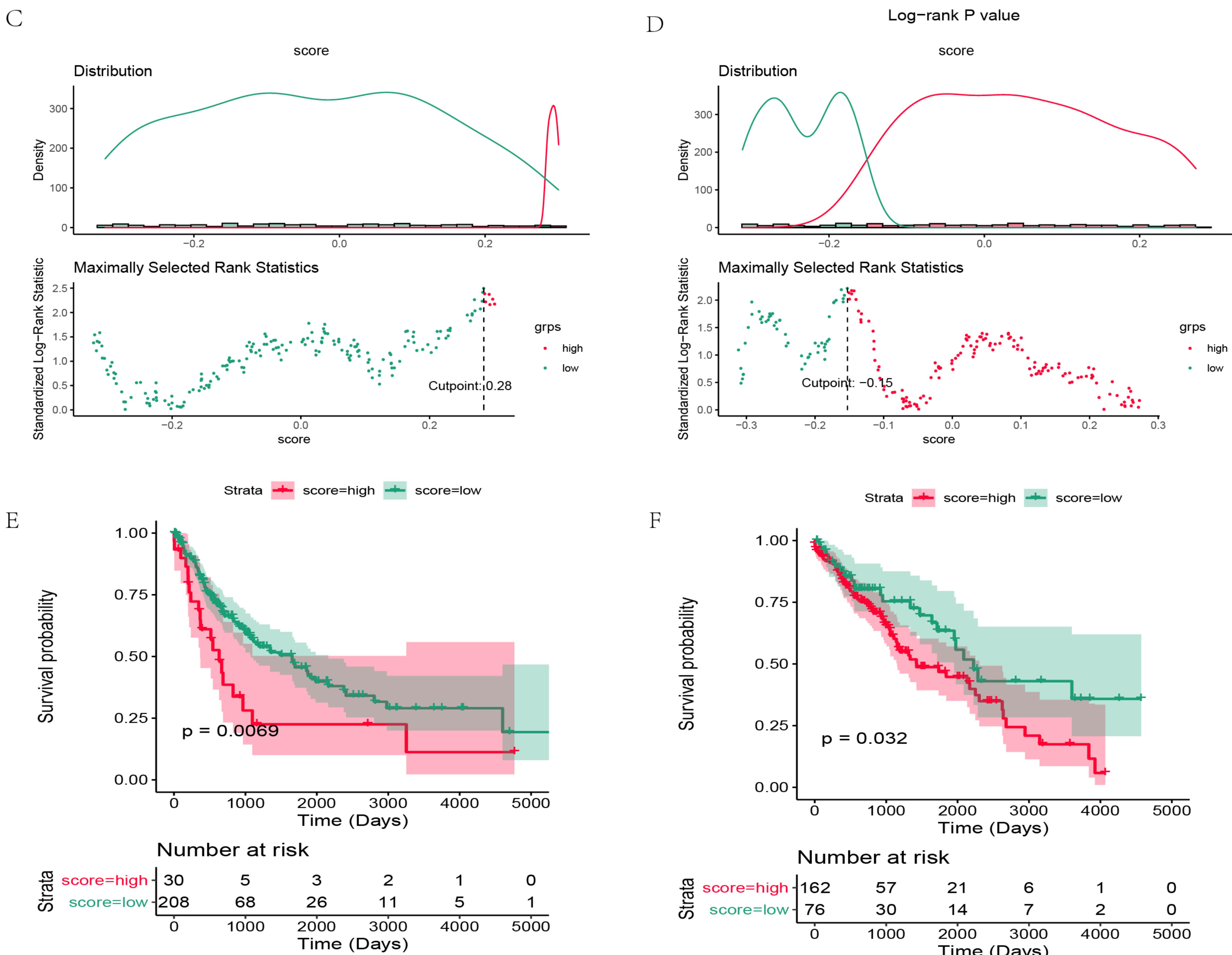
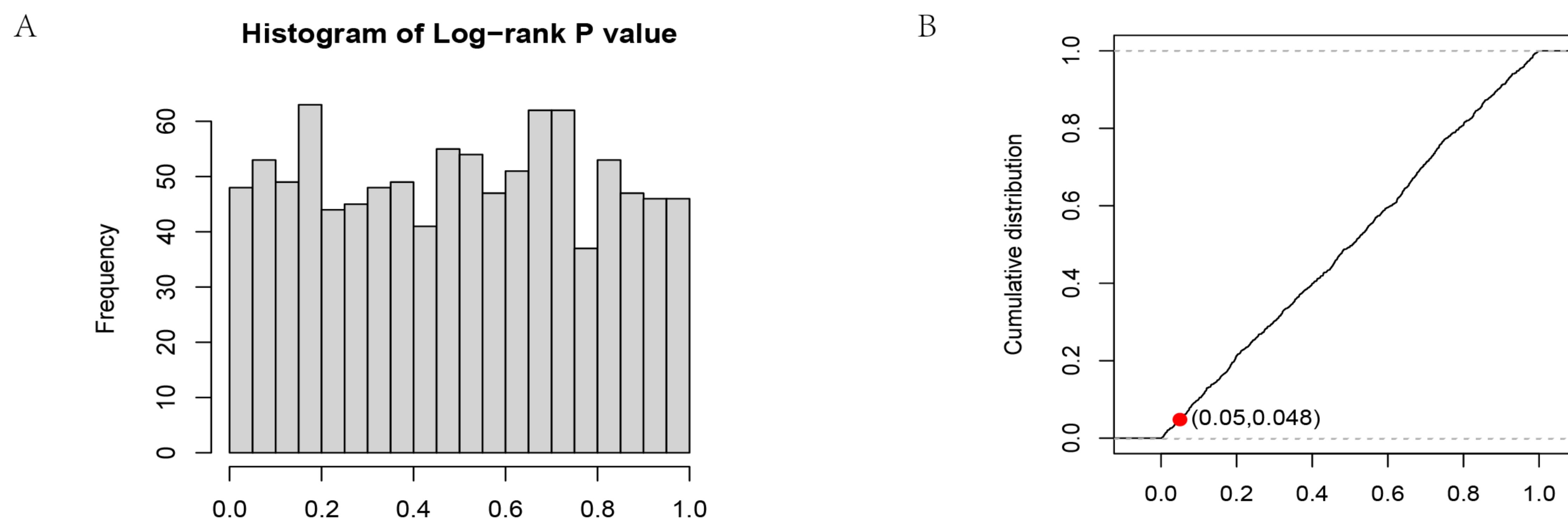


Supplementary materials



Supplementary Figure 1: Results of analysis of two groups of TCGA-LUSC samples.

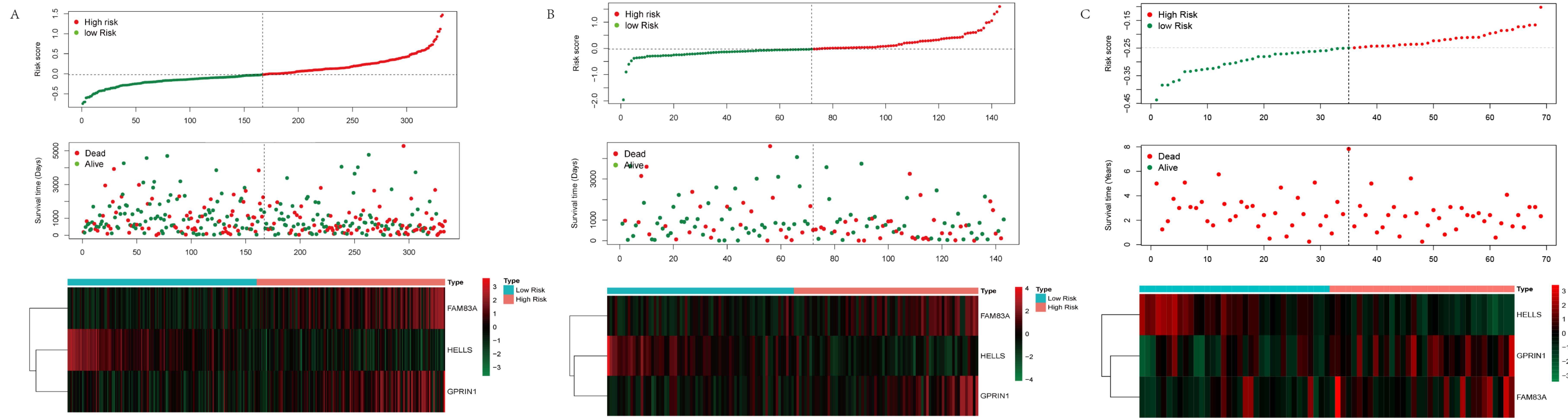
(A,B) The samples are divided into a training set and a test set based on frequency and cumulative distribution.

(C) The training set was divided into two groups of high and low hypoxia.

(D) The test set was divided into two groups of high and low hypoxia.

(E) Survival differences between the two groups of high and low hypoxia in the training set.

(F) Survival differences between the two groups of high and low hypoxia in the test set.



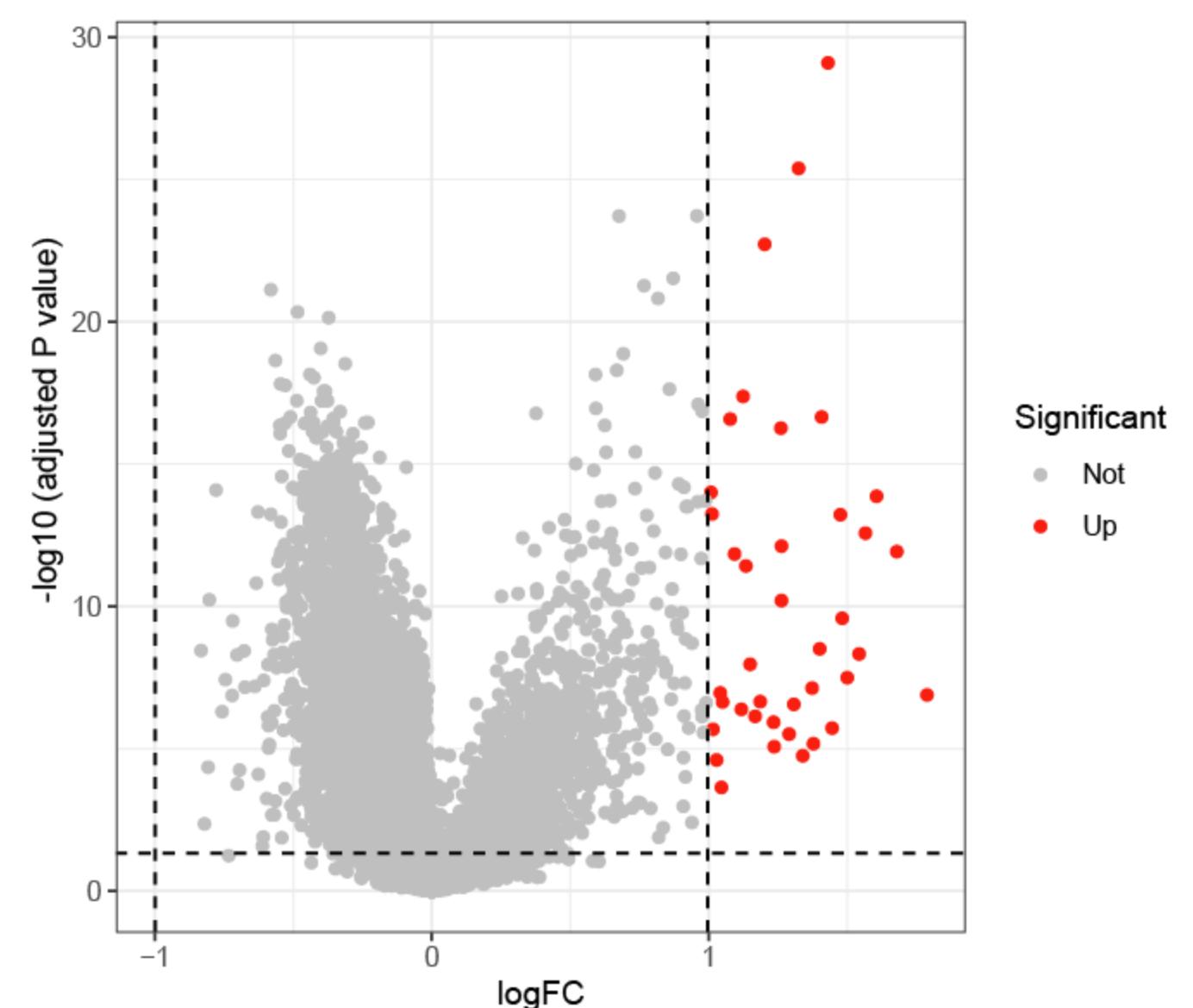
Supplementary Figure 2: The risk score, survival status, and 3 gene expression profiles of TCGA-training set, TCGA-internal testing set and GEO-external validation set.

(A)The risk score, survival status, and 3 gene expression profiles of TCGA-training set.

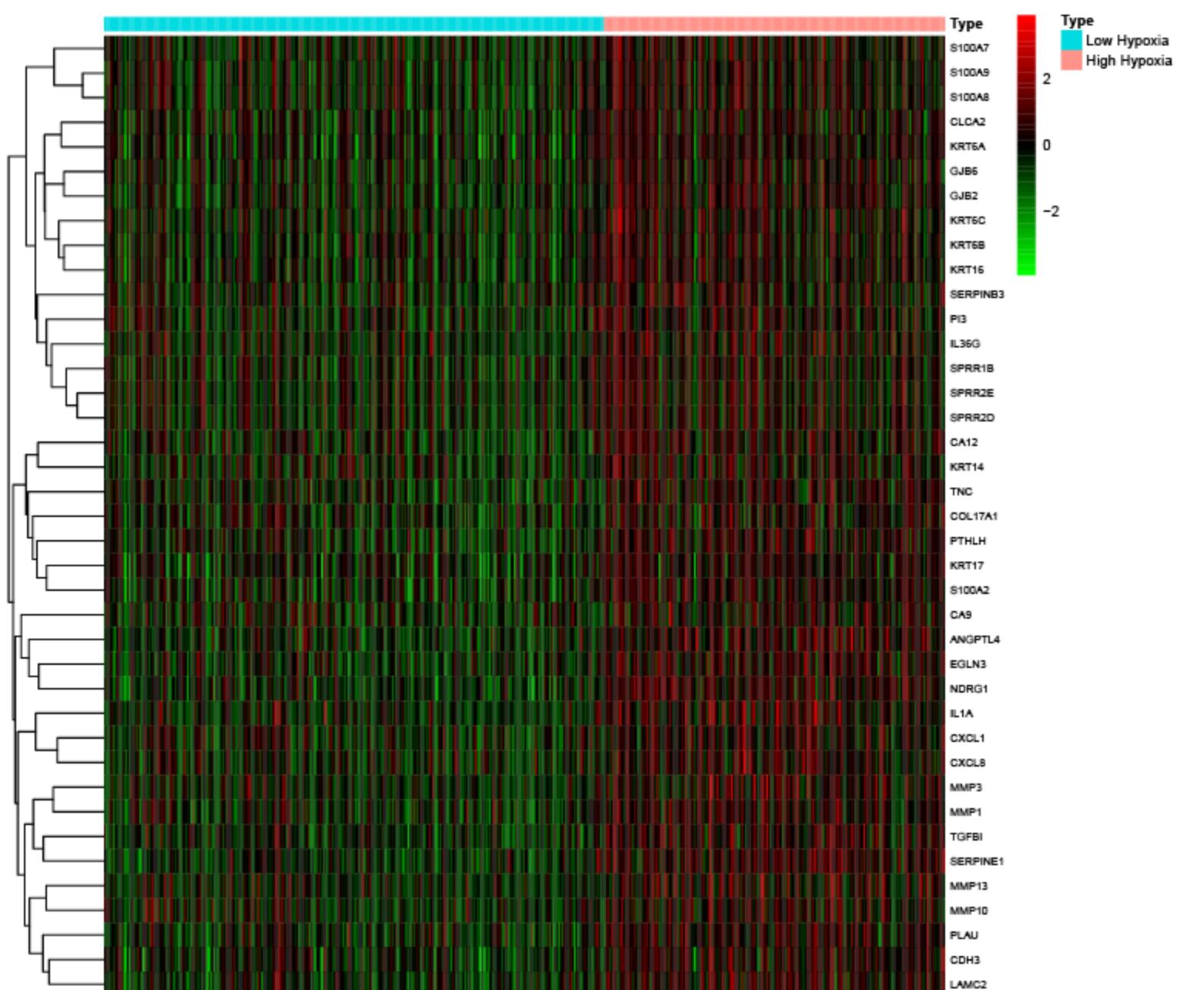
(B)The risk score, survival status, and 3 gene expression profiles of TCGA-internal testing set.

(C)The risk score, survival status, and 3 gene expression profiles of GEO-external validation set.

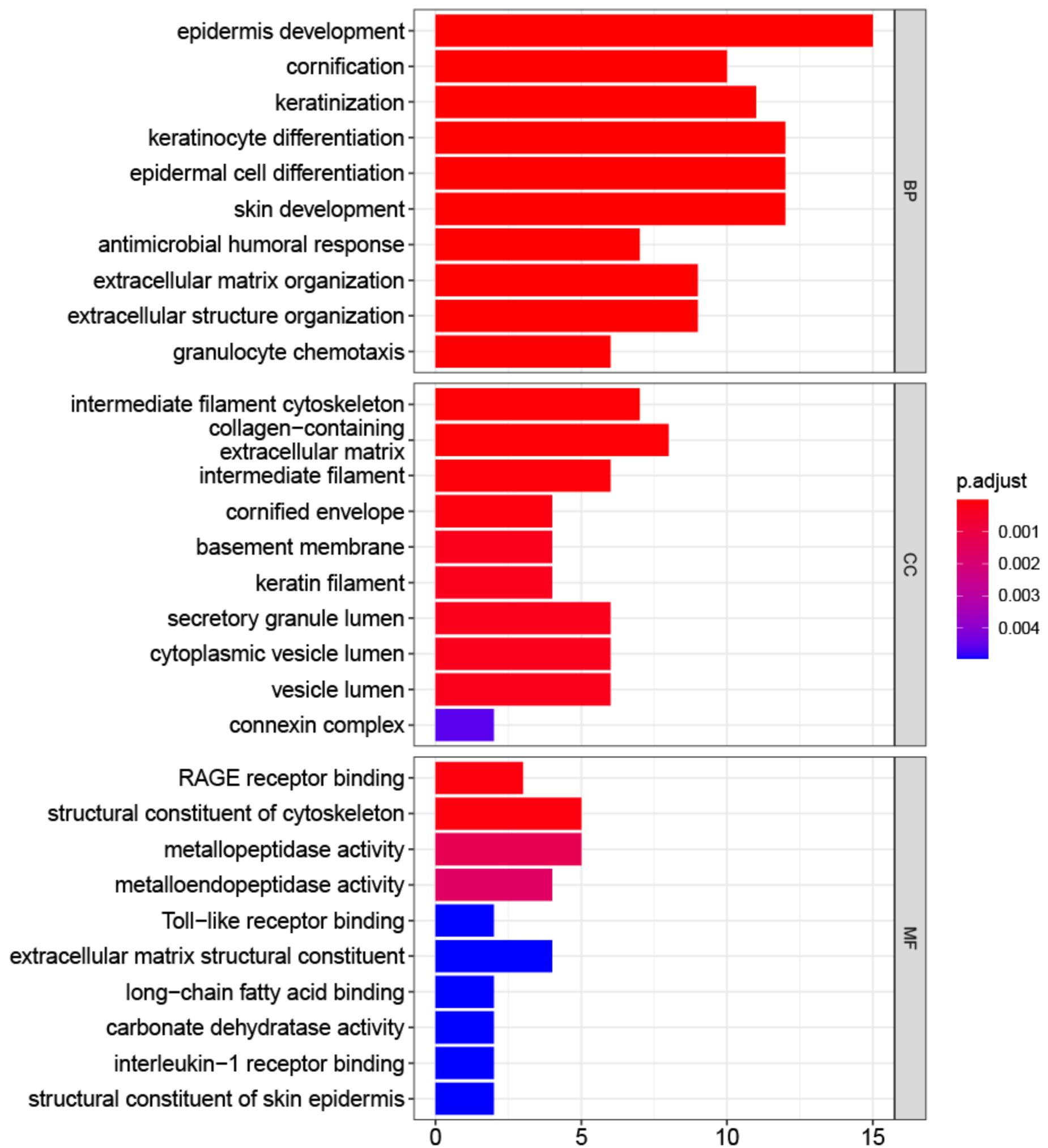
A



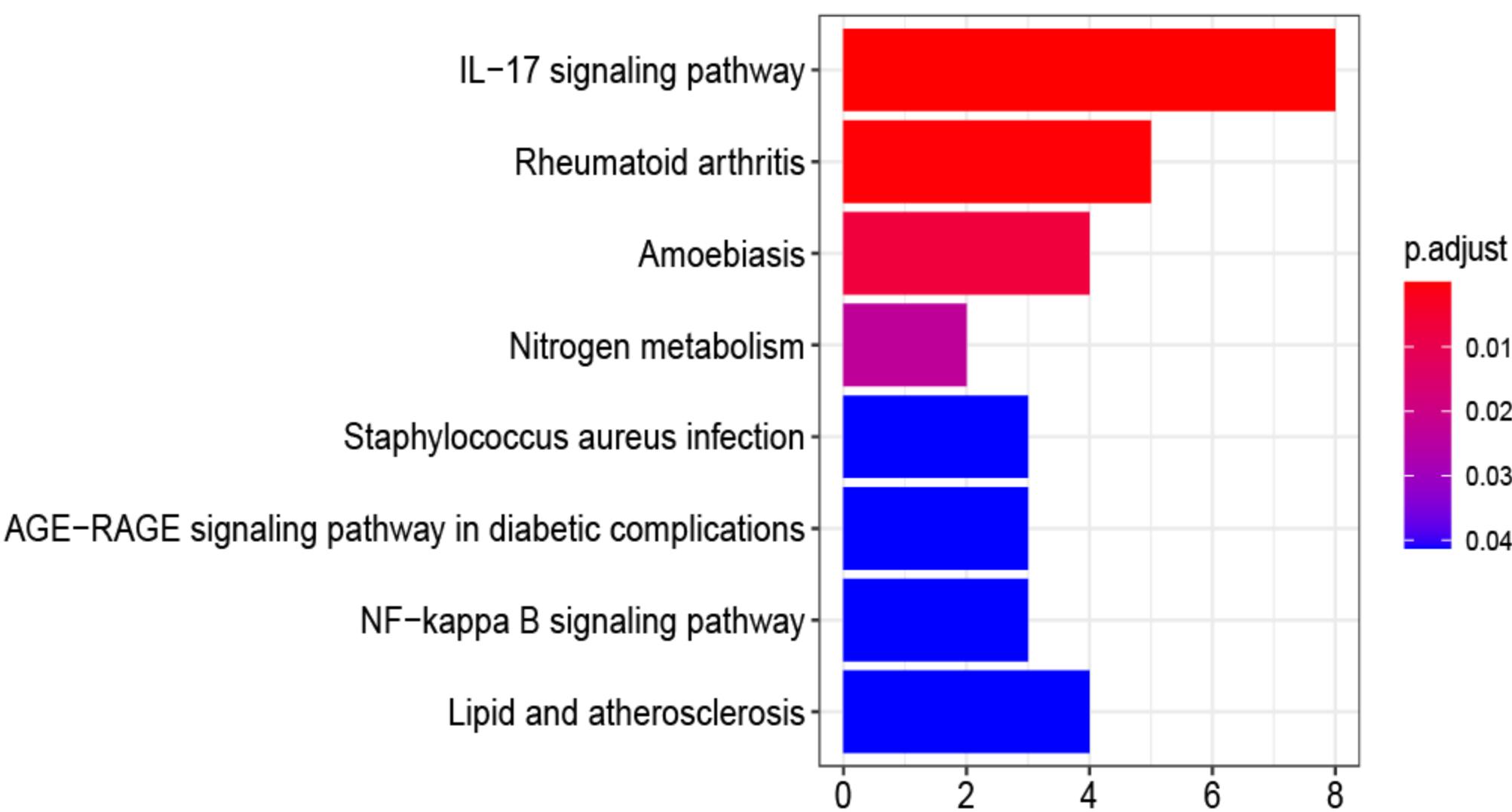
B



C

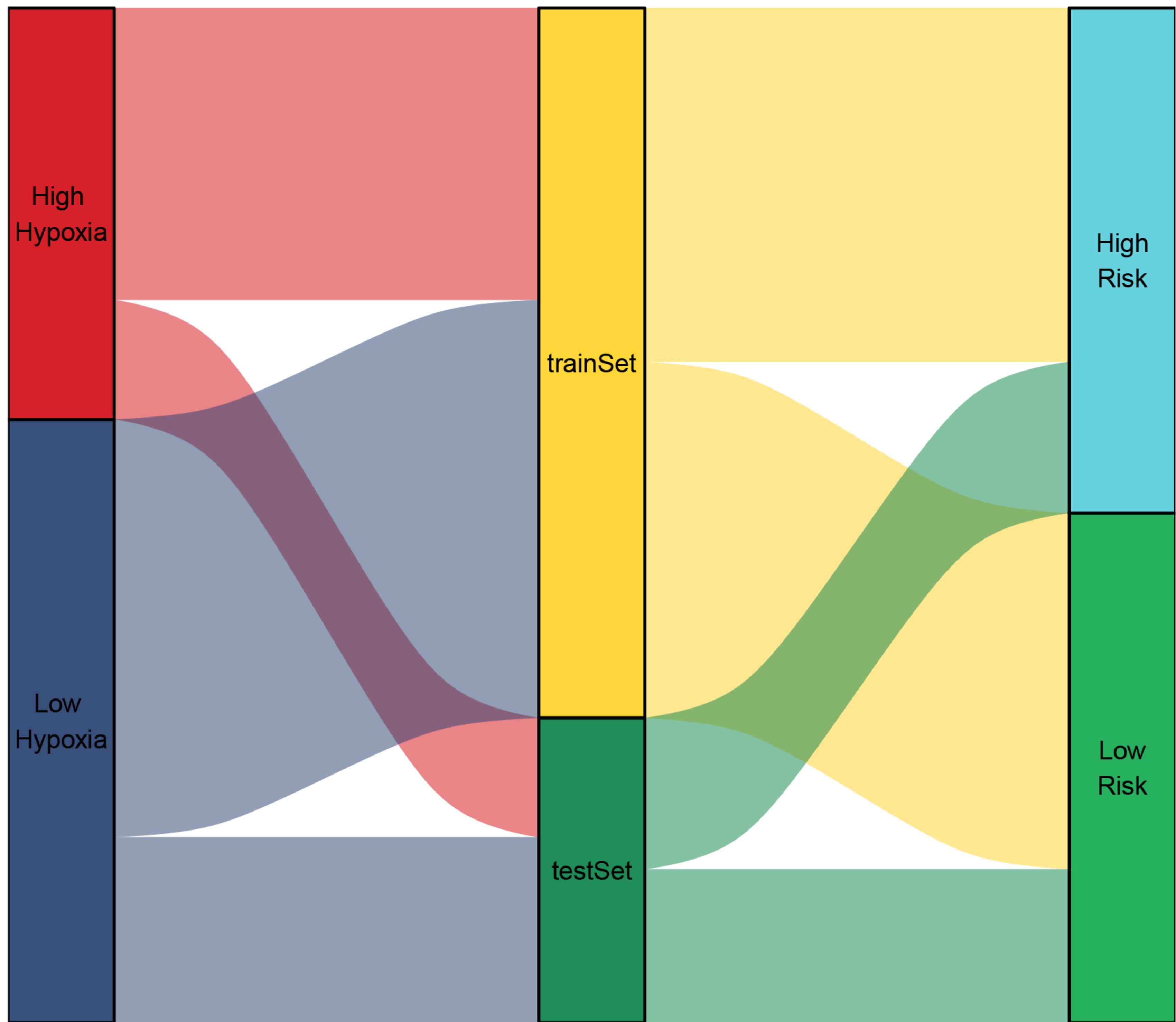


D



Supplementary Figure 3: The results of the analysis of the 39 DEGs between the high and low hypoxia score groups.

- (A) Volcano plot of hypoxia score-related DEGs. Red represented upregulated genes, and blue indicated downregulated genes.
- (B) Expression differences of DEGs. Red represented high expression, green represented low expression.
- (C) Gene Ontology analysis of the hypoxia score-related DEGs regarding biological process, cellular component, and molecular function.
- (D) All significant KEGG pathways. The x-axis showed the number of genes enriched in this term.



Supplementary Figure 4: Sankey plots of hypoxia score group and risk score group.
Correlation between hypoxia score group and risk score group

Supplementary Table 1

The 200 hypoxia-related genes were obtained from the HALLMARK_HYPOXIA

HALLMARK_HYPOXIA

ACKR3

ADM

ADORA2B

AK4

AKAP12

ALDOA

ALDOB

ALDOC

AMPD3

ANGPTL4

ANKZF1

ANXA2

ATF3

ATP7A

B3GALT6

B4GALNT2

BCAN

BCL2

BGN

BHLHE40

BNIP3L

BRS3

BTG1

CA12

CASP6

CAV1

CAVIN1

CAVIN3

CCN1

CCN2

CCN5

CCNG2

CDKN1A

CDKN1B

CDKN1C

CHST2

CHST3

CITED2

COL5A1

CP

CSRP2

CXCR4

DCN

DDIT3

DDIT4

DPYSL4
DTNA
DUSP1
EDN2
EFNA1
EFNA3
EGFR
EN01
EN02
EN03
ER01A
ERRFI1
ETS1
EXT1
F3
FAM162A
FBP1
FOS
FOSL2
FOXO3
GAA
GALK1
GAPDH
GAPDHS
GBE1
GCK
GCNT2
GLRX
GPC1
GPC3
GPC4
GPI
GRHPR
GYS1
HAS1
HDLBP
HEXA
HK1
HK2
HMOX1
HOXB9
HS3ST1
HSPA5
IDS
IER3
IGFBP1
IGFBP3
IL6

ILVBL
INHA
IRS2
ISG20
JMJD6
JUN
KDELR3
KDM3A
KIF5A
KLF6
KLF7
KLHL24
LALBA
LARGE1
LDHA
LDHC
LOX
LXN
MAFF
MAP3K1
MIF
MT1E
MT2A
MXI1
MYH9
NAGK
NCAN
NDRG1
NDST1
NDST2
NEDD4L
NFIL3
NOCT
NR3C1
P4HA1
P4HA2
PAM
PCK1
PDGFB
PDK1
PDK3
PFKFB3
PFKL
PFKP
PGAM2
PGF
PGK1
PGM1

PGM2
PHKG1
PIM1
PKLR
PKP1
PLAC8
PLAUR
PLIN2
PNRC1
PPARGC1A
PPFIA4
PPP1R15A
PPP1R3C
PRDX5
PRKCA
PYGM
RBPJ
RORA
RRAGD
S100A4
SAP30
SCARB1
SDC2
SDC3
SDC4
SELENBP1
SERPINE1
SIAH2
SLC25A1
SLC2A1
SLC2A3
SLC2A5
SLC37A4
SLC6A6
SRPX
STBD1
STC1
STC2
SULT2B1
TES
TGFB3
TGFBI
TGM2
TIPARP
TKTL1
TMEM45A
TNFAIP3
TPBG

TPD52
TPI1
TPST2
UGP2
VEGFA
VHL
VLDLR
WSB1
XPNPEP1
ZFP36
ZNF292

Supplementary Table 2

hypoxia scores of TCGA-LUSC samples calculated by GSVA
based on 200 hypoxia-related gene expression profiles

id	score
TCGA-63-512	0.559826
TCGA-60-270	0.506366
TCGA-85-848	0.501353
TCGA-77-813	0.496299
TCGA-43-677	0.48709
TCGA-85-835	0.481722
TCGA-60-272	0.467371
TCGA-60-270	0.4563
TCGA-51-407	0.417266
TCGA-18-341	0.415003
TCGA-56-773	0.410372
TCGA-77-813	0.399891
TCGA-85-858	0.398081
TCGA-85-679	0.397511
TCGA-85-A53	0.391164
TCGA-77-814	0.388473
TCGA-68-775	0.383812
TCGA-34-592	0.38325
TCGA-43-664	0.376064
TCGA-63-A5M	0.374932
TCGA-66-278	0.373052
TCGA-77-800	0.370266
TCGA-85-866	0.367494
TCGA-66-273	0.364993
TCGA-21-A5D	0.357286
TCGA-56-830	0.356458
TCGA-39-503	0.351882
TCGA-NK-A5C	0.349109
TCGA-43-677	0.347153
TCGA-66-278	0.343161

TCGA-66-280 0.340675
TCGA-56-589 0.336086
TCGA-77-733 0.332375
TCGA-22-548 0.332233
TCGA-22-460 0.32932
TCGA-02-A52 0.328452
TCGA-77-800 0.324739
TCGA-52-781 0.314111
TCGA-77-733 0.311858
TCGA-43-A47 0.311058
TCGA-56-654 0.308274
TCGA-22-547 0.307669
TCGA-NK-A5C 0.307578
TCGA-18-340 0.306461
TCGA-52-781 0.306298
TCGA-77-714 0.30386
TCGA-66-276 0.301314
TCGA-21-107 0.301048
TCGA-46-376 0.298099
TCGA-63-A5M 0.293722
TCGA-66-274 0.29264
TCGA-02-A52 0.290614
TCGA-85-617 0.290036
TCGA-66-278 0.289615
TCGA-34-524 0.287039
TCGA-18-559 0.285646
TCGA-18-341 0.283953
TCGA-85-784 0.282626
TCGA-66-275 0.281766
TCGA-60-272 0.278986
TCGA-90-683 0.278463
TCGA-96-754 0.272657
TCGA-85-805 0.271196
TCGA-18-340 0.27051
TCGA-77-815 0.269777
TCGA-56-862 0.266183
TCGA-98-A53 0.26615
TCGA-77-684 0.263558
TCGA-46-602 0.263423
TCGA-77-813 0.262286
TCGA-77-814 0.260687
TCGA-68-A59 0.259874
TCGA-21-107 0.258644
TCGA-77-813 0.257443
TCGA-60-270 0.256512
TCGA-92-734 0.251635
TCGA-60-270 0.251211
TCGA-63-A5M 0.250694

TCGA-21-107 0.246502
TCGA-63-702 0.243187
TCGA-22-460 0.240128
TCGA-58-839 0.233077
TCGA-43-765 0.232098
TCGA-66-277 0.231753
TCGA-NK-A5C 0.229487
TCGA-85-A50 0.228978
TCGA-21-578 0.228836
TCGA-33-673 0.225468
TCGA-56-782 0.220916
TCGA-85-A4J 0.217009
TCGA-56-722 0.214127
TCGA-22-547 0.213798
TCGA-18-340 0.211837
TCGA-56-758 0.210355
TCGA-33-458 0.210083
TCGA-21-578 0.205898
TCGA-33-AAS 0.204661
TCGA-56-830 0.203424
TCGA-85-A4J 0.20303
TCGA-22-101 0.202623
TCGA-18-559 0.198776
TCGA-56-A4Z 0.197368
TCGA-56-850 0.195279
TCGA-66-279 0.189336
TCGA-85-771 0.187957
TCGA-63-702 0.186892
TCGA-63-702 0.184348
TCGA-66-279 0.183177
TCGA-85-828 0.180242
TCGA-98-802 0.175807
TCGA-85-804 0.175376
TCGA-94-A5I 0.174438
TCGA-66-275 0.174402
TCGA-39-502 0.171075
TCGA-85-784 0.170939
TCGA-NC-A5H 0.166949
TCGA-66-276 0.165669
TCGA-56-589 0.16449
TCGA-39-501 0.163003
TCGA-77-A5G 0.161761
TCGA-33-AAS 0.161275
TCGA-85-795 0.15538
TCGA-66-274 0.154722
TCGA-33-458 0.15365
TCGA-NC-A5H 0.145325
TCGA-90-796 0.144929

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TCGA-66-277 0.140617
TCGA-22-094 0.140359
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TCGA-02-A52 0.139696
TCGA-85-A4C 0.138243
TCGA-68-A59 0.136882
TCGA-56-830 0.135433
TCGA-94-A5I 0.13244
TCGA-85-A50 0.131193
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TCGA-37-379 0.123609
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TCGA-70-672 0.122012
TCGA-85-835 0.120234
TCGA-60-271 0.119634
TCGA-22-459 0.115308
TCGA-56-862 0.112663
TCGA-66-276 0.111005
TCGA-66-278 0.110983
TCGA-37-378 0.110594
TCGA-85-A4Q 0.110244
TCGA-39-502 0.106211
TCGA-34-523 0.105585
TCGA-22-101 0.104509
TCGA-85-835 0.10398
TCGA-63-620 0.1028
TCGA-58-838 0.101748
TCGA-60-271 0.100445
TCGA-58-A46 0.095333
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TCGA-98-A53 0.090361
TCGA-77-A5G 0.089864
TCGA-L3-A52 0.089296
TCGA-22-460 0.088264
TCGA-90-776 0.088232
TCGA-66-275 0.086232
TCGA-37-413 0.084738
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TCGA-92-806 0.082895
TCGA-77-746 0.082571
TCGA-56-758 0.08253

TCGA-37-378 0.081694
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TCGA-85-A51 0.074879
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TCGA-43-339 0.059021
TCGA-46-376 0.058996
TCGA-85-847 0.05886
TCGA-43-A56 0.055408
TCGA-XC-AA0 0.05448
TCGA-22-459 0.052342
TCGA-60-269 0.051094
TCGA-85-769 0.050228
TCGA-68-825 0.048484
TCGA-37-A5E 0.045188
TCGA-60-272 0.043547
TCGA-18-340 0.042078
TCGA-22-548 0.041777
TCGA-34-A5I 0.040124
TCGA-43-677 0.037824
TCGA-60-270 0.037136
TCGA-77-812 0.036298
TCGA-77-A5G 0.035869
TCGA-96-816 0.035387
TCGA-60-271 0.035282
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TCGA-33-458 0.032211
TCGA-63-513 0.03217
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TCGA-37-413 -0.02003
TCGA-85-807 -0.02004
TCGA-56-862 -0.02252
TCGA-NC-A5H -0.02415
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TCGA-33-456 -0.029
TCGA-22-549 -0.03056
TCGA-33-453 -0.031
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TCGA-56-A4B -0.03393
TCGA-66-278 -0.03485
TCGA-22-460 -0.03775
TCGA-77-713 -0.03826
TCGA-96-754 -0.03944
TCGA-94-A4V -0.042
TCGA-63-A5M -0.04202
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TCGA-70-672 -0.0516
TCGA-56-830 -0.05209
TCGA-60-269 -0.05291
TCGA-22-547 -0.05387
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TCGA-58-A46 -0.0557
TCGA-39-502 -0.05685
TCGA-63-A5M -0.0608

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TCGA-52-762 -0. 0623
TCGA-66-279 -0. 06231
TCGA-22-094 -0. 06252
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TCGA-43-257 -0. 06725
TCGA-21-578 -0. 06745
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TCGA-NC-A5H -0. 07111
TCGA-MF-A52 -0. 07195
TCGA-18-341 -0. 07282
TCGA-L3-A4E -0. 07297
TCGA-56-808 -0. 07365
TCGA-51-408 -0. 07595
TCGA-77-800 -0. 0769
TCGA-21-578 -0. 07783
TCGA-22-A5C -0. 08008
TCGA-6A-AB4 -0. 08328
TCGA-39-501 -0. 08373
TCGA-22-547 -0. 08397
TCGA-33-673 -0. 08409
TCGA-98-802 -0. 08712
TCGA-22-459 -0. 08739
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TCGA-33-AAS -0. 0886
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TCGA-98-802 -0. 11416
TCGA-85-858 -0. 11418
TCGA-34-845 -0. 11452
TCGA-60-271 -0. 11454

TCGA-56-820 -0.1154
TCGA-66-276 -0.11717
TCGA-21-107 -0.12136
TCGA-58-A46 -0.12162
TCGA-46-376 -0.12652
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TCGA-33-AAS -0.13042
TCGA-39-503 -0.13233
TCGA-22-548 -0.13299
TCGA-77-814 -0.13329
TCGA-39-503 -0.13526
TCGA-66-277 -0.13669
TCGA-94-703 -0.14018
TCGA-22-101 -0.14031
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TCGA-33-458 -0.14282
TCGA-56-A5D -0.14322
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TCGA-98-A53 -0.14664
TCGA-34-845 -0.14667
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TCGA-39-503 -0.15069
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TCGA-85-807 -0. 18586
TCGA-22-100 -0. 18639
TCGA-85-A5B -0. 18825
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TCGA-77-714 -0. 19977
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TCGA-56-A49 -0. 266
TCGA-63-702 -0. 26619
TCGA-43-614 -0. 26676

TCGA-56-A4B -0.26806
TCGA-39-502 -0.27128
TCGA-85-656 -0.27249
TCGA-21-107 -0.27278
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TCGA-22-461 -0.30834
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TCGA-85-835 -0.31154
TCGA-34-592 -0.31239
TCGA-43-811 -0.31245
TCGA-22-549 -0.31311
TCGA-77-714 -0.31322
TCGA-22-547 -0.3161
TCGA-90-A59 -0.31617
TCGA-60-271 -0.31633
TCGA-43-811 -0.31752
TCGA-85-769 -0.32034
TCGA-90-A4E -0.32195
TCGA-NC-A5H -0.32334
TCGA-22-548 -0.32478
TCGA-77-815 -0.32837
TCGA-94-849 -0.33265
TCGA-63-A5M -0.3411
TCGA-98-A53 -0.34149
TCGA-66-275 -0.34593

TCGA-LA-A7S -0. 34689
TCGA-66-275 -0. 3557
TCGA-77-813 -0. 35577
TCGA-58-A46 -0. 35619
TCGA-43-765 -0. 35715
TCGA-63-A5M -0. 35754
TCGA-NC-A5H -0. 36378
TCGA-77-746 -0. 36967
TCGA-56-722 -0. 37105
TCGA-21-108 -0. 3735
TCGA-43-A47 -0. 37432
TCGA-56-808 -0. 37708
TCGA-34-523 -0. 3782
TCGA-37-412 -0. 37956
TCGA-85-A4F -0. 38131
TCGA-58-A46 -0. 38314
TCGA-37-A5E -0. 38469
TCGA-37-414 -0. 38566
TCGA-66-279 -0. 386
TCGA-02-A52 -0. 39049
TCGA-56-A5D -0. 3966
TCGA-56-830 -0. 39971
TCGA-60-272 -0. 40014
TCGA-60-271 -0. 40034
TCGA-85-A51 -0. 4023
TCGA-98-A53 -0. 40697
TCGA-21-108 -0. 40803
TCGA-92-806 -0. 40902
TCGA-90-776 -0. 41178
TCGA-51-408 -0. 4236
TCGA-43-765 -0. 44241
TCGA-52-780 -0. 44656
TCGA-60-271 -0. 46762
TCGA-96-A4J -0. 48677

Supplementary Table 3

The obvious outliers samples above the red line were removed by clustering

TCGA-33-A5GW-01A-11R-A27Q-07
TCGA-63-A5MG-01A-12R-A27Q-07
TCGA-39-5011-01A-01R-1443-07
TCGA-56-A49D-01A-11R-A24H-07
TCGA-66-2727-01A-01R-0980-07
TCGA-77-8009-01A-11R-2187-07
TCGA-92-8065-01A-11R-2247-07
TCGA-60-2726-01A-01R-0851-07
TCGA-90-A59Q-01A-11R-A26W-07

TCGA-NK-A7XE-01A-12R-A405-07
TCGA-56-A4BW-01A-11R-A24H-07
TCGA-94-7033-01A-11R-1949-07
TCGA-60-2709-01A-21R-1820-07
TCGA-33-AASL-01A-11R-A405-07
TCGA-39-5027-01A-21R-1820-07
TCGA-37-4132-01A-01R-1100-07
TCGA-NC-A5HR-01A-21R-A26W-07
TCGA-33-AASI-01A-22R-A405-07
TCGA-18-3419-01A-01R-0980-07
TCGA-66-2754-01A-01R-0980-07
TCGA-18-3411-01A-01R-0980-07
TCGA-85-A4CL-01A-41R-A26W-07
TCGA-85-8354-01A-31R-2326-07
TCGA-33-4589-01A-01R-1443-07
TCGA-18-3406-01A-01R-0980-07
TCGA-77-7140-01A-41R-2045-07
TCGA-22-4591-01A-01R-1201-07
TCGA-34-A5IX-01A-12R-A27Q-07
TCGA-85-A50Z-01A-21R-A262-07
TCGA-37-3783-01A-01R-1201-07
TCGA-77-A5GA-01A-11R-A27Q-07
TCGA-02-A52W-01A-11R-A26W-07
TCGA-18-3421-01A-01R-0980-07

Supplementary Table 4

Genes from the black module

AAAS

AADAT

AAGAB

AAR2

AARSD1

AATF

ABCA5

ABCA7

ABCB10

ABCB7

ABCC4

ABCD4

ABCE1

ABCF1

ABHD13

ABHD15

ABHD16A

ABHD17A

ABHD5

ABHD8
ABI2
ACACA
ACAD10
ACAD8
ACADVL
ACAP3
ACBD3
ACBD4
ACCS
ACD
ACER3
ACIN1
ACLY
ACOX1
ACOX3
ACP6
ACSS1
ACTB
ACTR2
ACTR3B
ACTR5
ACVR1B
ACY1
ACYP1
ADA
ADAL
ADAM10
ADAR
ADAT1
ADAT2
ADAT3
ADCK3
ADCY6
ADHFE1
ADIPO1
ADM5
ADNP
ADNP2
ADO
ADRA2B
ADRM1
ADSS
AEN
AES
AFTPH
AGA
AGAP1

