRrrOd-deNovo-meme3: width=15, sites=20, llr=259, E=1.1e+07

Figure 178: De novo motifs for the filtered AR DHT vs GR DEX overlaps (down) sequences.

Table 148: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	66.9449	0.1445	0.0021	30	1	73.29E-14	0.06862
FOXA1pAR	4.3151	0.1367	0.0316	29	13	2.737E-06	0.09132
ARMotifTH	2.8575	0.0664	0.0232	17	11	56.79E-04	0.03694
FOXA1	2.7252	0.7188	0.2637	128	102	16.01E-22	0.50782
Foxa2	2.6421	0.5742	0.2173	113	82	18.56E-20	0.45869
GRMotifTH	2.2112	0.3359	0.1519	70	66	20.61E-08	0.23293
ARMotifT	2.0233	0.5977	0.2954	111	115	1.173E-12	0.47928
NR3C1	1.9063	0.4062	0.2131	81	88	27.16E-08	0.30375
GABPA	1.8506	0.0781	0.0422	20	20	4.509E-02	0.05186
FOXF2	1.6660	0.1406	0.0844	33	38	1.958E-02	0.10712
Stat3	1.6085	0.2070	0.1287	39	52	3.847E-02	0.19780
GR	1.5936	0.2656	0.1667	60	74	6.275E-04	0.19945
ARMotifHH	1.5133	0.3672	0.2426	71	96	4.464E-04	0.33630
GRMotifT	1.5082	2.0938	1.3882	218	342	30.08E-34	2.09201
EBF1	1.4915	0.6797	0.4557	111	144	47.69E-10	0.81707
Foxq1	1.4785	0.4336	0.2932	84	105	4.572E-06	0.45320
NFE2L2	1.4574	0.1445	0.0992	35	45	4.268E-02	0.11294
FOXI1	1.4409	0.7539	0.5232	126	166	31.82E-12	0.90616
NFIC	1.4378	2.4297	1.6899	220	358	58.18E-34	2.69290
FOXD1	1.4193	0.8594	0.6055	142	203	1.089E-12	0.81328
ARMotifH	1.3999	7.5430	5.3882	253	462	4.891E-46	13.08902
Gata1	1.3908	0.6250	0.4494	117	160	38.74E-10	0.59865
MAX	1.3885	0.1875	0.1350	37	49	4.495E-02	0.20688
Hand1::Tcfe2a	1.3149	1.0625	0.8080	157	246	6.039E-14	1.08271
NR4A2	1.2604	1.5742	1.2489	196	323	22.5E-24	1.60329
GRMotifH	1.2519	5.0156	4.0063	251	448	12.16E-46	6.69170
Myb	1.2390	0.6875	0.5549	120	192	32.44E-08	0.67627
FEV	1.2127	0.5117	0.4219	102	153	6.419E-06	0.49508
FOXO3	1.2044	1.3594	1.1287	176	290	21.18E-18	1.68578
YY1	0.8207	2.5781	3.1414	230	434	80.83E-34	5.41111
Pdx1	0.8173	1.5742	1.9262	161	350	1.673E-08	3.63182
MZF1_5-13	0.7935	0.9141	1.1519	142	300	4.037E-06	1.47130
Prrx2	0.7418	1.4336	1.9325	168	343	62.62E-12	3.41027
FOXL1	0.6930	4.0000	5.7722	228	419	1.013E-32	33.01704
Foxd3	0.6034	1.3125	2.1751	146	293	20.16E-08	10.09212
Ddit3::Cebpa	0.4055	0.1445	0.3565	35	129	1.113E-02	0.34001

15.56 AR DHT vs GR DEX overlaps (stable)

Chromosome specific statistics are shown in Table 149. A histogram of sequence lengths is shown in Figure 179.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	180	15	371	862	66775	0.000268
10	67	77	307	654	20539	0.000152
11	102	89	341	779	34766	0.000258
12	57	4	308	602	17576	0.000131
13	35	131	410	850	14346	0.000125
14	63	28	346	848	21779	0.000203
15	55	13	334	804	18389	0.000179
16	41	168	319	517	13080	0.000145
17	74	0	322	840	23851	0.000294
18	26	157	395	984	10266	0.000131
19	41	75	319	746	13065	0.000221
2	118	53	327	659	38571	0.000159
20	47	135	323	599	15184	0.000241
21	28	18	354	600	9907	0.000206
22	21	159	290	465	6088	0.000119
3	108	1	368	873	39738	0.000201
4	65	12	338	725	21955	0.000115
5	94	35	342	658	32108	0.000177
6	88	20	299	691	26278	0.000154
7	73	100	348	684	25436	0.00016
8	77	19	339	703	26104	0.000178
9	60	64	316	557	18963	0.000134
X	26	145	316	667	8225	5.3e-05
all 23	1546	0	338	984	522989	0.000169

Table 149: Chromosome specific distribution of the regions. The last line represents the overall statistics.

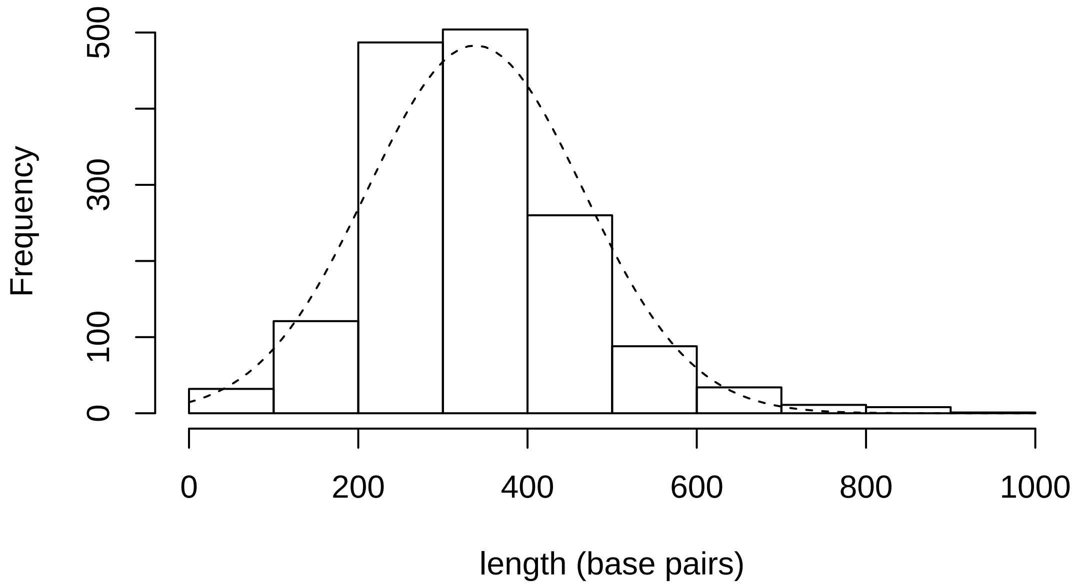
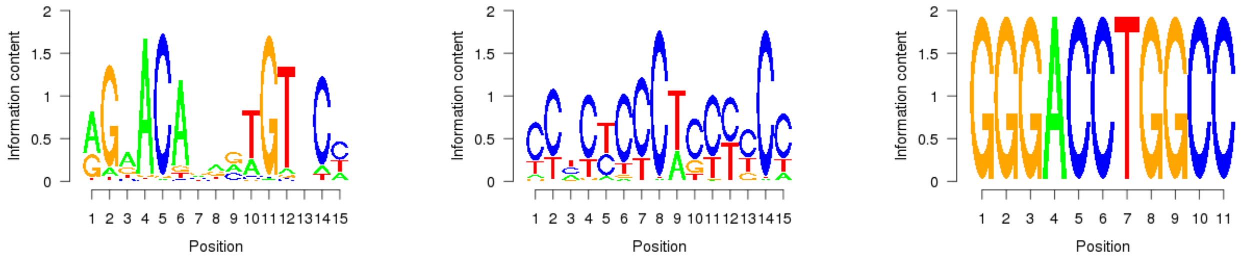


Figure 179: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrOs-gCount** component.

property	value
genes	1463



(a) ARGRrrOs-deNovo-meme1: width=15, sites=339, llr=3201, E=2.5e-233

(b) ARGRrrOs-deNovo-meme2: width=15, sites=93, llr=1011, E=2.3e-15

(c) ARGRrrOs-deNovo-meme3: width=11, sites=2, llr=32, E=6.8e+08

Figure 180: De novo motifs for the filtered AR DHT vs GR DEX overlaps (stable) sequences.

Table 150: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	16.6630	0.1562	0.0093	220	24	4.448E-78	0.06802
TLX1::NFIC	6.9916	0.0220	0.0031	28	6	1.383E-08	0.01365
FOXA1	3.1041	0.8633	0.2781	893	679	4.727E-168	0.57606
FOXF2	2.7471	0.2553	0.0929	347	258	1.039E-42	0.15595
Foxa2	2.7068	0.7285	0.2691	782	620	98.87E-130	0.58305
ESR2	2.3935	0.0207	0.0086	29	21	8.145E-04	0.01629
Tal1::Gata1	2.1782	0.0557	0.0256	82	72	63.71E-08	0.03746
ARMotifT	2.1294	0.6701	0.3147	725	743	13.95E-84	0.50903
FOXA1pAR	2.1188	0.1128	0.0532	158	139	32.67E-14	0.08649
GRMotifTH	2.0583	0.3584	0.1741	454	443	14.16E-42	0.27885
ARMotifTH	2.0505	0.0680	0.0332	103	95	7.304E-08	0.04460
NR3C1	1.9046	0.3889	0.2041	478	518	13.41E-38	0.30096
FOXD1	1.8110	1.0454	0.5772	965	1196	5.082E-116	0.90014
Stat3	1.7984	0.1957	0.1088	235	245	50.52E-16	0.18869
Foxq1	1.7499	0.4854	0.2774	557	663	64.22E-42	0.41678
GABPA	1.7177	0.0706	0.0411	109	115	2.388E-06	0.05055
ARMotifHH	1.7025	0.3752	0.2204	462	534	17.57E-32	0.31942
Esrrb	1.6840	0.1082	0.0642	158	181	11.96E-08	0.07954
Tcfcp2l1	1.6450	0.0648	0.0394	88	104	5.24E-04	0.05627
STAT1	1.5664	0.0428	0.0273	49	60	2.327E-02	0.04829
GRMotifT	1.5624	2.2333	1.4294	1337	2126	8.563E-204	2.24698
AR	1.5343	0.0525	0.0342	79	98	30.75E-04	0.04027
TEAD1	1.5159	0.0765	0.0504	114	142	2.081E-04	0.05957
Gata1	1.4804	0.6643	0.4487	714	973	14.17E-52	0.61461
GRMotifHH	1.4636	0.2139	0.1461	280	360	21.11E-12	0.20627
Evi1	1.4511	0.0421	0.0290	61	82	3.627E-02	0.03561
ARMotifH	1.4453	7.7589	5.3682	1527	2804	15.87E-274	13.34562
GR	1.4429	0.2677	0.1855	356	473	62.28E-16	0.22778
NHLH1	1.4193	0.1108	0.0781	102	148	1.67E-02	0.15675
FOXI1	1.3981	0.8056	0.5762	747	1090	4.505E-50	1.00419
NFIC	1.3538	2.3785	1.7568	1310	2208	68.99E-182	2.91746
Arnt	1.3448	0.1575	0.1171	174	229	8.196E-06	0.20908
EBF1	1.2765	0.5366	0.4204	554	861	4.074E-22	0.65330
NFYA	1.2762	0.0428	0.0335	66	89	2.892E-02	0.04170
GRMotifH	1.2601	5.1698	4.1026	1499	2754	52.93E-258	8.17634
NFE2L2	1.2507	0.1063	0.0850	153	237	74.81E-04	0.09378
FOXO3	1.2366	1.4900	1.2048	1113	1858	1.067E-112	1.80549
Myf	1.2360	0.1990	0.1610	237	371	1.181E-04	0.25070
Hand1::Tcfe2a	1.2173	1.0298	0.8459	945	1580	1.14E-70	1.06963
MZF1_5-13	0.8258	0.9145	1.1074	845	1774	88.87E-32	1.45499
CREB1	0.8091	0.5120	0.6328	592	1249	45.23E-10	0.69797
Pdx1	0.7932	1.7122	2.1585	1106	2213	1.27E-84	3.91412
YY1	0.7908	2.5859	3.2701	1363	2650	24.42E-178	5.29285
Foxd3	0.7497	1.5321	2.0435	972	1787	88.13E-66	8.82217
Prrx2	0.7311	1.4984	2.0494	1020	2151	1.76E-58	3.55720
Zfx	0.7151	0.0914	0.1278	117	315	1.425E-02	0.14428
FOXL1	0.7046	4.5742	6.4922	1371	2597	10.53E-186	62.12523
Ddit3::Cebpa	0.4848	0.1601	0.3302	224	679	1.34E-04	0.36261
RREB1	0.2612	0.0162	0.0622	19	66	2.644E-02	1.23767

15.57 AR DHT vs GR DEX unique for ARDHTrrO

Chromosome specific statistics are shown in Table 151. A histogram of sequence lengths is shown in Figure 181.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	223	12	422	832	94056	0.000377
10	72	192	394	636	28400	0.00021
11	110	214	418	800	46029	0.000341
12	91	3	386	933	35111	0.000262
13	44	197	422	1081	18584	0.000161
14	64	51	412	771	26392	0.000246
15	65	76	442	673	28717	0.00028
16	61	51	407	784	24797	0.000274
17	60	144	399	656	23912	0.000295
18	38	200	401	914	15241	0.000195
19	19	202	331	436	6287	0.000106
2	137	130	395	915	54056	0.000222
20	50	254	407	898	20337	0.000323
21	23	212	430	702	9883	0.000205
22	25	208	384	640	9591	0.000187
3	147	218	458	994	67324	0.00034
4	100	198	406	954	40579	0.000212
5	104	236	407	808	42343	0.000234
6	127	69	389	673	49415	0.000289
7	101	214	413	854	41722	0.000262
8	79	217	422	731	33344	0.000228
9	77	223	394	669	30310	0.000215
X	40	214	380	647	15208	9.8e-05
Y	3	199	285	345	856	1.4e-05
all 24	1860	3	410	1081	762494	0.000246

Table 151: Chromosome specific distribution of the regions. The last line represents the overall statistics.

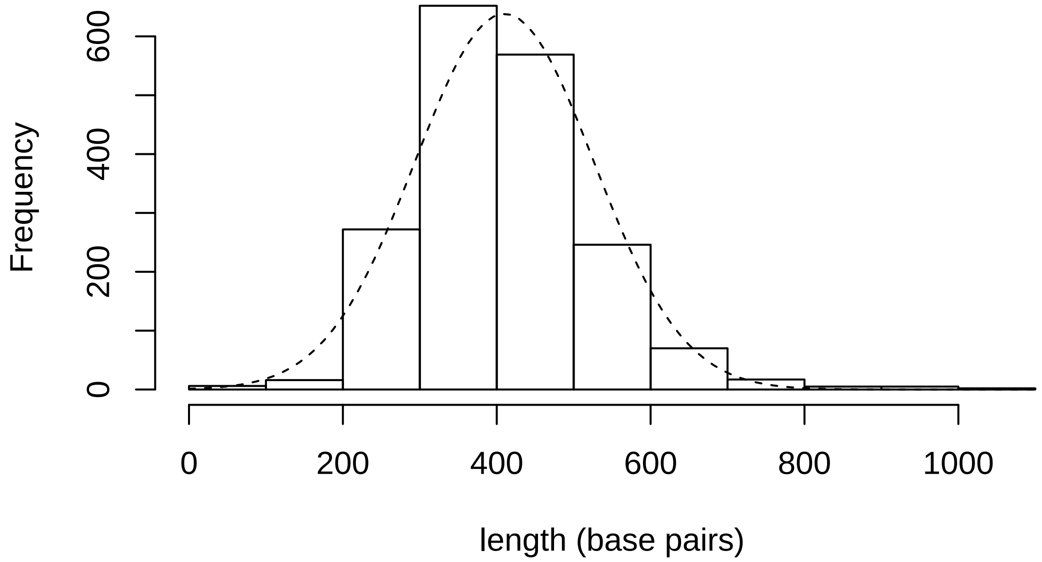
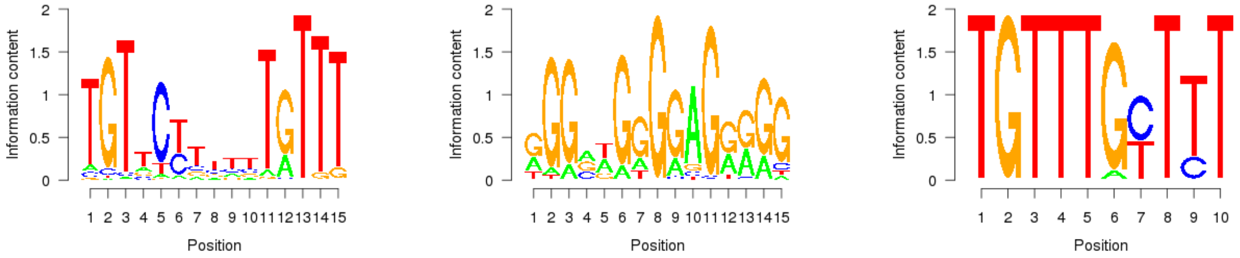


Figure 181: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU1-gCount** component.

property	value
genes	5694



(a) ARGRrrU1-deNovo-meme1: width=15, sites=204, llr=2116, E=7.8e-119

(b) ARGRrrU1-deNovo-meme2: width=15, sites=57, llr=684, E=1.9e-08

(c) ARGRrrU1-deNovo-meme3: width=10, sites=33, llr=397, E=4700

Figure 182: De novo motifs for the filtered AR DHT vs GR DEX unique for ARDHTrrO sequences.

Table 152: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
FOXA1pAR	4.8895	0.3141	0.0642	528	199	9.167E-126	0.16336
Ar	4.0038	0.0301	0.0075	54	25	5.256E-10	0.01627
FOXA1	3.0947	1.0382	0.3354	1261	959	11.17E-268	0.67276
CTCF	2.7640	0.0065	0.0023	12	8	3.286E-02	0.00374
Foxa2	2.7609	0.9016	0.3265	1153	838	6.206E-236	0.69164
FOXF2	2.7336	0.3244	0.1186	519	374	4.876E-70	0.20630
TLX1::NFIC	2.7297	0.0134	0.0049	20	12	18.38E-04	0.01157
ARMotifTT	1.9578	0.0108	0.0055	20	18	3.135E-02	0.00764
STAT1	1.8665	0.0468	0.0251	70	68	65.64E-06	0.04771
FOXD1	1.8427	1.3249	0.7190	1354	1643	2.745E-202	1.14764
Foxq1	1.7668	0.6477	0.3665	873	960	4.469E-90	0.56805
Tal1::Gata1	1.7632	0.0549	0.0311	97	105	33.71E-06	0.04084
GABPA	1.6940	0.0893	0.0527	150	170	46.72E-08	0.07431
ELK4	1.6242	0.0360	0.0222	59	68	52.19E-04	0.03604
Stat3	1.5844	0.2044	0.1290	291	353	1.016E-12	0.21223
FOXI1	1.4193	1.0172	0.7167	1116	1509	6.997E-112	1.22942
ARMotifT	1.4097	0.5062	0.3591	748	1010	1.913E-46	0.44085
AR	1.4006	0.0533	0.0380	95	131	1.164E-02	0.04333
ARMotifTH	1.3810	0.0565	0.0409	101	136	52.14E-04	0.04831
GRMotifTH	1.3077	0.2711	0.2073	430	635	98.77E-14	0.24067
Esrrb	1.2906	0.1022	0.0792	178	254	3.363E-04	0.09237
Gata1	1.2783	0.7122	0.5572	919	1398	17.95E-58	0.69538
GRMotifT	1.2340	2.0726	1.6795	1611	2724	8.739E-230	2.14868
ELK1	1.2247	0.8908	0.7273	1046	1716	57.65E-70	0.92177
SP1	0.8211	0.9715	1.1831	753	1598	3.014E-12	4.98467
CREB1	0.8187	0.6487	0.7924	836	1713	5.044E-20	0.96378
Pdx1	0.8113	2.1856	2.6939	1472	2899	2.448E-144	4.99447
Prrx2	0.7944	2.0151	2.5367	1445	2829	1.046E-136	4.56062
FOXL1	0.7724	5.8849	7.6185	1756	3221	76.19E-282	45.18138
Zfx	0.6733	0.1173	0.1742	189	477	3.694E-02	0.20784
NFYA	0.6198	0.0334	0.0538	58	168	1.02E-02	0.05391
Ddit3::Cebpa	0.5740	0.2238	0.3899	362	978	2.929E-02	0.42402

15.58 AR DHT vs GR DEX unique for ARDHTrrO (up)

Chromosome specific statistics are shown in Table 153. A histogram of sequence lengths is shown in Figure 183.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	31	220	445	789	13809	5.5e-05
10	7	221	339	391	2376	1.8e-05
11	9	303	403	694	3625	2.7e-05
12	7	347	417	477	2918	2.2e-05
13	7	262	339	464	2371	2.1e-05
14	7	232	374	480	2616	2.4e-05
15	6	254	376	505	2257	2.2e-05
16	7	304	376	484	2629	2.9e-05
17	14	266	416	519	5831	7.2e-05
18	1	444	444	444	444	6e-06
19	5	223	333	428	1667	2.8e-05
2	21	245	389	515	8166	3.4e-05
20	9	296	383	456	3449	5.5e-05
21	2	212	236	259	471	1e-05
22	3	208	319	390	957	1.9e-05
3	12	267	463	704	5561	2.8e-05
4	20	253	411	954	8221	4.3e-05
5	16	310	398	516	6365	3.5e-05
6	17	211	405	673	6881	4e-05
7	12	288	496	854	5957	3.7e-05
8	8	292	376	518	3007	2.1e-05
9	8	264	395	530	3157	2.2e-05
X	1	382	382	382	382	2e-06
all 23	230	208	405	954	93117	3e-05

Table 153: Chromosome specific distribution of the regions. The last line represents the overall statistics.

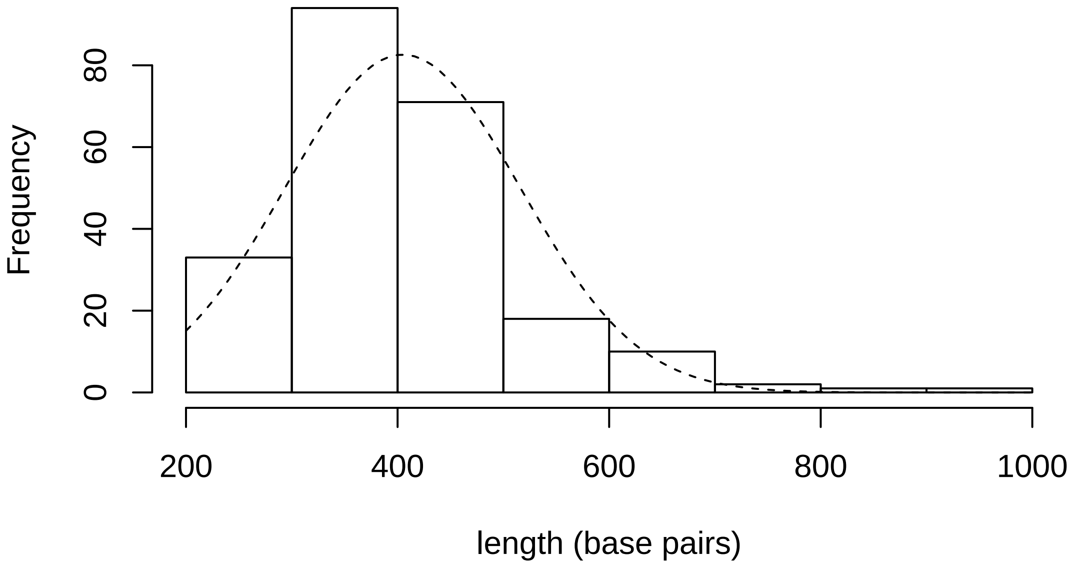
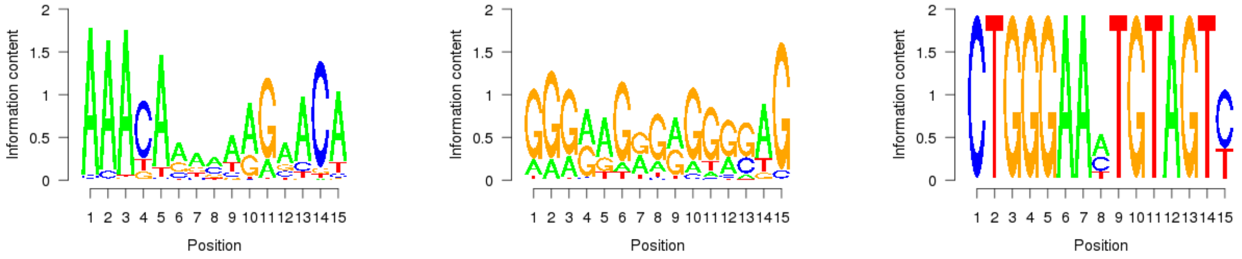


Figure 183: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU1u-gCount** component.

property	value
genes	198



(a) ARGRrrU1u-deNovo-meme1: width=15, sites=89, llr=915, E=5.9e-29

(b) ARGRrrU1u-deNovo-meme2: width=15, sites=66, llr=687, E=0.0015

(c) ARGRrrU1u-deNovo-meme3: width=15, sites=6, llr=115, E=2700

Figure 184: De novo motifs for the filtered AR DHT vs GR DEX unique for ARDHTrrO (up) sequences.

Table 154: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
FOXA1pAR	5.3246	0.2739	0.0514	63	20	19.05E-18	0.11875
FOXF2	3.0509	0.3565	0.1168	66	44	71.73E-12	0.23671
FOXA1	2.7135	0.9130	0.3364	145	116	82.89E-30	0.59597
Foxa2	2.4627	0.7826	0.3178	129	96	42.39E-26	0.71574
AR	2.1074	0.0739	0.0350	17	15	3.36E-02	0.04634
Stat3	1.7087	0.1957	0.1145	37	42	73.35E-04	0.17134
NR2F1	1.7009	0.1391	0.0818	31	33	1.043E-02	0.10073
FOXD1	1.6447	1.1913	0.7243	154	210	60.2E-20	1.04061
NHLH1	1.5085	0.1304	0.0864	22	22	2.923E-02	0.17987
FOXI1	1.4533	0.9304	0.6402	129	165	5.838E-14	1.26953
Foxq1	1.3985	0.5261	0.3762	91	118	41.96E-08	0.52533
GRMotifTH	1.3615	0.2609	0.1916	53	76	1.157E-02	0.20906
Hand1::Tcfe2a	1.2862	1.2261	0.9533	161	256	18.43E-18	1.08743
INSM1	1.2842	0.2130	0.1659	44	61	2.483E-02	0.19804
Gata1	1.2830	0.6565	0.5117	105	166	1.841E-06	0.65136
NFIC	1.2771	2.6826	2.1005	208	344	3.035E-34	3.47216
TFAP2A	1.2741	1.9826	1.5561	153	246	44.74E-16	5.80031
RUNX1	1.2610	0.3565	0.2827	68	101	19.87E-04	0.32629
ARMotifT	1.2483	0.4696	0.3762	85	132	1.831E-04	0.42470
GRMotifT	1.2038	2.0870	1.7336	200	349	56.17E-30	2.14699
ARID3A	0.8274	3.0565	3.6939	192	357	5.797E-24	9.83250
Pdx1	0.7682	1.9870	2.5864	169	342	1.831E-14	5.14236
Prrx2	0.7594	1.7957	2.3645	163	331	76.09E-14	4.61940
FOXL1	0.7351	5.5304	7.5234	212	397	1.433E-32	39.61377
Foxd3	0.6691	1.7478	2.6121	148	297	9.479E-10	10.96005

15.59 AR DHT vs GR DEX unique for ARDHTrrO (down)

Chromosome specific statistics are shown in Table 155. A histogram of sequence lengths is shown in Figure 185.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	16	263	475	774	7598	3e-05
10	9	250	415	566	3733	2.8e-05
11	7	382	503	800	3520	2.6e-05
12	8	281	356	514	2846	2.1e-05
13	2	495	586	677	1172	1e-05
14	4	232	359	513	1436	1.3e-05
15	5	335	484	565	2419	2.4e-05
16	11	269	387	560	4255	4.7e-05
17	11	312	424	628	4661	5.7e-05
19	2	295	362	428	723	1.2e-05
2	11	218	368	501	4045	1.7e-05
20	6	268	422	576	2534	4e-05
21	1	474	474	474	474	1e-05
22	2	243	298	353	596	1.2e-05
3	13	267	437	592	5678	2.9e-05
4	4	320	410	475	1641	9e-06
5	2	422	445	468	890	5e-06
6	11	196	388	579	4263	2.5e-05
7	11	287	352	408	3874	2.4e-05
8	4	418	506	589	2026	1.4e-05
9	9	270	373	502	3354	2.4e-05
X	1	283	283	283	283	2e-06
all 22	150	196	413	800	62021	2e-05

Table 155: Chromosome specific distribution of the regions. The last line represents the overall statistics.

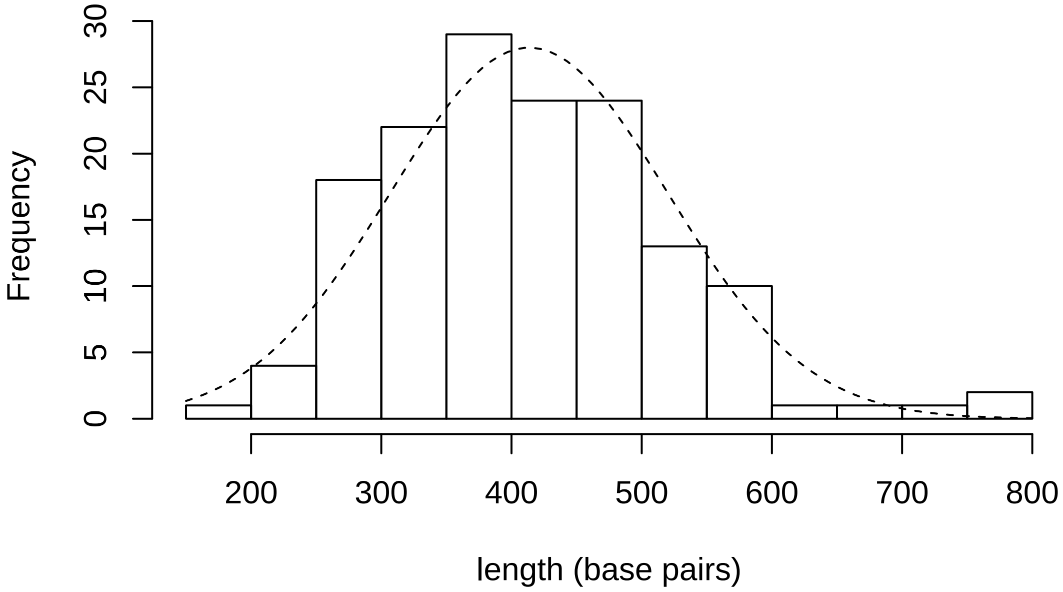
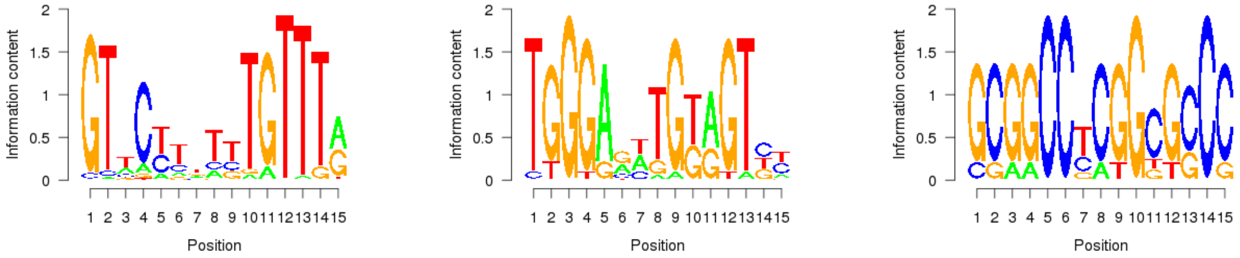


Figure 185: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU1d-gCount** component.

property	value
genes	131



(a) ARGRrrU1d-deNovo-meme1: width=15, sites=52, llr=571, E=1.4e-16

(b) ARGRrrU1d-deNovo-meme2: width=15, sites=20, llr=253, E=150000

(c) ARGRrrU1d-deNovo-meme3: width=15, sites=7, llr=113, E=1200000

Figure 186: De novo motifs for the filtered AR DHT vs GR DEX unique for ARDHTrrO (down) sequences.

Table 156: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
CTCF	667.6667	0.0333	0.0000	5	0	86.17E-04	0.01139
Evi1	9.3806	0.0333	0.0035	5	1	3.505E-02	0.01363
FOXA1pAR	3.4469	0.3267	0.0947	42	21	19.58E-10	0.23208
ELK4	3.4131	0.0600	0.0175	9	5	3.27E-02	0.03122
FOXF2	3.1248	0.3400	0.1088	44	28	3.234E-08	0.20402
GABPA	2.7850	0.1467	0.0526	22	15	8.471E-04	0.07800
FOXA1	2.6941	1.1533	0.4281	104	93	24.34E-22	0.91922
Foxa2	2.1090	0.8067	0.3825	86	81	1.90E-14	0.83500
Stat3	2.0834	0.2267	0.1088	24	26	2.08E-02	0.20573
FOXD1	1.8399	1.2267	0.6667	104	126	3.743E-16	1.17614
Myb	1.4548	0.8933	0.6140	90	127	6.172E-10	0.84217
Foxq1	1.4509	0.5600	0.3860	65	83	3.468E-06	0.50111
Myf	1.4332	0.2867	0.2000	33	41	1.243E-02	0.35717
ARMotifHH	1.3635	0.4067	0.2982	48	71	50.23E-04	0.36635
FOXI1	1.3612	0.9600	0.7053	88	110	46.56E-12	1.57922
ELK1	1.3585	0.9533	0.7018	88	142	7.817E-08	0.94134
BRCA1	1.3169	2.1533	1.6351	132	211	3.574E-22	2.47907
Nr2e3	1.3153	0.4800	0.3649	44	69	2.114E-02	0.62855
NFIC	1.2990	2.6800	2.0632	131	232	9.083E-20	3.24631
Gata1	1.2876	0.5467	0.4246	54	102	3.55E-02	0.53978
TFAP2A	1.2572	2.0733	1.6491	95	174	8.838E-08	6.63777
ARMotifH	1.2212	8.0600	6.6000	150	282	1.361E-28	12.02844
Gfi	0.8253	0.8600	1.0421	93	190	3.748E-06	0.94197
YY1	0.8145	3.3067	4.0596	140	275	4.118E-22	5.82396
ARID3A	0.8057	2.8667	3.5579	121	238	5.631E-14	9.06586
Pdx1	0.7586	2.1133	2.7860	105	236	16.07E-08	5.44120
Prrx2	0.7543	1.9533	2.5895	111	237	11.64E-10	4.36270
Sox5	0.7366	1.4267	1.9368	112	223	65.57E-12	2.56944
Foxd3	0.6927	1.6600	2.3965	101	192	1.166E-08	8.90130
FOXL1	0.6494	4.8533	7.4737	127	266	35.8E-16	61.27791

15.60 AR DHT vs GR DEX unique for ARDHTrrO (stable)

Chromosome specific statistics are shown in Table 157. A histogram of sequence lengths is shown in Figure 187.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	126	12	426	832	53712	0.000215
10	44	250	409	636	18001	0.000133
11	59	214	417	800	24603	0.000182
12	42	200	398	933	16732	0.000125
13	17	265	436	1081	7410	6.4e-05
14	37	238	404	757	14959	0.000139
15	30	238	446	673	13390	0.000131
16	35	259	414	784	14494	0.00016
17	32	228	409	656	13075	0.000161
18	16	258	389	632	6221	8e-05
19	12	202	334	428	4008	6.8e-05
2	72	130	368	567	26490	0.000109
20	22	255	377	530	8298	0.000132
21	15	212	377	486	5648	0.000117
22	24	208	381	640	9152	0.000178
3	73	218	451	704	32936	0.000166
4	51	198	415	689	21188	0.000111
5	45	236	406	589	18268	0.000101
6	54	180	394	591	21253	0.000124
7	47	214	392	590	18436	0.000116
8	29	217	414	663	12006	8.2e-05
9	45	234	383	596	17221	0.000122
X	12	218	371	647	4452	2.9e-05
Y	2	312	328	345	657	1.1e-05
all 24	941	12	407	1081	382610	0.000124

Table 157: Chromosome specific distribution of the regions. The last line represents the overall statistics.

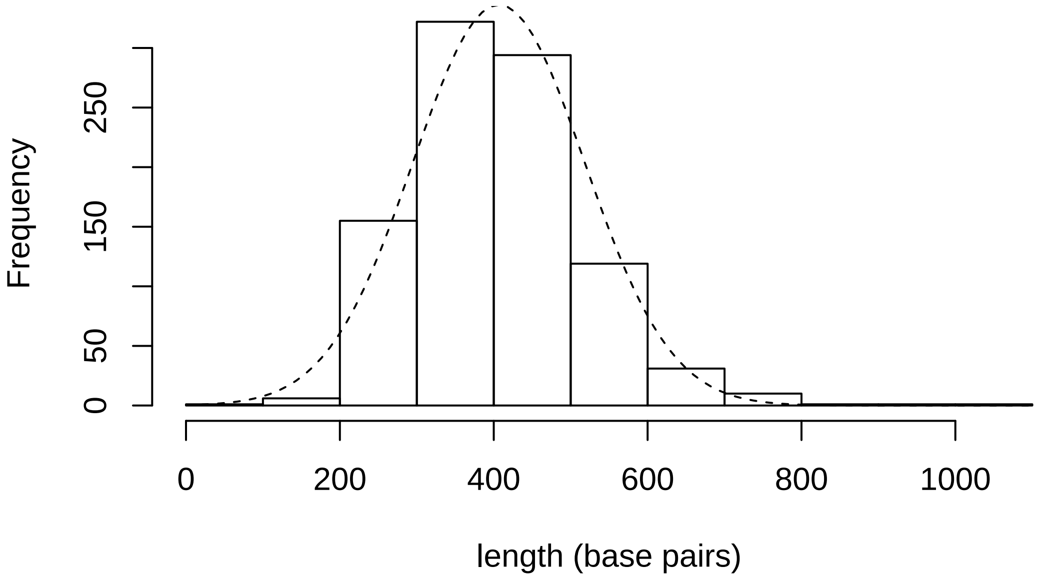
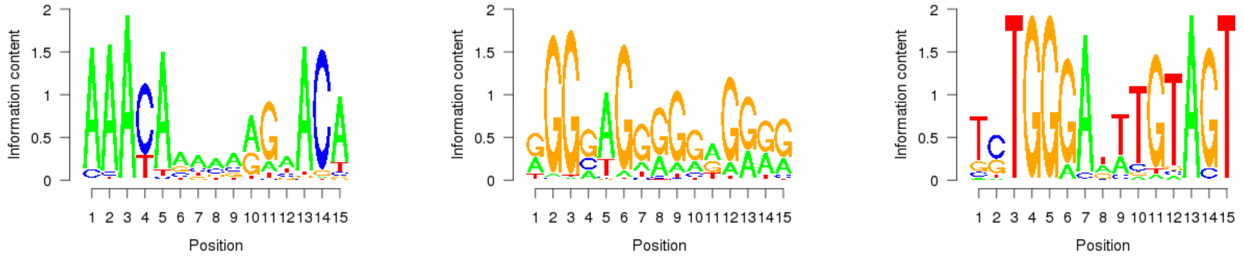


Figure 187: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU1s-gCount** component.

property	**value**
genes	1075



(a) ARGRrrU1s-deNovo-meme1: width=15, sites=196, llr=1983, E=3.3e-92 (b) ARGRrrU1s-deNovo-meme2: width=15, sites=87, llr=943, E=6.1e-08 (c) ARGRrrU1s-deNovo-meme3: width=15, sites=25, llr=362, E=8.3e-07

Figure 188: De novo motifs for the filtered AR DHT vs GR DEX unique for ARDHTrrO (stable) sequences.

Table 158: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	4.5020	0.0308	0.0068	28	12	4.959E-06	0.01568
FOXA1pAR	3.7049	0.2922	0.0788	251	115	1.683E-52	0.17337
FOXA1	3.0123	1.0287	0.3415	632	478	72.75E-136	0.68680
FOXF2	2.9703	0.3337	0.1123	264	178	19.85E-40	0.21497
Foxa2	2.5506	0.8725	0.3420	581	423	15.57E-120	0.80062
GABPA	2.2108	0.1041	0.0471	87	78	19.23E-08	0.07654
ELK4	1.9184	0.0436	0.0227	36	39	1.596E-02	0.03425
FOXD1	1.8750	1.2891	0.6875	674	815	5.565E-100	1.12106
ARMotifTH	1.7336	0.0531	0.0306	49	53	35.87E-04	0.03848
STAT1	1.7137	0.0574	0.0335	42	45	71.25E-04	0.06448
Foxq1	1.6956	0.6079	0.3585	425	499	31.37E-40	0.50681
Tal1::Gata1	1.5174	0.0499	0.0329	45	57	3.821E-02	0.03956
Stat3	1.5060	0.2179	0.1446	159	200	37.74E-08	0.22854
Egr1	1.4271	0.0850	0.0596	71	94	1.079E-02	0.08004
GRMotifTH	1.3887	0.2710	0.1951	221	306	80.37E-10	0.22875
ARMotifT	1.3226	0.4644	0.3511	359	497	74.77E-22	0.40681
Gata1	1.3047	0.6801	0.5213	434	687	18.51E-24	0.65636
NHLH1	1.2943	0.1211	0.0936	73	107	4.562E-02	0.17396
ELK1	1.2879	0.9256	0.7187	552	848	73.85E-46	0.95876
FEV	1.2826	0.6227	0.4855	431	655	33.27E-26	0.59305
Myb	1.2647	0.8013	0.6336	509	789	4.803E-36	0.76966
GRMotifT	1.2599	2.0967	1.6642	820	1388	20.09E-120	2.11845
FOXI1	1.2519	0.9267	0.7402	533	781	1.798E-44	1.33122
GR	1.2303	0.2561	0.2082	215	322	1.043E-06	0.23207
Arnt	1.2131	0.1796	0.1480	125	175	5.836E-04	0.24403
NFIC	1.2059	2.5855	2.1441	825	1456	82.36E-118	3.42484
SPI1	1.2034	1.8799	1.5621	785	1322	40.63E-106	2.27057
Pdx1	0.8119	2.0659	2.5445	725	1464	18.94E-66	4.64437
Prrx2	0.7861	1.9649	2.4997	712	1420	1.118E-62	4.48837
CREB1	0.7686	0.6387	0.8310	430	905	1.617E-10	0.95134
FOXL1	0.7274	5.5112	7.5763	875	1635	6.126E-134	51.11808
Foxd3	0.7072	1.8247	2.5803	646	1255	18.05E-48	9.46199

15.61 AR DHT vs GR DEX unique for GRDEXrrO

Chromosome specific statistics are shown in Table 159. A histogram of sequence lengths is shown in Figure 189.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	1293	1	289	1031	373102	0.001497
10	570	25	274	949	156157	0.001152
11	541	16	266	804	144012	0.001067
12	500	2	274	989	137111	0.001024
13	411	1	300	1787	123187	0.00107
14	421	2	279	1050	117313	0.001093
15	425	18	279	752	118451	0.001155
16	358	3	277	1638	99028	0.001096
17	459	47	263	670	120793	0.001488
18	279	3	287	1991	80132	0.001026
19	149	64	230	703	34299	0.00058
2	953	14	277	1946	263660	0.001084
20	314	21	258	1249	80960	0.001285
21	164	31	271	1440	44459	0.000924
22	179	5	251	845	44927	0.000876
3	928	2	298	920	276375	0.001396
4	597	0	259	2287	154460	0.000808
5	906	16	288	939	260548	0.00144
6	622	6	262	1818	163113	0.000953
7	720	0	278	1103	200008	0.001257
8	653	1	277	956	180870	0.001236
9	561	7	267	806	149975	0.001062
X	319	43	237	624	75495	0.000486
Y	49	109	252	408	12349	0.000208
all 24	12371	0	276	2287	3410784	0.001102

Table 159: Chromosome specific distribution of the regions. The last line represents the overall statistics.

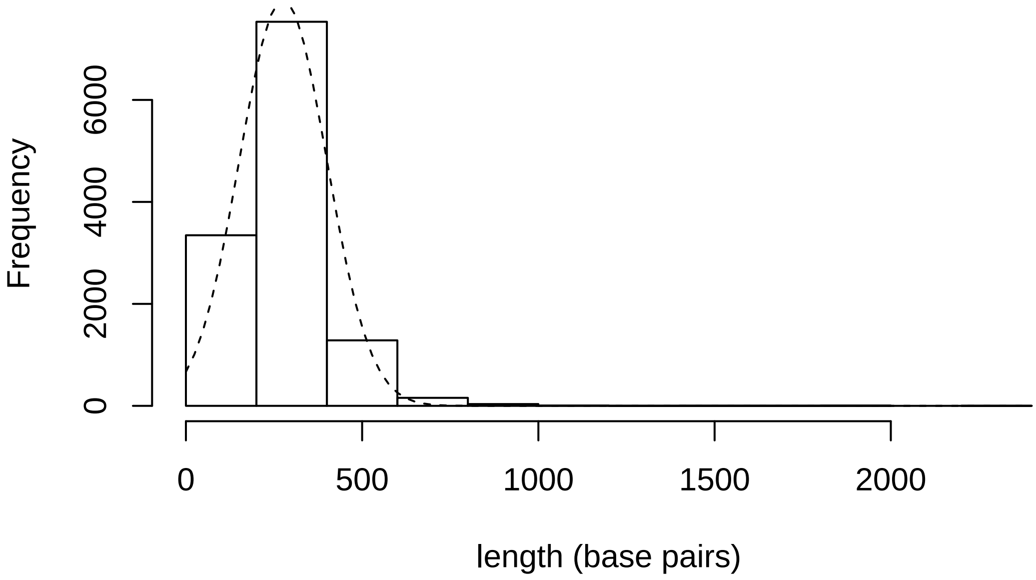
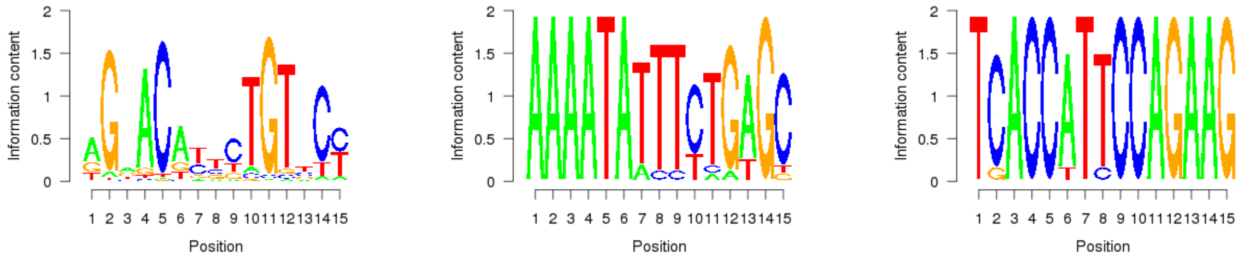


Figure 189: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU2-gCount** component.

property	value
genes	19247



(a) ARGRrrU2-deNovo-meme1: width=15, sites=293, llr=2726, E=2.9e-134

(b) ARGRrrU2-deNovo-meme2: width=15, sites=15, llr=260, E=5.1e-08

(c) ARGRrrU2-deNovo-meme3: width=15, sites=10, llr=198, E=5.8e-07

Figure 190: De novo motifs for the filtered AR DHT vs GR DEX unique for GRDEXrrO sequences.

