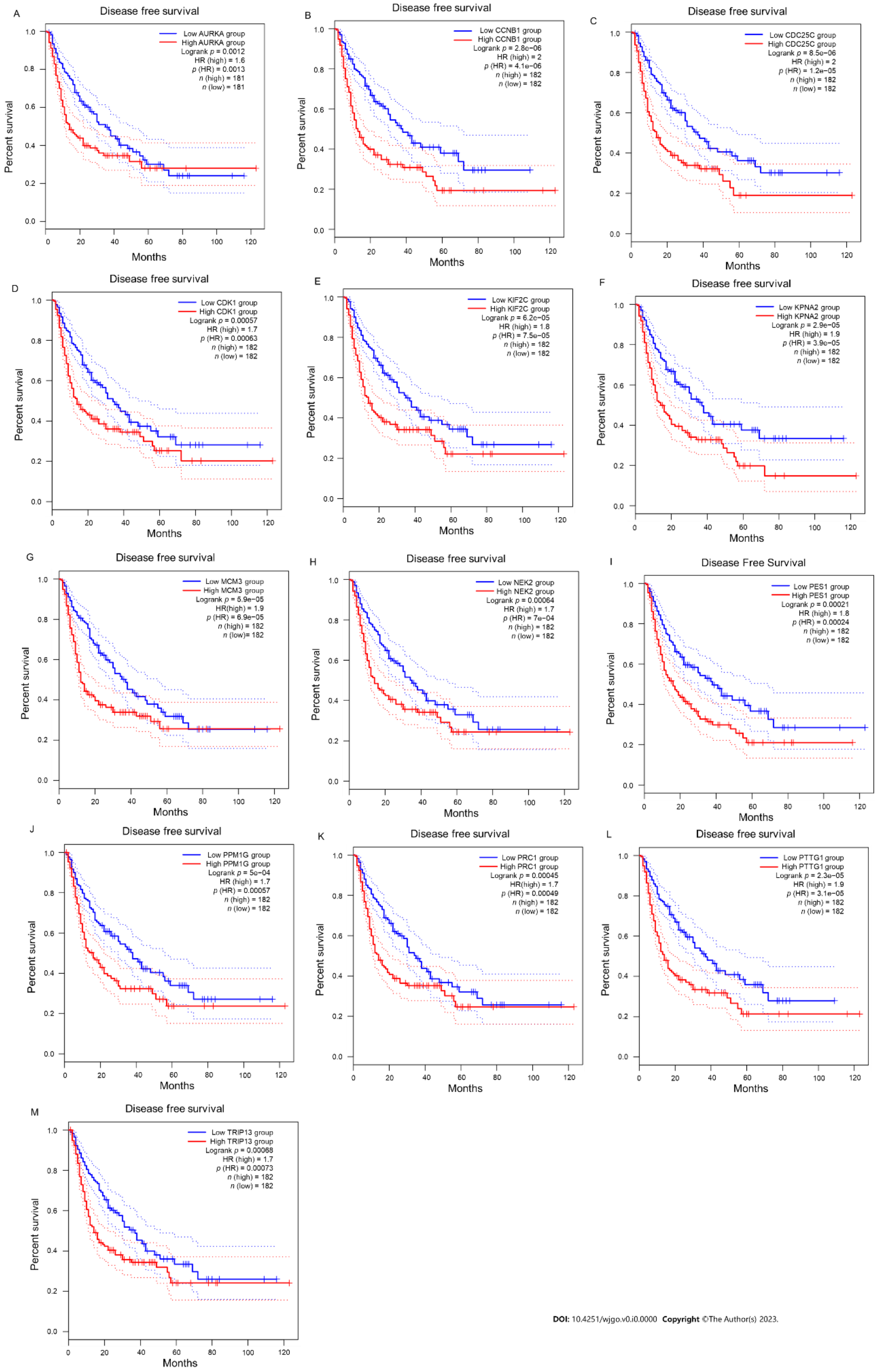