AGAP10
AGAP3
AGAP6
AGFG1
AGGF1
AGO1
AGO3
AGO4
AGPAT1
AGTRAP
AHCTF1
AHCYL1
AHR
AHSA2
AKAP1
AKAP17A
AKAP8
AKAP8L
AKIRIN1
AKT3
ALDH18A1
ALDH5A1
ALG1
ALG10B
ALKBH2
ALKBH7
ALMS1
ALS2
ALS2CL
AMBRA1
AMDHD2
AMER1
AMFR
AMMECR1L
AMN
AMT
ANAPC1
ANAPC7
ANGEL2
ANK3
ANKDD1A
ANKLE2
ANKRA2
ANKRD10
ANKRD12
ANKRD13B
ANKRD13C
ANKRD13D

ANKRD17
ANKRD26
ANKRD32
ANKRD40
ANKRD42
ANKRD52
ANKRD54
ANKS1A
ANKS3
ANKZF1
ANLN
AN08
ANP32A
ANP32E
ANXA2
ANXA8
ANXA8L1
AP1G2
AP1M1
AP1M2
AP1S3
AP2B1
AP3D1
AP3M1
AP3S1
AP3S2
AP4E1
AP4M1
AP5B1
AP5Z1
APAF1
APBA2
APBA3
APBB3
APC
API5
APOOL
APPBP2
APPL1
AQR
ARAP1
ARF3
ARF4
ARFGAP1
ARFGAP2
ARFGEF2
ARFRP1
ARGLU1

ARHGAP11A
ARHGAP11B
ARHGAP12
ARHGAP19
ARHGAP27
ARHGDIA
ARHGEF11
ARHGEF18
ARHGEF19
ARHGEF2
ARHGEF25
ARHGEF7
ARID1A
ARID2
ARID3A
ARID3B
ARID4B
ARIH1
ARL2BP
ARL5B
ARL8A
ARL8B
ARL9
ARMC5
ARMC6
ARMC7
ARMCX2
ARMCX3
ARMCX5
ARNT
ARPC2
ARPP19
ARSG
ASAP1
ASAP2
ASB1
ASB7
ASCL2
ASF1B
ASH1L
ASL
ASPM
ASTN2
ASXL2
ATAD1
ATAD2
ATAD2B
ATAD3B

ATAD3C
ATAD5
ATAT1
ATF6B
ATF7
ATF7IP
ATG16L1
ATG16L2
ATG2A
ATG4B
ATG4D
ATG9B
ATHL1
ATIC
ATL3
ATP11C
ATP13A1
ATP5B
ATP5D
ATP5I
ATP6V0A1
ATP6V0A2
ATP6V0C
ATP6V0D1
ATP6V0E1
ATP6V1B1
ATP7A
ATP9A
ATRX
ATXN2
ATXN2L
ATXN7L1
ATXN7L2
ATXN7L3
ATXN7L3B
AUNIP
AURKA
AUTS2
AVEN
AVIL
AVL9
AVPI1
AXIN1
B3GALNT2
B3GALT4
B3GAT3
B3GNT3
B3GNT8

B4GALNT4
B4GALT7
BABAM1
BAG6
BAHCC1
BAHD1
BAI2
BAK1
BANP
BAP1
BARD1
BAZ1B
BAZ2A
BAZ2B
BBS5
BCAS3
BCHE
BCKDK
BCL10
BCL11A
BCL11B
BCL2
BCL2L2
BCL7A
BCL9
BCLAF1
BCOR
BCORL1
BCS1L
BDKRB2
BDP1
BECN1
BEND3
BEND5
BFAR
BHLHB9
BIK
BIRC6
BIVM
BLM
BLMH
BLOC1S6
BMF
BMP3
BMPR1A
BMS1
BNIP2
BOD1L1

BORA
BPGM
BPTF
BRAF
BRAP
BRAT1
BRCA1
BRCA2
BRCC3
BRD2
BRD4
BRD8
BRI3BP
BRICD5
BRIP1
BROX
BRPF1
BRPF3
BRWD1
BRWD3
BSCL2
BSDC1
BSG
BTAF1
BTBD1
BTBD2
BTN2A1
BUB1
BUB1B
BUD13
BVES
BZRAP1
BZW1
C11orf30
C11orf49
C11orf68
C11orf80
C11orf95
C12orf43
C12orf65
C14orf93
C15orf40
C15orf41
C15orf62
C16orf13
C16orf58
C16orf59
C16orf62

C16orf72
C16orf87
C16orf91
C17orf53
C17orf70
C17orf80
C17orf96
C18orf25
C18orf54
C18orf8
C19orf24
C19orf25
C19orf43
C19orf44
C19orf52
C19orf53
C19orf60
C19orf70
C19orf71
C1orf109
C1orf112
C1orf122
C1orf131
C1orf216
C1orf27
C1orf35
C20orf96
C21orf2
C21orf58
C21orf59
C22orf46
C2CD3
C2orf44
C2orf68
C3orf62
C4orf19
C4orf3
C5orf45
C6orf106
C6orf136
C6orf47
C6orf48
C6orf62
C6orf89
C7orf26
C7orf43
C7orf55-LUC7L2
C8orf44

CA2
CABIN1
CABLES2
CACNB1
CACNB3
CACTIN
CACUL1
CAD
CAMK1D
CAMKK2
CAMSAP3
CAMTA2
CANX
CAPN10
CAPN12
CAPN15
CAPN2
CAPN7
CAPRIN1
CARD6
CARHSP1
CARKD
CARM1
CARS
CARS2
CASC3
CASC5
CASKIN2
CASP2
CASP8AP2
CASP9
CAST
CASZ1
CAV2
CBFA2T2
CBLL1
CBR4
CBX1
CBX2
CBX4
CBX5
CBX8
CC2D1A
CC2D1B
CCAR1
CCDC101
CCDC102A
CCDC112

CCDC117
CCDC12
CCDC120
CCDC124
CCDC130
CCDC137
CCDC138
CCDC14
CCDC142
CCDC159
CCDC163P
CCDC174
CCDC18
CCDC22
CCDC23
CCDC24
CCDC43
CCDC47
CCDC57
CCDC64B
CCDC66
CCDC74A
CCDC77
CCDC82
CCDC84
CCDC85B
CCDC93
CCDC94
CCHCR1
CCNA2
CCNB1
CCNB2
CCNE2
CCNF
CCNJ
CCNL1
CCNL2
CCNT1
CCNT2
CCNYL1
CCP110
CCS
CCSAP
CD151
CD2BP2
CD320
CD59
CDAN1

CDC16
CDC20
CDC23
CDC25A
CDC25C
CDC27
CDC34
CDC37
CDC40
CDC42BPA
CDC42BPG
CDC42EP1
CDC42SE1
CDC6
CDC7
CDC73
CDCA2
CDCA5
CDCA7
CDCA7L
CDCA8
CDH26
CDIP1
CDIPT
CDK10
CDK11A
CDK12
CDK13
CDK19
CDK2
CDK20
CDK2AP1
CDK5RAP1
CDK5RAP3
CDKAL1
CDKN1A
CDKN1B
CDKN2C
CDKN2D
CDPF1
CDT1
CEBDP
CEBPZ
CELF1
CENPA
CENPBD1
CENPC
CENPE

CENPF
CENPH
CENPI
CENPJ
CENPO
CENPT
CENPU
CEP104
CEP131
CEP152
CEP162
CEP164
CEP192
CEP250
CEP290
CEP295
CEP350
CEP55
CEP57
CEP68
CEP83
CEP85
CEP95
CERS5
CES3
CFAP97
CHAF1A
CHAF1B
CHAMP1
CHD1
CHD1L
CHD2
CHD4
CHD6
CHD7
CHEK1
CHERP
CHIC1
CHKB
CHML
CHMP4A
CHP1
CHRNA5
CHST10
CHST14
CHTF18
CHTF8
CHTOP

CIB1
CIRBP
CIT
CKAP2L
CKAP5
CLASP1
CLASRP
CLCC1
CLCN3
CLCN6
CLCN7
CLDN15
CLDN23
CLGN
CLIC6
CLK1
CLK2
CLK3
CLK4
CLMN
CLN3
CLN6
CLPP
CLPX
CLSPN
CLTB
CLTC
CLUAP1
CMTR1
CNIH2
CNKSR1
CNKSR3
CNN2
CNNM3
CNNM4
CNOT10
CNOT6
CNP
CNST
CNTLN
COA7
COASY
COG1
COG2
COG4
COG7
COG8
COL9A2

COL9A3
COLCA2
COLGALT1
COMM4
COPE
COPG2
COPS2
COPS7B
COQ7
CORO1B
CORO6
COX19
CP
CPNE1
CPNE8
CPSF6
CPSF7
CPT2
CRAMP1L
CRB3
CREB1
CREB3L4
CREBBP
CREBZF
CRIPTAK
CRLF3
CRNL1
CROCC
CRTCK2
CRTCK3
CRY1
CRYBB3
CRYGS
CS
CSAD
CSDE1
CSNK1A1
CSNK1D
CSNK1E
CSNK1G1
CSNK1G2
CSNK1G3
CSNK2B
CSPP1
CST3
CST6
CSTF1
CSTF2T

CSTF3
CTBP1
CTC1
CTCF
CTDP1
CTDSP1
CTDSPL2
CTF1
CTNNB1
CTNNBL1
CTPS1
CTPS2
CTR9
CTSC
CTXN1
CUEDC1
CUL3
CUL4B
CWC22
CWC25
CWC27
CXorf23
CXXC1
CYB5R1
CYFIP1
CYP20A1
CYP2J2
CYP4X1
CYTH1
D2HGDH
DAPK3
DARS2
DAXX
DAZAP1
DBF4B
DCAF15
DCAF16
DCAF17
DCAF7
DCAF8
DCAKD
DCLRE1B
DCP1B
DCTN5
DDA1
DDAH2
DDB1
DDI2

DDRGK1
DDTL
DDX17
DDX18
DDX19A
DDX20
DDX21
DDX23
DDX26B
DDX27
DDX39A
DDX39B
DDX3X
DDX41
DDX42
DDX46
DDX49
DDX5
DDX50
DDX51
DDX52
DDX54
DDX55
DDX6
DECR2
DEF8
DEGS1
DEK
DENND4A
DENND4B
DENND6A
DENR
DEPDC1B
DEPDC5
DEPTOR
DESI2
DET1
DEXI
DFFA
DFFB
DFNB31
DGKA
DGKE
DGKQ
DHFR
DHODH
DHPS
DHRS11

DHRS13
DHRS3
DHTKD1
DHX15
DHX16
DHX30
DHX32
DHX37
DHX38
DHX57
DHX8
DHX9
DIAPH3
DID01
DIEXF
DIP2A
DIS3
DIS3L
DIS3L2
DLEC1
DLG3
DLL1
DLX4
DMAP1
DMPK
DMTF1
DNA2
DNAAF5
DNAJA3
DNAJA4
DNAJB1
DNAJC11
DNAJC14
DNAJC16
DNAJC17
DNAJC24
DNAJC27
DNAJC7
DNAJC9
DNAL4
DNALI1
DNASE1L1
DNASE2
DNM2
DNMT1
DNMT3A
DOCK6
DOCK7

DOHH
DONSON
DOPEY1
DOT1L
DPF2
DPP8
DPP9
DSCC1
DSN1
DSTN
DSTYK
DTL
DTNBP1
DTX3
DUS1L
DUS3L
DUSP28
DXO
DYM
DYNC2LI1
DYNLL2
DYRK1A
DZIP1
DZIP3
E2F1
E2F2
E2F3
E2F4
E2F7
E2F8
E4F1
EARS2
EBF4
ECHDC2
ECI1
ECSIT
EDC3
EDC4
EDEM3
EDRF1
EEF2
EEF2K
EEF2KMT
EFCAB7
EFNA5
EFTUD1
EFTUD2
EHF

EHMT2
EID1
EIF2AK1
EIF2AK4
EIF2B1
EIF2B4
EIF2S3
EIF3C
EIF3G
EIF3J
EIF4A1
EIF4B
EIF4ENIF1
EIF4G2
ELAVL1
ELF2
ELK1
ELK4
ELL
ELL2
ELMO2
ELMOD3
ELOF1
ELOVL1
ELP2
EME1
EME2
EML3
EML4
EMP1
EN1
ENAH
ENDOV
ENGASE
ENKD1
ENOSF1
ENTHD2
ENTPD6
EP400
EPB41
EPC1
EPC2
EPG5
EPHB4
EPM2AIP1
EPRS
EPS15L1
EPS8L2

ERAL1
ERBB2
ERBB3
ERCC3
ERCC4
ERCC5
ERCC6
ERCC6L
ERI2
ERMAP
ERMARD
ERV3-1
ESCO1
ESPL1
ETAA1
ETHE1
ETV3
EVC2
EVI5L
EWSR1
EX01
EXOC2
EXOC4
EXOC7
EXOC8
EXOG
EXOSC10
EXOSC9
EYA2
EYA3
EZH1
EZH2
F3
FAAH
FABP5
FAF1
FAF2
FAHD1
FAM111A
FAM111B
FAM114A1
FAM118A
FAM120B
FAM120C
FAM122B
FAM126B
FAM134C
FAM13A

FAM160A2
FAM160B2
FAM161A
FAM168A
FAM168B
FAM171A1
FAM171A2
FAM173A
FAM174A
FAM189B
FAM193A
FAM193B
FAM195A
FAM207A
FAM208B
FAM210B
FAM212B
FAM219B
FAM222B
FAM24B
FAM32A
FAM50A
FAM50B
FAM53C
FAM63A
FAM63B
FAM73A
FAM76B
FAM83A
FAM83E
FAM98A
FAM98B
FAN1
FANCA
FANCB
FANCD2
FANCF
FANCI
FARP1
FARSA
FASN
FASTK
FBRS
FBRSL1
FBXL12
FBXL19
FBXL20
FBXL4

FBXL8
FBXO11
FBXO21
FBXO28
FBXO41
FBXO42
FBXO44
FBXO5
FBXW4
FBXW8
FBXW9
FCHSD1
FDX1L
FEM1B
FEN1
FEZ1
FEZF1
FGD1
FGD6
FGFR3
FHL3
FIGNL1
FKBP8
FKBPL
FLVCR1
FLYWCH2
FMNL2
FMR1
FNBP1L
FNBP4
FNIP1
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FOXC1
FOXI1
FOXJ3
FOXK2
FOXO3
FOXRED1
FOXRED2
FRA10AC1
FRG1B
FRK
FRS3
FTHL17
FTSJ3
FUBP1
FUK
FUS

FZR1
G3BP1
GABBR1
GABPA
GABPB1
GABPB2
GABRE
GADD45GIP1
GAK
GAL
GALK2
GANAB
GAREML
GART
GAS8
GATAD2A
GATAD2B
GATS
GBE1
GCC2
GCDH
GCFC2
GCN1L1
GDE1
GDF11
GDI1
GDPD3
GDPGP1
GEMIN5
GEN1
GET4
GFER
GFOD2
GGA1
GGA3
GGNBP2
GID8
GIGYF1
GIGYF2
GIPC1
GIT1
GJC1
GLB1L
GLCE
GLYR1
GMDS
GMEB1
GMEB2

GNA11
GNA15
GNAS
GNAZ
GNB1
GNB5
GNG12
GNL1
GNL2
GNL3
GNL3L
GNPTG
GOLGA8A
GOLGA8B
GON4L
GOSR1
GPANK1
GPATCH11
GPATCH2
GPATCH3
GPATCH4
GPATCH8
GPBP1L1
GPCPD1
GPKOW
GPN2
GPR108
GPR115
GPR125
GPR137
GPR161
GPRC5B
GPRIN1
GPS2
GPX4
GRB7
GRIPAP1
GSDMB
GSPT1
GSTCD
GSTT2B
GTF2F1
GTF2H3
GTF2H4
GTF2I
GTF3C1
GTF3C2
GTPBP1

GTPBP3
GTPBP6
GTSE1
GUCD1
GUF1
GXYLT1
GYG2
GZF1
HADHA
HAGHL
HAP1
HARS
HARS2
HAUS2
HAUS3
HAUS6
HAUS8
HBEGF
HBS1L
HCFC1
HCFC1R1
HCN3
HDAC10
HDAC11
HDAC2
HDAC4
HDAC5
HDAC6
HDAC7
HDAC8
HDGF
HDGFRP2
HDGFRP3
HDHD2
HEATR1
HEATR5B
HEATR6
HECTD4
HELLS
HELZ
HENMT1
HERC1
HERC2
HEXDC
HEXIM1
HEXIM2
HGS
HHAT

HHLA3
HIF1AN
HIF3A
HINFP
HIP1R
HIPK1
HIPK2
HIRIP3
HIST1H1E
HIST1H3E
HIST1H4E
HJURP
HLCS
HMG20A
HMG20B
HMGB2
HMGN1
HMGN5
HMMR
HMOX2
HN1L
HNRNPA0
HNRNPA1
HNRNPA1L2
HNRNPA2B1
HNRNPA3
HNRNPD
HNRNPDL
HNRNPH1
HNRNPH2
HNRNPH3
HNRNPM
HNRNPR
HNRNPU
HNRNPUL2
HOMER3
HOOK1
HOOK2
HOXA3
HOXC4
HOXC6
HOXC9
HOXD9
HP1BP3
HPS6
HSBP1L1
HSD11B2
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THAP9
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THOC2
THOC6
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TRAPP12

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 ZXDB
 ZYG11B
 ZZZ3

Supplementary Table 5

In the TCGA-LUSC dataset, 3055 DEGs were identified between LUSC and normal samples

gene	logFC	AveExpr	t	P.Value
RS1	-1.12103	0.1565535	-50.772	1.52E-208
F11	-1.62278	0.2607507	-46.239	1.34E-190
CNTN6	-1.67884	0.2576835	-46.022	1.03E-189
CA4	-3.66625	0.7201767	-44.214	3.06E-182
GPM6A	-2.65464	0.4319557	-43.704	4.21E-180
GPD1	-3.37826	0.7482394	-42.958	6.04E-177
ADAMTS8	-3.24325	0.7005306	-41.829	4.09E-172
TCF21	-3.07836	0.821453	-41.57	5.39E-171
ASPA	-1.01154	0.2166221	-40.748	2.01E-167
GKN2	-4.29209	0.8891224	-40.076	1.79E-164
GGTLC1	-4.2424	0.8693885	-39.89	1.19E-163
CLIC5	-4.35607	1.2191097	-39.078	4.76E-160
C1QTNF7	-1.80992	0.4421089	-38.68	2.88E-158
FXYD1	-1.52	0.425901	-38.434	3.65E-157

CD300LG	-1.80015	0.2406313	-38.358	8.04E-157
MYZAP	-2.48359	0.6658852	-38.34	9.71E-157
AGRP	-2.11519	0.4389865	-38.295	1.55E-156
GPA33	-2.19472	0.3905341	-38.267	2.06E-156
FHL5	-2.5355	0.7546523	-37.824	2.05E-154
GPIHBP1	-3.87202	0.97572	-37.763	3.89E-154
GDF10	-3.08592	0.6893279	-37.689	8.47E-154
ABCA8	-2.31429	0.582122	-37.213	1.23E-151
FIGF	-3.91713	1.0649117	-37.029	8.55E-151
GPR133	-2.30037	0.6673924	-36.815	8.19E-150
RSP01	-1.3815	0.2830019	-36.785	1.12E-149
CPB2	-3.55989	0.6599361	-36.7	2.75E-149
TNXB	-2.93043	0.7854951	-36.69	3.04E-149
SCN7A	-2.86971	0.7847397	-36.689	3.07E-149
LRRC36	-2.14255	0.4851883	-36.669	3.81E-149
VEPH1	-3.06461	0.8408367	-36.513	1.99E-148
NOSTRIN	-2.15235	0.8834813	-36.384	7.77E-148
ANGPT4	-1.0066	0.1767395	-36.052	2.65E-146
USHBP1	-1.3506	0.4952578	-35.914	1.15E-145
ACOXL	-1.53505	0.4443737	-35.485	1.13E-143
SLC46A2	-2.55029	0.64686	-35.324	6.35E-143
FAM107A	-4.45138	1.3170415	-35.152	4.04E-142
UBE2C	4.242785	5.1555366	34.9585	3.24E-141
TEK	-3.16659	1.394596	-34.779	2.26E-140
MCEMP1	-4.8631	1.5594233	-34.63	1.12E-139
SLC6A4	-3.59731	0.642643	-34.009	9.52E-137
TPX2	3.916819	4.7042883	33.9691	1.46E-136
KANK3	-2.35803	0.9688312	-33.847	5.57E-136
ROB04	-2.97966	1.6822738	-33.594	8.81E-135
RTKN2	-3.17265	1.4468409	-33.579	1.04E-134
CDC20	3.880438	4.6711697	33.5615	1.25E-134
EFCC1	-2.40374	0.8502186	-33.357	1.18E-133
GRIA1	-1.70204	0.2904511	-33.211	5.87E-133
EMCN	-2.86551	1.2557417	-33.207	6.13E-133
PTPRB	-2.73224	1.3787806	-33.195	6.94E-133
KHDRBS2	-1.6908	0.3643827	-33.151	1.13E-132
NMUR1	-1.2919	0.3625597	-32.893	1.92E-131
INMT	-4.58826	1.8891227	-32.81	4.79E-131
EDNRB	-3.63049	1.6041122	-32.805	5.11E-131
NPR1	-3.03699	1.312607	-32.777	6.91E-131
TNNC1	-4.58615	1.4820395	-32.773	7.24E-131
CLEC3B	-4.53061	2.250195	-32.683	1.95E-130
HIGD1B	-3.00899	1.5815931	-32.678	2.06E-130
SLC51B	-2.03589	0.6496172	-32.653	2.73E-130
MYBL2	4.05792	4.7454698	32.6256	3.68E-130
GYPE	-1.08809	0.2593785	-32.484	1.75E-129
PLA2G1B	-3.87203	0.9906843	-32.416	3.74E-129
RETN	-3.75575	1.0867228	-32.244	2.50E-128

ARHGEF15	-2.43041	1.2384433	-32.188	4.67E-128
ECSCR	-2.0305	1.0432975	-32.095	1.32E-127
HSD17B6	-3.43367	1.8487131	-31.754	5.82E-126
ANKRD1	-4.2082	1.0182992	-31.559	5.12E-125
PRX	-2.92844	1.3390714	-31.321	7.30E-124
SCUBE1	-1.7727	0.3522968	-31.308	8.49E-124
PGM5	-2.03759	0.6431316	-31.236	1.89E-123
CCDC85A	-1.28745	0.3632339	-31.15	4.94E-123
SEC14L6	-2.27712	0.7100039	-31.128	6.30E-123
LDB2	-2.66224	1.6306594	-30.891	9.08E-122
CLDN18	-6.38493	1.8484716	-30.883	9.90E-122
DLC1	-3.40995	1.7855599	-30.883	9.90E-122
SHE	-2.25547	0.8808817	-30.845	1.52E-121
BIRC5	3.694737	4.1971198	30.7388	5.00E-121
ITLN2	-3.36374	0.8509741	-30.48	9.19E-120
CACNA2D2	-4.14923	1.5446702	-30.448	1.31E-119
ANGPTL1	-1.8189	0.5723519	-30.442	1.42E-119
TMEM100	-4.18244	1.1938403	-30.326	5.20E-119
NOVA2	-1.27642	0.4913328	-30.318	5.73E-119
CCNB1	3.170407	4.4478034	30.2751	9.28E-119
CCNB2	3.153522	3.7583678	30.2439	1.32E-118
ARHGAP6	-1.47825	0.5017046	-30.207	2.00E-118
LRRN4	-2.99107	0.8538441	-30.158	3.48E-118
WWC2	-2.42628	1.5417967	-30.114	5.73E-118
CDCA5	2.923039	3.4436903	30.0571	1.09E-117
JAM2	-2.33994	1.3301396	-30.038	1.35E-117
SOX17	-2.02916	0.7970736	-30.023	1.60E-117
FAM189A2	-3.19377	1.18807	-30.004	1.99E-117
ADH1B	-4.8428	1.5438687	-29.808	1.84E-116
MYCT1	-2.43432	1.4583905	-29.79	2.24E-116
PLK1	2.821911	3.2395238	29.7351	4.18E-116
PREX2	-1.45247	0.4974607	-29.437	1.24E-114
MS4A15	-4.06221	1.0155368	-29.399	1.89E-114
KIF2C	2.957567	3.3360588	29.3896	2.11E-114
AGER	-6.86456	3.3946619	-29.318	4.76E-114
CDCA8	2.935191	3.6161276	29.167	2.66E-113
DPCR1	-1.39909	0.2962588	-29.132	3.97E-113
SYNE1	-1.86329	0.8297107	-29.073	7.73E-113
PLAC9	-2.82632	1.6243129	-29.055	9.57E-113
LYVE1	-3.05556	1.3734285	-28.98	2.24E-112
LRRN3	-1.72307	0.444079	-28.886	6.53E-112
ATOH8	-2.83683	0.9889126	-28.837	1.15E-111
SLC19A3	-1.90237	0.605048	-28.758	2.83E-111
GPR146	-1.14457	0.5859824	-28.637	1.12E-110
KL	-1.64157	0.4813796	-28.536	3.58E-110
RASGRP4	-1.47031	0.6885062	-28.469	7.73E-110
SLC2A1	5.146643	6.8759795	28.3325	3.67E-109
ACVRL1	-2.89175	2.5892402	-28.31	4.75E-109

NUSAP1	3. 000711	4. 1517743	28. 3084	4. 85E-109
KIF4A	2. 623382	2. 8339745	28. 2822	6. 54E-109
CDH5	-3. 2431	2. 5956871	-28. 277	6. 91E-109
ANLN	3. 007369	3. 4177038	28. 2604	8. 40E-109
CEP55	3. 020814	3. 517753	28. 2435	1. 02E-108
UBE2T	3. 22155	4. 3927635	28. 1568	2. 76E-108
NLRC4	-1. 66261	0. 8967756	-28. 153	2. 89E-108
C8B	-1. 96115	0. 3245238	-28. 041	1. 04E-107
CCNA2	2. 980344	3. 6299498	28. 0344	1. 12E-107
FRMD3	-1. 3314	0. 5175203	-28. 016	1. 38E-107
MAP1LC3C	-1. 97301	0. 5357281	-28. 006	1. 55E-107
TOP2A	3. 651254	4. 5025836	27. 986	1. 96E-107
ACKR4	-1. 37535	0. 5415855	-27. 946	3. 09E-107
F8	-1. 87619	1. 2054987	-27. 876	6. 90E-107
PRC1	2. 815981	3. 6218346	27. 8449	9. 90E-107
LRP2BP	-1. 0105	0. 4238522	-27. 837	1. 09E-106
ITGA8	-2. 53154	1. 0998094	-27. 817	1. 36E-106
CD5L	-1. 0179	0. 1605879	-27. 638	1. 07E-105
KIF11	2. 551304	3. 1794723	27. 6317	1. 15E-105
RGCC	-3. 49482	4. 8818614	-27. 589	1. 88E-105
PTPN21	-2. 10637	1. 5958609	-27. 531	3. 66E-105
C10orf67	-1. 01485	0. 24671	-27. 475	6. 97E-105
GLDN	-1. 73767	0. 7134716	-27. 448	9. 57E-105
PHACTR1	-1. 89998	0. 9729136	-27. 32	4. 18E-104
MCM4	2. 678041	4. 3923217	27. 2993	5. 30E-104
RRM2	3. 221112	3. 993664	27. 2735	7. 14E-104
NCAPH	2. 742363	3. 1117166	27. 233	1. 14E-103
FFAR4	-1. 49056	0. 4282236	-27. 202	1. 63E-103
PTTG1	2. 701329	4. 16172	27. 1745	2. 24E-103
RAMP2	-2. 98023	3. 4094925	-27. 159	2. 67E-103
DLGAP5	2. 635661	2. 8575096	27. 1246	3. 98E-103
LIMS2	-2. 35996	1. 4844129	-27. 108	4. 82E-103
SUSD2	-4. 75505	2. 4868871	-27. 075	7. 09E-103
RASGRF1	-2. 35978	0. 7189388	-27. 04	1. 05E-102
MYRF	-2. 5112	1. 1199984	-27. 002	1. 65E-102
SEMA3G	-2. 3752	1. 3481066	-26. 981	2. 10E-102
TK1	3. 3843	5. 5772342	26. 9639	2. 55E-102
ACADL	-1. 98681	0. 724306	-26. 937	3. 46E-102
KCNT2	-1. 08454	0. 3263683	-26. 904	5. 10E-102
GPR116	-3. 7825	2. 745133	-26. 879	6. 81E-102
AFF3	-1. 53366	0. 4431046	-26. 871	7. 43E-102
SH2D3C	-2. 46587	1. 979976	-26. 856	8. 89E-102
FOXM1	3. 398718	3. 8873311	26. 8285	1. 22E-101
PKNOX2	-1. 48902	0. 5953653	-26. 81	1. 50E-101
STARD8	-2. 11056	1. 287865	-26. 795	1. 79E-101
FCN3	-4. 59924	1. 9528089	-26. 788	1. 95E-101
CENPA	2. 615578	2. 7066405	26. 715	4. 53E-101
COL4A3	-2. 17929	0. 6894064	-26. 702	5. 25E-101

FHL1	-3.80076	2.3842238	-26.684	6.51E-101
HMGA1	2.836248	7.1634723	26.6638	8.19E-101
ZWINT	2.775629	4.1359774	26.6563	8.94E-101
CCM2L	-1.88158	0.9789068	-26.63	1.21E-100
SERTM1	-1.92923	0.4016937	-26.621	1.34E-100
HJURP	2.673895	2.7932183	26.5734	2.33E-100
HSPA12B	-2.25843	1.4468447	-26.571	2.39E-100
KIF23	2.300596	2.6665523	26.5691	2.45E-100
FAM110D	-1.6408	0.7555798	-26.557	2.83E-100
ESAM	-2.9359	3.2253854	-26.534	3.67E-100
KIFC1	2.729139	3.5641514	26.4892	6.18E-100
MAMDC2	-3.25891	1.1867157	-26.48	6.90E-100
HHIP	-2.57691	0.6692361	-26.479	6.98E-100
SLC39A8	-3.77549	2.9642118	-26.472	7.56E-100
NEK2	2.727751	2.8888764	26.4349	1.16E-99
AURKB	3.090247	3.4607137	26.428	1.26E-99
HNF1B	-1.95012	0.5120561	-26.39	1.95E-99
SCARA5	-2.37264	0.5950777	-26.364	2.65E-99
AURKA	2.521402	3.4108354	26.362	2.70E-99
BUB1B	2.582098	2.78124	26.3471	3.21E-99
SIGLEC11	-1.14361	0.3106546	-26.311	4.87E-99
CD302	-2.14121	1.4118279	-26.307	5.08E-99
KIF20A	2.537543	2.9861056	26.2531	9.54E-99
GRK5	-2.25387	1.9351008	-26.251	9.83E-99
CAPN9	-2.00781	0.6812885	-26.247	1.02E-98
CDC45	2.975425	3.2476942	26.2087	1.60E-98
S1PR1	-3.33316	2.6328937	-26.12	4.49E-98
CCL23	-2.46953	0.8585197	-25.989	2.05E-97
GUCY1A2	-1.40933	0.6423477	-25.96	2.85E-97
NCKAP5	-2.00488	0.8517371	-25.882	7.08E-97
CDK1	2.784246	3.8415557	25.8706	8.09E-97
PTCRA	-1.11019	0.3986937	-25.723	4.50E-96
TROAP	2.742743	2.8526624	25.6345	1.26E-95
AK1	-1.96273	1.9517566	-25.582	2.31E-95
PCDH12	-2.06781	1.480252	-25.542	3.69E-95
APOH	-2.26336	0.4499635	-25.501	5.91E-95
GIMAP8	-2.72398	1.8350299	-25.396	2.01E-94
ZBTB16	-1.80214	0.4222341	-25.382	2.37E-94
LONRF3	-1.59936	0.6122968	-25.361	3.03E-94
SLC1A1	-2.83008	1.5386688	-25.334	4.16E-94
TAL1	-1.54053	0.5585648	-25.312	5.37E-94
TRIP13	2.822137	3.4904816	25.1939	2.12E-93
KPNA2	2.500403	5.6100768	25.1682	2.86E-93
BUB1	2.221744	2.6968138	25.1201	5.01E-93
ARHGAP44	-2.05476	1.0492728	-25.115	5.34E-93
ARRB1	-2.68146	1.8842394	-25.109	5.70E-93
COL6A6	-2.14913	0.7356105	-25.059	1.02E-92
CCL14	-1.35274	0.3586049	-25.033	1.39E-92

PRAM1	-1.85123	0.9840465	-24.976	2.70E-92
SLC5A9	-1.26625	0.3182256	-24.963	3.12E-92
LPL	-3.81934	2.0581363	-24.955	3.44E-92
CLEC14A	-2.86816	2.9426168	-24.948	3.73E-92
CDC6	2.609447	2.9176304	24.9377	4.19E-92
NCAPG	2.099617	2.3412386	24.9259	4.81E-92
MCM2	2.961089	4.6437065	24.9154	5.44E-92
SECISBP2L	-1.83558	2.5850408	-24.909	5.87E-92
DES	-3.9643	1.608905	-24.903	6.31E-92
LM07	-2.61389	2.7486186	-24.862	1.02E-91
CDT1	2.592755	3.0934401	24.7889	2.38E-91
KCNK3	-2.71109	0.9622633	-24.772	2.88E-91
CHIA	-1.62021	0.3433338	-24.705	6.32E-91
HSPB6	-3.23005	1.7299485	-24.684	8.12E-91
SHC3	-1.33997	0.5850507	-24.669	9.66E-91
SIRPB1	-1.89702	0.761471	-24.667	9.81E-91
FAXDC2	-2.48685	1.3879922	-24.611	1.89E-90
GINS1	2.514845	2.8322081	24.6095	1.92E-90
SHROOM4	-2.03209	1.1758485	-24.601	2.13E-90
PDLIM2	-1.58241	1.4073973	-24.588	2.47E-90
CSRNP1	-2.99193	3.3737746	-24.553	3.73E-90
RBP2	-1.59784	0.4391591	-24.533	4.72E-90
TTK	2.414044	2.5044524	24.5301	4.86E-90
ZNF385B	-2.41616	0.8659002	-24.504	6.61E-90
DPEP2	-2.0179	1.0638889	-24.487	8.00E-90
SNX25	-1.86484	2.2895036	-24.479	8.80E-90
HBA1	-1.35264	0.2309049	-24.469	9.89E-90
OGN	-2.56279	0.8365536	-24.442	1.36E-89
FAM162B	-2.30152	1.3344424	-24.417	1.81E-89
FILIP1	-1.81694	0.8378988	-24.371	3.10E-89
VIPR1	-2.57946	1.4190004	-24.368	3.22E-89
ZNF366	-1.0616	0.4612302	-24.356	3.72E-89
PTH1R	-1.55803	0.7054781	-24.351	3.94E-89
TIE1	-2.35733	1.874441	-24.343	4.31E-89
ATP1A2	-1.23391	0.2990834	-24.303	6.87E-89
RAMP3	-3.18211	2.9793568	-24.259	1.15E-88
RHOJ	-2.11548	1.6476633	-24.234	1.54E-88
MMP24	-1.88563	0.8965884	-24.223	1.76E-88
SSTR1	-1.82166	0.4973258	-24.221	1.80E-88
IL1RL1	-2.53669	0.7118695	-24.205	2.16E-88
PRKCE	-1.47562	1.3946515	-24.197	2.38E-88
ROR1	-1.78885	0.7523091	-24.194	2.45E-88
HECW2	-1.4229	0.941648	-24.165	3.44E-88
WFDC1	-1.076	0.5020421	-24.125	5.47E-88
RACGAP1	2.04263	3.7090542	24.1078	6.72E-88
CKAP2L	2.003433	2.1265617	24.0343	1.58E-87
RAD51	2.10072	2.4695798	24.0277	1.71E-87
CGNL1	-2.62886	1.649002	-24.019	1.89E-87

GAPDH	2. 513182	10. 283514	23. 9666	3. 49E-87
CPAMD8	-2. 2555	0. 9886863	-23. 885	9. 09E-87
MMRN1	-2. 29988	0. 9932505	-23. 865	1. 15E-86
MELK	2. 86788	3. 1147314	23. 8637	1. 16E-86
DSP	3. 726828	6. 2201692	23. 8561	1. 27E-86
ABI3BP	-2. 80122	1. 4109962	-23. 821	1. 91E-86
CASS4	-1. 84966	0. 9714623	-23. 799	2. 47E-86
GTSE1	2. 208668	2. 4113203	23. 7985	2. 49E-86
ASF1B	2. 691811	3. 746421	23. 7793	3. 11E-86
TNS2	-2. 26934	2. 6595635	-23. 774	3. 32E-86
C1QTNF2	-1. 14295	0. 5703199	-23. 747	4. 53E-86
LEPR	-1. 82591	1. 0624723	-23. 733	5. 35E-86
SYNDIG1L	-1. 07656	0. 2609142	-23. 72	6. 23E-86
HPGDS	-1. 73798	0. 9487279	-23. 701	7. 78E-86
LIMCH1	-3. 22954	2. 2226005	-23. 688	9. 04E-86
TMEM88	-2. 14196	1. 4730531	-23. 68	9. 90E-86
EXO1	2. 119381	2. 1967674	23. 6575	1. 29E-85
CDCA4	2. 353473	4. 0519056	23. 6256	1. 87E-85
ADCY4	-1. 42328	0. 853033	-23. 596	2. 65E-85
AATK	-1. 8112	0. 9425129	-23. 577	3. 31E-85
NDNF	-4. 20332	2. 0242582	-23. 575	3. 40E-85
KIAA1462	-2. 5402	1. 9869659	-23. 57	3. 57E-85
AOC3	-3. 65788	2. 8001927	-23. 539	5. 13E-85
ADRB1	-2. 34134	0. 9249379	-23. 537	5. 25E-85
SORBS1	-1. 92202	1. 1730989	-23. 491	9. 05E-85
ESYT3	-1. 59826	0. 6825713	-23. 475	1. 09E-84
CST5	-1. 1392	0. 250013	-23. 458	1. 33E-84
CCBE1	-2. 03205	0. 6700737	-23. 457	1. 34E-84
GNG11	-2. 84018	2. 5636123	-23. 433	1. 78E-84
FGFR4	-2. 65156	1. 6045268	-23. 379	3. 35E-84
TNS1	-2. 96204	3. 2615709	-23. 354	4. 47E-84
WISP2	-2. 48506	1. 2160581	-23. 343	5. 11E-84
CFP	-1. 54461	0. 7235768	-23. 342	5. 16E-84
DCDC2	-1. 36437	0. 4503083	-23. 335	5. 57E-84
KANK2	-2. 35095	2. 8259608	-23. 334	5. 66E-84
ALDH3B1	-3. 02886	2. 0000439	-23. 329	6. 02E-84
CX3CR1	-1. 81225	0. 7266458	-23. 322	6. 50E-84
NUF2	2. 559245	2. 7152013	23. 3004	8. 37E-84
F10	-1. 64082	0. 839157	-23. 295	8. 93E-84
ERG	-1. 92818	1. 5439251	-23. 239	1. 72E-83
SNRK	-1. 30434	2. 4703852	-23. 22	2. 15E-83
CD34	-2. 24453	2. 2056644	-23. 215	2. 27E-83
SPN	-2. 58778	1. 5155988	-23. 214	2. 31E-83
SKA3	2. 001383	2. 1341556	23. 2018	2. 65E-83
AGTR1	-1. 4198	0. 419954	-23. 183	3. 32E-83
SGCA	-2. 18572	0. 9642781	-23. 169	3. 87E-83
FZD4	-2. 00083	1. 7055982	-23. 141	5. 37E-83
EPAS1	-3. 3096	5. 0642474	-23. 112	7. 56E-83

IHH	-1.31978	0.2596273	-23.111	7.63E-83
DENND2A	-1.83113	1.1100921	-23.083	1.06E-82
PECAM1	-3.01875	4.1287034	-23.071	1.22E-82
SPTBN1	-1.97267	4.2399413	-23.046	1.63E-82
TDRD10	-1.4395	0.4825837	-22.933	6.13E-82
HSPB7	-1.5944	0.7431706	-22.874	1.21E-81
EMP2	-2.70887	4.6641917	-22.846	1.70E-81
FGD5	-2.22627	1.6088608	-22.845	1.70E-81
BCL6B	-2.01069	1.6837029	-22.843	1.74E-81
CCDC68	-1.72428	0.8304616	-22.819	2.33E-81
PF4	-1.46626	0.3771952	-22.792	3.18E-81
FM05	-2.06369	0.9703188	-22.785	3.45E-81
RAD54L	2.157214	2.2639818	22.7667	4.27E-81
ARHGAP31	-2.35897	1.9727754	-22.751	5.14E-81
CXorf36	-1.73408	1.2297726	-22.728	6.69E-81
GIMAP1	-1.76043	1.0383987	-22.725	6.91E-81
MAD2L1	2.224798	2.6939015	22.7231	7.11E-81
CHRM1	-1.00029	0.2067454	-22.714	7.87E-81
NDC80	2.274565	2.5591549	22.6855	1.10E-80
LRRK2	-3.38594	1.6981468	-22.685	1.11E-80
PERP	3.281308	7.8201302	22.6843	1.12E-80
PSAT1	3.777385	4.6629138	22.6608	1.47E-80
TBX4	-2.48055	1.2805688	-22.627	2.18E-80
UBE2S	2.470645	3.8723026	22.5801	3.78E-80
PRG4	-2.49637	0.6251871	-22.569	4.30E-80
EMR3	-1.09709	0.3576553	-22.565	4.51E-80
FANCI	2.262244	3.089187	22.5585	4.86E-80
CDCA3	2.129437	2.2535599	22.5443	5.74E-80
DOCK4	-1.72101	1.4805282	-22.542	5.89E-80
RXRG	-1.37923	0.3967951	-22.54	6.04E-80
CYP4B1	-5.11875	2.3440561	-22.54	6.05E-80
FAM105A	-2.38093	1.9587941	-22.51	8.60E-80
PDK4	-3.66466	1.9200461	-22.501	9.50E-80
FEN1	2.085063	4.310271	22.4824	1.18E-79
CHEK1	1.728881	2.1852484	22.4807	1.21E-79
CHRDL1	-3.41486	1.6320689	-22.475	1.29E-79
FOXF1	-2.31928	1.6377663	-22.456	1.61E-79
FAM83D	3.114349	4.1315832	22.4398	1.94E-79
PRR11	2.108299	2.8283376	22.4367	2.02E-79
CENPF	2.593603	2.879923	22.4356	2.04E-79
DPYSL2	-2.78049	3.420166	-22.422	2.39E-79
NXPH3	-1.27773	0.4720149	-22.387	3.61E-79
RFC4	2.708152	3.9689477	22.3659	4.61E-79
STARD13	-1.72105	1.2241423	-22.361	4.87E-79
ST6GALNAC6	-1.51478	3.2718105	-22.337	6.44E-79
PBK	2.646356	2.9129377	22.3145	8.39E-79
HBA2	-4.26594	2.3101434	-22.311	8.75E-79
FRY	-1.6202	1.0056604	-22.3	9.91E-79

PKMYT1	2.19456	2.3442945	22.2758	1.32E-78
SHMT2	1.945829	4.9914597	22.2553	1.68E-78
CENPM	2.355491	3.2580625	22.2356	2.11E-78
HYAL1	-2.64501	1.9604017	-22.217	2.62E-78
PDE2A	-1.41549	0.7389474	-22.14	6.44E-78
SNX30	-1.66282	2.0653475	-22.121	7.99E-78
SVEP1	-1.89594	1.306188	-22.118	8.27E-78
FCN1	-2.31343	1.1739341	-22.114	8.71E-78
SKA1	2.129781	2.2518492	22.1067	9.49E-78
CDKN3	2.496903	3.0127899	22.0977	1.05E-77
KLF2	-2.87049	2.6597728	-22.083	1.26E-77
LIMD1	-1.34097	2.0541548	-22.074	1.39E-77
MKI67	2.578326	3.1267616	22.0712	1.44E-77
HYAL2	-1.48512	3.6993691	-22.067	1.52E-77
NECAB1	-1.40457	0.547427	-22.034	2.20E-77
DEPDC1	1.907322	1.9296501	22.0178	2.68E-77
CDKL2	-1.4351	0.6803989	-22.011	2.91E-77
MS4A2	-1.56102	0.7173375	-21.999	3.33E-77
ORC1	1.987562	2.2646452	21.99	3.70E-77
ARHGAP11A	1.930202	2.4461903	21.9593	5.29E-77
KIF18B	2.476878	2.5387621	21.9521	5.76E-77
IL3RA	-1.88074	1.7704953	-21.889	1.20E-76
PVRL1	3.890937	5.4167226	21.8873	1.23E-76
DAPK2	-1.57254	0.9342622	-21.878	1.37E-76
PEBP4	-4.73486	1.972742	-21.86	1.68E-76
FPR2	-2.08508	0.8282413	-21.852	1.84E-76
GRAMD2	-2.09467	1.2568576	-21.851	1.88E-76
SLIT3	-2.57775	1.395289	-21.848	1.94E-76
SPC25	2.046305	2.4635908	21.8387	2.16E-76
ORC6	1.974403	2.107915	21.8361	2.23E-76
SYNC	-1.04713	0.6899589	-21.78	4.29E-76
CD93	-2.93848	3.2281416	-21.769	4.90E-76
CPED1	-1.81418	0.9670581	-21.738	6.99E-76
ADRB2	-2.39227	1.3633625	-21.729	7.81E-76
TGFBR2	-2.86073	4.2299416	-21.725	8.14E-76
NME1	2.098664	4.2352723	21.725	8.14E-76
GINS2	2.395259	2.8096464	21.7186	8.77E-76
RGN	-1.81415	0.8059087	-21.709	9.85E-76
UHFR1	2.188181	2.4050517	21.7027	1.06E-75
RSP02	-1.39007	0.3076162	-21.677	1.42E-75
RBMS3	-1.44027	1.0907458	-21.673	1.49E-75
WFS1	-1.98142	3.5099921	-21.672	1.51E-75
COX4I2	-2.63319	2.3214807	-21.659	1.76E-75
AHCYL2	-2.29367	2.7142728	-21.644	2.08E-75
SPAG5	2.416664	2.9978095	21.6408	2.17E-75
SMAD6	-1.73663	1.0877889	-21.628	2.51E-75
STAC	-2.0785	0.9125257	-21.613	2.99E-75
ECT2	2.640763	4.0325059	21.5832	4.25E-75