Table 160: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	24.3663	0.1357	0.0055	1477	122	0.00E00	0.06878
ESR1	4.8663	0.0004	0.0000	5	1	3.953E-02	0.00017
TLX1::NFIC	3.8743	0.0153	0.0039	153	73	56.19E-26	0.01083
ARMotifTH	3.5578	0.0857	0.0240	885	542	67.15E-112	0.06931
ARMotifTT	2.7487	0.0129	0.0047	156	107	1.035E-16	0.00764
GRMotifTT	2.6906	0.0340	0.0126	404	287	4.978E-40	0.02133
ARMotifT	2.6433	0.6525	0.2468	5568	4803	0.00E00	0.62118
GRMotifTH	2.6263	0.3618	0.1377	3433	2903	0.00E00	0.34617
CTCF	2.5900	0.0047	0.0018	58	40	76.06E-08	0.00285
NR3C1	2.3830	0.3764	0.1579	3661	3256	0.00E00	0.29511
ESR2	2.3014	0.0180	0.0078	187	160	8.957E-14	0.01512
FOXA1	2.2941	0.5291	0.2306	4838	4512	0.00E00	0.39601
ARMotifHH	2.1549	0.4059	0.1883	3702	3663	8.983E-318	0.68892
Foxa2	2.1507	0.4709	0.2189	4322	3903	0.00E00	0.44962
AR	2.1227	0.0590	0.0278	689	625	73.19E-46	0.04139
RXRA::VDR	2.1184	0.0070	0.0033	75	75	1.372E-04	0.00770
FOXF2	2.0274	0.1656	0.0817	1839	1772	4.923E-124	0.11842
GR	1.8005	0.2625	0.1458	2745	2980	12.27E-168	0.26610
Tal1::Gata1	1.7999	0.0362	0.0201	441	452	35.97E-22	0.02630
GRMotifT	1.7860	2.0497	1.1477	10283	14908	0.00E00	2.70002
Stat3	1.7558	0.1514	0.0862	1430	1608	3.867E-62	0.14919
GRMotifHH	1.7093	0.2102	0.1230	2114	2484	6.541E-94	0.20285
STAT1	1.6552	0.0326	0.0197	311	371	12.5E-10	0.03376
GABPA	1.6359	0.0599	0.0366	686	790	3.329E-24	0.05096
FOXD1	1.6331	0.7760	0.4751	6163	8041	0.00E00	0.74323
MIZF	1.6092	0.0224	0.0139	245	316	6.976E-06	0.03160
ARMotifH	1.5770	6.8601	4.3501	12194	21839	0.00E00	16.54519
PPARG::RXRA	1.5475	0.0141	0.0091	171	207	20.56E-06	0.01106
Foxq1	1.5233	0.3690	0.2422	3476	4503	2.48E-162	0.36487
Esrrb	1.5100	0.0810	0.0536	937	1182	20.62E-26	0.06802
Tcfcp2l1	1.4833	0.0486	0.0327	541	688	29.19E-14	0.04632
RORA_2	1.4722	0.0181	0.0123	219	277	9.667E-06	0.01476
ELK4	1.4123	0.0184	0.0130	217	285	58.97E-06	0.01619
TAL1::TCF3	1.4096	0.1899	0.1347	1769	2282	1.506E-54	0.22230
GRMotifH	1.3959	4.5786	3.2800	11804	20999	0.00E00	8.62387
Evi1	1.3808	0.0296	0.0214	341	476	11.67E-06	0.02756
TEAD1	1.3745	0.0598	0.0435	702	972	2.737E-12	0.05077
RXR::RAR_DR5	1.3722	0.0202	0.0147	248	337	78.66E-06	0.01661
Arnt	1.3349	0.1296	0.0971	1064	1486	11.98E-20	0.20458
Gata1	1.3032	0.4746	0.3641	4397	6587	2.378E-176	0.47645
NHLH1	1.2917	0.0860	0.0666	699	989	50.51E-12	0.12791
FEV	1.2915	0.4535	0.3511	4339	6478	77.5E-174	0.46062
Myc	1.2859	0.0983	0.0764	948	1322	47.16E-18	0.13326
NFIC	1.2753	1.7829	1.3980	9506	15599	0.00E00	2.49398
FOXI1	1.2581	0.5988	0.4759	4802	7262	3.819E-210	0.85258
Hand1::Tcfe2a	1.2528	0.8383	0.6691	6593	10687	0.00E00	0.91238
Mycn	1.2514	0.0780	0.0623	731	1076	18.77E-10	0.10524
NR2F1	1.2352	0.0809	0.0655	935	1428	2.146E-10	0.07496
FOXC1	1.2232	5.0304	4.1124	11641	21504	0.00E00	13.00668
NR4A2	1.2226	1.2639	1.0338	8419	13806	0.00E00	1.58114
ELK1	1.2218	0.5927	0.4851	5180	8281	6.142E-218	0.67078
MYC::MAX	1.2115	0.0439	0.0362	432	664	3.214E-04	0.05403
Myf	1.2102	0.1598	0.1320	1503	2378	51.43E-18	0.25377
FOXO3	1.2078	1.1838	0.9801	7766	12978	0.00E00	1.56423
Myb	1.2027	0.5350	0.4448	4854	7874	8.762E-178	0.56378
YY1	0.8308	2.2012	2.6494	10310	20028	0.00E00	4.95514
CREB1	0.8044	0.4359	0.5420	4059	8642	78.0E-32	0.66193
Klf4	0.8042	0.1084	0.1348	1153	2604	1.14E-02	0.16778
Pdx1	0.7898	1.4112	1.7868	7899	16448	0.00E00	3.39607
FOXL1	0.7774	3.9866	5.1285	10240	19715	0.00E00	37.54040
SP1	0.7754	0.5969	0.7698	3446	8137	1.72E-04	3.02946
MZF1_5-13	0.7675	0.7003	0.9124	5628	12551	34.64E-92	1.44142
Zfp423	0.7598	0.0272	0.0358	283	659	59.2E-04	0.04640
PBX1	0.7401	0.0548	0.0741	641	1457	29.52E-04	0.11511
NFKB1	0.7363	0.0276	0.0375	268	641	21.29E-04	0.05458
NF-kappaB	0.7217	0.1007	0.1395	901	2547	25.69E-18	0.20837
Prrx2	0.7192	1.2207	1.6972	7269	16016	49.49E-264	3.02204
IRF1	0.7069	0.1154	0.1633	1262	3146	20.11E-08	0.18676
Lhx3	0.6915	0.1533	0.2217	1388	3397	6.001E-06	0.35873
Zfx	0.6708	0.0722	0.1077	713	2104	28.42E-20	0.14192
Foxd3	0.6705	1.1250	1.6779	6237	12801	12.88E-184	6.81326
PLAG1	0.6148	0.0063	0.0103	76	225	6.654E-04	0.00968
IRF2	0.5637	0.0024	0.0043	30	98	88.11E-04	0.00378
RREB1	0.5334	0.0147	0.0275	137	405	6.052E-06	0.05872
Ddit3::Cebpa	0.5032	0.1353	0.2690	1520	4726	17.88E-34	0.28549
EWSR1-FLI1	0.2316	0.0023	0.0103	16	59	1.915E-02	0.04827

15.62 AR DHT vs GR DEX unique for GRDEXrrO (up)

Chromosome specific statistics are shown in Table 161. A histogram of sequence lengths is shown in Figure 191.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	241	22	297	901	71682	0.000288
10	90	128	291	686	26165	0.000193
11	86	108	309	763	26600	0.000197
12	79	58	282	571	22282	0.000166
13	46	86	290	1434	13342	0.000116
14	76	102	277	646	21024	0.000196
15	84	104	298	752	25055	0.000244
16	83	3	285	579	23631	0.000262
17	76	47	261	665	19833	0.000244
18	49	103	358	1991	17546	0.000225
19	24	64	282	703	6779	0.000115
2	146	60	285	664	41558	0.000171
20	65	105	281	811	18279	0.00029
21	9	31	377	1440	3389	7e-05
22	44	125	273	845	12014	0.000234
3	135	71	297	837	40151	0.000203
4	102	0	269	646	27475	0.000144
5	183	16	284	939	52010	0.000287
6	136	10	272	799	37046	0.000216
7	99	0	270	705	26700	0.000168
8	75	115	275	525	20648	0.000141
9	86	32	280	551	24088	0.000171
X	47	92	251	624	11787	7.6e-05
all 23	2061	0	286	1991	589084	0.00019

Table 161: Chromosome specific distribution of the regions. The last line represents the overall statistics.

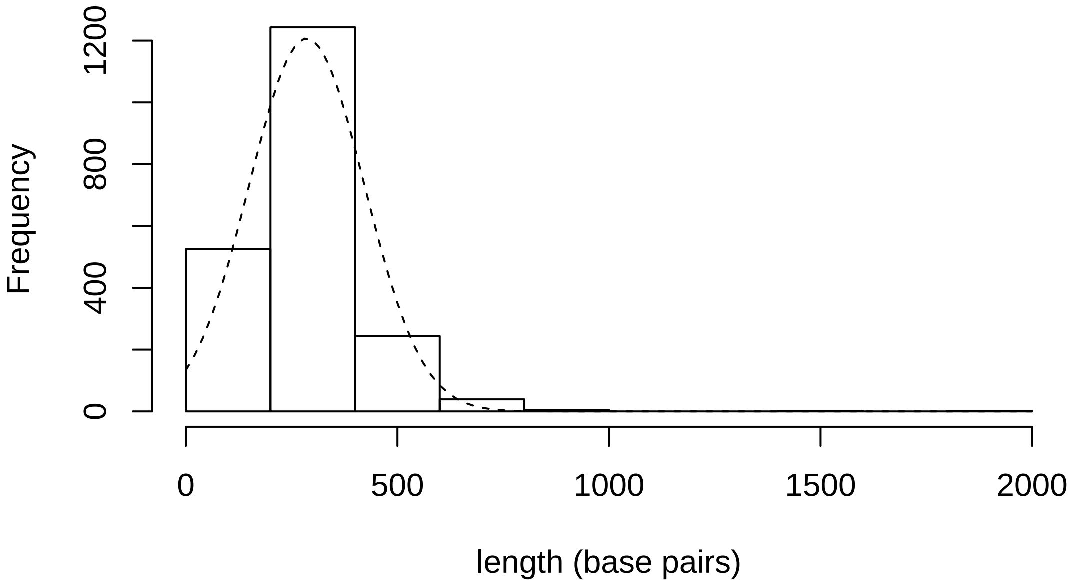
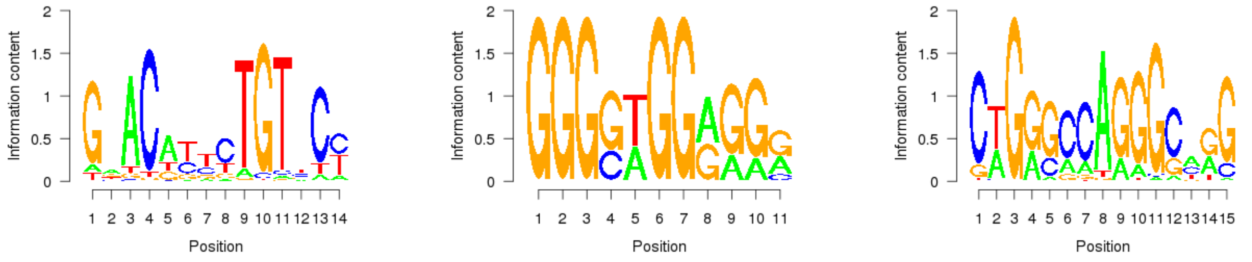


Figure 191: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU2u-gCount** component.

property	value
genes	611



(a) ARGRrrU2u-deNovo-meme1: width=14, sites=324, llr=2787, E=1.4e-108 (b) ARGRrrU2u-deNovo-meme2: width=11, sites=46, llr=527, E=9900 (c) ARGRrrU2u-deNovo-meme3: width=15, sites=43, llr=517, E=1200000

Figure 192: De novo motifs for the filtered AR DHT vs GR DEX unique for GRDEXrrO (up) sequences.

Table 162: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	22.8362	0.1386	0.0060	264	23	10.19E-96	0.05681
CTCF	3.6313	0.0058	0.0016	12	6	99.39E-04	0.00305
ARMotifTH	3.6260	0.0846	0.0233	158	86	6.343E-24	0.05466
ESR2	3.1442	0.0248	0.0079	37	28	2.849E-04	0.02414
GRMotifTH	2.7325	0.4113	0.1505	642	522	77.04E-78	0.41305
ARMotifT	2.6826	0.6748	0.2515	929	800	77.5E-128	0.63473
GRMotifTT	2.6772	0.0379	0.0141	75	53	1.583E-08	0.02332
TLX1::NFIC	2.6515	0.0160	0.0060	28	19	6.437E-04	0.01250
ARMotifHH	2.5057	0.4978	0.1986	686	629	9.208E-72	1.74071
NR3C1	2.4271	0.3996	0.1646	637	558	1.439E-68	0.34862
AR	2.3488	0.0579	0.0246	114	93	3.375E-10	0.03799
PPARG::RXRA	2.3003	0.0199	0.0086	39	32	5.483E-04	0.01379
GABPA	1.9413	0.0666	0.0343	127	128	12.8E-08	0.04795
MIZF	1.9344	0.0233	0.0120	47	46	18.14E-04	0.01608
GR	1.8868	0.2790	0.1479	480	476	31.26E-38	0.24303
GRMotifT	1.8811	2.2066	1.1730	1752	2508	8.991E-282	3.15202
ARMotifTT	1.8515	0.0131	0.0071	27	26	1.998E-02	0.00944
FOXA1	1.7869	0.4439	0.2484	696	794	46.03E-52	0.37165
GRMotifHH	1.7274	0.2329	0.1348	391	445	58.09E-22	0.26304
ELK4	1.7148	0.0238	0.0139	47	49	43.78E-04	0.01910
Tcfcp2l1	1.6818	0.0515	0.0306	98	108	66.67E-06	0.04433
ARMotifH	1.6789	7.5314	4.4857	2028	3649	0.00E00	24.61356
FOXF2	1.6298	0.1463	0.0898	276	323	2.35E-12	0.11289
Foxa2	1.6151	0.3792	0.2348	592	699	3.053E-36	0.42174
NFYA	1.5911	0.0438	0.0275	84	100	14.63E-04	0.03616
Mycn	1.5860	0.0967	0.0610	152	184	8.827E-06	0.10452
Stat3	1.5695	0.1458	0.0929	232	287	1.392E-08	0.15042
RORA_2	1.5323	0.0185	0.0120	37	44	4.935E-02	0.01511
Myc	1.5225	0.1128	0.0741	183	229	2.357E-06	0.11909
Arnt	1.5013	0.1415	0.0942	192	249	5.43E-06	0.18018
MYC::MAX	1.5012	0.0554	0.0369	89	113	39.05E-04	0.06022
NR2F1	1.4765	0.0943	0.0639	181	236	15.84E-06	0.07612
Myf	1.4719	0.1949	0.1324	294	398	1.028E-08	0.23908
TEAD1	1.4219	0.0651	0.0458	125	171	27.02E-04	0.05492
NHLH1	1.4170	0.1001	0.0707	131	168	3.154E-04	0.14624
GRMotifH	1.3833	4.7078	3.4033	1975	3502	0.00E00	10.63068
FOXD1	1.3363	0.6767	0.5064	948	1374	1.573E-58	0.71803
TAL1::TCF3	1.3282	0.1915	0.1442	297	408	2.079E-08	0.23398
EBF1	1.3182	0.4813	0.3651	650	988	97.93E-24	0.65327
NFE2L2	1.3021	0.0924	0.0709	169	254	45.22E-04	0.08692
Egr1	1.2900	0.0685	0.0531	124	188	2.976E-02	0.06838
Myb	1.2889	0.5620	0.4360	841	1279	6.264E-40	0.56069
ELK1	1.2863	0.6480	0.5038	897	1456	12.77E-40	0.66670
NR4A2	1.2857	1.3807	1.0738	1434	2350	68.36E-138	1.70190
HIF1A::ARNT	1.2805	0.3053	0.2384	421	708	1.677E-06	0.48461
Esrrb	1.2803	0.0788	0.0615	153	220	25.67E-04	0.07184
FEV	1.2707	0.4706	0.3703	748	1139	1.412E-30	0.46059
Foxq1	1.2648	0.3257	0.2575	522	788	50.88E-16	0.35879
Hand1::Tcfe2a	1.2543	0.8663	0.6907	1124	1822	39.91E-72	0.94842
MAX	1.2271	0.1599	0.1303	248	400	18.75E-04	0.27984
NFIC	1.2192	1.8206	1.4933	1602	2656	2.401E-186	3.12491
Klf4	1.2166	0.1633	0.1343	268	432	7.756E-04	0.19268
HOXA5	0.8297	3.6111	4.3525	1845	3533	29.86E-250	11.50861
Nobox	0.8265	0.8542	1.0335	971	1924	2.984E-28	1.89467
Nkx2-5	0.7961	3.3106	4.1583	1744	3365	2.379E-204	12.96589
ARID3A	0.7553	1.9096	2.5281	1448	2889	3.851E-104	6.65867
PBX1	0.7177	0.0520	0.0725	99	258	1.975E-02	0.07570
Pdx1	0.7041	1.2956	1.8401	1249	2770	11.89E-50	3.54365
FOXL1	0.6723	3.4847	5.1832	1632	3281	62.43E-156	35.52614
Prrx2	0.6586	1.1313	1.7176	1170	2709	2.811E-34	3.09522
IRF1	0.6112	0.1099	0.1798	202	565	4.711E-04	0.19282
Foxd3	0.6097	1.0535	1.7278	977	2148	3.361E-20	7.09565
Lhx3	0.5753	0.1337	0.2324	194	561	1.049E-04	0.40886
MEF2A	0.5540	0.1376	0.2484	233	690	20.99E-06	0.30114
Ddit3::Cebpa	0.5119	0.1444	0.2821	265	811	2.407E-06	0.30481
Pou5f1	0.4556	0.0049	0.0107	10	41	3.289E-02	0.00860
IRF2	0.2201	0.0015	0.0068	3	26	98.78E-04	0.00491

15.63 AR DHT vs GR DEX unique for GRDEXrrO (down)

Chromosome specific statistics are shown in Table 163. A histogram of sequence lengths is shown in Figure 193.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	109	10	273	666	29706	0.000119
10	37	39	223	459	8252	6.1e-05
11	41	31	264	546	10804	8e-05
12	29	149	285	660	8272	6.2e-05
13	13	150	266	429	3459	3e-05
14	36	92	335	700	12056	0.000112
15	35	18	274	573	9588	9.4e-05
16	58	130	274	1638	15895	0.000176
17	53	68	243	606	12896	0.000159
18	7	153	214	257	1499	1.9e-05
19	34	139	236	428	8029	0.000136
2	68	48	272	623	18497	7.6e-05
20	22	119	232	455	5110	8.1e-05
21	17	122	248	379	4212	8.8e-05
22	10	117	273	663	2729	5.3e-05
3	74	131	296	909	21920	0.000111
4	31	117	246	447	7620	4e-05
5	130	30	328	910	42675	0.000236
6	36	35	244	523	8785	5.1e-05
7	52	70	278	496	14465	9.1e-05
8	43	63	247	442	10628	7.3e-05
9	44	5	259	481	11394	8.1e-05
X	6	161	238	290	1427	9e-06
all 23	985	5	274	1638	269918	8.7e-05

Table 163: Chromosome specific distribution of the regions. The last line represents the overall statistics.

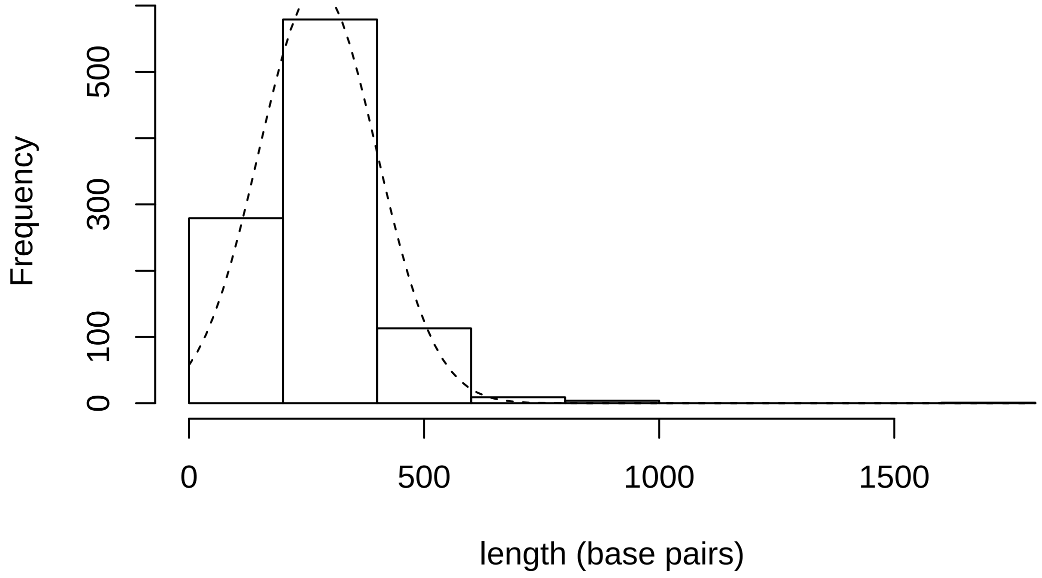
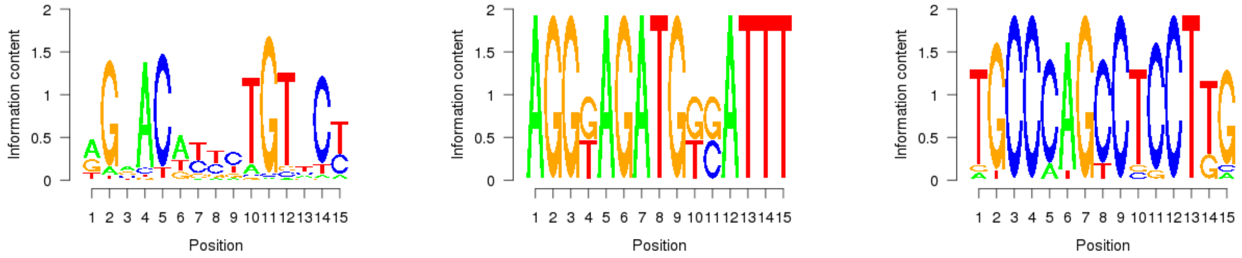


Figure 193: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU2d-gCount** component.

property	value
genes	400



(a) ARGRrrU2d-deNovo-meme1: width=15, sites=282, llr=2531, E=9.5e-122
(b) ARGRrrU2d-deNovo-meme2: width=15, sites=17, llr=315, E=1.4e-24
(c) ARGRrrU2d-deNovo-meme3: width=15, sites=16, llr=286, E=5.9e-17

Figure 194: De novo motifs for the filtered AR DHT vs GR DEX unique for GRDEXrrO (down) sequences.

Table 164: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	31.3537	0.1211	0.0038	106	7	1.291E-40	0.05620
TLX1::NFIC	5.2803	0.0203	0.0038	16	4	58.04E-06	0.01446
ARMotifTT	3.2077	0.0193	0.0060	19	11	18.41E-04	0.01053
GRMotifTT	3.1037	0.0356	0.0114	34	20	19.14E-06	0.02090
AR	2.6202	0.0600	0.0229	58	42	70.38E-08	0.03527
PPARG::RXRA	2.5248	0.0193	0.0076	19	12	33.41E-04	0.01370
GRMotifTH	2.5051	0.3316	0.1324	254	219	62.93E-28	0.34924
ARMotifT	2.3142	0.5534	0.2391	408	379	39.24E-50	0.40675
STAT1	2.2256	0.0376	0.0169	27	28	3.15E-02	0.03277
Foxa2	2.2031	0.4608	0.2092	332	304	3.351E-36	0.41181
ARMotifTH	2.1935	0.0682	0.0310	63	56	16.67E-06	0.04562
NR3C1	2.1090	0.3286	0.1558	248	249	1.898E-20	0.35679
FOXA1	2.0732	0.5025	0.2424	361	369	43.43E-36	0.41030
ARMotifHH	1.8422	0.3693	0.2004	270	307	2.26E-18	0.35324
Stat3	1.7994	0.1617	0.0899	127	133	3.772E-08	0.15286
GABPA	1.7921	0.0732	0.0408	67	71	3.16E-04	0.05796
Tcfcp2l1	1.7762	0.0600	0.0338	52	60	70.38E-04	0.04819
FOXF2	1.7739	0.1353	0.0763	119	132	1.035E-06	0.10382
HNF1B	1.7314	0.0651	0.0376	57	66	45.56E-04	0.05207
GR	1.6583	0.2258	0.1362	191	218	40.38E-12	0.19126
GRMotifT	1.6390	1.8739	1.1432	786	1181	39.97E-110	2.06509
Esrrb	1.6108	0.0895	0.0556	85	98	2.26E-04	0.06785
NR2F1	1.5778	0.1109	0.0703	105	125	54.8E-06	0.08300
ARMotifH	1.4931	6.5025	4.3551	967	1743	37.29E-174	13.34086
FOXD1	1.4897	0.7497	0.5033	472	673	59.31E-34	0.76306
GRMotifHH	1.4647	0.2035	0.1389	155	213	29.01E-06	0.20992
NFIC	1.3911	1.8881	1.3573	777	1256	18.57E-98	2.31571
FEV	1.3448	0.4710	0.3502	371	515	56.86E-22	0.43083
GRMotifH	1.3163	4.3245	3.2854	923	1684	51.36E-148	7.60937
Foxq1	1.2825	0.3255	0.2538	251	374	1.993E-08	0.34026
Myc	1.2709	0.0997	0.0784	80	111	1.452E-02	0.11754
ELK1	1.2486	0.6094	0.4880	433	677	2.26E-22	0.61610
MAX	1.2451	0.1322	0.1062	105	156	1.187E-02	0.15313
EBF1	1.2394	0.4415	0.3562	286	458	1.417E-08	0.60329
Hand1::Tcfe2a	1.2313	0.8464	0.6874	549	846	71.25E-42	1.00445
NR4A2	1.2294	1.2696	1.0327	679	1103	5.511E-66	1.53355
TFAP2A	1.2093	1.2014	0.9935	526	826	17.81E-36	2.78699
Sox17	1.2079	0.9237	0.7647	550	902	1.164E-36	1.07162
CREB1	0.8299	0.4588	0.5528	330	711	11.07E-04	0.63932
YY1	0.8169	2.1373	2.6166	816	1613	6.565E-90	4.66911
Pdx1	0.7931	1.3835	1.7446	600	1297	65.5E-28	3.23529
FOXL1	0.7755	3.8311	4.9401	777	1550	24.08E-76	28.55668
MZF1_5-13	0.7645	0.6907	0.9036	446	1023	11.64E-08	1.18770
Prrx2	0.7182	1.1994	1.6699	534	1293	1.088E-12	2.93849
Foxd3	0.7044	1.1648	1.6536	481	1019	28.84E-14	7.16109
Ddit3::Cebpa	0.5105	0.1343	0.2631	122	382	6.857E-04	0.26644

15.64 AR DHT vs GR DEX unique for GRDEXrrO (stable)

Chromosome specific statistics are shown in Table 165. A histogram of sequence lengths is shown in Figure 195.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	646	28	287	1031	185641	0.000745
10	293	25	269	843	78746	0.000581
11	295	16	272	763	80187	0.000594
12	220	10	270	989	59306	0.000443
13	145	1	292	1434	42397	0.000368
14	188	2	280	1050	52701	0.000491
15	199	29	277	684	55092	0.000537
16	210	15	277	1638	58091	0.000643
17	239	84	259	670	61867	0.000762
18	83	127	301	1991	24970	0.00032
19	112	64	229	703	25597	0.000433
2	431	14	270	773	116329	0.000478
20	155	21	258	1249	40060	0.000636
21	77	31	285	643	21956	0.000456
22	114	5	250	845	28478	0.000555
3	384	3	293	920	112463	0.000568
4	258	0	255	2287	65696	0.000344
5	319	16	278	755	88675	0.00049
6	251	14	251	1181	62908	0.000368
7	314	19	278	1103	87224	0.000548
8	285	32	274	956	78087	0.000534
9	251	8	266	659	66808	0.000473
X	136	43	247	624	33656	0.000217
Y	28	109	258	408	7238	0.000122
all 24	5633	0	272	2287	1534173	0.000496

Table 165: Chromosome specific distribution of the regions. The last line represents the overall statistics.

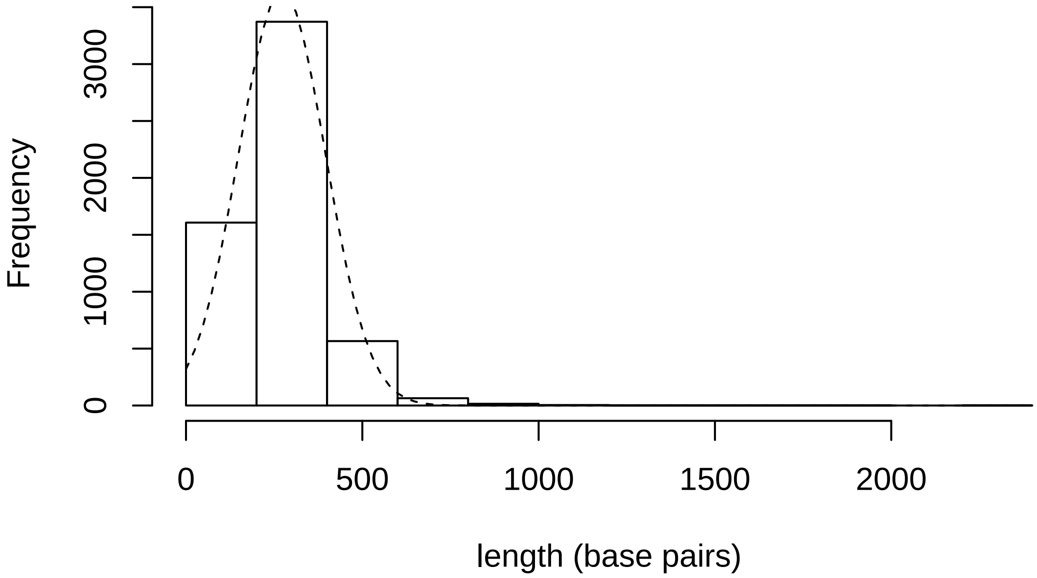
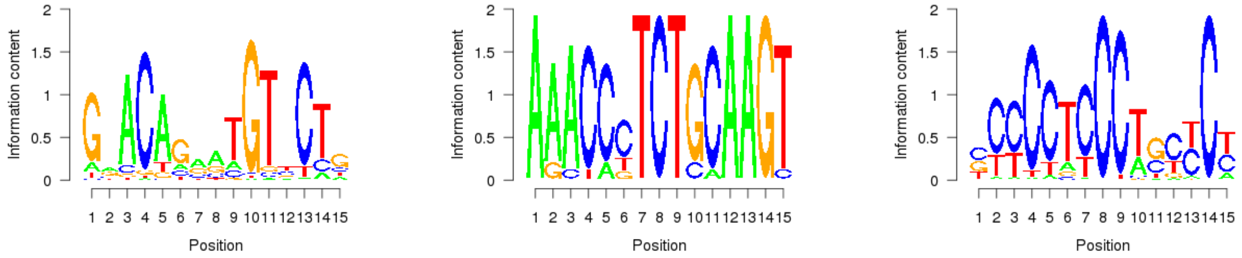


Figure 195: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARGRrrU2s-gCount** component.

property	value
genes	3381



(a) ARGRrrU2s-deNovo-meme1: width=15, sites=329, llr=2874, E=4.1e-130 (b) ARGRrrU2s-deNovo-meme2: width=15, sites=14, llr=246, E=6.8e-08 (c) ARGRrrU2s-deNovo-meme3: width=15, sites=70, llr=804, E=4.6e-10

Figure 196: De novo motifs for the filtered AR DHT vs GR DEX unique for GRDEXrrO (stable) sequences.

Table 166: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	23.0223	0.1418	0.0061	696	62	52.62E-250	0.08162
TLX1::NFIC	3.7315	0.0158	0.0042	72	32	36.07E-14	0.01180
ESR2	3.3184	0.0201	0.0060	97	59	1.07E-12	0.01330
ARMotifTH	3.2398	0.0821	0.0253	398	256	14.17E-48	0.06325
GRMotifTH	2.6640	0.3682	0.1382	1564	1304	6.27E-170	0.38788
ARMotifT	2.5983	0.6423	0.2472	2518	2192	0.00E00	0.62487
NR3C1	2.4188	0.3680	0.1521	1640	1421	4.207E-172	0.30254
GRMotifTT	2.3669	0.0322	0.0136	171	138	1.961E-14	0.02265
FOXA1	2.3291	0.5257	0.2257	2195	2012	15.76E-250	0.39040
CTCF	2.2648	0.0057	0.0025	32	26	18.89E-04	0.00359
ARMotifHH	2.2600	0.4233	0.1873	1685	1649	5.041E-148	0.96772
ARMotifTT	2.1821	0.0117	0.0053	65	53	5.745E-06	0.00802
FOXF2	2.1789	0.1640	0.0753	825	743	4.533E-64	0.11388
Foxa2	2.1275	0.4619	0.2171	1964	1754	1.834E-216	0.43334
AR	2.0293	0.0551	0.0271	296	278	1.471E-18	0.03927
RORA_2	1.9448	0.0195	0.0100	108	105	1.19E-06	0.01343
GRMotifT	1.8255	2.0690	1.1333	4671	6818	0.00E00	3.12414
Stat3	1.7793	0.1521	0.0855	667	725	97.09E-34	0.14702
GR	1.7636	0.2650	0.1502	1246	1388	1.741E-72	0.34645
GRMotifHH	1.7322	0.2111	0.1219	985	1101	42.94E-52	0.18506
GABPA	1.7081	0.0620	0.0363	322	371	4.114E-12	0.04908
FOXD1	1.6281	0.7562	0.4644	2769	3648	12.04E-220	0.71377
RXR::RAR_DR5	1.6276	0.0226	0.0138	125	144	52.33E-06	0.01698
Tcfcp2l1	1.6229	0.0499	0.0308	259	297	7.749E-10	0.04438
Tal1::Gata1	1.6064	0.0350	0.0218	195	225	23.3E-08	0.02633
ARMotifH	1.5973	6.9129	4.3278	5558	9922	0.00E00	18.08667
MIZF	1.5716	0.0224	0.0142	124	145	89.83E-06	0.01766
Foxq1	1.5329	0.3540	0.2309	1535	1976	7.758E-72	0.34726
T	1.4946	0.0117	0.0078	65	80	1.375E-02	0.00948
STAT1	1.4892	0.0315	0.0211	146	182	1.642E-04	0.03294
Evi1	1.4579	0.0297	0.0203	151	206	21.28E-04	0.03026
Esrrb	1.4497	0.0816	0.0563	437	568	22.81E-12	0.06708
TAL1::TCF3	1.4300	0.1782	0.1246	771	996	5.757E-24	0.19861
GRMotifH	1.3736	4.5076	3.2816	5366	9578	0.00E00	8.58294
PPARG::RXRA	1.3719	0.0165	0.0120	90	124	2.728E-02	0.01417
FEV	1.3249	0.4503	0.3399	1976	2915	4.451E-82	0.42274
Arnt	1.3004	0.1246	0.0958	478	668	17.48E-10	0.17579
NFYA	1.2953	0.0375	0.0289	202	279	4.141E-04	0.03601
NHLH1	1.2744	0.0889	0.0697	329	459	2.906E-06	0.13419
Gata1	1.2723	0.4669	0.3669	1975	3027	11.78E-74	0.48179
ELK1	1.2661	0.6103	0.4820	2399	3752	3.616E-110	0.74914
NFIC	1.2652	1.7768	1.4044	4348	7085	0.00E00	2.47023
Myf	1.2506	0.1759	0.1407	737	1133	49.78E-12	0.25136
Myb	1.2448	0.5408	0.4344	2224	3504	6.293E-90	0.57300
TEAD1	1.2442	0.0567	0.0456	301	463	13.75E-04	0.05135
FOXI1	1.2427	0.5799	0.4666	2141	3268	14.21E-90	0.81008
Hand1::Tcfe2a	1.2282	0.8322	0.6776	2983	4868	77.77E-176	0.96109
NR2F1	1.2248	0.0791	0.0646	419	648	59.04E-06	0.07287
NR4A2	1.2154	1.2655	1.0413	3841	6250	0.00E00	1.65879
FOXC1	1.2067	4.8967	4.0579	5284	9791	0.00E00	13.22517
Myc	1.2062	0.0940	0.0779	415	629	18.53E-06	0.12317
Mycn	1.2056	0.0739	0.0613	321	468	52.57E-06	0.10154
YY1	0.8259	2.1692	2.6265	4660	9147	0.00E00	4.97177
CREB1	0.8094	0.4326	0.5344	1821	3871	4.476E-14	0.67742
MZF1_5-13	0.8041	0.7242	0.9006	2619	5637	35.64E-54	1.63703
SP1	0.7943	0.6350	0.7994	1624	3685	54.8E-06	3.96633
NF-kappaB	0.7897	0.1116	0.1413	445	1148	31.07E-06	0.24228
FOXL1	0.7587	3.7782	4.9801	4556	8965	0.00E00	33.62282
Pdx1	0.7479	1.2963	1.7333	3449	7404	9.738E-150	3.21663
MEF2A	0.7228	0.1580	0.2186	683	1705	7.48E-04	0.30022
Zfx	0.7225	0.0784	0.1085	360	947	13.95E-06	0.14329
IRF1	0.6903	0.1123	0.1627	568	1443	1.004E-04	0.18122
Prrx2	0.6848	1.1249	1.6428	3119	7216	2.184E-82	2.85836
NFKB1	0.6633	0.0295	0.0445	133	339	57.06E-04	0.06468
Foxd3	0.6610	1.0823	1.6373	2766	5770	87.42E-74	6.67557
PLAG1	0.6388	0.0068	0.0106	37	109	2.126E-02	0.00954
PBX1	0.6374	0.0471	0.0739	252	652	2.105E-04	0.13878
Lhx3	0.6017	0.1372	0.2281	580	1575	18.57E-08	0.36750
Pou5f1	0.5475	0.0043	0.0078	24	81	1.348E-02	0.00667
Ddit3::Cebpa	0.5366	0.1374	0.2560	695	2084	21.99E-14	0.27613
RREB1	0.5067	0.0144	0.0285	67	193	33.6E-04	0.06436

15.65 AR LNCaP vs VCaP DHT overlaps

Chromosome specific statistics are shown in Table 167. A histogram of sequence lengths is shown in Figure 197.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	552	2	422	975	232829	0.000934
10	227	8	402	931	91264	0.000673
11	257	23	421	1090	108295	0.000802
12	210	12	396	875	83099	0.000621
13	141	197	426	1097	60051	0.000521
14	174	38	403	829	70068	0.000653
15	192	5	437	1065	83873	0.000818
16	136	18	375	1042	50944	0.000564
17	185	7	410	918	75917	0.000935
18	110	200	441	1125	48527	0.000622
19	64	202	401	947	25680	0.000434
2	380	12	413	963	156895	0.000645
20	134	237	423	1134	56667	0.000899
21	72	196	449	768	32295	0.000671
22	59	12	371	545	21885	0.000427
3	420	9	428	1030	179915	0.000909
4	259	0	405	1056	104946	0.000549
5	335	12	416	1129	139247	0.00077
6	320	69	393	918	125801	0.000735
7	299	158	425	1124	127069	0.000798
8	282	4	432	934	121820	0.000832
9	208	105	416	812	86541	0.000613
X	101	57	370	717	37323	0.00024
Y	4	199	282	344	1129	1.9e-05
all 24	5121	0	414	1134	2122080	0.000685

Table 167: Chromosome specific distribution of the regions. The last line represents the overall statistics.

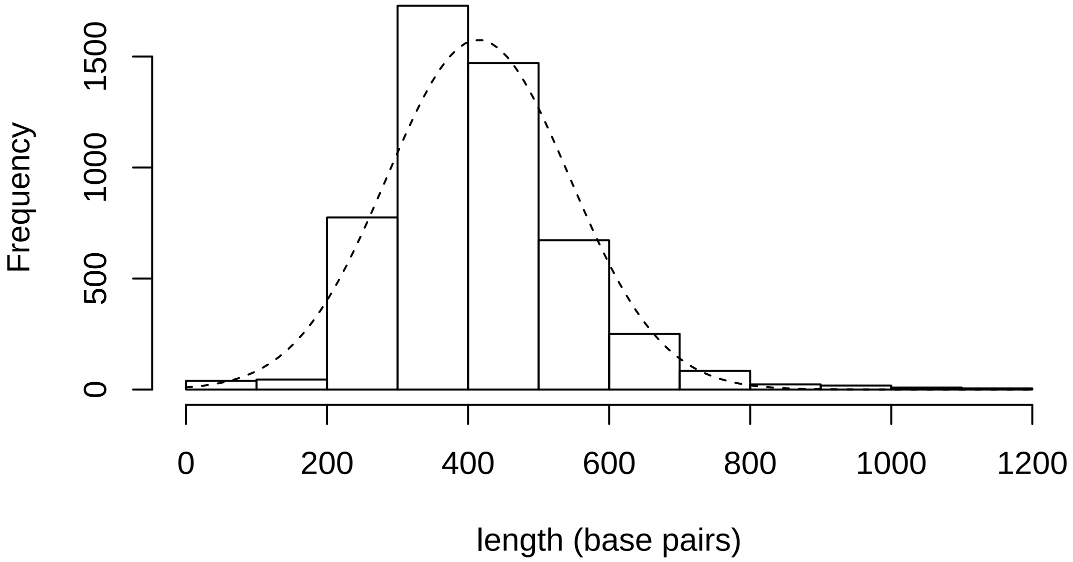
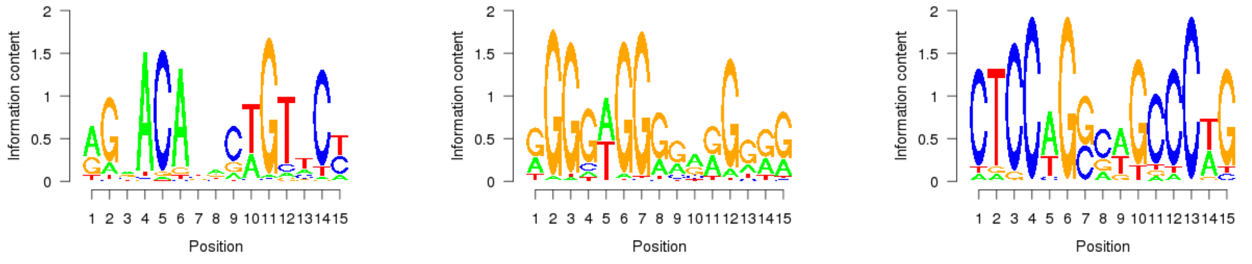


Figure 197: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrO-gCount** component.

property	value
genes	11228



(a) ARvsAR2rrO-deNovo-meme1: width=15, sites=303, llr=2712, E=9.4e-86 (b) ARvsAR2rrO-deNovo-meme2: width=15, sites=87, llr=991, E=6.5e-23 (c) ARvsAR2rrO-deNovo-meme3: width=15, sites=17, llr=244, E=2.7e+08

Figure 198: De novo motifs for the filtered AR LNCaP vs VCaP DHT overlaps sequences.

Table 168: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	13.6618	0.1177	0.0086	548	80	6.489E-176	0.05245
TLX1::NFIC	3.1657	0.0190	0.0060	77	47	2.362E-10	0.01446
FOXA1	2.7610	1.0029	0.3632	3317	2782	0.00E00	0.68840
FOXA1pAR	2.6271	0.1975	0.0751	930	625	12.68E-120	0.13521
Foxa2	2.5708	0.8637	0.3359	3013	2369	0.00E00	0.70808
FOXF2	2.4663	0.3019	0.1224	1326	1063	8.569E-150	0.20056
ARMotifTT	2.3180	0.0129	0.0055	66	52	1.885E-06	0.00817
ESR2	2.2994	0.0239	0.0103	106	92	2.714E-08	0.01823
Tal1::Gata1	1.9545	0.0630	0.0322	308	299	1.878E-18	0.04420
ARMotifTH	1.9112	0.0721	0.0377	357	352	75.7E-22	0.05038
FOXD1	1.7986	1.3024	0.7241	3659	4582	0.00E00	1.14299
ARMotifT	1.7933	0.6780	0.3781	2472	2882	9.781E-238	0.54228
Stat3	1.7085	0.2225	0.1302	850	971	10.4E-42	0.22671
GRMotifTH	1.6691	0.3640	0.2181	1508	1827	5.265E-88	0.29740
Foxq1	1.6397	0.6143	0.3746	2286	2678	4.845E-202	0.56929
PPARG::RXRA	1.5997	0.0233	0.0145	112	138	7.105E-04	0.01862
NR3C1	1.5852	0.3851	0.2429	1549	1994	3.293E-80	0.32463
GRMotifTT	1.5850	0.0262	0.0165	131	152	31.93E-06	0.02072
GABPA	1.5670	0.0848	0.0541	416	499	99.74E-16	0.06581
RXRA::VDR	1.5483	0.0086	0.0055	44	53	3.532E-02	0.00656
AR	1.4801	0.0645	0.0436	315	409	2.623E-08	0.05142
Gata1	1.4142	0.7754	0.5483	2650	3848	48.85E-192	0.71963
Esrrb	1.4134	0.1191	0.0842	569	753	15.4E-16	0.10070
GRMotifT	1.3970	2.4532	1.7560	4598	7694	0.00E00	2.50143
NHLH1	1.3919	0.1347	0.0968	425	605	4.606E-08	0.19091
Tcfcp2l1	1.3834	0.0661	0.0478	309	406	8.551E-08	0.06374
RORA_2	1.3563	0.0217	0.0160	109	152	1.495E-02	0.01806
ARMotifHH	1.3428	0.3873	0.2884	1567	2220	5.129E-64	0.37649
FOXI1	1.3346	0.9656	0.7235	2953	4192	4.05E-258	1.22553
STAT1	1.3212	0.0452	0.0342	181	264	41.78E-04	0.05249
ELK4	1.3165	0.0233	0.0177	114	160	1.43E-02	0.02127
ARMotifH	1.3001	8.5668	6.5896	5097	9456	0.00E00	14.97801
GR	1.2987	0.2960	0.2279	1299	1845	2.711E-44	0.27508
RXR::RAR_DR5	1.2878	0.0285	0.0222	144	197	24.19E-04	0.03223
NFIC	1.2848	2.7148	2.1130	4518	7864	0.00E00	3.52254
GRMotifHH	1.2501	0.2295	0.1836	1001	1484	8.993E-24	0.22868
Arnt	1.2472	0.1756	0.1408	634	895	4.622E-14	0.25428
Pax5	1.2274	0.0530	0.0432	263	399	14.14E-04	0.04741
FEV	1.2192	0.6401	0.5250	2385	3696	14.83E-130	0.64023
FOXO3	1.2171	1.7934	1.4735	4075	6740	0.00E00	2.17457
Hand1::Tcfe2a	1.2164	1.2223	1.0048	3477	5837	94.81E-308	1.26190
ELK1	1.2130	0.8698	0.7170	2871	4674	73.13E-190	0.89205
Myf	1.2093	0.2370	0.1959	928	1434	16.45E-18	0.31450
MIZF	1.2041	0.0276	0.0229	140	213	3.786E-02	0.02487
Pdx1	0.8151	2.1865	2.6825	4069	7950	0.00E00	5.06659
MZF1_5-13	0.8124	1.1198	1.3785	3242	6677	94.87E-172	1.84512
SP1	0.7981	0.9810	1.2292	2101	4420	2.412E-34	5.85800
HLF	0.7956	0.3906	0.4910	1463	3332	1.544E-04	0.63367
NF-kappaB	0.7954	0.1709	0.2148	655	1568	3.017E-02	0.29552
CREB1	0.7714	0.6370	0.8257	2270	4918	2.454E-40	0.97009
Prrx2	0.7639	1.9554	2.5597	3940	7831	0.00E00	4.48933
Klf4	0.7468	0.1582	0.2118	667	1612	2.002E-02	0.26480
NFYA	0.7465	0.0405	0.0542	201	469	3.942E-02	0.06103
FOXL1	0.7362	5.7312	7.7850	4824	8878	0.00E00	64.22970
Foxd3	0.7239	1.8676	2.5798	3678	6680	59.0E-324	10.64626
Zfx	0.6736	0.1128	0.1675	488	1306	4.547E-06	0.19820
Ddit3::Cebpa	0.5126	0.2104	0.4104	944	2750	1.451E-08	0.45852
EWSR1-FLI1	0.1231	0.0045	0.0369	12	51	1.297E-02	0.29504

15.66 AR LNCaP vs VCaP DHT overlaps (up)

Chromosome specific statistics are shown in Table 169. A histogram of sequence lengths is shown in Figure 199.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	46	34	441	789	20298	8.1e-05
10	10	349	476	581	4763	3.5e-05
11	27	282	463	922	12501	9.3e-05
12	12	230	399	668	4790	3.6e-05
13	8	257	385	576	3083	2.7e-05
14	8	232	386	501	3092	2.9e-05
15	28	5	408	672	11417	0.000111
16	11	234	359	493	3947	4.4e-05
17	29	201	428	702	12404	0.000153
18	9	200	452	609	4066	5.2e-05
19	4	555	640	779	2558	4.3e-05
2	24	237	453	689	10867	4.5e-05
20	7	340	454	623	3181	5e-05
21	10	212	417	570	4174	8.7e-05
22	4	377	430	545	1720	3.4e-05
3	16	220	416	645	6652	3.4e-05
4	22	231	454	873	9985	5.2e-05
5	16	41	396	841	6332	3.5e-05
6	36	242	424	680	15251	8.9e-05
7	14	275	454	854	6350	4e-05
8	16	133	412	655	6588	4.5e-05
9	14	296	426	619	5958	4.2e-05
X	1	406	406	406	406	3e-06
all 23	372	5	431	922	160383	5.2e-05

Table 169: Chromosome specific distribution of the regions. The last line represents the overall statistics.