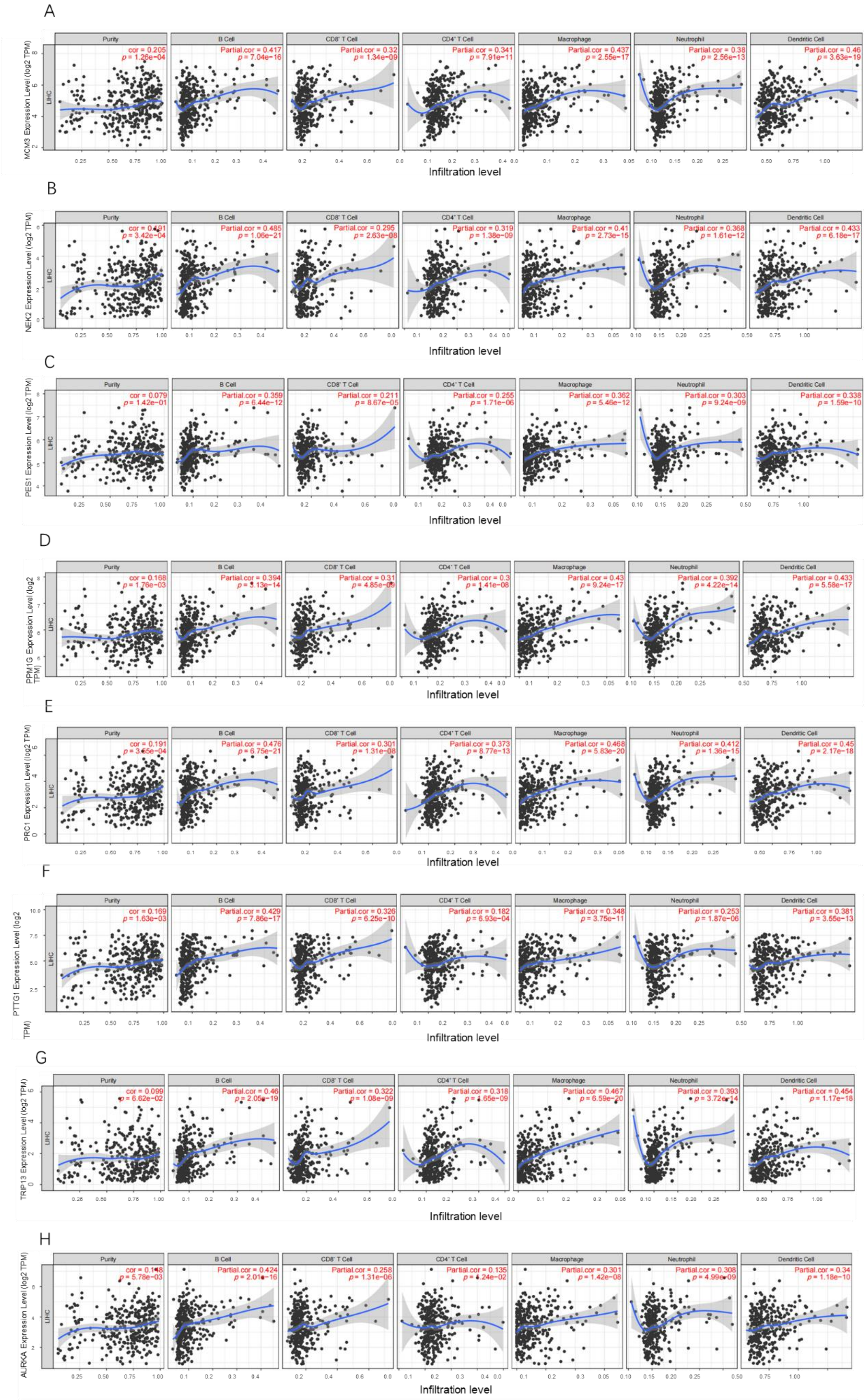