AQP4	-4.74391	2.0948468	-21.578	4.50E-75
IQSEC3	-1.09662	0.3711458	-21.559	5.66E-75
ACE	-2.17361	2.0790796	-21.527	8.22E-75
SLC4A4	-1.95185	0.8463857	-21.477	1.46E-74
TMEM132A	2.616219	3.8759007	21.4692	1.60E-74
ABCC6	-1.41225	0.8471162	-21.409	3.25E-74
VWF	-3.09489	3.8261795	-21.395	3.79E-74
OIP5	2.049298	2.3747797	21.3857	4.24E-74
ART4	-1.01712	0.2349605	-21.385	4.28E-74
FBLN5	-2.80102	2.541252	-21.375	4.80E-74
TIMELESS	2.002371	3.6199266	21.3593	5.76E-74
PGC	-5.65568	2.2858688	-21.358	5.88E-74
ATAD2	1.864477	3.2405752	21.3351	7.65E-74
ANGPT1	-2.08907	1.1424782	-21.302	1.12E-73
TFAP2A	2.5442	2.5197604	21.2785	1.48E-73
PNMA2	-1.70435	0.8523722	-21.226	2.71E-73
PEAR1	-1.65858	1.1446969	-21.225	2.76E-73
RPS6KA2	-2.35031	2.5275034	-21.207	3.38E-73
STIL	1.493043	1.7487718	21.1844	4.41E-73
SPC24	2.132617	2.4745733	21.1707	5.18E-73
CFAP221	-1.28702	0.4580943	-21.162	5.73E-73
ZWILCH	1.459314	2.675983	21.1445	7.02E-73
SDPR	-3.83502	3.1330432	-21.096	1.24E-72
CENPW	2.618656	4.480317	21.0653	1.76E-72
SGMS2	-2.32023	2.0650051	-21.065	1.77E-72
RECQL4	2.519422	3.0614602	21.0404	2.36E-72
SCARF1	-1.73278	1.6031784	-21.022	2.91E-72
CD300C	-2.03666	1.4057666	-21.012	3.27E-72
CACNA1D	-1.04363	0.4021775	-21.006	3.53E-72
C19orf48	2.017938	4.4573647	20.9913	4.17E-72
SFTA3	-3.90252	1.5894855	-20.976	5.01E-72
SERPINB5	4.785573	4.7497331	20.9699	5.35E-72
GATA6	-2.15833	1.6026968	-20.949	6.79E-72
KLB	-1.02578	0.255693	-20.929	8.57E-72
MRC1	-3.82079	2.7426715	-20.925	9.04E-72
SLC9A3R2	-2.20596	3.6400113	-20.911	1.06E-71
MCM10	1.786001	1.8597717	20.9053	1.13E-71
STX11	-2.54777	2.3962752	-20.898	1.23E-71
RAD51AP1	2.301332	2.983829	20.8537	2.06E-71
CA3	-1.9164	0.7103239	-20.85	2.14E-71
BTNL9	-2.63101	1.0996983	-20.786	4.54E-71
PPP1R14B	1.968568	5.5613097	20.7712	5.38E-71
FOXA2	-2.91783	1.2142773	-20.764	5.82E-71
KIAA0101	2.374572	2.8284911	20.7498	6.89E-71
PTPRM	-2.11414	1.9460497	-20.748	7.02E-71
TUBA1C	1.862729	5.6269387	20.7425	7.50E-71
P2RY14	-1.35737	0.8614581	-20.706	1.15E-70
SPOCK2	-3.64186	3.0600765	-20.702	1.19E-70

MMRN2	-2.236	2.099123	-20.662	1.91E-70
A2M	-3.71865	6.1248167	-20.647	2.28E-70
DAAM2	-1.84714	1.2848475	-20.636	2.59E-70
CCT3	1.429306	6.3530622	20.6323	2.70E-70
KDR	-2.19119	2.1249177	-20.631	2.73E-70
GPX3	-3.70852	4.9046308	-20.606	3.66E-70
RAPGEF2	-1.32045	1.628925	-20.571	5.49E-70
SORBS2	-1.34307	0.6491013	-20.57	5.56E-70
CASQ2	-1.35135	0.4303081	-20.565	5.91E-70
CKS1B	2.176069	4.1370095	20.5561	6.52E-70
RBMS2	-1.74608	2.4978404	-20.537	8.12E-70
SHCBP1	1.589813	2.0654978	20.5148	1.05E-69
NOTCH4	-1.85903	1.6005276	-20.498	1.27E-69
DNASE2B	-1.29315	0.4160256	-20.497	1.29E-69
PEAK1	-1.3841	1.4237076	-20.492	1.37E-69
PHACTR2	-1.45794	1.8032143	-20.465	1.88E-69
CRY2	-1.49573	2.6286034	-20.465	1.88E-69
SLC26A9	-2.36469	0.9986251	-20.46	1.99E-69
CCRL2	-1.82228	1.305755	-20.458	2.04E-69
C1orf198	-1.49136	4.0185162	-20.456	2.09E-69
CENPU	2.272546	3.0461436	20.4552	2.10E-69
SFTPC	-9.24869	4.1507706	-20.446	2.34E-69
ALDH18A1	1.322832	4.6641721	20.4336	2.70E-69
LTA4H	-1.54479	4.1001793	-20.397	4.10E-69
CKAP2	1.74978	3.362724	20.3848	4.75E-69
CCNF	1.680278	2.3274761	20.371	5.58E-69
MRPL3	1.664622	5.585577	20.334	8.56E-69
OSCAR	-2.50656	2.1520438	-20.321	9.89E-69
FLT4	-1.62564	1.3061843	-20.302	1.24E-68
MRGBP	1.466287	3.6627291	20.2949	1.35E-68
IQGAP3	2.21459	2.4976061	20.2748	1.70E-68
CDCA2	1.732113	1.8384455	20.2598	2.02E-68
DEPDC1B	1.887363	1.968913	20.2557	2.12E-68
RCC1	1.681648	4.093303	20.2537	2.17E-68
PCNA	1.891793	6.538978	20.2434	2.44E-68
CD01	-1.9088	0.7697752	-20.243	2.45E-68
PPBP	-2.60537	0.6881274	-20.239	2.57E-68
CLDN5	-2.91636	2.5138977	-20.223	3.08E-68
RAI2	-2.24954	2.0039113	-20.19	4.55E-68
SELENBP1	-3.85687	3.2211772	-20.159	6.50E-68
AQP1	-3.8925	4.9934985	-20.154	6.84E-68
RASL12	-2.03574	1.922975	-20.146	7.52E-68
GGCT	1.893103	5.03487	20.1421	7.89E-68
LRRC32	-2.58164	2.8946923	-20.128	9.24E-68
CAT	-2.0495	4.5770879	-20.128	9.28E-68
GLIPR2	-2.39099	3.3446944	-20.125	9.65E-68
ASPM	1.852048	1.9226047	20.1152	1.08E-67
ATP10A	-1.80289	1.1025444	-20.112	1.11E-67

WDHD1	1. 537015	2. 1807994	20. 1097	1. 15E-67
FAM184A	-1. 39266	0. 6856701	-20. 094	1. 37E-67
CASC5	1. 349514	1. 4920486	20. 0669	1. 88E-67
KIAA1524	1. 852219	2. 3455183	20. 0638	1. 95E-67
MND1	1. 753889	1. 9438233	20. 053	2. 21E-67
MITF	-1. 32652	1. 1791654	-20. 046	2. 41E-67
CSE1L	1. 505723	5. 3759422	20. 0355	2. 71E-67
CD33	-1. 16492	0. 7400223	-20. 034	2. 76E-67
4-Sep	-1. 29728	0. 9929688	-20. 027	2. 98E-67
FLAD1	1. 44062	3. 9449408	20. 0132	3. 50E-67
DENND3	-1. 88447	1. 6415563	-19. 999	4. 12E-67
CENPH	1. 866946	2. 8868674	19. 9851	4. 84E-67
FAM64A	2. 093167	2. 2407024	19. 9713	5. 68E-67
CFL2	-1. 47958	1. 9201124	-19. 971	5. 71E-67
ICAM2	-2. 02234	1. 6423813	-19. 965	6. 12E-67
CD36	-2. 7438	1. 7078907	-19. 932	8. 95E-67
PAICS	2. 013925	4. 3974497	19. 9177	1. 05E-66
TPI1	1. 760094	8. 187058	19. 8947	1. 37E-66
RNASEH2A	2. 004576	4. 1897873	19. 8916	1. 43E-66
HMMR	1. 951884	2. 3397907	19. 8794	1. 64E-66
FERMT1	3. 02246	3. 5897453	19. 8736	1. 75E-66
PI16	-1. 72487	0. 471998	-19. 854	2. 21E-66
EFNA4	1. 733005	3. 6597669	19. 8482	2. 35E-66
EZH2	2. 210181	2. 8990653	19. 8257	3. 05E-66
RCC2	1. 696152	5. 9518175	19. 7989	4. 15E-66
TNFSF13	-1. 93837	2. 5347419	-19. 792	4. 50E-66
C17orf53	1. 869462	2. 1388407	19. 7808	5. 12E-66
KCNA3	-1. 69804	0. 7953516	-19. 78	5. 19E-66
DKC1	1. 727443	4. 7971104	19. 7664	6. 04E-66
CD55	-2. 51195	4. 7033235	-19. 752	7. 16E-66
FABP4	-4. 63098	1. 9511669	-19. 746	7. 67E-66
CBLC	3. 110618	4. 0265711	19. 7261	9. 62E-66
COBL	-1. 77738	0. 8241206	-19. 724	9. 85E-66
NPM3	2. 191728	5. 1310207	19. 7128	1. 12E-65
AOX1	-1. 76704	0. 9210477	-19. 709	1. 17E-65
ESPL1	1. 720674	1. 8856468	19. 7082	1. 18E-65
AMICA1	-1. 99535	1. 4167669	-19. 706	1. 22E-65
DISP1	-1. 46443	1. 2511175	-19. 704	1. 24E-65
DENR	1. 123798	4. 6996594	19. 6914	1. 43E-65
AUNIP	1. 582661	1. 7053269	19. 6876	1. 50E-65
MCM7	1. 985948	5. 4279958	19. 6742	1. 75E-65
2-Mar	-1. 74466	2. 4374927	-19. 665	1. 95E-65
FLVCR2	-1. 73876	1. 4623031	-19. 658	2. 12E-65
GNAQ	-1. 39055	3. 4315327	-19. 627	3. 01E-65
MARCO	-4. 55212	3. 2194908	-19. 626	3. 05E-65
RMI2	2. 308604	3. 093851	19. 6208	3. 24E-65
EXOC3L1	-1. 06531	1. 2604883	-19. 604	3. 91E-65
IL6ST	-1. 83442	3. 6244604	-19. 603	3. 96E-65

UNG	1. 628089	4. 708874	19. 576	5. 42E-65
OLR1	-3. 49691	2. 613162	-19. 568	5. 94E-65
COLEC12	-2. 57306	1. 9527843	-19. 566	6. 10E-65
C2orf40	-2. 25648	0. 7620593	-19. 565	6. 17E-65
CAV1	-3. 48848	4. 964544	-19. 558	6. 64E-65
DRAM1	-2. 53148	3. 6215228	-19. 558	6. 70E-65
TMEM139	-2. 23095	0. 94551	-19. 55	7. 28E-65
FOLR1	-4. 68857	2. 7310203	-19. 531	9. 11E-65
EPB41L5	-1. 39785	1. 9587867	-19. 523	9. 98E-65
VSIG2	-3. 55225	2. 0071368	-19. 499	1. 32E-64
SGOL1	1. 322448	1. 3849148	19. 4941	1. 39E-64
HBB	-5. 07755	3. 6610484	-19. 491	1. 44E-64
DTL	1. 943223	2. 6902054	19. 4703	1. 83E-64
GIMAP6	-2. 44746	2. 2351033	-19. 469	1. 87E-64
TM6SF1	-1. 38576	0. 9908448	-19. 451	2. 29E-64
ST6GALNAC5	-1. 66437	1. 2341847	-19. 445	2. 45E-64
IGFALS	-1. 01761	0. 3474431	-19. 443	2. 51E-64
CDC25A	1. 617293	1. 8323872	19. 4415	2. 55E-64
FLI1	-1. 8204	1. 5772174	-19. 423	3. 14E-64
FKBP4	2. 018618	5. 3185284	19. 4203	3. 25E-64
CFD	-2. 91696	3. 5619789	-19. 411	3. 62E-64
GPR87	4. 282762	4. 2979797	19. 4069	3. 79E-64
CENPI	1. 408451	1. 5636166	19. 3965	4. 28E-64
ENG	-2. 37317	4. 5797476	-19. 393	4. 48E-64
SLC6A8	3. 744899	5. 1674351	19. 3907	4. 57E-64
CD101	-1. 39819	1. 1489904	-19. 39	4. 62E-64
KNSTRN	1. 621434	2. 9892895	19. 3845	4. 91E-64
LILRA2	-1. 16412	0. 5590005	-19. 37	5. 77E-64
PLK4	1. 44958	1. 8978888	19. 3701	5. 79E-64
CYYR1	-2. 14337	2. 1090474	-19. 36	6. 49E-64
COL4A4	-1. 95502	0. 9343566	-19. 355	6. 93E-64
SEMA3B	-2. 54132	1. 6548828	-19. 35	7. 34E-64
RAE1	1. 314361	3. 343711	19. 3359	8. 58E-64
CALCRL	-2. 33645	2. 6073243	-19. 325	9. 68E-64
RECK	-1. 42483	1. 3809757	-19. 319	1. 04E-63
C16orf59	1. 802868	1. 9010621	19. 3105	1. 15E-63
KRT6A	7. 586193	8. 3771548	19. 3044	1. 23E-63
GNA14	-1. 81854	1. 0117282	-19. 264	1. 96E-63
C10orf128	-1. 80901	1. 4360257	-19. 26	2. 04E-63
UCK2	1. 787371	3. 2185475	19. 2593	2. 07E-63
RHOBTB2	-2. 57086	2. 402257	-19. 256	2. 16E-63
C1orf162	-2. 35852	2. 4122494	-19. 252	2. 24E-63
PIP5K1B	-1. 96623	1. 1923717	-19. 248	2. 35E-63
ACOX2	-1. 36638	0. 8605135	-19. 245	2. 44E-63
MCM6	1. 695786	4. 1523013	19. 2294	2. 92E-63
C16orf89	-4. 51788	2. 5251879	-19. 229	2. 94E-63
SASH1	-1. 71805	2. 0785327	-19. 226	3. 03E-63
CCT5	1. 762599	5. 8338968	19. 2089	3. 69E-63

TMEM220	-1.12913	0.915316	-19.185	4.83E-63
NR3C2	-1.67812	0.9363903	-19.137	8.39E-63
SLC6A20	-1.12401	0.3425058	-19.128	9.35E-63
SELP	-2.2374	1.4213563	-19.121	1.01E-62
MGME1	1.647015	3.9590556	19.1176	1.05E-62
KIF14	1.586084	1.5982805	19.1096	1.15E-62
ITIH5	-2.00526	0.8321594	-19.109	1.16E-62
LGI3	-2.93181	1.332731	-19.108	1.17E-62
RANBP1	1.732562	4.5401896	19.0699	1.82E-62
ACACB	-1.05021	0.8427508	-19.063	1.97E-62
PID1	-2.28938	1.8789312	-19.053	2.21E-62
DSCC1	1.721641	2.427219	19.029	2.90E-62
CHEK2	1.686805	2.7246523	19.0187	3.27E-62
STEAP4	-3.14818	1.8164761	-19.014	3.46E-62
UBL3	-1.5954	3.3950633	-19.005	3.84E-62
ASAHI	-1.82802	5.061945	-18.999	4.08E-62
RILP	-1.43089	2.2244259	-18.995	4.28E-62
ZEB2	-1.52594	1.3629503	-18.986	4.77E-62
FAM83B	2.8418	2.7033999	18.9807	5.05E-62
LHFPL3	-1.10848	0.3602466	-18.977	5.29E-62
ADARB1	-1.6431	1.5298902	-18.966	5.96E-62
TAPT1	-1.14595	1.9246881	-18.965	6.07E-62
CD97	-2.4032	3.5839538	-18.955	6.80E-62
TRPV2	-2.23105	2.6999006	-18.949	7.28E-62
CDCA7	2.398691	2.9405131	18.9392	8.12E-62
CELF2	-2.27667	2.0124497	-18.939	8.15E-62
PAFAH1B3	2.120674	4.5186408	18.9288	9.14E-62
PLA1A	-2.02458	1.2511493	-18.923	9.76E-62
MYOZ1	-1.55882	0.688556	-18.923	9.83E-62
TYMS	2.195922	3.7951397	18.9218	9.90E-62
ST8SIA6	-1.46603	0.6277447	-18.905	1.20E-61
MAGI1	-1.23526	1.2411782	-18.881	1.58E-61
FM02	-3.32293	2.3427323	-18.88	1.60E-61
MFAP4	-4.0324	4.4960953	-18.867	1.86E-61
MIS18A	1.603917	3.3328633	18.8657	1.88E-61
GMNN	1.805326	3.4779461	18.8654	1.89E-61
ARC	-1.50161	0.5417364	-18.865	1.90E-61
ATP11A	-2.05641	2.5622619	-18.843	2.44E-61
NCAPG2	1.636941	2.6715064	18.802	3.90E-61
GPER1	-1.42697	0.8345939	-18.8	4.00E-61
ACTL6A	2.166361	5.1336935	18.7994	4.02E-61
TMEM125	-3.34348	2.8146802	-18.793	4.33E-61
KIF15	1.482643	1.6994466	18.7912	4.41E-61
NR0B2	-1.93287	0.4756525	-18.753	6.81E-61
SLIT2	-2.18635	1.6899495	-18.749	7.15E-61
GPD1L	-1.83503	2.7335252	-18.744	7.57E-61
ATP8A1	-1.81189	1.1879963	-18.727	9.14E-61
LMNB1	1.901161	4.019947	18.7001	1.25E-60

CDC25C	1. 429563	1. 4599543	18. 6921	1. 37E-60
MAGI3	-1. 48541	1. 8510611	-18. 67	1. 75E-60
ESRP1	1. 605281	4. 7656822	18. 6689	1. 78E-60
BOP1	1. 94699	4. 4096916	18. 6209	3. 08E-60
ARHGAP29	-1. 84254	1. 3621474	-18. 614	3. 35E-60
LM03	-2. 53793	1. 1453363	-18. 584	4. 68E-60
VAMP2	-1. 44339	3. 841039	-18. 563	5. 97E-60
HSD17B4	-1. 16646	3. 5510852	-18. 562	6. 06E-60
SERINC1	-1. 2665	5. 7310867	-18. 558	6. 28E-60
TRAIP	1. 277465	1. 6961428	18. 5368	8. 03E-60
PLLP	-1. 67085	1. 670248	-18. 529	8. 74E-60
TRIM29	3. 954693	4. 950835	18. 4996	1. 23E-59
SKP2	2. 218234	3. 6955939	18. 4977	1. 26E-59
B4GALT2	1. 371579	4. 2947532	18. 4938	1. 31E-59
ZMYND15	-1. 28326	1. 126934	-18. 493	1. 33E-59
SAPCD2	2. 567997	2. 7105108	18. 4897	1. 37E-59
LMOD1	-2. 31232	1. 8904758	-18. 473	1. 66E-59
NCAPD2	1. 956991	4. 6771108	18. 464	1. 84E-59
C1orf116	-2. 88501	3. 0488099	-18. 463	1. 87E-59
PRDM16	-1. 19845	0. 5296369	-18. 447	2. 24E-59
PPIF	1. 836993	5. 3587083	18. 4436	2. 32E-59
HELLS	1. 528219	1. 7879069	18. 4385	2. 46E-59
PRPF19	1. 173695	5. 9176656	18. 4126	3. 30E-59
HPCAL1	-1. 57042	3. 1070507	-18. 409	3. 43E-59
RHOV	3. 541973	4. 3888203	18. 3801	4. 78E-59
SRPK1	1. 34334	3. 7071479	18. 3351	7. 98E-59
TSPAN12	-2. 51592	2. 327498	-18. 329	8. 53E-59
ABCA3	-4. 16551	3. 0902844	-18. 328	8. 66E-59
TBRG4	1. 356289	3. 8648589	18. 3216	9. 30E-59
ASUN	1. 471494	3. 6264502	18. 3188	9. 60E-59
DCAF13	1. 270256	2. 9387068	18. 2922	1. 30E-58
SNRPA1	1. 31228	3. 6372332	18. 2817	1. 46E-58
STX12	-1. 1762	3. 8916788	-18. 277	1. 54E-58
SPATS2	1. 133245	2. 7444168	18. 2437	2. 25E-58
UPK3B	-3. 6859	2. 1809823	-18. 205	3. 51E-58
FBP1	-3. 51562	3. 9871396	-18. 203	3. 57E-58
C12orf49	-1. 23779	3. 0912334	-18. 201	3. 67E-58
IGSF9	2. 974075	3. 2121493	18. 1927	4. 02E-58
MS4A7	-2. 66604	2. 5376663	-18. 186	4. 35E-58
WDR75	1. 192438	3. 5546495	18. 1732	5. 01E-58
MSR1	-2. 83393	2. 4253145	-18. 172	5. 11E-58
PSMG3	1. 555626	4. 4209429	18. 1506	6. 48E-58
POLR2H	1. 867943	4. 7627383	18. 1506	6. 48E-58
MYOC	-1. 35984	0. 2308394	-18. 128	8. 34E-58
TMEM150B	-1. 74086	1. 1898113	-18. 115	9. 72E-58
PKP3	2. 191879	4. 847903	18. 1076	1. 05E-57
SPNS2	-2. 09465	1. 9371394	-18. 097	1. 19E-57
PYCR1	2. 576785	4. 4462431	18. 0966	1. 20E-57

H2AFX	1. 931913	5. 181317	18. 0833	1. 39E-57
POC1A	1. 322574	2. 4261486	18. 0765	1. 50E-57
ACSS3	-1. 13899	0. 6072189	-18. 07	1. 61E-57
ALOX5AP	-3. 00463	3. 6718002	-18. 061	1. 78E-57
CITED2	-2. 37909	4. 248057	-18. 06	1. 81E-57
NUDT1	1. 675457	3. 6574888	18. 0559	1. 90E-57
ALG3	2. 007677	4. 9166675	18. 0521	1. 98E-57
ADAMTSL3	-1. 53602	0. 7285172	-18. 048	2. 07E-57
CAMP	-1. 60698	0. 6096772	-18. 042	2. 21E-57
KIF22	1. 519051	3. 8956132	18. 0388	2. 30E-57
EPN3	2. 188778	2. 5107845	18. 0337	2. 44E-57
CNRIP1	-1. 46913	1. 4259367	-18. 032	2. 48E-57
PPP1R14A	-2. 19645	2. 0291699	-18. 026	2. 66E-57
LMNB2	1. 962621	4. 7232806	18. 0227	2. 76E-57
FBXO45	1. 761967	3. 310239	18. 0058	3. 34E-57
TNFSF12	-1. 8901	3. 2197688	-18. 005	3. 37E-57
SMIM6	-1. 39181	0. 524109	-18. 002	3. 47E-57
NDC1	1. 356715	3. 3336882	17. 9867	4. 15E-57
SLC25A39	1. 333515	5. 7141132	17. 9821	4. 37E-57
TMEM204	-2. 04726	2. 9165471	-17. 973	4. 86E-57
DTYMK	1. 49947	3. 9204359	17. 9612	5. 53E-57
RFC5	1. 495501	3. 2614983	17. 9449	6. 66E-57
RAB37	-1. 15379	0. 7799265	-17. 944	6. 72E-57
SLC11A1	-2. 06304	1. 9464238	-17. 94	7. 06E-57
CENPN	1. 608603	2. 6372287	17. 9381	7. 18E-57
FNIP2	-1. 45106	1. 9060186	-17. 938	7. 20E-57
FAT4	-1. 24248	0. 6913764	-17. 931	7. 83E-57
ERCC6L	1. 39611	1. 4365721	17. 9163	9. 20E-57
SPRY4	-1. 99008	2. 6771923	-17. 914	9. 44E-57
KNTC1	1. 460329	2. 0729235	17. 9119	9. 67E-57
CD300LF	-2. 14544	1. 7783596	-17. 906	1. 04E-56
EIF4E3	-1. 24361	1. 4308497	-17. 905	1. 05E-56
HDGF	1. 288657	6. 8361623	17. 8888	1. 26E-56
CCDC58	1. 731219	3. 6755783	17. 8794	1. 39E-56
ALG1L	3. 125609	3. 6634369	17. 8784	1. 41E-56
SLC7A5	3. 204391	5. 5167163	17. 8712	1. 53E-56
ECE2	2. 08884	2. 4494871	17. 8559	1. 82E-56
TSPAN4	-1. 93266	2. 526856	-17. 852	1. 89E-56
NEXN	-1. 69226	1. 5186419	-17. 849	1. 96E-56
COX7A1	-2. 03235	2. 2537964	-17. 849	1. 97E-56
PITX1	3. 864353	3. 7895457	17. 8475	2. 00E-56
DNAJC9	1. 123307	2. 7349114	17. 8458	2. 04E-56
DBF4	1. 465261	2. 4117174	17. 8421	2. 13E-56
CCNE1	2. 154907	2. 4499696	17. 8403	2. 17E-56
CYBRD1	-2. 3581	4. 1877457	-17. 833	2. 35E-56
CABLES1	-1. 80121	1. 5332458	-17. 823	2. 62E-56
FGR	-2. 29192	2. 559622	-17. 818	2. 78E-56
NCMAP	-1. 49374	0. 8710278	-17. 81	3. 04E-56

BMP5	-2.20485	1.0012912	-17.81	3.06E-56
GPR4	-1.40362	1.584982	-17.808	3.11E-56
AGTR2	-2.51431	0.8294824	-17.802	3.33E-56
CCDC69	-2.27401	2.6702509	-17.802	3.35E-56
CCDC34	1.685305	2.512936	17.7976	3.51E-56
TREM1	-2.69957	2.0301079	-17.794	3.67E-56
MT1M	-2.72918	1.6950102	-17.79	3.84E-56
OCLN	-1.47834	1.2710199	-17.784	4.11E-56
UTRN	-1.7886	2.6231146	-17.764	5.14E-56
GJB5	3.720163	3.8892252	17.7613	5.29E-56
ALOX5	-2.7451	2.9964189	-17.757	5.56E-56
MACROD2	-1.62526	0.8234736	-17.755	5.66E-56
SFXN1	1.60913	3.1887444	17.7516	5.90E-56
SFTA2	-5.17072	2.919949	-17.745	6.34E-56
XRCC2	1.575919	1.6609984	17.745	6.36E-56
KAT2B	-1.35671	1.9618115	-17.732	7.39E-56
MYO19	1.386281	2.4723948	17.7223	8.21E-56
DOK2	-2.3152	2.5422105	-17.722	8.28E-56
RXFP1	-1.13214	0.3856716	-17.719	8.56E-56
ALDH1A2	-1.34046	0.5535528	-17.706	9.88E-56
PNPLA6	-1.36052	3.3843323	-17.704	1.00E-55
MFNG	-1.96558	2.1758609	-17.703	1.02E-55
ITGA1	-1.51013	1.743177	-17.701	1.05E-55
ZFP64	1.273486	2.5779363	17.6966	1.10E-55
TUBG1	1.359013	4.4958839	17.6906	1.17E-55
CENPE	1.350637	1.5311677	17.6855	1.24E-55
GIPC3	-1.08018	0.8899555	-17.672	1.45E-55
CYSTM1	-1.43045	4.1774715	-17.662	1.63E-55
LAD1	2.484721	5.9625886	17.6599	1.66E-55
CHAF1B	1.501134	2.1386603	17.6355	2.18E-55
ADPRH	-1.53449	1.9423509	-17.633	2.24E-55
SULT1A2	-1.47781	0.6961647	-17.614	2.77E-55
S1PR4	-1.95767	1.6394682	-17.6	3.27E-55
TM4SF18	-1.31507	0.9443519	-17.58	4.07E-55
YWHAZ	1.279885	7.1551503	17.5617	5.01E-55
ARHGAP18	-1.84658	2.8248439	-17.552	5.60E-55
GADD45B	-2.41894	4.2306049	-17.539	6.47E-55
MAP3K3	-1.19345	2.672697	-17.536	6.69E-55
TMEM177	1.29305	2.461472	17.5198	8.02E-55
CYB5A	-2.04603	3.0116499	-17.494	1.07E-54
BYSL	1.399707	3.9175986	17.4899	1.12E-54
CHI3L2	-2.81338	1.6547938	-17.484	1.20E-54
LHFP	-1.98779	3.4327192	-17.481	1.24E-54
TTLL12	1.999642	4.687626	17.4632	1.52E-54
IRF6	2.543677	5.5845342	17.457	1.62E-54
BRIX1	1.588906	3.6746727	17.4559	1.64E-54
INCENP	1.528201	3.1091751	17.4489	1.78E-54
TMEM243	-1.36148	2.6262541	-17.443	1.90E-54

FANCD2	1. 227097	1. 8668742	17. 4397	1. 97E-54
SCN4B	-1. 80546	1. 1447749	-17. 429	2. 23E-54
MBIP	-1. 56248	3. 0959484	-17. 412	2. 69E-54
DLL4	-1. 59772	1. 8755926	-17. 411	2. 73E-54
HN1	1. 617717	5. 3189223	17. 4058	2. 88E-54
SH3BP5	-1. 62026	1. 56913	-17. 404	2. 95E-54
TNS4	3. 695961	4. 0286791	17. 3926	3. 34E-54
CORO2B	-1. 38846	0. 811573	-17. 389	3. 48E-54
CRTAC1	-3. 48305	2. 0442176	-17. 384	3. 67E-54
GJB3	3. 361766	3. 6532805	17. 3745	4. 10E-54
S100A4	-2. 37967	6. 2241972	-17. 373	4. 18E-54
LILRA5	-1. 97393	1. 5520328	-17. 358	4. 93E-54
AK4	1. 992909	2. 563491	17. 3482	5. 50E-54
ABLIM3	-1. 78001	1. 315432	-17. 34	6. 04E-54
SCTR	-2. 01966	0. 9976095	-17. 332	6. 57E-54
SOD3	-2. 50541	3. 0500457	-17. 326	7. 04E-54
PDE5A	-1. 47923	1. 4530303	-17. 323	7. 30E-54
MTFR2	1. 40373	1. 8664347	17. 3163	7. 87E-54
CFTR	-1. 73155	0. 8417745	-17. 309	8. 54E-54
PPAT	1. 53189	2. 4320945	17. 3028	9. 15E-54
BTBD9	-1. 24927	1. 6870567	-17. 3	9. 42E-54
RNASE1	-3. 12419	6. 1816194	-17. 299	9. 54E-54
RUVBL1	1. 433173	3. 769924	17. 2869	1. 09E-53
TMEM69	1. 122255	3. 8002712	17. 2816	1. 16E-53
TACC3	1. 647304	3. 324069	17. 2671	1. 36E-53
TARS	1. 493196	4. 7351637	17. 2661	1. 38E-53
CENPO	1. 169953	2. 1408529	17. 2651	1. 40E-53
BLM	1. 351061	1. 666435	17. 2573	1. 52E-53
PARPBP	1. 514046	1. 8086292	17. 2432	1. 78E-53
CD52	-3. 25202	4. 5484024	-17. 242	1. 80E-53
PLA2G4F	-2. 26926	1. 6836545	-17. 242	1. 80E-53
GGH	2. 127429	3. 9065683	17. 2382	1. 88E-53
HPRT1	1. 63532	5. 0492692	17. 2347	1. 96E-53
PKM	1. 472735	7. 6969165	17. 2307	2. 05E-53
SRSF9	1. 013521	4. 8757736	17. 2158	2. 42E-53
RANGAP1	1. 463142	5. 0742271	17. 2055	2. 72E-53
RPP40	1. 386118	2. 3566711	17. 2015	2. 84E-53
KRT17	6. 019522	8. 4431673	17. 1923	3. 15E-53
CRIP1	-1. 18027	0. 7337185	-17. 176	3. 79E-53
TBX5	-1. 56009	1. 3272401	-17. 173	3. 91E-53
LAMP3	-3. 14061	4. 4285227	-17. 171	4. 01E-53
ELTD1	-1. 68243	2. 1115137	-17. 166	4. 24E-53
C1orf112	1. 193607	1. 6702002	17. 1612	4. 46E-53
DCUN1D5	1. 52952	4. 5089554	17. 1572	4. 66E-53
POLQ	1. 432693	1. 4236363	17. 1564	4. 71E-53
NUP155	1. 480635	3. 1455344	17. 1555	4. 75E-53
HOPX	-2. 90456	2. 7564129	-17. 145	5. 35E-53
RFC2	1. 300093	4. 4096797	17. 1383	5. 76E-53

TUBB	1. 344517	8. 1400537	17. 1379	5. 78E-53
FERMT2	-1. 77428	2. 2231874	-17. 135	6. 00E-53
CCDC86	1. 428003	4. 201122	17. 1338	6. 06E-53
KRT5	6. 78383	8. 5839946	17. 1319	6. 19E-53
KAL1	-2. 49983	2. 1394402	-17. 121	6. 95E-53
IGIP	-1. 13272	1. 5111084	-17. 115	7. 46E-53
ADCY9	-1. 33373	2. 0298586	-17. 114	7. 56E-53
BZW2	1. 470888	4. 8539193	17. 0883	1. 01E-52
EME1	1. 536728	1. 675357	17. 0841	1. 05E-52
MMP12	4. 120883	4. 5380724	17. 0778	1. 13E-52
ALDH2	-2. 11237	3. 5811115	-17. 076	1. 15E-52
DOCK11	-1. 66334	1. 7815305	-17. 071	1. 23E-52
RFWD3	1. 306726	3. 2645479	17. 0616	1. 35E-52
CEACAM21	-1. 35933	0. 9156682	-17. 054	1. 47E-52
PGAM5	1. 375887	4. 2353801	17. 0421	1. 68E-52
RBPMS	-1. 62033	2. 2050598	-17. 032	1. 88E-52
GMPS	1. 572356	3. 9849028	17. 0104	2. 40E-52
ITPR1	-1. 27986	1. 5877883	-17. 005	2. 54E-52
DNAJB11	1. 558716	4. 5975312	17. 004	2. 57E-52
VSIG4	-3. 35385	3. 6226862	-16. 996	2. 83E-52
WDR72	2. 511152	2. 5180811	16. 9917	2. 95E-52
CADM1	-2. 49844	2. 0862977	-16. 991	2. 97E-52
TICRR	1. 558617	1. 5634711	16. 9869	3. 12E-52
SLC27A3	-1. 3199	2. 6464671	-16. 984	3. 23E-52
ATP13A4	-2. 49922	1. 5080825	-16. 981	3. 33E-52
MTIF2	1. 163376	3. 8601177	16. 9682	3. 84E-52
EFNA3	2. 09537	2. 3474112	16. 9586	4. 27E-52
CBX7	-1. 44275	2. 121455	-16. 958	4. 29E-52
AFAP1L1	-1. 5474	1. 8267376	-16. 948	4. 78E-52
ADAMTSL4	-2. 18139	1. 8624651	-16. 942	5. 12E-52
ARHGEF10	-1. 36645	1. 5219367	-16. 939	5. 28E-52
MCM8	1. 455375	2. 232791	16. 9348	5. 57E-52
CALCOC01	-1. 43593	2. 9367152	-16. 931	5. 78E-52
PPM1G	1. 092306	5. 4279883	16. 9215	6. 45E-52
SLC16A1	2. 363018	4. 0359813	16. 921	6. 49E-52
NOL10	1. 069409	3. 6496864	16. 919	6. 63E-52
ACKR1	-3. 14319	2. 1132209	-16. 903	7. 90E-52
KIAA1324L	-1. 52054	1. 8711912	-16. 903	7. 91E-52
ARHGEF6	-1. 7718	1. 8858503	-16. 898	8. 39E-52
FYC01	-1. 2397	2. 332852	-16. 894	8. 74E-52
TCF19	1. 55827	3. 4483208	16. 894	8. 75E-52
CISH	-1. 55992	2. 134808	-16. 89	9. 12E-52
CCDC173	-1. 00208	0. 4086373	-16. 886	9. 60E-52
RAB27A	-1. 44722	2. 782631	-16. 884	9. 75E-52
GYPC	-2. 17232	2. 4845338	-16. 871	1. 13E-51
RILPL2	-1. 13794	2. 3338606	-16. 853	1. 39E-51
PARD6B	-1. 33432	1. 6437579	-16. 845	1. 51E-51
CENPL	1. 176363	1. 7928005	16. 8401	1. 59E-51

KLF6	-1. 99813	4. 5311543	-16. 839	1. 62E-51
CLEC12A	-1. 64241	1. 050378	-16. 83	1. 79E-51
HMGB3	2. 25658	4. 631006	16. 8264	1. 86E-51
GRASP	-2. 06857	2. 0215161	-16. 825	1. 89E-51
HSPD1	1. 56918	6. 4732617	16. 82	1. 99E-51
MLPH	-2. 78477	1. 9959838	-16. 819	2. 02E-51
GIMAP7	-2. 4479	2. 8395214	-16. 799	2. 51E-51
ITLN1	-2. 09504	0. 4779526	-16. 799	2. 52E-51
COQ3	1. 403472	3. 0846007	16. 7924	2. 71E-51
PTGIR	-1. 32313	1. 1486706	-16. 792	2. 71E-51
ARNTL2	2. 440087	3. 3170156	16. 7921	2. 72E-51
SNRPB	1. 445032	7. 5270059	16. 7842	2. 97E-51
C5AR1	-2. 29605	3. 0565054	-16. 779	3. 14E-51
LATS2	-1. 32675	2. 2819278	-16. 777	3. 20E-51
HSPE1	1. 631471	5. 7015739	16. 7746	3. 30E-51
TP63	4. 403168	5. 1176141	16. 7719	3. 40E-51
DSG2	2. 107261	5. 5079679	16. 7623	3. 78E-51
MTX2	1. 133894	4. 6623953	16. 7611	3. 83E-51
UNC13B	-1. 89772	3. 0873953	-16. 756	4. 05E-51
CTHRC1	2. 919308	4. 8099286	16. 7497	4. 35E-51
E2F7	1. 698502	1. 7098405	16. 7483	4. 42E-51
NKX2-1	-3. 49732	1. 9342783	-16. 736	5. 09E-51
RASSF3	-1. 4279	3. 2767221	-16. 731	5. 35E-51
AHCY	1. 647295	6. 0528632	16. 7237	5. 80E-51
IFT57	-1. 57097	3. 8102062	-16. 717	6. 25E-51
SCIMP	-1. 61785	1. 1722595	-16. 714	6. 47E-51
SLC16A4	-1. 86532	1. 4684475	-16. 707	6. 95E-51
RBP4	-2. 81265	1. 4078248	-16. 702	7. 41E-51
PLEKHH2	-1. 50736	1. 163998	-16. 696	7. 91E-51
ALDOA	1. 418553	7. 9487067	16. 6952	7. 95E-51
GSTM5	-1. 29345	0. 5941187	-16. 695	8. 01E-51
EIF3B	1. 207404	4. 9786493	16. 6802	9. 39E-51
FOSB	-3. 91365	3. 0346714	-16. 663	1. 13E-50
FAM220A	1. 211386	3. 7326328	16. 6631	1. 14E-50
FIGNL1	1. 437516	2. 4562418	16. 6613	1. 16E-50
PSMD2	1. 699966	6. 4728717	16. 6585	1. 19E-50
SUV39H2	1. 17634	2. 2026156	16. 6558	1. 23E-50
REPS2	-1. 05219	1. 0744094	-16. 652	1. 28E-50
NRGN	-2. 98146	2. 9124587	-16. 642	1. 43E-50
TFAP4	1. 144279	1. 8283629	16. 6376	1. 51E-50
EXOSC5	1. 581285	4. 1622545	16. 6337	1. 57E-50
DUSP1	-2. 80552	6. 1984623	-16. 632	1. 60E-50
YDJC	1. 775268	4. 1551534	16. 6292	1. 65E-50
HN1L	1. 204172	5. 0563895	16. 6253	1. 73E-50
KNDC1	-1. 23312	0. 5611728	-16. 61	2. 05E-50
GJA4	-1. 83328	2. 244364	-16. 604	2. 18E-50
C5	-1. 54802	1. 2246187	-16. 596	2. 38E-50
ITGA9	-1. 67357	1. 409969	-16. 586	2. 65E-50

LYPD3	4. 168825	4. 7475288	16. 5857	2. 67E-50
PUS7	1. 47873	3. 0831994	16. 5759	2. 98E-50
TMEM163	-1. 64719	1. 1181904	-16. 57	3. 17E-50
POP7	1. 347412	5. 083391	16. 5698	3. 19E-50
C7	-3. 72287	2. 6956041	-16. 567	3. 29E-50
MCM5	1. 496779	3. 9553002	16. 5659	3. 33E-50
MIF	2. 066091	5. 7747289	16. 5421	4. 33E-50
CXCL16	-1. 79169	4. 8975853	-16. 539	4. 49E-50
XXYLT1	1. 899814	3. 4415742	16. 538	4. 53E-50
FAM167A	-1. 96738	1. 1407153	-16. 528	5. 07E-50
DDX39A	1. 522488	4. 6022239	16. 5241	5. 28E-50
CASKIN2	-1. 44324	2. 9245399	-16. 508	6. 28E-50
ILF2	1. 256225	6. 8048824	16. 507	6. 38E-50
EFR3B	-1. 00517	0. 4911301	-16. 498	7. 01E-50
AKAP13	-1. 44003	2. 9598033	-16. 494	7. 33E-50
DSC3	4. 384058	4. 527472	16. 4943	7. 34E-50
JADE1	-1. 15466	1. 7104034	-16. 494	7. 36E-50
RARA	-1. 34991	3. 1292573	-16. 49	7. 73E-50
C10orf32	-1. 21248	2. 6615711	-16. 489	7. 81E-50
BRIP1	1. 25492	1. 36038	16. 4784	8. 74E-50
FGD4	-1. 08507	1. 3567536	-16. 471	9. 50E-50
SNRPE	1. 351669	5. 2191603	16. 4588	1. 08E-49
E2F2	1. 359658	1. 6042691	16. 4559	1. 12E-49
PKP1	5. 040338	5. 9589273	16. 4476	1. 23E-49
PTGFRN	2. 115985	4. 9221503	16. 4269	1. 54E-49
FAM136A	1. 275131	4. 0589411	16. 4207	1. 65E-49
DNA2	1. 303431	1. 686002	16. 4161	1. 74E-49
PDIA4	1. 577705	6. 8903488	16. 4141	1. 78E-49
FAM167B	-1. 41509	2. 1611326	-16. 402	2. 04E-49
SIDT2	-1. 20863	2. 7119602	-16. 395	2. 20E-49
SPTBN2	1. 98445	2. 781417	16. 3911	2. 29E-49
MRPL47	1. 663541	5. 4081601	16. 3861	2. 42E-49
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HLA-E	-1. 70346	7. 857537	-16. 38	2. 57E-49
FARSB	1. 146513	4. 147861	16. 378	2. 64E-49
TONSL	1. 693373	2. 3250216	16. 3731	2. 79E-49
MTURN	-1. 59301	2. 0865655	-16. 37	2. 88E-49
DSG3	5. 023111	4. 8133401	16. 3683	2. 94E-49
GPRC5A	-3. 46106	4. 0613387	-16. 365	3. 03E-49
RPL39L	2. 92143	4. 4753311	16. 3598	3. 23E-49
MGLL	-2. 31006	2. 8499629	-16. 353	3. 48E-49
CCT7	1. 094139	6. 3843704	16. 3461	3. 75E-49
CPM	-2. 70189	2. 5487517	-16. 346	3. 77E-49
HDAC1	1. 22145	5. 5004411	16. 3412	3. 96E-49
TSKU	2. 065583	4. 6144475	16. 3329	4. 34E-49
PRIM2	1. 213278	2. 4256494	16. 3272	4. 62E-49
ALOX15B	-2. 94828	2. 2633373	-16. 318	5. 11E-49
ANKRD29	-1. 92802	1. 5613796	-16. 314	5. 35E-49