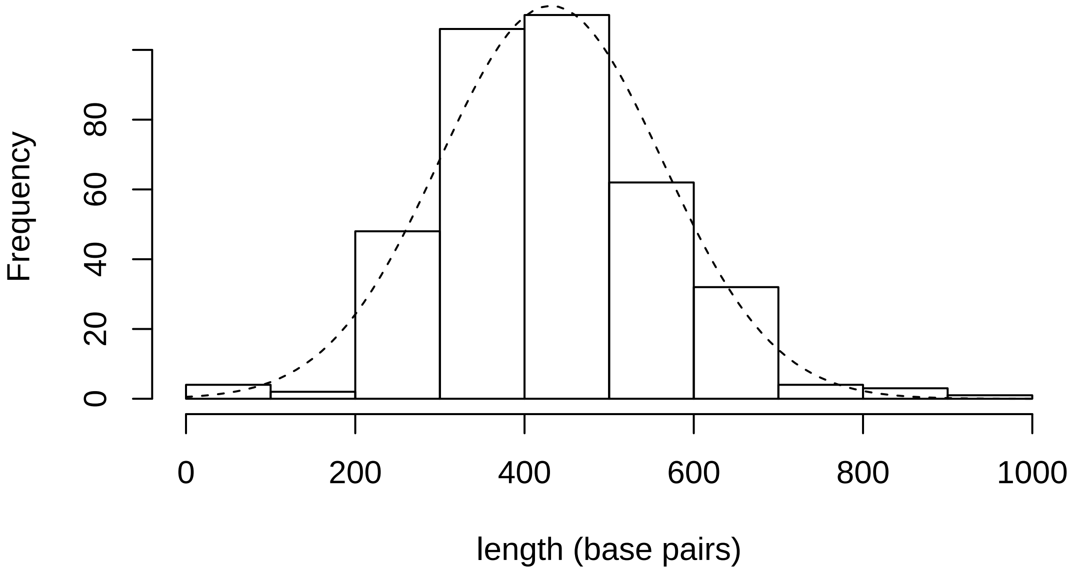
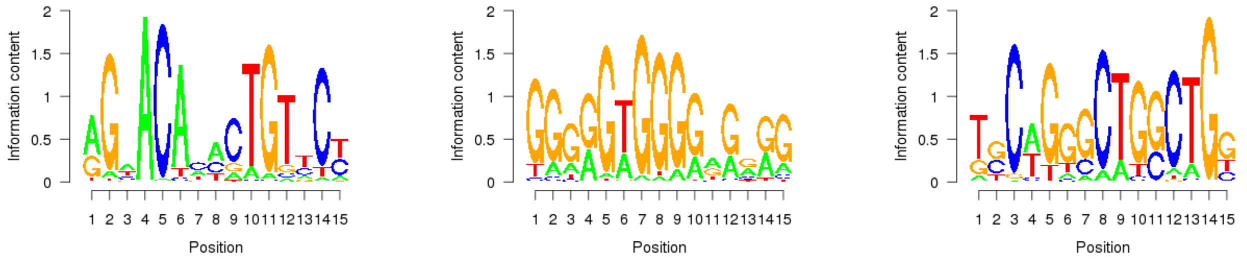


Figure 199: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrOu-gCount** component.

property	value
genes	171



(a) ARvsAR2rrOu-deNovo-meme1: width=15, sites=93, llr=1001, E=5.6e-23
(b) ARvsAR2rrOu-deNovo-meme2: width=15, sites=56, llr=645, E=0.00059
(c) ARvsAR2rrOu-deNovo-meme3: width=15, sites=37, llr=455, E=4000

Figure 200: De novo motifs for the filtered AR LNCaP vs VCaP DHT overlaps (up) sequences.

Table 170: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	17.3195	0.1267	0.0073	43	5	14.02E-16	0.05619
ESR2	6.6372	0.0485	0.0073	15	5	3.637E-04	0.02694
E2F1	3.3220	0.0243	0.0073	9	5	4.108E-02	0.01306
MYC::MAX	2.7778	0.0647	0.0233	18	14	1.516E-02	0.05150
FOXA1	2.7000	0.9380	0.3474	231	193	84.81E-44	0.61969
FOXA1pAR	2.6037	0.1590	0.0610	56	40	18.18E-08	0.09581
Foxa2	2.4503	0.7978	0.3256	200	150	94.47E-38	0.72842
NFKB1	2.4283	0.1024	0.0422	28	26	78.35E-04	0.08768
FOXF2	2.2889	0.2695	0.1177	83	73	82.58E-10	0.19288
Esrrb	1.8539	0.1375	0.0741	47	46	4.568E-04	0.10414
Pax5	1.8535	0.0836	0.0451	31	30	68.86E-04	0.05706
NR3C1	1.8232	0.4744	0.2602	132	158	3.004E-10	0.36106
Egr1	1.8074	0.1051	0.0581	33	38	2.768E-02	0.08611
ARMotifT	1.7906	0.6819	0.3808	182	212	72.96E-20	0.53171
GABPA	1.7750	0.1213	0.0683	40	41	29.36E-04	0.10209
GRMotifTH	1.6987	0.3531	0.2078	109	122	1.354E-08	0.29027
FOXD1	1.6697	1.2426	0.7442	259	333	48.8E-36	1.10304
Stat3	1.5868	0.2399	0.1512	67	76	1.648E-04	0.26638
Foxq1	1.5501	0.5768	0.3721	160	195	7.377E-14	0.58923
Tcfcp2l1	1.5031	0.0809	0.0538	28	32	4.665E-02	0.07633
GRMotifT	1.4749	2.6819	1.8183	334	556	36.59E-54	2.86061
ARMotifHH	1.4498	0.4636	0.3198	135	171	13.21E-10	0.41862
Hand1::Tcfe2a	1.4267	1.3396	0.9390	256	407	3.43E-26	1.29049
NFIC	1.4080	3.0863	2.1919	335	559	15.56E-54	4.04794
MAX	1.3998	0.2075	0.1483	66	84	16.58E-04	0.21053
ARMotifH	1.3956	9.6334	6.9026	369	679	31.25E-68	16.67111
Arnt	1.3372	0.2022	0.1512	51	71	3.30E-02	0.28615
NR2F1	1.3208	0.1402	0.1061	51	65	1.089E-02	0.12311
TFAP2A	1.3202	1.9784	1.4985	263	391	1.169E-30	5.46251
GRMotifHH	1.3034	0.2615	0.2006	79	124	1.366E-02	0.25033
INSM1	1.2795	0.1860	0.1453	59	89	4.449E-02	0.17961
RUNX1	1.2491	0.3504	0.2805	113	167	39.14E-06	0.31993
Gata1	1.2438	0.7466	0.6003	189	297	1.737E-12	0.73764
GRMotifH	1.2351	6.3801	5.1657	366	675	25.58E-66	9.75043
Myb	1.2311	0.8571	0.6962	198	335	3.927E-12	0.86123
ELK1	1.2252	0.9973	0.8140	228	352	3.035E-20	1.05226
BRCA1	1.2242	2.0836	1.7020	320	542	6.146E-46	2.20738
GR	1.2236	0.2615	0.2137	86	126	17.71E-04	0.24554
Arnt::Ahr	1.2070	1.5930	1.3198	250	402	3.355E-24	5.23553
Nkx2-5	0.7988	5.0647	6.3401	355	655	50.63E-60	17.90826
ARID3A	0.7960	3.1159	3.9142	324	582	48.05E-46	9.86349
Pdx1	0.7601	2.1024	2.7660	277	587	4.557E-22	5.16783
Foxd3	0.7316	1.8248	2.4942	261	474	60.61E-24	9.70471
Prrx2	0.6915	1.8302	2.6468	269	569	4.923E-20	4.84329
FOXL1	0.6886	5.2075	7.5625	343	637	1.999E-52	44.27885
CREB1	0.6746	0.5795	0.8590	157	360	74.16E-04	1.02888

15.67 AR LNCaP vs VCaP DHT overlaps (down)

Chromosome specific statistics are shown in Table 171. A histogram of sequence lengths is shown in Figure 201.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	16	287	451	695	7219	2.9e-05
10	2	354	414	473	827	6e-06
11	18	254	418	799	7532	5.6e-05
12	13	220	445	612	5781	4.3e-05
14	13	232	421	710	5471	5.1e-05
15	2	421	499	577	998	1e-05
17	7	187	412	591	2883	3.6e-05
19	3	281	312	351	937	1.6e-05
2	18	229	442	833	7949	3.3e-05
20	15	300	436	778	6547	0.000104
21	1	284	284	284	284	6e-06
22	3	359	380	405	1141	2.2e-05
3	22	228	451	795	9930	5e-05
4	10	144	337	487	3371	1.8e-05
5	12	239	406	621	4866	2.7e-05
6	8	139	377	731	3016	1.8e-05
7	15	160	393	577	5895	3.7e-05
8	11	314	443	533	4877	3.3e-05
9	2	252	358	464	716	5e-06
X	1	472	472	472	472	3e-06
all 20	192	139	420	833	80712	2.6e-05

Table 171: Chromosome specific distribution of the regions. The last line represents the overall statistics.

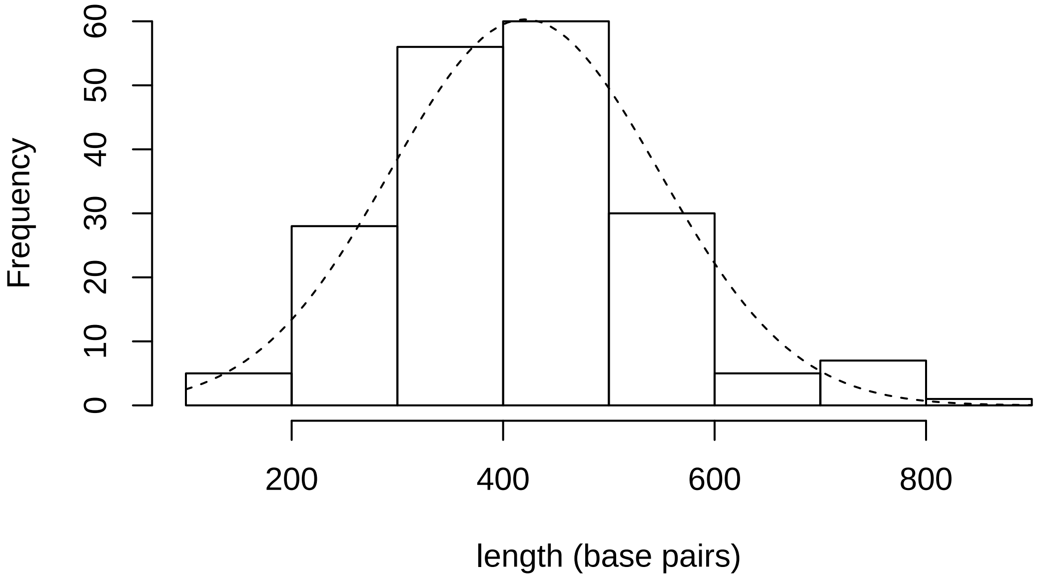
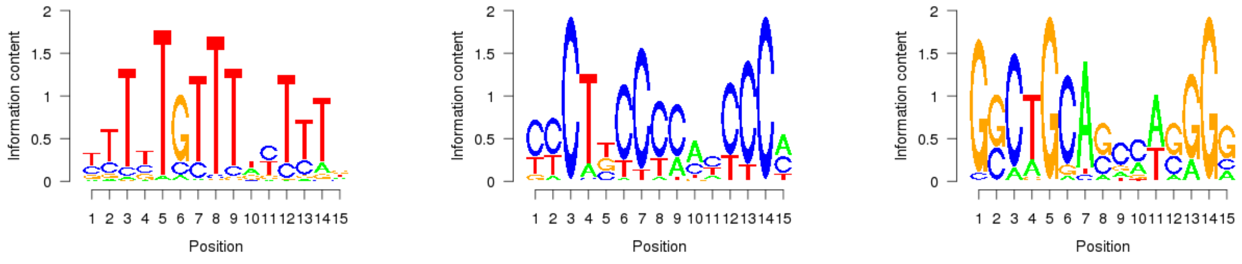


Figure 201: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrOd-gCount** component.

property	value
genes	109



(a) ARvsAR2rrOd-deNovo-meme1: width=15, sites=114, llr=1012, E=1e-05 (b) ARvsAR2rrOd-deNovo-meme2: width=15, sites=40, llr=463, E=0.012 (c) ARvsAR2rrOd-deNovo-meme3: width=15, sites=21, llr=270, E=670000

Figure 202: De novo motifs for the filtered AR LNCaP vs VCaP DHT overlaps (down) sequences.

Table 172: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	6.5376	0.0729	0.0111	13	4	5.935E-04	0.03523
ARMotifTH	3.2761	0.0729	0.0222	14	8	63.36E-04	0.03834
FOXF2	2.9115	0.3802	0.1306	62	46	10.12E-10	0.22852
FOXA1	2.8938	1.1094	0.3833	129	120	3.617E-24	0.75102
Foxa2	2.8287	0.8958	0.3167	118	93	10.33E-24	0.74014
FOXA1pAR	2.3990	0.1667	0.0694	28	25	25.5E-04	0.11091
Tal1::Gata1	2.3059	0.0833	0.0361	14	12	4.884E-02	0.06076
Foxq1	2.0109	0.6927	0.3444	93	99	13.68E-12	0.54328
FOXD1	1.9588	1.3385	0.6833	139	181	2.014E-20	0.97759
GRMotifTH	1.7498	0.3646	0.2083	54	65	2.838E-04	0.29203
ARMotifT	1.6708	0.6823	0.4083	93	114	13.03E-10	0.57712
Stat3	1.6224	0.2344	0.1444	34	41	1.495E-02	0.23222
Gata1	1.5608	0.8281	0.5306	105	145	2.991E-10	0.71158
GRMotifT	1.5124	2.5417	1.6806	177	282	11.06E-32	2.52410
NR3C1	1.4422	0.3646	0.2528	56	76	12.86E-04	0.33401
NFIC	1.4112	2.9635	2.1000	172	298	43.33E-28	3.75412
ARMotifHH	1.3980	0.4427	0.3167	66	86	62.52E-06	0.43060
GR	1.3351	0.2448	0.1833	41	58	2.723E-02	0.22118
ARMotifH	1.3186	8.8385	6.7028	192	356	3.321E-36	15.48524
Hand1::Tcfe2a	1.3076	1.3802	1.0556	136	223	78.8E-16	1.45432
RUNX1	1.3010	0.3542	0.2722	54	80	67.95E-04	0.33771
FEV	1.2701	0.6562	0.5167	96	140	7.595E-08	0.57650
FOXI1	1.2500	0.9375	0.7500	111	166	2.794E-10	1.19265
FOXO3	1.2158	1.7292	1.4222	155	251	20.49E-22	1.94834
ARID3A	0.8216	3.0104	3.6639	160	310	20.44E-20	8.63844
SP1	0.8083	1.1562	1.4306	93	170	78.47E-06	6.85844
Gfi	0.8036	0.8281	1.0306	97	213	14.95E-04	1.25431
Pdx1	0.7857	2.0625	2.6250	143	295	1.276E-12	5.15289
Prrx2	0.7641	1.8698	2.4472	143	289	55.31E-14	4.42195
FOXL1	0.7071	5.0417	7.1306	182	338	2.045E-30	41.68223
Foxd3	0.6415	1.6198	2.5250	140	258	8.429E-14	10.19895

15.68 AR LNCaP vs VCaP DHT overlaps (stable)

Chromosome specific statistics are shown in Table 173. A histogram of sequence lengths is shown in Figure 203.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	358	2	425	975	152134	0.00061
10	122	178	398	830	48507	0.000358
11	172	23	415	922	71431	0.000529
12	111	75	390	700	43276	0.000323
13	84	228	439	1097	36859	0.00032
14	111	38	396	824	43993	0.00041
15	143	5	432	1065	61745	0.000602
16	97	211	387	1042	37540	0.000415
17	139	201	416	918	57825	0.000712
18	70	209	433	923	30291	0.000388
19	51	202	416	947	21205	0.000359
2	252	12	409	918	103095	0.000424
20	92	238	421	1134	38747	0.000615
21	45	196	433	644	19475	0.000405
22	54	12	367	545	19831	0.000387
3	243	9	423	1006	102897	0.00052
4	146	0	401	873	58573	0.000306
5	190	12	424	1129	80512	0.000445
6	204	69	394	918	80473	0.00047
7	171	158	423	1124	72370	0.000455
8	156	4	431	829	67178	0.000459
9	115	169	408	679	46915	0.000332
X	59	57	365	717	21521	0.000139
Y	2	311	328	344	655	1.1e-05
all 24	3187	0	413	1134	1317048	0.000425

Table 173: Chromosome specific distribution of the regions. The last line represents the overall statistics.

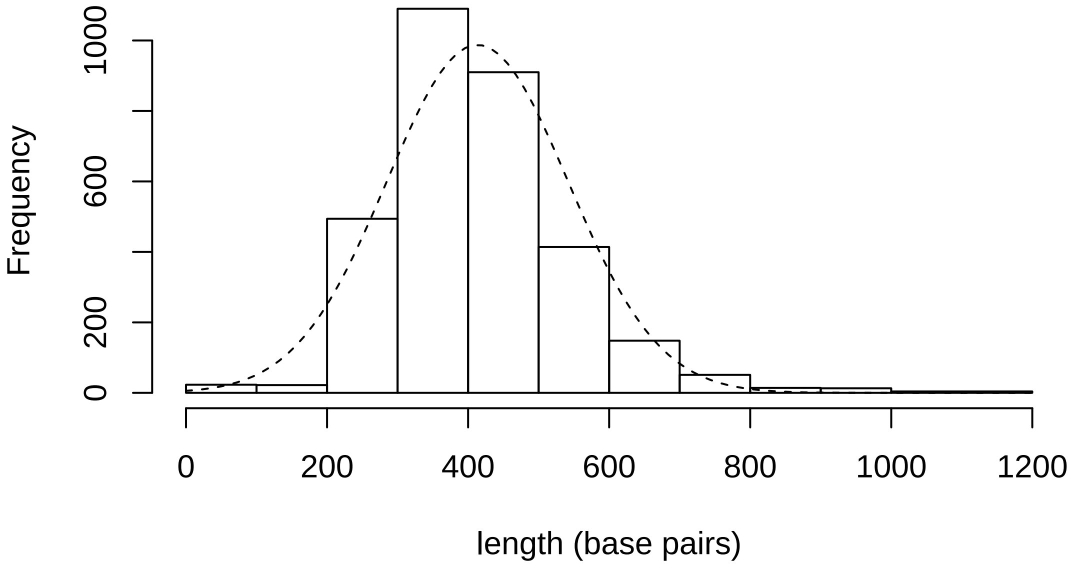
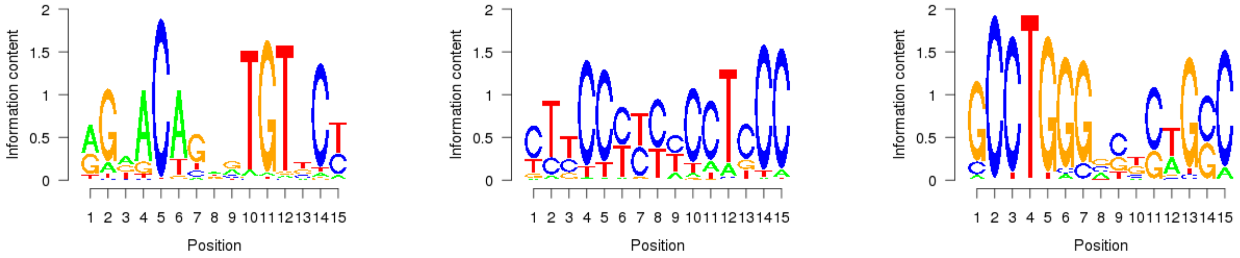


Figure 203: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrOs-gCount** component.

property	value
genes	3202



(a) ARvsAR2rrOs-deNovo-meme1: width=15, sites=194, llr=1904, E=1.6e-55 (b) ARvsAR2rrOs-deNovo-meme2: width=15, sites=87, llr=968, E=2.2e-13 (c) ARvsAR2rrOs-deNovo-meme3: width=15, sites=23, llr=316, E=62000

Figure 204: De novo motifs for the filtered AR LNCaP vs VCaP DHT overlaps (stable) sequences.

Table 174: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	20.4954	0.1153	0.0056	336	32	1.862E-118	0.04951
TLX1::NFIC	3.3024	0.0185	0.0056	48	29	70.89E-08	0.01331
FOXA1	2.7912	0.9843	0.3526	2049	1653	0.00E00	0.68273
FOXF2	2.6112	0.3007	0.1151	838	616	3.93E-106	0.19203
FOXA1pAR	2.5365	0.1879	0.0740	554	379	78.81E-70	0.12773
Foxa2	2.4416	0.8511	0.3485	1853	1463	0.00E00	0.73811
ESR2	2.2862	0.0283	0.0123	78	65	83.65E-08	0.02265
ARMotifTT	2.0512	0.0129	0.0063	41	37	14.72E-04	0.00850
ARMotifTH	1.8249	0.0704	0.0385	219	224	5.034E-12	0.04941
ARMotifT	1.8011	0.6500	0.3609	1490	1711	51.42E-142	0.51656
GABPA	1.7680	0.0927	0.0524	284	293	14.1E-16	0.06845
PPARG::RXRA	1.7640	0.0242	0.0137	70	79	19.78E-04	0.01948
CTCF	1.7594	0.0063	0.0035	20	18	3.354E-02	0.00515
FOXD1	1.7465	1.2633	0.7233	2258	2804	11.38E-314	1.12473
Tal1::Gata1	1.7261	0.0578	0.0335	176	192	3.024E-08	0.04330
GRMotifTH	1.7169	0.3698	0.2153	961	1130	1.677E-60	0.29444
Stat3	1.7156	0.2265	0.1320	542	643	2.006E-24	0.22225
AR	1.7064	0.0603	0.0353	184	203	2.274E-08	0.04521
NR3C1	1.5987	0.3732	0.2334	930	1190	33.22E-48	0.31894
Foxq1	1.5900	0.5822	0.3661	1382	1635	6.101E-116	0.53306
GRMotifTT	1.5291	0.0264	0.0172	82	100	35.5E-04	0.02091
GRMotifT	1.4603	2.4524	1.6793	2867	4676	0.00E00	2.48297
Tcfcp2l1	1.4530	0.0710	0.0489	208	256	61.07E-08	0.06593
ELK4	1.4326	0.0254	0.0177	76	102	2.674E-02	0.02200
Pax5	1.4298	0.0556	0.0389	172	226	1.174E-04	0.04493
GR	1.4255	0.2937	0.2061	802	1033	6.911E-36	0.25963
STAT1	1.4059	0.0440	0.0313	110	156	1.829E-02	0.04764
ARMotifHH	1.4026	0.4031	0.2874	1003	1341	1.068E-48	0.39954
Esrrb	1.3803	0.1206	0.0874	359	487	29.92E-10	0.10132
NHLH1	1.3605	0.1348	0.0991	261	376	53.54E-06	0.20046
ARMotifH	1.3283	8.6472	6.5100	3170	5852	0.00E00	14.90483
Evi1	1.3153	0.0449	0.0341	137	192	48.97E-04	0.04044
Gata1	1.3015	0.7333	0.5634	1576	2402	4.925E-96	0.72604
NFIC	1.2975	2.7301	2.1041	2829	4857	0.00E00	3.44977
RXR::RAR_DR5	1.2564	0.0295	0.0235	93	133	3.883E-02	0.02715
Arnt	1.2538	0.1778	0.1418	398	563	48.58E-10	0.25457
GRMotifHH	1.2464	0.2297	0.1842	625	914	8.321E-16	0.22736
ELK1	1.2303	0.8944	0.7270	1822	2853	5.752E-132	0.93105
FEV	1.2215	0.6422	0.5257	1485	2358	10.13E-76	0.61207
FOXI1	1.2184	0.9189	0.7542	1781	2661	28.78E-136	1.23850
EBF1	1.2166	0.6638	0.5456	1329	2118	59.19E-58	0.90282
TEAD1	1.2082	0.0823	0.0681	250	390	25.4E-04	0.07325
Hand1::Tcfe2a	1.2062	1.2215	1.0127	2172	3612	3.318E-194	1.26414
Myf	1.2031	0.2381	0.1979	579	893	31.57E-12	0.30403
MZF1_5-13	0.8130	1.1376	1.3993	2012	4130	48.86E-106	1.85869
HLF	0.7949	0.3864	0.4861	904	2018	14.34E-04	0.60597
CREB1	0.7859	0.6255	0.7960	1396	2938	66.45E-28	0.96642
Pdx1	0.7847	2.1219	2.7042	2521	4926	1.071E-246	4.97458
Prrx2	0.7428	1.8960	2.5526	2419	4859	3.147E-206	4.46201
Foxd3	0.7260	1.8256	2.5147	2260	4104	11.31E-192	9.55293
FOXL1	0.7089	5.5573	7.8396	2993	5512	0.00E00	55.83794
Zfx	0.6794	0.1118	0.1646	303	804	3.543E-04	0.18197
MEF2A	0.6730	0.2218	0.3296	549	1384	4.038E-02	0.44567
Pou5f1	0.5682	0.0079	0.0139	23	81	92.52E-04	0.01228
Ddit3::Cebpa	0.5067	0.2096	0.4136	586	1758	24.69E-08	0.44299

15.69 AR LNCaP vs VCaP DHT unique for ARDHTrrO

Chromosome specific statistics are shown in Table 175. A histogram of sequence lengths is shown in Figure 205.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	43	12	383	650	16480	6.6e-05
10	5	250	349	482	1744	1.3e-05
11	26	222	378	579	9831	7.3e-05
12	13	3	432	933	5614	4.2e-05
13	10	200	363	536	3628	3.2e-05
14	9	51	302	459	2720	2.5e-05
15	8	350	421	565	3368	3.3e-05
16	20	295	404	565	8089	9e-05
17	16	286	391	524	6261	7.7e-05
18	6	256	376	475	2253	2.9e-05
19	5	235	326	400	1630	2.8e-05
2	21	218	355	495	7448	3.1e-05
20	10	268	484	898	4837	7.7e-05
22	1	640	640	640	640	1.2e-05
3	21	300	451	636	9479	4.8e-05
4	11	253	412	629	4527	2.4e-05
5	24	213	383	568	9186	5.1e-05
6	20	180	357	565	7141	4.2e-05
7	11	282	456	620	5015	3.2e-05
8	17	224	359	535	6100	4.2e-05
9	5	270	347	446	1733	1.2e-05
X	3	281	335	416	1006	6e-06
all 22	305	3	389	933	118730	3.8e-05

Table 175: Chromosome specific distribution of the regions. The last line represents the overall statistics.

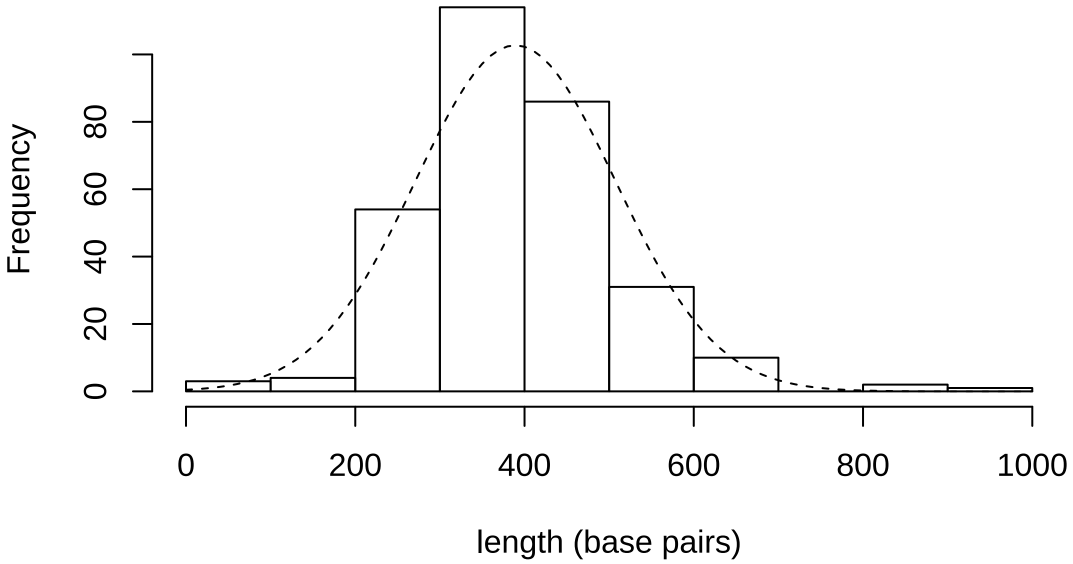
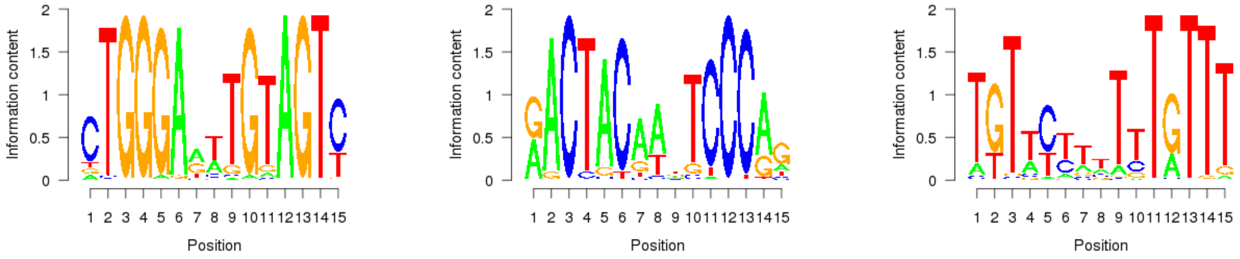


Figure 205: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU1-gCount** component.

property	value
genes	1293



(a) ARvsAR2rrU1-deNovo-meme1: width=15, sites=46, llr=718, E=5.1e-81

(b) ARvsAR2rrU1-deNovo-meme2: width=15, sites=41, llr=550, E=7.2e-29

(c) ARvsAR2rrU1-deNovo-meme3: width=15, sites=56, llr=640, E=7.5e-11

Figure 206: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARDHTrrO sequences.

Table 176: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	3.7925	0.0526	0.0138	16	8	14.41E-04	0.02650
ELK4	3.5258	0.0855	0.0242	22	14	8.487E-04	0.05469
FOXA1pAR	3.4775	0.2829	0.0813	74	36	11.88E-16	0.19857
STAT1	3.3513	0.0987	0.0294	24	15	3.755E-04	0.08229
FOXA1	2.4548	0.7730	0.3149	159	154	39.77E-24	0.55374
GABPA	2.4506	0.1612	0.0657	40	37	3.853E-04	0.12079
Stat3	2.4289	0.3026	0.1246	63	57	77.9E-08	0.27413
Egr1	2.3641	0.1678	0.0709	43	33	11.49E-06	0.15483
Foxa2	2.0943	0.6776	0.3235	141	137	88.39E-20	0.58103
TFAP2A	1.8147	2.6184	1.4429	186	326	2.944E-14	10.26066
FOXF2	1.8009	0.2368	0.1315	62	70	99.36E-06	0.17839
Arnt	1.7524	0.1941	0.1107	43	39	1.462E-04	0.23138
Myb	1.6230	0.9211	0.5675	180	238	4.508E-20	0.75696
HIF1A::ARNT	1.5994	0.5230	0.3270	96	120	55.07E-08	0.71361
FOXD1	1.4871	1.0395	0.6990	173	271	2.654E-14	1.06044
EBF1	1.4345	0.6875	0.4792	125	182	3.594E-08	0.89013
Foxq1	1.4259	0.5230	0.3668	113	163	64.88E-08	0.55045
Klf4	1.4259	0.2763	0.1938	66	92	23.96E-04	0.30924
Gata1	1.4241	0.6480	0.4550	128	202	28.09E-08	0.61531
Esrrb	1.3967	0.1184	0.0848	35	46	4.839E-02	0.09626
FEV	1.3889	0.6776	0.4879	147	197	60.2E-14	0.65380
ELK1	1.3600	0.9671	0.7111	174	285	17.91E-14	1.01190
ARMotifHH	1.3357	0.3651	0.2734	88	127	1.404E-04	0.35977
NFIC	1.3207	2.5592	1.9377	267	451	28.53E-42	3.46384
ARMotifH	1.2841	7.5888	5.9100	302	569	22.96E-56	13.45560
FOXI1	1.2260	0.8421	0.6869	145	251	7.515E-08	1.10731
SPI1	1.2178	1.8520	1.5208	251	414	27.51E-36	2.04818
Nobox	0.8241	1.1776	1.4291	179	374	31.1E-10	2.29579
Nkx3-2	0.8017	1.4079	1.7561	220	458	10.38E-18	2.01609
FOXL1	0.7675	5.3553	6.9775	260	540	86.65E-32	56.52511
Pdx1	0.7505	1.8257	2.4325	218	481	10.7E-16	4.21680
YY1	0.7337	2.7928	3.8062	275	546	71.98E-40	6.30745
Prrx2	0.7203	1.6711	2.3201	214	468	57.47E-16	3.67629
Foxd3	0.6987	1.7467	2.5000	184	411	95.91E-10	12.63456

15.70 AR LNCaP vs VCaP DHT unique for ARDHTrrO (up)

Chromosome specific statistics are shown in Table 177. A histogram of sequence lengths is shown in Figure 207.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	8	255	401	597	3210	1.3e-05
2	1	437	437	437	437	2e-06
3	2	389	412	435	824	4e-06
5	1	312	312	312	312	2e-06
6	1	538	538	538	538	3e-06
8	2	339	408	478	817	6e-06
11	4	302	365	458	1461	1.1e-05
12	1	419	419	419	419	3e-06
13	1	454	454	454	454	4e-06
14	1	459	459	459	459	4e-06
17	1	352	352	352	352	4e-06
all 11	23	255	404	597	9283	3e-06

Table 177: Chromosome specific distribution of the regions. The last line represents the overall statistics.

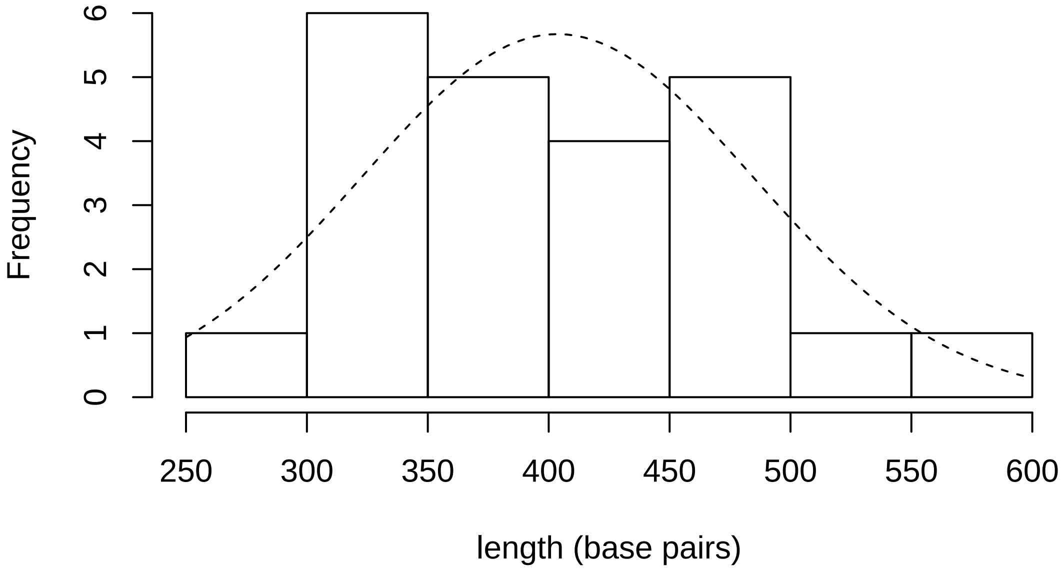
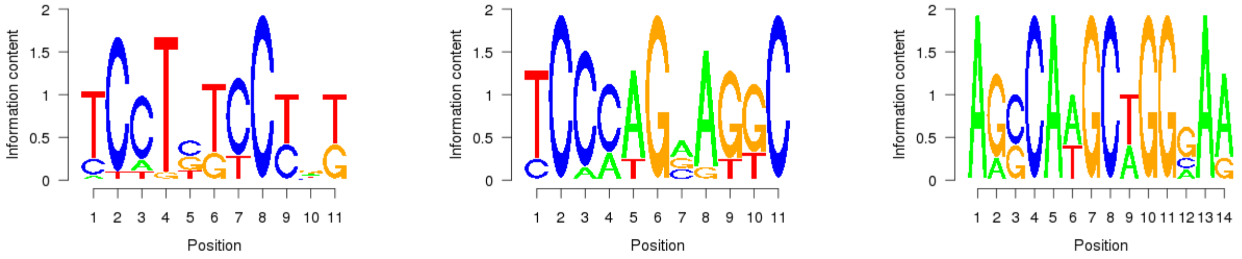


Figure 207: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU1u-gCount** component.

property	value
genes	27



(a) ARvsAR2rrU1u-deNovo-meme1: width=11, sites=22, llr=191, E=44000
(b) ARvsAR2rrU1u-deNovo-meme2: width=11, sites=11, llr=121, E=84000
(c) ARvsAR2rrU1u-deNovo-meme3: width=14, sites=5, llr=77, E=1400000

Figure 208: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARDHTrrO (up) sequences.

Table 178: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Stat3	7.8210	0.5217	0.0667	7	3	1.745E-02	0.35360
NHLH1	2.7945	0.4348	0.1556	8	4	1.289E-02	0.33955
Foxa2	2.2824	0.6087	0.2667	11	10	1.589E-02	0.38894
HIF1A::ARNT	1.9564	0.5652	0.2889	11	11	2.367E-02	0.38894
NFIC	1.8327	3.2174	1.7556	23	35	5.245E-06	3.17537
Myb	1.6770	1.0435	0.6222	16	21	35.29E-04	0.71993
SPI1	1.6555	2.3913	1.4444	21	32	76.07E-06	2.21247
BRCA1	1.5351	2.2174	1.4444	22	36	36.92E-06	1.43459
FEV	1.4461	0.7391	0.5111	13	17	2.516E-02	0.54434
Mafb	1.3294	2.3043	1.7333	19	35	22.75E-04	2.72586
ELF5	1.2601	1.6522	1.3111	18	31	36.0E-04	1.77063
SOX10	0.8289	5.9130	7.1333	22	44	1.579E-04	17.60733
Arnt::Ahr	0.8131	1.3913	1.7111	17	26	39.86E-04	18.27283
Fos	0.8041	1.3043	1.6222	16	30	2.466E-02	3.71620
MZF1_5-13	0.7881	1.2609	1.6000	17	34	1.782E-02	1.92515
GATA2	0.7642	9.3913	12.2889	23	45	35.82E-06	28.96291
YY1	0.7391	2.9565	4.0000	21	43	6.017E-04	4.73924
Pdx1	0.7337	1.6957	2.3111	16	33	3.928E-02	4.45193
SPIB	0.7337	2.2174	3.0222	19	42	67.21E-04	4.10075
FOXL1	0.4467	4.0000	8.9556	19	42	67.21E-04	56.44315
MEF2A	0.0001	0.0000	0.4444	0	14	2.517E-02	0.47937

15.71 AR LNCaP vs VCaP DHT unique for ARDHTrrO (down)

Chromosome specific statistics are shown in Table 179. A histogram of sequence lengths is shown in Figure 209.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	4	241	351	442	1403	6e-06
2	2	437	466	495	932	4e-06
3	1	399	399	399	399	2e-06
6	1	509	509	509	509	3e-06
7	2	398	509	620	1018	6e-06
8	2	243	276	308	551	4e-06
11	2	222	312	401	623	5e-06
12	1	462	462	462	462	3e-06
14	1	394	394	394	394	4e-06
17	3	305	392	456	1175	1.4e-05
all 10	19	222	393	620	7466	2e-06

Table 179: Chromosome specific distribution of the regions. The last line represents the overall statistics.

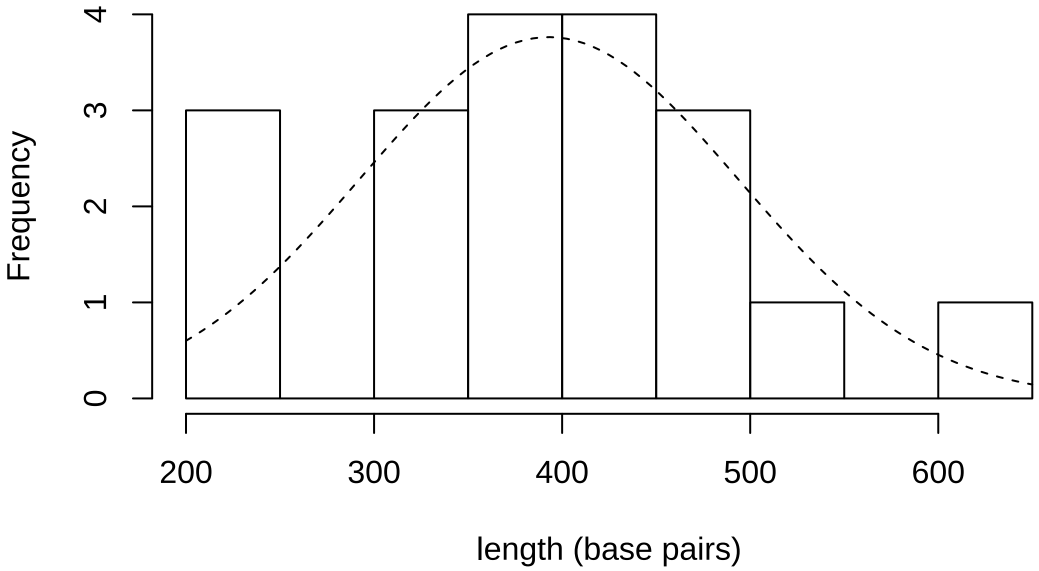
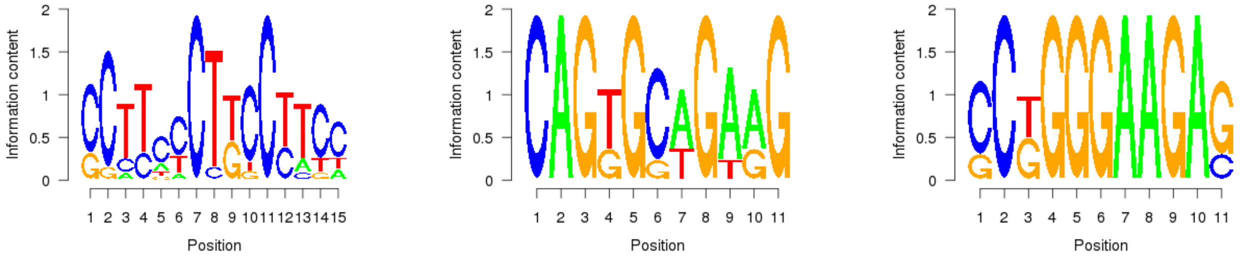


Figure 209: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU1d-gCount** component.

property	value
genes	16



(a) ARvsAR2rrU1d-deNovo-meme1: width=15, sites=11, llr=136, E=1900

(b) ARvsAR2rrU1d-deNovo-meme2: width=11, sites=6, llr=76, E=2e+05

(c) ARvsAR2rrU1d-deNovo-meme3: width=11, sites=4, llr=55, E=450000

Figure 210: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARDHTrrO (down) sequences.

Table 180: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
FOXA1	2.4998	0.7895	0.3158	10	11	3.36E-02	0.50376
Foxa2	2.2665	0.8947	0.3947	12	12	56.45E-04	0.60777
ELF5	1.4737	2.2105	1.5000	16	27	25.91E-04	2.80451
NR4A2	1.3877	1.7895	1.2895	15	29	1.296E-02	1.32393
GRMotifT	1.3226	2.1579	1.6316	19	28	28.38E-06	1.87281
NFIC	1.3077	2.6842	2.0526	17	31	14.09E-04	2.87594
SPI1	1.2787	2.0526	1.6053	18	32	3.726E-04	1.47431
FOXC1	1.2754	6.9474	5.4474	18	37	8.769E-04	11.83647
ETS1	1.2212	6.6842	5.4737	18	38	10.2E-04	11.00251
Pdx1	1.2048	2.6316	2.1842	17	30	11.67E-04	3.86905
ZNF354C	0.8246	2.4737	3.0000	16	34	87.11E-04	5.50439
Pax2	0.7312	1.7895	2.4474	17	36	32.14E-04	2.57206
Mafb	0.7302	1.2105	1.6579	14	31	4.984E-02	1.39724
Foxd3	0.6885	2.2105	3.2105	14	25	1.932E-02	16.85965
Nkx3-2	0.6250	1.3158	2.1053	15	30	1.525E-02	2.38534

15.72 AR LNCaP vs VCaP DHT unique for ARDHTrrO (stable)

Chromosome specific statistics are shown in Table 181. A histogram of sequence lengths is shown in Figure 211.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	34	12	362	597	12324	4.9e-05
10	6	244	389	555	2334	1.7e-05
11	19	222	370	579	7030	5.2e-05
12	9	3	404	933	3637	2.7e-05
13	6	266	447	536	2680	2.3e-05
14	6	101	300	458	1799	1.7e-05
15	6	350	453	668	2719	2.7e-05
16	17	295	418	565	7107	7.9e-05
17	17	286	401	637	6817	8.4e-05
18	6	256	370	475	2221	2.8e-05
19	4	267	349	400	1395	2.4e-05
2	16	218	359	518	5746	2.4e-05
20	8	268	382	589	3059	4.9e-05
22	1	640	640	640	640	1.2e-05
3	19	300	436	580	8285	4.2e-05
4	8	253	391	629	3129	1.6e-05
5	17	246	409	736	6945	3.8e-05
6	14	211	377	538	5272	3.1e-05
7	9	282	447	620	4027	2.5e-05
8	11	230	391	588	4299	2.9e-05
9	3	270	375	446	1125	8e-06
X	1	281	281	281	281	2e-06
all 22	237	3	392	933	92871	3e-05

Table 181: Chromosome specific distribution of the regions. The last line represents the overall statistics.

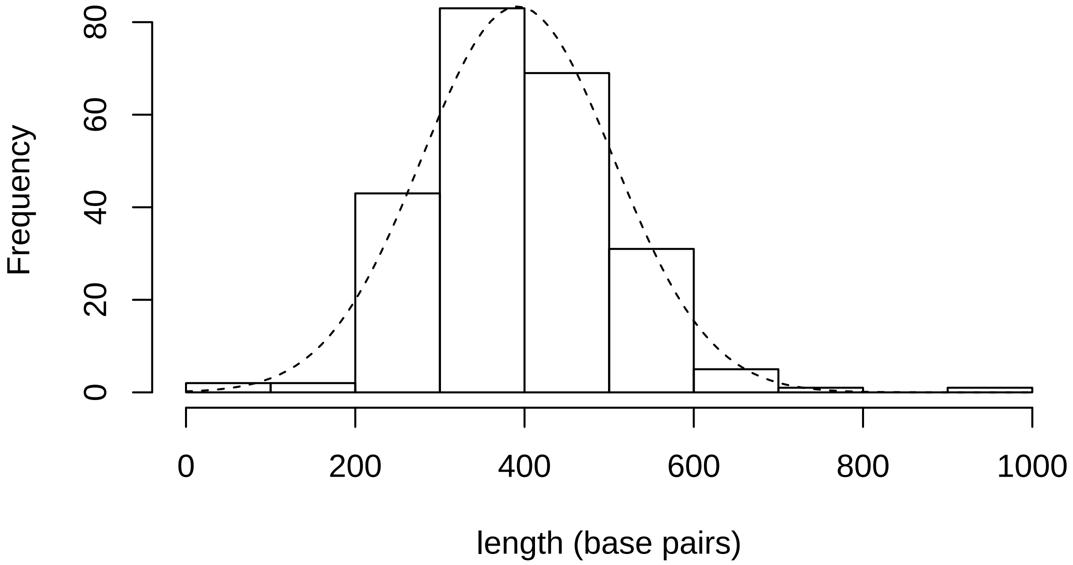
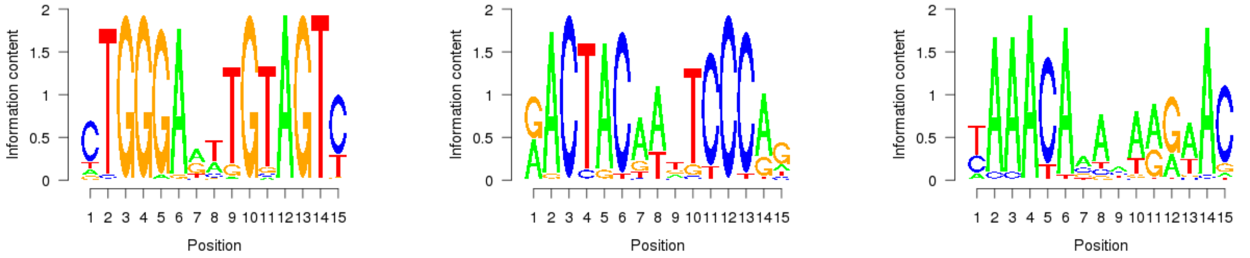


Figure 211: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU1s-gCount** component.

property	value
genes	430



(a) ARvsAR2rrU1s-deNovo-meme1: width=15, sites=39, llr=615, E=1.3e-70

(b) ARvsAR2rrU1s-deNovo-meme2: width=15, sites=31, llr=431, E=2.9e-22

(c) ARvsAR2rrU1s-deNovo-meme3: width=15, sites=43, llr=495, E=0.00094

Figure 212: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARDHTrrO (stable) sequences.