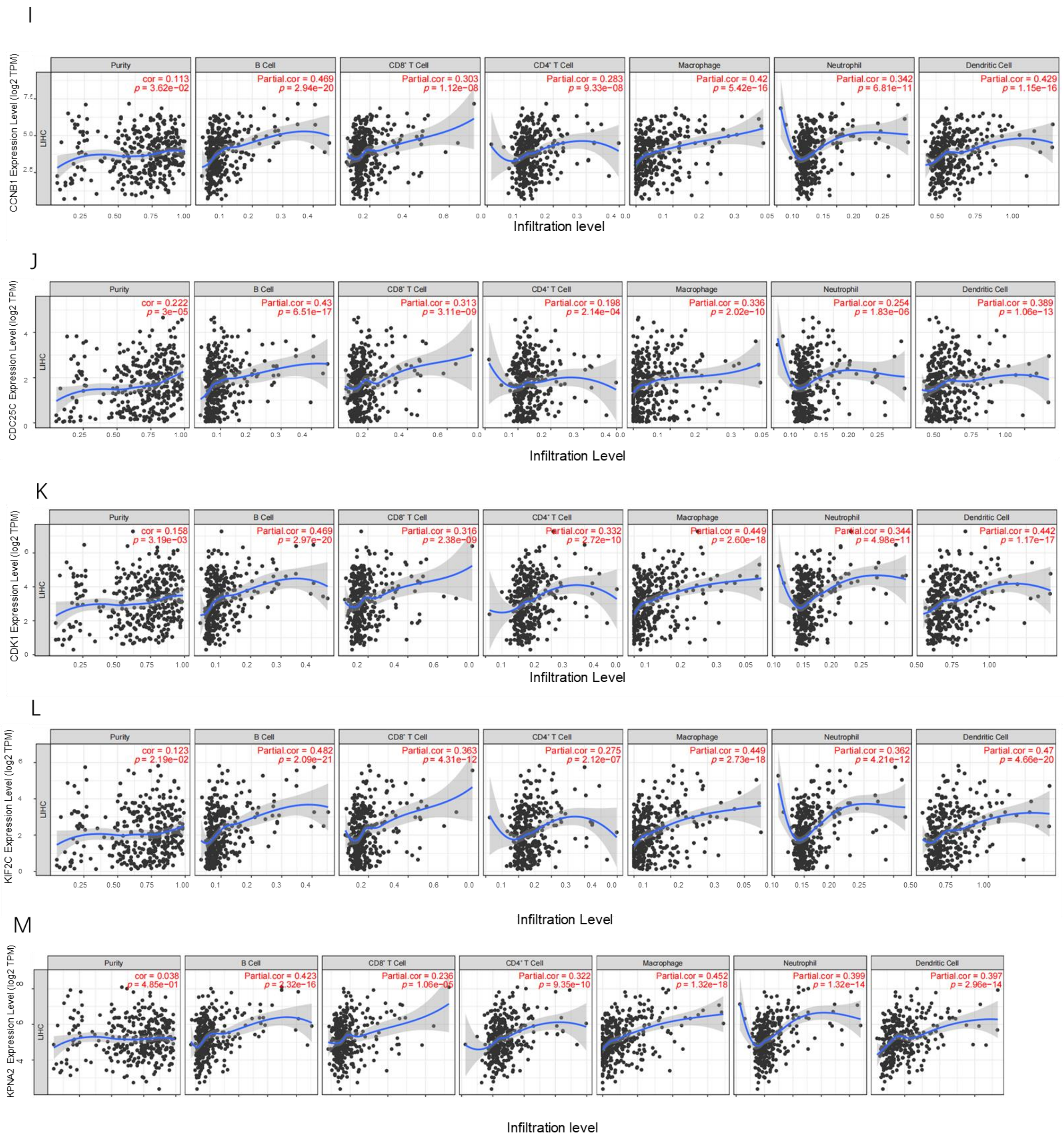