TOMM40	1. 368754	4. 6431602	16. 3137	5. 36E-49
XPOT	1. 505478	4. 5019033	16. 3073	5. 75E-49
C10orf107	-1. 49201	0. 5602183	-16. 306	5. 84E-49
E2F8	1. 297788	1. 4481874	16. 3053	5. 88E-49
DIXDC1	-1. 08233	1. 2948485	-16. 304	5. 96E-49
NOP2	1. 50007	3. 9259004	16. 304	5. 97E-49
ZEB1	-1. 3769	1. 7188493	-16. 302	6. 10E-49
MRPL36	1. 512087	4. 3327623	16. 2975	6. 40E-49
TRAF7	1. 160264	4. 9155156	16. 2936	6. 69E-49
TMPRSS4	3. 649304	3. 8600721	16. 2897	6. 98E-49
ANG	-1. 53517	1. 9865574	-16. 283	7. 47E-49
PSMD14	1. 167289	3. 7092024	16. 2758	8. 13E-49
GYLTL1B	2. 486445	3. 8233398	16. 2687	8. 79E-49
FANCE	1. 667325	3. 3187234	16. 259	9. 78E-49
ANKRD44	-1. 14591	1. 1236833	-16. 248	1. 10E-48
POLE2	1. 421507	1. 8273054	16. 2407	1. 20E-48
OTUD1	-1. 51128	3. 0485901	-16. 24	1. 20E-48
KLF9	-2. 01307	3. 0687535	-16. 24	1. 21E-48
HGF	-1. 41279	0. 8117973	-16. 238	1. 23E-48
RAN	1. 186509	6. 1684181	16. 2369	1. 25E-48
SIAH2	1. 82335	4. 895393	16. 2301	1. 34E-48
RSRC1	1. 328391	3. 1753502	16. 2279	1. 38E-48
PRKCZ	-1. 20655	2. 1338349	-16. 219	1. 52E-48
LRP2	-1. 19543	0. 4358131	-16. 215	1. 59E-48
EMR1	-1. 47318	0. 6782534	-16. 214	1. 60E-48
PTPRN2	-1. 59187	1. 1162288	-16. 21	1. 68E-48
COL7A1	3. 711215	3. 9030007	16. 2	1. 87E-48
TPPP3	-2. 99675	3. 1068016	-16. 2	1. 87E-48
MRPL37	1. 087656	5. 0101108	16. 1976	1. 92E-48
WDR53	1. 421106	3. 4167001	16. 1943	1. 99E-48
APBB1	-1. 61703	1. 8988519	-16. 169	2. 62E-48
WWC1	-1. 32989	2. 0380513	-16. 162	2. 83E-48
HPGD	-2. 75326	1. 9877425	-16. 156	3. 03E-48
SNX22	-1. 15243	0. 883497	-16. 149	3. 28E-48
RCCD1	1. 329079	2. 198444	16. 1427	3. 50E-48
CPSF3	1. 072446	3. 9750098	16. 1415	3. 55E-48
POLD2	1. 303382	5. 0928355	16. 1361	3. 76E-48
COL6A5	-1. 01192	0. 4631507	-16. 132	3. 92E-48
RHN01	1. 386794	4. 1766112	16. 1322	3. 93E-48
CXCL2	-3. 63787	3. 1224939	-16. 132	3. 94E-48
CSF3R	-2. 26715	1. 8995408	-16. 129	4. 07E-48
R3HDM1	1. 033742	2. 7135079	16. 1241	4. 29E-48
TMPRSS2	-2. 84281	2. 1437525	-16. 114	4. 77E-48
NINJ2	-1. 88595	1. 9790607	-16. 111	4. 94E-48
C10orf131	1. 021258	2. 0783181	16. 1102	5. 00E-48
DNALI1	-2. 06503	1. 2319553	-16. 102	5. 46E-48
MZT2A	1. 408052	3. 0728956	16. 1019	5. 48E-48
MEF2C	-1. 36553	1. 3485523	-16. 099	5. 66E-48

KIF1C	-1.3547	3.9372309	-16.092	6.12E-48
TNFRSF10C	-1.28927	0.9023313	-16.091	6.15E-48
WDR43	1.172505	4.2013065	16.0815	6.85E-48
C6	-1.23238	0.3604489	-16.079	7.01E-48
TRAP1	1.241767	3.7778977	16.0774	7.16E-48
ESC02	1.070163	1.123962	16.0694	7.81E-48
PXMP4	-1.35546	2.30423	-16.063	8.38E-48
THOC3	1.655095	2.6206933	16.0617	8.50E-48
XP01	1.172217	4.4548696	16.05	9.66E-48
ARHGEF19	1.878862	3.6532089	16.0419	1.06E-47
PAG1	-1.33656	1.478814	-16.037	1.12E-47
LILRB3	-1.17483	0.9947432	-16.034	1.15E-47
NTN4	-2.32902	2.9573798	-16.026	1.26E-47
GINS3	1.224922	1.8947298	16.0199	1.34E-47
MARS	1.015457	4.3898234	16.0196	1.35E-47
KIAA1683	-1.14829	0.6128896	-16.014	1.43E-47
BRI3BP	1.325095	2.8195212	16.0142	1.43E-47
APOBR	-1.82724	2.0235415	-16.013	1.44E-47
GSG2	1.187254	1.420241	16.0124	1.46E-47
RGS5	-1.8343	2.2601677	-16.009	1.51E-47
NOP56	1.358509	4.784925	16.0053	1.57E-47
SCEL	-3.02631	2.149527	-16.004	1.59E-47
HSD17B11	-1.78636	4.0710473	-16.004	1.61E-47
GRHL2	1.533012	3.7706743	16.0002	1.67E-47
NUP37	1.130662	3.1438906	15.9796	2.08E-47
CLIC3	-2.86178	2.7738504	-15.977	2.15E-47
XP05	1.261391	3.3640423	15.9766	2.15E-47
GPI	1.865013	6.0419578	15.9698	2.32E-47
PTPLAD2	-1.30162	1.4374954	-15.969	2.33E-47
TRAK2	-1.17012	2.6953114	-15.967	2.38E-47
PRICKLE2	-1.19104	1.263215	-15.965	2.45E-47
CHAF1A	1.721427	3.1264756	15.9634	2.49E-47
OLA1	1.290788	4.1433091	15.9507	2.86E-47
KIF18A	1.281421	1.798706	15.9488	2.92E-47
MRT04	1.165664	4.3269479	15.945	3.04E-47
STIP1	1.112756	5.5238273	15.9398	3.22E-47
EIF4EBP1	2.555801	6.1072684	15.9389	3.25E-47
MTHFD2	1.868266	4.5912101	15.9209	3.96E-47
FSCN1	2.534954	6.3516893	15.9191	4.03E-47
DONSON	1.275583	2.5194355	15.897	5.13E-47
MVB12B	-1.43506	1.7073045	-15.895	5.25E-47
P3H4	1.823786	3.5054268	15.8906	5.50E-47
KCTD12	-1.92867	3.6933624	-15.89	5.53E-47
TFG	1.213427	5.0539668	15.8772	6.37E-47
EPT1	1.684926	3.4218901	15.8744	6.57E-47
CMSS1	1.448938	3.1731479	15.8715	6.77E-47
SFTP4	-5.38522	4.256863	-15.858	7.83E-47
DDO	-1.25737	0.8244603	-15.854	8.16E-47

NIFK	1.	190146	4.	4307595	15.	8519	8.	38E-47
GPT2	1.	914256	2.	7338912	15.	8483	8.	72E-47
TPBG	1.	784331	3.	1918327	15.	8401	9.	54E-47
GPRIN3	-1.	15754	0.	9634443	-15.	839	9.	66E-47
SGOL2	1.	188408	1.	7339468	15.	8114	1.	30E-46
C2	-2.	10788	2.	8488545	-15.	808	1.	35E-46
CSTF2	1.	297222	3.	6830414	15.	8038	1.	42E-46
NR2F1	-1.	80086	2.	1416695	-15.	792	1.	61E-46
FGF18	-1.	08177	0.	498466	-15.	792	1.	61E-46
GJB2	4.	545829	5.	1811637	15.	778	1.	87E-46
PPAP2C	1.	961662	3.	2067046	15.	7761	1.	91E-46
SLC35A1	-1.	20226	2.	5284477	-15.	763	2.	19E-46
NXPH4	3.	242636	3.	1796814	15.	7634	2.	20E-46
MYADM	-2.	65475	4.	7503766	-15.	763	2.	20E-46
TLR3	-1.	20821	1.	0920363	-15.	762	2.	24E-46
BMPR2	-1.	23565	3.	1235984	-15.	759	2.	30E-46
MRPL30	1.	03959	3.	7745875	15.	7581	2.	33E-46
APOLD1	-1.	56602	1.	7761123	-15.	748	2.	60E-46
NELFCD	1.	16684	4.	2234069	15.	7454	2.	67E-46
NR4A3	-2.	14872	1.	2563525	-15.	741	2.	81E-46
ATP1B2	-1.	05883	0.	6186763	-15.	74	2.	84E-46
NABP2	1.	044173	4.	145579	15.	7358	2.	96E-46
ZNF106	-1.	15644	2.	7583143	-15.	733	3.	05E-46
MRPL12	1.	638641	4.	6765069	15.	7331	3.	05E-46
TIMM8A	1.	153068	2.	2711328	15.	7324	3.	08E-46
NIPSNAP1	1.	514137	5.	0423712	15.	7314	3.	11E-46
COL13A1	-1.	02747	0.	7908881	-15.	728	3.	24E-46
SPDL1	1.	017114	1.	9140007	15.	7224	3.	43E-46
CFLAR	-1.	22547	2.	6419208	-15.	721	3.	50E-46
USP5	1.	096616	5.	2688953	15.	7202	3.	51E-46
CCT6A	1.	527583	6.	1533635	15.	7193	3.	54E-46
CD81	-1.	06223	5.	959527	-15.	709	3.	97E-46
ENPP4	-1.	9687	2.	0460809	-15.	709	3.	98E-46
ARHGEF3	-1.	14861	2.	5027347	-15.	708	3.	99E-46
TFB2M	1.	229342	3.	7698008	15.	7078	4.	01E-46
PRICKLE3	1.	303505	2.	9785339	15.	7035	4.	21E-46
GID8	1.	037163	4.	6505197	15.	699	4.	42E-46
OLFML1	-1.	69416	1.	7422921	-15.	696	4.	55E-46
B3GNT7	-2.	1869	2.	3396354	-15.	689	4.	94E-46
F2RL3	-1.	42707	1.	0355929	-15.	688	4.	96E-46
CKAP4	1.	510598	5.	8517791	15.	687	5.	03E-46
CBX3	1.	149181	5.	4075765	15.	6799	5.	44E-46
NAA50	1.	340765	5.	1457402	15.	6796	5.	45E-46
SASS6	1.	019816	1.	7376546	15.	679	5.	49E-46
LMCD1	-1.	42255	2.	1678716	-15.	678	5.	52E-46
SMUG1	1.	013723	2.	9498229	15.	6638	6.	47E-46
C10orf2	1.	216994	2.	6354875	15.	6588	6.	83E-46
MFSD2A	-2.	12065	2.	9027043	-15.	658	6.	90E-46

SH3D19	-1.25461	2.9463857	-15.65	7.49E-46
SHROOM3	-1.56186	1.7983354	-15.646	7.88E-46
MSRA	-1.09913	1.3940859	-15.636	8.78E-46
TDG	1.035701	3.0480279	15.6315	9.19E-46
LILRA6	-1.08808	0.8130775	-15.63	9.36E-46
SNRPA	1.022237	4.8912227	15.6258	9.76E-46
CD83	-1.92916	3.4342329	-15.624	9.95E-46
DDAH1	-1.92362	2.4117694	-15.615	1.10E-45
PAPSS2	-2.4858	3.4109294	-15.607	1.20E-45
PFKP	1.719076	4.8405737	15.6058	1.21E-45
METTL1	1.171068	3.3626915	15.5956	1.36E-45
SLC02A1	-2.69794	2.68596	-15.59	1.44E-45
H2AFZ	1.432393	6.5951142	15.5808	1.59E-45
BTK	-1.67023	1.5954021	-15.574	1.72E-45
TOPBP1	1.449659	3.6060384	15.5737	1.72E-45
MMP11	3.466125	3.6770518	15.5712	1.76E-45
S100A2	5.428683	6.9582751	15.5676	1.83E-45
JUP	2.042485	7.3488418	15.5653	1.88E-45
GSS	1.191202	5.2493491	15.5635	1.92E-45
RASGEF1B	-1.36017	1.5118995	-15.55	2.22E-45
PSME4	1.035208	3.813128	15.5496	2.23E-45
SYNPO	-2.05422	3.3248395	-15.547	2.29E-45
B4GALNT4	2.602158	2.5417746	15.5414	2.43E-45
CDK4	1.442372	5.225062	15.5394	2.49E-45
WDR12	1.034952	2.3474324	15.5353	2.60E-45
SRPRB	1.341242	4.7302248	15.5348	2.61E-45
CDH3	3.070105	4.7359816	15.5307	2.73E-45
NEDD9	-2.1345	3.3088283	-15.526	2.89E-45
PSRC1	1.382258	2.2870863	15.5234	2.96E-45
CARD16	-1.35672	2.3608179	-15.513	3.29E-45
C11orf84	1.3215	3.7245679	15.5121	3.34E-45
KRT16	5.790174	6.0241142	15.4974	3.92E-45
C9orf152	-1.77483	0.9086675	-15.462	5.71E-45
PCDH17	-1.52373	1.6197049	-15.457	6.06E-45
DCSTAMP	-1.10795	0.5428448	-15.45	6.54E-45
SELPLG	-2.25975	3.3925773	-15.445	6.90E-45
CENPK	1.242241	1.5688787	15.4436	6.99E-45
ANXA3	-2.38516	2.8306723	-15.431	8.02E-45
ALDH3B2	2.986006	3.3530159	15.4266	8.40E-45
TWF1	1.254646	4.3777454	15.4265	8.41E-45
DOCK8	-1.64511	1.5952712	-15.426	8.49E-45
FLRT3	-2.63498	2.133307	-15.425	8.54E-45
GPRIN2	-2.02744	1.6682373	-15.42	9.04E-45
FAM83H	1.71138	4.8369168	15.4184	9.18E-45
C11orf96	-2.53583	2.9517147	-15.418	9.24E-45
TRPC6	-1.59855	1.2469886	-15.418	9.24E-45
ARRB2	-1.2437	3.5171585	-15.414	9.67E-45
CSF3	-2.84793	1.1847112	-15.405	1.06E-44

PIFO	-1. 88233	0. 9611828	-15. 404	1. 07E-44
GNAI2	-1. 08476	5. 1801324	-15. 387	1. 29E-44
MTERF3	1. 178225	3. 8562975	15. 3834	1. 34E-44
PPIL6	-1. 10931	0. 6610775	-15. 378	1. 42E-44
METAP1	1. 266317	4. 3540637	15. 3702	1. 54E-44
PVRL4	2. 55106	4. 4280808	15. 3586	1. 75E-44
PDK1	1. 360082	2. 132908	15. 3572	1. 77E-44
FAM189B	1. 198799	3. 6121019	15. 341	2. 11E-44
NAPSA	-5. 33622	4. 1057425	-15. 34	2. 13E-44
PIGR	-4. 26611	3. 4638732	-15. 338	2. 17E-44
NCBP2	1. 32712	4. 8576661	15. 3365	2. 22E-44
ITM2A	-2. 3395	2. 7778801	-15. 334	2. 27E-44
TLR8	-1. 5961	1. 1054081	-15. 33	2. 38E-44
FCH02	-1. 13937	2. 5388887	-15. 329	2. 41E-44
TMTC3	1. 449423	3. 3994517	15. 3215	2. 60E-44
SMAD9	-1. 27981	0. 9870673	-15. 321	2. 61E-44
DPP3	1. 051837	4. 2686978	15. 3198	2. 65E-44
RORC	-1. 78802	0. 9645283	-15. 319	2. 67E-44
CCT4	1. 431199	6. 5266931	15. 3176	2. 71E-44
RRM1	1. 464074	4. 6051352	15. 2912	3. 61E-44
MORC2	1. 114193	3. 5779453	15. 2905	3. 63E-44
SNRPD1	1. 227596	3. 7484147	15. 2804	4. 05E-44
CPOX	1. 300177	3. 3394092	15. 2573	5. 19E-44
HDAC2	1. 086519	3. 2779394	15. 2531	5. 43E-44
ROS1	-2. 60132	1. 661944	-15. 252	5. 47E-44
RASIP1	-1. 92794	1. 8556662	-15. 25	5. 61E-44
SGPL1	1. 083749	4. 0459432	15. 2392	6. 30E-44
ST3GAL5	-1. 7024	1. 9175747	-15. 235	6. 62E-44
DNASE1L3	-1. 78102	1. 1366577	-15. 228	7. 12E-44
MAPK6	1. 430554	4. 0491539	15. 2249	7. 35E-44
C4BPA	-4. 42269	2. 8896942	-15. 219	7. 83E-44
GMFG	-2. 10635	3. 4541437	-15. 218	7. 87E-44
MRPS12	1. 568811	4. 462112	15. 206	8. 99E-44
PARD3B	-1. 22718	0. 9395398	-15. 206	9. 02E-44
RNF187	1. 028039	5. 7191725	15. 2013	9. 46E-44
HRCT1	-1. 56753	0. 8166871	-15. 198	9. 81E-44
NR4A1	-2. 65966	3. 1266007	-15. 18	1. 18E-43
ZMYND19	1. 338458	3. 5026969	15. 1668	1. 37E-43
EXOSC4	1. 340911	4. 2723047	15. 1663	1. 38E-43
GNG7	-1. 26235	1. 0003369	-15. 155	1. 55E-43
LPCAT1	-2. 34618	4. 5726906	-15. 152	1. 60E-43
SLC5A6	1. 4798	3. 3572011	15. 1515	1. 61E-43
FAM216B	-1. 9432	0. 6393061	-15. 151	1. 62E-43
WIF1	-4. 12356	1. 9537409	-15. 149	1. 66E-43
FANCA	1. 202568	1. 6465484	15. 1422	1. 78E-43
PRR29	-1. 25791	0. 7158778	-15. 132	1. 98E-43
CTSH	-2. 42059	5. 0959396	-15. 118	2. 30E-43
GATA2	-1. 77433	1. 6391805	-15. 114	2. 40E-43

GNGT1	1. 224997	1. 1250543	15. 112	2. 46E-43
FAM150B	-1. 41537	0. 6816448	-15. 109	2. 54E-43
C5orf34	1. 145109	1. 4496623	15. 0911	3. 08E-43
TBX2	-1. 80601	2. 1749367	-15. 076	3. 60E-43
TMEM79	2. 034025	3. 0942932	15. 0691	3. 89E-43
ABCC9	-1. 11746	0. 8924099	-15. 067	4. 00E-43
LIFR	-2. 10482	1. 8661227	-15. 061	4. 22E-43
SGCG	-1. 52764	0. 6375171	-15. 056	4. 48E-43
GAB2	-1. 80265	2. 174184	-15. 054	4. 56E-43
ANAPC7	1. 002656	3. 5782399	15. 0493	4. 80E-43
SLC22A31	-2. 90599	1. 8226079	-15. 047	4. 91E-43
CTSV	2. 374953	2. 6222609	15. 0395	5. 34E-43
TLR4	-1. 88748	1. 883229	-15. 039	5. 34E-43
CYP27A1	-2. 54896	3. 6492143	-15. 032	5. 78E-43
CTSO	-1. 57975	3. 4108518	-15. 03	5. 89E-43
YARS2	1. 067583	3. 5191011	15. 0242	6. 28E-43
DSN1	1. 227867	3. 4690945	15. 0206	6. 52E-43
ZBTB47	-1. 12186	2. 0821154	-15. 014	6. 97E-43
PLSCR4	-1. 58461	2. 4542993	-15. 014	6. 98E-43
NEIL3	1. 334842	1. 3530811	15. 0029	7. 88E-43
MARK1	1. 807407	2. 5870014	14. 9955	8. 52E-43
ORC5	1. 107155	2. 8469632	14. 9942	8. 64E-43
CLSPN	1. 261463	1. 4767264	14. 9896	9. 08E-43
CYSLTR1	-1. 01111	0. 7303146	-14. 984	9. 63E-43
NME5	-1. 12051	0. 5088119	-14. 966	1. 17E-42
KAT2A	1. 540918	4. 2297548	14. 9646	1. 18E-42
LY86	-2. 06939	2. 3473546	-14. 96	1. 24E-42
SLC7A7	-1. 92669	2. 4189558	-14. 959	1. 26E-42
ZBTB4	-1. 11101	3. 9842999	-14. 951	1. 37E-42
NDUFS6	1. 427204	5. 6405184	14. 9506	1. 38E-42
CAD	1. 428371	3. 6095915	14. 9489	1. 40E-42
ERICH2	-1. 72005	1. 3863379	-14. 936	1. 60E-42
EN01	1. 335012	8. 9397198	14. 9344	1. 63E-42
ADRM1	1. 009941	5. 9423787	14. 9333	1. 65E-42
NFE2	-1. 16032	0. 6088551	-14. 931	1. 70E-42
DOK4	-1. 25857	2. 6914252	-14. 915	2. 01E-42
RHBDD3	1. 236521	3. 4282005	14. 8959	2. 46E-42
SMARCB1	1. 110122	5. 4547026	14. 8938	2. 52E-42
NPC2	-1. 63167	6. 4731927	-14. 871	3. 21E-42
STXBP6	-1. 67265	1. 1023788	-14. 87	3. 24E-42
MLF2	1. 128384	6. 1669275	14. 8671	3. 34E-42
SHFM1	1. 34497	3. 4815197	14. 8593	3. 63E-42
SPP1	4. 34958	7. 2212832	14. 8509	3. 97E-42
PPAP2B	-1. 46904	3. 6517161	-14. 849	4. 06E-42
NLRP3	-1. 07453	0. 809546	-14. 834	4. 73E-42
MNDA	-2. 21778	2. 5879118	-14. 834	4. 76E-42
SLC34A2	-4. 95363	4. 7099051	-14. 834	4. 77E-42
CAB39L	-1. 28704	1. 5665119	-14. 827	5. 09E-42

CALML3	5. 380621	5. 1103502	14. 8126	5. 96E-42
SPI1	-2. 18838	3. 7949859	-14. 809	6. 20E-42
FAM11B	1. 780457	2. 1692224	14. 8063	6. 37E-42
SLC25A10	1. 323785	1. 9355097	14. 7981	6. 95E-42
TCF3	1. 335622	4. 1326362	14. 7977	6. 98E-42
C20orf24	1. 498206	4. 7072437	14. 7964	7. 08E-42
BORA	1. 081667	1. 816919	14. 7946	7. 22E-42
LST1	-1. 92315	2. 4282705	-14. 794	7. 27E-42
NOL11	1. 034167	3. 8398805	14. 7896	7. 60E-42
MICALCL	-1. 36704	0. 9798181	-14. 789	7. 63E-42
CCDC170	-1. 35682	0. 6535309	-14. 782	8. 26E-42
ALYREF	1. 344708	5. 7113867	14. 7745	8. 92E-42
FAM83F	1. 701926	1. 6906641	14. 7729	9. 08E-42
DAPK1	-2. 04516	2. 3686322	-14. 769	9. 49E-42
OPA1	1. 283368	3. 8902398	14. 7662	9. 75E-42
SSRP1	1. 010663	5. 2068998	14. 7563	1. 08E-41
GAB3	-1. 00357	0. 9803651	-14. 756	1. 09E-41
HEATR1	1. 07942	2. 9077555	14. 748	1. 18E-41
DPH2	1. 094839	3. 6072693	14. 7386	1. 30E-41
RFTN1	-1. 91408	2. 8486602	-14. 728	1. 45E-41
CCDC137	1. 32119	3. 8774906	14. 7237	1. 53E-41
UMPS	1. 130885	2. 989901	14. 7183	1. 62E-41
AGR3	-3. 50176	2. 7111044	-14. 718	1. 62E-41
PES1	1. 186751	4. 7388365	14. 708	1. 80E-41
GEN1	1. 089564	1. 6232272	14. 7049	1. 86E-41
MDH2	1. 038944	6. 0869904	14. 7044	1. 87E-41
IGSF10	-1. 47965	0. 9714031	-14. 703	1. 90E-41
FANCG	1. 532084	3. 0581855	14. 6998	1. 97E-41
PILRA	-1. 84509	2. 3578481	-14. 698	2. 01E-41
QKI	-1. 02827	2. 8177087	-14. 69	2. 18E-41
NCF2	-1. 98181	3. 5789577	-14. 685	2. 31E-41
HK3	-1. 97356	2. 0108656	-14. 672	2. 64E-41
NDE1	1. 243159	2. 8868778	14. 6695	2. 71E-41
OMG	-1. 2863	0. 5430395	-14. 669	2. 72E-41
SIK2	-1. 02981	2. 6121063	-14. 667	2. 78E-41
CHTF18	1. 594734	2. 2945313	14. 6611	2. 96E-41
PDZD2	-1. 78115	1. 2112067	-14. 658	3. 05E-41
RUSC1	1. 092055	3. 4896658	14. 6583	3. 05E-41
GARS	1. 179046	5. 1323825	14. 6577	3. 07E-41
LSG1	1. 475559	4. 4021907	14. 6545	3. 17E-41
WDYHV1	1. 050092	3. 0357097	14. 6493	3. 35E-41
CEP85	1. 216107	2. 6558188	14. 6492	3. 36E-41
TMEM117	1. 668492	2. 3359178	14. 6489	3. 37E-41
CYS1	-1. 47284	1. 1128723	-14. 648	3. 39E-41
LAMB2	-1. 6318	4. 1247776	-14. 641	3. 67E-41
NDST1	-1. 32924	3. 5625114	-14. 635	3. 92E-41
SF3B6	1. 063211	5. 909136	14. 6344	3. 92E-41
CYC1	1. 389243	6. 2142021	14. 6309	4. 07E-41

FAM162A	1. 716177	4. 6199556	14. 6267	4. 25E-41
C1orf35	1. 054153	2. 6796941	14. 6217	4. 49E-41
GINS4	1. 440905	1. 6425266	14. 6136	4. 88E-41
MYH10	-1. 80865	3. 4273137	-14. 606	5. 29E-41
CLEC1A	-1. 52889	1. 0242311	-14. 605	5. 34E-41
FCGRT	-1. 5247	4. 6098087	-14. 595	5. 96E-41
PDCD5	1. 454314	4. 8557517	14. 5913	6. 18E-41
RCAN2	-1. 67501	1. 7951324	-14. 589	6. 36E-41
GART	1. 036946	3. 5710393	14. 5806	6. 92E-41
ITGB4	2. 580287	5. 8486058	14. 58	6. 96E-41
PFN2	2. 729978	5. 7462263	14. 5755	7. 30E-41
PAK1IP1	1. 171023	4. 0444326	14. 5706	7. 69E-41
REM1	-1. 10501	0. 7325495	-14. 57	7. 70E-41
NR2C2AP	1. 327229	3. 9095805	14. 5702	7. 71E-41
PAK1	1. 56551	4. 2431325	14. 5702	7. 72E-41
APOBEC3B	2. 368228	3. 1460063	14. 558	8. 78E-41
WDR62	1. 351201	1. 5754016	14. 5579	8. 78E-41
TRIM59	1. 249359	1. 6427787	14. 5435	1. 02E-40
KCNK17	-1. 05687	0. 5817029	-14. 541	1. 05E-40
MSRB3	-1. 83506	2. 2310169	-14. 541	1. 05E-40
PDIA6	1. 221709	6. 2903625	14. 5385	1. 08E-40
DVL3	1. 731685	5. 2636433	14. 5324	1. 15E-40
TFAP2C	1. 859146	3. 4801604	14. 5293	1. 19E-40
PMAIP1	1. 946039	3. 6603497	14. 524	1. 26E-40
PYCRL	1. 285814	3. 0607028	14. 5217	1. 29E-40
NUP205	1. 156378	3. 8039927	14. 5205	1. 30E-40
DDR1	1. 603803	5. 6367397	14. 5147	1. 38E-40
SLC02B1	-2. 25387	2. 5465027	-14. 507	1. 50E-40
MARVELD3	1. 160161	1. 9802381	14. 5067	1. 50E-40
PTGDS	-3. 0626	3. 8995002	-14. 506	1. 51E-40
SFTPAP1	-7. 16124	6. 0592293	-14. 504	1. 55E-40
CDK2AP1	1. 038995	5. 0030704	14. 4977	1. 65E-40
CCDC167	1. 391615	4. 7712392	14. 4891	1. 81E-40
ZFP36	-2. 31806	6. 605073	-14. 487	1. 86E-40
THOP1	1. 047896	2. 7779419	14. 4749	2. 10E-40
ECM2	-1. 42064	1. 4360329	-14. 473	2. 14E-40
DYSF	-1. 53777	1. 92883	-14. 467	2. 27E-40
DGUOK	1. 000819	5. 1997585	14. 4666	2. 29E-40
KLF15	-1. 54309	1. 2353069	-14. 436	3. 16E-40
MYO1C	-1. 17373	4. 5215986	-14. 435	3. 18E-40
E2F1	1. 610245	3. 3256224	14. 4182	3. 81E-40
MRPL51	1. 14243	6. 0299271	14. 4176	3. 83E-40
PKIG	-1. 60001	3. 5909553	-14. 412	4. 08E-40
GIPC2	-1. 2042	0. 6216127	-14. 408	4. 24E-40
LDHA	1. 436796	7. 0846868	14. 4075	4. 26E-40
MMP19	-2. 05234	2. 187785	-14. 407	4. 28E-40
RFC3	1. 227421	2. 9481266	14. 4048	4. 38E-40
KCNJ8	-1. 58462	2. 1553924	-14. 402	4. 50E-40

FCER1A	-1. 92782	1. 2559624	-14. 384	5. 47E-40
CXCR1	-1. 50156	0. 6304004	-14. 379	5. 76E-40
MEOX2	-1. 44888	1. 0627399	-14. 366	6. 59E-40
APLN	-1. 91788	1. 912916	-14. 364	6. 76E-40
NOB1	1. 016904	4. 6928296	14. 3606	6. 97E-40
PIEZ02	-1. 02856	0. 6680289	-14. 358	7. 14E-40
PDE4D	-1. 02477	1. 3456442	-14. 356	7. 28E-40
CAPN8	-1. 97015	1. 0914863	-14. 352	7. 64E-40
CYP4V2	-1. 04106	1. 2977298	-14. 347	8. 00E-40
TGFBR3	-1. 76382	1. 8278543	-14. 336	8. 97E-40
MED10	1. 209298	4. 553373	14. 3293	9. 66E-40
FBL	1. 550676	6. 3929922	14. 329	9. 69E-40
RGS3	-1. 07312	1. 9267287	-14. 328	9. 82E-40
GPC1	2. 649448	5. 4404663	14. 3199	1. 07E-39
MGP	-2. 74354	4. 9469391	-14. 311	1. 18E-39
SFXN4	1. 130221	3. 6739488	14. 307	1. 22E-39
CTPS1	1. 166501	3. 4125611	14. 3021	1. 28E-39
SMIM10	-1. 31372	1. 3528846	-14. 301	1. 30E-39
MAPRE2	-1. 30241	2. 6103894	-14. 3	1. 32E-39
JDP2	-1. 33975	2. 3069873	-14. 286	1. 51E-39
JUND	-1. 52835	5. 7891477	-14. 276	1. 68E-39
MRPS34	1. 060559	5. 773109	14. 2723	1. 75E-39
NME1-NME2	1. 389985	3. 9747011	14. 2666	1. 86E-39
IRAK1	1. 234122	5. 4814289	14. 2613	1. 96E-39
IQSEC1	-1. 2005	2. 8696269	-14. 26	2. 00E-39
GIMAP4	-2. 09348	3. 2626753	-14. 254	2. 12E-39
C1orf74	1. 261308	1. 8009408	14. 2456	2. 31E-39
PODXL	-1. 80736	3. 0808169	-14. 243	2. 37E-39
NSUN2	1. 25084	4. 4928283	14. 2409	2. 43E-39
CECR5	1. 241344	3. 5898762	14. 2409	2. 43E-39
RAB8B	-1. 16157	2. 731105	-14. 23	2. 71E-39
ACP5	-1. 97118	5. 0071965	-14. 228	2. 79E-39
LSM4	1. 255058	5. 2101216	14. 2271	2. 81E-39
RASSF2	-1. 95867	2. 3039561	-14. 224	2. 89E-39
SDCBP	-1. 16622	5. 2297694	-14. 223	2. 94E-39
GNGT2	-1. 02275	1. 0376115	-14. 19	4. 11E-39
TCP1	1. 053875	5. 4930779	14. 1791	4. 63E-39
RFX2	-1. 08067	1. 3682828	-14. 172	5. 00E-39
C16orf54	-1. 55131	1. 3667138	-14. 171	5. 03E-39
LRFN4	1. 519191	3. 0066055	14. 1706	5. 06E-39
ETV1	-1. 70142	1. 7508049	-14. 17	5. 08E-39
C10orf10	-2. 4045	4. 6265575	-14. 166	5. 29E-39
AIMP2	1. 096891	3. 7486125	14. 1534	6. 05E-39
KRT6B	5. 229196	5. 2773028	14. 1468	6. 48E-39
PTPRG	-1. 11895	1. 6979712	-14. 147	6. 48E-39
CLIC2	-1. 92273	2. 6656258	-14. 145	6. 61E-39
BOLA3	1. 238568	2. 821642	14. 141	6. 88E-39
AKAP12	-1. 99826	1. 9558201	-14. 139	6. 99E-39

ASNS	1. 836135	3. 6847584	14. 1386	7. 05E-39
LIG1	1. 24752	2. 9791527	14. 1321	7. 54E-39
SNRPF	1. 175336	4. 1470204	14. 1301	7. 70E-39
PRMT3	1. 056412	2. 3638976	14. 1298	7. 72E-39
LM02	-1. 74812	2. 1213904	-14. 126	8. 02E-39
EIF6	1. 113534	6. 544109	14. 1257	8. 06E-39
PPP1R15A	-1. 6173	4. 9430964	-14. 125	8. 11E-39
BMP2	-2. 18319	2. 3566572	-14. 121	8. 44E-39
UQCRH	1. 216381	6. 3990744	14. 1185	8. 69E-39
PRELP	-2. 60181	3. 0739345	-14. 118	8. 75E-39
SAC3D1	1. 169825	2. 9336323	14. 1076	9. 72E-39
PPME1	1. 116325	3. 5032873	14. 1071	9. 77E-39
REEP4	1. 432948	4. 6314427	14. 1033	1. 02E-38
PSMG1	1. 076739	3. 6149348	14. 1022	1. 03E-38
MAOB	-2. 17922	2. 3379791	-14. 1	1. 05E-38
PTPRE	-1. 20132	1. 8278597	-14. 084	1. 24E-38
PSMB4	1. 021965	6. 875064	14. 0799	1. 30E-38
PUS1	1. 10707	2. 5536253	14. 0781	1. 32E-38
ALPL	-2. 92617	3. 81599	-14. 073	1. 39E-38
PABPC1	1. 223096	8. 4036373	14. 0665	1. 49E-38
PPIL1	1. 254066	4. 5998207	14. 0594	1. 60E-38
GLRX3	1. 246914	4. 0153016	14. 0567	1. 65E-38
HEG1	-1. 84634	3. 2217264	-14. 053	1. 71E-38
C10orf54	-1. 64839	3. 4096205	-14. 052	1. 73E-38
SMAD7	-1. 45004	2. 7132223	-14. 05	1. 76E-38
GRHL3	2. 572001	2. 4784302	14. 0427	1. 91E-38
SUV39H1	1. 054169	2. 5114099	14. 0317	2. 14E-38
CPSF4	1. 11179	3. 2634636	14. 0304	2. 17E-38
SFN	2. 877769	8. 5523601	14. 0293	2. 19E-38
SLC22A3	-2. 22692	1. 6637017	-14. 028	2. 21E-38
EIF4A3	1. 044464	4. 6750315	14. 0281	2. 22E-38
PSMD11	1. 245174	4. 5818625	14. 0223	2. 36E-38
PALD1	-1. 49156	1. 8822873	-14. 01	2. 68E-38
TNFAIP8L3	-1. 21512	1. 3786027	-14. 008	2. 73E-38
MRPL13	1. 143858	3. 4246935	14. 0066	2. 77E-38
NOP58	1. 106253	4. 7371444	14. 0017	2. 92E-38
DDIAS	1. 323153	1. 947782	14. 0009	2. 94E-38
TMEM47	-1. 75565	2. 307381	-13. 993	3. 19E-38
RRAD	-2. 82357	2. 5632313	-13. 977	3. 75E-38
SH3BP1	1. 435434	3. 4717753	13. 9705	4. 03E-38
MMP28	-2. 51878	1. 85367	-13. 967	4. 15E-38
PLEKHG2	-1. 3715	3. 6472115	-13. 967	4. 19E-38
LSM5	1. 024498	3. 2330698	13. 9655	4. 24E-38
PLEKHG6	1. 86552	2. 596322	13. 9632	4. 34E-38
FAT2	2. 882483	2. 8308227	13. 9614	4. 42E-38
VSTM4	-1. 33979	1. 3384439	-13. 955	4. 75E-38
SAMHD1	-1. 72227	4. 2978408	-13. 949	5. 05E-38
CCND3	-1. 40985	3. 7342435	-13. 944	5. 31E-38

SERPING1	-2.07506	5.9931956	-13.926	6.40E-38
FOXP1	-1.08752	2.0124128	-13.898	8.52E-38
C19orf40	1.154262	1.9471295	13.8925	9.00E-38
NOP16	1.06064	3.1245233	13.8897	9.26E-38
PIK3R5	-1.33843	1.3177625	-13.889	9.34E-38
PN01	1.18827	4.0877865	13.8874	9.48E-38
HOXA5	-1.34787	1.9121021	-13.887	9.49E-38
CARM1	1.093853	3.9204287	13.881	1.01E-37
CKS2	1.762788	5.8216279	13.8796	1.03E-37
N4BP2L1	-1.12967	1.468787	-13.879	1.03E-37
DAW1	-1.02549	0.3658128	-13.877	1.05E-37
STMN1	1.698151	5.0808525	13.8741	1.09E-37
TMEM130	-1.37262	0.8772489	-13.867	1.17E-37
ATAD5	1.018695	1.391152	13.8611	1.24E-37
BRCA1	1.164919	1.8234637	13.8527	1.36E-37
LPAR2	1.096986	3.1148183	13.8394	1.55E-37
MSH6	1.257091	3.3872938	13.8382	1.57E-37
RASGRP2	-1.22268	0.8885691	-13.835	1.63E-37
PER1	-1.7494	3.2569187	-13.827	1.78E-37
ZMYND10	-1.75323	0.7921171	-13.817	1.95E-37
EIF5A	1.061867	7.3169914	13.8118	2.07E-37
PRKDC	1.382375	4.2997428	13.8073	2.16E-37
ALPK3	-1.27997	0.9353965	-13.805	2.22E-37
CLNS1A	1.105125	4.3430921	13.7923	2.52E-37
KIF13B	-1.20286	1.6841274	-13.792	2.54E-37
SIX4	1.327331	1.8662107	13.7834	2.77E-37
SORD	1.521171	2.6777912	13.7734	3.06E-37
TEKT1	-1.55511	0.5102045	-13.758	3.58E-37
RAP2B	1.426757	4.4286791	13.7566	3.64E-37
C5orf49	-1.58559	0.7189016	-13.744	4.13E-37
PARP1	1.187977	5.0257719	13.7424	4.21E-37
ICAM1	-2.6658	4.8243478	-13.734	4.58E-37
ZCCHC24	-1.46395	2.3227281	-13.723	5.15E-37
PAQR5	-1.29094	1.3314651	-13.717	5.45E-37
CSRP1	-1.20481	4.4136777	-13.717	5.45E-37
VGLL3	-1.43842	1.1619792	-13.714	5.64E-37
CRABP2	3.556883	5.3438755	13.7119	5.76E-37
DDX49	1.075741	4.4069493	13.7036	6.27E-37
LAMC3	-1.56865	1.5926189	-13.689	7.27E-37
FAM60A	1.427262	4.1435359	13.6866	7.46E-37
XAGE2B	-1.66293	0.6241136	-13.682	7.81E-37
GPR65	-1.11286	0.9846771	-13.68	8.01E-37
SLC9A3R1	2.297364	6.12088	13.6787	8.09E-37
RAC3	2.048678	3.2530266	13.6752	8.39E-37
ATAD3A	1.202535	3.3245915	13.6713	8.72E-37
SFTPA2	-6.84425	6.3964907	-13.671	8.76E-37
PPARG	-1.75815	2.021617	-13.662	9.55E-37
RPUSD1	1.107227	3.3693982	13.659	9.89E-37

PPM1M	-1.07173	2.8006828	-13.659	9.94E-37
MASTL	1.091955	2.8346911	13.6579	1.00E-36
UBXN10	-1.52191	0.861671	-13.655	1.03E-36
TMEM40	2.078831	2.2766728	13.6553	1.03E-36
LAT2	-1.38135	1.8957729	-13.647	1.12E-36
NATD1	-1.15111	1.8448964	-13.644	1.15E-36
EGFL7	-1.75249	3.51121	-13.635	1.26E-36
GJA5	-2.08366	2.5405933	-13.631	1.32E-36
UQCC3	1.205234	3.364365	13.6291	1.34E-36
CELSR2	1.909621	2.8770897	13.6261	1.39E-36
SLC52A2	1.181781	4.5457443	13.6243	1.41E-36
PDCD2L	1.305367	2.7997881	13.6209	1.46E-36
RIOK1	1.019245	3.664874	13.6105	1.62E-36
CMAS	1.271225	4.7579236	13.608	1.67E-36
SIRPB2	-1.06165	0.9283165	-13.608	1.67E-36
VRK1	1.244579	3.080263	13.6048	1.72E-36
CDK5R1	1.425742	1.8957681	13.604	1.74E-36
CD69	-1.85778	1.7683206	-13.592	1.96E-36
KCNQ1	-1.82316	2.3019857	-13.583	2.16E-36
PIF1	1.219417	1.398632	13.575	2.33E-36
KDM5B	1.094209	3.4579696	13.5671	2.53E-36
STOM	-1.47529	6.2399508	-13.555	2.85E-36
F12	1.654866	1.8445485	13.5457	3.14E-36
LRRFIP1	-1.06177	3.4647496	-13.544	3.21E-36
RHOB	-1.75958	6.1236965	-13.539	3.36E-36
PFDN2	1.196889	6.3801997	13.5335	3.56E-36
USP54	-1.11843	2.2475536	-13.532	3.61E-36
KCTD1	1.808767	2.6490297	13.5287	3.74E-36
FPR1	-2.16123	2.375049	-13.522	4.01E-36
KRT15	4.526964	5.3377927	13.5194	4.11E-36
MAZ	1.070071	4.2800527	13.5167	4.22E-36
MACF1	-1.28867	2.6305866	-13.511	4.47E-36
PTS	1.177258	2.9776654	13.5083	4.60E-36
CAV2	-1.76475	3.97162	-13.505	4.77E-36
SESN1	-1.11578	2.3946459	-13.496	5.21E-36
C9orf171	-1.15625	0.4001109	-13.487	5.72E-36
FXR1	1.414645	4.1928697	13.4855	5.80E-36
SULT1A1	-1.25077	1.4756693	-13.48	6.12E-36
TMEM189	1.166893	3.7118201	13.479	6.20E-36
SULT1C4	-1.38138	0.8080342	-13.478	6.25E-36
TRMT6	1.051476	3.3465529	13.4702	6.77E-36
RND1	-2.47091	1.8697622	-13.468	6.96E-36
DARS2	1.240378	3.5222959	13.4648	7.16E-36
MP RIP	-1.05211	2.8751445	-13.456	7.86E-36
RAB11FIP1	-1.9495	3.0671715	-13.455	7.89E-36
PLA2G12B	-1.13055	0.3114544	-13.452	8.15E-36
SPATA18	-1.48247	1.2624962	-13.45	8.35E-36
GOT2	1.110374	5.1045913	13.4486	8.43E-36

TBL1XR1	1. 470304	4. 6498404	13. 4343	9. 75E-36
DOCK9	-1. 19271	2. 5794109	-13. 429	1. 03E-35
GRHL1	1. 776221	2. 4834785	13. 4274	1. 05E-35
FBXO5	1. 024159	2. 1529706	13. 4237	1. 09E-35
HOXA1	1. 223469	1. 4103731	13. 4184	1. 15E-35
C1orf194	-1. 80293	0. 7292666	-13. 415	1. 18E-35
DOLPP1	1. 018519	3. 5533886	13. 4111	1. 23E-35
POLA2	1. 041445	2. 7043982	13. 4086	1. 26E-35
KIAA0040	-1. 53799	3. 2535363	-13. 408	1. 27E-35
AP2M1	1. 237953	7. 0398287	13. 4047	1. 32E-35
MOCS1	-1. 23313	1. 7070124	-13. 395	1. 45E-35
PIGX	1. 670402	3. 7307344	13. 3917	1. 50E-35
MDK	2. 263385	6. 1018446	13. 3899	1. 53E-35
CACYBP	1. 180252	4. 2919242	13. 3896	1. 53E-35
AARD	-1. 15227	0. 5829952	-13. 388	1. 56E-35
CDC7	1. 206761	2. 2729541	13. 3857	1. 60E-35
NRP1	-1. 46006	2. 8380685	-13. 382	1. 66E-35
RSPH4A	-1. 42132	0. 7085887	-13. 372	1. 84E-35
DQX1	1. 688902	1. 6169348	13. 3704	1. 86E-35
ABCF3	1. 206425	4. 3755019	13. 3679	1. 91E-35
ABCC5	2. 674047	4. 1821592	13. 3664	1. 94E-35
SENP5	1. 100476	3. 4261433	13. 363	2. 01E-35
CD300E	-1. 32505	1. 0493015	-13. 363	2. 01E-35
DUOX1	-1. 89152	2. 8935729	-13. 361	2. 05E-35
SCGB3A1	-4. 52686	3. 5771109	-13. 358	2. 12E-35
SAMD1	1. 05223	4. 46981	13. 346	2. 38E-35
SMC4	1. 392992	3. 4337206	13. 3457	2. 39E-35
ATP2A2	1. 037506	5. 1809243	13. 3325	2. 73E-35
TBXAS1	-1. 36027	1. 8276234	-13. 332	2. 74E-35
SOX2	4. 05981	5. 0221942	13. 3228	3. 02E-35
TYSND1	1. 162387	3. 1899278	13. 3174	3. 18E-35
ATIC	1. 003292	4. 4620024	13. 3119	3. 37E-35
FABP3	-1. 70345	2. 5545928	-13. 287	4. 33E-35
FOLR3	-1. 29482	0. 4804041	-13. 285	4. 40E-35
HOXA10	1. 4812	1. 4257036	13. 2827	4. 52E-35
MYO5C	-1. 34605	1. 7647565	-13. 281	4. 58E-35
FBXL19	1. 286208	2. 9323555	13. 279	4. 69E-35
FAM81B	-1. 21641	0. 4694672	-13. 275	4. 87E-35
CTDSPL	-1. 00608	3. 1519755	-13. 275	4. 89E-35
TIMP3	-1. 77412	1. 4853494	-13. 274	4. 94E-35
DGKA	1. 535296	2. 9803231	13. 2715	5. 06E-35
GTF2IRD1	1. 127211	2. 8550464	13. 2698	5. 15E-35
KIAA1244	-1. 23093	1. 5248199	-13. 261	5. 62E-35
PARD6G	1. 53181	2. 7525143	13. 2546	6. 00E-35
BIK	2. 086138	3. 2957438	13. 2541	6. 03E-35
KLRF1	-1. 036	0. 6624238	-13. 247	6. 49E-35
PGAM1	1. 169113	4. 7504575	13. 2323	7. 51E-35
C1orf106	1. 491288	2. 7137655	13. 2177	8. 70E-35