Table 182: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	24.0009	0.0551	0.0022	13	1	13.88E-06	0.02016
FOXA1pAR	7.8863	0.2839	0.0360	53	14	6.824E-16	0.17189
STAT1	6.9846	0.1102	0.0157	21	6	3.466E-06	0.08147
ELK4	5.8789	0.1059	0.0180	21	8	23.93E-06	0.06088
E2F1	3.3835	0.0381	0.0112	9	5	3.627E-02	0.02016
GABPA	2.8595	0.1864	0.0652	34	27	1.833E-04	0.14290
Stat3	2.5027	0.3263	0.1303	53	46	2.569E-06	0.29447
Foxa2	2.4874	0.6653	0.2674	107	95	11.07E-16	0.53844
Egr1	2.3284	0.1780	0.0764	36	29	1.239E-04	0.13459
FOXA1	2.2167	0.7373	0.3326	120	115	23.02E-18	0.56139
FOXF2	1.9270	0.1949	0.1011	40	43	19.54E-04	0.14535
Esrrb	1.8849	0.1144	0.0607	27	27	1.068E-02	0.07311
TFAP2A	1.6595	2.6441	1.5933	155	246	15.11E-16	8.92613
HIF1A::ARNT	1.6374	0.5593	0.3416	78	104	26.41E-06	0.69347
FOXD1	1.5153	0.9364	0.6180	122	188	28.41E-10	0.98050
EBF1	1.4574	0.7500	0.5146	103	145	10.54E-08	1.06463
ELK1	1.4372	0.9915	0.6899	139	210	78.39E-14	1.08415
NF-kappaB	1.4329	0.2415	0.1685	42	60	3.911E-02	0.28296
Arnt	1.4303	0.1864	0.1303	34	39	1.181E-02	0.22165
ARMotifHH	1.4218	0.3898	0.2742	72	100	2.41E-04	0.35993
Myb	1.4142	0.9280	0.6562	139	219	4.859E-12	0.74642
Foxq1	1.4021	0.4915	0.3506	82	122	1.261E-04	0.47847
FEV	1.3995	0.7076	0.5056	116	180	3.238E-08	0.61817
NFIC	1.3043	2.7288	2.0921	213	351	16.84E-36	3.50938
Klf4	1.3038	0.2754	0.2112	52	74	1.075E-02	0.30570
Gata1	1.2599	0.6314	0.5011	98	173	2.014E-04	0.61881
SPI1	1.2397	1.9195	1.5483	192	336	1.128E-24	2.18960
Mafb	1.2349	2.0424	1.6539	198	331	2.634E-28	2.47581
Hand1::Tcfe2a	1.2327	1.0720	0.8697	148	252	1.801E-12	1.07725
ARMotifH	1.2287	7.8305	6.3730	235	440	16.9E-44	13.11895
FOXI1	1.2126	0.7712	0.6360	107	186	16.02E-06	0.96984
ARMotifT	1.2067	0.4068	0.3371	80	116	1.102E-04	0.44285
Sox5	0.8176	1.5085	1.8449	163	349	20.77E-12	2.63050
ARID3A	0.7734	2.6314	3.4022	179	376	6.848E-16	8.36113
HOXA5	0.7729	4.6568	6.0247	222	427	25.13E-36	14.92427
Nkx3-2	0.7667	1.4110	1.8404	171	360	11.57E-14	2.12830
YY1	0.7414	2.8305	3.8180	217	417	80.19E-34	6.83802
Pdx1	0.7316	1.7246	2.3573	167	355	1.781E-12	4.41915
Nobox	0.7280	1.1059	1.5191	137	281	28.54E-08	2.88789
Foxd3	0.7252	1.6737	2.3079	140	302	54.09E-08	8.59811
Prrx2	0.6905	1.5890	2.3011	160	356	4.611E-10	3.99851
FOXL1	0.6349	4.9068	7.7281	201	403	1.552E-24	180.10818

15.73 AR LNCaP vs VCaP DHT unique for ARvcap

Chromosome specific statistics are shown in Table 183. A histogram of sequence lengths is shown in Figure 213.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	4421	136	405	2499	1788623	0.007176
10	2450	136	404	1582	990336	0.007307
11	2533	141	434	2589	1100307	0.00815
12	2655	119	420	3062	1116256	0.008339
13	1442	137	438	3219	631022	0.005479
14	1619	136	400	1287	647544	0.006032
15	1959	133	427	2278	835551	0.008149
16	925	132	373	1230	344730	0.003815
17	1603	129	429	1238	687159	0.008463
18	1228	129	408	2400	501427	0.006422
19	880	153	441	1549	388199	0.006565
2	4269	118	401	1721	1712797	0.007043
20	1390	145	442	1617	614227	0.009746
21	906	157	502	1826	454506	0.009443
22	723	159	430	2433	310820	0.006058
3	3757	126	407	1864	1530546	0.007729
4	3101	140	410	2478	1270528	0.006647
5	2924	108	409	2597	1194681	0.006604
6	2977	112	407	5734	1210705	0.007075
7	3230	111	422	1821	1362371	0.008561
8	2860	119	439	2097	1255247	0.008576
9	2547	123	427	1741	1087793	0.007703
X	1422	117	383	7354	544611	0.003507
Y	269	161	376	1031	101129	0.001703
all 24	52090	108	416	7354	21681115	0.007004

Table 183: Chromosome specific distribution of the regions. The last line represents the overall statistics.

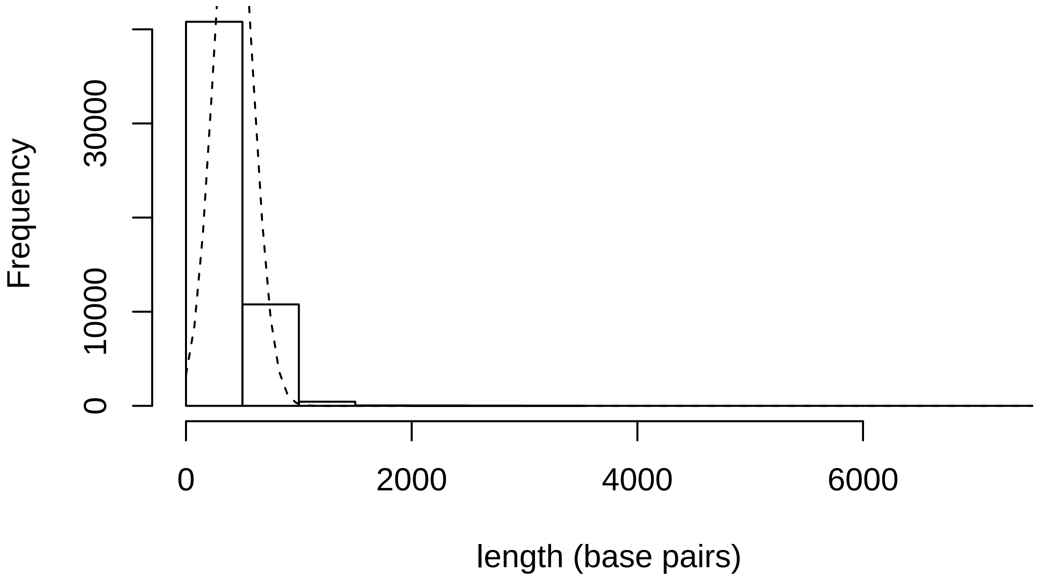
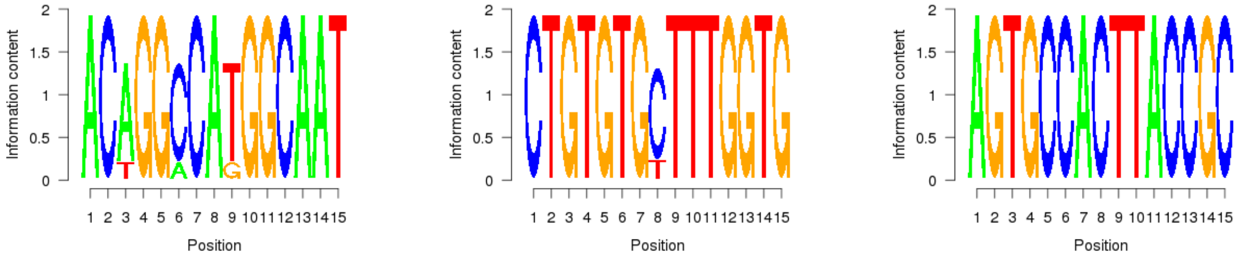


Figure 213: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU2-gCount** component.

property	value
genes	31656



(a) ARvsAR2rrU2-deNovo-meme1: width=15, sites=7, llr=139, E=180 (b) ARvsAR2rrU2-deNovo-meme2: width=15, sites=6, llr=124, E=650 (c) ARvsAR2rrU2-deNovo-meme3: width=15, sites=5, llr=107, E=5000

Figure 214: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARvcap sequences.

Table 184: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	10.6546	0.0867	0.0081	4079	767	0.00E00	0.04294
TLX1::NFIC	3.3422	0.0209	0.0062	819	483	17.11E-102	0.01649
CTCF	2.6676	0.0088	0.0033	455	308	52.75E-48	0.00578
FOXA1	1.9628	0.7084	0.3609	25984	27781	0.00E00	0.62840
ARMotifTH	1.9250	0.0738	0.0383	3631	3608	84.75E-194	0.05543
Tal1::Gata1	1.8041	0.0552	0.0306	2777	2910	5.825E-124	0.03997
Foxa2	1.7906	0.6073	0.3391	23093	24009	0.00E00	0.63681
ARMotifT	1.7861	0.6721	0.3762	24587	28973	0.00E00	0.58036
ESR2	1.7580	0.0225	0.0128	1025	1108	26.53E-40	0.02082
FOXF2	1.7576	0.2123	0.1208	9834	10760	0.00E00	0.16468
GRMotifTH	1.6844	0.3587	0.2129	15193	18097	0.00E00	0.30729
ARMotifTT	1.6627	0.0115	0.0069	591	658	78.68E-22	0.00876
AR	1.6506	0.0661	0.0400	3280	3777	27.79E-114	0.05148
GABPA	1.5663	0.0826	0.0527	3970	4827	1.072E-118	0.07148
GRMotifTT	1.5603	0.0301	0.0193	1534	1834	1.215E-42	0.02358
ARMotifHH	1.5259	0.4443	0.2912	17290	22498	0.00E00	0.57699
ELK4	1.5238	0.0292	0.0191	1423	1768	5.719E-34	0.02741
FOXA1pAR	1.4941	0.1071	0.0717	5107	6122	17.54E-172	0.10524
NR3C1	1.4905	0.3566	0.2393	14842	20030	0.00E00	0.31930
FOXD1	1.4491	1.0491	0.7239	32558	46134	0.00E00	1.07300
Stat3	1.4433	0.1916	0.1328	7643	10194	1.036E-208	0.21224
GRMotifT	1.4339	2.4939	1.7392	46483	77044	0.00E00	2.98488
Arnt	1.4287	0.2060	0.1442	6756	9214	1.577E-158	0.51394
RXRA::VDR	1.4160	0.0074	0.0052	382	502	14.37E-08	0.00616
PPARG::RXRA	1.3849	0.0228	0.0165	1174	1560	1.011E-20	0.01918
GR	1.3659	0.3041	0.2226	13057	18376	0.00E00	0.28452
Myc	1.3464	0.1644	0.1221	6172	8983	34.84E-104	0.41328
Tcfcp2l1	1.3394	0.0670	0.0500	3138	4422	71.05E-48	0.06503
ARMotifH	1.3241	8.7301	6.5932	52006	96134	0.00E00	20.68022
Mycn	1.3240	0.1295	0.0978	4773	7054	2.871E-64	0.37155
E2F1	1.3023	0.0150	0.0115	759	1087	41.67E-10	0.01321
MIZF	1.3013	0.0267	0.0205	1357	1965	36.08E-16	0.02315
GRMotifHH	1.2974	0.2433	0.1875	10448	15328	11.37E-246	0.24791
NHLH1	1.2912	0.1320	0.1022	4575	6296	90.78E-88	0.20004
Esrrb	1.2898	0.1088	0.0843	5267	7683	6.699E-80	0.09743
Foxq1	1.2802	0.4691	0.3665	18430	27013	0.00E00	0.52029
Gata1	1.2659	0.6966	0.5502	24650	38553	0.00E00	0.72536
TAL1::TCF3	1.2406	0.2547	0.2053	9607	14396	2.597E-192	0.32391
Arnt::Ahr	1.2364	1.6229	1.3126	33768	56399	0.00E00	7.16254
STAT1	1.2286	0.0387	0.0315	1626	2472	23.3E-14	0.04686
TEAD1	1.2211	0.0872	0.0714	4279	6611	11.69E-42	0.08034
MYC::MAX	1.2124	0.0687	0.0567	2745	4342	1.245E-18	0.09814
MAX	1.2109	0.2199	0.1816	8666	13924	14.52E-112	0.39682
PBX1	0.8299	0.0897	0.1081	4257	9027	3.224E-02	0.15632
ARID3A	0.8256	3.0908	3.7435	45210	83427	0.00E00	10.25417
HLF	0.7965	0.3864	0.4852	15067	33190	1.672E-52	0.63604
NF-kappaB	0.7950	0.1670	0.2101	6553	15579	12.93E-12	0.29123
Pdx1	0.7901	2.1300	2.6959	41151	80692	0.00E00	5.51674
IRF2	0.7722	0.0055	0.0072	285	696	2.141E-04	0.00662
Zfx	0.7401	0.1214	0.1641	5117	13001	8.655E-32	0.20272
Prrx2	0.7356	1.8716	2.5443	39122	79088	0.00E00	4.86364
IRF1	0.7215	0.1815	0.2516	8109	19672	1.44E-10	0.28818
NFIL3	0.7213	0.1433	0.1987	6096	14307	1.866E-10	0.32411
FOXL1	0.7175	5.5682	7.7608	48332	90349	0.00E00	61.20657
RREB1	0.6984	0.0283	0.0406	1070	2535	40.18E-10	0.11427
Foxd3	0.6520	1.6421	2.5185	33743	67066	0.00E00	10.79996
Lhx3	0.6396	0.2201	0.3441	8356	21017	4.111E-18	0.56488
MEF2A	0.6356	0.2140	0.3367	8516	22740	10.22E-38	0.49447
Ddit3::Cebpa	0.6067	0.2434	0.4012	10736	27667	1.067E-12	0.46771
EWSR1-FLI1	0.2610	0.0064	0.0246	115	452	55.03E-14	0.18453

15.74 AR LNCaP vs VCaP DHT unique for ARvcap (up)

Chromosome specific statistics are shown in Table 185. A histogram of sequence lengths is shown in Figure 215.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	243	177	406	1107	98613	0.000396
10	107	190	425	926	45431	0.000335
11	123	204	562	2589	69076	0.000512
12	78	196	448	1008	34908	0.000261
13	52	189	391	623	20322	0.000176
14	51	190	432	1047	22034	0.000205
15	194	168	463	1018	89870	0.000877
16	31	181	395	1230	12248	0.000136
17	120	165	441	1129	52925	0.000652
18	39	196	447	1109	17439	0.000223
19	86	187	579	1549	49820	0.000843
2	173	154	418	1212	72275	0.000297
20	55	160	431	812	23680	0.000376
21	57	258	541	1367	30816	0.00064
22	36	216	430	759	15484	0.000302
3	165	150	427	952	70393	0.000355
4	165	169	430	1098	70937	0.000371
5	113	166	471	1182	53249	0.000294
6	117	191	448	2031	52415	0.000306
7	104	173	453	1142	47104	0.000296
8	103	185	495	1004	50940	0.000348
9	122	123	439	1125	53617	0.00038
X	20	215	429	683	8586	5.5e-05
all 23	2354	123	451	2589	1062182	0.000343

Table 185: Chromosome specific distribution of the regions. The last line represents the overall statistics.

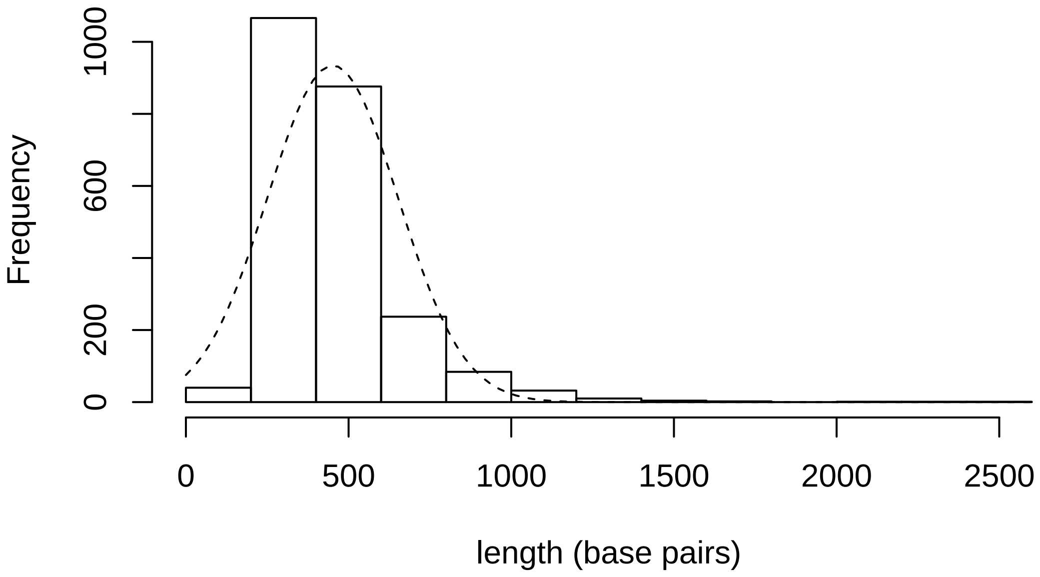
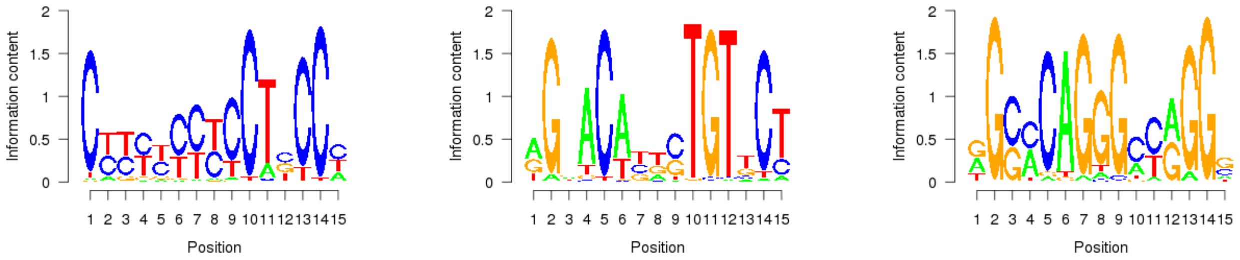


Figure 215: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU2u-gCount** component.

property	value
genes	297



(a) ARvsAR2rrU2u-deNovo-meme1: width=15, sites=129, llr=1338, E=7.7e-09

(b) ARvsAR2rrU2u-deNovo-meme2: width=15, sites=90, llr=991, E=0.00019

(c) ARvsAR2rrU2u-deNovo-meme3: width=15, sites=30, llr=400, E=350000

Figure 216: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARvcap (up) sequences.

Table 186: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	8.4951	0.0858	0.0101	187	41	5.766E-52	0.04058
TLX1::NFIC	4.0447	0.0297	0.0073	54	29	1.198E-08	0.02058
CTCF	2.9008	0.0140	0.0048	33	21	89.09E-06	0.00796
RXRA::VDR	2.6032	0.0102	0.0039	24	17	25.16E-04	0.00606
PPARG::RXRA	2.1243	0.0370	0.0174	86	76	84.33E-08	0.02394
ARMotifTH	2.1180	0.0828	0.0391	180	167	1.318E-12	0.05739
E2F1	2.0120	0.0217	0.0107	51	47	4.375E-04	0.01435
Tal1::Gata1	1.9569	0.0667	0.0341	154	144	1.368E-10	0.04579
AR	1.8355	0.0709	0.0386	154	159	1.381E-08	0.05845
ARMotifT	1.7780	0.7141	0.4016	1155	1372	38.4E-110	0.60277
GABPA	1.7664	0.1066	0.0603	220	250	7.30E-10	0.09090
GRMotifTH	1.7444	0.4031	0.2311	742	881	12.46E-48	0.32418
ESR2	1.7216	0.0272	0.0158	56	60	26.43E-04	0.02621
FOXA1	1.6640	0.6470	0.3888	1096	1323	11.56E-96	0.54895
FOXF2	1.6273	0.1946	0.1195	419	486	94.0E-22	0.14863
Foxa2	1.5718	0.5590	0.3557	970	1141	97.42E-80	0.58594
ELK4	1.5504	0.0408	0.0263	85	111	93.12E-04	0.03484
GRMotifTT	1.5475	0.0319	0.0206	73	90	68.01E-04	0.02452
ARMotifHH	1.5203	0.5081	0.3342	880	1130	28.11E-56	0.58176
Tcfcp2l1	1.5147	0.0956	0.0631	199	234	4.578E-08	0.09211
FOXA1pAR	1.4865	0.1088	0.0731	224	279	9.075E-08	0.10831
NR3C1	1.4802	0.3857	0.2606	713	970	2.266E-32	0.33869
GRMotifT	1.4599	2.7681	1.8960	2139	3522	0.00E00	3.29889
MIZF	1.4466	0.0344	0.0238	79	101	88.84E-04	0.02823
Arnt	1.4291	0.2489	0.1742	363	495	1.247E-10	0.38882
Mycn	1.4226	0.1623	0.1141	274	373	23.07E-08	0.20655
Myc	1.4137	0.1958	0.1385	327	459	2.631E-08	0.25562
GR	1.4125	0.3364	0.2382	638	867	1.737E-26	0.31542
NFKB1	1.3671	0.0875	0.0640	155	202	1.359E-04	0.11904
Esrrb	1.3539	0.1300	0.0960	271	395	12.79E-06	0.11499
RELA	1.3376	0.1266	0.0946	244	360	1.052E-04	0.13357
ARMotifH	1.3375	9.7447	7.2859	2352	4335	0.00E00	27.20948
Stat3	1.3200	0.2145	0.1625	381	537	3.624E-10	0.25420
NHLH1	1.2956	0.1457	0.1125	233	296	12.16E-08	0.21691
GRMotifHH	1.2845	0.2596	0.2021	509	736	95.78E-16	0.26321
HIF1A::ARNT	1.2756	0.5327	0.4176	788	1208	1.671E-28	0.90016
MAX	1.2646	0.2370	0.1874	407	637	17.9E-08	0.30170
TAL1::TCF3	1.2589	0.2676	0.2126	462	673	3.295E-12	0.33507
Pax5	1.2575	0.0667	0.0530	145	215	1.022E-02	0.07201
FOXD1	1.2572	0.9673	0.7694	1414	2154	1.489E-116	1.04143
ELK1	1.2470	0.9911	0.7947	1385	2221	43.55E-102	1.11526
EBF1	1.2467	0.7332	0.5881	1010	1621	1.175E-44	1.09549
NR2F1	1.2229	0.1300	0.1063	279	422	53.37E-06	0.13387
Arnt::Ahr	1.2197	1.8105	1.4843	1627	2676	6.238E-152	8.54563
Myb	1.2128	0.8895	0.7335	1309	2136	4.652E-84	0.96430
TFAP2A	1.2121	2.0637	1.7026	1578	2575	70.02E-142	8.12725
Myf	1.2117	0.2897	0.2391	483	750	2.367E-10	0.71793
Gfi	0.8263	0.8879	1.0745	1281	2654	17.73E-46	1.32572
NKX3-1	0.8043	0.6342	0.7886	977	2001	1.085E-18	1.24137
Nobox	0.7963	1.3432	1.6869	1485	2972	9.405E-82	3.09548
Nkx2-5	0.7881	5.1597	6.5472	2220	4141	0.00E00	21.86716
ARID3A	0.7540	2.9970	3.9749	2006	3802	1.379E-242	10.91968
Pdx1	0.7080	2.0387	2.8793	1835	3667	4.009E-168	5.91311
Prrx2	0.6778	1.8449	2.7218	1746	3579	2.064E-136	5.25323
FOXL1	0.6620	5.3607	8.0983	2149	4093	2.272E-304	61.28969
NFIL3	0.6617	0.1381	0.2087	264	660	2.415E-02	0.28006
Foxd3	0.6537	1.7549	2.6846	1481	3056	5.164E-76	12.71241
Lhx3	0.5484	0.2052	0.3742	347	996	56.44E-06	0.60197
MEF2A	0.5415	0.1916	0.3538	349	1071	43.52E-08	0.45974

15.75 AR LNCaP vs VCaP DHT unique for ARvcap (down)

Chromosome specific statistics are shown in Table 187. A histogram of sequence lengths is shown in Figure 217.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	105	168	409	1945	42981	0.000172
10	41	240	434	926	17805	0.000131
11	188	185	493	2589	92640	0.000686
12	105	190	406	994	42656	0.000319
13	29	179	381	702	11043	9.6e-05
14	84	175	406	885	34107	0.000318
15	23	158	461	832	10614	0.000104
16	17	220	413	867	7018	7.8e-05
17	76	165	432	958	32796	0.000404
18	27	199	362	603	9762	0.000125
19	35	181	434	1064	15173	0.000257
2	151	188	410	1721	61852	0.000254
20	101	174	429	1086	43316	0.000687
21	14	399	576	895	8063	0.000168
22	19	203	377	653	7163	0.00014
3	129	194	415	1268	53546	0.00027
4	129	161	436	1114	56289	0.000294
5	70	183	446	1100	31241	0.000173
6	106	212	422	1017	44736	0.000261
7	84	151	418	1136	35084	0.00022
8	134	168	437	1056	58545	4e-04
9	14	229	409	607	5727	4.1e-05
X	62	193	658	7354	40778	0.000263
all 23	1743	151	438	7354	762935	0.000246

Table 187: Chromosome specific distribution of the regions. The last line represents the overall statistics.

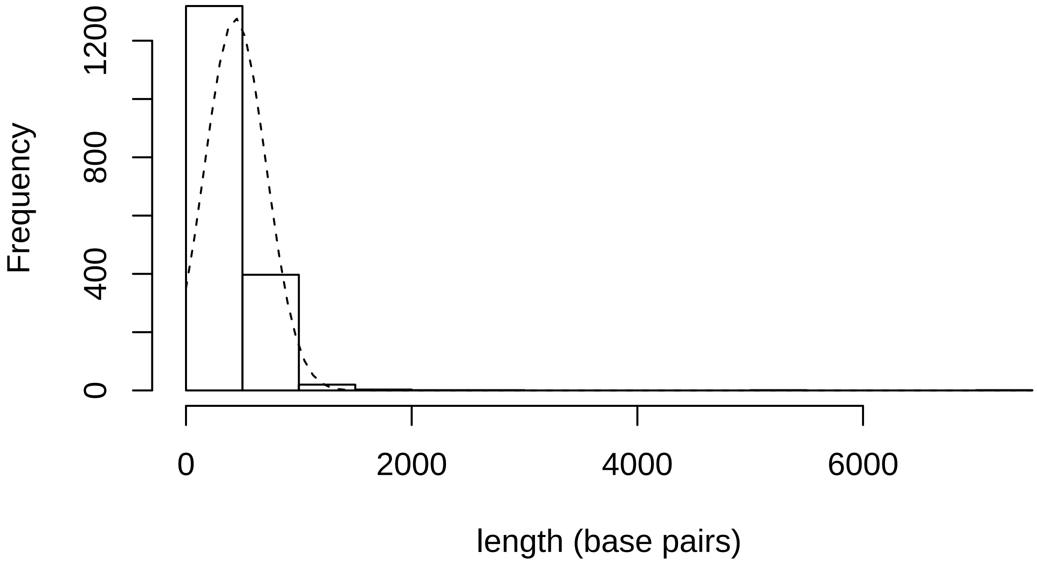
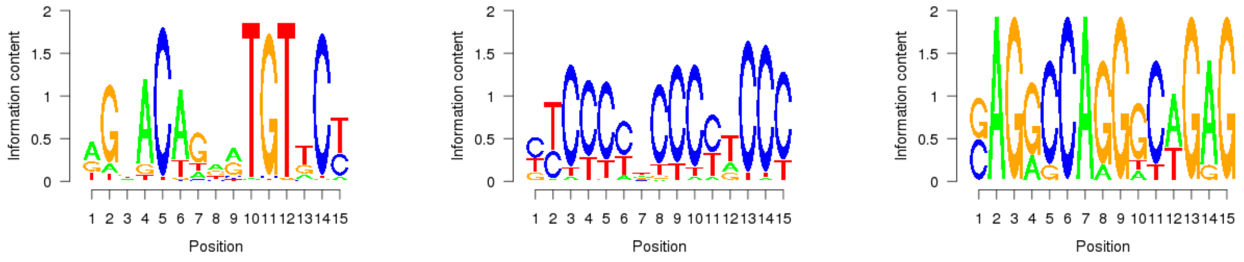


Figure 217: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU2d-gCount** component.

property	value
genes	256



(a) ARvsAR2rrU2d-deNovo-meme1: width=15, sites=109, llr=1174, E=6.1e-16 (b) ARvsAR2rrU2d-deNovo-meme2: width=15, sites=56, llr=665, E=120 (c) ARvsAR2rrU2d-deNovo-meme3: width=15, sites=8, llr=139, E=1.6e+08

Figure 218: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARvcap (down) sequences.

Table 188: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	11.9080	0.0906	0.0076	142	25	3.835E-44	0.04129
TLX1::NFIC	6.3424	0.0310	0.0048	39	14	40.1E-10	0.02042
ESR2	2.9857	0.0281	0.0094	45	29	2.502E-06	0.01798
Tal1::Gata1	2.1643	0.0597	0.0275	100	90	4.502E-08	0.03913
ARMotifTH	2.1309	0.0723	0.0339	121	104	1.638E-10	0.05168
ELK4	1.7266	0.0356	0.0206	60	66	16.38E-04	0.02668
FOXA1	1.7145	0.6741	0.3932	816	1008	3.451E-72	0.61499
ARMotifT	1.6879	0.6483	0.3841	811	980	6.62E-74	0.60616
MIZF	1.6452	0.0304	0.0185	53	60	51.81E-04	0.02248
GABPA	1.6436	0.0975	0.0593	158	184	23.78E-08	0.07718
Foxa2	1.6296	0.5944	0.3647	750	882	2.052E-66	0.62068
Myc	1.6175	0.2071	0.1280	263	309	56.07E-14	0.24380
GRMotifTH	1.5912	0.3511	0.2206	516	624	1.964E-32	0.29225
MYC::MAX	1.5874	0.0918	0.0578	117	140	44.52E-06	0.11268
AR	1.5585	0.0585	0.0375	94	122	23.79E-04	0.04714
Egr1	1.5349	0.1027	0.0669	155	198	13.52E-06	0.09598
FOXF2	1.5308	0.1928	0.1259	302	372	8.328E-14	0.16051
Pax5	1.5131	0.0637	0.0421	102	135	21.71E-04	0.05224
NR3C1	1.4987	0.3706	0.2473	499	690	2.448E-22	0.42349
Arnt	1.4580	0.2352	0.1613	261	329	1.106E-10	0.40920
Esrrb	1.4526	0.1337	0.0920	211	283	82.67E-08	0.11531
Tcfcp2l1	1.4428	0.0769	0.0533	123	155	1.263E-04	0.07153
GR	1.4374	0.3133	0.2179	438	607	11.43E-18	0.30131
Mycn	1.4347	0.1555	0.1084	202	246	1.418E-08	0.20741
ARMotifHH	1.4253	0.4504	0.3160	581	819	2.857E-28	0.46179
GRMotifT	1.4248	2.5714	1.8048	1562	2629	3.56E-244	3.74447
Stat3	1.4225	0.2020	0.1419	270	372	1.43E-08	0.21749
FOXA1pAR	1.4022	0.1044	0.0745	164	197	47.07E-08	0.12162
FOXD1	1.3791	1.0327	0.7488	1067	1604	1.611E-96	1.18918
NR2F1	1.3376	0.1348	0.1008	213	308	24.02E-06	0.12011
ARMotifH	1.3242	9.2278	6.9685	1742	3269	72.49E-318	32.92260
Arnt::Ahr	1.3111	1.7476	1.3329	1172	1955	7.086E-106	7.16228
TAL1::TCF3	1.2868	0.2765	0.2149	348	517	10.32E-10	0.34017
MAX	1.2764	0.2484	0.1946	330	491	70.5E-10	0.30769
HIF1A::ARNT	1.2489	0.4676	0.3744	528	834	51.94E-18	0.75499
RELA	1.2354	0.1256	0.1017	192	293	7.484E-04	0.13079
Gata1	1.2249	0.7063	0.5766	824	1324	1.169E-44	0.87147
GRMotifHH	1.2243	0.2438	0.1992	333	543	2.423E-06	0.27400
USF1	1.2220	0.6277	0.5136	569	888	1.264E-20	1.12437
EBF1	1.2176	0.7028	0.5772	727	1213	6.485E-30	1.07895
Hand1::Tcfe2a	1.2168	1.2937	1.0633	1177	2023	2.05E-102	1.74435
TFAP2A	1.2082	1.8302	1.5148	1102	1894	87.73E-86	6.08610
NKX3-1	0.8316	0.6403	0.7700	722	1466	7.873E-16	1.33330
Nkx2-5	0.8091	5.3236	6.5796	1660	3138	8.641E-268	33.38103
Pdx1	0.7766	2.1773	2.8036	1358	2736	31.43E-128	7.90474
ARID3A	0.7692	3.0046	3.9062	1475	2830	4.158E-178	15.22164
Prrx2	0.7175	1.9082	2.6595	1302	2696	5.886E-106	6.60034
FOXL1	0.6596	5.4928	8.3278	1611	3078	6.624E-240	85.48360
IRF1	0.6556	0.1750	0.2669	251	690	76.71E-04	0.32894
MEF2A	0.6244	0.2220	0.3556	290	807	81.42E-04	0.50864
Foxd3	0.6208	1.6386	2.6395	1101	2282	12.12E-60	12.50837
Lhx3	0.6175	0.2301	0.3726	281	746	3.911E-02	0.73727
NFIL3	0.6017	0.1331	0.2212	182	503	41.21E-04	0.44099

15.76 AR LNCaP vs VCaP DHT unique for ARvcap (stable)

Chromosome specific statistics are shown in Table 189. A histogram of sequence lengths is shown in Figure 219.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	3021	136	403	2499	1217340	0.004884
10	1454	136	405	1323	588249	0.00434
11	1713	141	440	2589	753112	0.005578
12	1604	119	418	1065	671091	0.005014
13	934	137	411	2959	384276	0.003337
14	1093	136	402	1287	439747	0.004096
15	1500	133	423	2278	633788	0.006181
16	715	132	377	1230	269334	0.002981
17	1218	129	433	1238	527573	0.006498
18	690	129	410	2400	283080	0.003626
19	749	153	432	1490	323262	0.005467
2	2663	118	400	1395	1066284	0.004384
20	940	145	445	1617	418057	0.006633
21	629	157	506	1826	318013	0.006607
22	645	159	426	2293	274508	0.005351
3	2170	130	409	1864	887815	0.004483
4	1800	140	410	2478	738626	0.003864
5	1749	108	411	2597	718943	0.003974
6	1737	112	404	5734	700895	0.004096
7	2052	111	423	1343	868899	0.00546
8	1565	119	436	2097	681576	0.004657
9	1553	135	433	1318	671851	0.004758
X	932	136	370	1585	345054	0.002222
Y	176	172	375	1031	66033	0.001112
all 24	33302	108	416	5734	13847406	0.004473

Table 189: Chromosome specific distribution of the regions. The last line represents the overall statistics.

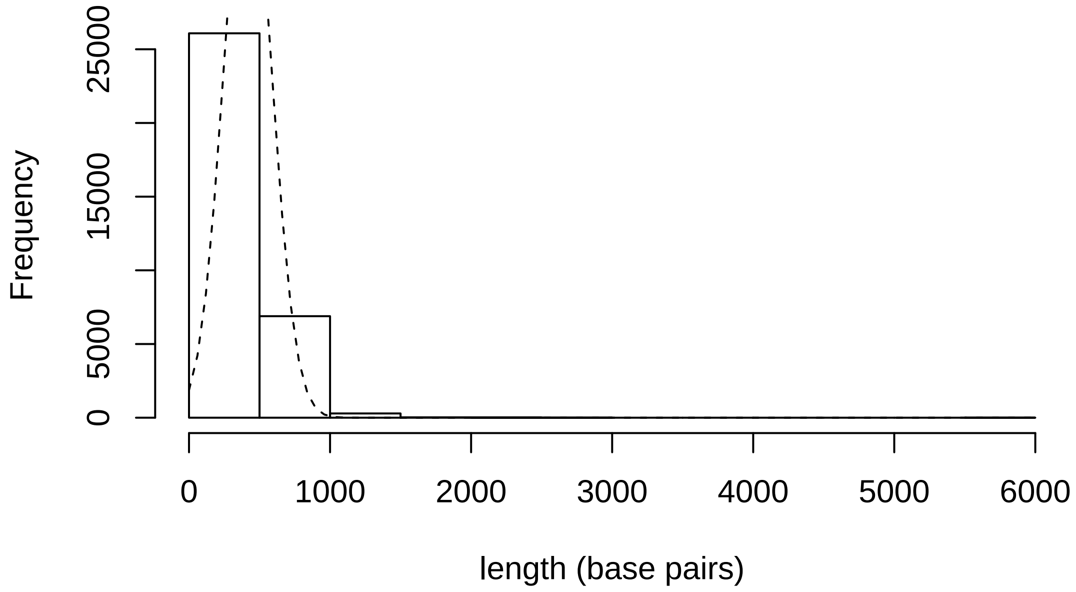
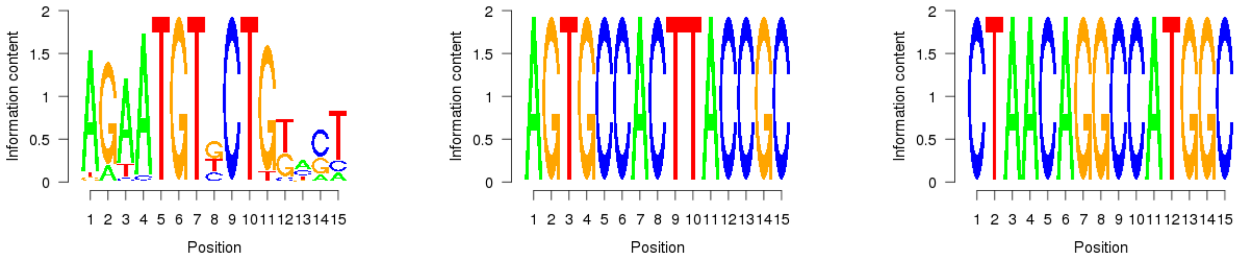


Figure 219: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **ARvsAR2rrU2s-gCount** component.

property	value
genes	9402



(a) ARvsAR2rrU2s-deNovo-meme1: width=15, sites=31, llr=439, E=1.2e-06 (b) ARvsAR2rrU2s-deNovo-meme2: width=15, sites=7, llr=149, E=0.0037 (c) ARvsAR2rrU2s-deNovo-meme3: width=15, sites=7, llr=149, E=0.0037

Figure 220: De novo motifs for the filtered AR LNCaP vs VCaP DHT unique for ARvcap (stable) sequences.

Table 190: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	10.5386	0.0894	0.0084	2681	508	0.00E00	0.04569
TLX1::NFIC	3.7498	0.0227	0.0060	550	288	1.855E-78	0.01798
ESR1	3.2558	0.0005	0.0001	16	7	10.99E-04	0.00024
CTCF	2.8306	0.0099	0.0035	325	212	11.93E-36	0.00592
FOXA1	2.0019	0.7039	0.3516	16521	17401	0.00E00	0.65668
ARMotifTH	1.9191	0.0734	0.0382	2289	2275	1.033E-120	0.05841
ESR2	1.8356	0.0223	0.0121	653	686	17.36E-28	0.01903
ARMotifT	1.7959	0.6659	0.3708	15645	18269	0.00E00	0.57646
Foxa2	1.7847	0.5998	0.3360	14607	15133	0.00E00	0.67206
Tal1::Gata1	1.7352	0.0550	0.0317	1770	1916	7.012E-72	0.04081
FOXF2	1.7253	0.2088	0.1210	6199	6857	0.00E00	0.16286
GRMotifTH	1.6975	0.3607	0.2125	9742	11511	0.00E00	0.31101
AR	1.6965	0.0656	0.0387	2079	2336	33.45E-78	0.04961
ARMotifTT	1.6393	0.0114	0.0069	373	420	48.31E-14	0.00866
GRMotifTT	1.6245	0.0295	0.0181	959	1096	22.58E-32	0.02275
GABPA	1.6004	0.0866	0.0541	2644	3165	7.666E-84	0.07538
ELK4	1.5868	0.0306	0.0192	936	1138	1.389E-24	0.02991
ARMotifHH	1.5425	0.4545	0.2946	11181	14501	0.00E00	0.67180
FOXA1pAR	1.5122	0.1089	0.0720	3304	3907	12.66E-116	0.10988
PPARG::RXRA	1.4887	0.0247	0.0166	815	1005	3.312E-20	0.01974
NR3C1	1.4860	0.3539	0.2381	9435	12652	0.00E00	0.31668
FOXD1	1.4505	1.0344	0.7131	20567	29140	0.00E00	1.06026
Arnt	1.4455	0.2155	0.1490	4406	5991	71.96E-106	0.64881
Stat3	1.4447	0.1924	0.1332	4893	6509	6.992E-134	0.21379
RXRA::VDR	1.4360	0.0076	0.0053	248	327	33.69E-06	0.00615
GRMotifT	1.4349	2.4955	1.7392	29762	49011	0.00E00	2.99816
E2F1	1.3936	0.0157	0.0113	511	683	39.94E-10	0.01330
GR	1.3921	0.3021	0.2170	8320	11442	10.89E-294	0.27976
Myc	1.3898	0.1737	0.1250	4043	5761	33.96E-76	0.54341
Mycn	1.3716	0.1381	0.1007	3139	4590	36.06E-46	0.49591
Tcfcp2l1	1.3401	0.0695	0.0519	2079	2891	14.2E-34	0.06835
ARMotifH	1.3271	8.8188	6.6450	33245	61264	0.00E00	20.92642
MIZF	1.3094	0.0278	0.0212	903	1291	32.95E-12	0.02415
Foxq1	1.2749	0.4598	0.3607	11540	16907	0.00E00	0.52657
Esrrb	1.2696	0.1092	0.0860	3387	4993	1.922E-48	0.09901
GRMotifHH	1.2692	0.2442	0.1924	6710	9969	50.16E-150	0.25376
STAT1	1.2686	0.0397	0.0313	1075	1592	69.63E-12	0.04627
NHLH1	1.2599	0.1362	0.1081	2997	4267	1.667E-48	0.20319
TEAD1	1.2351	0.0859	0.0695	2692	4123	17.07E-28	0.07802
MYC::MAX	1.2346	0.0706	0.0572	1775	2799	1.384E-12	0.10572
NR2F1	1.2307	0.1196	0.0972	3687	5614	3.139E-46	0.11229
TAL1::TCF3	1.2307	0.2510	0.2039	6101	9162	46.75E-120	0.31753
Gata1	1.2273	0.6804	0.5544	15479	24766	0.00E00	0.72392
Arnt::Ahr	1.2260	1.6456	1.3423	21760	36089	0.00E00	7.51890
Pax5	1.2239	0.0569	0.0465	1784	2762	1.583E-14	0.05326
RORA_2	1.2134	0.0217	0.0179	715	1096	9.471E-06	0.01929
MAX	1.2124	0.2256	0.1861	5557	8972	45.62E-70	0.48765
Myf	1.2092	0.2565	0.2121	6176	9768	21.05E-96	0.39780
Sox2	1.2066	0.0081	0.0067	269	413	1.188E-02	0.00723
ELK1	1.2037	0.8777	0.7291	18275	29947	0.00E00	0.97936
Nkx2-5	0.8333	5.1068	6.1283	31528	58473	0.00E00	20.29656
ARID3A	0.8047	2.9809	3.7044	28467	52803	0.00E00	10.05552
NF-kappaB	0.8027	0.1713	0.2134	4286	9993	8.418E-06	0.29622
HLF	0.7956	0.3797	0.4772	9512	20990	2.626E-30	0.59065
Zfx	0.7728	0.1332	0.1723	3567	8709	7.021E-14	0.21112
Pdx1	0.7723	2.0536	2.6591	25958	51079	0.00E00	5.43860
RREB1	0.7358	0.0291	0.0395	699	1581	1.683E-04	0.11019
IRF1	0.7214	0.1784	0.2473	5081	12296	9.854E-08	0.28516
Prrx2	0.7203	1.8169	2.5225	24641	50059	0.00E00	4.83249
NFIL3	0.7050	0.1379	0.1956	3762	9005	1.949E-10	0.30424
FOXL1	0.7029	5.3857	7.6623	30594	57326	0.00E00	60.57011
Foxd3	0.6440	1.6149	2.5078	21303	42354	0.00E00	11.06050
MEF2A	0.6170	0.2048	0.3319	5258	14284	15.92E-32	0.48809
Lhx3	0.6027	0.2071	0.3437	5077	13301	1.081E-22	0.55644
Ddit3::Cebpa	0.6000	0.2438	0.4063	6870	17606	3.112E-08	0.48365
EWSR1-FLI1	0.2611	0.0063	0.0243	71	287	32.88E-10	0.18650

15.77 GR LNCaP vs VCaP DEX overlaps

Chromosome specific statistics are shown in Table 191. A histogram of sequence lengths is shown in Figure 221.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	287	3	217	568	62268	0.00025
10	103	6	199	451	20460	0.000151
11	164	6	233	596	38223	0.000283
12	129	2	212	748	27343	0.000204
13	52	17	189	431	9827	8.5e-05
14	105	4	196	484	20599	0.000192
15	123	7	218	587	26855	0.000262
16	67	45	187	490	12523	0.000139
17	123	0	228	515	28054	0.000346
18	60	18	198	539	11883	0.000152
19	61	31	210	671	12786	0.000216
2	207	12	202	495	41892	0.000172
20	80	17	242	463	19347	0.000307
21	65	1	234	588	15194	0.000316
22	56	13	216	491	12077	0.000235
3	178	9	220	532	39153	0.000198
4	152	8	200	491	30418	0.000159
5	155	11	205	439	31826	0.000176
6	145	6	191	621	27645	0.000162
7	199	9	210	756	41732	0.000262
8	176	5	219	594	38611	0.000264
9	147	0	220	512	32409	0.00023
X	34	8	168	327	5722	3.7e-05
Y	9	12	84	142	752	1.3e-05
all 24	2877	0	211	756	607599	0.000196

Table 191: Chromosome specific distribution of the regions. The last line represents the overall statistics.