DOI: 10.4251/wjgo.v0.i0.0000 **Copyright** ©The Author(s) 2023.

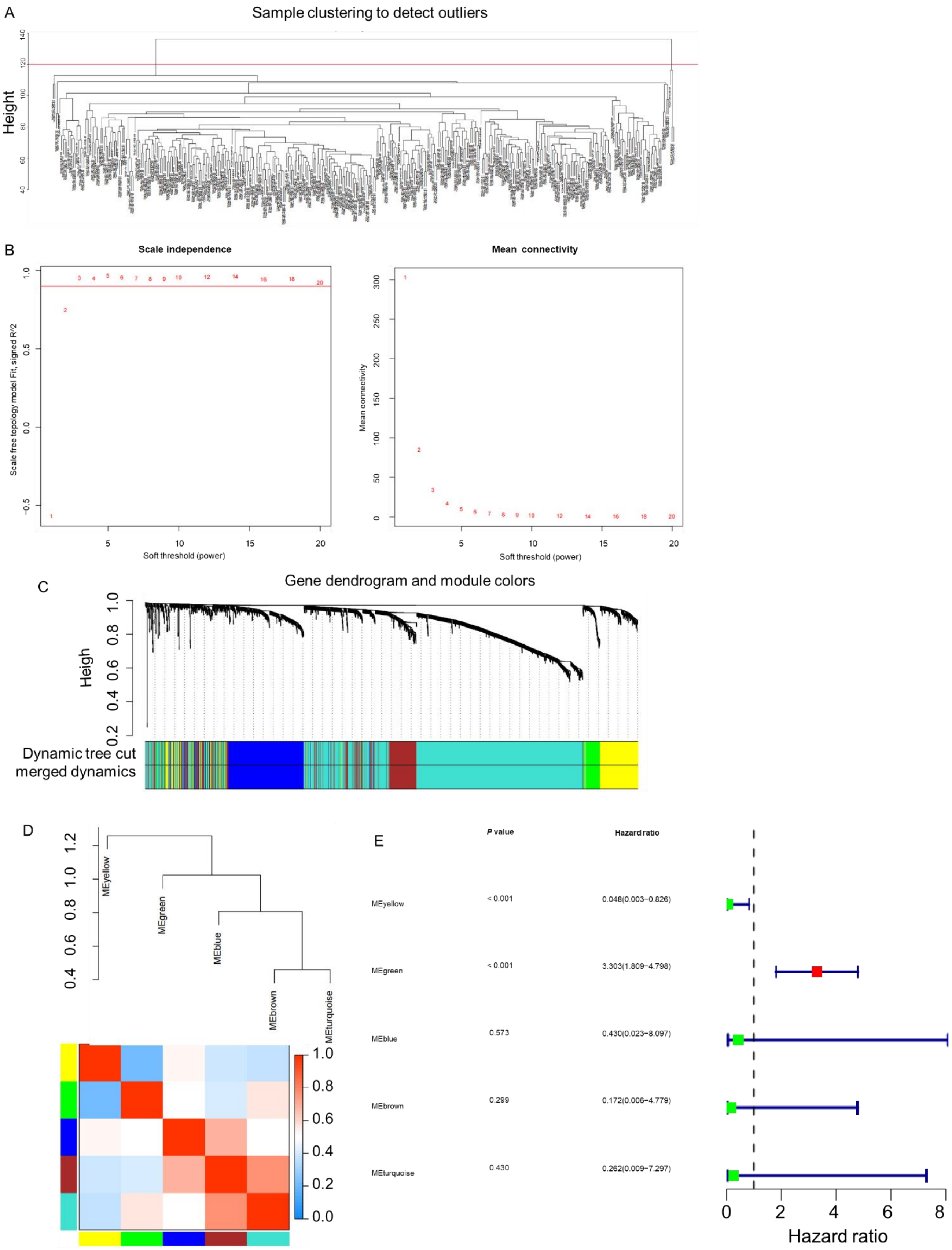
Supplementary Figure 1 Identification of tumor antigens associated with hepatocellular carcinoma **prognosis.** A-M: Kaplan−Meier curves showing that high expression of *AURKA* (A), *CCNB1* (B), *CDC25C* (C), *CDK1* (D), *KIF2C* (E), *KPNA2* (F), *MCM3* (G), *NEK2* (H), *PES1* (I), *PPM1G* (J), *PRC1* (K), *PTTG1* (L), and *TRIP13* (M) indicates worse recurrence-free survival in hepatocellular carcinoma patients.