PTHLH	4. 081308	4. 2163645	13. 2133	9. 09E-35
HMBS	1. 057311	2. 9413396	13. 211	9. 31E-35
TJP1	-1. 05172	3. 2841878	-13. 211	9. 33E-35
IDH2	1. 297186	5. 7621805	13. 2022	1. 02E-34
CGN	-1. 86999	2. 6809818	-13. 2	1. 04E-34
ACSL4	-1. 39661	3. 665189	-13. 197	1. 07E-34
SORT1	-1. 50014	3. 4096294	-13. 196	1. 08E-34
NCS1	1. 462058	3. 197066	13. 1937	1. 11E-34
RGL1	-1. 35184	2. 71098	-13. 192	1. 13E-34
DKK2	-1. 43474	0. 8806519	-13. 189	1. 16E-34
PTGES2	1. 021696	4. 084325	13. 1885	1. 17E-34
CFAP52	-1. 15121	0. 4735769	-13. 186	1. 19E-34
SSX2IP	1. 007685	2. 0599242	13. 1851	1. 21E-34
TFPI	-2. 04754	2. 4977088	-13. 177	1. 31E-34
PRKG1	-1. 11621	1. 1971571	-13. 171	1. 40E-34
MMP1	4. 142545	5. 1078985	13. 1701	1. 40E-34
PDCD6	1. 119747	3. 8717045	13. 1687	1. 42E-34
P2RX7	-1. 09929	1. 1917615	-13. 169	1. 42E-34
CRYM	-1. 49286	0. 7020278	-13. 164	1. 49E-34
STS	-1. 24022	1. 7360487	-13. 157	1. 60E-34
CXCL3	-1. 89623	1. 4941664	-13. 155	1. 63E-34
SNRPG	1. 346795	5. 1045741	13. 1526	1. 67E-34
TMEM194A	1. 218022	3. 1379736	13. 1521	1. 68E-34
PTRF	-1. 74232	5. 9123031	-13. 149	1. 74E-34
AQP9	-1. 91783	1. 904293	-13. 146	1. 80E-34
VIM	-2. 00822	6. 6002153	-13. 145	1. 81E-34
SNED1	-1. 00715	1. 0811951	-13. 143	1. 84E-34
MFN1	1. 235349	3. 8120878	13. 1412	1. 88E-34
ER01L	1. 689189	4. 6312691	13. 1276	2. 15E-34
PMP22	-1. 75306	4. 3435042	-13. 123	2. 25E-34
ETNK2	1. 555183	2. 5014952	13. 1164	2. 40E-34
SNTN	-1. 318	0. 46983	-13. 115	2. 45E-34
MCM3	1. 302176	5. 2027346	13. 1127	2. 50E-34
FAM65B	-1. 26461	1. 123791	-13. 112	2. 51E-34
DHX34	1. 060891	2. 807566	13. 1096	2. 58E-34
SHISA3	-1. 4601	0. 612998	-13. 09	3. 13E-34
SEMA4B	2. 038546	5. 2335383	13. 0864	3. 25E-34
MT1A	-2. 40678	1. 2518333	-13. 079	3. 51E-34
MFI2	2. 177019	2. 5155343	13. 0746	3. 66E-34
CDHR3	-1. 35154	0. 8303787	-13. 075	3. 66E-34
PRAME	3. 425389	3. 1916173	13. 0741	3. 67E-34
ARTN	2. 432705	2. 4559181	13. 0718	3. 76E-34
PAQR4	1. 333139	2. 8408377	13. 0672	3. 94E-34
GPX2	5. 075959	5. 7255644	13. 0651	4. 02E-34
ACSL5	-2. 17992	2. 6701488	-13. 062	4. 16E-34
DDX11	1. 372196	2. 2557395	13. 0569	4. 36E-34
UNC119	1. 071635	3. 1413581	13. 0552	4. 44E-34
SIGLEC9	-1. 15629	1. 2733003	-13. 044	4. 99E-34

BAIAP2L1	1.	116646	4.	1171911	13.	0429	5.	02E-34
NES	-1.	93505	2.	938056	-13.	035	5.	45E-34
TIMMDC1	1.	018017	5.	0798117	13.	0331	5.	53E-34
ZP3	1.	443786	1.	9593147	13.	033	5.	54E-34
MYO1F	-1.	4231	1.	9407826	-13.	028	5.	83E-34
P4HB	1.	01484	7.	7159185	13.	0276	5.	85E-34
SPARCL1	-2.	3846	5.	5373201	-13.	027	5.	88E-34
SIGLEC1	-1.	6895	1.	7445908	-13.	022	6.	18E-34
CDH24	1.	402216	2.	4668611	13.	0189	6.	38E-34
TNS3	-1.	71946	3.	1368044	-13.	016	6.	59E-34
TMEM14A	1.	605959	5.	4279346	13.	015	6.	63E-34
NCKAP1L	-1.	67669	1.	9937742	-13.	011	6.	88E-34
TTF2	1.	002409	2.	0420152	13.	009	7.	04E-34
FAM65A	-1.	10803	3.	4084336	-13.	007	7.	16E-34
LSM7	1.	082123	4.	6647408	13.	0024	7.	52E-34
STYK1	1.	314801	1.	8010167	13.	0024	7.	52E-34
RRAS	-1.	63572	5.	0912595	-13		7.	69E-34
TYROBP	-2.	2148	5.	7187479	-12.	998	7.	86E-34
EPHB3	2.	257886	3.	9217308	12.	9975	7.	90E-34
IL6R	-1.	4603	2.	5547104	-12.	997	7.	95E-34
MRPL15	1.	129577	5.	3148733	12.	9961	8.	01E-34
SNTB1	-1.	61028	1.	9933379	-12.	985	8.	93E-34
PDRG1	1.	109246	3.	8867634	12.	9642	1.	10E-33
TACC1	-1.	67234	3.	2664043	-12.	957	1.	18E-33
SCNN1B	-2.	32812	2.	4845611	-12.	956	1.	19E-33
TGM2	-2.	44997	4.	6824966	-12.	94	1.	40E-33
CPA3	-2.	45768	3.	174167	-12.	938	1.	43E-33
CBX1	1.	228999	5.	0100853	12.	9362	1.	45E-33
FAM49A	-1.	29557	2.	0485232	-12.	936	1.	46E-33
AP1S1	1.	204311	5.	1593969	12.	9275	1.	59E-33
STRAP	1.	048043	6.	2216119	12.	9268	1.	60E-33
WWC3	-1.	16766	3.	2311377	-12.	923	1.	66E-33
KCNJ5	-1.	32971	1.	049354	-12.	918	1.	75E-33
TOP1MT	1.	213382	2.	8587585	12.	9146	1.	80E-33
MSH2	1.	172159	3.	4741419	12.	9129	1.	83E-33
DMBT1	-3.	42568	2.	2931049	-12.	893	2.	24E-33
PALMD	-1.	3544	1.	5001247	-12.	889	2.	32E-33
WDR5	1.	026633	4.	1212859	12.	8859	2.	40E-33
NCAPD3	1.	081349	2.	5426631	12.	8849	2.	42E-33
C6orf118	-1.	02363	0.	3208213	-12.	881	2.	51E-33
ARHGEF17	-1.	24792	2.	3402971	-12.	877	2.	63E-33
GJB6	4.	225388	4.	0189884	12.	8652	2.	95E-33
MTFR1	1.	109208	3.	093111	12.	8651	2.	95E-33
BMPER	-1.	13003	0.	5499994	-12.	862	3.	04E-33
FRMD6	1.	695213	3.	2516569	12.	8512	3.	38E-33
HGH1	1.	038131	3.	6524632	12.	8504	3.	41E-33
ADCK5	1.	190639	2.	443306	12.	8503	3.	41E-33
YWHAG	1.	001019	6.	483836	12.	8468	3.	53E-33

RCSD1	-1.44755	1.6712104	-12.844	3.62E-33
SRD5A1	1.363747	2.3750985	12.8422	3.70E-33
ITGAL	-1.85437	2.2298825	-12.841	3.73E-33
TTYH3	1.375955	4.6774371	12.8385	3.84E-33
SLC39A6	1.201179	4.8521831	12.8358	3.94E-33
TMEM206	1.236912	2.808634	12.8243	4.42E-33
RRP1	1.022209	3.369502	12.8188	4.67E-33
C16orf74	1.889124	2.4548121	12.8147	4.86E-33
SLC1A5	1.391373	6.0787752	12.814	4.89E-33
PTGER2	-1.18923	1.0415311	-12.812	4.97E-33
CXCR2	-1.36087	0.8390753	-12.809	5.12E-33
CABLES2	1.077749	2.5048816	12.8069	5.25E-33
PCDHGB7	-1.12013	0.7688163	-12.806	5.30E-33
MYL9	-2.01994	5.6421326	-12.805	5.35E-33
SERPIN A1	-3.19687	5.121993	-12.8	5.60E-33
UBE2O	1.019648	3.3474976	12.8002	5.61E-33
TMEM213	-1.17434	0.3582889	-12.796	5.86E-33
SOX15	2.920921	3.3533365	12.7943	5.95E-33
PHYHD1	-1.72616	1.7596976	-12.785	6.53E-33
DNAJC2	1.000229	2.8416561	12.7771	7.05E-33
COL17A1	3.906727	4.251406	12.7726	7.37E-33
LAIR1	-1.58493	2.0501882	-12.772	7.45E-33
CLCN2	1.509592	2.2208956	12.7588	8.44E-33
TRIM28	1.113185	6.5247335	12.746	9.59E-33
PPP1R16B	-1.45556	1.4157815	-12.746	9.62E-33
TNFRSF18	2.321883	3.20488	12.7432	9.85E-33
SLAIN1	-1.19657	1.0498801	-12.735	1.07E-32
PSPH	1.68433	3.3756378	12.7349	1.07E-32
KLC3	1.650415	1.9471095	12.7341	1.08E-32
RAPGEFL1	2.50501	3.3666592	12.7329	1.09E-32
SLC12A8	1.36	2.7484786	12.7328	1.09E-32
PNPT1	1.016555	3.4774572	12.73	1.12E-32
UNC13D	-1.74652	2.3108996	-12.728	1.14E-32
GPM6B	-1.24111	1.5164225	-12.724	1.19E-32
CYR61	-2.2324	5.4704099	-12.72	1.23E-32
SNRPD2	1.156789	6.7277769	12.7132	1.32E-32
PARL	1.35656	5.4805457	12.712	1.34E-32
SMOX	1.501953	2.9398773	12.712	1.34E-32
UQCC2	1.130901	3.1094308	12.7063	1.42E-32
STEAP1	1.95391	3.7137826	12.7048	1.44E-32
SLC7A1	1.341411	3.6227267	12.7028	1.47E-32
TMC5	-2.08903	1.78023	-12.699	1.53E-32
TOMM22	1.11038	5.5913609	12.6985	1.53E-32
LSR	1.318951	6.1394117	12.6911	1.65E-32
DOCK2	-1.37948	1.4836076	-12.684	1.76E-32
IRAK3	-1.31899	1.5008235	-12.681	1.82E-32
CKAP5	1.104987	4.0461075	12.6768	1.90E-32
LTBP4	-1.90047	3.9472649	-12.663	2.18E-32

NEBL	-1.49726	2.1907422	-12.661	2.21E-32
IFITM2	-1.77412	5.3794511	-12.66	2.24E-32
TSPAN13	-1.58185	5.6429575	-12.655	2.34E-32
DYNLRB2	-1.11029	0.5419505	-12.643	2.64E-32
PLEKHB1	-1.73166	1.437008	-12.634	2.88E-32
CTSG	-1.30726	0.7619658	-12.634	2.89E-32
WDR4	1.054878	2.67192	12.6326	2.93E-32
DLX5	2.675478	2.6136475	12.6318	2.95E-32
FAM174B	-1.55304	2.1289151	-12.632	2.95E-32
VASH1	-1.20859	1.9762971	-12.631	2.97E-32
BMP7	2.721344	3.3509786	12.6293	3.02E-32
ENTPD7	1.157398	2.7259024	12.6269	3.10E-32
EIF4G1	1.292245	6.5566173	12.6201	3.31E-32
MAP6	-1.07616	0.8318842	-12.619	3.35E-32
SLC25A13	1.000881	3.3833484	12.6172	3.41E-32
PPP1R12B	-1.12775	1.4893743	-12.615	3.49E-32
PREX1	-1.56897	2.7157856	-12.613	3.56E-32
DLG5	1.349226	2.9184861	12.6064	3.79E-32
WDFY4	-1.15585	0.9707886	-12.605	3.84E-32
PSMC4	1.190356	5.6943629	12.6039	3.88E-32
SPTLC3	-1.09718	0.8880033	-12.601	4.00E-32
OCIAD2	1.321197	4.4737923	12.5973	4.14E-32
RTKN	1.163726	3.4015882	12.5948	4.25E-32
OTX1	1.737567	1.7437768	12.5917	4.38E-32
TMEM237	1.04924	2.6021186	12.5809	4.87E-32
EIF2B5	1.23138	4.1390534	12.5782	5.00E-32
PDCD10	1.288763	4.5421498	12.5743	5.19E-32
TSC22D3	-1.76682	4.7170044	-12.572	5.31E-32
MRPS26	1.194274	5.4137151	12.5719	5.31E-32
GPRIN1	1.328477	1.7399566	12.5708	5.37E-32
RNF145	-1.04883	4.8642063	-12.57	5.43E-32
CLCA2	4.253263	4.5659576	12.5638	5.75E-32
RAB17	-1.60343	1.4960199	-12.564	5.77E-32
TPD52	1.235937	3.8421213	12.5618	5.87E-32
BANK1	-1.1711	1.0674437	-12.554	6.33E-32
SCNN1G	-1.82857	1.5977187	-12.551	6.49E-32
NDUFB4	1.10628	5.7569774	12.5474	6.75E-32
GNG2	-1.1946	1.536874	-12.542	7.10E-32
CCT2	1.123832	5.3906569	12.5403	7.24E-32
GTPBP3	1.112057	2.5618888	12.5335	7.74E-32
CFAP43	-1.03878	0.4499276	-12.527	8.25E-32
GAS6	-1.76356	4.0396746	-12.523	8.61E-32
ETS1	-1.81585	3.5645431	-12.522	8.69E-32
PNPLA2	-1.16514	3.7743465	-12.52	8.83E-32
PRPS2	1.132557	4.5840203	12.5137	9.40E-32
C1orf115	-1.40521	2.9584932	-12.514	9.40E-32
LDLRAD1	-1.72074	0.7773221	-12.512	9.55E-32
HSPB8	-2.23407	3.223306	-12.506	1.02E-31

PLCE1	-1.01877	1.0849445	-12.493	1.15E-31
SH2B3	-1.33297	2.6515561	-12.491	1.17E-31
HRAS	1.228042	4.6990368	12.4908	1.18E-31
ARHGAP30	-1.44649	2.8505203	-12.484	1.26E-31
ARHGEF39	1.078487	1.2596173	12.4765	1.35E-31
CRIM1	-1.27044	3.707247	-12.476	1.36E-31
APOL3	-1.67601	2.3909084	-12.475	1.37E-31
IL33	-2.40422	2.7585152	-12.473	1.40E-31
CTSW	-1.8552	2.1031822	-12.463	1.54E-31
ANKRD22	1.817239	2.9661264	12.4587	1.61E-31
TMEM41A	1.10368	3.1604031	12.4523	1.71E-31
STXBP1	-1.38041	2.605988	-12.449	1.77E-31
MGAT3	-2.01238	1.5542997	-12.448	1.78E-31
PHF5A	1.099092	5.1578256	12.4469	1.80E-31
MORN5	-1.57131	0.613012	-12.444	1.85E-31
GABRA3	1.489903	1.3747279	12.4442	1.85E-31
PGK1	1.257028	7.2349134	12.4418	1.89E-31
HLA-DMA	-2.04483	4.6676172	-12.441	1.92E-31
TPSAB1	-2.11971	3.1068674	-12.436	2.00E-31
CAMK2N1	-2.14675	2.8800661	-12.434	2.04E-31
AMMECR1	1.037187	2.4724055	12.4268	2.19E-31
POLE3	1.058033	5.2366545	12.4202	2.34E-31
RARG	1.398337	3.912492	12.4168	2.42E-31
PLXNB3	1.453578	1.730984	12.4168	2.42E-31
ADAMTSL2	-1.32277	1.681637	-12.414	2.50E-31
LGR4	1.581838	2.8345212	12.4058	2.69E-31
ZNF367	1.238207	1.9409256	12.399	2.88E-31
C7orf73	1.044867	4.1659547	12.3977	2.91E-31
RTN1	-1.15567	0.9182131	-12.396	2.97E-31
U2SURP	1.124917	3.7903656	12.3777	3.54E-31
STX2	-1.05195	2.0498028	-12.377	3.56E-31
HLA-D0A	-2.12954	3.0942695	-12.374	3.67E-31
TNFAIP8L2	-1.47441	2.1615807	-12.374	3.68E-31
NET1	1.297773	5.0924552	12.3732	3.70E-31
PTGIS	-1.81099	2.0702771	-12.372	3.75E-31
MUC1	-2.66244	4.5855302	-12.367	3.94E-31
SLC15A3	-1.61448	2.7662363	-12.353	4.51E-31
CHAC2	1.449484	2.5680728	12.3518	4.55E-31
LRRC8D	1.194106	3.4468145	12.345	4.86E-31
SRM	1.009354	5.1864072	12.3384	5.18E-31
DUSP9	2.011594	1.8849764	12.3354	5.34E-31
KCNAB2	-1.12068	2.0407955	-12.334	5.40E-31
ARHGEF2	-1.05812	3.1686997	-12.333	5.46E-31
TXNIP	-1.99627	6.507128	-12.333	5.47E-31
SOX12	1.474348	3.133368	12.3322	5.51E-31
FOS	-2.48467	5.6585227	-12.32	6.20E-31
CERS6	1.193496	2.8704669	12.3156	6.47E-31
DNAI2	-1.12994	0.4211317	-12.314	6.54E-31

NEK7	-1.01681	3.6019167	-12.305	7.15E-31
RNF7	1.114408	5.003855	12.2984	7.63E-31
FBXO32	1.571528	3.0730034	12.2942	7.96E-31
DACH1	-1.36542	1.0345624	-12.285	8.71E-31
SPAST	1.160949	3.3466213	12.2845	8.73E-31
PGM2	1.212219	4.0218432	12.2814	9.00E-31
SMC2	1.134391	2.8719459	12.28	9.12E-31
MAP3K8	-1.30393	2.4855093	-12.277	9.43E-31
SLA	-1.52823	1.9619945	-12.273	9.80E-31
ZNF331	-1.2073	1.8345241	-12.256	1.15E-30
GAREML	1.316795	1.7204024	12.2556	1.16E-30
WASF3	-1.35523	1.4243591	-12.251	1.20E-30
ARL6IP5	-1.22085	5.3378561	-12.248	1.24E-30
HOMER3	1.36018	3.4774074	12.2471	1.25E-30
TBCCD1	1.09888	3.0638161	12.2468	1.26E-30
TMEM2	-1.28257	3.0426762	-12.245	1.28E-30
CBX2	1.979441	2.4837758	12.2314	1.46E-30
FILIP1L	-1.53402	2.6615568	-12.23	1.48E-30
FAM57A	1.299439	4.0468257	12.219	1.65E-30
FGD3	-1.04135	1.7260381	-12.218	1.67E-30
YEATS2	1.437322	3.5942505	12.217	1.68E-30
TMPO	1.103815	3.9984007	12.2048	1.89E-30
STK10	-1.04579	2.3384546	-12.199	2.00E-30
PLOD2	1.705161	3.9091192	12.1961	2.05E-30
RMI1	1.1166	2.6140733	12.1894	2.19E-30
LRRC25	-1.39675	2.0622935	-12.188	2.21E-30
ARAP3	-1.12522	2.1213862	-12.183	2.32E-30
SCGB1A1	-5.32524	4.322032	-12.182	2.36E-30
C1QTNF6	1.453048	2.3678833	12.1787	2.43E-30
RSP04	-1.49563	0.8342124	-12.179	2.43E-30
CYBB	-2.27263	3.7014323	-12.172	2.58E-30
ZC3HAV1L	1.312359	2.2957757	12.1683	2.68E-30
ABCG2	-1.20589	0.9710895	-12.161	2.87E-30
METTL7A	-2.05833	3.9027825	-12.156	3.01E-30
VANGL2	1.971251	3.7468729	12.1532	3.10E-30
JARID2	1.082385	3.1996437	12.1529	3.11E-30
TPD52L1	1.802338	3.2237137	12.1444	3.38E-30
C19orf38	-1.06207	1.2367367	-12.141	3.50E-30
PPIH	1.017145	4.3352252	12.1375	3.61E-30
FAM46B	-1.9019	2.0518975	-12.135	3.71E-30
ALKBH2	1.036044	2.940481	12.1287	3.93E-30
ABRACL	1.432706	5.4526473	12.1264	4.01E-30
HNMT	-1.43905	2.3591345	-12.126	4.04E-30
LPIN2	-1.3849	2.7059696	-12.121	4.22E-30
PHGDH	2.016191	3.8971805	12.1139	4.53E-30
IL7R	-2.13225	3.0261232	-12.109	4.72E-30
CD37	-1.73863	2.6338282	-12.109	4.77E-30
FOXE1	3.358296	3.1718411	12.0997	5.19E-30

BDH1	1. 520129	2. 3451647	12. 0975	5. 30E-30
PLXND1	-1. 36898	3. 4931211	-12. 097	5. 34E-30
MZT2B	1. 223577	4. 9934075	12. 0911	5. 63E-30
MRPL4	1. 022504	3. 8825463	12. 0789	6. 33E-30
ST14	1. 343236	5. 7518523	12. 078	6. 39E-30
HS6ST1	1. 269577	4. 184729	12. 0637	7. 33E-30
MS4A8	-1. 89733	0. 7460451	-12. 054	8. 02E-30
CD1C	-1. 33054	1. 187432	-12. 053	8. 10E-30
ID4	-1. 92221	2. 6719492	-12. 052	8. 19E-30
IL16	-1. 10953	1. 2763163	-12. 049	8. 42E-30
TTC25	-1. 08282	0. 8352982	-12. 047	8. 63E-30
NPNT	-2. 05283	3. 4478841	-12. 044	8. 82E-30
PTPRZ1	2. 634382	2. 8210164	12. 0443	8. 82E-30
DCTPP1	1. 255901	4. 8512145	12. 0415	9. 06E-30
RCN2	1. 136186	3. 5821759	12. 0272	1. 04E-29
FAM107B	-1. 58244	3. 0861302	-12. 02	1. 11E-29
SMO	1. 897236	3. 3200241	12. 0102	1. 22E-29
CCDC42B	-1. 26151	0. 5885119	-12. 01	1. 23E-29
CEP72	1. 073812	1. 9245133	12. 0087	1. 24E-29
STAP2	1. 401373	3. 985204	12. 0041	1. 30E-29
MRAS	-1. 21878	1. 8744128	-12. 003	1. 31E-29
DSC2	1. 866171	3. 4723682	11. 9985	1. 37E-29
ATP5G1	1. 155542	4. 6876743	11. 9924	1. 45E-29
DUS1L	1. 060003	4. 0656362	11. 9898	1. 49E-29
TMEM158	2. 153142	2. 8302152	11. 9859	1. 54E-29
C17orf89	1. 142289	3. 8608818	11. 9821	1. 60E-29
RSPH1	-1. 63707	0. 8864435	-11. 976	1. 70E-29
MFSD7	-1. 13878	1. 6493141	-11. 973	1. 74E-29
MSLN	-3. 27893	2. 6058373	-11. 966	1. 86E-29
ESPN	1. 75269	2. 1983221	11. 9644	1. 89E-29
EDN1	-2. 11544	3. 2720636	-11. 959	1. 99E-29
PROS1	-1. 70004	3. 1702023	-11. 955	2. 06E-29
ARPC1A	1. 001121	6. 1473579	11. 954	2. 09E-29
TTC28	-1. 01904	1. 5242429	-11. 948	2. 22E-29
UBA2	1. 080393	5. 1448401	11. 9429	2. 32E-29
RPH3AL	-1. 20239	1. 2709468	-11. 942	2. 35E-29
SMC6	1. 022535	2. 7041368	11. 9415	2. 35E-29
HEYL	-1. 35147	2. 392442	-11. 935	2. 51E-29
PARVG	-1. 12649	1. 3916066	-11. 934	2. 53E-29
C12orf56	1. 062471	0. 9815375	11. 9319	2. 58E-29
P2RY13	-1. 26159	1. 2492502	-11. 929	2. 65E-29
CTSS	-2. 08023	4. 863046	-11. 923	2. 82E-29
EHD1	-1. 16466	3. 3696702	-11. 92	2. 89E-29
GCLC	2. 490182	4. 1905335	11. 9192	2. 91E-29
WASF1	1. 844581	2. 9037685	11. 9096	3. 19E-29
GRTP1	1. 387679	2. 5604943	11. 9064	3. 29E-29
BTBD11	1. 605067	1. 7098025	11. 9055	3. 32E-29
ARRDC2	-1. 11629	2. 841136	-11. 904	3. 35E-29

IGF2BP3	1. 692103	1. 6693834	11. 9026	3. 41E-29
LAGE3	1. 208922	4. 4382187	11. 8954	3. 65E-29
BIN2	-1. 36036	1. 7789227	-11. 893	3. 74E-29
BCL11A	1. 745863	2. 1703305	11. 8885	3. 90E-29
FAM213A	1. 175013	4. 0548702	11. 8832	4. 10E-29
CSF1	-1. 43974	3. 1355114	-11. 869	4. 69E-29
TRAF4	1. 068704	4. 2874048	11. 8661	4. 82E-29
GBP6	3. 327295	3. 6037353	11. 8637	4. 93E-29
EGLN3	2. 298298	3. 2940428	11. 8562	5. 30E-29
EFEMP1	-2. 25577	4. 3519917	-11. 852	5. 52E-29
LAMA4	-1. 42211	2. 4606475	-11. 849	5. 68E-29
HSPB1	1. 838023	8. 8881595	11. 8446	5. 92E-29
BNC1	2. 427397	2. 5593907	11. 8427	6. 02E-29
ROPN1L	-1. 34117	0. 6874572	-11. 839	6. 25E-29
C1QA	-2. 26552	6. 5446662	-11. 837	6. 37E-29
ANPEP	-1. 64303	2. 463637	-11. 837	6. 38E-29
ITGAM	-1. 66805	2. 1107537	-11. 834	6. 52E-29
EVI2B	-1. 90981	3. 0534123	-11. 832	6. 66E-29
PLCB2	-1. 20719	1. 7324697	-11. 829	6. 86E-29
NFATC2	-1. 20886	1. 3322598	-11. 824	7. 16E-29
CKMT1B	1. 504735	1. 508905	11. 8178	7. 63E-29
PRIM1	1. 071796	2. 5514029	11. 8077	8. 39E-29
HLF	-1. 53214	1. 4739287	-11. 806	8. 55E-29
GLRX	-1. 28463	1. 9740783	-11. 802	8. 84E-29
C20orf85	-2. 89191	1. 4314341	-11. 8	8. 99E-29
SFRP5	-1. 59877	0. 7688286	-11. 793	9. 62E-29
HLA-DPB1	-2. 1567	6. 0254914	-11. 793	9. 67E-29
PLAU	2. 266486	5. 6425019	11. 7903	9. 89E-29
VSNL1	2. 191474	2. 914838	11. 7845	1. 04E-28
THEMIS2	-1. 61635	3. 0100953	-11. 779	1. 10E-28
ITGB8	1. 613518	2. 4966485	11. 7779	1. 11E-28
C9orf24	-1. 80398	1. 0154457	-11. 775	1. 14E-28
EMP3	-1. 50259	4. 252862	-11. 773	1. 16E-28
KCNJ15	-1. 60997	2. 1429932	-11. 773	1. 16E-28
PRDX4	1. 146298	5. 7010474	11. 7697	1. 20E-28
C11orf88	-1. 04736	0. 4931486	-11. 769	1. 21E-28
TCEAL2	-1. 41552	0. 6891451	-11. 76	1. 32E-28
RIN3	-1. 09697	2. 0531558	-11. 756	1. 37E-28
PPP1R35	1. 106075	3. 7556187	11. 7507	1. 44E-28
CADPS2	-1. 3326	2. 0386172	-11. 75	1. 45E-28
NFAM1	-1. 36442	1. 628614	-11. 748	1. 48E-28
APOA1BP	1. 131474	5. 8920593	11. 7442	1. 53E-28
ZNF217	1. 007631	3. 7623851	11. 7435	1. 54E-28
HLA-DPA1	-2. 29692	5. 2199245	-11. 743	1. 55E-28
MEX3A	1. 748603	1. 9291001	11. 7428	1. 55E-28
DUSP8	-1. 17901	1. 5759914	-11. 741	1. 58E-28
KRI1	1. 080655	3. 649027	11. 7396	1. 60E-28
RHOU	-1. 52612	2. 3311516	-11. 734	1. 68E-28

SLC38A1	1.	193471	4.	0585649	11.	7259	1.	82E-28
RAPGEF5	-1.	01175	2.	3630572	-11.	72	1.	92E-28
NR4A2	-1.	65227	2.	2547006	-11.	711	2.	09E-28
OVOL1	1.	695985	1.	9055664	11.	7094	2.	12E-28
SNAI2	1.	750574	4.	1746734	11.	7088	2.	13E-28
PTDSS1	1.	310278	4.	80834	11.	7084	2.	14E-28
DAB2	-1.	54063	2.	9588221	-11.	708	2.	15E-28
CNFN	2.	73619	3.	2146921	11.	7032	2.	25E-28
SLC1A4	1.	784121	3.	7346551	11.	6937	2.	46E-28
SIGLEC14	-1.	41878	1.	3970291	-11.	693	2.	47E-28
PHLDB3	1.	09998	2.	0740754	11.	6917	2.	51E-28
SOX18	-1.	38253	1.	9591398	-11.	678	2.	85E-28
CCR1	-1.	61963	2.	3762738	-11.	676	2.	90E-28
CNN1	-1.	64903	2.	2256124	-11.	676	2.	90E-28
WDR38	-1.	68207	0.	7520367	-11.	675	2.	93E-28
B4GALT4	1.	585372	3.	2302956	11.	6752	2.	93E-28
EMC9	1.	008916	3.	1958871	11.	6731	2.	99E-28
UBTD1	-1.	04926	3.	6448982	-11.	669	3.	10E-28
CYCS	1.	058387	5.	1108625	11.	6645	3.	24E-28
ATP13A3	1.	030326	3.	9189658	11.	6468	3.	82E-28
SLC25A20	-1.	03892	2.	7072742	-11.	639	4.	10E-28
SLC16A5	-1.	48555	2.	5904422	-11.	63	4.	49E-28
SDR16C5	-2.	21455	2.	5558244	-11.	622	4.	85E-28
MRPL24	1.	019812	5.	1250573	11.	6184	4.	99E-28
PFDN4	1.	036957	3.	5512925	11.	6154	5.	13E-28
PLP2	1.	249819	7.	3672565	11.	6126	5.	27E-28
HIST1H2BH	2.	158512	2.	2007636	11.	6098	5.	41E-28
SIGLEC7	-1.	00557	1.	1185743	-11.	607	5.	55E-28
SAMD4A	-1.	07916	1.	3383356	-11.	602	5.	81E-28
PRR5	1.	001403	2.	0665594	11.	6011	5.	87E-28
SERPINB6	-1.	24054	4.	0013623	-11.	599	5.	96E-28
SPAG6	-1.	3957	0.	6280172	-11.	594	6.	26E-28
RAB20	-1.	29185	3.	6045811	-11.	579	7.	25E-28
IQGAP2	-1.	14613	1.	4126363	-11.	574	7.	59E-28
GALNT14	2.	12873	2.	3765811	11.	5692	7.	91E-28
SMIM14	-1.	08442	3.	3141084	-11.	568	8.	00E-28
SEMA5A	-1.	82913	1.	5207328	-11.	564	8.	32E-28
ZNF385A	1.	258642	4.	9257742	11.	5596	8.	65E-28
ETV4	2.	154724	2.	9148396	11.	558	8.	78E-28
ZNF146	1.	072345	4.	7980142	11.	5561	8.	95E-28
CCDC64	1.	312073	2.	2729711	11.	5521	9.	29E-28
NFKBIA	-1.	37955	6.	271578	-11.	547	9.	72E-28
SLC44A5	1.	425408	1.	580357	11.	5355	1.	08E-27
NOC2L	1.	009901	4.	2856306	11.	5348	1.	09E-27
RASAL1	1.	309097	1.	3510444	11.	5334	1.	11E-27
HLA-DRB5	-2.	56915	6.	2103272	-11.	532	1.	12E-27
RASSF8	-1.	22283	1.	8548271	-11.	519	1.	26E-27
TMEM171	1.	322087	1.	4261724	11.	5181	1.	28E-27

SPRR1B	5.165124	5.4973456	11.5167	1.29E-27
TLR2	-1.24698	2.8740895	-11.516	1.29E-27
CRIP2	-1.93601	3.4243298	-11.513	1.34E-27
LPHN2	-1.58258	2.725921	-11.504	1.46E-27
LIN7A	-1.22888	0.8633845	-11.497	1.56E-27
SLC46A3	-1.12272	2.0354408	-11.489	1.68E-27
GAS7	-1.34865	1.8883796	-11.488	1.68E-27
CAPSL	-1.56882	0.7386119	-11.487	1.71E-27
APLP2	-1.0633	6.5399736	-11.485	1.74E-27
HMGB2	1.257002	5.2550851	11.4831	1.77E-27
APBB1IP	-1.36412	1.8840169	-11.48	1.82E-27
PODXL2	2.229257	3.6907284	11.4768	1.87E-27
DLK2	1.748831	2.3029748	11.4738	1.93E-27
KIAA1211L	-1.3053	1.3601708	-11.473	1.95E-27
DLG1	1.075317	3.582527	11.4688	2.02E-27
VAMP5	-1.6384	4.71934	-11.455	2.30E-27
SLC12A4	-1.01587	2.770579	-11.454	2.32E-27
MAD2L2	1.079084	3.6096897	11.4533	2.33E-27
HAUS5	1.079239	2.6912912	11.4527	2.34E-27
TEKT2	-1.34328	0.7689202	-11.451	2.38E-27
FBXO27	2.142947	3.4003846	11.4507	2.39E-27
PRKCQ	-1.16681	1.3187673	-11.445	2.51E-27
HLA-DRB1	-2.29081	7.9993651	-11.442	2.59E-27
TFDP1	1.149784	4.9433109	11.442	2.59E-27
MS4A4A	-1.79469	2.7334755	-11.43	2.89E-27
SLC44A4	-2.28102	2.3086861	-11.427	2.97E-27
KIF3C	1.194645	2.4172706	11.4207	3.16E-27
MTFP1	1.008243	2.1664087	11.4202	3.17E-27
CLEC4E	-1.31417	1.2352584	-11.418	3.24E-27
GCHFR	-1.16777	2.1708536	-11.413	3.40E-27
XPR1	1.153831	3.6108018	11.4113	3.45E-27
SFTPB	-5.41294	6.7117029	-11.406	3.61E-27
FCER1G	-1.84682	5.2418164	-11.405	3.66E-27
C9orf135	-1.1559	0.4270766	-11.402	3.76E-27
SLC44A2	-1.05056	5.0685631	-11.399	3.85E-27
FZD5	-1.18303	2.1229489	-11.399	3.85E-27
MID1IP1	-1.04044	4.0564608	-11.398	3.91E-27
CDHR4	-1.18273	0.4512628	-11.396	3.97E-27
YEATS4	1.146825	3.8044643	11.3955	3.99E-27
TMEM173	-1.33095	4.194268	-11.395	4.01E-27
CERS3	2.172643	2.0114204	11.3912	4.15E-27
KIAA0907	1.250266	3.3054528	11.3823	4.50E-27
ATG4D	1.100714	3.6652517	11.3751	4.82E-27
FHOD1	-1.06889	2.6268885	-11.371	4.99E-27
FIBIN	-1.81857	2.3260201	-11.368	5.16E-27
FAM134B	-1.26161	1.7734269	-11.359	5.60E-27
SMS	1.294163	5.6431879	11.3382	6.78E-27
PRPF4	1.007801	3.9799955	11.3369	6.86E-27

AP00	1. 07294	3. 8301399	11. 3343	7. 02E-27
SNRNP25	1. 034134	3. 4440794	11. 3296	7. 34E-27
LDLR	-1. 53241	4. 1888027	-11. 328	7. 47E-27
CXCL12	-1. 76105	2. 4828335	-11. 322	7. 88E-27
JAG1	1. 868614	4. 8843278	11. 3211	7. 93E-27
PPP2R2C	1. 962086	1. 8520639	11. 3161	8. 31E-27
LRRC46	-1. 37075	0. 9826536	-11. 315	8. 42E-27
GSDMC	2. 122581	2. 3733036	11. 3118	8. 65E-27
EPHA1	1. 362507	2. 9512046	11. 2971	9. 90E-27
ARHGDI1B	-1. 52996	5. 7781311	-11. 297	9. 91E-27
UPF3B	1. 024619	3. 1832537	11. 2959	1. 00E-26
CD74	-2. 13733	8. 9314099	-11. 293	1. 02E-26
RPLP0	1. 043568	8. 6429563	11. 2859	1. 10E-26
SPINT2	1. 336752	6. 7048223	11. 2851	1. 11E-26
DROSHA	1. 043535	3. 4781399	11. 279	1. 17E-26
RPL22L1	1. 554091	4. 1506285	11. 2787	1. 17E-26
FSTL3	-1. 74554	3. 1861996	-11. 277	1. 19E-26
SLC04C1	-1. 40552	1. 4114533	-11. 276	1. 21E-26
MMP14	1. 460824	6. 4891349	11. 2698	1. 27E-26
E2F3	1. 036341	2. 7491423	11. 2646	1. 34E-26
COA6	1. 541343	4. 5240864	11. 2427	1. 63E-26
DDR2	-1. 2994	1. 7303338	-11. 241	1. 67E-26
FOXD1	1. 394844	1. 4484251	11. 2366	1. 73E-26
NFIX	-1. 42502	3. 5974229	-11. 234	1. 77E-26
H1F0	1. 376997	6. 97657	11. 2314	1. 81E-26
PCOLCE2	-1. 67157	1. 8216772	-11. 228	1. 88E-26
ACSL1	-1. 18818	4. 0243427	-11. 227	1. 89E-26
NUDT8	1. 463314	2. 9477356	11. 2215	1. 99E-26
LAMA2	-1. 33773	1. 723891	-11. 221	1. 99E-26
MARCKSL1	1. 523428	6. 342301	11. 2207	2. 00E-26
TMEM99	1. 064351	2. 983667	11. 2178	2. 05E-26
SLC43A2	-1. 05798	2. 2887502	-11. 217	2. 07E-26
PDGFB	-1. 37795	2. 963519	-11. 216	2. 10E-26
FGF7	-1. 16597	1. 1308195	-11. 213	2. 14E-26
STX1A	1. 079328	1. 7209624	11. 2102	2. 20E-26
C1QB	-2. 29083	6. 498757	-11. 193	2. 59E-26
HIST3H2A	2. 193985	3. 318858	11. 191	2. 63E-26
PRKCB	-1. 02973	1. 130749	-11. 19	2. 65E-26
IL1R1	-1. 39674	3. 8378792	-11. 189	2. 67E-26
PALM3	-1. 20674	0. 9394991	-11. 18	2. 90E-26
AIF1	-1. 64582	4. 0080704	-11. 175	3. 05E-26
CLSTN1	1. 284845	6. 170928	11. 1682	3. 24E-26
DPP4	-1. 68272	1. 8189113	-11. 167	3. 26E-26
ADAM12	1. 664622	2. 1337595	11. 1625	3. 41E-26
HIP1	-1. 0187	2. 8796559	-11. 16	3. 49E-26
PLK3	-1. 12682	2. 6453357	-11. 159	3. 52E-26
DAPL1	3. 576955	3. 5697399	11. 1573	3. 58E-26
FAM92B	-1. 45921	0. 8489219	-11. 153	3. 72E-26

PROM2	2. 304388	3. 739771	11. 149	3. 86E-26
SRRM3	1. 202914	1. 3031369	11. 1386	4. 24E-26
BTN3A3	-1. 21962	2. 4560896	-11. 138	4. 27E-26
ADM2	1. 378659	1. 7542709	11. 1335	4. 45E-26
NME4	1. 102162	4. 376047	11. 1328	4. 47E-26
HIST1H2BD	1. 729681	3. 8146295	11. 1319	4. 51E-26
MATN3	-1. 49376	1. 513525	-11. 129	4. 64E-26
KIAA1522	1. 130704	5. 1252476	11. 1253	4. 79E-26
RBBP8NL	1. 155737	1. 4392248	11. 1161	5. 21E-26
TMEM54	1. 067117	5. 5826565	11. 1086	5. 58E-26
SOX4	1. 457846	4. 8118744	11. 0954	6. 30E-26
TLE2	-1. 57917	2. 3769399	-11. 095	6. 34E-26
POLD1	1. 008731	3. 2141806	11. 093	6. 44E-26
MZT1	1. 078074	3. 7527522	11. 0927	6. 45E-26
SIX1	1. 351217	1. 9703358	11. 0903	6. 60E-26
LAPTM4B	1. 293283	6. 2032157	11. 0874	6. 77E-26
VAT1	-1. 04114	5. 5190633	-11. 082	7. 13E-26
ENPP2	-1. 62121	2. 6460903	-11. 076	7. 54E-26
TARBP1	1. 048922	3. 0237407	11. 07	7. 94E-26
DPYD	-1. 43361	2. 5301048	-11. 07	7. 94E-26
DCUN1D1	1. 336335	3. 3235855	11. 0655	8. 27E-26
ELMO1	-1. 0457	1. 798402	-11. 062	8. 50E-26
BST1	-1. 27436	1. 4304405	-11. 062	8. 57E-26
HOXC13	1. 480839	1. 3555247	11. 0582	8. 84E-26
EMILIN2	-1. 1714	2. 4225645	-11. 046	9. 92E-26
HOXB7	1. 83662	3. 0411407	11. 0445	1. 00E-25
MYO1G	-1. 25105	1. 6652132	-11. 044	1. 01E-25
GOLT1A	-1. 71918	1. 353066	-11. 039	1. 05E-25
LPXN	-1. 45935	2. 9953878	-11. 037	1. 07E-25
TRPV4	1. 585959	2. 9625715	11. 0302	1. 14E-25
GALC	-1. 08075	2. 3999461	-11. 019	1. 26E-25
BMP6	-1. 40315	1. 4702083	-11. 011	1. 35E-25
MFAP2	1. 726153	3. 8697119	11. 0098	1. 37E-25
IRF8	-1. 52091	2. 0796627	-11. 004	1. 44E-25
C1QBP	1. 110017	5. 3041342	11. 0015	1. 48E-25
ARHGAP25	-1. 00195	2. 1537879	-10. 994	1. 58E-25
FES	-1. 06336	2. 2698954	-10. 992	1. 61E-25
LTBP2	-1. 67005	4. 1015975	-10. 983	1. 75E-25
QSOX1	-1. 00218	4. 7567043	-10. 977	1. 85E-25
LSM2	1. 050411	5. 334115	10. 9708	1. 95E-25
NKD1	-1. 0965	0. 652674	-10. 968	2. 00E-25
ZNF692	1. 205901	2. 8787197	10. 9673	2. 02E-25
GPSM3	-1. 49225	3. 7301213	-10. 967	2. 02E-25
CKMT1A	1. 291951	1. 3208068	10. 9637	2. 08E-25
C3	-2. 18058	5. 4127157	-10. 963	2. 10E-25
DUSP6	-1. 72502	3. 9973117	-10. 961	2. 14E-25
GPR115	1. 724531	1. 7053335	10. 9598	2. 16E-25
HLA-DRA	-2. 31534	8. 9230226	-10. 954	2. 28E-25