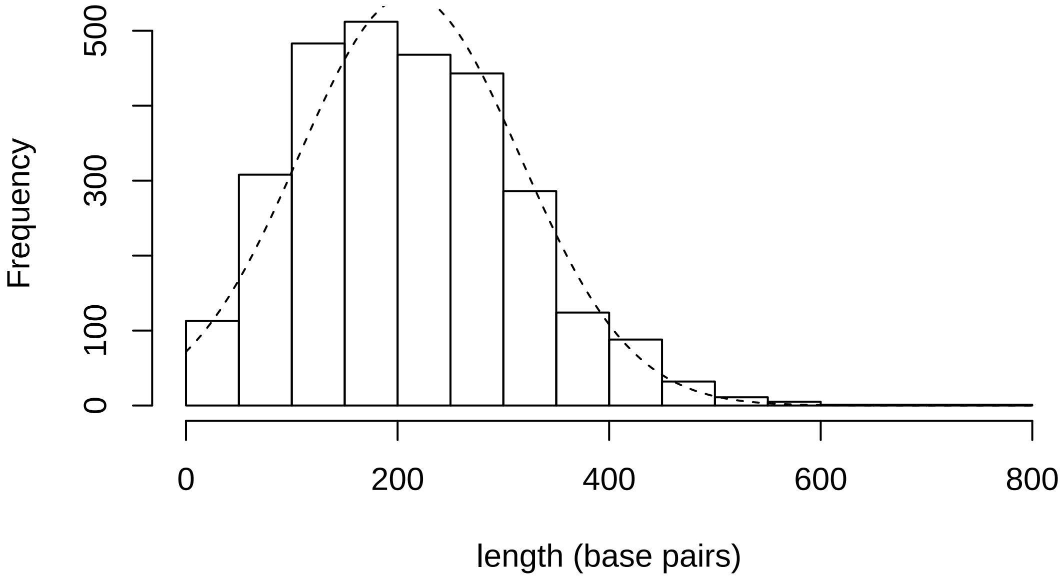
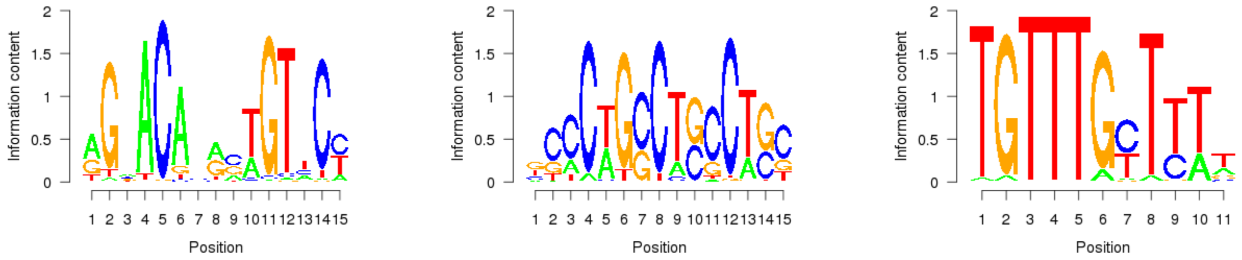


Figure 221: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrO-gCount** component.

property	value
genes	7485



(a) GRvsGR2rrO-deNovo-meme1: width=15, sites=221, llr=2174, E=3.9e-130

(b) GRvsGR2rrO-deNovo-meme2: width=15, sites=56, llr=636, E=1.8

(c) GRvsGR2rrO-deNovo-meme3: width=11, sites=59, llr=653, E=4.8e-07

Figure 222: De novo motifs for the filtered GR LNCaP vs VCaP DEX overlaps sequences.

Table 192: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	28.6308	0.0661	0.0023	176	12	1.002E-64	0.02743
TLX1::NFIC	14.6757	0.0283	0.0019	64	10	3.126E-20	0.01518
RXRA::VDR	4.0754	0.0063	0.0015	18	8	5.342E-04	0.00317
Tal1::Gata1	3.1421	0.0392	0.0124	108	65	1.967E-14	0.02254
FOXA1	3.1227	0.5423	0.1736	1163	814	95.29E-188	0.35750
Foxa2	2.9374	0.4664	0.1588	1024	674	47.38E-166	0.36148
ESR2	2.3623	0.0161	0.0068	40	33	5.287E-04	0.01239
FOXF2	2.3157	0.1497	0.0646	388	323	1.229E-34	0.10114
NHLH1	2.2859	0.1189	0.0520	214	181	19.39E-18	0.13436
Stat3	2.1059	0.1325	0.0629	296	262	83.47E-24	0.12226
Tcfcp2l1	2.0106	0.0587	0.0292	148	141	14.0E-10	0.04899
GRMotifTH	2.0055	0.1972	0.0983	494	479	19.46E-36	0.14661
Esrrb	1.9533	0.0839	0.0429	238	223	4.368E-16	0.05572
MIZF	1.8828	0.0220	0.0117	63	62	3.061E-04	0.01507
NFIC	1.8446	1.9829	1.0750	2225	3086	37.12E-316	2.36462
AR	1.7866	0.0367	0.0205	103	108	14.18E-06	0.02624
ARMotifTH	1.7755	0.0392	0.0220	108	114	10.09E-06	0.02945
GABPA	1.7488	0.0573	0.0328	161	161	22.27E-10	0.04505
FOXD1	1.7453	0.6364	0.3646	1277	1518	42.05E-110	0.55102
ARMotifT	1.7370	0.3357	0.1932	778	886	56.31E-50	0.27779
ELK4	1.7087	0.0206	0.0121	57	58	11.18E-04	0.01826
Myf	1.6580	0.1696	0.1023	367	439	87.65E-16	0.19007
RXR::RAR_DR5	1.5846	0.0185	0.0117	52	61	1.493E-02	0.01437
NR2F1	1.5502	0.0762	0.0492	205	250	36.98E-08	0.06181
ARMotifHH	1.5489	0.2378	0.1535	542	693	65.55E-22	0.23203
Hand1::Tcfe2a	1.5216	0.7766	0.5104	1463	1990	16.86E-116	0.73166
GRMotifT	1.5006	1.3353	0.8898	1942	2912	15.12E-200	1.40199
NFE2L2	1.4899	0.0825	0.0554	220	279	80.7E-08	0.06851
STAT1	1.4754	0.0245	0.0166	55	69	2.944E-02	0.02754
Myc	1.4723	0.0899	0.0610	203	255	1.826E-06	0.09863
Mycn	1.4588	0.0706	0.0484	159	199	38.18E-06	0.08021
TAL1::TCF3	1.4496	0.1570	0.1083	330	430	6.036E-10	0.18554
Gata1	1.4242	0.3871	0.2718	861	1208	21.76E-36	0.35232
TFAP2A	1.4214	1.1248	0.7913	1536	2041	3.617E-134	2.32831
Pax5	1.3917	0.0346	0.0249	97	129	82.45E-04	0.02870
Foxq1	1.3871	0.2531	0.1825	615	816	72.64E-24	0.24411
GR	1.3844	0.1538	0.1111	391	521	16.68E-12	0.14594
Mafb	1.3820	1.2514	0.9055	1833	2702	13.86E-176	1.58419
Arnt	1.3805	0.1126	0.0815	226	300	5.135E-06	0.14803
ARMotifH	1.3736	4.7423	3.4524	2692	4762	0.00E00	8.87986
NR3C1	1.3509	0.1654	0.1224	420	588	1.123E-10	0.14942
Myb	1.3506	0.4741	0.3510	1028	1501	12.79E-46	0.45280
MYC::MAX	1.3485	0.0381	0.0282	88	121	2.318E-02	0.04368
Egr1	1.3381	0.0542	0.0405	148	205	19.95E-04	0.04765
FOXA1pAR	1.3168	0.0444	0.0337	121	157	13.09E-04	0.04389
ELK1	1.3139	0.5164	0.3930	1084	1589	1.191E-50	0.52140
EBF1	1.3115	0.3853	0.2938	753	1127	1.951E-22	0.48092
HIF1A::ARNT	1.3028	0.2427	0.1863	547	775	25.84E-16	0.27669
TEAD1	1.2801	0.0490	0.0382	133	200	2.733E-02	0.04267
NR4A2	1.2360	1.0154	0.8215	1673	2742	12.8E-116	1.14481
RORA_1	1.2333	0.1315	0.1066	340	533	64.22E-06	0.11965
GRMotifHH	1.2329	0.1224	0.0992	312	452	2.949E-06	0.12644
BRCA1	1.2140	1.0654	0.8776	1746	2855	1.178E-130	1.24749
MAX	1.2122	0.1164	0.0960	271	425	10.96E-04	0.13172
FEV	1.2106	0.3329	0.2750	785	1221	21.76E-22	0.32243
NF-kappaB	0.8276	0.0832	0.1006	183	438	4.35E-02	0.13356
Cebpa	0.8224	0.3500	0.4256	755	1634	28.79E-04	0.51578
YY1	0.8081	1.6248	2.0107	2104	4144	1.175E-170	3.14208
Sox5	0.7858	0.7507	0.9554	1365	2820	61.94E-36	1.31663
En1	0.7852	1.8336	2.3350	2197	4357	11.81E-196	3.53154
HOXA5	0.7513	2.3759	3.1625	2328	4541	15.37E-244	6.35230
Nobox	0.7395	0.5626	0.7608	1045	2216	4.072E-12	1.19563
ARID3A	0.6956	1.2423	1.7859	1694	3481	44.25E-76	3.67901
Nkx2-5	0.6769	2.0385	3.0115	2133	4269	1.703E-174	7.21189
PBX1	0.6760	0.0360	0.0533	100	258	1.667E-02	0.05506
HLF	0.6231	0.1563	0.2508	354	1039	91.15E-08	0.28910
Pdx1	0.5906	0.7734	1.3096	1345	3242	8.833E-18	2.05932
IRF1	0.5863	0.0689	0.1175	182	537	8.608E-06	0.12247
NFIL3	0.5635	0.0531	0.0944	124	393	3.579E-06	0.11737
Prrx2	0.5351	0.6685	1.2493	1208	3148	2.073E-06	1.88379
Ddit3::Cebpa	0.5268	0.1031	0.1959	277	850	4.665E-08	0.19719
Foxd3	0.5111	0.6161	1.2055	1087	2468	13.49E-10	4.45207
FOXL1	0.4998	1.8706	3.7431	1993	4140	11.34E-130	20.39188
Lhx3	0.4469	0.0717	0.1605	164	590	32.55E-12	0.23507
MEF2A	0.4319	0.0720	0.1669	165	656	34.81E-16	0.21790
EWSR1-FLI1	0.0707	0.0007	0.0105	2	17	4.624E-02	0.04940

15.78 GR LNCaP vs VCaP DEX overlaps (up)

Chromosome specific statistics are shown in Table 193. A histogram of sequence lengths is shown in Figure 223.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	52	38	240	524	12496	5e-05
10	10	61	259	550	2586	1.9e-05
11	22	93	273	596	6015	4.5e-05
12	12	25	231	358	2770	2.1e-05
13	5	99	163	254	813	7e-06
14	8	156	280	484	2242	2.1e-05
15	5	104	269	340	1343	1.3e-05
16	9	78	160	276	1442	1.6e-05
17	10	100	173	255	1728	2.1e-05
18	4	110	188	364	754	1e-05
19	6	109	173	310	1036	1.8e-05
2	28	48	211	429	5919	2.4e-05
20	14	82	221	436	3092	4.9e-05
21	1	156	156	156	156	3e-06
22	5	78	164	271	820	1.6e-05
3	14	38	211	354	2952	1.5e-05
4	28	8	238	491	6656	3.5e-05
5	32	85	237	420	7570	4.2e-05
6	32	59	177	447	5652	3.3e-05
7	10	96	198	261	1975	1.2e-05
8	12	15	260	480	3117	2.1e-05
9	17	14	255	419	4339	3.1e-05
X	2	100	164	229	329	2e-06
all 23	338	8	224	596	75802	2.4e-05

Table 193: Chromosome specific distribution of the regions. The last line represents the overall statistics.

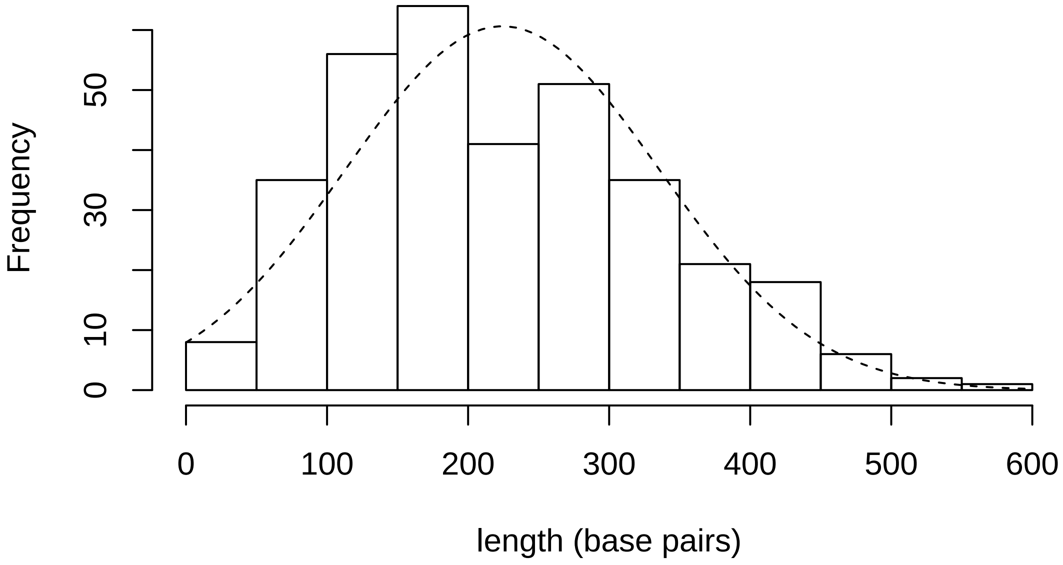
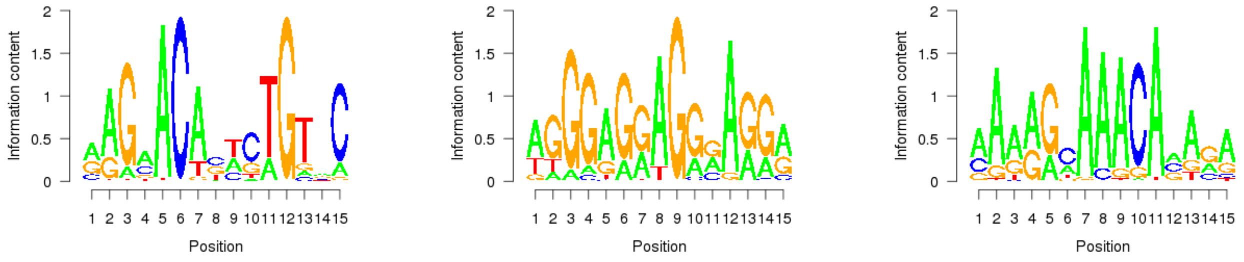


Figure 223: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrOu-gCount** component.

property	value
genes	179



(a) GRvsGR2rrOu-deNovo-meme1: width=15, sites=72, llr=747, E=4.9e-07 (b) GRvsGR2rrOu-deNovo-meme2: width=15, sites=38, llr=449, E=7.4 (c) GRvsGR2rrOu-deNovo-meme3: width=15, sites=55, llr=593, E=15

Figure 224: De novo motifs for the filtered GR LNCaP vs VCaP DEX overlaps (up) sequences.

Table 194: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
RXRA::VDR	238.3887	0.0119	0.0000	4	0	2.503E-02	0.00407
Ar	18.2592	0.0861	0.0047	27	3	2.381E-10	0.03775
TLX1::NFIC	4.7400	0.0297	0.0062	8	4	3.798E-02	0.01818
Egr1	3.4533	0.0861	0.0249	26	16	1.687E-04	0.04998
GRMotifTH	2.8928	0.2700	0.0933	76	54	33.54E-12	0.17950
FOXA1	2.5194	0.5134	0.2037	133	105	1.586E-20	0.36741
AR	2.4242	0.0415	0.0171	14	11	3.257E-02	0.02488
ARMotifTH	2.4242	0.0415	0.0171	14	11	3.257E-02	0.02488
NR3C1	2.2651	0.2255	0.0995	69	60	8.024E-08	0.14505
Tal1::Gata1	2.1986	0.0445	0.0202	15	12	2.817E-02	0.02983
ARMotifT	2.1731	0.3887	0.1788	104	98	10.89E-12	0.29239
Klf4	1.9374	0.1929	0.0995	54	57	1.859E-04	0.15528
Foxa2	1.9351	0.4214	0.2177	113	89	2.224E-16	0.50955
Stat3	1.9072	0.1039	0.0544	31	28	21.8E-04	0.09091
NR2F1	1.9072	0.1009	0.0529	31	32	85.82E-04	0.07690
Esrrb	1.9069	0.0801	0.0420	26	24	74.03E-04	0.06029
GABPA	1.8113	0.0564	0.0311	19	19	4.688E-02	0.04029
FOXF2	1.7830	0.1276	0.0715	42	40	4.195E-04	0.09695
NFIC	1.6722	2.0623	1.2333	265	412	2.275E-36	2.58495
GRMotifT	1.6643	1.5608	0.9378	245	356	5.995E-32	1.67553
FOXD1	1.6562	0.6053	0.3655	143	189	20.84E-12	0.52538
TFAP2A	1.6333	1.3056	0.7994	197	248	43.61E-24	2.35272
Gata1	1.5779	0.4540	0.2877	111	151	57.94E-08	0.43251
ARMotifH	1.5269	5.5163	3.6128	327	576	6.26E-60	9.87329
Myb	1.5071	0.5579	0.3701	131	200	24.69E-08	0.47479
RUNX1	1.4972	0.1840	0.1229	58	73	18.24E-04	0.14373
EBF1	1.4912	0.4036	0.2706	92	142	6.715E-04	0.42486
Arnt::Ahr	1.4556	0.8783	0.6034	170	228	14.61E-16	1.45924
Hand1::Tcfe2a	1.4476	0.7745	0.5350	166	237	21.77E-14	0.81461
INSM1	1.4405	0.1098	0.0762	34	44	4.964E-02	0.09852
ARMotifHH	1.4387	0.2730	0.1897	78	99	81.05E-06	0.26075
ELK1	1.4226	0.5045	0.3546	124	181	27.83E-08	0.47432
NR4A2	1.3199	1.1454	0.8678	212	339	13.91E-20	1.29181
Mafb	1.2928	1.2908	0.9984	218	354	1.483E-20	1.71134
Foxq1	1.2871	0.2522	0.1960	78	112	11.14E-04	0.22428
SP1	1.2815	0.7953	0.6205	123	198	8.963E-06	2.02965
USF1	1.2762	0.2938	0.2302	66	85	8.178E-04	0.42160
FOXO3	1.2597	0.9110	0.7232	188	307	4.565E-14	1.00291
ZNF354C	1.2316	1.8694	1.5179	261	445	19.7E-32	2.65999
SPI1	1.2253	1.0119	0.8258	205	316	48.86E-20	1.13187
BRCA1	1.2078	1.1157	0.9238	217	342	32.81E-22	1.39928
FEV	1.2033	0.3294	0.2737	91	135	3.18E-04	0.35031
SRY	0.8324	1.4214	1.7076	220	447	97.23E-16	3.12698
GATA3	0.8133	2.5816	3.1742	281	547	9.488E-34	7.01342
En1	0.7852	1.9258	2.4526	261	546	2.626E-24	3.66067
Sox5	0.7656	0.7715	1.0078	156	345	2.598E-04	1.43280
HOXA5	0.7291	2.4481	3.3577	275	555	3.404E-30	7.54037
Nkx2-5	0.6217	2.0653	3.3219	247	521	4.895E-20	8.59867
ARID3A	0.5531	1.1157	2.0171	194	438	5.479E-08	4.30332
Foxd3	0.5075	0.6677	1.3157	131	310	4.102E-02	5.15276
Prrx2	0.5015	0.7003	1.3966	148	386	4.266E-02	2.32870
IRF1	0.4940	0.0653	0.1322	20	78	1.473E-02	0.11983
Ddit3::Cebpa	0.4904	0.1098	0.2240	34	117	2.394E-02	0.22224
MEF2A	0.4816	0.0801	0.1664	22	83	1.716E-02	0.18557
FOXL1	0.4369	1.7062	3.9051	224	516	2.048E-12	16.07993
Lhx3	0.2648	0.0564	0.2131	16	87	3.501E-04	0.29537

15.79 GR LNCaP vs VCaP DEX overlaps (down)

Chromosome specific statistics are shown in Table 195. A histogram of sequence lengths is shown in Figure 225.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	4	172	254	339	1015	4e-06
2	8	73	201	340	1609	7e-06
3	9	24	133	306	1197	6e-06
4	4	155	182	209	726	4e-06
5	9	11	165	435	1484	8e-06
6	6	64	124	204	746	4e-06
7	3	89	150	182	449	3e-06
8	3	56	143	262	428	3e-06
9	1	237	237	237	237	2e-06
10	2	129	217	305	434	3e-06
12	4	138	230	327	920	7e-06
14	11	113	249	391	2740	2.6e-05
15	2	130	216	303	433	4e-06
16	4	112	142	171	567	6e-06
17	2	320	341	362	682	8e-06
19	4	149	237	398	948	1.6e-05
all 16	76	11	192	435	14615	5e-06

Table 195: Chromosome specific distribution of the regions. The last line represents the overall statistics.

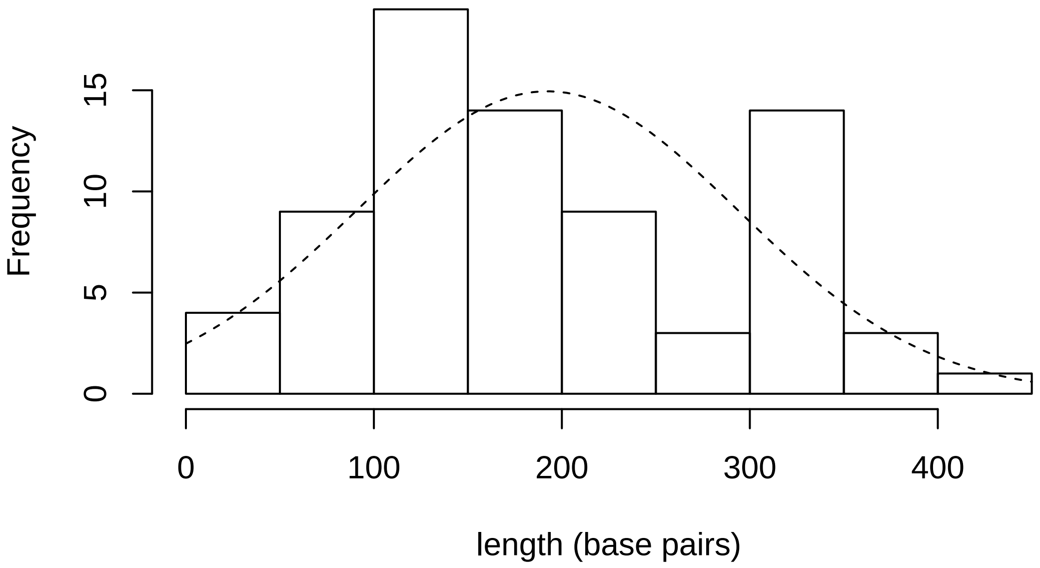
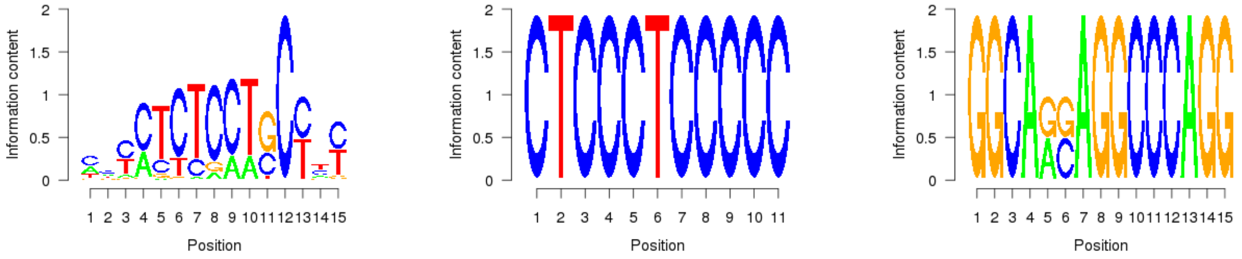


Figure 225: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrOd-gCount** component.

property	value
genes	34



(a) GRvsGR2rrOd-deNovo-meme1: width=15, sites=39, llr=359, E=0.37 (b) GRvsGR2rrOd-deNovo-meme2: width=11, sites=2, llr=31, E=3600000 (c) GRvsGR2rrOd-deNovo-meme3: width=15, sites=2, llr=40, E=5200000

Figure 226: De novo motifs for the filtered GR LNCaP vs VCaP DEX overlaps (down) sequences.

Table 196: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Tcfcp2l1	11.3722	0.0789	0.0069	5	1	3.288E-02	0.03990
FOXA1	4.7680	0.5263	0.1103	33	16	79.77E-10	0.25368
FOXF2	4.4434	0.0921	0.0207	7	3	3.374E-02	0.04340
Foxa2	4.1958	0.4342	0.1034	29	15	29.58E-08	0.20716
ARMotifT	2.8607	0.2368	0.0828	15	12	1.294E-02	0.14513
GRMotifT	1.9078	1.3289	0.6966	46	70	34.11E-06	1.36076
FOXD1	1.8688	0.6316	0.3379	35	39	1.007E-04	0.50193
NFIC	1.8118	1.7368	0.9586	56	85	5.442E-08	1.87585
ELK1	1.8099	0.4868	0.2690	28	26	2.828E-04	0.49938
NR4A2	1.7901	1.0000	0.5586	40	57	2.471E-04	1.01575
FOXO3	1.7561	1.0658	0.6069	46	62	5.249E-06	1.00802
TFAP2A	1.6237	1.0526	0.6483	43	54	9.484E-06	1.39548
Hand1::Tcfe2a	1.5727	0.8026	0.5103	38	60	19.47E-04	0.71152
Myb	1.4990	0.4342	0.2897	25	32	1.545E-02	0.43431
AP1	1.3999	1.6316	1.1655	59	86	21.31E-10	2.18429
ARMotifH	1.3892	4.1579	2.9931	70	123	2.005E-12	7.94887
GATA2	0.8216	4.2895	5.2207	69	135	68.46E-12	14.49914
YY1	0.7717	1.4211	1.8414	55	103	4.783E-06	3.01222
ARID3A	0.7600	1.2632	1.6621	43	92	96.73E-04	3.57779
GATA3	0.6884	1.8421	2.6759	58	116	1.911E-06	4.95697
Nkx2-5	0.5913	1.5658	2.6483	46	114	1.625E-02	6.69165
FOXL1	0.5814	1.7763	3.0552	54	112	45.52E-06	8.12867

15.80 GR LNCaP vs VCaP DEX overlaps (stable)

Chromosome specific statistics are shown in Table 197. A histogram of sequence lengths is shown in Figure 227.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	173	17	219	439	37807	0.000152
10	62	6	195	377	12112	8.9e-05
11	110	6	239	596	26338	0.000195
12	71	2	199	405	14119	0.000105
13	15	67	183	426	2739	2.4e-05
14	44	27	203	469	8936	8.3e-05
15	64	10	213	587	13661	0.000133
16	44	45	174	414	7669	8.5e-05
17	86	11	228	515	19620	0.000242
18	15	33	175	535	2623	3.4e-05
19	55	31	207	671	11396	0.000193
2	114	14	206	495	23505	9.7e-05
20	53	17	225	411	11911	0.000189
21	36	31	232	446	8367	0.000174
22	42	13	218	491	9162	0.000179
3	98	24	203	463	19902	0.000101
4	70	18	214	487	14997	7.8e-05
5	84	11	206	508	17292	9.6e-05
6	82	15	199	415	16337	9.5e-05
7	119	9	207	756	24621	0.000155
8	90	8	228	486	20524	0.00014
9	65	25	240	407	15606	0.000111
X	18	8	134	312	2409	1.6e-05
Y	5	62	84	107	419	7e-06
all 24	1615	2	212	756	342072	0.00011

Table 197: Chromosome specific distribution of the regions. The last line represents the overall statistics.

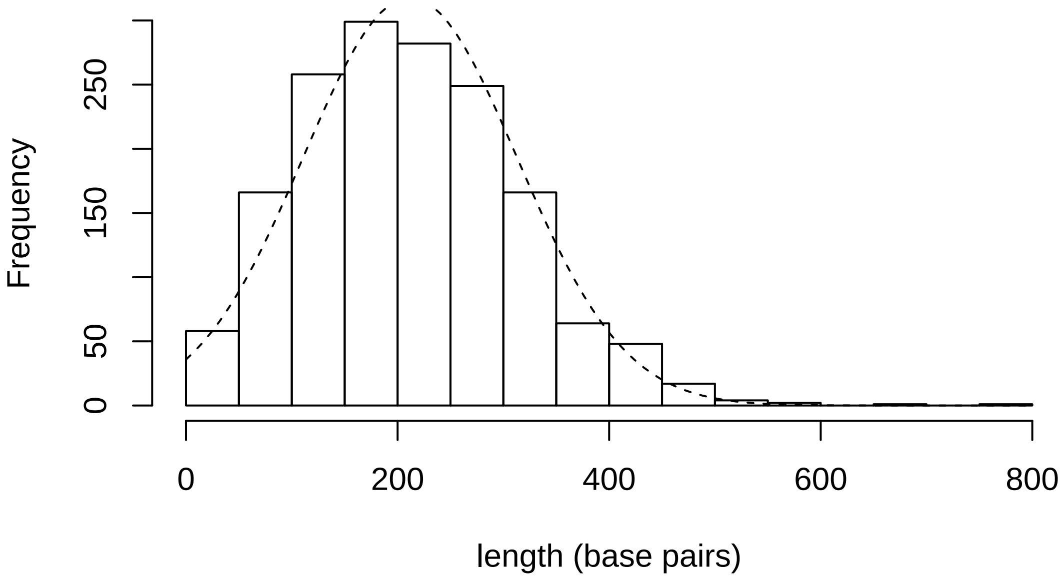
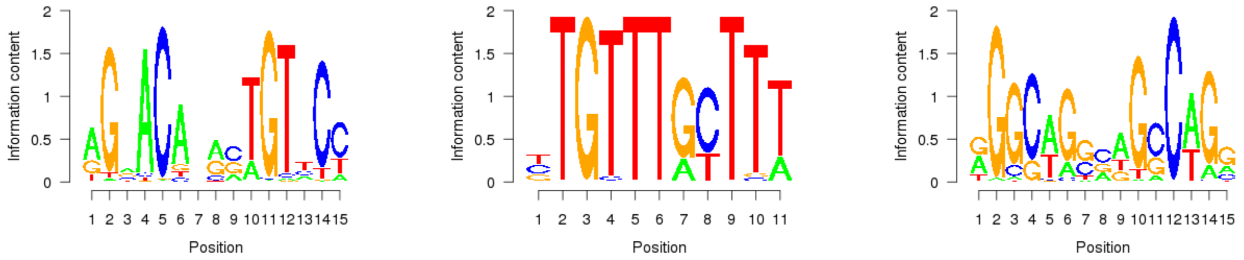


Figure 227: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrOs-gCount** component.

property	value
genes	1576



(a) GRvsGR2rrOs-deNovo-meme1: width=15, sites=140, llr=1439, E=5.8e-62
(b) GRvsGR2rrOs-deNovo-meme2: width=11, sites=38, llr=452, E=0.00013
(c) GRvsGR2rrOs-deNovo-meme3: width=15, sites=69, llr=745, E=15

Figure 228: De novo motifs for the filtered GR LNCaP vs VCaP DEX overlaps (stable) sequences.

Table 198: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	9.7323	0.0590	0.0060	88	17	5.476E-26	0.02787
TLX1::NFIC	5.6508	0.0286	0.0050	37	13	1.315E-08	0.01787
ESR2	3.5110	0.0236	0.0067	33	18	13.57E-06	0.01593
ELK4	2.9607	0.0248	0.0084	39	24	10.23E-06	0.01480
FOXA1	2.9120	0.5317	0.1825	641	477	2.985E-96	0.35495
NHLH1	2.6642	0.1168	0.0438	115	90	31.32E-12	0.12150
FOXF2	2.6368	0.1491	0.0565	216	162	27.47E-24	0.09492
Foxa2	2.5818	0.4472	0.1732	553	417	3.119E-76	0.36367
GABPA	2.3571	0.0584	0.0247	91	70	34.69E-10	0.03823
Tal1::Gata1	2.1562	0.0311	0.0144	48	42	2.687E-04	0.02111
ARMotifTH	2.1111	0.0410	0.0194	64	58	38.37E-06	0.02710
MIZF	2.0271	0.0217	0.0107	35	32	37.45E-04	0.01435
Tcfcp2l1	1.8772	0.0559	0.0298	80	83	81.41E-06	0.04436
Stat3	1.8753	0.1280	0.0682	161	168	23.36E-10	0.12206
NFIC	1.8387	2.0366	1.1077	1276	1766	9.631E-188	2.47683
Esrrb	1.7933	0.0876	0.0488	139	141	1.597E-08	0.06154
Mycn	1.7187	0.0696	0.0405	86	96	2.314E-04	0.07157
STAT1	1.6974	0.0267	0.0157	32	34	2.557E-02	0.03049
ARMotifHH	1.6780	0.2323	0.1384	310	364	8.305E-16	0.19762
Myc	1.6646	0.0913	0.0548	117	129	5.948E-06	0.09391
Egr1	1.6622	0.0584	0.0351	90	100	1.376E-04	0.04530
FOXD1	1.6496	0.6056	0.3671	700	865	29.49E-56	0.52761
ARMotifT	1.6427	0.3323	0.2023	436	524	52.0E-26	0.28033
Pax5	1.6204	0.0342	0.0211	54	62	78.25E-04	0.02586
GRMotifTH	1.5958	0.1932	0.1210	272	333	6.974E-12	0.15925
MYC::MAX	1.5766	0.0385	0.0244	50	63	3.557E-02	0.03805
Myf	1.5508	0.1634	0.1053	207	263	15.02E-08	0.16639
Arnt	1.5165	0.1106	0.0729	124	145	19.06E-06	0.14216
Hand1::Tcfe2a	1.5118	0.7764	0.5135	824	1149	40.87E-64	0.71457
NR2F1	1.5000	0.0783	0.0522	116	151	8.604E-04	0.06450
Foxq1	1.4824	0.2478	0.1672	339	425	29.05E-16	0.22942
ELK1	1.4813	0.5354	0.3614	636	867	12.11E-38	0.47793
NFE2L2	1.4768	0.0820	0.0555	121	163	15.13E-04	0.06711
AR	1.4571	0.0385	0.0264	60	77	2.419E-02	0.03145
RELA	1.4571	0.0634	0.0435	90	113	22.78E-04	0.06267
GRMotifT	1.4319	1.3180	0.9204	1107	1691	3.903E-114	1.34993
TFAP2A	1.4175	1.1621	0.8198	887	1184	2.606E-80	2.43026
EBF1	1.4148	0.3969	0.2805	436	609	34.95E-18	0.47679
ARMotifH	1.4070	4.7379	3.3674	1524	2673	32.1E-254	8.49180
TAL1::TCF3	1.3916	0.1429	0.1026	177	243	63.31E-06	0.16137
Mafb	1.3803	1.2516	0.9067	1046	1538	12.25E-104	1.53316
NR3C1	1.3514	0.1509	0.1117	219	314	17.75E-06	0.12970
Gata1	1.3444	0.3677	0.2735	470	682	10.15E-18	0.34476
FOXA1pAR	1.3442	0.0472	0.0351	70	93	2.245E-02	0.04823
GRMotifHH	1.3185	0.1261	0.0956	182	260	1.983E-04	0.11675
Myb	1.3066	0.4609	0.3527	568	835	59.18E-26	0.46068
GR	1.2907	0.1584	0.1227	228	334	24.42E-06	0.14868
RUNX1	1.2886	0.1702	0.1321	251	357	92.72E-08	0.15385
INSM1	1.2826	0.1081	0.0843	161	222	2.269E-04	0.10795
HIF1A::ARNT	1.2537	0.2385	0.1902	303	440	2.759E-08	0.28122
FEV	1.2524	0.3342	0.2668	448	675	1.923E-14	0.31088
BRCA1	1.2453	1.0621	0.8529	976	1541	19.88E-78	1.26628
NR4A2	1.2232	1.0093	0.8251	935	1565	3.791E-62	1.10302
Klf4	1.2069	0.1267	0.1050	171	263	41.14E-04	0.14993
Gfi	0.8330	0.4155	0.4988	511	1083	1.105E-04	0.56783
SRY	0.8120	1.3571	1.6713	1033	2024	3.57E-62	3.01672
YY1	0.8097	1.6652	2.0565	1191	2345	86.41E-100	3.21179
NF-kappaB	0.8005	0.0851	0.1063	103	261	4.856E-02	0.14000
En1	0.7789	1.8130	2.3276	1237	2464	2.153E-110	3.52278
HOXA5	0.7300	2.2975	3.1474	1280	2530	27.35E-126	6.54142
Sox5	0.7226	0.7050	0.9756	728	1543	17.57E-16	1.43277
Nobox	0.7093	0.5478	0.7723	587	1268	1.035E-06	1.15163
ARID3A	0.6556	1.2056	1.8388	941	1987	1.611E-38	3.84326
Nkx2-5	0.6419	1.9913	3.1023	1186	2418	2.443E-92	7.88705
HLF	0.6101	0.1509	0.2474	190	590	15.76E-06	0.28413
IRF1	0.5923	0.0677	0.1143	105	292	51.07E-04	0.12322
NFIL3	0.5659	0.0547	0.0966	74	228	9.62E-04	0.11742
Pdx1	0.5599	0.7590	1.3557	750	1823	7.824E-10	2.27276
Ddit3::Cebpa	0.5192	0.1106	0.2130	166	494	1.605E-04	0.22318
Prrx2	0.5137	0.6640	1.2925	681	1754	1.609E-04	2.07864
FOXL1	0.4712	1.7950	3.8094	1103	2315	2.854E-68	20.49233
Foxd3	0.4663	0.5944	1.2748	595	1404	2.954E-04	5.11278
MEF2A	0.4394	0.0702	0.1598	88	365	7.973E-10	0.18937
Lhx3	0.3969	0.0665	0.1675	87	350	52.2E-10	0.22514

15.81 GR LNCaP vs VCaP DEX unique for GRDEXrrO

Chromosome specific statistics are shown in Table 199. A histogram of sequence lengths is shown in Figure 229.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	1383	1	304	995	420899	0.001689
10	599	20	282	949	168687	0.001245
11	551	16	276	804	151835	0.001125
12	501	2	282	989	141528	0.001057
13	459	1	325	1787	149072	0.001294
14	441	2	292	848	128933	0.001201
15	441	29	283	752	124967	0.001219
16	396	3	288	1638	113988	0.001262
17	462	30	279	670	129095	0.00159
18	296	3	304	1991	89851	0.001151
19	146	64	244	973	35609	0.000602
2	1005	14	289	1946	290371	0.001194
20	326	21	273	1249	88963	0.001412
21	152	31	278	1440	42330	0.000879
22	160	5	249	845	39894	0.000778
3	1035	0	314	969	324788	0.00164
4	633	0	270	2287	170671	0.000893
5	1019	16	300	939	305993	0.001691
6	701	6	281	1818	196928	0.001151
7	725	0	285	1103	206757	0.001299
8	682	1	294	956	200550	0.00137
9	550	7	274	806	150974	0.001069
X	348	50	245	646	85386	0.00055
Y	43	109	252	408	10825	0.000182
all 24	13054	0	289	2287	3768894	0.001217

Table 199: Chromosome specific distribution of the regions. The last line represents the overall statistics.

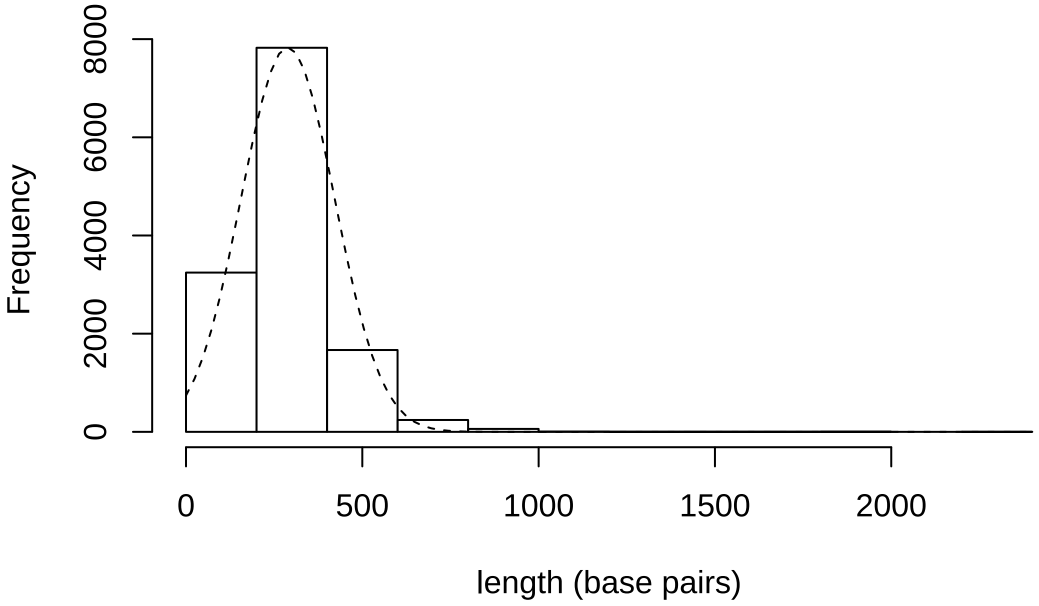
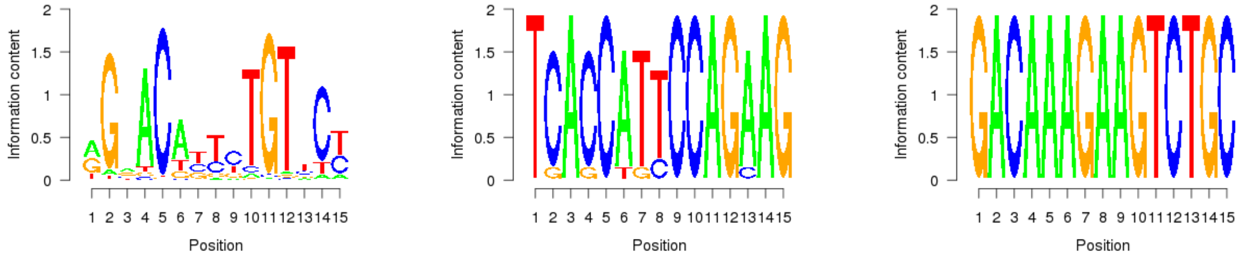


Figure 229: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU1-gCount** component.

property	value
genes	19638



(a) GRvsGR2rrU1-deNovo-meme1: width=15, sites=333, llr=3178, E=7.9e-212 (b) GRvsGR2rrU1-deNovo-meme2: width=15, sites=11, llr=207, E=6.5e-06 (c) GRvsGR2rrU1-deNovo-meme3: width=15, sites=9, llr=187, E=5.6e-07

Figure 230: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRDEXrrO sequences.

Table 200: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	29.5192	0.1541	0.0052	1761	121	0.00E00	0.07607
TLX1::NFIC	3.7214	0.0125	0.0033	132	66	73.52E-22	0.00910
ARMotifTH	3.6189	0.0872	0.0241	960	569	3.19E-126	0.06897
ARMotifTT	2.9705	0.0141	0.0047	180	113	10.58E-22	0.00825
ESR2	2.8603	0.0189	0.0066	208	144	8.315E-22	0.01443
ARMotifT	2.6475	0.6968	0.2631	6172	5355	0.00E00	0.64937
GRMotifTH	2.6009	0.3773	0.1450	3783	3197	0.00E00	0.35696
GRMotifTT	2.5350	0.0355	0.0140	444	335	2.932E-40	0.02276
NR3C1	2.4840	0.4094	0.1648	4156	3586	0.00E00	0.31179
AR	2.3889	0.0622	0.0260	769	623	45.27E-64	0.04090
FOXA1	2.3253	0.5716	0.2458	5375	5057	0.00E00	0.43718
CTCF	2.3039	0.0046	0.0020	60	48	9.301E-06	0.00288
Foxa2	2.1917	0.5089	0.2322	4853	4400	0.00E00	0.47681
FOXF2	2.1457	0.1791	0.0835	2084	1911	15.32E-160	0.12520
ARMotifHH	2.0371	0.4130	0.2027	4006	4110	0.00E00	0.67962
RXRA::VDR	2.0346	0.0070	0.0034	80	83	1.686E-04	0.00763
Tal1::Gata1	1.8301	0.0375	0.0205	480	493	40.36E-24	0.02658
GR	1.7953	0.2718	0.1514	2989	3236	2.252E-188	0.27407
GRMotifT	1.7782	2.1365	1.2014	11007	16120	0.00E00	2.78785
Stat3	1.7567	0.1559	0.0887	1555	1741	10.03E-70	0.15508
FOXD1	1.6632	0.8419	0.5062	6827	8972	0.00E00	0.80380
GRMotifHH	1.6505	0.2224	0.1347	2346	2828	1.179E-100	0.21882
GABPA	1.6332	0.0602	0.0368	730	858	2.061E-24	0.04968
STAT1	1.6135	0.0326	0.0202	331	406	22.04E-10	0.03398
Foxq1	1.5844	0.4099	0.2587	3989	5067	7.117E-212	0.39632
ARMotifH	1.5584	7.1394	4.5812	12873	23208	0.00E00	17.63290
RORA_2	1.4925	0.0190	0.0127	240	307	4.936E-06	0.01513
PPARG::RXRA	1.4722	0.0140	0.0095	179	227	71.41E-06	0.01151
MIZF	1.4439	0.0212	0.0147	246	353	7.976E-04	0.03087
Evi1	1.3996	0.0319	0.0227	384	529	85.64E-08	0.03065
Esrrb	1.3919	0.0801	0.0576	971	1325	21.39E-20	0.07238
GRMotifH	1.3907	4.8417	3.4814	12501	22474	0.00E00	9.43988
RXR::RAR_DR5	1.3893	0.0207	0.0149	268	352	5.286E-06	0.01755
FOXA1pAR	1.3636	0.0638	0.0468	754	1026	1.612E-14	0.06398
Gata1	1.3406	0.5155	0.3845	4915	7264	5.106E-222	0.51068
TAL1::TCF3	1.3314	0.1880	0.1412	1857	2561	20.69E-46	0.22404
Tcfcp2l1	1.3300	0.0445	0.0335	523	747	9.734E-08	0.04667
FOXI1	1.3228	0.6654	0.5030	5440	8116	20.53E-274	0.89802
NR2F1	1.3212	0.0820	0.0620	996	1449	88.61E-16	0.07214
Arnt	1.3148	0.1296	0.0985	1136	1612	7.368E-20	0.20266
FEV	1.2884	0.4740	0.3679	4731	7197	1.711E-188	0.47339
TEAD1	1.2666	0.0586	0.0462	728	1096	2.473E-08	0.05177
ELK4	1.2635	0.0160	0.0127	200	299	1.055E-02	0.01473
FOXC1	1.2425	5.4247	4.3658	12387	22858	0.00E00	14.38589
FOXO3	1.2185	1.2721	1.0440	8478	14102	0.00E00	1.70455
NR4A2	1.2063	1.3082	1.0845	9019	14906	0.00E00	1.67138
Hand1::Tcfe2a	1.2009	0.8427	0.7018	6948	11652	0.00E00	0.94037
YY1	0.8325	2.2990	2.7615	10998	21468	0.00E00	5.13244
FOXL1	0.8258	4.4772	5.4216	11100	21135	0.00E00	40.55681
Pdx1	0.8254	1.5637	1.8945	8716	17768	0.00E00	3.66583
INSM1	0.8161	0.0862	0.1056	1012	2290	54.74E-04	0.11626
RELA	0.8019	0.0573	0.0715	644	1487	10.01E-04	0.08755
PBX1	0.7960	0.0583	0.0732	717	1571	2.945E-02	0.09728
CREB1	0.7883	0.4439	0.5632	4311	9336	2.145E-30	0.69916
SRF	0.7864	0.0093	0.0118	101	248	2.898E-02	0.01419
MZF1_5-13	0.7682	0.7211	0.9387	6076	13408	2.475E-112	1.47720
Klf4	0.7668	0.1050	0.1370	1177	2769	2.327E-04	0.18247
IRF1	0.7588	0.1275	0.1680	1453	3456	2.417E-04	0.19136
Prrx2	0.7584	1.3574	1.7898	8049	17274	0.00E00	3.24652
Zfp423	0.7486	0.0289	0.0387	317	744	31.18E-04	0.05190
Lhx3	0.7483	0.1777	0.2374	1684	3864	3.537E-02	0.38807
Foxd3	0.7273	1.2610	1.7337	7037	13969	10.75E-272	6.98380
SP1	0.7228	0.5871	0.8122	3592	8744	1.204E-02	3.36052
NF-kappaB	0.7201	0.1058	0.1470	1012	2771	45.28E-16	0.22216
NFKB1	0.6219	0.0270	0.0435	285	760	2.322E-06	0.06264
IRF2	0.6026	0.0031	0.0053	41	128	53.7E-04	0.00450
Zfx	0.5993	0.0682	0.1138	701	2323	11.03E-32	0.14617
RREB1	0.5991	0.0154	0.0257	154	396	14.88E-04	0.06475
PLAG1	0.5256	0.0059	0.0113	74	254	5.367E-06	0.01173
Ddit3::Cebpa	0.5159	0.1418	0.2750	1668	5099	13.94E-32	0.29456
EWSR1-FLI1	0.1473	0.0025	0.0175	20	83	15.1E-04	0.12345

15.82 GR LNCaP vs VCaP DEX unique for GRDEXrrO (up)

Chromosome specific statistics are shown in Table 201. A histogram of sequence lengths is shown in Figure 231.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	194	15	320	927	62125	0.000249
10	74	128	292	737	21581	0.000159
11	76	63	311	698	23633	0.000175
12	47	58	290	583	13621	0.000102
13	20	86	276	544	5530	4.8e-05
14	41	102	300	646	12287	0.000114
15	33	113	292	523	9647	9.4e-05
16	76	3	301	585	22842	0.000253
17	51	73	286	665	14584	0.00018
18	11	131	423	1991	4656	6e-05
19	10	101	315	703	3150	5.3e-05
2	110	98	315	879	34619	0.000142
20	51	105	301	811	15351	0.000244
21	5	31	446	1440	2228	4.6e-05
22	25	125	271	440	6765	0.000132
3	138	64	311	837	42965	0.000217
4	60	0	285	686	17076	8.9e-05
5	112	16	302	939	33841	0.000187
6	124	14	301	799	37311	0.000218
7	35	70	302	678	10582	6.6e-05
8	63	115	312	931	19661	0.000134
9	58	32	268	492	15563	0.00011
X	47	102	275	624	12908	8.3e-05
all 23	1461	0	303	1991	442526	0.000143

Table 201: Chromosome specific distribution of the regions. The last line represents the overall statistics.