A
MCM3 Expression Level (log2 TPM)
LIHC
Purity
cor = 0.205
p = 1.26e-04
B Cell
Partial.cor = 0.417
p = 7.04e-16
CD8⁺ T Cell
Partial.cor = 0.32
p = 1.34e-09
CD4⁺ T Cell
Partial.cor = 0.341
p = 7.91e-11
Macrophage
Partial.cor = 0.437
p = 2.55e-17
Neutrophil
Partial.cor = 0.38
p = 2.56e-13
Dendritic Cell
Partial.cor = 0.46
p = 3.63e-19
Infiltration level
B
NEK2 Expression Level (log2 TPM)
LIHC
Purity
cor = 0.191
p = 3.42e-04
B Cell
Partial.cor = 0.485
p = 1.06e-21
CD8⁺ T Cell
Partial.cor = 0.295
p = 2.63e-08
CD4⁺ T Cell
Partial.cor = 0.319
p = 1.38e-09
Macrophage
Partial.cor = 0.41
p = 2.73e-15
Neutrophil
Partial.cor = 0.368
p = 1.61e-12
Dendritic Cell
Partial.cor = 0.433
p = 6.18e-17
Infiltration level
C
PES1 Expression Level (log2 TPM)
LIHC
Purity
cor = 0.079
p = 1.42e-01
B Cell
Partial.cor = 0.359
p = 6.44e-12
CD8⁺ T Cell
Partial.cor = 0.211
p = 8.67e-05
CD4⁺ T Cell
Partial.cor = 0.255
p = 1.71e-06
Macrophage
Partial.cor = 0.362
p = 5.46e-12
Neutrophil
Partial.cor = 0.303
p = 9.24e-09
Dendritic Cell
Partial.cor = 0.338
p = 1.59e-10
Infiltration level
D
PPM1G Expression Level (log2 TPM)
LIHC
Purity
cor = 0.168
p = 1.76e-03
B Cell
Partial.cor = 0.394
p = 3.13e-14
CD8⁺ T Cell
Partial.cor = 0.31
p = 4.85e-09
CD4⁺ T Cell
Partial.cor = 0.3
p = 1.41e-08
Macrophage
Partial.cor = 0.43
p = 9.24e-17
Neutrophil
Partial.cor = 0.392
p = 4.22e-14
Dendritic Cell
Partial.cor = 0.433
p = 5.58e-17
Infiltration level
E
PRC1 Expression Level (log2 TPM)
LIHC
Purity
cor = 0.191
p = 3.65e-04
B Cell
Partial.cor = 0.476
p = 6.75e-21
CD8⁺ T Cell
Partial.cor = 0.301
p = 1.31e-08
CD4⁺ T Cell
Partial.cor = 0.373
p = 8.77e-13
Macrophage
Partial.cor = 0.468
p = 5.83e-20
Neutrophil
Partial.cor = 0.412
p = 1.36e-15
Dendritic Cell
Partial.cor = 0.45
p = 2.17e-18
Infiltration level
F
PTTG1 Expression Level (log2 TPM)
LIHC
Purity
cor = 0.169
p = 1.63e-03
B Cell
Partial.cor = 0.429
p = 7.86e-17
CD8⁺ T Cell
Partial.cor = 0.326
p = 6.25e-10
CD4⁺ T Cell
Partial.cor = 0.182
p = 6.93e-04
Macrophage
Partial.cor = 0.348
p = 3.75e-11
Neutrophil
Partial.cor = 0.253
p = 1.87e-06
Dendritic Cell
Partial.cor = 0.381
p = 3.55e-13
Infiltration level
G
TRIP13 Expression Level (log2 TPM)
LIHC
Purity
cor = 0.099
p = 6.62e-02
B Cell
Partial.cor = 0.46
p = 2.05e-19
CD8⁺ T Cell
Partial.cor = 0.322
p = 1.08e-09
CD4⁺ T Cell
Partial.cor = 0.318
p = 1.65e-09
Macrophage
Partial.cor = 0.467
p = 6.59e-20
Neutrophil
Partial.cor = 0.393
p = 3.72e-14
Dendritic Cell
Partial.cor = 0.454
p = 1.17e-18
Infiltration level
H
AURKA Expression Level (log2 TPM)
LIHC
Purity
cor = 0.148
p = 5.78e-03
B Cell
Partial.cor = 0.424
p = 2.01e-16
CD8⁺ T Cell
Partial.cor = 0.258
p = 1.31e-06
CD4⁺ T Cell
Partial.cor = 0.135
p = 1.24e-02
Macrophage
Partial.cor = 0.301
p = 1.42e-08
Neutrophil
Partial.cor = 0.308
p = 4.99e-09
Dendritic Cell
Partial.cor = 0.34
p = 1.18e-10
Infiltration level