MGAT4A	-1.18265	1.880769	-10.953	2.30E-25
EFS	1.563868	3.9496135	10.933	2.75E-25
ZNF639	1.122927	3.2898685	10.9257	2.94E-25
SYNM	-1.09117	1.6720402	-10.925	2.95E-25
HCST	-1.50907	2.8196363	-10.921	3.07E-25
ABCA12	1.526249	1.4412597	10.9109	3.36E-25
AKR1B10	4.946703	4.9709952	10.8973	3.79E-25
SLC14A1	-1.17704	0.4274616	-10.894	3.91E-25
RRS1	1.040867	4.071247	10.8924	3.97E-25
SH3BGRL	-1.35548	5.1054372	-10.888	4.13E-25
SDC1	1.599253	7.8487867	10.8856	4.22E-25
FOXRED2	1.28002	3.1698381	10.8818	4.36E-25
FJX1	1.363685	2.5357844	10.8782	4.51E-25
EPDR1	-1.64595	2.8330373	-10.877	4.56E-25
GJB1	-1.29865	0.5698204	-10.867	4.97E-25
C4A	-1.07476	0.9590419	-10.866	5.02E-25
SLC50A1	1.031509	4.7885138	10.8662	5.02E-25
GSAP	-1.00381	1.8778417	-10.865	5.07E-25
ABCB6	1.242832	1.6862975	10.8648	5.09E-25
C1orf189	-1.32211	0.6464206	-10.859	5.35E-25
GCAT	1.305759	3.195517	10.854	5.61E-25
CA9	3.171165	3.2489781	10.8512	5.75E-25
FCGR2A	-1.56743	3.0574179	-10.848	5.89E-25
FRRS1	1.26124	2.3555884	10.8475	5.94E-25
ADAMTS1	-1.73375	3.1452189	-10.844	6.14E-25
FBXO41	1.035306	1.6462791	10.8395	6.39E-25
PRF1	-1.64513	2.5471778	-10.831	6.87E-25
BTG2	-1.35941	5.6447802	-10.829	7.02E-25
TMEM106C	1.184211	4.5796679	10.8253	7.26E-25
AHNAK	-1.50864	5.4597671	-10.825	7.30E-25
MAP6D1	1.247791	1.7633318	10.8207	7.57E-25
TENM4	1.23188	1.5367088	10.8007	9.05E-25
DCHS1	-1.18295	1.5259134	-10.801	9.05E-25
CD163	-2.05573	3.3231649	-10.799	9.19E-25
MLLT11	1.783159	2.7788118	10.7978	9.29E-25
RAET1L	2.371361	2.1990659	10.7945	9.57E-25
SERpine2	1.88742	3.0916658	10.7924	9.75E-25
CST3	-1.05529	5.6686343	-10.785	1.05E-24
PLEKHG3	1.185414	2.6082461	10.7733	1.16E-24
DLX6	1.482514	1.361445	10.7541	1.37E-24
ACN9	1.13704	3.0811269	10.7473	1.46E-24
DIP2B	1.059438	3.439293	10.7458	1.48E-24
C8orf4	-2.3324	5.1113728	-10.744	1.50E-24
PARM1	-2.12457	3.2554839	-10.744	1.51E-24
DNMT3B	1.146085	1.4882483	10.738	1.59E-24
TOM1L2	-1.00557	2.9195029	-10.729	1.73E-24
OXLD1	1.00654	3.8181165	10.7277	1.74E-24
EHD2	-1.60967	4.9524338	-10.721	1.85E-24

NRROS	-1.10335	1.8730644	-10.715	1.95E-24
THSD1	-1.18018	1.5777759	-10.711	2.02E-24
PNCK	1.986154	1.8884357	10.7068	2.10E-24
DTX4	-1.29197	2.7739243	-10.693	2.37E-24
MEX3D	1.019344	3.2635608	10.693	2.37E-24
MDFI	1.682515	3.7104761	10.6906	2.42E-24
CD151	-1.06239	5.7095003	-10.687	2.50E-24
RGL3	-1.2697	0.9926433	-10.685	2.54E-24
SCRIB	1.165442	4.2494119	10.6838	2.57E-24
PRR15L	-2.04246	2.4734807	-10.683	2.59E-24
TTC22	1.278258	2.4381237	10.6766	2.74E-24
FAM84A	1.862725	3.0364266	10.6562	3.29E-24
COL11A1	2.361725	2.3374919	10.6513	3.44E-24
JAM3	-1.29621	2.1617124	-10.644	3.67E-24
SERPINB13	3.210227	3.060997	10.6366	3.92E-24
CAPNS2	2.983787	2.9508277	10.6247	4.35E-24
TLN1	-1.13266	5.0459717	-10.624	4.36E-24
COL10A1	2.202684	2.8085773	10.6152	4.73E-24
ZNF608	-1.03936	1.3344904	-10.614	4.79E-24
HSPA4L	1.090748	1.6797596	10.6132	4.82E-24
CYFIP2	-1.19618	1.7022634	-10.607	5.11E-24
ALPP	-1.0184	0.319242	-10.601	5.39E-24
FAM101B	-1.24482	2.5678292	-10.598	5.52E-24
CD4	-1.67041	3.9552063	-10.592	5.80E-24
RBBP8	1.18916	3.8303526	10.5914	5.85E-24
BAIAP2L2	1.346668	1.5377967	10.5802	6.45E-24
MTL5	1.115937	1.2034041	10.5772	6.63E-24
SLFN11	-1.37732	2.6018846	-10.576	6.73E-24
PTPRF	1.196602	5.9527318	10.5708	7.02E-24
CFI	-1.59614	2.9226772	-10.558	7.84E-24
IKBKE	1.159711	2.8621291	10.5561	7.99E-24
ZIC2	1.585447	1.4980028	10.5546	8.09E-24
MPEG1	-1.64051	2.875529	-10.553	8.20E-24
LAPTM5	-1.82671	5.9170938	-10.547	8.67E-24
MT-ND6	-1.86001	9.3190261	-10.545	8.80E-24
TRIT1	1.034605	3.4835037	10.5452	8.80E-24
MFSD3	1.054693	3.3781914	10.5423	9.02E-24
ADA	1.489193	3.0436606	10.5354	9.59E-24
RPL35A	1.109501	7.7723588	10.5348	9.64E-24
FCGR3A	-1.96286	4.4547483	-10.533	9.77E-24
TSC22D1	-1.09201	4.4781427	-10.525	1.06E-23
TMOD1	-1.30228	0.8777697	-10.504	1.27E-23
HIST1H2BG	1.625375	1.8622349	10.5025	1.28E-23
ANXA6	-1.45145	3.9971374	-10.5	1.31E-23
TPPP	-1.55251	1.9147892	-10.497	1.35E-23
GIMAP2	-1.30513	2.1388371	-10.485	1.50E-23
STAT5A	-1.10403	2.5400182	-10.478	1.59E-23
CFAP45	-1.12351	0.9450632	-10.47	1.70E-23

EVA1A	-1. 65273	2. 0901937	-10. 465	1. 78E-23
CXCL5	-2. 09639	1. 6134747	-10. 462	1. 83E-23
SELE	-1. 60785	1. 0201064	-10. 445	2. 13E-23
RNF168	1. 261982	3. 4327396	10. 4421	2. 18E-23
HIF3A	-1. 33068	0. 8606749	-10. 429	2. 45E-23
PXDC1	-1. 1492	3. 7440485	-10. 427	2. 50E-23
IQCB1	1. 014715	3. 6661986	10. 4206	2. 63E-23
HIST1H2AE	1. 774287	2. 1395603	10. 4195	2. 66E-23
STOML2	1. 1458	5. 9025938	10. 4194	2. 66E-23
ID2	-1. 35124	4. 0211751	-10. 413	2. 82E-23
PLD1	1. 267717	2. 3477321	10. 4115	2. 85E-23
CTGF	-1. 97748	5. 7493984	-10. 411	2. 87E-23
SCGB3A2	-3. 89989	4. 2509421	-10. 41	2. 90E-23
FERMT3	-1. 4663	3. 3250991	-10. 403	3. 07E-23
HILPDA	1. 658383	4. 1260014	10. 3871	3. 53E-23
TPSB2	-2. 02628	2. 9872272	-10. 383	3. 65E-23
S100A16	1. 623065	7. 2280689	10. 3807	3. 73E-23
DPT	-2. 06159	3. 1597011	-10. 377	3. 85E-23
C17orf96	1. 205261	1. 9313174	10. 3737	3. 97E-23
IGSF6	-1. 43468	2. 3097587	-10. 373	4. 01E-23
DNPH1	1. 027853	4. 4245296	10. 3694	4. 12E-23
PACSI3	1. 252498	4. 0456552	10. 3601	4. 47E-23
PLEKHN1	1. 223289	1. 5308274	10. 3582	4. 54E-23
NMU	1. 987493	2. 0531078	10. 3576	4. 57E-23
PTGER4	-1. 29503	2. 4120933	-10. 345	5. 11E-23
CADM4	1. 477122	3. 8995954	10. 3439	5. 15E-23
SEMA3E	-1. 08536	0. 57688	-10. 335	5. 55E-23
ARHGEF26	-1. 62335	2. 4052049	-10. 335	5. 58E-23
FGG	-2. 92771	1. 9198533	-10. 334	5. 62E-23
STK26	1. 054318	3. 4892826	10. 3326	5. 68E-23
SULF1	1. 86778	3. 9202306	10. 3282	5. 91E-23
MAL	-1. 76827	1. 7397425	-10. 325	6. 08E-23
HLTF	1. 167319	3. 3472261	10. 3219	6. 24E-23
MAN1A1	-1. 41962	3. 2438159	-10. 318	6. 43E-23
WAS	-1. 31494	2. 584505	-10. 306	7. 18E-23
SOCS3	-1. 45355	5. 7458017	-10. 304	7. 27E-23
NCF4	-1. 39608	2. 8943336	-10. 299	7. 60E-23
SLC4A3	1. 271802	1. 7406354	10. 2896	8. 26E-23
ZNF750	1. 937268	3. 0550872	10. 2892	8. 29E-23
FAM166B	-1. 241	0. 8983491	-10. 28	9. 00E-23
H2AFY2	1. 483517	3. 9966496	10. 2692	9. 87E-23
TXNDC17	1. 06481	3. 7549156	10. 2603	1. 07E-22
TMSB4X	-1. 20651	9. 4862504	-10. 26	1. 07E-22
MICALL1	1. 245868	4. 0879362	10. 2495	1. 17E-22
PTPRC	-1. 66155	2. 772478	-10. 244	1. 23E-22
PLA2G16	-1. 82256	2. 6960833	-10. 244	1. 23E-22
CDCP1	1. 164176	3. 8528437	10. 2386	1. 29E-22
GPR56	1. 317617	4. 532382	10. 2386	1. 29E-22

TET3	1. 01083	2. 6384391	10. 2278	1. 41E-22
CD47	-1. 12602	4. 2246818	-10. 225	1. 45E-22
TSPAN6	1. 024491	3. 7287631	10. 2211	1. 50E-22
SRPX	-1. 71333	2. 4874945	-10. 212	1. 62E-22
MSI2	1. 017857	2. 2542699	10. 2024	1. 76E-22
WNK2	1. 684109	1. 8213026	10. 2011	1. 78E-22
SPRR1A	4. 663568	5. 1054932	10. 1941	1. 89E-22
MBNL2	-1. 02286	3. 3672213	-10. 192	1. 93E-22
NAA20	1. 019108	5. 1302365	10. 1845	2. 05E-22
COX5B	1. 01904	6. 1117017	10. 1808	2. 12E-22
IGFBP2	2. 683421	6. 1297436	10. 1772	2. 19E-22
AXIN2	-1. 11983	1. 4892535	-10. 176	2. 21E-22
HS6ST2	1. 670769	2. 1895819	10. 1731	2. 27E-22
PODN	-1. 54712	2. 4912726	-10. 173	2. 27E-22
NDUFB5	1. 112451	4. 3360976	10. 1724	2. 28E-22
ACAA2	-1. 29844	2. 7283379	-10. 169	2. 34E-22
ATP11B	1. 319479	4. 058961	10. 1689	2. 35E-22
FCGR3B	-1. 47038	0. 997508	-10. 167	2. 38E-22
SFXN3	-1. 04772	3. 1182117	-10. 164	2. 44E-22
SPRY1	-1. 16109	2. 9937321	-10. 164	2. 45E-22
PGF	1. 485689	2. 3985564	10. 1598	2. 54E-22
IGSF11	1. 212841	1. 1844916	10. 1476	2. 82E-22
SLC4A11	1. 885733	2. 5481639	10. 1475	2. 83E-22
SLC3A2	1. 128955	5. 7410389	10. 1403	3. 01E-22
ANKRD13B	1. 360521	2. 1114406	10. 1357	3. 13E-22
FAM3C	1. 128395	4. 2346773	10. 1356	3. 13E-22
HLA-DQB1	-2. 04588	4. 5529247	-10. 128	3. 33E-22
S100A11	1. 193382	10. 134782	10. 126	3. 40E-22
SOX21	2. 28527	2. 3963275	10. 1248	3. 44E-22
CERCAM	1. 240702	3. 4957217	10. 1213	3. 54E-22
FMNL1	-1. 0976	2. 41787	-10. 12	3. 57E-22
TRIB1	-1. 31665	4. 086915	-10. 117	3. 68E-22
GREM1	1. 724112	1. 9541072	10. 1159	3. 71E-22
STOML3	-1. 01254	0. 497103	-10. 114	3. 78E-22
KRT14	4. 943162	5. 3494374	10. 0971	4. 36E-22
TPRXL	1. 130404	1. 0882206	10. 0962	4. 39E-22
ARRDC3	-1. 1548	4. 3693545	-10. 096	4. 39E-22
HIST1H3D	1. 274152	1. 4944798	10. 0926	4. 53E-22
CMKLR1	-1. 24713	1. 7649171	-10. 092	4. 55E-22
HBEGF	-1. 74894	3. 7224424	-10. 07	5. 50E-22
GALNT5	-1. 47608	1. 7011637	-10. 067	5. 63E-22
ARHGEF16	1. 182509	2. 5705493	10. 0671	5. 64E-22
C2orf54	-1. 64992	1. 8294867	-10. 063	5. 83E-22
SDC4	-1. 43505	6. 7133969	-10. 059	6. 06E-22
FXYD6	-1. 49047	2. 3477421	-10. 054	6. 30E-22
RNF144B	-1. 21071	3. 1188557	-10. 054	6. 32E-22
PLEK2	1. 95366	3. 1937911	10. 052	6. 41E-22
SEPP1	-1. 91522	3. 9056921	-10. 05	6. 53E-22

SERTAD1	-1.19936	3.6342022	-10.046	6.74E-22
SASH3	-1.51999	2.9147504	-10.044	6.85E-22
CCL2	-1.94233	4.1155677	-10.03	7.73E-22
ZNF488	1.031902	1.0870189	10.0224	8.27E-22
ERP27	-1.40345	1.5583282	-10.022	8.30E-22
GBP4	-1.63409	2.9874325	-10.019	8.47E-22
MT-ND5	-1.47716	9.2800685	-10.018	8.58E-22
ATP1B3	1.485944	6.8865149	10.015	8.80E-22
RCOR2	1.554731	1.7156064	10.0145	8.84E-22
TRIM22	-1.36644	3.3261773	-10.008	9.35E-22
LY6K	1.774413	1.8168925	10.0035	9.71E-22
AXL	-1.38128	3.2005031	-10.001	9.93E-22
ACTG2	-1.55858	2.1267044	-9.9995	1.00E-21
UCHL1	3.176045	4.5164103	9.99885	1.01E-21
IGFBP3	2.272398	6.122672	9.99271	1.06E-21
SERPIN1D	-1.48481	0.8143222	-9.9918	1.07E-21
MPP1	-1.06662	2.2884973	-9.9844	1.14E-21
IL20RB	2.583119	2.7593266	9.98368	1.15E-21
UGT1A6	1.791187	1.7366916	9.98251	1.16E-21
TWIST1	1.621282	1.8793574	9.98171	1.17E-21
ELN	-2.02951	2.8786837	-9.9803	1.18E-21
MUC15	-1.59811	1.5864515	-9.9799	1.19E-21
GPR126	-1.29671	1.7221383	-9.9684	1.31E-21
CLDN1	2.712072	6.361702	9.9634	1.37E-21
FCGR1A	-1.05782	1.4189409	-9.9623	1.38E-21
C3AR1	-1.56021	2.8844135	-9.9612	1.39E-21
CLDND1	1.008897	4.5442879	9.95883	1.42E-21
UBA7	-1.26525	3.0793277	-9.9537	1.48E-21
SRGN	-1.93021	6.1956854	-9.9525	1.50E-21
SPHK1	1.298272	3.0355726	9.94912	1.54E-21
NTM	-1.25648	1.5682072	-9.9489	1.55E-21
PRRX2	1.615289	2.4305152	9.93362	1.76E-21
NRARP	1.661066	3.4420049	9.92169	1.95E-21
FAM83G	1.110572	2.7519866	9.90213	2.30E-21
CTSD	-1.11663	8.1030991	-9.8926	2.49E-21
LYZ	-2.62322	6.567656	-9.8906	2.53E-21
FST	2.34005	3.5556391	9.88311	2.70E-21
NCOA7	-1.31988	3.5724637	-9.8747	2.90E-21
DHCR24	-1.15857	7.0220114	-9.8746	2.90E-21
SPOCK1	1.543414	1.8849201	9.87429	2.91E-21
SEC14L4	-1.10693	1.0873395	-9.8699	3.02E-21
KLRB1	-1.18727	1.5180353	-9.8694	3.03E-21
EPB41L2	-1.07791	2.646025	-9.8626	3.21E-21
SHOX2	1.16196	1.1113393	9.8623	3.22E-21
TNFRSF1B	-1.41757	3.6387203	-9.8573	3.36E-21
CD53	-1.73774	4.4946565	-9.8515	3.53E-21
LRP8	1.209228	2.0262313	9.84852	3.62E-21
PDLIM3	-1.18149	1.9937007	-9.8381	3.95E-21

PAX9	1. 63539	1. 8942717	9. 83738	3. 97E-21
S1PR5	1. 564045	2. 4799875	9. 82843	4. 29E-21
TNFRSF25	1. 316675	2. 1879944	9. 82064	4. 58E-21
AKNA	-1. 05817	2. 0647959	-9. 8204	4. 59E-21
ITGAX	-1. 29692	2. 4942387	-9. 82	4. 60E-21
BCL2L10	1. 098252	1. 0587308	9. 81357	4. 86E-21
MAGEF1	1. 342264	5. 4854314	9. 81212	4. 92E-21
CEACAM6	-3. 0811	4. 7834537	-9. 8121	4. 92E-21
CPQ	-1. 14516	2. 9517588	-9. 8044	5. 25E-21
NETO2	1. 143044	2. 2689783	9. 80009	5. 44E-21
CLDN23	-1. 03994	1. 7651948	-9. 799	5. 49E-21
TMPRSS11E	2. 650345	2. 5363442	9. 79487	5. 69E-21
STON2	1. 323553	2. 4936554	9. 79216	5. 82E-21
VWA5A	-1. 07708	2. 3487555	-9. 7742	6. 77E-21
SIGMAR1	1. 055992	5. 0747475	9. 77333	6. 81E-21
TMEM190	-1. 57241	0. 9916809	-9. 7731	6. 83E-21
LRRC10B	-1. 25335	0. 7697577	-9. 7723	6. 87E-21
SERPINH1	1. 110265	5. 90141	9. 76269	7. 45E-21
KRT6C	3. 095742	2. 964896	9. 7478	8. 44E-21
AMOTL2	-1. 11082	3. 3035724	-9. 7411	8. 93E-21
CYGB	-1. 01084	2. 7258134	-9. 7403	8. 99E-21
SEC61G	1. 124879	5. 194124	9. 73656	9. 28E-21
RCAN1	-1. 09233	3. 0096552	-9. 7348	9. 42E-21
EDARADD	1. 438036	1. 7532671	9. 73457	9. 43E-21
HLA-DQB2	-1. 97715	3. 2192319	-9. 7312	9. 70E-21
POLB	1. 076893	3. 0120903	9. 7287	9. 91E-21
CXCL14	3. 021297	4. 8136148	9. 72236	1. 04E-20
CLEC10A	-1. 21917	1. 4787543	-9. 7169	1. 09E-20
MYLK	-1. 20573	2. 5165465	-9. 7055	1. 20E-20
SUSD4	1. 79188	2. 7557236	9. 6962	1. 30E-20
MYH11	-2. 28199	2. 5084834	-9. 6951	1. 31E-20
C15orf52	-1. 01202	1. 2891857	-9. 6857	1. 42E-20
HPDL	1. 376481	1. 432639	9. 67385	1. 57E-20
SLC43A3	-1. 28245	2. 70475	-9. 6716	1. 60E-20
PC	1. 35637	2. 7371715	9. 66278	1. 72E-20
RPS7	1. 004543	6. 7061221	9. 66149	1. 74E-20
TOX	-1. 10207	1. 392163	-9. 6601	1. 76E-20
TUFT1	1. 388674	4. 0375667	9. 65853	1. 78E-20
LILRB2	-1. 06506	1. 7181637	-9. 6435	2. 02E-20
LGALS3	-1. 13221	6. 4130201	-9. 6433	2. 02E-20
SH3BGRL2	-1. 27665	2. 3967922	-9. 6354	2. 16E-20
HR	1. 813019	2. 1032085	9. 624	2. 37E-20
CST6	-2. 11068	2. 2312452	-9. 618	2. 49E-20
ERVMER34-1	1. 328159	1. 6916003	9. 61569	2. 54E-20
EYA2	2. 047806	3. 1033764	9. 61405	2. 58E-20
MRPL21	1. 011844	3. 7672967	9. 60065	2. 88E-20
TCTEX1D2	1. 23585	2. 5864121	9. 59443	3. 03E-20
WNT7A	-1. 10442	0. 7816041	-9. 5913	3. 11E-20

KRT13	4.441592	5.0271824	9.58728	3.22E-20
SPRR2A	4.350431	4.5054473	9.58617	3.25E-20
EIF5A2	1.117944	2.0325975	9.57522	3.56E-20
SLC6A14	-1.96081	2.3145723	-9.5705	3.70E-20
PTAFR	-1.30603	2.7322295	-9.5676	3.79E-20
CECR1	-1.58081	3.5128136	-9.5624	3.95E-20
ZNF703	1.619899	3.9820916	9.55641	4.16E-20
IFI16	1.057713	5.2819317	9.54994	4.38E-20
PCDH1	-1.32815	2.6526666	-9.5478	4.46E-20
CABYR	1.871935	1.9368548	9.54593	4.53E-20
FUT2	1.300682	2.0183902	9.53778	4.85E-20
EDNRA	-1.28376	2.3927975	-9.5375	4.86E-20
NGEF	1.098923	1.3100887	9.53339	5.03E-20
HLA-DMB	-1.63238	3.3393413	-9.53	5.17E-20
IKZF1	-1.04348	1.4418122	-9.519	5.66E-20
AKR1C2	3.479018	4.4701955	9.51871	5.67E-20
LCP2	-1.16863	2.3263231	-9.5145	5.87E-20
GMPR	-1.16596	1.7715599	-9.5084	6.18E-20
LCP1	-1.6523	4.9613441	-9.5057	6.32E-20
WNT2	-1.28149	1.6690007	-9.5053	6.34E-20
PIR	1.536267	3.8503009	9.49551	6.87E-20
ABI3	-1.12571	2.4489753	-9.4955	6.87E-20
MTCL1	1.037434	1.4655704	9.49202	7.07E-20
CIITA	-1.19129	1.4962909	-9.4912	7.12E-20
SH3KBP1	-1.0715	2.7745316	-9.4815	7.71E-20
CGREF1	1.297472	1.4360964	9.47711	7.99E-20
MYO1B	-1.01079	3.9722018	-9.475	8.13E-20
HOXD11	1.268075	1.1598021	9.47322	8.25E-20
PPAPDC1A	1.197454	1.2263506	9.47113	8.39E-20
RHCG	3.263861	3.1190613	9.45174	9.84E-20
TNFRSF21	1.362401	5.2850274	9.43079	1.17E-19
SLC7A2	-1.48996	1.6680394	-9.4191	1.29E-19
HRASLS	1.586356	1.6987671	9.41126	1.37E-19
CACNG4	-1.68143	1.3773727	-9.403	1.47E-19
LYPD6B	1.523877	1.9382827	9.39535	1.56E-19
RTN4R	1.109498	2.154373	9.39328	1.59E-19
UCN2	1.298683	1.2307334	9.39275	1.60E-19
GJB4	1.392877	1.3733073	9.37626	1.83E-19
EGR1	-1.74381	5.954428	-9.3705	1.91E-19
LIPA	-1.16068	4.5976027	-9.3689	1.94E-19
ALDOC	1.422557	4.1543961	9.36197	2.05E-19
FZD6	1.019521	4.8899157	9.35975	2.09E-19
PLN	-1.37264	1.5398287	-9.3538	2.19E-19
TAGAP	-1.12511	1.7454431	-9.3452	2.35E-19
PLCH2	1.389922	1.673651	9.34477	2.36E-19
RGS2	-1.36083	4.3781519	-9.3443	2.37E-19
ATF3	-1.53559	3.8339589	-9.3388	2.48E-19
COL1A1	2.297655	7.6565185	9.33642	2.53E-19

P4HA1	1. 02737	5. 2252313	9. 32979	2. 67E-19
CIB2	1. 246267	2. 3264083	9. 31117	3. 10E-19
RHBDL1	1. 048409	1. 3102369	9. 30657	3. 22E-19
MRGPRF	-1. 09699	1. 6054321	-9. 3056	3. 24E-19
TOX2	-1. 15566	1. 8666195	-9. 2885	3. 73E-19
CSTA	2. 553989	6. 0402545	9. 28695	3. 77E-19
TMEM178A	-1. 00141	0. 7866077	-9. 285	3. 83E-19
NNMT	-1. 62298	4. 5742317	-9. 2808	3. 97E-19
LIPH	-1. 5514	2. 3282716	-9. 2806	3. 97E-19
FAM83A	2. 557906	2. 5480404	9. 2797	4. 00E-19
LPAR3	1. 5163	2. 559916	9. 27493	4. 16E-19
THBS2	1. 896795	4. 5042476	9. 27239	4. 25E-19
CIART	1. 191939	2. 0825952	9. 26086	4. 66E-19
SIX2	1. 994739	2. 2218516	9. 24311	5. 38E-19
RARRES3	-1. 67215	4. 4101477	-9. 2387	5. 58E-19
CCDC17	-1. 06528	0. 8738407	-9. 2333	5. 82E-19
IER5L	1. 095489	2. 3056576	9. 2327	5. 85E-19
OLFML3	-1. 37883	3. 4654661	-9. 214	6. 81E-19
USH1G	1. 252574	1. 15669	9. 21342	6. 84E-19
SEMA3F	1. 041786	4. 2053211	9. 20751	7. 17E-19
IGF2BP2	1. 910854	3. 8262076	9. 20394	7. 38E-19
ITGB2	-1. 5551	3. 9644825	-9. 2033	7. 42E-19
EPB41L3	-1. 13559	1. 7016415	-9. 1992	7. 67E-19
CYB5R2	1. 244243	2. 0754952	9. 19783	7. 75E-19
DCN	-1. 86411	4. 807894	-9. 1973	7. 79E-19
GGT1	-1. 15332	1. 916741	-9. 1963	7. 85E-19
SOCS2	-1. 33669	2. 2389076	-9. 1909	8. 20E-19
HPN	-1. 62396	1. 6666135	-9. 1875	8. 42E-19
C2CD4B	-1. 1745	1. 0412469	-9. 1872	8. 45E-19
SLC25A25	-1. 06853	2. 7644451	-9. 184	8. 67E-19
HOXC8	1. 238959	1. 2673808	9. 17847	9. 06E-19
B3GNT8	-1. 20126	2. 4179529	-9. 1536	1. 11E-18
SPON1	-1. 58737	2. 8290519	-9. 1357	1. 28E-18
CA12	2. 215254	3. 5422858	9. 13341	1. 30E-18
SPRR2D	3. 638119	3. 7670182	9. 13327	1. 30E-18
SLC15A2	-1. 19003	2. 3441768	-9. 1327	1. 31E-18
CST1	2. 715264	2. 6792419	9. 1271	1. 37E-18
SOX7	-1. 42088	2. 2246329	-9. 1224	1. 42E-18
ELOVL4	1. 198832	1. 3512289	9. 11613	1. 49E-18
DRC1	-1. 05082	0. 6193493	-9. 1142	1. 52E-18
HMCN1	-1. 01693	1. 2863512	-9. 1127	1. 53E-18
IL6	-2	2. 4821118	-9. 0974	1. 73E-18
KRT10	1. 599684	4. 3656893	9. 09666	1. 75E-18
CDH1	1. 065772	5. 9725001	9. 09596	1. 76E-18
MICAL2	-1. 13283	2. 319128	-9. 0952	1. 77E-18
PLXDC2	-1. 11934	2. 7833043	-9. 09	1. 84E-18
CHAC1	1. 055081	2. 0324331	9. 08604	1. 90E-18
HES1	1. 060172	4. 8786075	9. 07744	2. 04E-18

DI02	1. 408504	1. 6549271	9. 05357	2. 46E-18
SYNP02	-1. 26894	1. 2077292	-9. 0494	2. 55E-18
RGMA	1. 479224	1. 8814855	9. 03177	2. 93E-18
RAB38	1. 666565	3. 967298	9. 0278	3. 02E-18
KIFC2	1. 251083	2. 3334097	9. 02658	3. 05E-18
HIST1H2AD	1. 052381	1. 1461829	9. 02501	3. 09E-18
C1QC	-1. 76462	6. 539747	-9. 0232	3. 13E-18
B4GALNT1	1. 318282	1. 3966798	9. 01856	3. 25E-18
PANX2	1. 815342	2. 5760112	9. 01489	3. 35E-18
APOC1	-1. 96231	5. 3112046	-8. 9906	4. 06E-18
VPS37D	1. 023823	1. 6515327	8. 98107	4. 38E-18
HSPA1B	1. 14622	5. 4846673	8. 98069	4. 39E-18
NOTCH3	1. 334888	5. 0948571	8. 97744	4. 50E-18
TMEM184A	1. 215296	1. 814842	8. 9735	4. 65E-18
MEST	1. 306932	4. 1984529	8. 9695	4. 80E-18
HSD11B1	-1. 33189	2. 1319053	-8. 9689	4. 82E-18
HLA-DQA1	-1. 84451	4. 1580215	-8. 9663	4. 92E-18
RHBDL2	1. 132852	1. 7377533	8. 95938	5. 20E-18
IL10RA	-1. 23853	2. 3805913	-8. 9479	5. 69E-18
IVL	2. 734657	2. 7380592	8. 9453	5. 81E-18
PDLIM4	1. 369496	3. 1380744	8. 94262	5. 93E-18
CHPF	1. 136236	5. 4054934	8. 94191	5. 96E-18
MSN	-1. 03243	6. 5759303	-8. 9348	6. 31E-18
HES2	1. 605505	2. 1101331	8. 92846	6. 63E-18
PKP2	1. 179015	2. 0064781	8. 92371	6. 88E-18
PRTFDC1	1. 029785	2. 4192923	8. 91679	7. 27E-18
FGL2	-1. 41983	2. 6583843	-8. 9139	7. 44E-18
XDH	1. 183479	1. 327284	8. 9136	7. 46E-18
WDR76	1. 009529	2. 0859223	8. 91138	7. 59E-18
TXN	1. 380934	7. 7144953	8. 90872	7. 75E-18
TGFA	1. 324243	3. 202476	8. 90451	8. 01E-18
SAMD9L	-1. 16508	2. 2045024	-8. 896	8. 56E-18
ZBED2	-1. 382	1. 8461271	-8. 8921	8. 83E-18
GALNT18	-1. 12973	3. 3701097	-8. 8907	8. 93E-18
DYNC1I1	1. 208397	1. 5361746	8. 8869	9. 20E-18
LBH	-1. 11564	4. 8595201	-8. 8861	9. 26E-18
KLHL13	1. 238483	1. 7050253	8. 88575	9. 28E-18
NUDT11	1. 419523	1. 7245621	8. 88005	9. 71E-18
CCNJL	-1. 10044	1. 4832482	-8. 8717	1. 04E-17
SLC40A1	-1. 59835	4. 59576	-8. 8695	1. 05E-17
NKG7	-1. 60704	3. 3190089	-8. 8678	1. 07E-17
SGCE	-1. 32503	3. 115613	-8. 8633	1. 11E-17
NCALD	-1. 00645	1. 5886754	-8. 8558	1. 17E-17
CDKN1C	-1. 1301	2. 326567	-8. 8359	1. 37E-17
LPAR5	1. 015068	2. 1154212	8. 83033	1. 43E-17
A2ML1	2. 339962	2. 2053796	8. 8232	1. 52E-17
NDRG1	1. 694162	6. 8123025	8. 81785	1. 58E-17
HOXD10	1. 439529	1. 4065074	8. 81285	1. 64E-17

LSAMP	-1. 03296	1. 2376649	-8. 8024	1. 78E-17
CTNNAL1	-1. 23564	3. 6638062	-8. 7989	1. 83E-17
TUBA1A	-1. 40877	5. 1436535	-8. 7886	1. 98E-17
PGLYRP3	1. 993467	1. 8507374	8. 78389	2. 06E-17
C10orf99	2. 475853	2. 3187314	8. 77943	2. 13E-17
RERG	-1. 14476	1. 5529406	-8. 7622	2. 44E-17
WNT7B	1. 630225	3. 73304	8. 75492	2. 58E-17
TIMP2	-1. 37831	5. 2595638	-8. 7549	2. 58E-17
SYTL1	1. 067237	3. 4068648	8. 74987	2. 68E-17
MMP10	3. 319961	3. 5996619	8. 74924	2. 70E-17
FRZB	-1. 18534	1. 7804914	-8. 7355	3. 00E-17
ITGA6	1. 463903	5. 4639674	8. 72839	3. 17E-17
APLNR	-1. 16222	1. 8586523	-8. 7239	3. 28E-17
LTB4R	1. 410434	2. 7492288	8. 72197	3. 33E-17
HMGA2	1. 330908	1. 2364662	8. 71818	3. 43E-17
MALL	-1. 20792	1. 9178341	-8. 7118	3. 60E-17
ARL4C	1. 034399	4. 831371	8. 69811	4. 01E-17
THBS1	-1. 54808	4. 7428775	-8. 697	4. 04E-17
CHODL	1. 374368	1. 4969691	8. 6923	4. 19E-17
HAP1	1. 53404	1. 5116805	8. 69137	4. 22E-17
NMNAT3	1. 052507	2. 131549	8. 69097	4. 23E-17
CSF2RB	-1. 37978	2. 2773723	-8. 6909	4. 24E-17
PTGES	1. 711918	3. 8233953	8. 68905	4. 30E-17
PI3	3. 811371	5. 8392511	8. 68545	4. 42E-17
CST7	-1. 3336	2. 9789583	-8. 6839	4. 47E-17
SECTM1	-1. 23208	3. 1228045	-8. 6754	4. 77E-17
S100A3	-1. 23852	2. 1049165	-8. 6719	4. 91E-17
TPSD1	-1. 17259	1. 0170916	-8. 6699	4. 98E-17
B2M	-1. 24881	9. 2280057	-8. 6695	5. 00E-17
LGALS7B	2. 871236	2. 9081746	8. 6658	5. 14E-17
OPLAH	1. 091076	2. 7373529	8. 66557	5. 15E-17
GAMT	1. 273217	3. 2089779	8. 66511	5. 17E-17
HAVCR2	-1. 16809	2. 4341814	-8. 6624	5. 28E-17
NFKBIZ	-1. 28445	2. 9562597	-8. 6603	5. 37E-17
FAM20A	-1. 11946	2. 2491884	-8. 6504	5. 79E-17
CXCL17	-2. 43136	5. 1189237	-8. 648	5. 90E-17
DUSP14	1. 016946	3. 8575148	8. 64391	6. 09E-17
FOLR2	-1. 48166	3. 0830686	-8. 6147	7. 62E-17
TMEM119	-1. 41041	2. 8262498	-8. 6069	8. 09E-17
CD86	-1. 03428	2. 382178	-8. 6019	8. 40E-17
AHNAK2	1. 785106	2. 8267374	8. 59448	8. 90E-17
MME	-1. 62702	1. 7803917	-8. 5906	9. 17E-17
SBSRON	-1. 1526	1. 1112584	-8. 586	9. 50E-17
KCNG1	1. 234953	1. 2025231	8. 585	9. 57E-17
PPP1R1B	-1. 49765	1. 4759476	-8. 5824	9. 76E-17
RENBP	-1. 06748	2. 7759631	-8. 5797	9. 97E-17
KRT7	-2. 75753	4. 174103	-8. 5554	1. 20E-16
CREB3L1	-1. 37436	2. 6975389	-8. 5541	1. 21E-16

PLEKHG4	1.	202327	2.	3203529	8.	55044	1.	25E-16
KRT19	1.	957546	8.	791639	8.	53652	1.	39E-16
NFIB	-1.	02508	2.	4880256	-8.	536	1.	39E-16
SPRR3	3.	782627	3.	7969919	8.	53503	1.	40E-16
IRX2	-1.	44817	2.	441774	-8.	5319	1.	44E-16
PTPRH	1.	135568	1.	1953996	8.	5276	1.	48E-16
JAG2	1.	19753	3.	4749849	8.	51978	1.	57E-16
ARMCX1	-1.	06674	2.	5092449	-8.	5182	1.	59E-16
PKDCC	-1.	32702	1.	9157141	-8.	5035	1.	78E-16
HIST1H3H	1.	285373	1.	8221263	8.	49319	1.	93E-16
ADH7	3.	228703	3.	4143327	8.	48586	2.	04E-16
COL3A1	2.	051116	7.	9512592	8.	48582	2.	04E-16
SAMSN1	-1.	09908	2.	1306506	-8.	4763	2.	19E-16
BCL2A1	-1.	49203	3.	0885757	-8.	4534	2.	61E-16
SERINC2	1.	440036	5.	1620903	8.	45218	2.	63E-16
MSI1	1.	440209	1.	5762259	8.	45106	2.	65E-16
SLC29A4	1.	114316	1.	5219737	8.	44935	2.	69E-16
FAM117B	1.	012055	2.	712666	8.	4401	2.	88E-16
VNN2	-1.	16386	1.	3683386	-8.	4315	3.	08E-16
S100A7	3.	656767	3.	7644358	8.	43132	3.	08E-16
TREM2	-1.	45338	3.	5088814	-8.	4188	3.	39E-16
CCNO	1.	036274	1.	8034841	8.	41144	3.	58E-16
STRA6	1.	28651	1.	3509011	8.	40225	3.	84E-16
CCL26	1.	341826	1.	536584	8.	39384	4.	09E-16
ABCC1	1.	515921	4.	938654	8.	39108	4.	17E-16
SLPI	-2.	32595	7.	9652442	-8.	3847	4.	38E-16
LRP12	1.	00042	2.	1247963	8.	371	4.	86E-16
SYBU	-1.	01224	1.	2328267	-8.	3637	5.	13E-16
HCK	-1.	26143	3.	752528	-8.	3615	5.	22E-16
AZGP1	-2.	00302	1.	6953712	-8.	3558	5.	44E-16
RARRES2	-1.	49542	4.	8715428	-8.	3541	5.	51E-16
CTSE	-2.	54124	3.	1905236	-8.	3522	5.	59E-16
PLIN2	-1.	31348	3.	4089354	-8.	3517	5.	61E-16
KREMEN2	1.	735216	1.	6884654	8.	34901	5.	73E-16
ULBP2	1.	54817	2.	6983337	8.	33745	6.	25E-16
HOXC9	1.	019285	1.	0840113	8.	33504	6.	36E-16
HIST1H2BJ	1.	247913	1.	8488527	8.	33391	6.	41E-16
TNNI2	-1.	16459	1.	2876241	-8.	3301	6.	60E-16
PON3	-1.	25949	1.	5423515	-8.	3257	6.	82E-16
MMP9	1.	950939	4.	7762491	8.	32083	7.	07E-16
MAOA	-1.	41715	3.	9489431	-8.	3184	7.	21E-16
SLC7A11	1.	972559	2.	327854	8.	31313	7.	49E-16
MCAM	-1.	0427	3.	5944461	-8.	3053	7.	94E-16
VM01	-1.	21072	2.	2298755	-8.	2972	8.	44E-16
NPDC1	-1.	10241	3.	3526267	-8.	2935	8.	68E-16
FAM83C	1.	90539	1.	7666555	8.	28706	9.	11E-16
ADAM23	2.	387738	2.	8467164	8.	28549	9.	21E-16
RIPK4	1.	053634	3.	4607491	8.	27124	1.	02E-15

ADM	1. 587001	4. 6156509	8. 26913	1. 04E-15
KCNK5	-1. 07092	1. 6740154	-8. 2555	1. 15E-15
COL5A2	1. 598991	4. 6999774	8. 25151	1. 19E-15
TRIM16L	1. 877208	2. 7521031	8. 24833	1. 22E-15
JUN	-1. 07484	5. 7199277	-8. 2477	1. 22E-15
DUOXAL1	-1. 1768	2. 6707134	-8. 2461	1. 24E-15
LRP1	-1. 07864	4. 2442908	-8. 2335	1. 36E-15
EVI2A	-1. 19849	2. 3264735	-8. 2327	1. 36E-15
CLU	-1. 48629	4. 9217561	-8. 2209	1. 49E-15
TP73	1. 17563	1. 8028199	8. 21857	1. 52E-15
CBR3	1. 73552	3. 4485226	8. 21134	1. 60E-15
EGR2	-1. 20855	2. 5713872	-8. 2068	1. 65E-15
UGT8	1. 385154	1. 9170601	8. 20064	1. 73E-15
LEF1	1. 039569	2. 121338	8. 19306	1. 83E-15
HOXD13	1. 57661	1. 4419003	8. 18966	1. 88E-15
B3GNT3	1. 634926	2. 3724006	8. 17946	2. 02E-15
IGSF3	1. 205055	4. 1095032	8. 17009	2. 17E-15
CDKN2A	2. 136916	2. 5226756	8. 16084	2. 32E-15
CILP2	1. 0742	1. 3787544	8. 15978	2. 34E-15
ITGA2	1. 220206	3. 8459836	8. 15468	2. 43E-15
LY6D	3. 426336	3. 4692039	8. 1486	2. 54E-15
PRDX1	1. 061164	8. 1715944	8. 14187	2. 67E-15
MMP3	1. 826392	1. 807303	8. 12989	2. 92E-15
GBP3	-1. 08787	2. 7103951	-8. 1262	3. 00E-15
SORCS2	-1. 0801	1. 2195276	-8. 1187	3. 17E-15
SPAG4	1. 075323	2. 1781245	8. 1159	3. 23E-15
TMPRSS11D	2. 333395	2. 189424	8. 11036	3. 37E-15
TDRD5	1. 056038	1. 0542043	8. 10028	3. 63E-15
ARL4D	1. 489387	4. 1112373	8. 08382	4. 09E-15
GZMM	-1. 00667	1. 5679425	-8. 0812	4. 17E-15
TGFB2	-1. 10318	1. 4671476	-8. 0727	4. 44E-15
ORM1	-1. 40641	1. 2441629	-8. 0608	4. 84E-15
TRIB3	1. 28853	3. 5601076	8. 06014	4. 87E-15
KLF4	-1. 33432	4. 1560346	-8. 0553	5. 04E-15
RGS16	-1. 17268	3. 5618592	-8. 0539	5. 09E-15
CCL24	-1. 25784	1. 4035862	-8. 0491	5. 28E-15
ATF5	1. 226916	4. 5316613	8. 04642	5. 38E-15
LGALS2	-1. 03666	1. 6434185	-8. 0454	5. 42E-15
DDIT4	1. 44639	6. 1854562	8. 03946	5. 66E-15
CYP2S1	1. 962463	4. 782706	8. 03678	5. 77E-15
NKAIN2	1. 257066	1. 2035426	8. 02768	6. 17E-15
HAPLN3	1. 046207	2. 9430575	8. 02018	6. 51E-15
VTCN1	1. 942881	2. 2764781	8. 01449	6. 79E-15
GPR34	-1. 0469	1. 7215331	-8. 0133	6. 85E-15
TOR4A	-1. 08604	2. 2565979	-8. 0109	6. 97E-15
GZMH	-1. 32237	2. 2274409	-8. 0049	7. 28E-15
TSPAN8	-1. 4734	1. 630648	-8. 0002	7. 53E-15
B3GNT5	1. 145141	3. 6016918	7. 99831	7. 63E-15

MYCL	1.	410763	2.	4807514	7.	99808	7.	65E-15
TNNT1	1.	852505	2.	6245993	7.	99299	7.	94E-15
NCCRP1	1.	932669	2.	1733531	7.	99028	8.	09E-15
RAP1GAP	-1.	07457	2.	4650122	-7.	9901	8.	11E-15
PABPC1L	1.	198531	2.	3961496	7.	97639	8.	95E-15
PTX3	-1.	22456	1.	1707354	-7.	9705	9.	34E-15
CA2	-1.	54472	3.	2290563	-7.	9623	9.	91E-15
IL23A	1.	124718	1.	7534274	7.	95492	1.	05E-14
AC105009.1	1.	028585	1.	2059448	7.	95404	1.	05E-14
RNF128	-1.	37557	2.	0609588	-7.	9479	1.	10E-14
CNTNAP2	1.	667697	1.	6516285	7.	94748	1.	10E-14
BARX1	1.	934782	1.	7838374	7.	94642	1.	11E-14
DMRTA2	1.	198309	1.	1142469	7.	9464	1.	11E-14
CD109	1.	287525	3.	4662255	7.	93241	1.	23E-14
GNG4	1.	438553	1.	4093418	7.	91787	1.	37E-14
SERPINB4	2.	352313	2.	2754458	7.	90283	1.	52E-14
GAL	1.	565023	1.	5044016	7.	90157	1.	54E-14
CXCL13	2.	296819	3.	7431589	7.	89321	1.	63E-14
VASN	-1.	10023	2.	8287931	-7.	8888	1.	68E-14
IFIT2	-1.	13287	2.	4926321	-7.	8872	1.	70E-14
KDELR3	1.	038479	3.	8337434	7.	88389	1.	74E-14
ARHGEF4	1.	208468	2.	1955827	7.	87447	1.	87E-14
POF1B	1.	569801	2.	4374546	7.	86688	1.	97E-14
SESN3	1.	363243	3.	9295725	7.	86066	2.	06E-14
AIM1L	1.	119137	1.	791556	7.	85845	2.	09E-14
ADTRP	-1.	13057	1.	3227446	-7.	8541	2.	16E-14
SERPINB3	2.	72743	3.	3995964	7.	83187	2.	53E-14
IRF1	-1.	00834	3.	4249996	-7.	8293	2.	58E-14
SDK1	1.	188625	2.	5771386	7.	82344	2.	69E-14
CCL4	-1.	14708	2.	4610267	-7.	8216	2.	73E-14
ABCA13	1.	219584	1.	6361797	7.	81407	2.	88E-14
FOXJ1	-1.	71631	1.	6345246	-7.	8086	2.	99E-14
FOXN1	1.	402172	1.	4535924	7.	79433	3.	31E-14
CSF1R	-1.	23816	3.	3618165	-7.	7875	3.	48E-14
GSTA2	-1.	1927	0.	6469197	-7.	7863	3.	51E-14
NR1D1	1.	010325	3.	4701338	7.	78563	3.	52E-14
CPVL	-1.	28888	3.	1604559	-7.	7837	3.	57E-14
EPHB2	1.	01452	1.	685256	7.	77801	3.	72E-14
KIT	-1.	54915	1.	9369806	-7.	7691	3.	96E-14
COL4A6	1.	40874	1.	8226219	7.	76017	4.	22E-14
CDHR1	1.	103421	1.	1881532	7.	74826	4.	59E-14
TJP3	-1.	1542	1.	6126412	-7.	7411	4.	83E-14
PRKX	1.	200668	3.	3455269	7.	73238	5.	14E-14
ADAMDEC1	1.	469734	2.	1815237	7.	73157	5.	17E-14
GCLM	1.	629688	3.	9273647	7.	73097	5.	19E-14
MISP	-1.	33288	2.	7421045	-7.	721	5.	57E-14
SNRPN	-1.	00061	3.	4607635	-7.	7208	5.	58E-14
SLC24A3	-1.	01075	1.	7664508	-7.	7196	5.	63E-14