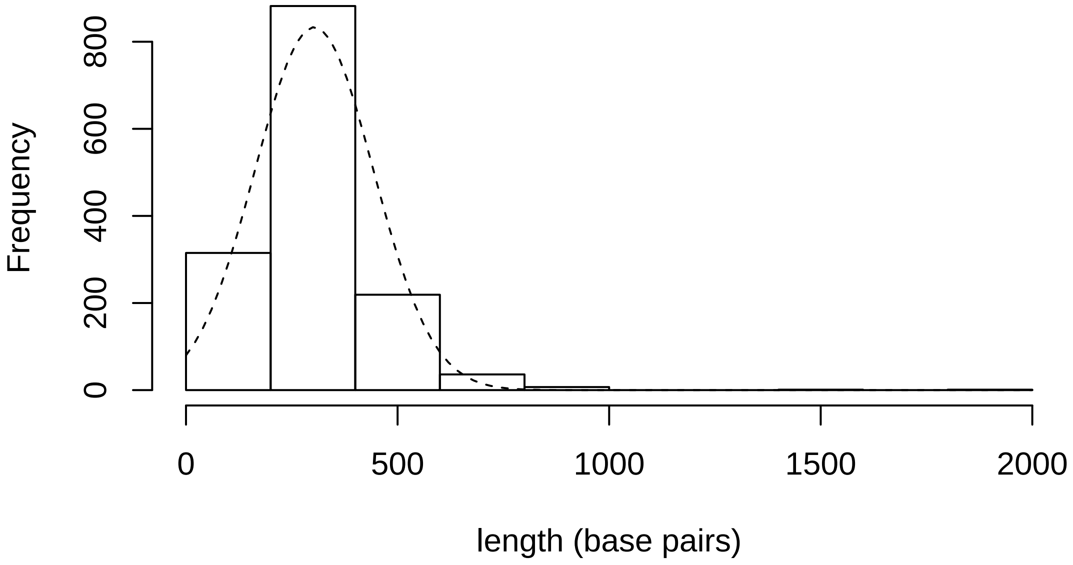
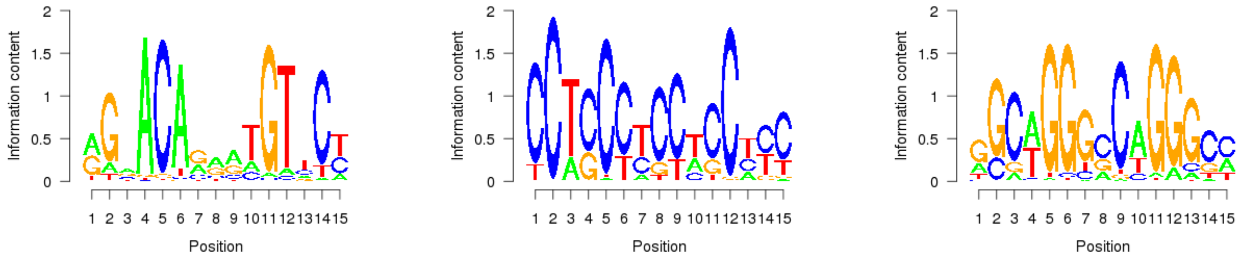


Figure 231: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU1u-gCount** component.

property	value
genes	367



(a) GRvsGR2rrU1u-deNovo-meme1: width=15, sites=351, llr=3261, E=8.2e-227 (b) GRvsGR2rrU1u-deNovo-meme2: width=15, sites=53, llr=648, E=1.1e-08 (c) GRvsGR2rrU1u-deNovo-meme3: width=15, sites=59, llr=674, E=110000

Figure 232: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRDEXrrO (up) sequences.

Table 202: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	43.7534	0.1768	0.0040	234	10	37.02E-96	0.07212
TLX1::NFIC	3.4600	0.0164	0.0047	19	11	17.08E-04	0.01203
ESR2	3.0120	0.0329	0.0109	35	27	3.895E-04	0.03289
CTCF	2.8014	0.0082	0.0029	12	8	3.056E-02	0.00472
ARMotifTH	2.5075	0.0747	0.0298	106	81	34.19E-12	0.04518
GRMotifTT	2.4792	0.0343	0.0138	49	37	13.25E-06	0.02140
GRMotifTH	2.4708	0.4010	0.1623	462	401	57.28E-54	0.31267
ARMotifTT	2.4539	0.0117	0.0047	17	12	1.10E-02	0.00754
ARMotifT	2.4306	0.6909	0.2842	678	657	1.974E-84	0.58434
NR3C1	2.4193	0.4400	0.1819	506	445	14.27E-60	0.29646
AR	2.3331	0.0644	0.0276	89	74	2.566E-08	0.04347
ARMotifHH	2.2393	0.4894	0.2185	492	499	2.831E-46	1.67743
GABPA	2.0866	0.0788	0.0377	107	103	10.74E-08	0.05403
PPARG::RXRA	1.9371	0.0254	0.0131	37	35	31.98E-04	0.01750
MIZF	1.8843	0.0212	0.0113	31	31	1.33E-02	0.01450
FOXA1	1.8824	0.4565	0.2425	509	557	39.94E-44	0.37401
RXR::RAR_DR5	1.8326	0.0240	0.0131	34	36	1.623E-02	0.01704
Stat3	1.7986	0.1659	0.0922	183	212	44.97E-10	0.15989
GRMotifT	1.7901	2.2748	1.2708	1265	1884	61.67E-208	2.87596
FOXF2	1.7747	0.1398	0.0788	191	201	7.036E-12	0.10371
Foxa2	1.7675	0.4016	0.2272	442	469	3.149E-36	0.43518
GRMotifHH	1.7628	0.2317	0.1314	289	304	6.257E-20	0.19552
GR	1.7550	0.2892	0.1648	348	406	73.59E-22	0.23781
ARMotifH	1.6460	7.8622	4.7764	1442	2634	3.594E-260	23.79836
STAT1	1.6222	0.0295	0.0181	39	39	47.04E-04	0.02918
NR2F1	1.5535	0.1083	0.0697	145	185	20.35E-06	0.08615
Egr1	1.5495	0.0754	0.0486	95	126	31.44E-04	0.06785
Myf	1.5045	0.2070	0.1376	227	303	4.54E-08	0.24091
Mycn	1.4833	0.0980	0.0661	110	132	75.47E-06	0.11819
Arnt	1.4761	0.1474	0.0998	139	178	39.67E-06	0.20295
NHLH1	1.4522	0.1097	0.0755	98	132	36.07E-04	0.15663
MYC::MAX	1.4113	0.0548	0.0388	63	88	4.821E-02	0.05951
FOXD1	1.3666	0.6984	0.5111	680	1012	2.022E-42	0.73705
GRMotifH	1.3555	4.9404	3.6446	1405	2572	2.818E-238	8.74255
ELK1	1.3266	0.6929	0.5223	675	1034	29.23E-40	0.72575
Foxq1	1.3191	0.3400	0.2577	375	555	95.56E-14	0.38283
NFE2L2	1.3014	0.0973	0.0748	126	199	2.701E-02	0.08907
Myc	1.3005	0.1138	0.0875	128	184	27.58E-04	0.14234
Klf4	1.2667	0.1830	0.1445	212	318	52.54E-06	0.22835
TEAD1	1.2586	0.0658	0.0523	93	138	3.103E-02	0.05989
Tcfcp2l1	1.2523	0.0459	0.0367	65	91	4.508E-02	0.04493
NR4A2	1.2501	1.4393	1.1514	1043	1739	34.58E-106	1.67253
FEV	1.2446	0.4798	0.3855	533	845	46.24E-22	0.47027
FOXA1pAR	1.2432	0.0555	0.0446	75	109	4.818E-02	0.05747
NFIC	1.2381	1.9328	1.5612	1159	1984	1.03E-138	2.69205
EBF1	1.2315	0.4949	0.4018	495	772	89.08E-20	0.66014
TFAP2A	1.2229	1.3276	1.0857	782	1293	2.64E-48	4.13174
HIF1A::ARNT	1.2014	0.3153	0.2624	309	541	90.8E-06	0.55516
HOXA5	0.8254	3.8293	4.6396	1306	2578	3.801E-174	11.47633
Nobox	0.8162	0.9424	1.1546	708	1514	1.275E-18	2.10545
Nkx2-5	0.7866	3.5648	4.5321	1235	2446	16.12E-144	14.41992
ARID3A	0.7753	2.0987	2.7071	1047	2162	24.32E-78	6.97400
Pdx1	0.7358	1.4277	1.9405	906	2050	1.338E-38	3.68103
Prrx2	0.6747	1.2659	1.8762	869	1982	2.299E-32	3.34937
IRF1	0.6704	0.1199	0.1789	152	415	1.143E-02	0.19371
FOXL1	0.6634	3.7025	5.5808	1169	2401	8.115E-114	42.15443
Foxd3	0.6045	1.0795	1.7858	712	1551	7.35E-18	6.78052
Lhx3	0.5567	0.1432	0.2574	155	474	1.946E-04	0.38880
Ddit3::Cebpa	0.5345	0.1528	0.2860	199	591	6.316E-04	0.32197

15.83 GR LNCaP vs VCaP DEX unique for GRDEXrrO (down)

Chromosome specific statistics are shown in Table 203. A histogram of sequence lengths is shown in Figure 233.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	27	10	282	662	7614	3.1e-05
10	3	127	195	302	585	4e-06
11	3	283	331	411	994	7e-06
12	10	103	262	415	2621	2e-05
13	2	150	234	318	468	4e-06
14	23	92	333	608	7666	7.1e-05
15	3	228	301	386	904	9e-06
16	18	130	315	1638	5676	6.3e-05
17	4	143	270	393	1078	1.3e-05
18	2	212	216	221	433	6e-06
19	8	154	236	342	1886	3.2e-05
2	15	193	300	533	4507	1.9e-05
22	2	179	248	316	495	1e-05
3	23	147	339	909	7793	3.9e-05
4	17	117	258	586	4387	2.3e-05
5	22	162	280	427	6163	3.4e-05
6	10	35	212	356	2119	1.2e-05
7	15	170	337	495	5057	3.2e-05
8	7	168	247	304	1731	1.2e-05
9	15	8	283	481	4248	3e-05
X	1	290	290	290	290	2e-06
all 21	230	8	290	1638	66715	2.2e-05

Table 203: Chromosome specific distribution of the regions. The last line represents the overall statistics.

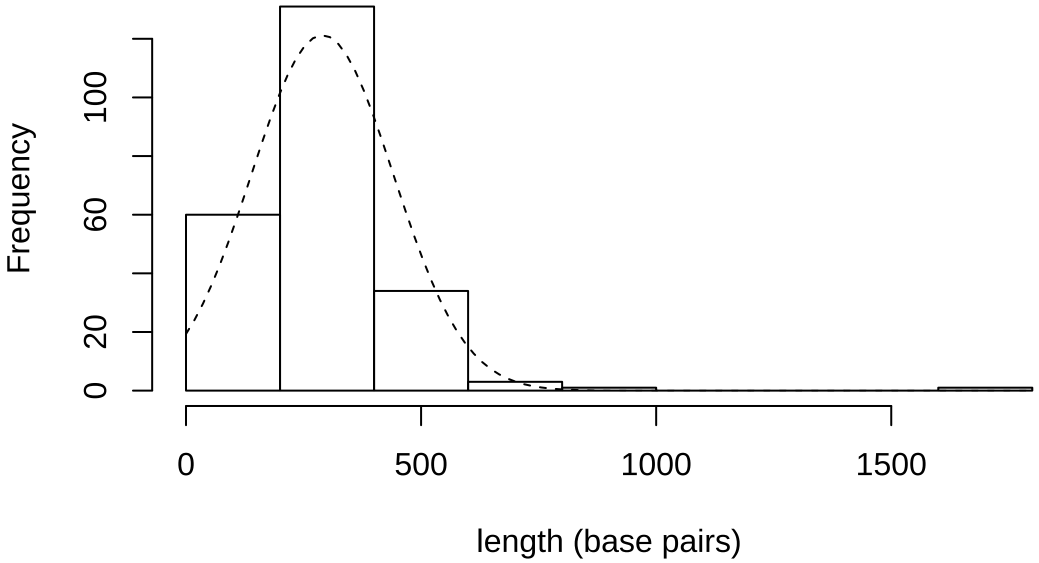
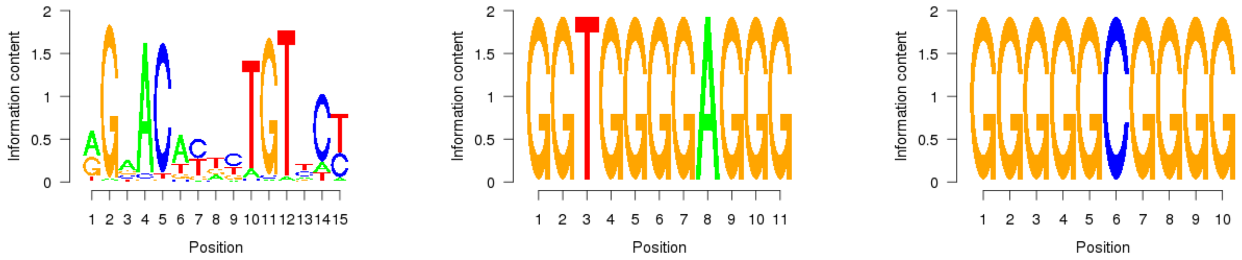


Figure 233: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU1d-gCount** component.

property	value
genes	77



(a) GRvsGR2rrU1d-deNovo-meme1: width=15, sites=81, llr=833, E=2.1e-34 (b) GRvsGR2rrU1d-deNovo-meme2: width=11, sites=2, llr=33, E=5e+07 (c) GRvsGR2rrU1d-deNovo-meme3: width=10, sites=2, llr=31, E=2.6e+07

Figure 234: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRDEXrrO (down) sequences.

Table 204: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	30.8047	0.1441	0.0046	32	2	25.62E-14	0.05325
SRF	12.9472	0.0306	0.0023	5	1	3.659E-02	0.01804
NR3C1	3.6035	0.4672	0.1296	73	53	14.9E-12	0.72546
Zfp423	2.6094	0.0786	0.0301	13	10	3.742E-02	0.06901
GRMotifTH	2.5336	0.3930	0.1551	58	57	5.469E-06	0.77835
HNF1B	2.5131	0.0873	0.0347	19	15	94.26E-04	0.05325
ARMotifT	2.3619	0.6288	0.2662	105	94	21.55E-16	0.46896
FOXA1	2.0372	0.4716	0.2315	81	86	2.383E-08	0.36447
GRMotifT	1.7938	2.1135	1.1782	193	287	33.34E-32	2.52007
Foxa2	1.7113	0.3843	0.2245	76	78	5.313E-08	0.33519
Stat3	1.6166	0.1310	0.0810	26	27	1.71E-02	0.12516
Gata1	1.5924	0.5677	0.3565	93	125	37.26E-08	0.50300
TAL1::TCF3	1.5581	0.1659	0.1065	31	39	4.126E-02	0.15352
FEV	1.5434	0.5502	0.3565	92	122	34.55E-08	0.49605
ARMotifHH	1.5091	0.3319	0.2199	62	79	2.973E-04	0.30722
GR	1.4821	0.2402	0.1620	48	63	59.87E-04	0.20812
ARMotifH	1.4605	6.8122	4.6644	227	411	1.087E-42	18.41775
FOXD1	1.4399	0.6900	0.4792	108	154	1.57E-08	0.68401
RORA_1	1.3719	0.2096	0.1528	43	63	4.252E-02	0.17021
FOXI1	1.3474	0.5895	0.4375	92	125	68.61E-08	0.70483
Foxq1	1.2916	0.3319	0.2569	62	89	23.36E-04	0.34863
GRMotifH	1.2788	4.5677	3.5718	215	398	30.3E-36	11.29761
AP1	1.2718	2.3581	1.8542	190	342	1.123E-24	3.77948
NR4A2	1.2525	1.4236	1.1366	158	274	31.38E-16	2.21997
NFIC	1.2391	1.7555	1.4167	185	295	5.869E-26	2.18255
FOXO3	1.2245	1.2926	1.0556	153	243	8.716E-16	1.67041
SPI1	1.2064	1.3013	1.0787	160	274	4.936E-16	1.25598
Prrx2	0.7848	1.4061	1.7917	139	296	16.43E-08	3.38595
MZF1_5-13	0.7811	0.7467	0.9560	105	241	87.75E-04	1.53944
FOXL1	0.6945	4.3712	6.2940	195	379	1.196E-24	123.20068
Foxd3	0.6610	1.1965	1.8102	123	246	5.017E-06	7.31963
Zfx	0.5111	0.0568	0.1111	10	42	4.772E-02	0.11420

15.84 GR LNCaP vs VCaP DEX unique for GRDEXrrO (stable)

Chromosome specific statistics are shown in Table 205. A histogram of sequence lengths is shown in Figure 235.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	796	2	300	927	239132	0.000959
10	291	20	281	949	81866	0.000604
11	324	16	275	804	89191	0.000661
12	255	4	279	989	71067	0.000531
13	147	27	317	1787	46554	0.000404
14	196	2	289	848	56660	0.000528
15	212	29	282	684	59874	0.000584
16	225	15	279	1638	62668	0.000694
17	257	106	272	670	69826	0.00086
18	70	115	313	1991	21930	0.000281
19	113	64	240	703	27098	0.000458
2	457	14	277	773	126403	0.00052
20	187	21	258	1249	48327	0.000767
21	63	101	265	613	16687	0.000347
22	108	106	257	845	27746	0.000541
3	433	3	298	895	128855	0.000651
4	295	0	276	2287	81492	0.000426
5	425	16	288	882	122409	0.000677
6	362	7	281	1181	101798	0.000595
7	365	19	285	1103	104141	0.000654
8	316	1	289	931	91413	0.000625
9	227	31	264	659	60041	0.000425
X	141	92	249	646	35070	0.000226
Y	29	109	264	408	7666	0.000129
all 24	6294	0	282	2287	1777914	0.000574

Table 205: Chromosome specific distribution of the regions. The last line represents the overall statistics.

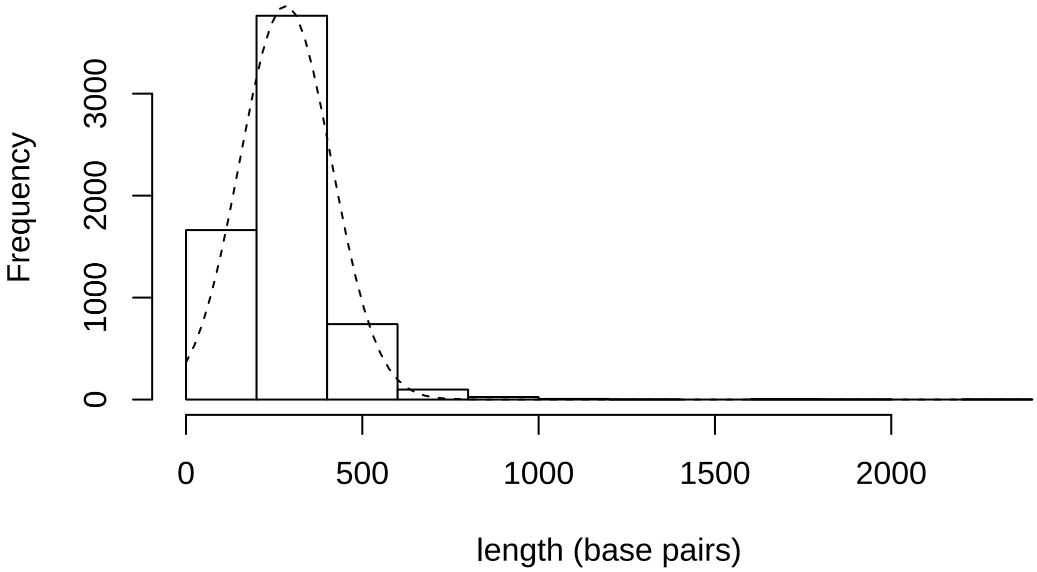
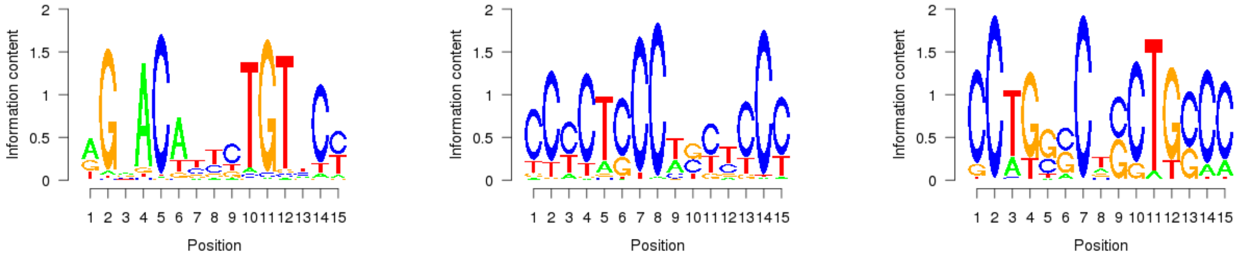


Figure 235: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU1s-gCount** component.

property	value
genes	3827



(a) GRvsGR2rrU1s-deNovo-meme1: width=15, sites=322, llr=3010, E=6.5e-191 (b) GRvsGR2rrU1s-deNovo-meme2: width=15, sites=89, llr=986, E=3.8e-16 (c) GRvsGR2rrU1s-deNovo-meme3: width=15, sites=37, llr=484, E=4e-05

Figure 236: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRDEXrrO (stable) sequences.

Table 206: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
Ar	27.4751	0.1559	0.0056	854	59	11.0E-320	0.08688
TLX1::NFIC	3.7813	0.0140	0.0037	73	39	26.08E-12	0.00933
ARMotifTH	3.5381	0.0807	0.0228	439	262	11.14E-58	0.05855
GRMotifTT	2.8052	0.0331	0.0118	197	133	8.081E-22	0.02183
CTCF	2.5919	0.0060	0.0023	38	26	64.52E-06	0.00371
ARMotifTT	2.5881	0.0118	0.0045	72	50	3.007E-08	0.00767
GRMotifTH	2.5777	0.3710	0.1439	1817	1533	2.542E-198	0.32666
ARMotifT	2.5726	0.6626	0.2575	2920	2537	0.00E00	0.50510
NR3C1	2.5037	0.4103	0.1638	2037	1698	1.666E-238	0.30087
RXRA::VDR	2.4485	0.0078	0.0032	38	37	56.8E-04	0.01097
ESR2	2.2709	0.0185	0.0081	101	88	8.449E-08	0.01413
FOXA1	2.2598	0.5514	0.2440	2543	2409	2.94E-284	0.41305
ARMotifHH	2.2436	0.4310	0.1921	1971	1882	7.728E-186	0.85343
Foxa2	2.2086	0.4922	0.2228	2315	1991	3.555E-278	0.46268
AR	2.0538	0.0552	0.0269	335	306	2.857E-22	0.03806
FOXF2	2.0392	0.1701	0.0834	959	912	4.448E-68	0.12158
GABPA	1.9119	0.0647	0.0338	378	386	10.77E-20	0.04830
GRMotifHH	1.8478	0.2278	0.1233	1147	1273	7.151E-62	0.21338
Stat3	1.7967	0.1573	0.0875	769	812	51.88E-42	0.15400
GR	1.7854	0.2679	0.1500	1393	1569	17.6E-80	0.33024
GRMotifT	1.7832	2.1252	1.1918	5308	7774	0.00E00	2.91467
STAT1	1.7624	0.0358	0.0203	181	198	5.713E-08	0.03481
PPARG::RXRA	1.6714	0.0167	0.0100	102	115	1.633E-04	0.01284
FOXD1	1.6594	0.8031	0.4839	3169	4147	37.18E-264	0.77147
ARMotifH	1.5942	7.1559	4.4886	6212	11141	0.00E00	18.17610
Foxq1	1.5285	0.3796	0.2483	1806	2326	1.838E-88	0.37991
Tal1::Gata1	1.4805	0.0331	0.0223	205	258	7.344E-06	0.02630
Evi1	1.4763	0.0302	0.0205	166	234	31.72E-04	0.03151
RXR::RAR_DR5	1.4388	0.0226	0.0157	140	181	7.006E-04	0.01832
Tcfcp2l1	1.4268	0.0492	0.0344	276	353	25.55E-08	0.05233
Esrrb	1.3904	0.0810	0.0582	477	650	2.852E-10	0.06978
GRMotifH	1.3894	4.7148	3.3935	6010	10783	0.00E00	8.41521
NR2F1	1.3422	0.0840	0.0626	491	697	64.33E-10	0.07469
FEV	1.3164	0.4671	0.3548	2275	3334	2.648E-100	0.44592
TAL1::TCF3	1.3052	0.1766	0.1353	850	1173	81.45E-22	0.21455
Arnt	1.2805	0.1339	0.1046	565	812	4.969E-10	0.20534
Gata1	1.2761	0.4782	0.3747	2241	3459	4.156E-84	0.48374
MIZF	1.2666	0.0202	0.0159	123	176	1.861E-02	0.01946
FOXI1	1.2389	0.6215	0.5017	2500	3835	3.413E-110	0.89144
FOXC1	1.2273	5.1939	4.2320	5942	10974	0.00E00	12.56593
NR4A2	1.2261	1.3121	1.0702	4371	7143	0.00E00	1.73005
NFIC	1.2256	1.7638	1.4391	4824	8098	0.00E00	2.50859
Hand1::Tcfe2a	1.2094	0.8341	0.6896	3333	5518	1.06E-190	0.96371
FOXO3	1.2090	1.2154	1.0053	3989	6683	3.439E-308	1.60928
Myb	1.2066	0.5425	0.4496	2493	4010	2.528E-96	0.57229
TEAD1	1.2026	0.0571	0.0475	347	540	8.167E-04	0.05170
ELK1	1.2025	0.6007	0.4995	2653	4279	12.82E-112	0.74736
SOX10	1.2007	5.7875	4.8202	6147	11286	0.00E00	12.49384
YY1	0.8264	2.2340	2.7032	5256	10232	0.00E00	5.20016
SP1	0.8074	0.6565	0.8131	1889	4183	1.565E-08	3.82639
MZF1_5-13	0.8073	0.7541	0.9340	2991	6427	15.59E-66	1.67936
FOXL1	0.7985	4.1882	5.2448	5207	10076	0.00E00	36.94964
CREB1	0.7971	0.4359	0.5468	2056	4428	39.24E-16	0.68179
Pdx1	0.7928	1.4354	1.8107	4038	8407	25.39E-214	3.40076
NF-kappaB	0.7545	0.1118	0.1482	506	1380	5.916E-08	0.25006
IRF1	0.7357	0.1254	0.1704	696	1649	1.231E-02	0.20026
Prrx2	0.7209	1.2467	1.7295	3724	8152	25.62E-142	3.05123
PBX1	0.7204	0.0506	0.0702	302	704	1.545E-02	0.10933
NFKB1	0.7107	0.0307	0.0432	156	375	2.036E-02	0.06199
Foxd3	0.6928	1.1906	1.7186	3269	6616	13.36E-110	7.10207
Zfx	0.6635	0.0759	0.1144	373	1153	55.07E-14	0.15638
PLAG1	0.6628	0.0072	0.0108	43	122	2.456E-02	0.01023
RREB1	0.5073	0.0142	0.0280	69	213	4.611E-04	0.06491
Ddit3::Cebpa	0.4736	0.1292	0.2728	730	2455	44.17E-26	0.28778

15.85 GR LNCaP vs VCaP DEX unique for GRvcap

Chromosome specific statistics are shown in Table 207. A histogram of sequence lengths is shown in Figure 237.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	1277	41	206	1705	262533	0.001053
10	500	35	184	795	92237	0.000681
11	901	39	300	2419	269878	0.001999
12	748	39	214	661	160377	0.001198
13	208	48	255	1462	53031	0.00046
14	321	44	174	486	56009	0.000522
15	508	48	217	633	110112	0.001074
16	258	50	183	886	47265	0.000523
17	599	44	236	1207	141121	0.001738
18	206	48	188	561	38759	0.000496
19	473	46	243	2831	114750	0.001941
2	1001	40	184	633	184623	0.000759
20	480	44	225	798	108008	0.001714
21	327	43	243	707	79615	0.001654
22	256	51	216	1021	55208	0.001076
3	802	40	196	666	157391	0.000795
4	772	43	203	3622	156674	0.00082
5	506	43	185	641	93619	0.000517
6	652	41	227	1176	147967	0.000865
7	778	45	205	600	159876	0.001005
8	744	40	226	892	167926	0.001147
9	747	37	210	729	156705	0.00111
X	213	57	226	2128	48062	0.00031
Y	45	58	166	470	7463	0.000126
all 24	13322	35	215	3622	2869209	0.000927

Table 207: Chromosome specific distribution of the regions. The last line represents the overall statistics.

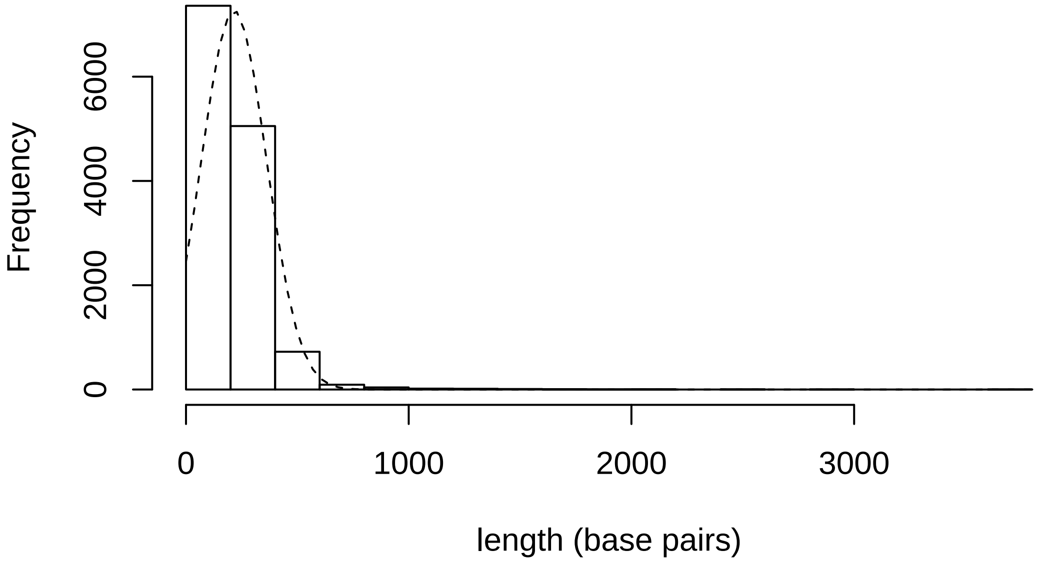
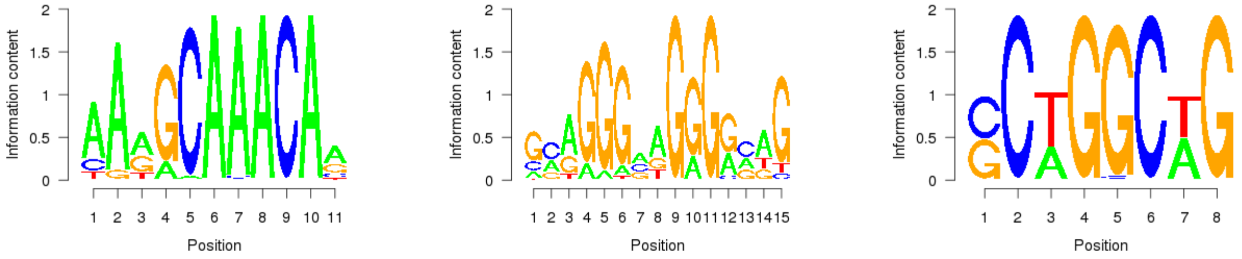


Figure 237: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU2-gCount** component.

property	value
genes	20735



(a) GRvsGR2rrU2-deNovo-meme1: width=11, sites=47, llr=535, E=15 (b) GRvsGR2rrU2-deNovo-meme2: width=15, sites=68, llr=753, E=0.17 (c) GRvsGR2rrU2-deNovo-meme3: width=8, sites=127, llr=1165, E=720000

Figure 238: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRvcap sequences.

Table 208: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
TLX1::NFIC	13.7718	0.0334	0.0024	338	51	34.86E-104	0.02218
CTCF	10.0983	0.0224	0.0022	291	52	3.881E-84	0.00970
ELK4	5.3284	0.0516	0.0096	599	230	4.61E-116	0.02984
E2F1	3.8040	0.0218	0.0057	270	140	7.678E-40	0.01281
GABPA	3.7919	0.0998	0.0263	1130	631	15.05E-160	0.06367
MIZF	3.2306	0.0314	0.0097	389	238	28.77E-48	0.01875
Tcfcp2l1	2.7225	0.0708	0.0260	818	592	2.718E-80	0.06047
Egr1	2.4102	0.0974	0.0404	1129	879	18.7E-102	0.09012
TFAP2A	2.3565	1.8231	0.7736	8109	9327	0.00E00	4.63452
NHLH1	2.3429	0.1302	0.0555	1101	884	12.26E-94	0.14415
Mycn	2.2414	0.1148	0.0512	1124	953	67.02E-88	0.12399
PPARG::RXRA	2.2075	0.0164	0.0074	217	184	4.658E-16	0.01057
Pax5	2.1780	0.0539	0.0247	678	595	84.79E-48	0.03700
Arnt	2.1581	0.1728	0.0800	1457	1326	2.459E-102	0.22232
Myf	2.1403	0.2295	0.1072	2166	2063	34.67E-154	0.25660
Klf4	2.0925	0.2246	0.1073	2231	2274	2.248E-138	0.22211
Myc	2.0707	0.1303	0.0629	1281	1188	1.363E-84	0.14462
HIF1A::ARNT	1.9755	0.3804	0.1925	3393	3567	18.99E-238	0.45272
Tal1::Gata1	1.9380	0.0293	0.0151	378	363	39.62E-22	0.02085
FOXA1	1.9353	0.3415	0.1764	3597	3767	5.944E-262	0.28087
NFIC	1.7671	1.9295	1.0919	10100	14229	0.00E00	2.73286
Stat3	1.7380	0.1200	0.0690	1261	1382	10.3E-56	0.11673
SP1	1.7174	1.1010	0.6410	5583	7298	0.00E00	3.32757
EBF1	1.6988	0.4776	0.2811	4012	5034	8.591E-214	0.59254
Zfp423	1.6910	0.0443	0.0262	479	536	7.013E-18	0.04682
Zfx	1.6737	0.1461	0.0873	1507	1872	7.708E-48	0.14907
INSM1	1.6571	0.1415	0.0854	1623	1887	64.88E-66	0.12696
Foxa2	1.6492	0.2831	0.1716	3075	3254	10.39E-202	0.31964
ESR2	1.6269	0.0107	0.0065	131	147	20.34E-06	0.00928
NFKB1	1.6267	0.0528	0.0324	509	598	2.574E-16	0.06473
Mafb	1.6221	1.4816	0.9134	9038	12675	0.00E00	2.13211
ELK1	1.6027	0.6063	0.3783	5419	7145	0.00E00	0.64242
Arnt::Ahr	1.5402	1.0663	0.6923	6565	9007	0.00E00	3.86588
NFYA	1.5303	0.0376	0.0246	434	561	8.304E-10	0.03698
MYC::MAX	1.5222	0.0459	0.0302	456	585	1.291E-10	0.05418
RELA	1.4804	0.0698	0.0471	805	1014	60.37E-22	0.06945
Hand1::Tcfe2a	1.4747	0.7621	0.5168	6354	9181	0.00E00	0.82496
MAX	1.4730	0.1401	0.0951	1340	1891	97.42E-26	0.17596
Esrrb	1.4471	0.0622	0.0430	783	1019	7.282E-18	0.05474
PLAG1	1.4273	0.0119	0.0083	155	193	1.52E-04	0.01056
Myb	1.4259	0.5019	0.3519	4869	6859	3.904E-236	0.50240
FOXF2	1.4190	0.0826	0.0582	1034	1345	65.41E-26	0.07180
ARMotifHH	1.4185	0.2104	0.1483	2337	3114	14.1E-72	0.20968
RXR::RAR_DR5	1.4078	0.0157	0.0111	204	275	3.141E-04	0.01288
MZF1_1-4	1.3195	2.5737	1.9506	10453	17389	0.00E00	7.55600
ZNF354C	1.2986	1.9693	1.5165	10193	16474	0.00E00	3.93018
NFE2L2	1.2969	0.0757	0.0584	958	1392	10.66E-14	0.06602
USF1	1.2876	0.3273	0.2542	2497	3568	3.969E-62	0.60048
ARMotifH	1.2782	4.3258	3.3844	12472	21872	0.00E00	11.85291
TAL1::TCF3	1.2680	0.1288	0.1016	1246	1902	67.81E-16	0.16748
NR2F1	1.2655	0.0654	0.0517	827	1222	1.993E-10	0.05951
RUNX1	1.2226	0.1784	0.1459	2094	3233	1.997E-32	0.17468
Fos	0.8279	0.6433	0.7770	5457	11732	18.9E-76	1.13107
NFATC2	0.8033	0.6554	0.8159	5936	12275	59.35E-124	1.11723
GATA3	0.7959	2.3349	2.9338	10615	21127	0.00E00	7.83927
FOXO3	0.7951	0.5872	0.7385	5341	11421	33.08E-72	1.05247
HNF1B	0.7815	0.0308	0.0394	389	931	3.295E-04	0.03873
Sox17	0.7810	0.4947	0.6335	4818	10580	5.48E-40	0.79268
FOXC1	0.7621	2.4274	3.1851	10701	21508	0.00E00	8.40456
GRMotifTT	0.7565	0.0074	0.0098	98	237	3.968E-02	0.00934
Gfi	0.7304	0.3671	0.5026	3769	8969	1.465E-04	0.59412
NR3C1	0.7235	0.0892	0.1233	1084	2740	41.27E-10	0.12629
En1	0.7162	1.7045	2.3799	9730	20420	0.00E00	4.75905
Cebpa	0.6665	0.2832	0.4249	2961	7531	1.417E-02	0.50988
T	0.6635	0.0049	0.0074	65	181	70.52E-04	0.00657
SOX9	0.6559	0.1935	0.2951	2217	5776	2.122E-08	0.32279
Pou5f1	0.6423	0.0035	0.0054	46	134	1.115E-02	0.00470
FOXA1pAR	0.6409	0.0225	0.0352	288	789	17.34E-08	0.03541
PBX1	0.6321	0.0324	0.0512	401	1092	38.54E-10	0.08156
HOXA5	0.6281	2.0338	3.2380	9919	21105	0.00E00	8.73754
TBP	0.5790	0.0824	0.1424	972	2921	11.25E-26	0.16136
HLF	0.5725	0.1395	0.2436	1532	4664	5.524E-32	0.28145
ARMotifTT	0.5690	0.0020	0.0035	26	83	2.053E-02	0.00309
Sox5	0.5673	0.5645	0.9951	5092	13092	2.847E-14	1.53092
SRY	0.5547	0.9433	1.7004	6749	16737	3.557E-98	3.48288
Nkx2-5	0.5154	1.6163	3.1360	8660	19842	0.00E00	9.67157
Ddit3::Cebpa	0.4798	0.1001	0.2088	1222	4086	2.048E-46	0.22164
Pdx1	0.4748	0.6478	1.3645	5232	15006	12.42E-04	2.54896
ARID3A	0.4745	0.8983	1.8931	6278	16292	3.011E-52	4.68907

Continued on next page...

motif	**ratio**	**fC**	**fR**	**n1C**	**n1R**	**p1**	**var**
NKX3-1	0.4549	0.1700	0.3738	1891	6454	16.88E-58	0.50926
IRF1	0.4518	0.0582	0.1290	715	2692	9.372E-52	0.13275
Prrx2	0.4361	0.5648	1.2951	4697	14622	1.513E-04	2.24628
NFIL3	0.3768	0.0378	0.1005	433	1915	15.13E-56	0.13228
FOXL1	0.3406	1.3233	3.8853	7285	19252	8.534E-110	26.21997
Foxd3	0.3398	0.4368	1.2855	3479	11479	1.562E-32	4.87726
MEF2A	0.2968	0.0504	0.1701	566	3152	4.56E-120	0.21812
Lhx3	0.2808	0.0491	0.1750	538	2942	1.214E-110	0.24200
EWSR1-FLI1	0.1455	0.0016	0.0111	13	68	5.736E-04	0.05101

15.86 GR LNCaP vs VCaP DEX unique for GRvcap (up)

Chromosome specific statistics are shown in Table 209. A histogram of sequence lengths is shown in Figure 239.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	101	55	233	1705	23559	9.5e-05
10	47	80	178	407	8375	6.2e-05
11	56	81	239	657	13379	9.9e-05
12	29	69	199	530	5766	4.3e-05
13	21	85	339	940	7125	6.2e-05
14	31	44	163	365	5039	4.7e-05
15	32	42	208	467	6646	6.5e-05
16	25	52	153	311	3822	4.2e-05
17	33	78	223	496	7359	9.1e-05
18	4	87	150	270	599	8e-06
19	26	76	217	572	5650	9.6e-05
2	64	77	181	374	11604	4.8e-05
20	43	50	209	431	8978	0.000142
21	2	53	98	143	196	4e-06
22	17	84	216	525	3675	7.2e-05
3	53	65	188	430	9965	5e-05
4	46	67	205	436	9421	4.9e-05
5	38	43	192	407	7309	4e-05
6	83	42	307	1176	25457	0.000149
7	33	79	230	540	7606	4.8e-05
8	25	94	315	892	7872	5.4e-05
9	45	78	201	595	9046	6.4e-05
X	13	82	158	365	2055	1.3e-05
all 23	867	42	220	1705	190503	6.2e-05

Table 209: Chromosome specific distribution of the regions. The last line represents the overall statistics.

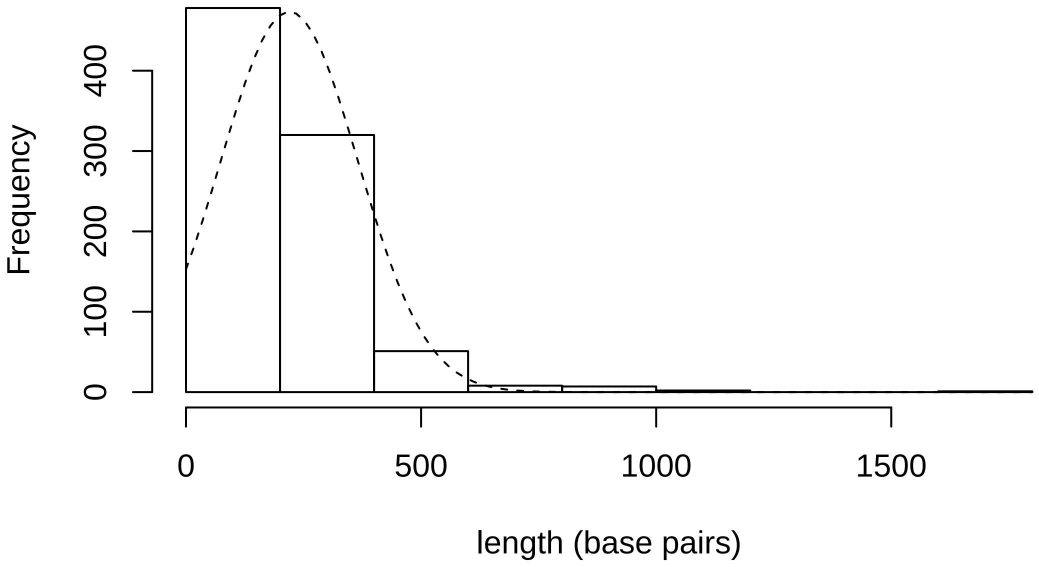
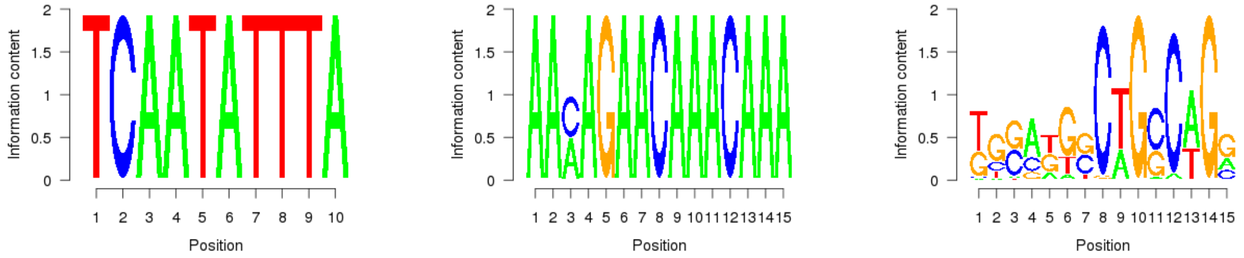


Figure 239: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU2u-gCount** component.

property	value
genes	313



(a) GRvsGR2rrU2u-deNovo-meme1: width=10, sites=2, llr=28, E=9.4e+08

(b) GRvsGR2rrU2u-deNovo-meme2: width=15, sites=2, llr=41, E=8.1e+08

(c) GRvsGR2rrU2u-deNovo-meme3: width=15, sites=56, llr=609, E=1.9e+08

Figure 240: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRvcap (up) sequences.