DOI: 10.4251/wjgo.v0.i0.0000 **Copyright** ©The Author(s) 2023.

Supplementary Figure 2 Correlation between candidate tumor antigens and infiltration levels of antigen-presenting cells. A-M: Correlation of *AURKA* (A), *CCNB1* (B), *CDC25C* (C), *CDK1* (D), *KIF2C* (E), *KPNA2* (F), *MCM3* (G), *NEK2* (H), *PES1* (I), *PPM1G* (J), *PRC1* (K), *PTTG1* (L), and *TRIP13* (M) expression levels with tumor purity and infiltration levels of B cells, CD8⁺ T cells, CD4⁺ T cells, macrophages, neutrophils, and dendritic cells in hepatocellular carcinoma.



	P value	Hazard ratio
MEyellow	< 0.001	0.048(0.003−0.826)
MEgreen	< 0.001	3.303(1.809−4.798)
MEblue	0.573	0.430(0.023−8.097)
MEbrown	0.299	0.172(0.006−4.779)
MEturquoise	0.430	0.262(0.009−7.297)

Supplementary Figure 3 Identification of the immune gene coexpression modules. A: Sample clustering diagram; B: Scale independence and mean connectivity for various soft-thresholding powers; C: Gene dendrogram and module colors; D: Heatmap of module correlations; E: Forest plots for univariate analysis of gene modules in hepatocellular carcinoma.

Supplementary Table 1 The accession numbers of TCGA and ICGC samples included in this study

TCGA	**ICGC**
TCGA-FV-A495-01	DO23508_SP50097
TCGA-CC-A3MB-01	DO23509_SP50099
TCGA-BC-A3KF-01	DO23510_SP50101
TCGA-DD-A4NV-01	DO23511_SP50103
TCGA-CC-A1HT-01	DO23512_SP50105
TCGA-BD-A3EP-01	DO23513_SP50107
TCGA-CC-A3MA-01	DO23514_SP50109
TCGA-ZP-A9CV-01	DO23515_SP50111
TCGA-DD-AACY-01	DO23516_SP50113
TCGA-XR-A8TG-01	DO23517_SP50115
TCGA-CC-A9FW-01	DO23518_SP50117
TCGA-BC-A10Y-01	DO23519_SP50119
TCGA-KR-A7K7-01	DO23521_SP50123
TCGA-ED-A459-01	DO23523_SP50127
TCGA-PD-A5DF-01	DO23524_SP50129
TCGA-ED-A5KG-01	DO23525_SP50131
TCGA-DD-AAVX-01	DO23526_SP50133
TCGA-ED-A7PY-01	DO23527_SP50135
TCGA-RC-A7SF-01	DO23528_SP50137
TCGA-DD-AAW0-01	DO23529_SP50139
TCGA-ED-A66X-01	DO23530_SP50141

TCGA-DD-AAC8-01	DO23531_SP50143
TCGA-FV-A3I1-01	DO23532_SP50145
TCGA-RC-A7S9-01	DO23533_SP50147
TCGA-ZP-A9D2-01	DO23534_SP50149
TCGA-G3-A5SL-01	DO23535_SP50151
TCGA-CC-A3M9-01	DO23536_SP50153
TCGA-BC-A216-01	DO23537_SP50155
TCGA-ED-A7XP-01	DO23538_SP50157
TCGA-DD-A11A-01	DO23539_SP50159
TCGA-DD-A73B-01	DO23540_SP50161
TCGA-DD-AACA-01	DO23541_SP50163
TCGA-DD-A1EH-01	DO23542_SP50165
TCGA-DD-AA3A-01	DO23543_SP50167
TCGA-RG-A7D4-01	DO23544_SP50169
TCGA-DD-A73F-01	DO23545_SP50171
TCGA-WX-AA46-01	DO23546_SP50173
TCGA-K7-AAU7-01	DO23547_SP50175
TCGA-DD-A3A2-01	DO23548_SP50177
TCGA-EP-A26S-01	DO23549_SP50179
TCGA-FV-A2QQ-01	DO23550_SP50181
TCGA-3K-AAZ8-01	DO23551_SP50183
TCGA-DD-A3A5-01	DO45091_SP98896
TCGA-DD-AADP-01	DO45092_SP98898
TCGA-CC-5259-01	DO45093_SP98900
TCGA-DD-AAD2-01	DO45094_SP98902
TCGA-ES-A2HT-01	DO45095_SP98904
TCGA-CC-A8HU-01	DO45096_SP98907
TCGA-ES-A2HS-01	DO45096_SP98909
TCGA-2Y-A9H0-01	DO45097_SP98913
TCGA-2V-A95S-01	DO45099_SP98915