BNIP3	1. 031698	3. 8677852	7. 71007	6. 02E-14
COCH	1. 523653	1. 6859804	7. 70867	6. 08E-14
TNFRSF10D	-1. 07156	1. 7563339	-7. 7052	6. 23E-14
UGDH	1. 201232	4. 6481725	7. 69125	6. 88E-14
KRTCAP3	1. 264488	4. 573872	7. 69009	6. 93E-14
FGFBP1	2. 348235	4. 7730817	7. 68536	7. 17E-14
TRIM16	1. 142938	2. 965119	7. 67465	7. 73E-14
C12orf54	1. 271988	1. 3683242	7. 67211	7. 87E-14
CYTIP	-1. 11274	2. 3770366	-7. 6632	8. 38E-14
F13A1	-1. 40459	2. 7939924	-7. 6537	8. 95E-14
TBX1	1. 13882	2. 0234157	7. 61159	1. 20E-13
BIRC3	-1. 29688	2. 5874773	-7. 6015	1. 29E-13
PGLYRP4	1. 259045	1. 2376705	7. 59902	1. 31E-13
RHOD	1. 164005	4. 2377349	7. 59724	1. 33E-13
TENM2	1. 591106	1. 6655168	7. 59266	1. 37E-13
C2CD4A	1. 2012	1. 489911	7. 58807	1. 42E-13
SIRPA	-1. 01977	3. 8493254	-7. 5743	1. 56E-13
CPXM1	1. 328493	2. 8947002	7. 57344	1. 57E-13
SLC35F2	1. 030232	2. 9939106	7. 57222	1. 58E-13
SLC2A3	-1. 34759	3. 4469146	-7. 5663	1. 65E-13
IL36RN	1. 563831	1. 4672053	7. 5608	1. 71E-13
WFDC5	1. 508248	1. 6509312	7. 53325	2. 08E-13
PLEK	-1. 28003	3. 3002931	-7. 5183	2. 30E-13
FZD10	1. 589057	2. 111691	7. 50876	2. 46E-13
SLC6A15	1. 139238	1. 0608334	7. 5015	2. 59E-13
OASL	-1. 19628	2. 1228616	-7. 4629	3. 38E-13
SLC16A9	1. 202532	1. 742691	7. 45928	3. 46E-13
F2RL1	1. 136721	3. 2905902	7. 45732	3. 51E-13
WISP1	1. 119391	2. 1517316	7. 45056	3. 68E-13
NFE2L3	1. 04444	3. 3188958	7. 43347	4. 13E-13
STC2	1. 250834	2. 8245347	7. 42321	4. 43E-13
FHL2	1. 201488	2. 8129175	7. 41888	4. 57E-13
CH25H	-1. 37556	2. 2955524	-7. 4099	4. 86E-13
SV2A	1. 042518	1. 7950503	7. 3972	5. 30E-13
SERPINB7	1. 481577	1. 5361295	7. 39429	5. 41E-13
FAM110C	1. 343113	2. 9163839	7. 36665	6. 53E-13
P3H3	1. 012402	2. 882261	7. 36616	6. 55E-13
C15orf48	1. 546178	3. 7099925	7. 36536	6. 59E-13
SPRR2E	2. 975555	3. 096919	7. 35914	6. 87E-13
SYT7	1. 120036	1. 97626	7. 35422	7. 11E-13
TNFRSF19	-1. 11441	2. 1567542	-7. 3518	7. 22E-13
IL36G	2. 068358	1. 9640962	7. 35144	7. 24E-13
AQP5	-1. 43686	1. 3464488	-7. 3453	7. 55E-13
PLA2G2A	-1. 44109	1. 2958743	-7. 3187	9. 05E-13
CRISPLD2	-1. 07486	2. 8325559	-7. 3158	9. 23E-13
EGR3	-1. 02778	1. 6678564	-7. 3114	9. 50E-13
SULF2	1. 316244	4. 1990605	7. 30939	9. 63E-13
AKR1B15	1. 461425	1. 3513978	7. 29449	1. 07E-12

HLA-C	-1.03257	8.377172	-7.2786	1.19E-12
HLA-DQA2	-1.94511	3.7238183	-7.2625	1.32E-12
HSD17B13	-1.00052	0.5456082	-7.2565	1.38E-12
HS3ST2	-1.04364	1.4298412	-7.2531	1.41E-12
C1QL1	1.044664	1.0877588	7.2407	1.53E-12
IFIT3	-1.27931	3.7844148	-7.2407	1.53E-12
IGFL1	1.885782	1.8256491	7.23148	1.63E-12
MAGEA4	2.832121	2.6540223	7.22899	1.66E-12
FGA	-1.44892	0.8866411	-7.2282	1.67E-12
ATP2C2	-1.01605	1.6661588	-7.2133	1.84E-12
XG	1.125049	1.4321546	7.19518	2.08E-12
SBSN	2.295228	2.3096486	7.18344	2.25E-12
FAM132A	1.243618	1.3954529	7.17968	2.31E-12
G6PD	1.335228	5.4772211	7.1769	2.35E-12
HOXC10	1.462709	1.3720198	7.17561	2.37E-12
AREG	-1.65792	3.2798095	-7.1624	2.59E-12
COL14A1	-1.27049	2.03919	-7.1297	3.22E-12
GOS2	-1.41282	3.7307701	-7.1219	3.39E-12
CEL	1.706722	1.8300544	7.11029	3.66E-12
KCNK1	1.123612	3.3195492	7.10353	3.83E-12
GDA	1.169019	1.1578504	7.10019	3.91E-12
GABRE	1.433862	2.4701946	7.09537	4.04E-12
MAP7D2	1.094184	1.2150337	7.08287	4.39E-12
CYP4F11	2.495102	2.8079242	7.07333	4.67E-12
PCDH19	1.194809	1.222504	7.06901	4.81E-12
SRPX2	1.044859	3.0068654	7.0525	5.36E-12
C5orf38	-1.05276	2.0153256	-7.0374	5.92E-12
CAPS	-1.23149	2.5424749	-7.0168	6.78E-12
KLF5	1.187636	5.6869354	7.0114	7.02E-12
PADI3	2.136157	2.0056847	7.00452	7.35E-12
CCL21	-1.67108	4.8410978	-7.0021	7.47E-12
HORMAD1	1.206952	1.233977	6.99352	7.90E-12
BARX2	1.398688	1.5702574	6.97803	8.74E-12
RBP1	1.501582	3.8534299	6.97671	8.81E-12
THBD	-1.49524	4.2556753	-6.9705	9.17E-12
IGFBP7	-1.03183	6.7660982	-6.9586	9.92E-12
STEAP1B	1.024798	1.1903096	6.95682	1.00E-11
MMP13	2.3501	2.3858791	6.94027	1.12E-11
PLAC8	-1.36053	2.0868478	-6.9323	1.18E-11
NDUFA4L2	1.863413	5.3018291	6.92271	1.25E-11
ANXA8	1.346359	2.4973925	6.88577	1.59E-11
ACKR3	1.604423	5.5015259	6.87704	1.68E-11
WNT5A	1.43706	3.3964405	6.87045	1.76E-11
CALML5	2.570219	2.4936281	6.84649	2.05E-11
KIAA1549L	1.018958	1.0279795	6.8294	2.29E-11
MXRA5	1.300638	3.7635599	6.7995	2.77E-11
NIPAL4	1.214773	1.3172376	6.78545	3.03E-11
SPTSSB	1.184751	1.167456	6.78524	3.03E-11

KRT80	1. 3286	3. 1113302	6. 76214	3. 52E-11
COL8A1	-1. 16884	2. 964202	-6. 7619	3. 52E-11
DMRT2	1. 437119	1. 8221755	6. 73549	4. 17E-11
TAGLN	-1. 15596	5. 2051326	-6. 7344	4. 20E-11
FKBP10	1. 207291	4. 6557259	6. 73131	4. 28E-11
EN02	1. 012795	4. 3067535	6. 73125	4. 28E-11
MRAP2	1. 533416	2. 2025625	6. 72704	4. 40E-11
FEZF1	1. 035029	0. 9775341	6. 72047	4. 58E-11
NRCAM	1. 421013	2. 2030156	6. 71617	4. 71E-11
PAPL	1. 165523	1. 1237166	6. 70695	4. 99E-11
BMP3	-1. 17607	1. 1962082	-6. 7068	5. 00E-11
PRSS22	1. 296957	3. 3515061	6. 68968	5. 57E-11
CD14	-1. 05728	5. 2258156	-6. 6894	5. 58E-11
ITGA11	1. 019547	1. 6542658	6. 67081	6. 27E-11
TMPRSS11A	1. 727089	1. 6039683	6. 66475	6. 51E-11
NDN	-1. 08901	3. 0742799	-6. 6617	6. 64E-11
IL32	-1. 13781	3. 9807403	-6. 654	6. 97E-11
TESC	-1. 01395	1. 2766511	-6. 6462	7. 32E-11
CYP24A1	1. 672948	1. 8897772	6. 62124	8. 56E-11
SERPINB2	1. 748465	2. 1228442	6. 60588	9. 42E-11
MAGEA3	2. 1549	1. 9801881	6. 58088	1. 10E-10
RASL11A	-1. 18538	2. 3997123	-6. 5766	1. 13E-10
SRXN1	1. 212043	1. 7624352	6. 57426	1. 15E-10
IL4I1	1. 011682	2. 4101554	6. 56687	1. 20E-10
RNASE7	1. 279701	1. 2729376	6. 56629	1. 21E-10
HES6	1. 130841	2. 2262921	6. 55085	1. 33E-10
KLK6	1. 626607	1. 5629032	6. 5371	1. 45E-10
HLA-B	-1. 03372	8. 8112285	-6. 5364	1. 45E-10
PGD	1. 186852	6. 8230682	6. 5271	1. 54E-10
MS4A6A	-1. 00229	2. 7555118	-6. 5236	1. 57E-10
NMB	1. 078884	3. 7132917	6. 52306	1. 58E-10
LRRC15	1. 274127	2. 0025963	6. 51896	1. 62E-10
KRT31	1. 68961	1. 5530962	6. 5077	1. 73E-10
ITGB6	-1. 31285	3. 7019549	-6. 4919	1. 91E-10
COL5A1	1. 338642	4. 5372493	6. 49191	1. 91E-10
HIST1H4H	1. 13974	2. 4844381	6. 48787	1. 96E-10
SOX9	1. 26239	3. 1730296	6. 48213	2. 03E-10
MAGEA6	2. 065477	1. 8959726	6. 45084	2. 46E-10
AIM2	1. 182521	1. 9440327	6. 44129	2. 61E-10
SLC35G1	1. 018344	1. 7342422	6. 42512	2. 88E-10
UPK1B	2. 802573	3. 1672185	6. 42193	2. 94E-10
AKR1C1	2. 407474	4. 1161226	6. 38973	3. 57E-10
LAMA1	1. 041058	1. 1810778	6. 38257	3. 73E-10
KLK8	1. 358406	1. 3252589	6. 36852	4. 06E-10
IRX4	1. 280524	1. 1733553	6. 36797	4. 08E-10
FXYD3	1. 461858	6. 4178079	6. 34212	4. 77E-10
EDIL3	-1. 0124	2. 7611979	-6. 2999	6. 15E-10
NTRK2	1. 86027	2. 9889247	6. 29334	6. 40E-10

NTS	3. 246686	4. 186566	6. 29035	6. 51E-10
GAST	1. 199926	1. 1201806	6. 27304	7. 23E-10
GSR	1. 019469	5. 2291214	6. 2544	8. 08E-10
GPR183	-1. 00338	2. 9422681	-6. 2518	8. 21E-10
A4GALT	1. 098407	4. 0968531	6. 23659	8. 99E-10
TMEM45A	1. 195497	2. 9522447	6. 22964	9. 37E-10
POSTN	1. 400873	5. 2687243	6. 22255	9. 77E-10
CLEC2L	1. 080298	1. 031513	6. 22094	9. 87E-10
COL4A5	1. 108966	3. 0753952	6. 20984	1. 05E-09
FPR3	-1. 02235	3. 0660278	-6. 2027	1. 10E-09
LY6G6C	1. 304388	1. 3292771	6. 1985	1. 13E-09
MT1E	-1. 40994	4. 2096606	-6. 1955	1. 15E-09
TP53AIP1	1. 039244	1. 0867565	6. 17652	1. 28E-09
FBN2	1. 508174	1. 5622556	6. 1756	1. 29E-09
KRT75	1. 368742	1. 2757707	6. 1634	1. 39E-09
POPDC3	1. 079363	1. 3794548	6. 14936	1. 51E-09
CCL18	-1. 59588	5. 280314	-6. 1421	1. 57E-09
HMOX1	-1. 06597	4. 5338219	-6. 1316	1. 67E-09
LAMB3	1. 228885	6. 3487288	6. 12609	1. 73E-09
NQ01	1. 770709	5. 0299754	6. 11937	1. 80E-09
CBR1	1. 347766	5. 5221371	6. 10449	1. 96E-09
HP	-1. 43084	1. 7955193	-6. 1025	1. 98E-09
SELL	-1. 07321	2. 4692823	-6. 0996	2. 02E-09
FAM46C	-1. 03896	2. 5473393	-6. 0836	2. 22E-09
MAGEA11	1. 329245	1. 2174352	6. 06851	2. 42E-09
ME1	1. 279002	4. 1370328	6. 04085	2. 84E-09
BASP1	1. 197479	4. 7938726	6. 03767	2. 90E-09
ECHDC3	-1. 08301	2. 457938	-6	3. 60E-09
TFRC	1. 127459	6. 1092447	5. 99085	3. 80E-09
LOXL2	1. 002836	3. 0849325	5. 9776	4. 10E-09
LGALS7	1. 694556	1. 6236665	5. 96514	4. 40E-09
COLCA2	1. 091319	2. 0922653	5. 95768	4. 60E-09
TSPAN7	-1. 42436	3. 444125	-5. 9568	4. 62E-09
GLYATL2	1. 152153	1. 1279489	5. 91698	5. 80E-09
CD24	1. 290012	6. 0598896	5. 90126	6. 35E-09
VSTM2L	-1. 17664	1. 8690544	-5. 8771	7. 28E-09
PTGS2	-1. 3712	3. 0466995	-5. 8691	7. 62E-09
CYP26A1	1. 193324	1. 162223	5. 84466	8. 75E-09
FNDC1	1. 074143	2. 1151644	5. 83511	9. 24E-09
CCL13	-1. 12228	2. 3477942	-5. 8324	9. 38E-09
SPRR2G	1. 641885	1. 6216011	5. 81754	1. 02E-08
ALDH3A1	2. 33386	4. 1760249	5. 76806	1. 35E-08
ACTA2	-1. 02945	5. 4397623	-5. 765	1. 37E-08
CLIC6	-1. 11649	2. 6135044	-5. 7411	1. 56E-08
MYEOV	1. 099871	1. 1005871	5. 7333	1. 63E-08
CYP4F3	1. 886692	2. 1936235	5. 73112	1. 65E-08
EEF1A2	1. 614482	1. 8437586	5. 71581	1. 80E-08
HOXB9	1. 050131	0. 9821708	5. 70022	1. 96E-08

PTGR1	1. 359287	4. 1817228	5. 66865	2. 34E-08
CLCA4	1. 315674	1. 2738542	5. 65225	2. 56E-08
FZD7	1. 024596	3. 6726453	5. 6313	2. 87E-08
AMTN	1. 738862	1. 6839223	5. 62243	3. 01E-08
FGFR3	1. 281977	4. 156094	5. 61602	3. 12E-08
BCAM	-1. 07349	5. 1060295	-5. 6114	3. 20E-08
KRTDAP	1. 887508	2. 0287953	5. 53694	4. 80E-08
AQP3	-1. 63674	5. 3178466	-5. 4968	5. 95E-08
CHP2	1. 035243	1. 151374	5. 45727	7. 36E-08
TSPAN18	-1. 04553	2. 6229002	-5. 4544	7. 47E-08
CRCT1	1. 228933	1. 1654556	5. 43765	8. 17E-08
NEFL	1. 273211	1. 3016634	5. 429	8. 55E-08
CHST2	1. 088639	3. 1371883	5. 42377	8. 79E-08
TUBB2B	1. 210518	1. 6061498	5. 4144	9. 24E-08
RAB6B	1. 199288	2. 3554497	5. 41166	9. 38E-08
SPRR2F	1. 499979	1. 676085	5. 4086	9. 53E-08
NPPC	1. 195997	1. 2147635	5. 36299	1. 21E-07
KRT23	1. 392364	1. 9157227	5. 31453	1. 56E-07
HAS3	1. 311691	4. 3573542	5. 30801	1. 62E-07
POMC	1. 064931	1. 6463122	5. 2981	1. 70E-07
UGT1A7	1. 375592	1. 2703044	5. 29358	1. 74E-07
BPIFB1	-1. 9686	2. 7200802	-5. 2791	1. 88E-07
DERL3	1. 002907	2. 8941378	5. 25245	2. 16E-07
MAGEA1	1. 509384	1. 3988979	5. 17723	3. 17E-07
NGFR	1. 133488	2. 1276504	5. 15068	3. 63E-07
FETUB	1. 198104	1. 1104788	5. 15047	3. 64E-07
TCN1	1. 176032	1. 2846458	5. 11463	4. 36E-07
LCE3D	1. 24822	1. 1696928	5. 09477	4. 82E-07
LRG1	-1. 02119	2. 692862	-5. 0754	5. 32E-07
LAMC2	1. 240092	5. 7208521	5. 06016	5. 74E-07
SOHLH1	1. 162132	1. 0681492	5. 04922	6. 06E-07
FN1	-1. 10197	6. 5287584	-5. 0126	7. 27E-07
F2RL2	1. 019756	1. 3223404	4. 97411	8. 80E-07
TNC	1. 288092	4. 9760629	4. 93847	1. 05E-06
KLHDC7B	1. 034324	1. 759781	4. 93185	1. 08E-06
SPRR2B	1. 087321	1. 0542751	4. 88186	1. 38E-06
SFRP2	1. 208624	5. 8738282	4. 86415	1. 51E-06
AKR1C3	1. 750114	4. 5501947	4. 84953	1. 62E-06
CRABP1	1. 012632	1. 0818048	4. 79022	2. 15E-06
C6orf15	1. 195629	1. 1624203	4. 76884	2. 38E-06
SCNN1A	-1. 04235	4. 2312864	-4. 7552	2. 54E-06
ZNF812	1. 099676	1. 7680945	4. 71268	3. 11E-06
KLK11	-1. 16278	2. 2210903	-4. 6918	3. 43E-06
CSAG1	1. 218662	1. 1436503	4. 66438	3. 90E-06
SOST	1. 416409	1. 4677675	4. 65175	4. 14E-06
GPNMB	1. 037995	7. 0233406	4. 64268	4. 32E-06
CLDN3	-1. 13037	2. 644451	-4. 6045	5. 15E-06
MAGEA10	1. 04613	0. 9590592	4. 58586	5. 62E-06

APOD	-1.0342	3.0002255	-4.5796	5.78E-06
SOSTDC1	-1.16199	2.516614	-4.576	5.88E-06
ALOX15	-1.1219	1.5002625	-4.5658	6.16E-06
GABRP	1.014226	1.3780728	4.41123	1.24E-05
PEG10	-1.07811	2.6971455	-4.3772	1.44E-05
NR0B1	1.098067	1.0181219	4.34616	1.65E-05
IGJ	-1.34684	6.7367101	-4.2572	2.44E-05
MAGEB2	1.065402	0.9839573	4.2423	2.60E-05
MAGEA12	1.021153	0.9455061	4.14061	4.01E-05
CXCL6	1.06034	2.1140628	4.01107	6.89E-05
FDCSP	1.569845	2.5871891	3.97213	8.08E-05
GPC3	-1.20397	4.4899794	-3.7896	0.00016774
SAA1	1.027686	3.8315772	3.54378	0.00042836
KRT4	-1.15805	2.2156732	-3.4321	0.00064443
CES1	-1.29732	5.101265	-3.0661	0.00227638
GSTM1	1.054726	1.776484	2.96095	0.00320073

Supplementary Table 6

376 overlapping genes

UBE2C

TPX2

CDC20

MYBL2

CCNB1

CCNB2

CDCA5

PLK1

KIF2C

CDCA8

NUSAP1

KIF4A

ANLN

CEP55

CCNA2

TOP2A

PRC1

KIF11

MCM4

RRM2

NCAPH

PTTG1

CENPA

ZWINT

HJURP

KIF23
KIFC1
AURKA
BUB1B
KIF20A
TROAP
KPNA2
BUB1
CDC6
NCAPG
MCM2
CDT1
TTK
RACGAP1
CKAP2L
RAD51
GTSE1
ASF1B
EXO1
SKA3
RAD54L
MAD2L1
NDC80
FANCI
FEN1
CHEK1
PRR11
CENPF
PKMYT1
SKA1
MKI67
ORC1
ARHGAP11A
KIF18B
SPC25
UHRF1
SPAG5
OIP5
TIMELESS
ATAD2
STIL
SPC24
ZWILCH
MCM10
SHCBP1
CENPU
ALDH18A1
CCNF

MRGBP
IQGAP3
CDCA2
DEPDC1B
RCC1
ASPM
CASC5
MND1
CENPH
RNASEH2A
HMMR
EZH2
RCC2
C17orf53
ESPL1
DENR
AUNIP
MCM7
UNG
SGOL1
DTL
CDC25A
CENPI
KNSTRN
PLK4
C16orf59
MCM6
KIF14
DSCC1
CDCA7
TYMS
MIS18A
NCAPG2
KIF15
LMNB1
CDC25C
LM03
TRAIP
PLLP
HELLS
SRPK1
IGSF9
POC1A
KIF22
LMNB2
NDC1
RFC5
ERCC6L

KNTC1
HDGF
DNAJC9
MT1M
UTRN
XRCC2
MYO19
PNPLA6
CENPE
CHAF1B
INCENP
FANCD2
MTFR2
TACC3
CENPO
BLM
PARPBP
SRSF9
C1orf112
TUBB
EME1
RFWD3
PGAM5
TICRR
MCM8
TCF19
E2F7
PLEKHH2
FIGNL1
TFAP4
HN1L
MCM5
DDX39A
CASKIN2
BRIP1
E2F2
DNA2
E2F8
TRAF7
R3HDM1
C1orf131
DNALI1
TRAP1
XP01
ARHGEF19
BRI3BP
CHAF1A
KIF18A

DONSON
SGOL2
NELFCD
ZNF106
SPDL1
GID8
SASS6
SNRPA
B4GALNT4
PSRC1
FAM189B
HDAC2
MAPK6
FANCA
ANAPC7
DSN1
NEIL3
CLSPN
KAT2A
CAD
ADRM1
RHBDD3
FAM111B
TCF3
BORA
NOL11
SSRP1
HEATR1
CCDC137
GEN1
IGSF10
NDE1
CHTF18
RUSC1
CEP85
C1orf35
GART
NR2C2AP
NUP205
CDK2AP1
THOP1
E2F1
CTPS1
MRPS34
IRAK1
LSM4
PUS1
SUV39H1

PSMD11
MMP28
CARM1
STMN1
ATAD5
BRCA1
LPAR2
MSH6
PRKDC
PARP1
PAQR5
DDX49
RAC3
RPUSD1
MASTL
PIF1
MAZ
MACF1
CAV2
DARS2
FBXO5
POLA2
CDC7
SAMD1
SMC4
ATIC
FBXL19
DGKA
BIK
PGAM1
TJP1
IDH2
SSX2IP
TMEM194A
PAQR4
TTF2
LSM7
CBX1
MSH2
CABLES2
UBE20
CKAP5
GPRIN1
GTPBP3
PLXNB3
ARHGEF2
NEK7
GAREML

HOMER3
CBX2
TMPO
PLOD2
VANGL2
ALKBH2
MRPL4
ID4
RCN2
STAP2
DUS1L
TTC28
BCL11A
PRIM1
ZNF217
MEX3A
KRI1
RAPGEF5
UBTD1
SLC16A5
HMGB2
KIF3C
MID1IP1
KIAA0907
ATG4D
SNRNP25
LDLR
UPF3B
E2F3
NFIX
MARCKSL1
PROM2
NME4
RBBP8NL
SOX4
TARBP1
ZNF692
GPR115
FOXRED2
FBXO41
CST3
THSD1
MEX3D
CD151
ZNF608
MTL5
ADA
TPPP

HIF3A
C17orf96
SLC4A3
TET3
MSI2
SLC4A11
ANKRD13B
HBEGF
SPHK1
TNFRSF25
CLDN23
LGALS3
CST6
EYA2
MRPL21
IFI16
MTCL1
UCN2
PLCH2
FAM83A
B3GNT8
KIFC2
VPS37D
NOTCH3
TMEM184A
WDR76
SYTL1
HAP1
MME
PLEKHG4
NFIB
SERINC2
MSI1
HOXC9
TNNI2
B3GNT3
LY6D
TDRD5
PABPC1L
CA2
IL23A
AC105009. 1
GAL
KDELR3
KIT
RHOD
GABRE
MAP7D2

PCDH19
 SRPX2
 ANXA8
 FEZF1
 BMP3
 PRSS22
 KRT31
 SOX9
 TMEM45A
 MT1E
 POPDC3
 LGALS7
 COLCA2
 CLIC6
 FGFR3

Supplementary Table 7

DE-HGs were remarkably enriched in nuclear division (BP)
 condensed chromosome (CC), and microtubule binding (MF)

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	Count
BP	GO:000028	nuclear division	70/344	407/18670	1.13E-47	70
BP	GO:004828	organelle	72/344	449/18670	7.08E-47	72
BP	GO:014001	mitotic nucleus	58/344	264/18670	9.78E-46	58
BP	GO:000705	chromosome	61/344	321/18670	4.02E-44	61
BP	GO:000007	mitotic si	41/344	151/18670	1.85E-36	41
BP	GO:000081	sister chr	43/344	189/18670	1.22E-34	43
BP	GO:009881	nuclear cl	48/344	262/18670	6.25E-34	48
BP	GO:000626	DNA replic	47/344	273/18670	5.98E-32	47
BP	GO:000007	cell cycle	41/344	216/18670	1.06E-29	41
BP	GO:000709	mitotic ce	35/344	165/18670	3.27E-27	35
BP	GO:190199	regulator	52/344	444/18670	6.46E-27	52
BP	GO:190198	regulator	53/344	480/18670	3.52E-26	53
BP	GO:000708	regulator	34/344	164/18670	4.16E-26	34
BP	GO:190285	microtubul	30/344	131/18670	1.64E-24	30
BP	GO:005178	regulator	34/344	188/18670	4.81E-24	34
BP	GO:000626	DNA-depenc	31/344	151/18670	9.38E-24	31
BP	GO:000705	spindle or	32/344	170/18670	2.99E-23	32
BP	GO:001094	negative r	43/344	361/18670	1.23E-22	43
BP	GO:005198	regulator	26/344	103/18670	1.45E-22	26
BP	GO:004593	negative r	40/344	338/18670	5.26E-21	40
BP	GO:003157	DNA integ	29/344	157/18670	6.28E-21	29
BP	GO:007110	DNA confor	41/344	364/18670	1.06E-20	41
BP	GO:190198	negative r	34/344	267/18670	5.33E-19	34
BP	GO:000631	DNA recom	35/344	292/18670	1.13E-18	35

BP	GO:000705 mitotic sp23/344	106/18670	1. 72E-18	23
BP	GO:004483 cell cycle33/344	266/18670	4. 03E-18	33
BP	GO:190199 negative r132/344	248/18670	4. 09E-18	32
BP	GO:001096 regulation18/344	57/18670	6. 22E-18	18
BP	GO:005130 chromosome21/344	90/18670	1. 09E-17	21
BP	GO:003304 regulation20/344	80/18670	1. 52E-17	20
BP	GO:004484 cell cycle34/344	298/18670	1. 70E-17	34
BP	GO:009006 positive r134/344	298/18670	1. 70E-17	34
BP	GO:000008 G1/S transition33/344	279/18670	1. 74E-17	33
BP	GO:005130 mitotic si18/344	60/18670	1. 76E-17	18
BP	GO:004478 cell cycle19/344	71/18670	2. 44E-17	19
BP	GO:190581 regulation18/344	62/18670	3. 41E-17	18
BP	GO:000709 metaphase17/344	54/18670	5. 57E-17	17
BP	GO:004478 metaphase17/344	56/18670	1. 12E-16	17
BP	GO:190304 meiotic ce27/344	188/18670	1. 19E-16	27
BP	GO:003304 regulation18/344	68/18670	2. 12E-16	18
BP	GO:004578 positive r137/344	389/18670	2. 48E-16	37
BP	GO:000008 G2/M transition30/344	247/18670	2. 58E-16	30
BP	GO:005132 meiotic ce30/344	249/18670	3. 23E-16	30
BP	GO:190274 regulation28/344	213/18670	3. 35E-16	28
BP	GO:003007 regulation16/344	51/18670	4. 99E-16	16
BP	GO:190209 regulation16/344	53/18670	9. 98E-16	16
BP	GO:003304 negative r115/344	44/18670	1. 00E-15	15
BP	GO:005198 negative r115/344	45/18670	1. 48E-15	15
BP	GO:200081 negative r14/344	39/18670	3. 98E-15	14
BP	GO:004477 mitotic DN20/344	106/18670	5. 42E-15	20
BP	GO:190581 negative r14/344	40/18670	6. 01E-15	14
BP	GO:014001 meiotic nr24/344	172/18670	1. 20E-14	24
BP	GO:003304 negative r14/344	42/18670	1. 33E-14	14
BP	GO:004583 negative r115/344	52/18670	1. 71E-14	15
BP	GO:000007 DNA damage22/344	145/18670	2. 67E-14	22
BP	GO:001038 regulation25/344	196/18670	2. 76E-14	25
BP	GO:004584 negative r13/344	36/18670	3. 55E-14	13
BP	GO:003288 regulation26/344	218/18670	4. 20E-14	26
BP	GO:190210 negative r13/344	37/18670	5. 39E-14	13
BP	GO:000072 double-st121/344	134/18670	5. 39E-14	21
BP	GO:000072 recombination21/344	135/18670	6. 28E-14	21
BP	GO:007050 regulation24/344	186/18670	7. 09E-14	24
BP	GO:005131 metaphase 15/344	57/18670	7. 74E-14	15
BP	GO:000630 double-st127/344	248/18670	1. 27E-13	27
BP	GO:003326 nuclear DN15/344	60/18670	1. 78E-13	15
BP	GO:005178 negative r115/344	60/18670	1. 78E-13	15
BP	GO:200125 negative r121/344	146/18670	3. 08E-13	21
BP	GO:005130 establishment16/344	75/18670	3. 98E-13	16
BP	GO:000709 mitotic si12/344	34/18670	4. 82E-13	12
BP	GO:003157 spindle ch12/344	34/18670	4. 82E-13	12
BP	GO:007117 spindle assembly12/344	34/18670	4. 82E-13	12
BP	GO:007117 mitotic si12/344	34/18670	4. 82E-13	12

BP	GO:005000 chromosome 16/344	76/18670	4. 96E-13	16
BP	GO:003239 DNA geometr 19/344	119/18670	6. 21E-13	19
BP	GO:000708 mitotic me 13/344	44/18670	6. 99E-13	13
BP	GO:000627 DNA replicat 12/344	37/18670	1. 55E-12	12
BP	GO:003304 regulation 30/344	342/18670	1. 57E-12	30
BP	GO:000632 DNA packag 25/344	247/18670	5. 39E-12	25
BP	GO:009032 regulation 13/344	54/18670	1. 26E-11	13
BP	GO:000627 regulation 17/344	108/18670	1. 32E-11	17
BP	GO:000709 centrosome 18/344	124/18670	1. 34E-11	18
BP	GO:003250 DNA duplec 17/344	110/18670	1. 79E-11	17
BP	GO:004477 mitotic DM 16/344	97/18670	2. 56E-11	16
BP	GO:006500 protein-DN 24/344	248/18670	3. 75E-11	24
BP	GO:003102 microtubul 18/344	133/18670	4. 47E-11	18
BP	GO:007240 signal tra 14/344	73/18670	5. 54E-11	14
BP	GO:007242 signal tra 14/344	73/18670	5. 54E-11	14
BP	GO:000091 cytokinesi 20/344	171/18670	5. 56E-11	20
BP	GO:007239 signal tra 14/344	74/18670	6. 71E-11	14
BP	GO:005122 spindle a 16/344	108/18670	1. 37E-10	16
BP	GO:007233 signal tra 24/344	267/18670	1. 75E-10	24
BP	GO:004660 regulation 12/344	58/18670	5. 27E-10	12
BP	GO:000028 mitotic cy 13/344	72/18670	6. 00E-10	13
BP	GO:006198 meiosis I 16/344	119/18670	6. 02E-10	16
BP	GO:007182 protein-DN 24/344	288/18670	8. 21E-10	24
BP	GO:001063 negative r 128/344	393/18670	1. 13E-09	28
BP	GO:004593 positive r 18/344	163/18670	1. 33E-09	18
BP	GO:005165 establishm 28/344	401/18670	1. 77E-09	28
BP	GO:004277 signal tra 16/344	133/18670	3. 17E-09	16
BP	GO:000860 attachment 9/344	32/18670	4. 26E-09	9
BP	GO:003450 centromere 11/344	56/18670	5. 03E-09	11
BP	GO:004000 establishm 9/344	33/18670	5. 76E-09	9
BP	GO:000007 DNA replicat 7/344	16/18670	6. 73E-09	7
BP	GO:190198 positive r 14/344	106/18670	9. 15E-09	14
BP	GO:004513 meiotic ch 13/344	90/18670	1. 03E-08	13
BP	GO:005165 spindle l 10/344	48/18670	1. 39E-08	10
BP	GO:000072 double-stri 6/344	11/18670	1. 60E-08	6
BP	GO:003157 mitotic G 11/344	63/18670	1. 85E-08	11
BP	GO:004481 mitotic G 11/344	63/18670	1. 85E-08	11
BP	GO:004478 G1 DNA dan 11/344	64/18670	2. 20E-08	11
BP	GO:005129 centrosome 11/344	67/18670	3. 62E-08	11
BP	GO:000008 regulation 8/344	29/18670	3. 75E-08	8
BP	GO:006164 cytoskelet 13/344	100/18670	3. 78E-08	13
BP	GO:003450 protein l 12/344	83/18670	3. 79E-08	12
BP	GO:190275 positive r 8/344	30/18670	5. 03E-08	8
BP	GO:005138 kinetochor 7/344	21/18670	6. 32E-08	7
BP	GO:005129 establishm 9/344	43/18670	7. 16E-08	9
BP	GO:007243 signal tra 10/344	57/18670	7. 93E-08	10
BP	GO:190240 intracellu 10/344	57/18670	7. 93E-08	10
BP	GO:003246 regulation 12/344	89/18670	8. 41E-08	12

BP	GO:000626 DNA unwinding/344	14/18670	9.93E-08	6
BP	GO:190199 positive regulation/344	91/18670	1.08E-07	12
BP	GO:007241 signal transduction/344	59/18670	1.12E-07	10
BP	GO:190240 signal transduction/344	59/18670	1.12E-07	10
BP	GO:190240 signal transduction/344	59/18670	1.12E-07	10
BP	GO:003110 microtubule/344	112/18670	1.48E-07	13
BP	GO:005105 regulation/344	351/18670	1.65E-07	23
BP	GO:000712 meiosis I/344	114/18670	1.83E-07	13
BP	GO:003105 chromatin/344	48/18670	1.96E-07	9
BP	GO:003114 anaphase-telophase/344	81/18670	2.72E-07	11
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BP	GO:000633 nucleosome/344	145/18670	4.94E-07	14
BP	GO:000689 retrograde transport/344	86/18670	11	
BP	GO:190275 negative regulation/344	105/18670	5.31E-07	12
BP	GO:005130 regulation/344	168/18670	5.33E-07	15
BP	GO:000633 DNA replication/344	54/18670	5.65E-07	9
BP	GO:190402 regulation/344	106/18670	5.90E-07	12
BP	GO:003472 DNA replication/344	55/18670	6.65E-07	9
BP	GO:004500 DNA-dependent/344	41/18670	6.89E-07	8
BP	GO:000013 establishment/344	29/18670	7.47E-07	7
BP	GO:000697 DNA damage response/344	56/18670	9	
BP	GO:009030 mitotic spindle/344	56/18670	7.79E-07	9
BP	GO:004481 mitotic G2/M/344	30/18670	9.59E-07	7
BP	GO:001082 regulation/344	43/18670	1.01E-06	8
BP	GO:003149 chromatin/16/344	202/18670	1.12E-06	16
BP	GO:003408 CENP-A core/344	44/18670	1.22E-06	8
BP	GO:006164 CENP-A core/344	44/18670	1.22E-06	8
BP	GO:000714 female meiosis/344	31/18670	1.22E-06	7
BP	GO:003157 G2 DNA damage/344	31/18670	1.22E-06	7
BP	GO:000729 female gamete/344	136/18670	1.42E-06	13
BP	GO:005198 regulation/5/344	12/18670	1.47E-06	5
BP	GO:190197 regulation/7/344	32/18670	1.54E-06	7
BP	GO:007145 protein localization/centromere/344	21/18670	6	
BP	GO:003026 chromosome/8/344	47/18670	2.06E-06	8
BP	GO:000706 sister chromatids/344	63/18670	2.17E-06	9
BP	GO:190466 regulation/6/344	22/18670	2.18E-06	6
BP	GO:000001 regulation/11/344	101/18670	2.57E-06	11
BP	GO:007115 positive regulation/10/344	82/18670	2.61E-06	10
BP	GO:005129 establishment/7/344	35/18670	2.93E-06	7
BP	GO:001021 response to/13/344	147/18670	3.41E-06	13
BP	GO:200013 negative regulation/12/344	125/18670	3.45E-06	12
BP	GO:000710 mitotic centromere/344	14/18670	3.60E-06	5
BP	GO:009023 regulation/5/344	14/18670	3.60E-06	5
BP	GO:009026 regulation/5/344	14/18670	3.60E-06	5
BP	GO:190350 regulation/5/344	14/18670	3.60E-06	5
BP	GO:003033 DNA damage response/11/344	11/18670	107/18670	11
BP	GO:007115 regulation/11/344	108/18670	4.97E-06	11

BP	GO:003629 interstruc8/344	53/18670	5.27E-06	8
BP	GO:005129 centrosome5/344	15/18670	5.32E-06	5
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BP	GO:190280 negative 12/344	131/18670	5.63E-06	12
BP	GO:000701 microtubule18/344	285/18670	6.20E-06	18
BP	GO:003472 nucleosome14/344	184/18670	8.37E-06	14
BP	GO:200004 regulation14/344	184/18670	8.37E-06	14
BP	GO:007031 negative 17/344	41/18670	8.90E-06	7
BP	GO:005198 positive 16/344	28/18670	1.00E-05	6
BP	GO:007116 protein 1c6/344	28/18670	1.00E-05	6
BP	GO:000707 mitotic cl5/344	17/18670	1.06E-05	5
BP	GO:003450 protein 1c5/344	17/18670	1.06E-05	5
BP	GO:001988 antigen pr10/344	98/18670	1.32E-05	10
BP	GO:002241 cellular p20/344	361/18670	1.34E-05	20
BP	GO:004348 histone e8/344	60/18670	1.36E-05	8
BP	GO:000701 microtubule7/344	44/18670	1.45E-05	7
BP	GO:000633 chromatin 15/344	220/18670	1.50E-05	15
BP	GO:007031 regulation7/344	45/18670	1.69E-05	7
BP	GO:000249 antigen pr10/344	101/18670	1.72E-05	10
BP	GO:000256 somatic di8/344	62/18670	1.74E-05	8
BP	GO:001644 somatic ce8/344	62/18670	1.74E-05	8
BP	GO:000250 antigen pr10/344	102/18670	1.88E-05	10
BP	GO:003287 regulation4/344	10/18670	2.18E-05	4
BP	GO:003331 mitotic DM4/344	10/18670	2.18E-05	4
BP	GO:005123 spindle el4/344	10/18670	2.18E-05	4
BP	GO:004502 G0 to G1 t7/344	47/18670	2.26E-05	7
BP	GO:003129 replication6/344	32/18670	2.26E-05	6
BP	GO:190280 regulation14/344	202/18670	2.41E-05	14
BP	GO:007019 chromosome8/344	65/18670	2.48E-05	8
BP	GO:004202 DNA endore4/344	11/18670	3.37E-05	4
BP	GO:004304 ATP-dependenc9/344	88/18670	3.50E-05	9
BP	GO:001644 somatic re7/344	52/18670	4.45E-05	7
BP	GO:200102 regulation14/344	214/18670	4.54E-05	14
BP	GO:004574 positive 16/344	36/18670	4.57E-05	6
BP	GO:000072 telomere n12/344	162/18670	4.80E-05	12
BP	GO:190466 positive 14/344	12/18670	4.99E-05	4
BP	GO:200010 positive 14/344	12/18670	4.99E-05	4
BP	GO:004584 positive 17/344	53/18670	5.05E-05	7
BP	GO:190342 regulation5/344	23/18670	5.28E-05	5
BP	GO:001097 negative 19/344	93/18670	5.44E-05	9
BP	GO:000220 somatic di8/344	75/18670	7.06E-05	8
BP	GO:000021 meiotic sr4/344	13/18670	7.10E-05	4
BP	GO:005131 attachment4/344	13/18670	7.10E-05	4
BP	GO:005130 meiotic cl5/344	25/18670	8.09E-05	5
BP	GO:200010 negative 15/344	25/18670	8.09E-05	5
BP	GO:000815 negative 16/344	40/18670	8.47E-05	6
BP	GO:200077 regulation8/344	77/18670	8.53E-05	8
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BP	GO:009022 regulation6/344	41/18670	9.77E-05	6
BP	GO:007242 signal tr ϵ 4/344	14/18670	9.80E-05	4
BP	GO:005110 regulation10/344	124/18670	0.000101	10
BP	GO:003220 telomere c12/344	175/18670	0.000101	12
BP	GO:003220 telomere n5/344	27/18670	0.000119	5
BP	GO:190296 mitotic D Δ 4/344	15/18670	0.000132	4
BP	GO:190179 regulation12/344	180/18670	0.000132	12
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BP	GO:001644 somatic d γ 7/344	64/18670	0.000171	7
BP	GO:005138 kinetochor ϵ 4/344	16/18670	0.000173	4
BP	GO:005178 positive r τ 7/344	66/18670	0.000208	7
BP	GO:005105 positive r τ 12/344	191/18670	0.00023	12
BP	GO:000931 response t τ 20/344	448/18670	0.000262	20
BP	GO:005144 regulation6/344	49/18670	0.000269	6
BP	GO:001644 somatic h γ 4/344	18/18670	0.000282	4
BP	GO:005178 negative r τ 4/344	18/18670	0.000282	4
BP	GO:004814 positive r τ 6/344	51/18670	0.000335	6
BP	GO:000256 somatic d γ 4/344	19/18670	0.000353	4
BP	GO:000709 regulation4/344	19/18670	0.000353	4
BP	GO:000914 pyrimidin ϵ 4/344	19/18670	0.000353	4
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BP	GO:005143 regulation6/344	52/18670	0.000373	6
BP	GO:000247 antigen p τ 11/344	175/18670	0.000414	11
BP	GO:000713 reciprocal6/344	53/18670	0.000415	6
BP	GO:003582 homologou ϵ 6/344	54/18670	0.000459	6
BP	GO:000705 cell cycl ϵ 13/344	237/18670	0.000476	13
BP	GO:000911 nucleobas ϵ 5/344	36/18670	0.000486	5
BP	GO:000716 establish12/344	210/18670	0.000543	12
BP	GO:000709 centriole 5/344	37/18670	0.000554	5
BP	GO:006023 regulation5/344	37/18670	0.000554	5
BP	GO:001988 antigen p τ 11/344	182/18670	0.000576	11
BP	GO:004514 homologou ϵ 6/344	57/18670	0.000616	6
BP	GO:000706 regulation4/344	22/18670	0.000637	4
BP	GO:004659 regulation4/344	22/18670	0.000637	4
BP	GO:000713 meiosis I β 3/344	10/18670	0.000676	3
BP	GO:005125 spindle m β 3/344	10/18670	0.000676	3
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BP	GO:003250 cytokineti β 5/344	39/18670	0.00071	5
BP	GO:000914 pyrimidin ϵ 4/344	23/18670	0.00076	4
BP	GO:200024 regulation10/344	160/18670	0.000784	10
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BP	GO:009853 centriole 5/344	40/18670	0.000799	5
BP	GO:004679 transport 6/344	60/18670	0.000812	6
BP	GO:004476 multi-org ϵ 6/344	61/18670	0.000886	6
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BP	GO:000188 liver deve δ 9/344	135/18670	0.000902	9
BP	GO:005126 protein de δ 8/344	109/18670	0.000926	8
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BP	GO:006100 hepaticobi9/344	138/18670	0.001054	9
BP	GO:000072 DNA double4/344	25/18670	0.001055	4
BP	GO:004654 developmer9/344	139/18670	0.001109	9
BP	GO:004847 oogenesis 7/344	87/18670	0.001122	7
BP	GO:000707 mitotic n3/344	12/18670	0.001206	3
BP	GO:001082 negative i3/344	12/18670	0.001206	3
BP	GO:005109 regulatioi3/344	12/18670	0.001206	3
BP	GO:006070 trophobla3/344	12/18670	0.001206	3
BP	GO:000155 oocyte mat4/344	26/18670	0.001229	4
BP	GO:000912 nucleoside5/344	44/18670	0.001242	5
BP	GO:000630 DNA modifi8/344	116/18670	0.001386	8
BP	GO:000157 microtubul7/344	91/18670	0.00146	7
BP	GO:004859 oocyte dev5/344	46/18670	0.001522	5
BP	GO:000220 somatic re5/344	47/18670	0.001677	5
BP	GO:000220 somatic di5/344	47/18670	0.001677	5
BP	GO:004519 isotype sv5/344	47/18670	0.001677	5
BP	GO:004846 cell matu10/344	177/18670	0.001685	10
BP	GO:004472 DNA methyl7/344	94/18670	0.001762	7
BP	GO:001594 nucleobase4/344	29/18670	0.001869	4
BP	GO:005164 centrosome4/344	29/18670	0.001869	4
BP	GO:004660 negative i3/344	14/18670	0.001941	3
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BP	GO:000231B cell act6/344	73/18670	0.002261	6
BP	GO:003110 animal org6/344	73/18670	0.002261	6
BP	GO:004362 cellular pi11/344	217/18670	0.00238	11
BP	GO:000132 formation 3/344	15/18670	0.002393	3
BP	GO:000920 pyrimidine3/344	15/18670	0.002393	3
BP	GO:003315 V(D)J recc3/344	15/18670	0.002393	3
BP	GO:009065 t-circle i3/344	15/18670	0.002393	3
BP	GO:009073 telomere n3/344	15/18670	0.002393	3
BP	GO:001045 exit from 4/344	31/18670	0.002406	4
BP	GO:000999 oocyte dif5/344	51/18670	0.002419	5
BP	GO:004678 microtubul6/344	76/18670	0.002773	6
BP	GO:000620 pyrimidine3/344	16/18670	0.002906	3
BP	GO:000920 pyrimidine3/344	16/18670	0.002906	3
BP	GO:003039 membrane c3/344	16/18670	0.002906	3
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BP	GO:000915 ribonuclec4/344	33/18670	0.003039	4
BP	GO:005144 positive i4/344	33/18670	0.003039	4
BP	GO:004339 negative i5/344	54/18670	0.003114	5
BP	GO:000863 intrinsic 7/344	104/18670	0.00313	7
BP	GO:001988 antigen pr11/344	226/18670	0.003252	11
BP	GO:003111 regulatioi6/344	79/18670	0.003368	6