Table 210: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
CTCF	13.3138	0.0334	0.0025	28	4	9.598E-10	0.01389
ELK4	9.1731	0.0796	0.0086	54	14	1.011E-14	0.04591
TLX1::NFIC	6.6164	0.0288	0.0043	20	5	5.055E-06	0.01832
GABPA	6.3798	0.1419	0.0222	101	35	17.82E-24	0.08314
E2F1	4.8717	0.0242	0.0049	21	8	42.71E-06	0.01152
MIZF	4.6559	0.0404	0.0086	32	14	1.125E-06	0.02172
Pax5	3.3530	0.0807	0.0240	66	39	5.922E-10	0.04511
Egr1	3.3374	0.1153	0.0345	84	52	5.334E-12	0.07726
Tcfcp2l1	3.1735	0.1038	0.0327	75	47	1.409E-10	0.07266
NHLH1	2.8621	0.1430	0.0499	83	52	10.64E-12	0.13831
TFAP2A	2.8323	2.1811	0.7700	577	612	9.884E-90	4.85640
PPARG::RXRA	2.7941	0.0208	0.0074	18	12	61.37E-04	0.01191
Klf4	2.7259	0.3160	0.1159	198	158	92.61E-24	0.29190
Mycn	2.5001	0.1373	0.0549	87	64	4.387E-10	0.12645
Myf	2.4778	0.2399	0.0968	156	127	1.562E-16	0.22407
Zfp423	2.4239	0.0554	0.0228	37	32	10.32E-04	0.04827
HIF1A::ARNT	2.3253	0.4187	0.1800	232	213	64.09E-24	0.48096
Stat3	2.2782	0.1223	0.0536	83	71	9.843E-08	0.10612
SP1	2.2416	1.4083	0.6282	425	477	31.0E-46	3.78701
Arnt	2.2226	0.1892	0.0851	100	84	12.82E-10	0.22884
EBF1	2.0631	0.5686	0.2756	297	326	79.14E-26	0.63143
Myc	2.0061	0.1361	0.0678	95	84	2.095E-08	0.13228
Tal1::Gata1	1.9605	0.0242	0.0123	21	19	2.534E-02	0.01701
Zfx	1.9482	0.1730	0.0888	123	121	32.81E-10	0.15485
MYC::MAX	1.9441	0.0600	0.0308	36	38	1.197E-02	0.06263
NFKB1	1.8400	0.0715	0.0388	44	46	40.06E-04	0.08711
Mafb	1.8291	1.6217	0.8866	624	814	9.507E-86	2.16574
ELK1	1.8254	0.6978	0.3822	380	470	24.55E-32	0.68653
INSM1	1.7566	0.1603	0.0912	116	129	95.99E-08	0.14225
NFIC	1.7227	1.9585	1.1369	673	971	41.14E-94	2.59466
Arnt::Ahr	1.7136	1.0819	0.6313	440	562	6.062E-40	2.84543
FOXA1	1.6915	0.2941	0.1739	205	241	2.75E-12	0.25126
ARMotifHH	1.6585	0.2526	0.1523	177	212	13.53E-10	0.23342
RELA	1.6161	0.0807	0.0499	58	69	54.41E-04	0.07952
Hand1::Tcfe2a	1.6019	0.8247	0.5148	442	602	2.532E-36	0.82024
Myb	1.5452	0.5202	0.3366	319	450	33.5E-18	0.47252
MZF1_1-4	1.5307	3.0161	1.9704	698	1148	24.96E-90	8.05073
MZF1_5-13	1.4257	0.9827	0.6893	455	692	5.872E-32	1.51478
Foxa2	1.4129	0.2457	0.1739	175	205	6.196E-10	0.33141
MAX	1.4055	0.1569	0.1116	95	145	2.55E-02	0.19157
ZNF354C	1.3942	2.1326	1.5296	688	1060	4.251E-92	3.93139
ARMotifH	1.3349	4.6021	3.4476	821	1429	38.56E-140	12.30458
GRMotifTH	1.3018	0.1373	0.1054	106	158	85.36E-04	0.12629
RUNX1	1.2361	0.1730	0.1400	134	202	16.3E-04	0.16475
USF1	1.2221	0.3368	0.2756	160	245	3.253E-04	0.58665
REL	1.2133	0.3576	0.2947	222	375	44.54E-06	0.41983
Spz1	1.2026	0.4152	0.3453	264	440	17.83E-08	0.45818
Fos	0.7883	0.6148	0.7799	343	794	4.415E-04	1.02458
YY1	0.7833	1.6574	2.1159	622	1273	1.97E-46	4.23080
GATA2	0.7723	4.6897	6.0721	802	1569	3.017E-116	21.53691
NFATC2	0.7305	0.6332	0.8668	379	814	7.437E-08	1.23530
GATA3	0.7133	2.1349	2.9932	666	1395	1.155E-56	7.04193
En1	0.6996	1.6886	2.4137	626	1349	12.4E-44	4.64003
FOXO3	0.6951	0.5386	0.7750	339	749	73.63E-06	1.00799
FOXC1	0.6938	2.2318	3.2170	671	1398	1.344E-58	8.15289
NR3C1	0.6106	0.0715	0.1171	58	172	1.554E-02	0.10872
HOXA5	0.5737	1.8973	3.3070	636	1373	5.067E-46	8.47577
IRF1	0.5144	0.0669	0.1301	49	173	6.466E-04	0.14467
FOXI1	0.5113	0.2065	0.4038	146	434	95.2E-04	0.59106
HLF	0.5057	0.1269	0.2509	92	308	2.355E-04	0.28119
SOX9	0.5032	0.1557	0.3095	127	392	24.29E-04	0.30465
Ddit3::Cebpa	0.4861	0.1073	0.2207	87	281	8.322E-04	0.22801
SRY	0.4453	0.7889	1.7719	406	1126	26.89E-04	3.29818
TBP	0.4427	0.0657	0.1486	52	195	97.61E-06	0.17939
Nkx2-5	0.4209	1.3749	3.2663	517	1287	23.1E-16	10.44353
NFIL3	0.4004	0.0427	0.1067	34	139	1.589E-04	0.11024
Pdx1	0.3777	0.5409	1.4322	293	987	3.627E-02	2.71548
NKX3-1	0.3585	0.1315	0.3668	97	427	7.655E-10	0.40315
Prrx2	0.3532	0.4821	1.3650	274	958	37.58E-04	2.36848
PBX1	0.3327	0.0219	0.0660	18	91	1.724E-04	0.06898
Foxd3	0.2744	0.3391	1.2361	191	753	10.18E-08	4.04401
MEF2A	0.2550	0.0438	0.1720	31	194	8.406E-10	0.25749
Lhx3	0.1709	0.0311	0.1825	24	194	3.871E-12	0.25445

15.87 GR LNCaP vs VCaP DEX unique for GRvcap (down)

Chromosome specific statistics are shown in Table 211. A histogram of sequence lengths is shown in Figure 241.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	34	115	255	1000	8682	3.5e-05
2	17	82	197	343	3352	1.4e-05
3	26	76	222	655	5760	2.9e-05
4	11	91	171	348	1885	1e-05
5	16	83	209	438	3345	1.8e-05
6	3	96	118	148	355	2e-06
7	2	117	162	208	325	2e-06
8	14	154	250	491	3499	2.4e-05
9	26	83	199	462	5175	3.7e-05
10	8	71	177	380	1418	1e-05
11	13	83	208	341	2698	2e-05
12	24	52	198	532	4752	3.6e-05
13	3	100	181	297	543	5e-06
14	11	58	157	294	1725	1.6e-05
15	20	85	259	633	5174	5e-05
16	21	87	146	282	3071	3.4e-05
17	12	110	200	351	2402	3e-05
18	6	95	172	237	1034	1.3e-05
19	9	97	213	397	1921	3.2e-05
20	3	44	119	199	358	6e-06
22	4	111	214	365	856	1.7e-05
all 21	283	44	206	1000	58330	1.9e-05

Table 211: Chromosome specific distribution of the regions. The last line represents the overall statistics.

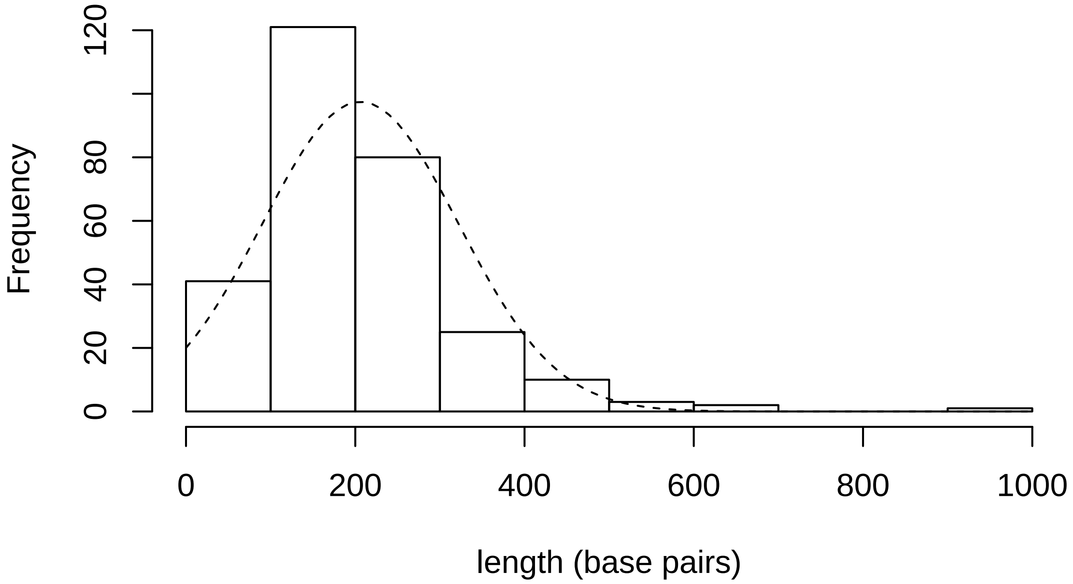
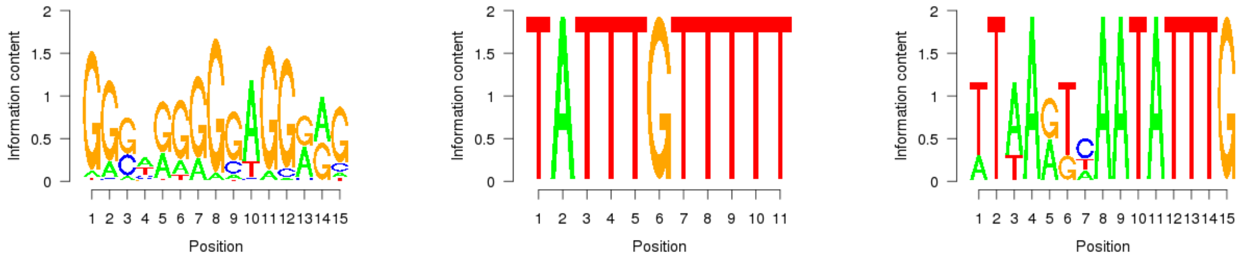


Figure 241: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU2d-gCount** component.

property	value
genes	95



(a) GRvsGR2rrU2d-deNovo-meme1: width=15, sites=44, llr=482, E=11000 (b) GRvsGR2rrU2d-deNovo-meme2: width=11, sites=2, llr=32, E=8.7e+07 (c) GRvsGR2rrU2d-deNovo-meme3: width=15, sites=4, llr=74, E=1.5e+08

Figure 242: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRvcap (down) sequences.

Table 212: Motif enrichments

motif	ratio	fC	fR	n1C	n1R	p1	var
TLX1::NFIC	849.0565	0.0424	0.0000	10	0	66.5E-06	0.01968
ESR2	354.3569	0.0177	0.0000	4	0	2.794E-02	0.00867
CTCF	21.5967	0.0424	0.0019	12	1	48.48E-06	0.01591
ELK4	15.2471	0.0883	0.0057	19	3	1.002E-06	0.05103
E2F1	7.2959	0.0283	0.0038	8	2	77.49E-04	0.01228
Pax5	5.8200	0.0671	0.0115	18	6	72.77E-06	0.03262
GABPA	5.6771	0.1307	0.0230	30	12	64.14E-08	0.08211
NFKB1	4.9102	0.1131	0.0230	24	10	16.84E-06	0.07910
Mycn	4.7908	0.1837	0.0383	35	14	5.239E-08	0.15119
Egr1	4.3349	0.1413	0.0326	37	13	38.24E-10	0.08578
Myc	3.6860	0.1625	0.0441	36	18	52.18E-08	0.11827
STAT1	3.6751	0.0353	0.0096	8	4	4.403E-02	0.02577
PLAG1	3.6659	0.0212	0.0057	6	2	4.481E-02	0.01356
Arnt	3.3799	0.2332	0.0690	40	24	1.272E-06	0.23019
Myf	3.1607	0.2544	0.0805	56	37	1.677E-08	0.19883
HIF1A::ARNT	2.6618	0.4947	0.1858	88	76	1.087E-10	0.46919
TFAP2A	2.4504	1.9576	0.7989	189	198	2.953E-30	4.76837
INSM1	2.4111	0.1802	0.0747	43	35	45.03E-06	0.13425
NHLH1	2.4107	0.1201	0.0498	20	15	70.05E-04	0.16608
EBF1	2.2603	0.5760	0.2548	96	96	6.887E-10	0.63328
SP1	2.2473	1.4982	0.6667	146	159	17.34E-18	4.10653
Tcfcp2l1	2.1682	0.0707	0.0326	18	16	3.315E-02	0.05137
Esrrb	2.1342	0.0777	0.0364	20	19	3.491E-02	0.05337
Stat3	2.0487	0.1413	0.0690	31	30	57.7E-04	0.12540
ARMotifHH	2.0418	0.3286	0.1609	68	74	19.32E-06	0.30607
MYC::MAX	1.9745	0.0530	0.0268	13	9	2.768E-02	0.05218
Klf4	1.9631	0.2332	0.1188	55	48	5.717E-06	0.22095
NFIC	1.9292	2.0106	1.0421	213	285	83.8E-32	2.73651
Arnt::Ahr	1.9280	1.2226	0.6341	158	199	78.22E-18	2.86275
Zfx	1.9278	0.1625	0.0843	39	35	4.745E-04	0.16659
Mafb	1.8782	1.5760	0.8391	200	241	12.88E-30	2.14583
USF1	1.7694	0.4170	0.2356	64	70	52.16E-06	0.63290
FOXA1	1.7650	0.3145	0.1782	59	77	29.91E-04	0.41648
ELK1	1.7371	0.6290	0.3621	115	151	1.576E-08	0.61404
Myb	1.7214	0.5442	0.3161	108	139	6.423E-08	0.49576
Foxa2	1.5369	0.2650	0.1724	51	67	98.66E-04	0.48405
ZNF354C	1.4866	2.0989	1.4119	228	335	24.29E-34	3.19192
MZF1_1-4	1.4842	2.9399	1.9808	235	393	8.614E-32	6.99824
MZF1_5-13	1.4092	0.9152	0.6494	153	224	1.512E-12	1.01962
Hand1::Tcfe2a	1.3815	0.6749	0.4885	119	190	3.333E-06	0.73495
REL	1.3701	0.3675	0.2682	77	102	2.007E-04	0.41796
ARMotifH	1.3235	4.4523	3.3640	264	468	57.97E-44	8.88097
Spz1	1.2955	0.4170	0.3218	89	141	11.14E-04	0.41840
Nkx3-2	0.7878	0.7350	0.9330	143	283	7.214E-06	1.17285
GATA2	0.7483	4.1661	5.5670	258	500	79.25E-38	16.47454
FOXC1	0.6547	2.0318	3.1034	215	452	3.175E-18	6.87049
GATA3	0.6529	1.9399	2.9713	209	449	4.784E-16	6.61162
SOX9	0.6188	0.1873	0.3027	39	132	2.525E-02	0.36280
En1	0.5619	1.3251	2.3582	188	433	7.058E-10	3.63182
HOXA5	0.5604	1.7208	3.0709	199	442	73.28E-14	6.63407
Ddit3::Cebpa	0.4442	0.0919	0.2069	25	86	3.352E-02	0.20609
NR3C1	0.4383	0.0671	0.1533	19	71	2.269E-02	0.13287
HLF	0.4349	0.1166	0.2682	29	111	62.74E-04	0.26595
Nkx2-5	0.4305	1.2650	2.9387	164	412	58.96E-06	7.48907
TBP	0.4022	0.0601	0.1494	13	61	56.32E-04	0.17884
NKX3-1	0.3374	0.1131	0.3352	28	127	3.827E-04	0.41763
IRF1	0.3329	0.0389	0.1169	11	53	79.1E-04	0.10144
Pdx1	0.3297	0.4099	1.2433	78	312	33.8E-04	1.84579
Prrx2	0.3119	0.3675	1.1782	72	306	5.464E-04	1.75723
Foxd3	0.2776	0.3286	1.1839	54	221	7.586E-04	5.21272
Lhx3	0.1422	0.0212	0.1494	5	56	38.83E-06	0.17318
NFIL3	0.0629	0.0071	0.1130	2	48	12.93E-06	0.09748
MEF2A	0.0408	0.0071	0.1743	2	66	12.64E-08	0.19932

15.88 GR LNCaP vs VCaP DEX unique for GRvcap (stable)

Chromosome specific statistics are shown in Table 213. A histogram of sequence lengths is shown in Figure 243.

		length				
chromosome	frequency	min	mean	max	total	coverage
1	841	41	209	1705	175585	0.000704
10	267	48	176	795	47116	0.000348
11	627	39	323	2419	202638	0.001501
12	473	43	220	661	104232	0.000779
13	60	61	178	740	10705	9.3e-05
14	196	53	181	503	35482	0.000331
15	292	52	222	588	64949	0.000633
16	192	45	187	886	35835	0.000397
17	453	46	236	1207	106694	0.001314
18	78	48	183	428	14249	0.000182
19	413	46	248	2831	102592	0.001735
2	547	45	183	633	100214	0.000412
20	287	44	225	798	64688	0.001026
21	203	43	257	707	52091	0.001082
22	192	51	219	1021	41957	0.000818
3	482	44	197	666	95155	0.000481
4	412	44	218	3622	89856	0.00047
5	260	43	183	622	47451	0.000262
6	402	41	223	1176	89599	0.000524
7	469	45	207	579	96864	0.000609
8	335	42	228	892	76474	0.000522
9	408	37	214	609	87144	0.000617
X	103	57	159	384	16407	0.000106
Y	12	58	188	300	2253	3.8e-05
all 24	8004	37	220	3622	1760230	0.000569

Table 213: Chromosome specific distribution of the regions. The last line represents the overall statistics.

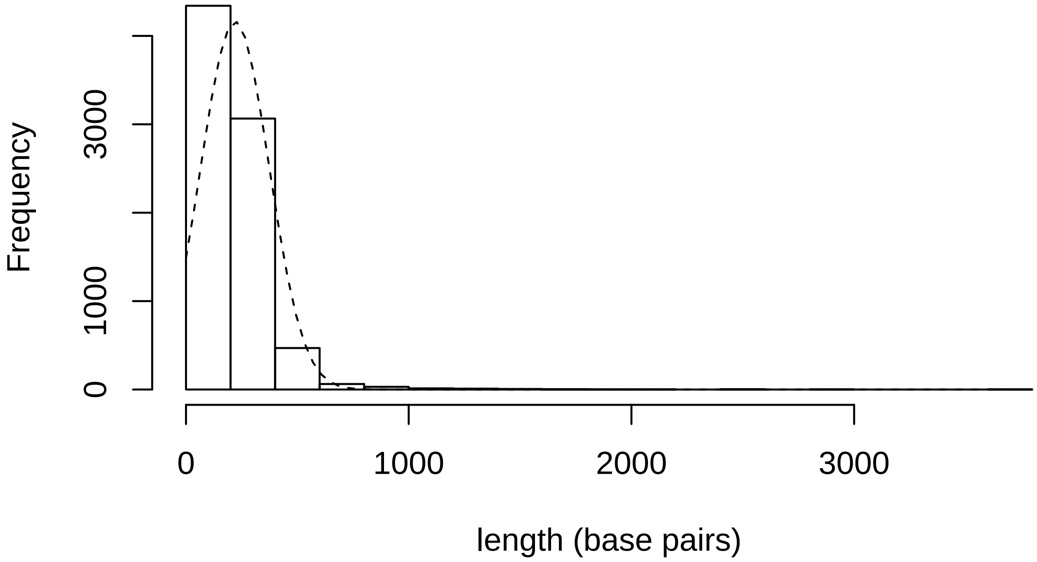
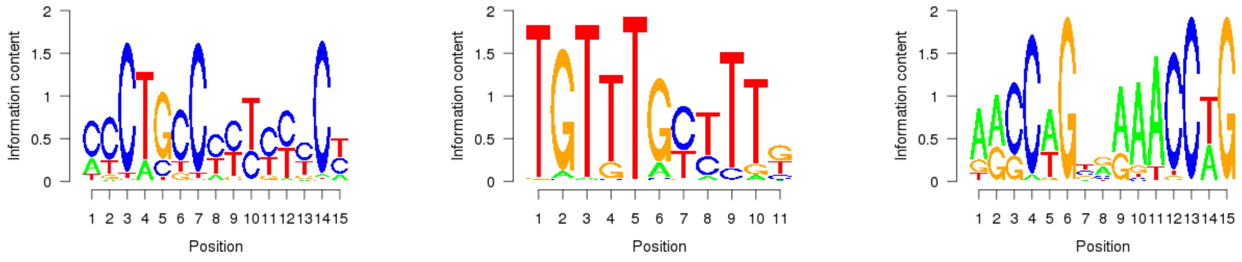


Figure 243: Sequence length distribution. Dashed line represents a normal distribution approximation that is based on the mean and the standard deviation of the sequece lengths.

The following table shows the properties of **GRvsGR2rrU2s-gCount** component.

property	value
genes	4573



(a) GRvsGR2rrU2s-deNovo-meme1: width=15, sites=101, llr=1023, E=5500 (b) GRvsGR2rrU2s-deNovo-meme2: width=11, sites=77, llr=788, E=5.9e+07 (c) GRvsGR2rrU2s-deNovo-meme3: width=15, sites=28, llr=361, E=2.2e+08

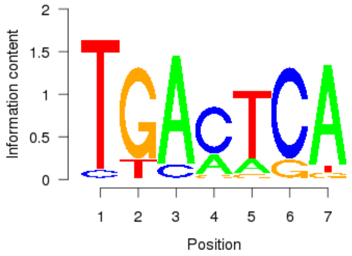
Figure 244: De novo motifs for the filtered GR LNCaP vs VCaP DEX unique for GRvcap (stable) sequences.

Table 214: Motif enrichments

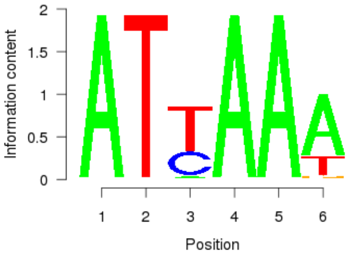
motif	ratio	fC	fR	n1C	n1R	p1	var
TLX1::NFIC	15.9587	0.0350	0.0021	209	25	1.639E-68	0.02529
CTCF	11.9512	0.0270	0.0022	209	33	14.53E-64	0.01136
ELK4	5.3941	0.0610	0.0113	414	154	34.55E-84	0.03854
E2F1	4.1274	0.0256	0.0062	191	92	63.59E-32	0.01488
GABPA	3.8552	0.1164	0.0302	765	433	2.089E-108	0.07717
MIZF	3.2234	0.0360	0.0111	267	162	17.82E-34	0.02168
Tcfcp2l1	2.6872	0.0781	0.0290	527	395	5.796E-50	0.07448
Egr1	2.6025	0.1098	0.0422	754	569	50.08E-74	0.08468
NHLH1	2.5752	0.1404	0.0545	716	526	7.303E-72	0.14953
TFAP2A	2.5063	2.0677	0.8250	5111	5867	0.00E00	5.66519
Pax5	2.4337	0.0568	0.0233	427	339	2.131E-36	0.03747
Klf4	2.3202	0.2639	0.1137	1521	1454	14.15E-114	0.26009
Tal1::Gata1	2.3128	0.0306	0.0132	235	191	39.28E-20	0.02057
Arnt	2.2521	0.1888	0.0838	951	818	1.731E-76	0.22576
Myf	2.2375	0.2368	0.1058	1353	1223	5.378E-108	0.24445
Mycn	2.1842	0.1248	0.0571	732	636	18.79E-56	0.12642
PPARG::RXRA	2.0939	0.0177	0.0084	140	119	80.53E-12	0.01321
HIF1A::ARNT	2.0433	0.4144	0.2028	2190	2242	57.93E-170	0.48138
Myc	1.9413	0.1333	0.0686	781	773	12.33E-46	0.14478
SP1	1.8398	1.2522	0.6806	3608	4510	1.63E-284	4.17767
FOXA1	1.8384	0.3306	0.1798	2088	2289	38.86E-138	0.28174
NFKB1	1.8367	0.0625	0.0340	356	378	3.291E-16	0.07316
INSM1	1.7716	0.1570	0.0886	1070	1137	72.65E-58	0.14593
NFIC	1.7428	1.9881	1.1408	6070	8686	0.00E00	2.94225
Zfx	1.7388	0.1675	0.0963	1004	1243	3.128E-34	0.17292
EBF1	1.7159	0.5067	0.2953	2487	3065	66.24E-144	0.66055
ELK1	1.7129	0.6478	0.3782	3360	4265	49.42E-240	0.70509
Stat3	1.7120	0.1246	0.0727	779	878	86.89E-34	0.12246
PLAG1	1.6877	0.0147	0.0087	115	124	17.03E-06	0.01149
Mafb	1.6508	1.5330	0.9286	5454	7662	0.00E00	2.27234
NFYA	1.6061	0.0407	0.0253	276	340	4.723E-08	0.04382
ESR2	1.5711	0.0102	0.0065	76	86	15.32E-04	0.00923
Foxa2	1.5582	0.2710	0.1739	1780	1970	53.31E-106	0.31759
RELA	1.5007	0.0730	0.0486	499	627	8.374E-14	0.07331
Zfp423	1.4999	0.0460	0.0306	295	376	13.16E-08	0.05006
MYC::MAX	1.4861	0.0459	0.0308	278	359	75.28E-08	0.05328
MAX	1.4757	0.1474	0.0999	841	1194	4.64E-16	0.17596
Arnt::Ahr	1.4676	1.0843	0.7388	4038	5565	30.86E-306	4.22445
Myb	1.4611	0.5151	0.3526	2978	4095	20.02E-158	0.51421
ARMotifHH	1.4527	0.2258	0.1554	1494	1951	11.52E-52	0.22507
RXR::RAR_DR5	1.4500	0.0167	0.0115	132	169	9.29E-04	0.01361
Hand1::Tcfe2a	1.3940	0.7632	0.5475	3795	5742	25.4E-220	0.88937
MZF1_1-4	1.3653	2.7955	2.0475	6376	10575	0.00E00	8.55790
FOXF2	1.3516	0.0828	0.0613	624	850	45.59E-14	0.07393
TAL1::TCF3	1.3385	0.1338	0.1000	768	1120	1.575E-12	0.17381
ZNF354C	1.3352	2.0785	1.5567	6239	9983	0.00E00	4.28902
RREB1	1.3022	0.0224	0.0172	133	182	53.34E-04	0.04410
NFE2L2	1.2990	0.0762	0.0587	574	835	94.71E-10	0.06810
NR2F1	1.2905	0.0656	0.0508	495	730	71.7E-08	0.05869
USF1	1.2868	0.3392	0.2636	1540	2231	6.433E-38	0.58409
ARMotifH	1.2852	4.5034	3.5041	7526	13252	0.00E00	13.10249
Esrrb	1.2746	0.0606	0.0475	456	673	3.005E-06	0.05584
MZF1_5-13	1.2056	0.8929	0.7406	3974	6823	20.74E-186	1.45696
Fos	0.8167	0.6354	0.7781	3212	7055	2.951E-38	1.19545
GATA2	0.8143	4.9058	6.0249	7464	14371	0.00E00	23.41405
NFATC2	0.7869	0.6448	0.8194	3517	7408	3.299E-66	1.10216
GATA3	0.7638	2.2782	2.9826	6311	12822	0.00E00	7.64470
Sox17	0.7498	0.4730	0.6309	2811	6248	3.327E-20	0.80945
FOXC1	0.7461	2.4127	3.2337	6441	12945	0.00E00	8.75404
HNF1B	0.7458	0.0290	0.0389	219	552	7.999E-04	0.03801
Foxq1	0.7432	0.1366	0.1838	959	2219	3.31E-02	0.22595
FOXO3	0.7389	0.5683	0.7692	3134	6949	87.66E-34	1.10149
En1	0.7142	1.7189	2.4067	5866	12248	0.00E00	5.01166
NR3C1	0.7028	0.0877	0.1248	630	1654	10.61E-08	0.13112
T	0.6422	0.0056	0.0088	45	129	1.708E-02	0.00779
Cebpa	0.6372	0.2695	0.4229	1701	4529	2.639E-04	0.50502
SOX9	0.6287	0.1884	0.2997	1280	3481	1.417E-08	0.33985
FOXI1	0.6243	0.2358	0.3777	1491	3744	72.08E-04	0.61296
HOXA5	0.6086	1.9843	3.2606	5881	12719	0.00E00	9.06211
FOXA1pAR	0.6052	0.0212	0.0351	162	464	9.879E-06	0.03835
PBX1	0.5999	0.0310	0.0517	226	675	1.367E-08	0.06447
Sox2	0.5584	0.0024	0.0043	19	64	2.998E-02	0.00361
TBP	0.5485	0.0773	0.1410	548	1741	8.162E-20	0.16054
Nobox	0.5457	0.4350	0.7973	2239	6229	1.33E-02	1.39772
ARMotifTT	0.5380	0.0022	0.0042	18	60	3.91E-02	0.00378
Sox5	0.5323	0.5364	1.0077	2947	7847	1.616E-04	1.64423
HLF	0.5319	0.1349	0.2537	887	2906	6.87E-28	0.30246
SRY	0.5227	0.8927	1.7077	3912	10002	47.95E-44	3.61644
Pou5f1	0.5067	0.0030	0.0060	24	86	57.31E-04	0.00525

Continued on next page...

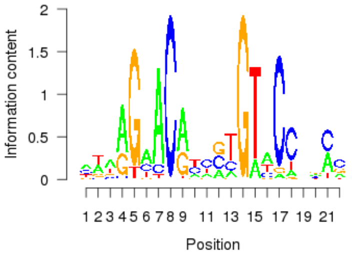
motif	**ratio**	**fC**	**fR**	**n1C**	**n1R**	**p1**	**var**
Nkx2-5	0.4863	1.5270	3.1400	5064	11891	9.478E-194	10.33531
Ddit3::Cebpa	0.4684	0.1002	0.2140	737	2532	9.987E-32	0.22400
IRF1	0.4440	0.0557	0.1256	407	1582	13.31E-34	0.13396
ARID3A	0.4414	0.8348	1.8913	3587	9738	45.33E-18	4.81033
NKX3-1	0.4341	0.1614	0.3719	1081	3814	4.034E-40	0.53651
Prrx2	0.4121	0.5380	1.3056	2730	8783	2.209E-06	2.35252
NFIL3	0.3367	0.0337	0.1003	237	1166	1.067E-40	0.12757
Foxd3	0.3219	0.4178	1.2981	2019	6844	24.59E-26	5.11287
FOXL1	0.3095	1.2245	3.9566	4214	11658	23.23E-44	29.29759
MEF2A	0.2799	0.0460	0.1644	316	1830	3.095E-74	0.19411
Lhx3	0.2676	0.0460	0.1720	304	1728	39.41E-70	0.24763
EWSR1-FLI1	0.1139	0.0007	0.0070	5	39	18.36E-04	0.01952



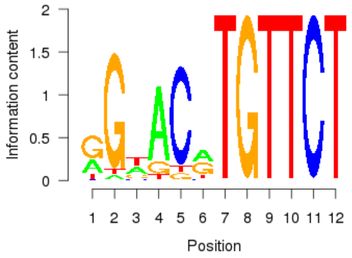
(a) AP1: class=Zipper-Type, family=Leucine Zipper, species=9606,10116,10090, type=COMPILED, acc=P05412,P01100, id=MA0099



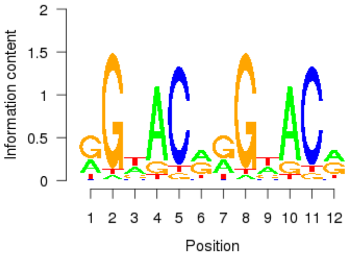
(b) ARID3A: class=Helix-Turn-Helix, family=Arid, species=10090, type=SELEX, acc=Q62431, id=MA0151



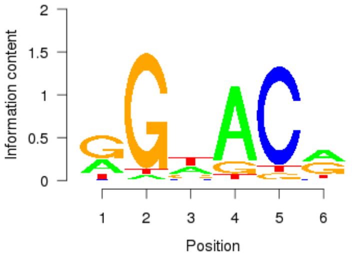
(c) Ar: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=10117, type=SELEX, acc=P15207, id=MA0007



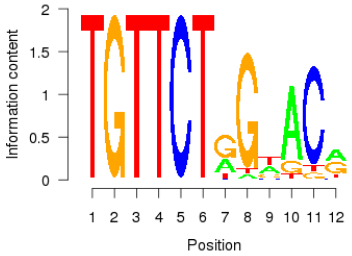
(d) AR



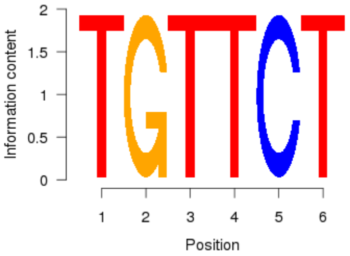
(e) ARMotifHH



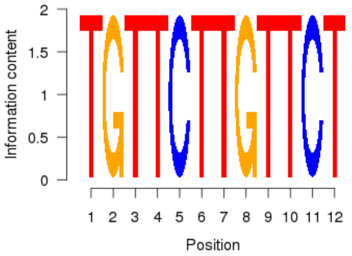
(f) ARMotifH



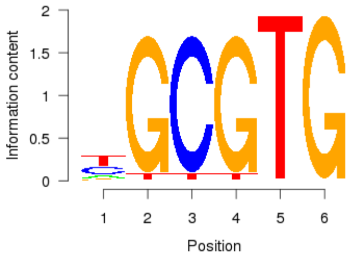
(g) ARMotifTH



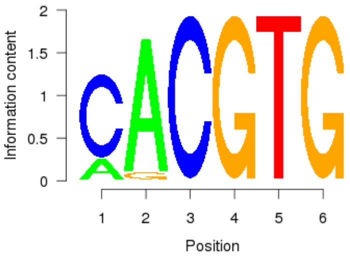
(h) ARMotifT



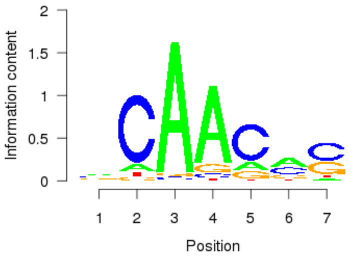
(i) ARMotifTT



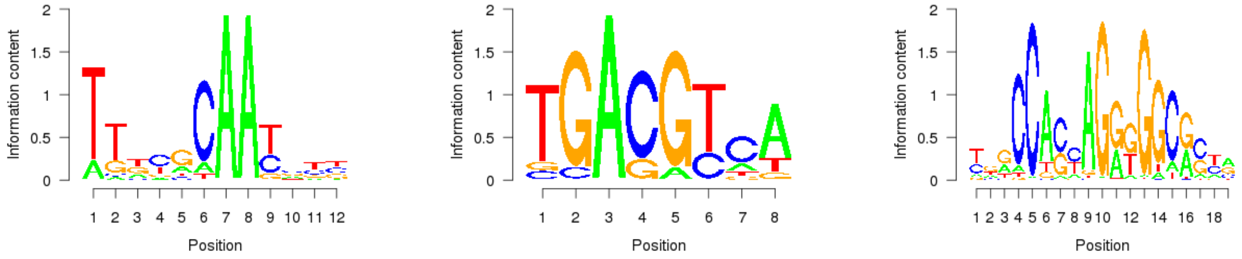
(j) Arnt::Ahr: class=Zipper-Type, family=Helix-Loop-Helix, species=10090, type=SELEX, acc=P30561,P53762, id=MA0006



(k) Arnt: class=Zipper-Type, family=Helix-Loop-Helix, species=10090, type=SELEX, acc=P53762, id=MA0004



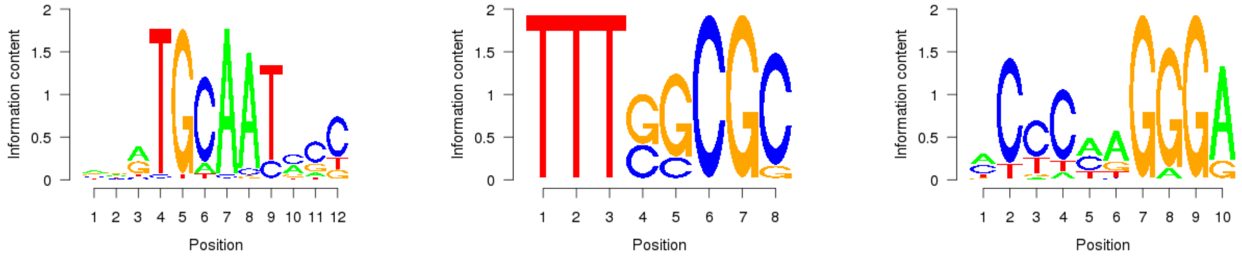
(l) BRCA1: class=Other, family=Other, species=9606, type=SELEX, acc=P38398, id=MA0133



(a) Cebpa: class=Zipper-Type, family=Leucine Zipper, species=10090,10116, type=COMPILED, id=MA0102

(b) CREB1: class=Zipper-Type, family=Leucine Zipper, species=10116,9606,10090, type=COMPILED, acc=P16220, id=MA0018

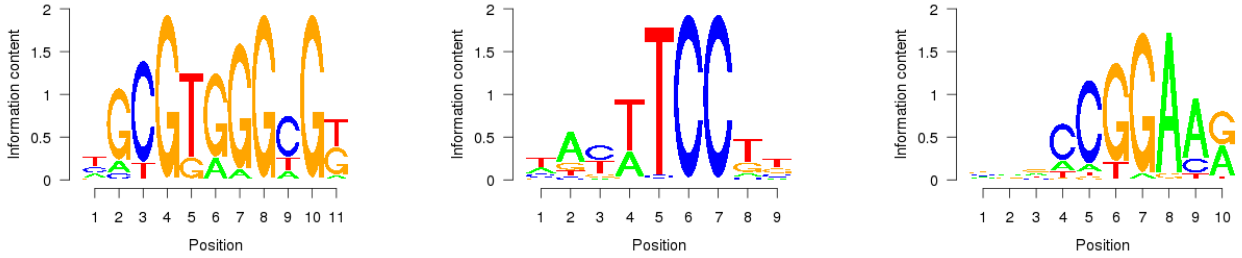
(c) CTCF: class=Zinc-coordinating , family=BetaBetaAlpha-zinc finger, species=9606, type=ChIP-seq, acc=P49711, id=MA0139



(d) Ddit3::Cebpa: class=Zipper-Type, family=Leucine Zipper, species=10116, type=SELEX, acc=Q62857,P05554, id=MA0019

(e) E2F1: class=Winged Helix-Turn-Helix, family=E2F, species=9606, type=COMPILED, acc=NP_005216, id=MA0024

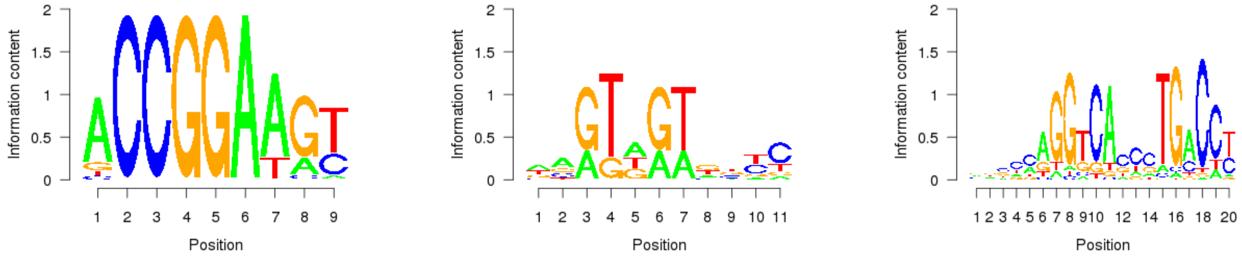
(f) EBF1: class=Zipper-Type, family=Helix-Loop-Helix, species=10090, type=COMPILED, acc=Q07802, id=MA0154



(g) Egr1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=10090, type=bacterial 1-hybrid, acc=P08046, id=MA0162

(h) ELF5: class=Winged Helix-Turn-Helix, family=Ets, species=10090, type=SELEX, id=MA0136

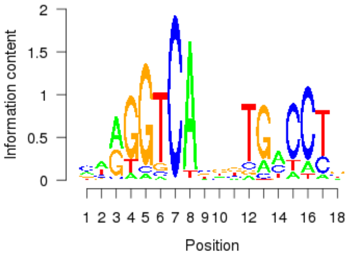
(i) ELK1: class=Winged Helix-Turn-Helix, family=Ets, species=9606, type=SELEX, acc=P19419, id=MA0028



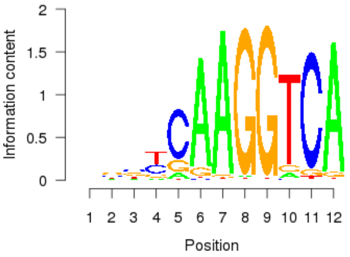
(j) ELK4: class=Winged Helix-Turn-Helix, family=Ets, species=9606, type=SELEX, acc=P28324, id=MA0076

(k) En1: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=P09065, id=MA0027

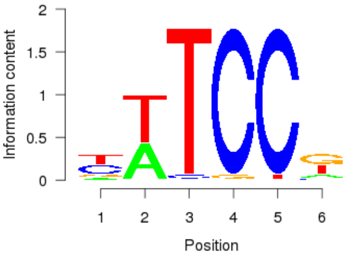
(l) ESR1: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=ChIP-seq, acc=P03372, id=MA0112



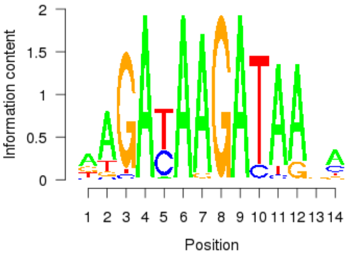
(a) ESR2: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=ChIP-chip, acc=Q92731, id=MA0258



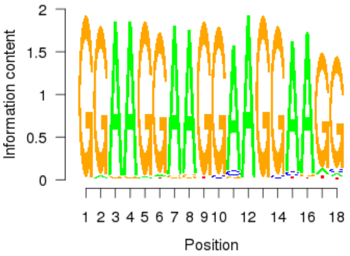
(b) Esrrb: class=Zinc-coordinating , family=Hormone-nuclear Receptor, species=10090, type=ChiP-seq, acc=Q61539, id=MA0141



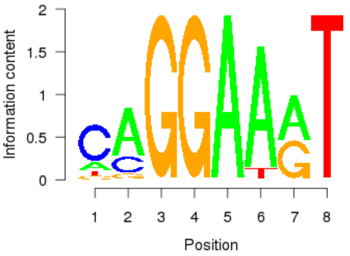
(c) ETS1: class=Winged Helix-Turn-Helix, family=Ets, species=9606, type=SELEX, acc=CAG47050, id=MA0098



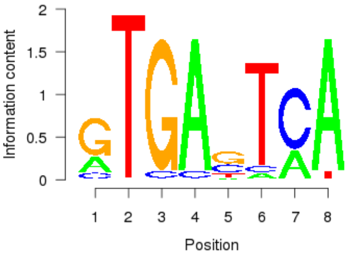
(d) Evi1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=10090, type=SELEX, acc=AAI39763, id=MA0029



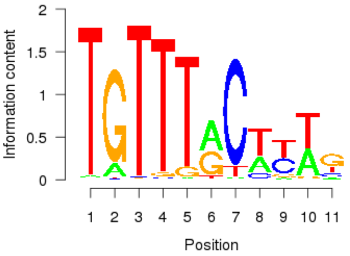
(e) EWSR1-FLI1: class=Winged Helix-Turn-Helix, family=Ets, species=9606, type=ChiP-seq, acc=Q9BZD1, id=MA0149



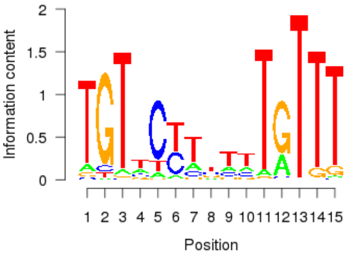
(f) FEV: class=Winged Helix-Turn-Helix, family=Ets, species=10116,9606, type=COMPILED, acc=Q99581, id=MA0156



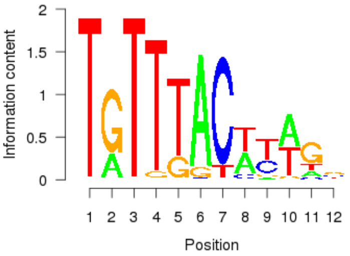
(g) Fos: class=Zipper-Type, family=Leucine Zipper, species=10090, type=SELEX, acc=P01101, id=MA0099



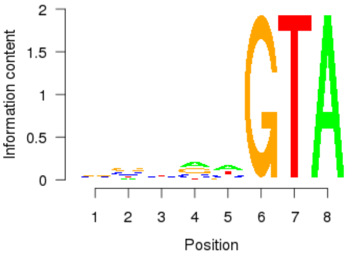
(h) FOXA1: class=Winged Helix-Turn-Helix, family=Forkhead, species=9606, type=ChiP-Seq, acc=P55317, id=MA0148



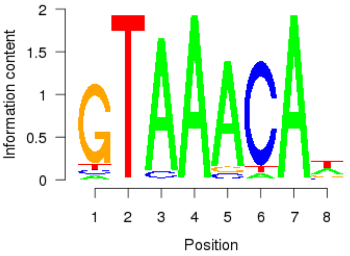
(i) FOXA1pAR



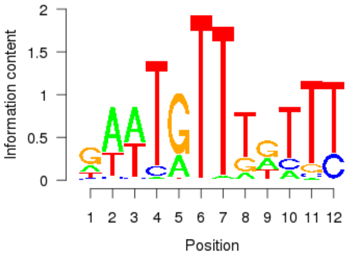
(j) Foxa2: class=Winged Helix-Turn-Helix, family=Forkhead, species=10090, type=ChiP-seq, acc=P35583, id=MA0047



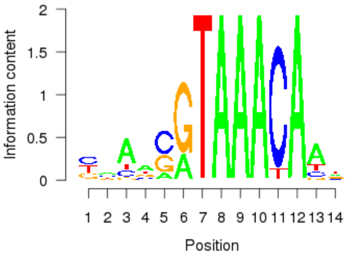
(k) FOXC1: class=Winged Helix-Turn-Helix, family=Forkhead, species=9606, type=SELEX, acc=Q12948, id=MA0032



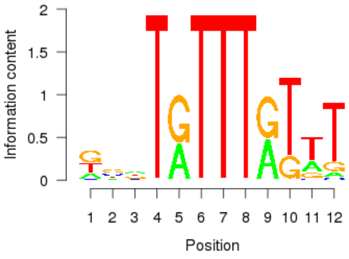
(l) FOXD1: class=Winged Helix-Turn-Helix, family=Forkhead, species=9606, type=SELEX, acc=Q16676, id=MA0031



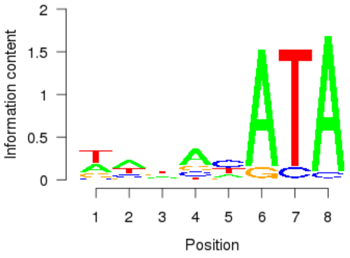
(a) Foxd3: class=Winged Helix-Turn-Helix, family=Forkhead, species=10116, type=SELEX, acc=Q63245, id=MA0041



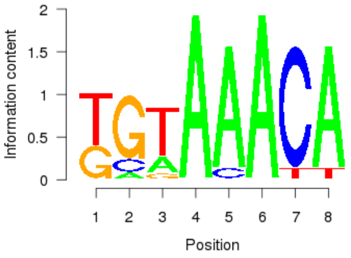
(b) FOXF2: class=Winged Helix-Turn-Helix, family=Forkhead, species=9606, type=SELEX, acc=Q12947, id=MA0030



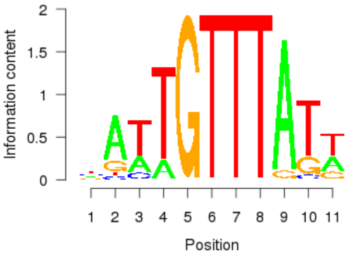
(c) FOXI1: class=Winged Helix-Turn-Helix, family=Forkhead, species=9606, type=SELEX, acc=Q12951, id=MA0042



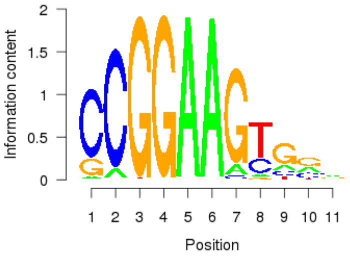
(d) FOXL1: class=Winged Helix-Turn-Helix, family=Forkhead, species=9606, type=SELEX, acc=Q12952, id=MA0033



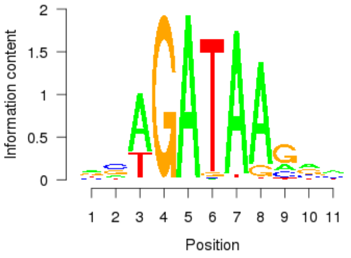
(e) FOXO3: class=Winged Helix-Turn-Helix, family=Forkhead, species=10090,9606, type=COMPILED, acc=O43524, id=MA0157