TCGA-2Y-A9GU-01	DO45101_SP98921
TCGA-RC-A7SB-01	DO45103_SP98925
TCGA-FV-A4ZP-01	DO45105_SP98927
TCGA-DD-AAD3-01	DO45107_SP98933
TCGA-DD-AAW2-01	DO45109_SP98937
TCGA-DD-A39V-01	DO45111_SP98941
TCGA-DD-AADD-01	DO45113_SP98945
TCGA-DD-AADW-01	DO45115_SP98949
TCGA-DD-AACS-01	DO45117_SP98953
TCGA-2Y-A9H4-01	DO45119_SP98955
TCGA-DD-AADV-01	DO45121_SP98959
TCGA-G3-A7M7-01	DO45123_SP98965
TCGA-DD-A4NK-01	DO45125_SP98967
TCGA-ED-A97K-01	DO45127_SP98973
TCGA-T1-A6J8-01	DO45129_SP98975
TCGA-DD-AACV-01	DO45131_SP98981
TCGA-DD-A4NF-01	DO45133_SP98985
TCGA-DD-A3A8-01	DO45135_SP98989
TCGA-G3-A25S-01	DO45137_SP98991
TCGA-DD-A1EL-01	DO45139_SP112184
TCGA-DD-AACH-01	DO45139_SP98997
TCGA-WQ-A9G7-01	DO45139_SP99265
TCGA-DD-A4NO-01	DO45141_SP99001
TCGA-G3-A7M9-01	DO45141_SP99003
TCGA-CC-5261-01	DO45143_SP99007
TCGA-ZS-A9CG-01	DO45145_SP99011
TCGA-CC-A123-01	DO45149_SP99019
TCGA-5R-AA1D-01	DO45153_SP99029
TCGA-BC-A69H-01	DO45155_SP99033
TCGA-DD-AAVZ-01	DO45157_SP99037

TCGA-DD-AAD0-01	DO45159_SP99041
TCGA-EP-A2KA-01	DO45161_SP99045
TCGA-2Y-A9HA-01	DO45163_SP99049
TCGA-DD-AACD-01	DO45165_SP99053
TCGA-DD-AAE7-01	DO45167_SP99057
TCGA-BC-A8YO-01	DO45169_SP99061
TCGA-DD-AAE2-01	DO45171_SP99065
TCGA-DD-AAEG-01	DO45173_SP99069
TCGA-XR-A8TF-01	DO45175_SP99073
TCGA-CC-A5UC-01	DO45177_SP99077
TCGA-KR-A7K0-01	DO45179_SP99081
TCGA-CC-5263-01	DO45181_SP99085
TCGA-K7-A5RG-01	DO45183_SP99089
TCGA-G3-AAV4-01	DO45185_SP99093
TCGA-ED-A627-01	DO45187_SP99097
TCGA-2Y-A9GZ-01	DO45189_SP99101
TCGA-DD-AACX-01	DO45191_SP99105
TCGA-DD-AAVR-01	DO45193_SP99109
TCGA-G3-A25T-01	DO45195_SP99113
TCGA-MR-A8JO-01	DO45197_SP99117
TCGA-DD-AAEK-01	DO45199_SP99121
TCGA-DD-A1EE-01	DO45201_SP99125
TCGA-DD-AACL-01	DO45203_SP99129
TCGA-KR-A7K8-01	DO45205_SP99133
TCGA-FV-A3I0-01	DO45207_SP99137
TCGA-DD-AADA-01	DO45209_SP99141
TCGA-G3-A5SM-01	DO45211_SP99145
TCGA-G3-A3CH-01	DO45213_SP99149
TCGA-G3-AAUZ-01	DO45215_SP99153
TCGA-DD-AAVV-01	DO45217_SP99157