BP	GO:003278 positive regulation of transcription from RNA polymerase II promoter	15/344	55/18670	0.003375	5
BP	GO:004438 protein localization to nucleus	15/344	55/18670	0.003375	5
BP	GO:000626 DNA ligase III	3/344	17/18670	0.00348	3
BP	GO:000627 DNA strand break repair	3/344	17/18670	0.00348	3
BP	GO:000834 determinant	3/344	17/18670	0.00348	3
BP	GO:007189 DNA biosynthesis	10/344	196/18670	0.003532	10
BP	GO:000728 germ cell development	12/344	262/18670	0.003537	12
BP	GO:004346 regulation of gene expression	6/344	80/18670	0.003586	6
BP	GO:000238 immunoglobulin	5/344	56/18670	0.003651	5
BP	GO:000926 deoxyribonucleic acid	4/344	35/18670	0.003779	4
BP	GO:007573 intracellular	5/344	57/18670	0.003943	5
BP	GO:007169 anatomical structure	11/344	232/18670	0.003964	11
BP	GO:005109 regulation of gene expression	15/344	373/18670	0.004062	15
BP	GO:004814 regulation of transcription	6/344	83/18670	0.004302	6
BP	GO:004814 fibroblast	6/344	84/18670	0.004563	6
BP	GO:200075 regulation of gene expression	5/344	59/18670	0.004576	5
BP	GO:000941 response to stimulus	8/344	141/18670	0.004658	8
BP	GO:003139 regulation of transcription	10/344	204/18670	0.00468	10
BP	GO:004327 response to growth factor	7/344	112/18670	0.004715	7
BP	GO:000912 purine nucleotide	3/344	19/18670	0.004826	3
BP	GO:000916 purine ribosom	3/344	19/18670	0.004826	3
BP	GO:004665 tetrahedron	3/344	19/18670	0.004826	3
CC	GO:009868 chromosome	62/354	347/19717	9.54E-44	62
CC	GO:000077 chromosome centromere	46/354	193/19717	4.60E-44	46
CC	GO:000079 condensed chromatin	46/354	223/19717	2.03E-35	46
CC	GO:000581 spindle pole	54/354	347/19717	7.86E-35	54
CC	GO:000077 kinetochore	35/354	135/19717	8.10E-31	35
CC	GO:000077 condensed centromere	32/354	118/19717	3.20E-31	32
CC	GO:000077 condensed chromatin	30/354	105/19717	5.99E-28	30
CC	GO:000092 spindle pole	27/354	164/19717	1.76E-18	27
CC	GO:007268 mitotic spindle	23/354	109/19717	1.95E-18	23
CC	GO:000587 microtubule	40/354	416/19717	4.15E-18	40
CC	GO:000587 kinesin complex	15/354	55/19717	3.00E-14	15
CC	GO:000094 condensed chromatin	9/354	14/19717	3.24E-13	9
CC	GO:000079 condensed chromatin	17/354	99/19717	2.07E-12	17
CC	GO:003049 midbody	21/354	173/19717	5.57E-12	21
CC	GO:000587 spindle midbody	13/354	59/19717	3.11E-11	13
CC	GO:000077 condensed centromere	8/354	15/19717	5.76E-11	8
CC	GO:005123 spindle midbody	10/354	34/19717	2.74E-10	10
CC	GO:000587 microtubule	18/354	152/19717	2.83E-10	18
CC	GO:000078 condensed centromere	9/354	26/19717	9.96E-10	9
CC	GO:000078 chromosome telomeric	17/354	158/19717	1.78E-09	17
CC	GO:004255 MCM complex	6/354	12/19717	2.71E-08	6
CC	GO:000078 nuclear envelope	14/354	123/19717	1.40E-07	14
CC	GO:004512 pronucleus	6/354	15/19717	1.40E-07	6
CC	GO:000565 replication	10/354	70/19717	4.67E-07	10
CC	GO:000079 heterochromatin	9/354	76/19717	8.66E-06	9
CC	GO:004517 intercellular junction	8/354	59/19717	9.96E-06	8

CC	GO:199075 microtubul6/354	29/19717	1. 08E-05	6
CC	GO:003537 microtubul5/354	20/19717	2. 25E-05	5
CC	GO:003215 cell divis8/354	68/19717	2. 89E-05	8
CC	GO:007268 meiotic sp4/354	11/19717	3. 05E-05	4
CC	GO:000079 nuclear ch19/354	376/19717	5. 47E-05	19
CC	GO:000080 lateral el4/354	13/19717	6. 43E-05	4
CC	GO:199002 mitotic sp4/354	13/19717	6. 43E-05	4
CC	GO:001036 chromocent4/354	14/19717	8. 87E-05	4
CC	GO:000015 nuclear ul6/354	43/19717	0. 000112	6
CC	GO:003439 nuclear pe10/354	131/19717	0. 000129	10
CC	GO:000581 centriole 10/354	139/19717	0. 00021	10
CC	GO:009073 site of DN7/354	73/19717	0. 000334	7
CC	GO:000572 pericentri4/354	20/19717	0. 000394	4
CC	GO:003215 cleavage f6/354	55/19717	0. 000443	6
CC	GO:000568 anaphase-t4/354	21/19717	0. 00048	4
CC	GO:007093 contractil3/354	10/19717	0. 000627	3
CC	GO:000079 synaptone5/354	40/19717	0. 000712	5
CC	GO:009908 synaptone5/354	40/19717	0. 000712	5
CC	GO:000565 nuclear le3/354	11/19717	0. 000851	3
CC	GO:009054 Flemming t4/354	28/19717	0. 001488	4
CC	GO:001899 host cell6/354	73/19717	0. 001989	6
CC	GO:004365 host cell 6/354	73/19717	0. 001989	6
CC	GO:000572 nuclear he4/354	33/19717	0. 002771	4
CC	GO:001636 nuclear ma7/354	109/19717	0. 003533	7
CC	GO:004257 DNA polym3/354	21/19717	0. 006004	3
CC	GO:004359 nuclear re4/354	41/19717	0. 006129	4
CC	GO:000030 cyclin-de4/354	42/19717	0. 006681	4
MF	GO:001688 ATPase act43/343	434/17696	1. 03E-18	43
MF	GO:000809 DNA-dependenc21/343	113/17696	4. 11E-15	21
MF	GO:000801 microtubul28/343	246/17696	4. 83E-14	28
MF	GO:014009 catalytic acting 25/343	25/343	213/17696	25
MF	GO:001711 single-st10/343	20/17696	1. 02E-12	10
MF	GO:001563 tubulin bi30/343	336/17696	3. 49E-12	30
MF	GO:000367 DNA helica15/343	81/17696	3. 87E-11	15
MF	GO:000438 helicase z20/343	163/17696	5. 58E-11	20
MF	GO:000368 DNA replic9/343	24/17696	3. 52E-10	9
MF	GO:000377 microtubul14/343	84/17696	7. 57E-10	14
MF	GO:000377 motor acti16/343	136/17696	8. 92E-09	16
MF	GO:000369 single-st14/343	113/17696	3. 94E-08	14
MF	GO:000021 DNA seconc7/343	24/17696	2. 52E-07	7
MF	GO:000040 four-way z6/343	16/17696	3. 45E-07	6
MF	GO:000368 damaged DN9/343	65/17696	4. 28E-06	9
MF	GO:007018 DNA polym5/343	19/17696	2. 47E-05	5
MF	GO:004313 3'-5' DNA 5/343	20/17696	3. 24E-05	5
MF	GO:001688 endodeoxyri produci4/343	16/17696	4	
MF	GO:004239 histone bi12/343	197/17696	0. 000478	12
MF	GO:003235 oxidized I3/343	10/17696	0. 000783	3
MF	GO:000028 magnesium 12/343	213/17696	0. 000952	12

MF	GO:000452 RNA-DNA hy3/343	11/17696	0. 001061	3
MF	GO:003240 mismatch 13/343	11/17696	0. 001061	3
MF	GO:000452 endodeoxyri5/343	41/17696	0. 001123	5
MF	GO:000857 ATP-depend plus-en4/343	26/17696	4	
MF	GO:001689 endonuclea active ·5/343	46/17696	5	

Supplementary Table 8

DE-HGs were remarkably enriched in KEGG pathway

ID	Description	GeneRatio	BgRatio	pvalue	Count
hsa04110	Cell cycle 29/159	124/8087	8. 32E-24		29
hsa03030	DNA repli 11/159	36/8087	4. 72E-11		11
hsa04914	Progester 12/159	100/8087	5. 20E-07		12
hsa04114	Oocyte me 13/159	129/8087	1. 32E-06		13
hsa03460	Fanconi a 8/159	54/8087	9. 04E-06		8
hsa03440	Homologou 7/159	41/8087	1. 28E-05		7
hsa05166	Human T-c 15/159	219/8087	2. 46E-05		15
hsa03430	Mismatch 4/159	23/8087	0. 00095175		4
hsa05219	Bladder c 5/159	41/8087	0. 00116715		5

Supplementary Table 9

Genes related to the OS of LUSC were selected after univariate Cox regression

gene	KM.Pvalue	HR	HR. 95L	HR. 95H	coxPvalue
HELLS	0. 000553	0. 8957804	0. 80277	0. 9995632	0. 049094
GPRIN1	0. 049042	1. 0673904	1. 00536	1. 13325041	0. 03277
TARBP1	0. 012165	0. 9536416	0. 91425	0. 9947306	0. 027423
CST3	0. 004145	1. 0053439	1. 00022	1. 01049497	0. 040952
FAM83A	0. 032133	1. 0076685	1. 00249	1. 01287268	0. 003654
LY6D	0. 016257	1. 0007576	1. 00009	1. 00142316	0. 025573

Supplementary Table 10

Genes related to the OS of LUSC were selected after multivariate Cox regression

id	coef	HR	HR. 95L	HR. 95H	pvalue
HELLS	-0. 10399	0. 9012382	0. 80527	1. 00864583	0. 070279
GPRIN1	0. 076852	1. 0798826	1. 01965	1. 14367723	0. 008682
FAM83A	0. 007378	1. 0074054	1. 00207	1. 0127665	0. 006438

Supplementary Table 11

Multivariate Cox regression analyses in the training set

id	HR	HR. 95L	HR. 95H	pvalue
age	1.016211	0.9992802	1.03343	0.060661
gender	1.198609	0.8663494	1.65829	0.27405442
pathologic_	1.265515	1.0712835	1.49496	0.00560681
pathologic_	1.306941	1.0890646	1.56841	0.00401599
pathologic_	1.277021	1.0540728	1.54712	0.0124928
pathologic_	1.110801	0.9292702	1.32779	0.24840964
riskScore	2.263156	1.5657418	3.27121	1.39E-05

Supplementary Table 12

Multivariate Cox regression analyses in the train				
id	HR	HR. 95L	HR. 95H	pvalue
pathologic_	1.172184	0.8839217	1.55445	0.26995184
pathologic_	1.210711	0.9453431	1.55057	0.12984786
pathologic_	1.27989	1.0511082	1.55847	0.01404717
riskScore	2.354673	1.6345907	3.39197	4.25E-06

Supplementary Table 13

14 up-regulated genes and 9 down-regulated genes between high- and low-risk groups based on the R package

ID	logFC	AveExpr	P. Value
FAM83A	1.662907	2.7541893	4.59E-23
NPPC	-1.19804	1.3296574	8.77E-18
GPC3	-1.56924	4.3693898	1.15E-15
PDZK1IP1	1.365348	3.8462034	1.86E-15
CST6	1.036455	2.0309571	7.73E-15
S100A7	2.031042	4.109029	5.58E-14
SOX2	-1.36366	5.3831897	3.69E-13
NTS	-2.24573	4.4667953	4.14E-12
MMP1	1.347209	5.4748693	7.06E-12
C19orf33	1.210843	4.7697111	1.10E-11
NTRK2	-1.23653	3.151525	1.35E-11
IGFBP2	-1.0557	6.3982762	5.33E-11
IVL	1.147262	2.9578188	1.82E-09
ALDH1A1	-1.02023	5.6523734	8.01E-09
S100A9	1.312119	9.098133	1.04E-08
GSTA1	-1.43012	4.0810748	1.30E-08
MMP13	1.175775	2.6011217	4.53E-08
S100A8	1.340535	6.6792063	7.87E-08
KRT14	1.623752	5.7987879	1.35E-07
LY6D	1.315552	3.7780165	7.36E-07
KRT15	-1.03507	5.7422588	8.57E-07

KRT16	1. 019139	6. 5461081	1. 26E-05
KRT6B	1. 008274	5. 738062	1. 41E-05

Supplementary Table 14

GO analysis was used to reveal the potential functions of risk score-related DEGs

ONTOLOGY	ID	Description	BgRatio	pvalue	Count
BP	GO:007026	cornification	112/1867	1. 72E-07	5
BP	GO:000854	epidermis	464/1867	6. 91E-07	7
BP	GO:005123	sequestering	16/18670	7. 87E-07	3
BP	GO:003021	keratinocyte	305/1867	1. 08E-06	6
BP	GO:000991	epidermal	358/1867	2. 74E-06	6
BP	GO:003142	keratinization	224/1867	5. 30E-06	5
BP	GO:004358	skin development	419/1867	6. 78E-06	6
BP	GO:007048	leukocyte	12/18670	8. 69E-05	2
BP	GO:000252	leukocyte	14/18670	0. 00011959	2
BP	GO:001701	protein	ni15/18670	0. 00013789	2
BP	GO:001811	peptidyl-prolyl	c15/18670	0. 00013789	2
BP	GO:005254	regulation	452/1867	0. 00015237	5
BP	GO:003296	collagen	n115/1867	0. 00032189	3
BP	GO:001973	antimicrobial	122/1867	0. 00038286	3
BP	GO:007162	granulocyte	123/1867	0. 00039213	3
BP	GO:009753	granulocyte	141/1867	0. 00058449	3
BP	GO:000341	growth	pl36/18670	0. 00081503	2
BP	GO:000688	cellular	z36/18670	0. 00081503	2
BP	GO:005506	zinc ion	l38/18670	0. 00090818	2
BP	GO:005083	defense	r40/18670	0. 00100621	2
BP	GO:000150	ossification	398/1867	0. 00109747	4
BP	GO:009009	negative	i178/1867	0. 00114834	3
BP	GO:000341	endochondral	44/18670	0. 00121688	2
BP	GO:001819	peptidyl-prolyl	c47/18670	0. 00138757	2
BP	GO:003057	collagen	c47/18670	0. 00138757	2
BP	GO:006035	cartilage	47/18670	0. 00138757	2
BP	GO:009886	bone growth	47/18670	0. 00138757	2
BP	GO:005254	regulation	425/1867	0. 00139877	4
BP	GO:004510	intermediary	50/18670	0. 00156905	2
BP	GO:004510	intermediary	51/18670	0. 00163193	2
BP	GO:000962	response	i52/18670	0. 00169599	2
BP	GO:001004	response	i53/18670	0. 00176125	2
BP	GO:003017	negative	i210/1867	0. 00184501	3
BP	GO:009752	myeloid	le210/1867	0. 00184501	3
BP	GO:004328	regulation	215/1867	0. 00197309	3
BP	GO:001000	glial cell	218/1867	0. 00205254	3
BP	GO:003059	leukocyte	224/1867	0. 00221739	3
BP	GO:200124	positive	i61/18670	0. 00232566	2
BP	GO:005090	leukocyte	499/1867	0. 00251528	4
BP	GO:200011	regulation	239/1867	0. 00266499	3

BP	GO:006035 endochondr	73/18670	0.00331138	2
BP	GO:006184 antimicrob	73/18670	0.00331138	2
CC	GO:004511 intermediate	251/1971	8.96E-06	5
CC	GO:000588 intermediate	214/1971	0.00010161	4
CC	GO:006202 collagen-	c406/1971	0.00115004	4
CC	GO:000153 cornified	65/1971	0.0025891	2
CC	GO:004509 keratin fi	95/1971	0.00544113	2
CC	GO:003477 secretory	321/1971	0.0059468	3
CC	GO:006020 cytoplasmic	325/1971	0.00615392	3
CC	GO:003198 vesicle li	327/1971	0.00625909	3
CC	GO:004367 axon termi	n119/1971	0.00841206	2
CC	GO:004430 neuron prc	138/1971	0.01117507	2
MF	GO:005078 RAGE recep	t11/17696	2.03E-07	3
MF	GO:000520 structural	102/17696	4.70E-06	4
MF	GO:003532 Toll-like 12/17696		7.96E-05	2
MF	GO:003604 long-chair	14/17696	0.00010954	2
MF	GO:190156 fatty acid	28/17696	0.00045071	2
MF	GO:000550 fatty acid	34/17696	0.00066619	2
MF	GO:003329 monocarbo	64/17696	0.00234588	2
MF	GO:001620 antioxidant	86/17696	0.00419025	2
MF	GO:000422 metalloen	103/17696	0.00595349	2

Supplementary Table 15

KEGG analysis of risk score-related DEGs

ID	Description	GeneRatio	BgRatio	pvalue	Count
hsa04657	IL-17 sig	5月15日	94/8086	5.23E-07	5
hsa05150	Staphyloc	3月15日	96/8086	0.00066535	3
hsa04915	Estrogen	3月15日	138/8086	0.00190411	3

Supplementary Table 16

The results of the GO enrichment analyses between the high and low hypoxia score groups

ONTOLOGY	ID	Description	BgRatio	pvalue	Count
BP	GO:000854 epidermis development	464/18670	9.92E-15	15	
BP	GO:007026 cornification	112/18670	2.20E-14	10	
BP	GO:003142 keratinization	224/18670	7.24E-13	11	
BP	GO:003021 keratinocyte differentiation	305/18670	7.68E-13	12	
BP	GO:000991 epidermal cell differentiation	358/18670	5.05E-12	12	
BP	GO:004358 skin development	419/18670	3.16E-11	12	
BP	GO:001973 antimicrobial humoral defense	122/18670	5.53E-09	7	
BP	GO:003019 extracellular matrix	368/18670	5.12E-08	9	
BP	GO:004306 extracellular structure	369/18670	5.24E-08	9	
BP	GO:007162 granulocyte chemotaxis	123/18670	1.98E-07	6	
BP	GO:009752 myeloid leukocyte differentiation	210/18670	2.34E-07	7	
BP	GO:003249 response to lipopolysaccharide	330/18670	3.34E-07	8	

BP	GO:003059 leukocyte chemotax	224/18670	3. 62E-07	7
BP	GO:006184 antimicrobial humo	73/18670	4. 13E-07	5
BP	GO:009753 granulocyte migrat	141/18670	4. 43E-07	6
BP	GO:000223 response to molecu	343/18670	4. 48E-07	8
BP	GO:003158 hemidesmosome asse	12/18670	1. 83E-06	3
BP	GO:003059 neutrophil chemota	104/18670	2. 41E-06	5
BP	GO:003057 collagen catabolic	47/18670	2. 72E-06	4
BP	GO:006032 cell chemotaxis	304/18670	2. 79E-06	7
BP	GO:004510 intermediate filam	50/18670	3. 49E-06	4
BP	GO:004510 intermediate filam	51/18670	3. 78E-06	4
BP	GO:199026 neutrophil migrati	118/18670	4. 49E-06	5
BP	GO:005123 sequestering of me	16/18670	4. 63E-06	3
BP	GO:001814 peptide cross-link	60/18670	7. 29E-06	4
BP	GO:005090 leukocyte migratio	499/18670	7. 30E-06	8
BP	GO:000695 humoral immune res	356/18670	7. 86E-06	7
BP	GO:002261 extracellular matr	81/18670	2. 41E-05	4
BP	GO:004211 neutrophil activat	498/18670	6. 76E-05	7
BP	GO:004230 molting cycle	112/18670	8. 58E-05	4
BP	GO:004263 hair cycle	112/18670	8. 58E-05	4
BP	GO:003296 collagen metabolic	115/18670	9. 51E-05	4
BP	GO:005254 regulation of endo	425/18670	0. 000232	6
BP	GO:007048 leukocyte aggregat	12/18670	0. 000277	2
BP	GO:005254 regulation of pept	452/18670	0. 000323	6
BP	GO:000252 leukocyte migratio	14/18670	0. 000381	2
BP	GO:001701 protein nitrosylat	15/18670	0. 000439	2
BP	GO:001811 peptidyl-cysteine	15/18670	0. 000439	2
BP	GO:003563 entry of bacterium	15/18670	0. 000439	2
BP	GO:004331 neutrophil degranu	485/18670	0. 000469	6
BP	GO:000228 neutrophil activat	488/18670	0. 000485	6
BP	GO:001095 positive regulatio	178/18670	0. 000506	4
BP	GO:000756 aging	321/18670	0. 000519	5
BP	GO:000244 neutrophil mediate	499/18670	0. 000545	6
BP	GO:004274 defense response t	330/18670	0. 000588	5
BP	GO:009002 positive regulatio	18/18670	0. 000637	2
BP	GO:001095 positive regulatio	197/18670	0. 000741	4
BP	GO:000691 activation of cyst	86/18670	0. 000765	3
BP	GO:005179 regulation of hair	20/18670	0. 000789	2
BP	GO:000269 positive regulatio	87/18670	0. 000791	3
BP	GO:004576 positive regulatio	204/18670	0. 000844	4
BP	GO:007122 cellular response	205/18670	0. 000859	4
BP	GO:000166 response to hypoxi	359/18670	0. 00086	5
BP	GO:007121 cellular response	212/18670	0. 000974	4
BP	GO:003629 response to decrea	370/18670	0. 000984	5
BP	GO:004510 intermediate filam	23/18670	0. 001046	2
BP	GO:000704 cell-substrate jun	97/18670	0. 001085	3
BP	GO:015011 cell-substrate jun	97/18670	0. 001085	3
BP	GO:007167 positive regulatio	24/18670	0. 00114	2
BP	GO:003163 plasminogen activa	25/18670	0. 001237	2

BP	GO:003246 positive regulation of monooxygenase activity	25/18670	0.001237	2
BP	GO:009002 regulation of monooxygenase activity	25/18670	0.001237	2
BP	GO:007048 response to oxygen	394/18670	0.001302	5
BP	GO:190401 positive regulation of monooxygenase activity	230/18670	0.001316	4
BP	GO:007162 positive regulation of monooxygenase activity	26/18670	0.001339	2
BP	GO:007121 cellular response to oxygen	236/18670	0.001447	4
BP	GO:003432 cell junction assembly	409/18670	0.001535	5
BP	GO:004263 regulation of hair	28/18670	0.001553	2
BP	GO:004273 fibrinolysis	28/18670	0.001553	2
BP	GO:000268 regulation of leukocyte migration	114/18670	0.001727	3
BP	GO:200035 negative regulation of monooxygenase activity	33/18670	0.002155	2
BP	GO:000268 positive regulation of monooxygenase activity	128/18670	0.002402	3
BP	GO:000688 cellular zinc ion homeostasis	36/18670	0.002561	2
BP	GO:004328 positive regulation of monooxygenase activity	132/18670	0.002621	3
BP	GO:005237 modulation by symbiont	37/18670	0.002704	2
BP	GO:004440 entry into host cell	134/18670	0.002735	3
BP	GO:005092 positive regulation of monooxygenase activity	135/18670	0.002794	3
BP	GO:005506 zinc ion homeostasis	38/18670	0.00285	2
BP	GO:005083 defense response to infection	40/18670	0.003154	2
BP	GO:001570 bicarbonate transporter	42/18670	0.003473	2
BP	GO:003245 regulation of protein modification process	43/18670	0.003637	2
BP	GO:200105 positive regulation of monooxygenase activity	149/18670	0.003689	3
BP	GO:007162 regulation of granule-mediated defense response	44/18670	0.003806	2
BP	GO:005072 positive regulation of monooxygenase activity	153/18670	0.003973	3
BP	GO:003362 regulation of cell adhesion	46/18670	0.004153	2
BP	GO:007167 regulation of monooxygenase activity	46/18670	0.004153	2
BP	GO:190403 negative regulation of monooxygenase activity	46/18670	0.004153	2
BP	GO:001819 peptidyl-cysteine modification	47/18670	0.004332	2
BP	GO:005212 movement in host cell	48/18670	0.004347	3
BP	GO:003030 positive regulation of monooxygenase activity	169/18670	0.005243	3
BP	GO:000962 response to fungus	52/18670	0.005278	2
BP	GO:001004 response to zinc ion	53/18670	0.005478	2
BP	GO:003019 negative regulation of monooxygenase activity	53/18670	0.005478	2
BP	GO:003163 zymogen activation	53/18670	0.005478	2
BP	GO:190004 negative regulation of monooxygenase activity	54/18670	0.005681	2
BP	GO:190464 response to amyloid	54/18670	0.005681	2
BP	GO:003158 cell-substrate adhesion	54/18670	0.006195	4
BP	GO:005081 negative regulation of monooxygenase activity	57/18670	0.006312	2
BP	GO:004586 positive regulation of monooxygenase activity	58/18670	0.006442	4
BP	GO:001003 response to metal ion	362/18670	0.006696	4
BP	GO:200035 regulation of endoplasmic reticulum membrane	59/18670	0.006749	2
BP	GO:200124 positive regulation of monooxygenase activity	61/18670	0.007199	2
CC	GO:004511 intermediate filament	251/19717	5.41E-07	7
CC	GO:006202 collagen-containing extracellular matrix	406/19717	1.06E-06	8
CC	GO:000588 intermediate filament	214/19717	3.69E-06	6
CC	GO:000153 cornified envelope	65/19717	8.11E-06	4
CC	GO:000560 basement membrane	95/19717	3.66E-05	4
CC	GO:004509 keratin filament	95/19717	3.66E-05	4

CC	GO:003477 secretory granule	321/19717	3. 69E-05	6
CC	GO:006020 cytoplasmic vesicle	1325/19717	3. 95E-05	6
CC	GO:003198 vesicle lumen	327/19717	4. 09E-05	6
CC	GO:000592 connexin complex	21/19717	0. 000782	2
CC	GO:000592 gap junction	32/19717	0. 001821	2
CC	GO:004517 basal part of cell	151/19717	0. 004572	2
CC	GO:003005 cell-substrate junction	412/19717	0. 008677	4
MF	GO:005078 RAGE receptor binding	11/17696	1. 49E-06	3
MF	GO:000520 structural constituent	102/17696	2. 49E-06	5
MF	GO:000823 metallopeptidase activity	181/17696	4. 04E-05	5
MF	GO:000422 metalloendopeptidase activity	103/17696	6. 86E-05	4
MF	GO:003532 Toll-like receptor activity	12/17696	0. 000292	2
MF	GO:000520 extracellular matrix protein	163/17696	0. 000401	4
MF	GO:003604 long-chain fatty acid binding	14/17696	0. 000402	2
MF	GO:000408 carbonate dehydratase activity	15/17696	0. 000463	2
MF	GO:000514 interleukin-1 receptor activity	16/17696	0. 000529	2
MF	GO:003028 structural constituent	16/17696	0. 000529	2
MF	GO:000486 serine-type endopeptidase activity	94/17696	0. 00107	3
MF	GO:000512 cytokine activity	220/17696	0. 001232	4
MF	GO:190156 fatty acid derivative binding	28/17696	0. 001639	2
MF	GO:000417 endopeptidase activity	427/17696	0. 002081	5
MF	GO:000550 fatty acid binding	34/17696	0. 002412	2
MF	GO:000512 cytokine receptor activity	286/17696	0. 0032	4
MF	GO:004801 receptor ligand activity	482/17696	0. 003511	5
MF	GO:003054 signaling receptor activity	487/17696	0. 003669	5
MF	GO:000425 serine-type endopeptidase activity	160/17696	0. 004853	3
MF	GO:000800 chemokine activity	49/17696	0. 004955	2
MF	GO:000486 endopeptidase inhibitor activity	175/17696	0. 006221	3
MF	GO:001683 hydro-lyase activity	56/17696	0. 006428	2
MF	GO:000823 serine-type peptidase activity	182/17696	0. 006931	3
MF	GO:003041 peptidase inhibitor activity	182/17696	0. 006931	3
MF	GO:006113 endopeptidase regulatory activity	182/17696	0. 006931	3
MF	GO:001682 hydrolase activity	186/17696	0. 007357	3
MF	GO:001717 serine hydrolase activity	186/17696	0. 007357	3
MF	GO:003140 carboxylic acid binding	193/17696	0. 00814	3
MF	GO:000485 enzyme inhibitor activity	375/17696	0. 008299	4
MF	GO:003329 monocarboxylic acid binding	64/17696	0. 008324	2
MF	GO:004237 chemokine receptor activity	66/17696	0. 008833	2
MF	GO:000551 collagen binding	67/17696	0. 009093	2
MF	GO:004317 organic acid binding	205/17696	0. 009593	3
MF	GO:001683 carbon-oxygen lyase activity	75/17696	0. 01129	2
MF	GO:006113 peptidase regulatory activity	219/17696	0. 011469	3
MF	GO:000801 microtubule binding	246/17696	0. 015649	3

Supplementary Table 17

The results of the KEGG enrichment analyses between the high and low hypoxia score groups

ID	Description	BgRatio	pvalue	geneID	Count
hsa04657	IL-17 signaling pathway	94/8086	3.24E-10	MMP1/MMP3	8
hsa05323	Rheumatoid arthritis	93/8086	9.82E-06	IL1A/MMP1	5
hsa05146	Amoebiasis	102/8086	0.00028824	LAMC2/CXC	4
hsa00910	Nitrogen metabolism	17/8086	0.00131264	CA12/CA9	2
hsa05150	Staphylococcus aureus	96/8086	0.00345905	KRT17/KRT	3
hsa04933	AGE-RAGE signaling	100/8086	0.00388151	SERpine1/	3
hsa04064	NF-kappa B signaling	104/8086	0.00433428	PLAU/CXCL	3
hsa05417	Lipid and atherosclerosis	1215/8086	0.00458856	MMP1/MMP3	4

Supplementary Table 18

39 DEGs between the high and low hypoxia score groups

ID	logFC	AveExpr	P. Value
SERpine1	1.430444	5.5729646	4.09E-34
NDRG1	1.324302	6.9650353	4.15E-30
ANGPTL4	1.202026	3.2669951	4.82E-27
EGLN3	1.124114	3.4919429	5.31E-21
LAMC2	1.407561	5.8486928	4.07E-20
TGFBI	1.077358	4.8770444	5.19E-20
IL1A	1.260405	1.9936476	1.35E-19
PLAU	1.007918	5.8369542	6.61E-17
PTHLH	1.605836	4.567594	9.57E-17
CDH3	1.011709	5.0077969	5.19E-16
GJB2	1.475109	5.5808251	5.59E-16
MMP1	1.565733	5.4748693	3.10E-15
TNC	1.262588	5.0735294	1.05E-14
S100A2	1.678985	7.4597917	1.79E-14
MMP3	1.093118	1.9767981	2.25E-14
CA12	1.134013	3.7405969	6.57E-14
CXCL8	1.26247	4.6895174	1.67E-12
MMP13	1.481851	2.6011217	8.66E-12
KRT17	1.40051	8.9993716	1.48E-10
MMP10	1.54279	3.9447388	2.41E-10
CXCL1	1.149361	4.6077995	6.32E-10
KRT6A	1.499981	9.0449326	2.20E-09
KRT16	1.373117	6.5461081	5.83E-09
IL36G	1.041521	2.1504238	9.15E-09
KRT14	1.788054	5.7987879	1.10E-08
GJB6	1.18579	4.377364	2.04E-08
CA9	1.049868	3.5376246	2.12E-08
KRT6B	1.307153	5.738062	2.64E-08
KRT6C	1.117808	3.2311955	4.14E-08
CLCA2	1.167555	4.952461	7.81E-08
S100A9	1.234035	9.098133	1.34E-07
S100A7	1.445374	4.109029	2.31E-07
COL17A1	1.015097	4.6131232	2.60E-07

S100A8	1.29018	6.6792063	4.04E-07
PI3	1.377925	6.1990377	9.80E-07
SPRR2D	1.236262	4.0778565	1.27E-06
SPRR1B	1.339443	5.935627	2.94E-06
SERPINB3	1.02824	3.6624151	4.34E-06
SPRR2E	1.045691	3.3392213	5.43E-05

Supplementary Table 19

The effect of a risk scoring system constructed based on 3 HRGs on the immune microenvironment of LUSC

gene	immune_ce	cor	p. value
HELLS	B cells	n	0.127432
HELLS	B cells	m	-0.093909
HELLS	Plasma	ce	-0.06627
HELLS	T cells	C	0.1193551
HELLS	T cells	C	0.0088478
HELLS	T cells	C	-0.130146
HELLS	T cells	C	0.0751889
HELLS	T cells	f	0.2448617
HELLS	T cells	r	0.0582558
HELLS	T cells	g	-0.02028
HELLS	NK cells	:0.0111346	0.81625
HELLS	NK cells	:0.1199588	0.01199
HELLS	Monocytes	-0.090008	0.05981
HELLS	Macrophag	0.0046711	0.92234
HELLS	Macrophag	0.1929842	4.79E-05
HELLS	Macrophag	-0.217826	4.20E-06
HELLS	Dendritic	-0.096311	0.04395
HELLS	Dendritic	-0.118878	0.01279
HELLS	Mast cell	-0.056378	0.23901
HELLS	Mast cell	-0.015378	0.74827
HELLS	Eosinophi	-0.062027	0.19509
HELLS	Neutrophi	-0.215546	5.32E-06
GPRIN1	B cells	n	-0.046767
GPRIN1	B cells	m	-0.050665
GPRIN1	Plasma	ce	-0.082384
GPRIN1	T cells	C	-0.048878
GPRIN1	T cells	C	0.0069623
GPRIN1	T cells	C	-0.005498
GPRIN1	T cells	C	0.0466967
GPRIN1	T cells	f	-0.027209
GPRIN1	T cells	r	0.024536
GPRIN1	T cells	g	-0.116928
GPRIN1	NK cells	:0.0313243	0.5132
GPRIN1	NK cells	:0.0686618	0.15141
GPRIN1	Monocytes	-0.108304	0.0234

GPRIN1	Macrophag	0.2181122	4.08E-06
GPRIN1	Macrophag	0.0020624	0.96567
GPRIN1	Macrophag	-0.11844	0.01312
GPRIN1	Dendritic	0.0033748	0.94385
GPRIN1	Dendritic	-0.100999	0.03459
GPRIN1	Mast cell	-0.136078	0.00433
GPRIN1	Mast cell	0.0271272	0.57125
GPRIN1	Eosinophi	-0.053003	0.26835
GPRIN1	Neutrophi	-0.30092	1.28E-10
FAM83A	B cells n	-0.19399	4.37E-05
FAM83A	B cells m	0.0239986	0.61645
FAM83A	Plasma ce	-0.00467	0.92236
FAM83A	T cells C	-0.175871	0.00022
FAM83A	T cells C	0.0062595	0.89607
FAM83A	T cells C	0.0312762	0.51385
FAM83A	T cells C	-0.1093	0.02215
FAM83A	T cells f	-0.007023	0.88348
FAM83A	T cells r	0.0265653	0.57925
FAM83A	T cells g	-0.070326	0.14172
FAM83A	NK cells	0.0937846	0.04982
FAM83A	NK cells	-0.030482	0.5246
FAM83A	Monocytes	0.0149781	0.75459
FAM83A	Macrophag	0.0698789	0.14427
FAM83A	Macrophag	-0.138008	0.0038
FAM83A	Macrophag	-0.039114	0.41418
FAM83A	Dendritic	-0.003326	0.94467
FAM83A	Dendritic	0.267443	1.31E-08
FAM83A	Mast cell	-0.088806	0.06332
FAM83A	Mast cell	0.1924612	5.03E-05
FAM83A	Eosinophi	0.0405566	0.39716
FAM83A	Neutrophi	0.3561563	1.52E-14

Supplementary Table 20

The sensitivity of patients in the high- and low-risk groups to current third-generation chemotherapeutic agents for LUSC using the GDSC database

ID	ChemicalI	ChemicalII	GeneSymbol
hells	14-deoxy-C495626		HELLS
hells	2, 3-bis(3 C029497		HELLS
hells	7, 8-Dihyd D015123		HELLS
hells	7-(benzyl C553817		HELLS
hells	Acetamino D000082		HELLS
hells	Acrolein D000171		HELLS
hells	Acrolein D000171		HELLS
hells	Aflatoxin D016604		HELLS
hells	Aflatoxin D016604		HELLS
hells	Aflatoxin D016604		HELLS

hells Aflatoxin D016607 HILLS
hells afuresert C00059326 HILLS
hells Air Pollu D000393 HILLS
hells alpha-pin C005451 HILLS
hells alpha-pin C005451 HILLS
hells Ascorbic D001205 HILLS
hells Azathiopr D001379 HILLS
hells bazedoxif C447119 HILLS
hells Benzo(a) p D001564 HILLS
hells beta-glyc C031463 HILLS
hells bisphenol C006780 HILLS
hells bisphenol C006780 HILLS
hells bisphenol C006780 HILLS
hells Calcitrio D002117 HILLS
hells Calcitrio D002117 HILLS
hells Cisplatin D002945 HILLS
hells Copper D003300 HILLS
hells Coumestro D003375 HILLS
hells Coumestro D003375 HILLS
hells Cyclospor D016572 HILLS
hells Dasatinib D00006943 HILLS
hells deguelin C107676 HILLS
hells Demecolci D003703 HILLS
hells Dexametha D003907 HILLS
hells dicrotoph C000944 HILLS
hells Dronabino D013759 HILLS
hells Estradiol D004958 HILLS
hells Formaldeh D005557 HILLS
hells GSK-J4 C00059303 HILLS
hells ICG 001 C492448 HILLS
hells incobotul C545476 HILLS
hells Irinoteca D00007714 HILLS
hells (+)-JQ1 c C561695 HILLS
hells K 7174 C410337 HILLS
hells lasiocarp C005136 HILLS
hells methacryl C039175 HILLS
hells methacryl C039175 HILLS
hells methylmer C004925 HILLS
hells Methyl Me D008741 HILLS
hells MLN7243 C00062263 HILLS
hells Nickel D009532 HILLS
hells NSC 68953 C558013 HILLS
hells Oxygen D010100 HILLS
hells Ozone D010126 HILLS
hells Ozone D010126 HILLS
hells Ozone D010126 HILLS
hells perfluoro C023036 HILLS

hells	phenethyl C058305	HELLS
hells	picoxystr C556557	HELLS
hells	pirinixic C006253	HELLS
hells	Progester D011374	HELLS
hells	Quercetin D011794	HELLS
hells	Resveratr D000077185	HELLS
hells	Resveratr D000077185	HELLS
hells	sodium ar C017947	HELLS
hells	Sunitinib D000077210	HELLS
hells	Testoster D013739	HELLS
hells	Testoster D013739	HELLS
hells	Tetrachlo D013749	HELLS
hells	Thimerosa D013849	HELLS
hells	Tobacco SD014028	HELLS
hells	tris(1, 3- C016805	HELLS
hells	Urethane D014520	HELLS
hells	Valproic D014635	HELLS
hells	Valproic D014635	HELLS
hells	Valproic D014635	HELLS
hells	Vincristi D014750	HELLS
hells	Volatile D055549	HELLS
hells	Vorinosta D000077337	HELLS
gprin1	4-(4-((5- C584509	GPRIN1
gprin1	Acetamino D000082	GPRIN1
gprin1	Benzo (a)p D001564	GPRIN1
gprin1	Benzo (a)p D001564	GPRIN1
gprin1	beta-meth C044887	GPRIN1
gprin1	butyralde C018475	GPRIN1
gprin1	Cadmium CD019256	GPRIN1
gprin1	Cisplatin D002945	GPRIN1
gprin1	dicrotoph C000944	GPRIN1
gprin1	Endosulfa D004726	GPRIN1
gprin1	Estradiol D004958	GPRIN1
gprin1	Folic Aci D005492	GPRIN1
gprin1	GSK-J4 C00059303(GPRIN1	
gprin1	jinfukang C544151	GPRIN1
gprin1	jinfukang C544151	GPRIN1
gprin1	methyleug C005223	GPRIN1
gprin1	N-Nitroso D009242	GPRIN1
gprin1	Plant Ext D010936	GPRIN1
gprin1	Resveratr D000077185	GPRIN1
gprin1	Tobacco SD014028	GPRIN1
gprin1	Tunicamyc D014415	GPRIN1
gprin1	Urethane D014520	GPRIN1
gprin1	Valproic D014635	GPRIN1
fam83a	1-Butanol D020001	FAM83A
fam83a	abrine C496492	FAM83A
fam83a	Aflatoxin D016604	FAM83A

fam83a	aflatoxin C029753	FAM83A
fam83a	arsenite C015001	FAM83A
fam83a	arsenite C015001	FAM83A
fam83a	Benzo(a)P D001564	FAM83A
fam83a	Benzo(a)P D001564	FAM83A
fam83a	butyralde C018475	FAM83A
fam83a	Cadmium C D019256	FAM83A
fam83a	chloropic C100187	FAM83A
fam83a	Decitabin D000077209	FAM83A
fam83a	Decitabin D000077209	FAM83A
fam83a	Diazinon D003976	FAM83A
fam83a	erucylpho C472787	FAM83A
fam83a	Estradiol D004958	FAM83A
fam83a	Gasoline D005742	FAM83A
fam83a	Gasoline D005742	FAM83A
fam83a	monomethyl C406082	FAM83A
fam83a	monomethyl C406082	FAM83A
fam83a	monomethyl C406082	FAM83A
fam83a	Particula D052638	FAM83A
fam83a	Particula D052638	FAM83A
fam83a	Polycycli D011084	FAM83A
fam83a	Polycycli D011084	FAM83A
fam83a	Silicon D D012822	FAM83A
fam83a	sodium ar C017947	FAM83A
fam83a	sodium ar C017947	FAM83A
fam83a	sodium ar C017947	FAM83A
fam83a	sodium ar C017947	FAM83A
fam83a	sodium ar C017947	FAM83A
fam83a	sulforaph C016766	FAM83A
fam83a	Tobacco S D014028	FAM83A
fam83a	Tobacco S D014028	FAM83A
fam83a	Tretinoin D014212	FAM83A
fam83a	trichosta C012589	FAM83A
fam83a	Valproic D014635	FAM83A