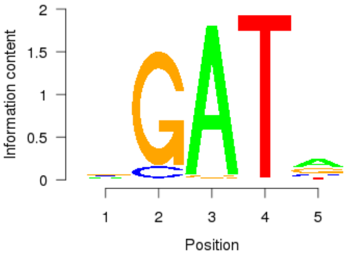
(f) Foxq1: class=Winged Helix-Turn-Helix, family=Forkhead, species=10116, type=SELEX, acc=Q63244, id=MA0040



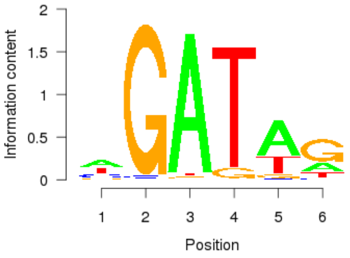
(g) GABPA: class=Winged Helix-Turn-Helix, family=Ets, species=10090, type=ChiP-seq, acc=Q91YY8, id=MA0062



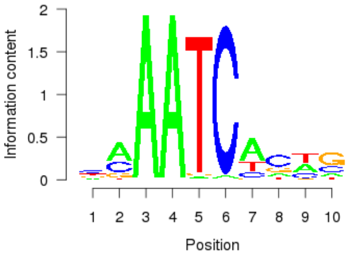
(h) Gata1: class=Zinc-coordinating , family=GATA, species=10090, type=ChiP-seq, acc=P17679, id=MA0035



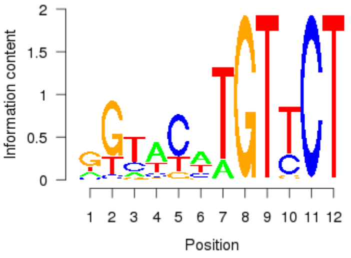
(i) GATA2: class=Zinc-coordinating, family=GATA, species=9606, type=SELEX, acc=P23769, id=MA0036



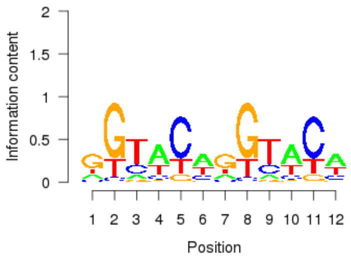
(j) GATA3: class=Zinc-coordinating, family=GATA, species=9606, type=SELEX, acc=P23771, id=MA0037



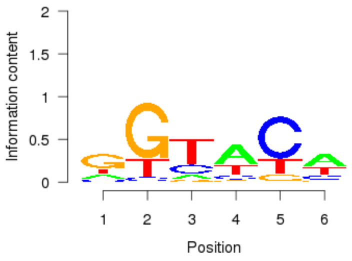
(k) Gfi: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=10116, type=SELEX, acc=Q07120, id=MA0038



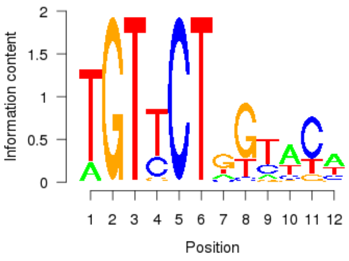
(l) GR



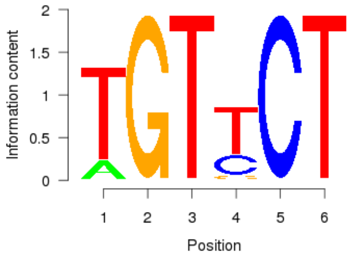
(a) GRMotifHH



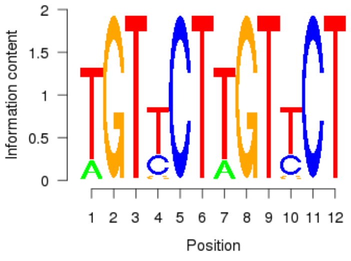
(b) GRMotifH



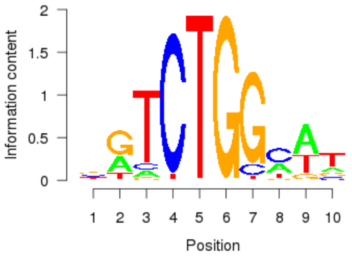
(c) GRMotifTH



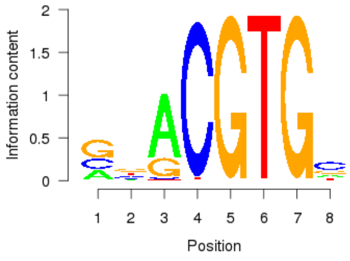
(d) GRMotifT



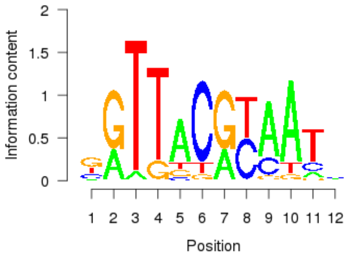
(e) GRMotifTT



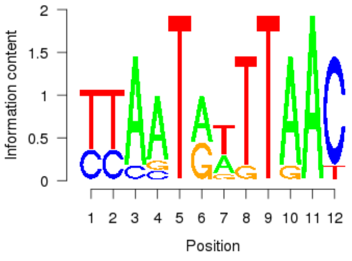
(f) Hand1::Tcfe2a: class=Zipper-Type, family=Helix-Loop-Helix, species=10090, type=SELEX, acc=Q64279,P15806, id=MA0092



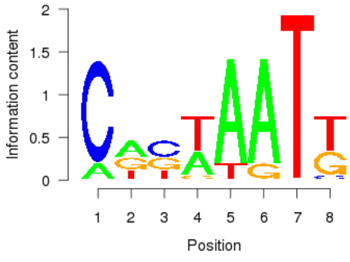
(g) HIF1A::ARNT: class=Zipper-Type, family=Helix-Loop-Helix, species=9606,10090,10117,9986, type=COMPILED, acc=EAW80806,EAW53510, id=MA0259



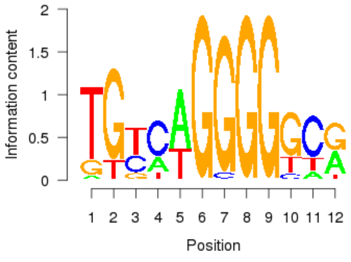
(h) HLF: class=Zipper-Type, family=Leucine Zipper, species=9606, type=SELEX, acc=Q16534, id=MA0043



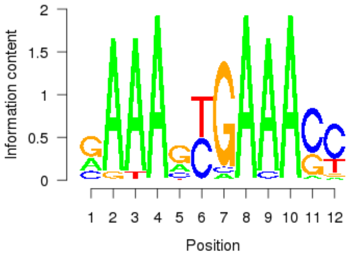
(i) HNF1B: class=Helix-Turn-Helix, family=Homeo, species=9606,10090, type=COMPILED, acc=P35680, id=MA0153



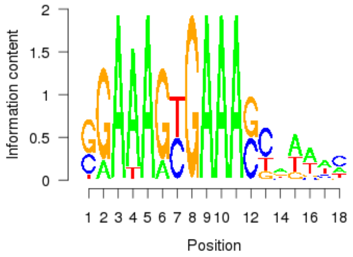
(j) HOXA5: class=Helix-Turn-Helix, family=Homeo, species=10090,9606, type=COMPILED, acc=P20719, id=MA0158



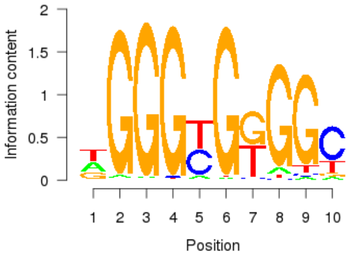
(k) INSM1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=COMPILED, acc=Q01101, id=MA0155



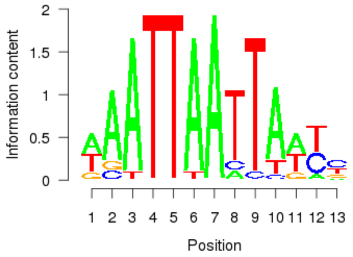
(l) IRF1: class=Winged Helix-Turn-Helix, family=IRF, species=9606, type=SELEX, acc=P10914, id=MA0050



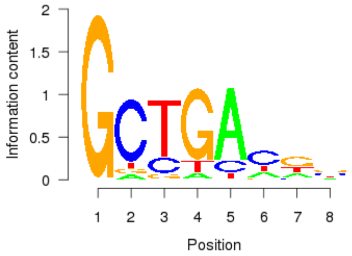
(a) IRF2: class=Winged Helix-Turn-Helix, family=IRF, species=9606, type=SELEX, acc=P14316, id=MA0051



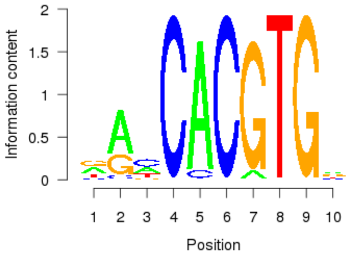
(b) Klf4: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=10090, type=ChiP-seq, acc=Q60793, id=MA0039



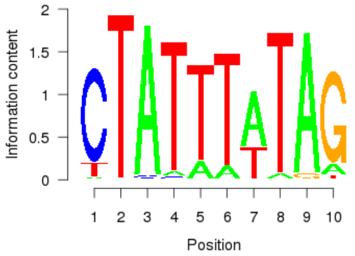
(c) Lhx3: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=P50481, id=MA0135



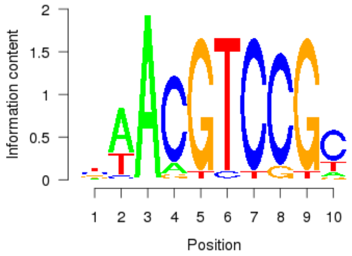
(d) Mafb: class=Zipper-Type, family=Leucine Zipper, species=10116, type=SELEX, acc=P54842, id=MA0117



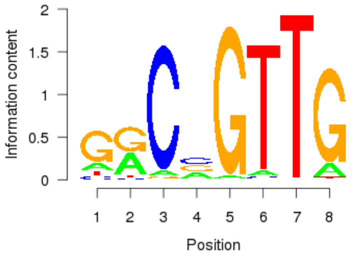
(e) MAX: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=SELEX, acc=AAH36092, id=MA0058



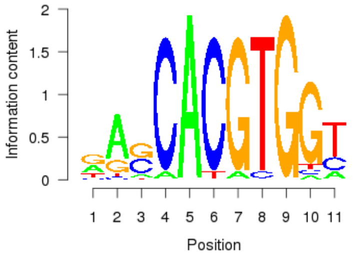
(f) MEF2A: class=Other Alpha-Helix, family=MADS, species=9606, type=SELEX, acc=EAX02249, id=MA0052



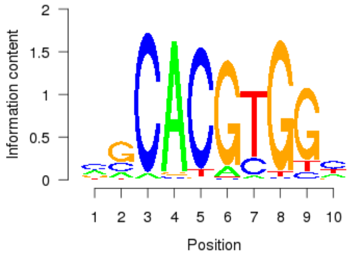
(g) MIZF: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=SELEX, acc=Q9BQA5, id=MA0131



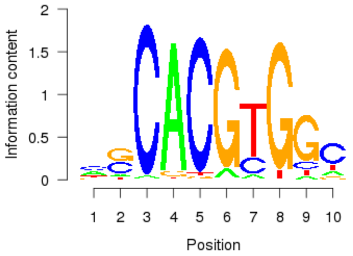
(h) Myb: class=Helix-Turn-Helix, family=Myb, species=10090, type=SELEX, acc=P06876, id=MA0100



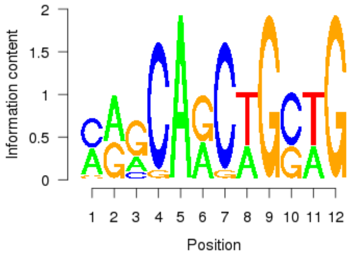
(i) MYC::MAX: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=SELEX, acc=AAH36092,Q6LBK7, id=MA0059



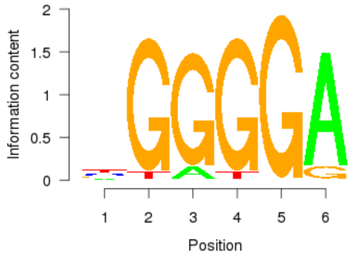
(j) Myc: class=Zipper-Type, family=Helix-Loop-Helix, species=10090, type=ChiP-seq, acc=P01108, id=MA0147



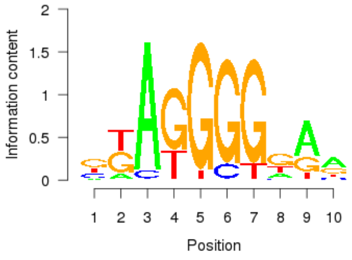
(k) Mycn: class=Zipper-Type, family=Helix-Loop-Helix, species=10090, type=ChiP-Seq, acc=P03966, id=MA0104



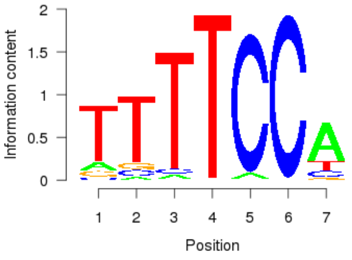
(l) Myf: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=COMPILED, id=MA0055



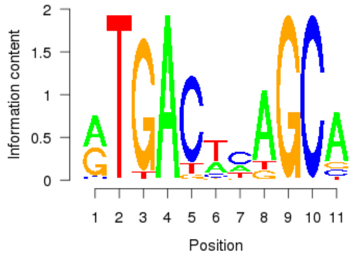
(a) MZF1_1-4: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=SELEX, acc=P28698, id=MA0056



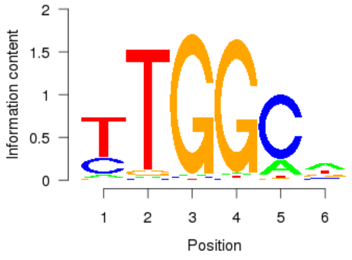
(b) MZF1_5-13: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=SELEX, acc=P28698, id=MA0057



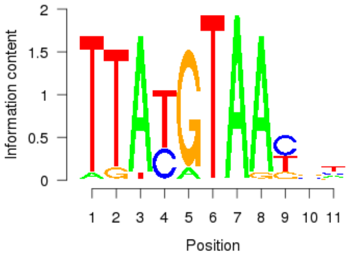
(c) NFATC2: class=Ig-fold, family=Rel, species=10090,9606,10116, type=COMPILED, acc=Q13469, id=MA0152



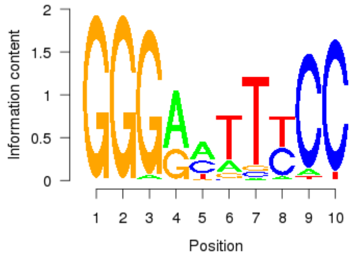
(d) NFE2L2: class=Zipper-Type, family=Leucine Zipper, species=9606, type=COMPILED, acc=Q16236, id=MA0150



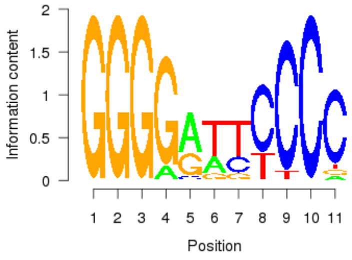
(e) NFIC: class=Other, family=NFI CCAAT-binding, species=9606, type=High-throughput SELEX SAGE, acc=P08651, id=MA0161



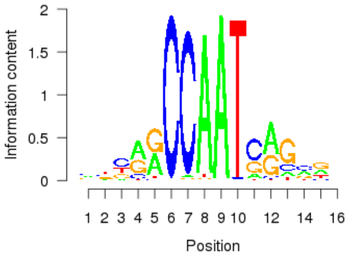
(f) NFIL3: class=Zipper-Type, family=Leucine Zipper, species=9606, type=SELEX, acc=NP_005375, id=MA0025



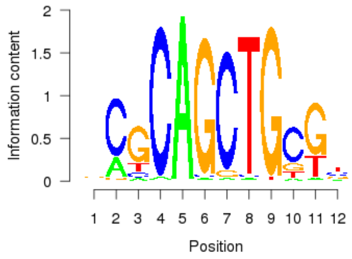
(g) NF-kappaB: class=Ig-fold, family=Rel, species=9606,10090,10116,9986, type=COMPILED, id=MA0061



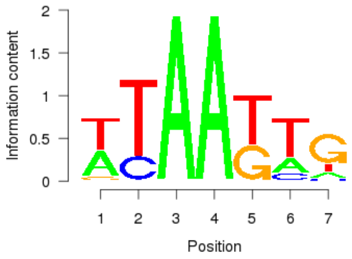
(h) NFKB1: class=Ig-fold, family=Rel, species=9606, type=SELEX, acc=P19838, id=MA0105



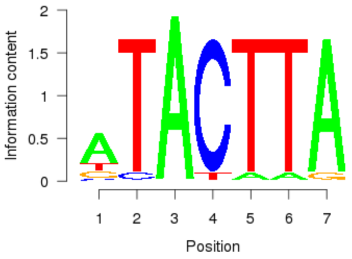
(i) NFYA: class=Other Alpha-Helix, family=NFY CCAAT-binding, species=9606,10090,10116,9031,8355,8364,9913,9986, type=COMPILED, acc=P23511, id=MA0060



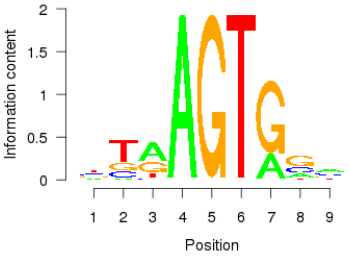
(j) NHLH1: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=SELEX, acc=Q02575, id=MA0048



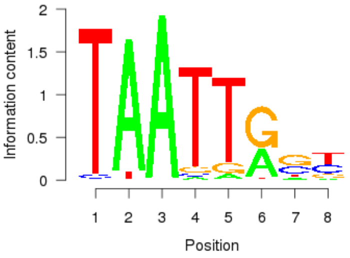
(k) Nkx2-5: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=P42582, id=MA0063



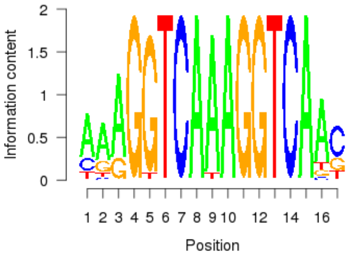
(l) NKX3-1: class=Helix-Turn-Helix, family=Homeo, species=9606, type=SELEX, acc=Q99801, id=MA0124



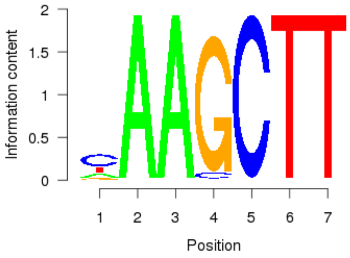
(a) Nkx3-2: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=P97503, id=MA0122



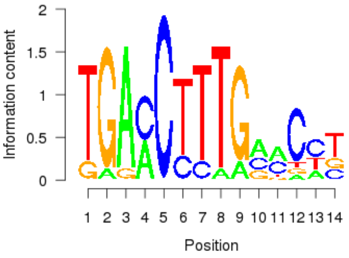
(b) Nobox: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=Q8VIH1, id=MA0125



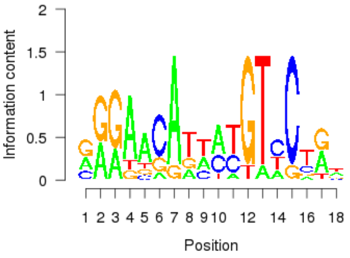
(c) NR1H2::RXRA: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=SELEX, acc=P55055,P19793, id=MA0115



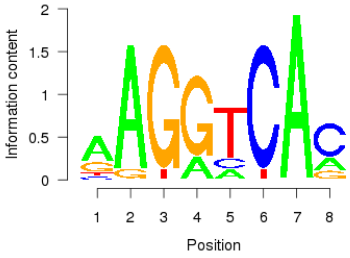
(d) Nr2e3: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=10090, type=SELEX, acc=Q9QXZ7, id=MA0164



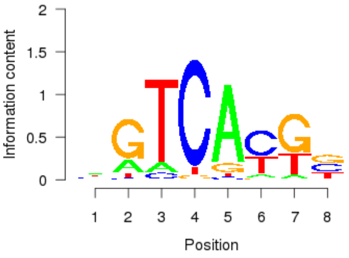
(e) NR2F1: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=COMPILED, acc=P10589, id=MA0017



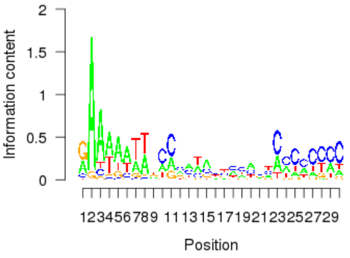
(f) NR3C1: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606,10090,10116,9031,8022, type=COMPILED, acc=P04150, id=MA0113



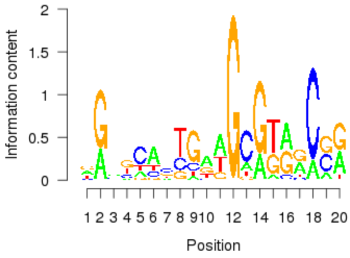
(g) NR4A2: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=10090,10116,9606, type=COMPILED, acc=P43354, id=MA0160



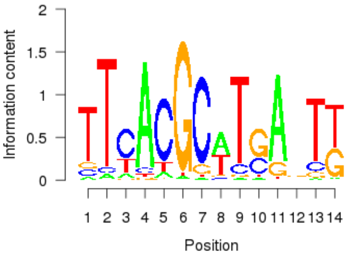
(h) Pax2: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=P32114, id=MA0067



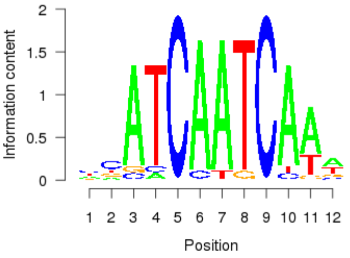
(i) Pax4: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=P32115, id=MA0068



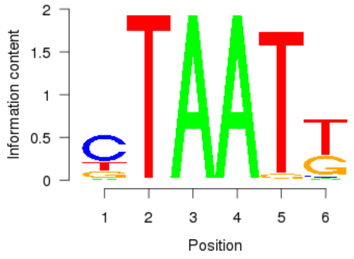
(j) Pax5: class=Helix-Turn-Helix, family=Homeo, species=10090, type=COMPILED, acc=Q02650, id=MA0014



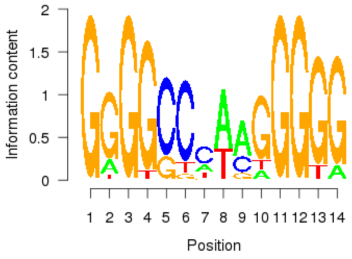
(k) Pax6: class=Helix-Turn-Helix, family=Homeo, species=9606, type=SELEX, acc=P26367, id=MA0069



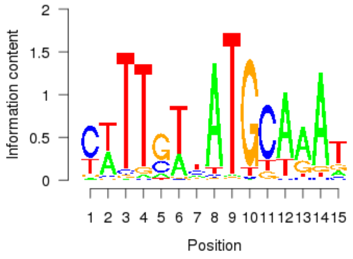
(l) PBX1: class=Helix-Turn-Helix, family=Homeo, species=9606, type=SELEX, acc=Q5T486, id=MA0070



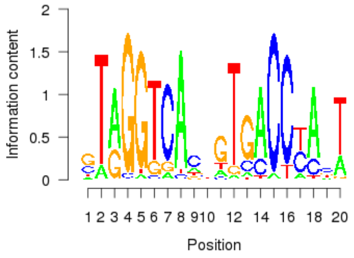
(a) Pdx1: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=NP_032840, id=MA0132



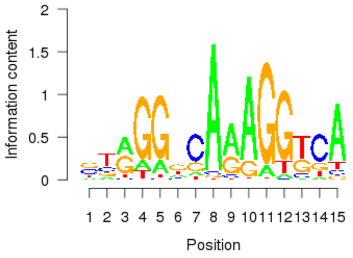
(b) PLAG1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=bacterial 1-hybrid, acc=Q6DJT9, id=MA0163



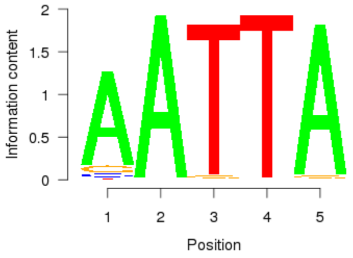
(c) Pou5f1: class=Helix-Turn-Helix, family=Homeo, species=10090, type=Chip-seq, acc=P20263, id=MA0142



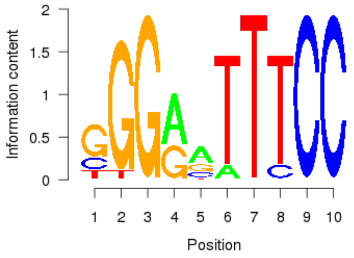
(d) PPARG: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=SELEX, acc=P37231, id=MA0066



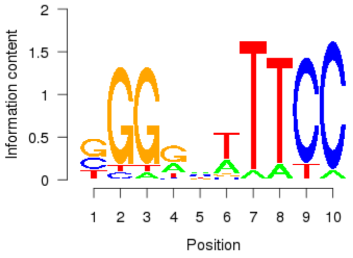
(e) PPARG::RXRA: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=10090, type=ChiP-seq, acc=P37238,P28700, id=MA0065



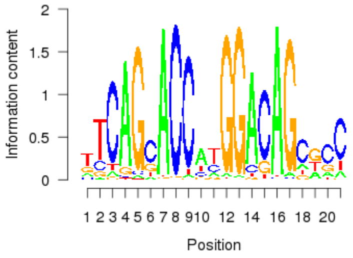
(f) Prrx2: class=Helix-Turn-Helix, family=Homeo, species=10090, type=SELEX, acc=Q06348, id=MA0075



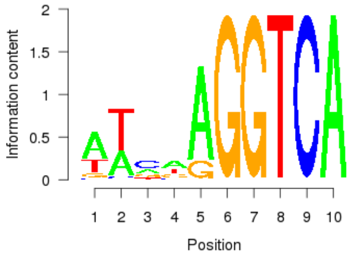
(g) RELA: class=Ig-fold, family=Rel, species=9606, type=SELEX, acc=Q04206, id=MA0107



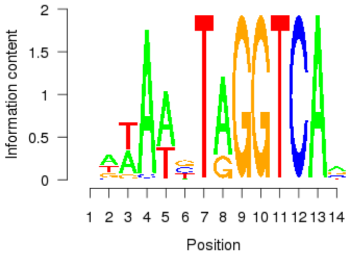
(h) REL: class=Ig-fold, family=Rel, species=9606, type=SELEX, acc=Q04864, id=MA0101



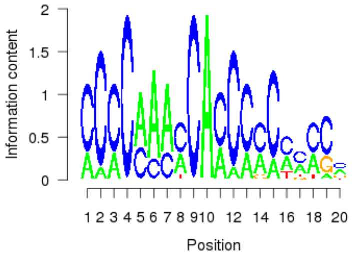
(i) REST: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=Chip-seq, acc=NP_005603, id=MA0138



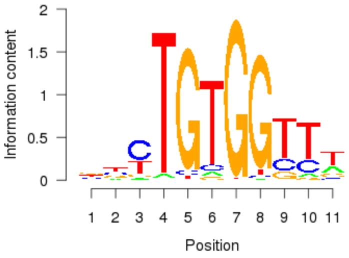
(j) RORA_1: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=SELEX, acc=NP_599023, id=MA0071



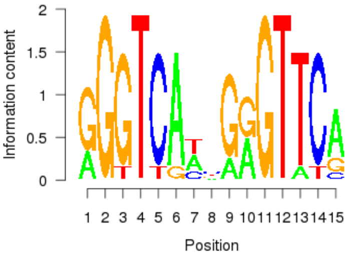
(k) RORA_2: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=SELEX, acc=NP_599022, id=MA0072



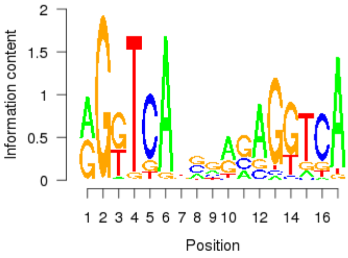
(l) RREB1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=SELEX, acc=Q92766, id=MA0073



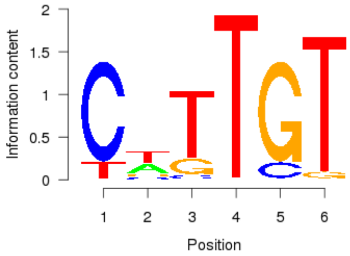
(a) RUNX1: class=Ig-fold, family=Runt, species=10090, type=ChiP-seq, acc=Q01196, id=MA0002



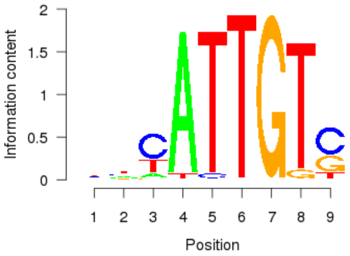
(b) RXRA::VDR: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=SELEX, acc=P19793,P11473, id=MA0074



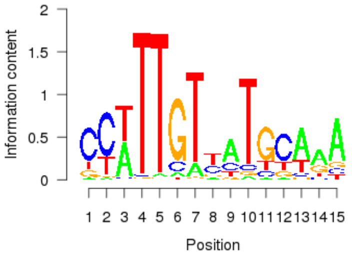
(c) RXR::RAR_DR5: class=Zinc-coordinating, family=Hormone-nuclear Receptor, species=9606, type=COMPILED, acc=P10276,P19793, id=MA0159



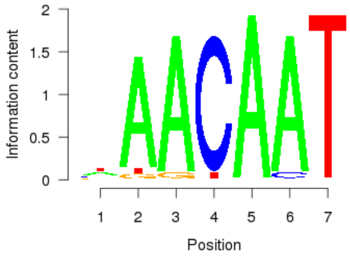
(d) SOX10: class=Other Alpha-Helix, family=High Mobility Group, species=10090,9606,10116, type=COMPILED, acc=P56693, id=MA0442



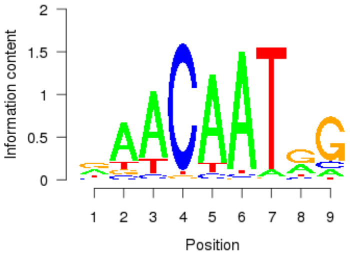
(e) Sox17: class=Other Alpha-Helix, family=High Mobility Group, species=10090, type=SELEX, acc=Q61473, id=MA0078



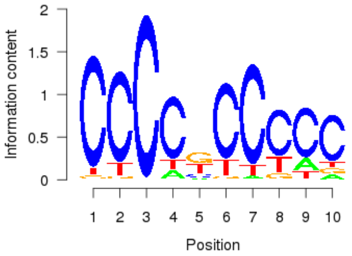
(f) Sox2: class=Other Alpha-Helix, family=High Mobility Group, species=10090, type=ChiP-seq, acc=P48432, id=MA0143



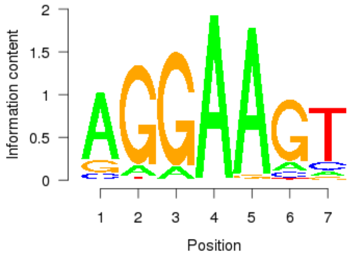
(g) Sox5: class=Other Alpha-Helix, family=High Mobility Group, species=10090, type=SELEX, acc=P35710, id=MA0087



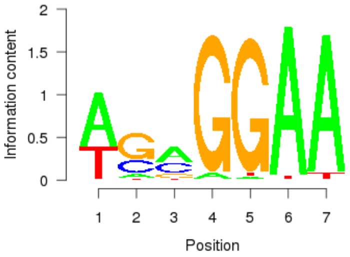
(h) SOX9: class=Other Alpha-Helix, family=High Mobility Group, species=9606, type=SELEX, acc=P48436, id=MA0077



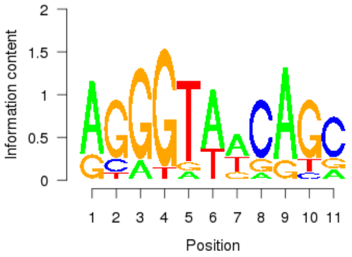
(i) SP1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606,10090,10116, type=COMPILED, acc=P08047, id=MA0079



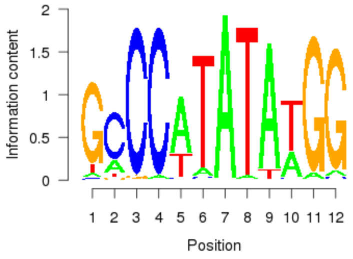
(j) SPI1: class=Winged Helix-Turn-Helix, family=Ets, species=9606, type=COMPILED, acc=P17947, id=MA0080



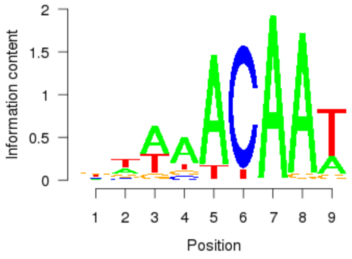
(k) SPIB: class=Winged Helix-Turn-Helix, family=Ets, species=9606, type=SELEX, acc=Q01892, id=MA0081



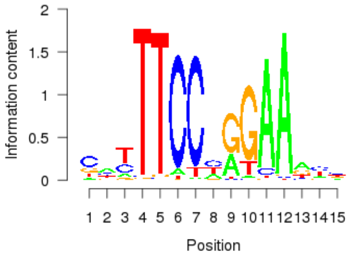
(l) Spz1: class=Other, family=Other, species=10090, type=SELEX, acc=AAK15458, id=MA0111



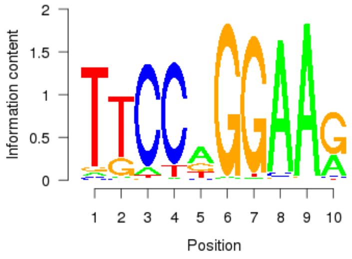
(a) SRF: class=Other Alpha-Helix, family=MADS, species=9606, type=SELEX, acc=P11831, id=MA0083



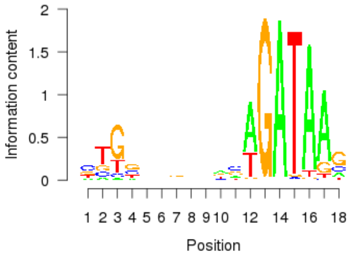
(b) SRY: class=Other Alpha-Helix, family=High Mobility Group, species=9606, type=SELEX, acc=Q05066, id=MA0084



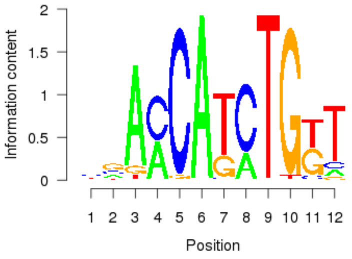
(c) STAT1: class=Ig-fold, family=Stat, species=9606, type=ChiP-seq, acc=Q53XW4, id=MA0137



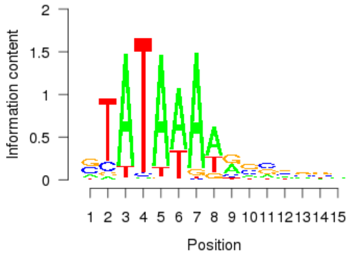
(d) Stat3: class=Ig-fold, family=Stat, species=10090, type=ChiP-seq, acc=P42227, id=MA0144



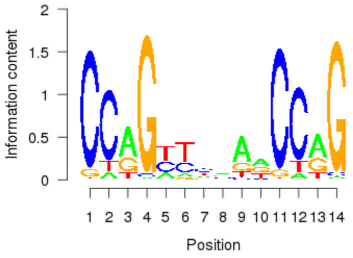
(e) Tal1::Gata1: class=Zipper-Type , family=Helix-Loop-Helix, species=10090, type=ChiP-seq, acc=P22091,P17679, id=MA0140



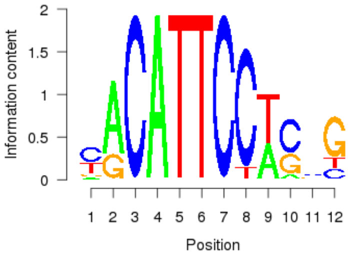
(f) TAL1::TCF3: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=SELEX, acc=P17542,P15923, id=MA0091



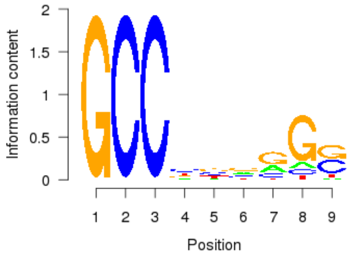
(g) TBP: class=Beta-sheet, family=TATA-binding, species=, id=MA0108



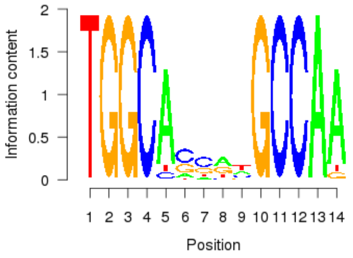
(h) Tcfcp2l1: class=Other, family=CP2, species=10090, type=ChiP-seq, acc=Q3UNW5, id=MA0145



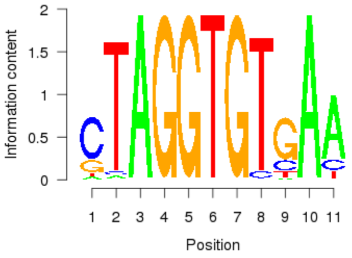
(i) TEAD1: class=Helix-Turn-Helix, family=Homeo, species=9606, type=COMPILED, acc=P28347, id=MA0090



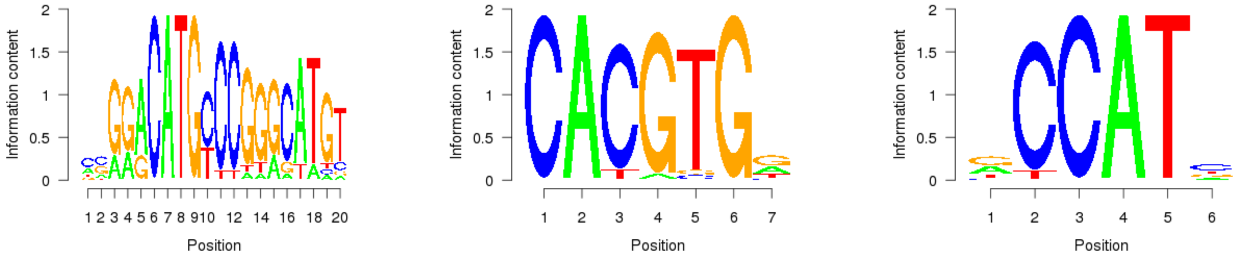
(j) TFAP2A: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=SELEX, acc=P05549, id=MA0003



(k) TLX1::NFIC: class=Helix-Turn-Helix::Other, family=Homeo::Nuclear Factor I-CCAAT-binding, species=9606, type=SELEX, acc=P31314,NP_995315.1, id=MA0119



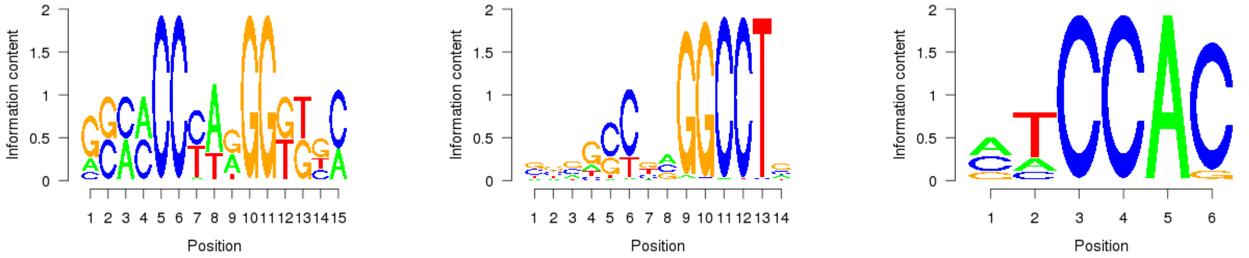
(l) T: class=Beta-Hairpin-Ribbon, family=T, species=10090, type=SELEX, acc=P20293, id=MA0009



(a) TP53: class=Zinc-coordinating, family=Loop-Sheet-Helix, species=9606, type=SELEX, acc=P04637, id=MA0106

(b) USF1: class=Zipper-Type, family=Helix-Loop-Helix, species=9606, type=SELEX, acc=P22415, id=MA0093

(c) YY1: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=COMPILED, acc=P25490, id=MA0095



(d) Zfp423: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=10116, type=SELEX, acc=O08961, id=MA0116

(e) Zfx: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=10090, type=ChIP-seq, acc=P17012, id=MA0146

(f) ZNF354C: class=Zinc-coordinating, family=BetaBetaAlpha-zinc finger, species=9606, type=SELEX, acc=Q86Y25, id=MA0130

Figure 245: Motifs in use

15.89 R configuration

base [12]

Version	2.14.2
Priority	base
Title	The R Base Package
Author	R Development Core Team and contributors worldwide
Maintainer	R Core Team <R-core@r-project.org>
Description	Base R functions
License	Part of R 2.14.2
Built	R 2.14.2; ; 2012-03-16 09:00:32 UTC; unix

csbl.go [10]

Version	1.3.7
Date	2011-12-19
Title	Semantic similarity based on Gene Ontology
Author	Kristian Ovaska <kristian.ovaska@helsinki.fi>, Marko Laakso <Marko.Laakso@Helsinki.FI>
Maintainer	Kristian Ovaska <kristian.ovaska@helsinki.fi>
Depends	methods, cluster, grDevices, Biobase, GO.db, annotate, RUnit
Namespace	csbl.go
Description	Compute semantic similarity for genes and proteins using Gene Ontology annotations.
License	GPL
Packaged	2011-12-19 08:03:33 UTC; kristian
Built	R 2.14.2; x86_64-unknown-linux-gnu; 2012-04-26 09:52:23 UTC; unix

15.90 System configurations

The following table shows the properties of **ensembl** component.

property	value
`database.driver`	com.mysql.jdbc.Driver
`database.recycle`	true
`database.timeout`	20
`database.url`	jdbc:mysql://deebee.giu.fi:3306/homo_sapiens_core_67_37
`database.user`	anonymous

The following table shows the properties of **ensemblPerl** component.

property	value
`database`	homo_sapiens_core_67_37
`driver`	mysql
`host`	deebee.giu.fi
`port`	3306
`user`	anonymous

The following table shows the properties of **moksiskaanInit-init** component.

property	value
`database.driver`	org.postgresql.Driver
`database.recycle`	true
`database.timeout`	20
`database.url`	jdbc:postgresql://narsil.fimm.fi:5432/moksiskaan
`database.user`	moksiskaan

The following table shows the properties of **illuDHTDEX-probeAnnot** component.

property	**value**
`dataset`	Homo sapiens genes (GRCh37.p7)
`version`	ENSEMBL GENES 67 (SANGER UK)

This analysis is based on Moksiskaan [9] (version 1.13) that is running on top of Hibernate with *org. hibernate.dialect.PostgreSQLDialect* to access the native database.

Database history:
`[2012-05-18]` EnsemblImport: *jdbc:mysql://ensembldb.ensembl.org:5306/mus_musculus_core_67_37 (37620 genes, 14820 proteins)* See also [4].
`[2012-05-18]` EnsemblImport: *jdbc:mysql://ensembldb.ensembl.org:5306/homo_sapiens_core_67_37 (53893 genes, 18831 proteins)* See also [4].
`[2012-05-18]` Keggonen: *KEGG pathway import from {SOAP/KEGG}KEGG: http://soap.genome.jp/keggapi/request_v6.2.cgi produced 253 Homo sapiens pathways.* See also [5, 6].
`[2012-05-18]` Keggonen: *KEGG pathway import from {SOAP/KEGG}KEGG: http://soap.genome.jp/keggapi/request_v6.2.cgi produced 249 Mus musculus pathways.* See also [5, 6].
`[2012-05-18]` Narggari: *Drug target import from the KEGG DRUG database.* See also [5, 6].
`[2012-05-18]` DrugBankImport: *Total of 1635 drugs identified from http://www.drugbank.ca/system/downloads/current/drugbank.xml.zip.* See also [8, 13].
`[2012-05-18]` DiseaseImport: *Imported 984 diseases from the KEGG DISEASE database.* See also [5, 6].
`[2012-05-18]` PINAImport: *Total of 3684 protein-protein interactions obtained from http://cbg.garvan.unsw.edu.au/pina/download/Mus%20musculus.txt.* See also [3].
`[2012-05-18]` PINAImport: *Total of 69122 protein-protein interactions obtained from http://cbg.garvan.unsw.edu.au/pina/download/Homo%20sapiens.txt.* See also [3].
`[2012-05-18]` PathwayCommonsImport: *Total of 27 new links obtained from http://www.pathwaycommons.org/pc-snapshot/current-release/tab_delim_network/by_species/mus-musculus-10090-edge-attributes.txt.zip.* See also [2].
`[2012-05-18]` PathwayCommonsImport: *Total of 66724 new links obtained from http://www.pathwaycommons.org/pc-snapshot/current-release/tab_delim_network/by_species/homo-sapiens-9606-edge-attributes.txt.zip.* See also [2].
`[2012-05-18]` WikiPathways: *WikiPathways import produced 127 Homo sapiens pathways.* See also [7].

References

[1] M. Ashburner, C. A. Ball, J. A. Blake, D. Botstein, H. Butler, J. M. Cherry, A. P. Davis, K. Dolinski, S. S. Dwight, and J. T. Eppig. Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat Genet*, 25(1):25–29, 2000.

[2] E. Cerami, B. Gross, E. Demir, I. Rodchenkov, Ö. Babur, N. Anwar, N. Schultz, G. Bader, and C. Sander. Pathway commons, a web resource for biological pathway data. *Nucleic Acids Research*, 2010.

[3] M. Cowley, M. Pinese, K. Kassahn, N. Waddell, J. Pearson, S. Grimmond, A. Biankin, S. Hautaniemi, and J. Wu. PINA v2. 0: mining interactome modules. *Nucleic acids research*, 40(D1):D862–D865, 2012.

[4] P. Flicek, M. Amode, D. Barrell, K. Beal, S. Brent, Y. Chen, P. Clapham, G. Coates, S. Fairley, S. Fitzgerald, et al. Ensembl 2011. *Nucleic acids research*, 39(suppl 1):D800, 2011.

[5] M. Kanehisa, S. Goto, M. Furumichi, M. Tanabe, and M. Hirakawa. KEGG for representation and analysis of molecular networks involving diseases and drugs. *Nucleic acids research*, 2009.

[6] M. Kanehisa, S. Goto, Y. Sato, M. Furumichi, and M. Tanabe. KEGG for integration and interpretation of large-scale molecular data sets. *Nucleic Acids Research*, 40(D1):D109–D114, 2012.

[7] T. Kelder, M. van Iersel, K. Hanspers, M. Kutmon, B. Conklin, C. Evelo, and A. Pico. Wikipathways: building research communities on biological pathways. *Nucleic Acids Research*, 40(D1):D1301–D1307, 2012.

[8] C. Knox, V. Law, T. Jewison, P. Liu, S. Ly, A. Frolkis, A. Pon, K. Banco, C. Mak, V. Neveu, et al. DrugBank 3.0: a comprehensive resource for Omics research on drugs. *Nucleic Acids Research*, 39(suppl 1):D1035, 2011.

[9] M. Laakso and S. Hautaniemi. Integrative platform to translate gene sets to networks. *Bioinformatics*, 26:1802–1803, 7 2010.

[10] K. Ovaska and M. Laakso. *csbl.go: Semantic similarity based on Gene Ontology*, 2011. R package version 1.3.7.

[11] K. Ovaska, M. Laakso, S. Haapa-Paananen, R. Louhimo, P. Chen, V. Aittomäki, E. Valo, J. Núñez-Fontarnau, V. Rantanen, S. Karinen, K. Nousiainen, A.-M. Lahesmaa-Korpinen, M. Miettinen, L. Saarinen, P. Kohonen, J. Wu, J. Westermarck, and S. Hautaniemi. Large-scale data integration framework provides a comprehensive view on glioblastoma multiforme. *Genome Medicine*, 2(9):65, September 2010.

[12] R Development Core Team. *R: A Language and Environment for Statistical Computing.* R Foundation for Statistical Computing, Vienna, Austria, 2012. ISBN 3-900051-07-0.

[13] D. Wishart, C. Knox, A. Guo, D. Cheng, S. Shrivastava, D. Tzur, B. Gautam, and M. Hassanali. DrugBank: a knowledgebase for drugs, drug actions and drug targets. *Nucleic acids research*, 36:D901–D906, 2008.