TCGA-DD-A4NP-01	DO45219_SP99161
TCGA-ED-A66Y-01	DO45221_SP99165
TCGA-LG-A6GG-01	DO45223_SP99169
TCGA-DD-AAE4-01	DO45225_SP99173
TCGA-HP-A5MZ-01	DO45227_SP99177
TCGA-G3-A5SI-01	DO45229_SP99181
TCGA-DD-A1EI-01	DO45231_SP99185
TCGA-G3-AAV1-01	DO45233_SP99189
TCGA-DD-A113-01	DO45235_SP99193
TCGA-DD-AACB-01	DO45237_SP99197
TCGA-CC-A9FS-01	DO45239_SP99201
TCGA-BC-A5W4-01	DO45241_SP99205
TCGA-2Y-A9H5-01	DO45243_SP99209
TCGA-BW-A5NO-01	DO45245_SP99213
TCGA-CC-A7IE-01	DO45247_SP99217
TCGA-KR-A7K2-01	DO45249_SP99221
TCGA-DD-AADM-01	DO45251_SP99225
TCGA-CC-5258-01	DO45253_SP99229
TCGA-BW-A5NQ-01	DO45255_SP99233
TCGA-2Y-A9GX-01	DO45257_SP99237
TCGA-LG-A9QC-01	DO45259_SP99241
TCGA-DD-A11C-01	DO45261_SP99245
TCGA-BC-A10Q-01	DO45263_SP99249
TCGA-4R-AA8I-01	DO45265_SP99253
TCGA-FV-A4ZQ-01	DO45267_SP99257
TCGA-BC-4073-01	DO45269_SP99261
TCGA-DD-AADQ-01	DO45273_SP99269
TCGA-DD-A1EA-01	DO45273_SP99271
TCGA-WQ-AB4B-01	DO45275_SP99275
TCGA-RC-A7SH-01	DO45277_SP99279

TCGA-BC-A10T-01	DO45279_SP99283
TCGA-DD-A39W-01	DO45281_SP99287
TCGA-RC-A6M5-01	DO45281_SP99289
TCGA-UB-A7MD-01	DO45283_SP99293
TCGA-2Y-A9H6-01	DO45285_SP99297
TCGA-5C-A9VG-01	DO45287_SP99301
TCGA-CC-5264-01	DO45289_SP99305
TCGA-DD-A4NS-01	DO45297_SP99321
TCGA-QA-A7B7-01	DO45299_SP99325
TCGA-DD-AAEB-01	DO45301_SP99329
TCGA-DD-A3A6-01	DO45303_SP99333
TCGA-UB-A7MF-01	DO45305_SP99337
TCGA-DD-AACW-01	DO45307_SP99341
TCGA-G3-A7M6-01	DO48672_SP106993
TCGA-GJ-A6C0-01	DO48674_SP106998
TCGA-DD-A3A3-01	DO48677_SP107004
TCGA-WX-AA44-01	DO48679_SP107007
TCGA-MR-A520-01	DO48681_SP107010
TCGA-DD-AADK-01	DO48682_SP107012
TCGA-DD-A73D-01	DO48693_SP107032
TCGA-BW-A5NP-01	DO48695_SP107037
TCGA-DD-A4NN-01	DO48697_SP107041
TCGA-ZP-A9CZ-01	DO48700_SP107044
TCGA-CC-A8HS-01	DO48701_SP107047
TCGA-G3-A6UC-01	DO48704_SP107052
TCGA-CC-A7IH-01	DO48706_SP107056
TCGA-BC-A69I-01	DO48712_SP107063
TCGA-K7-A6G5-01	DO48715_SP107068
TCGA-BC-A10U-01	DO48716_SP107071
TCGA-DD-A4NG-01	DO48717_SP107073

TCGA-UB-A7MC-01	DO48719_SP107076
TCGA-UB-AA0U-01	DO48720_SP107078
TCGA-DD-A4NB-01	DO48721_SP107080
TCGA-ED-A8O6-01	DO48723_SP107084
TCGA-DD-AACQ-01	DO48725_SP107088
TCGA-G3-AAV6-01	DO48727_SP107091
TCGA-DD-A3A4-01	DO48728_SP107094
TCGA-DD-A1EK-01	DO48730_SP107097
TCGA-FV-A3R2-01	DO48732_SP107101
TCGA-BC-A10Z-01	DO48733_SP107104
TCGA-WJ-A86L-01	DO48736_SP107109
TCGA-G3-A25Y-01	DO48737_SP107111
TCGA-ED-A82E-01	DO48741_SP107119
TCGA-DD-AACU-01	DO48742_SP107121
TCGA-DD-A4NJ-01	DO48743_SP107123
TCGA-2Y-A9H1-01	DO48746_SP107129
TCGA-FV-A496-01	DO48747_SP107132
TCGA-DD-A4ND-01	DO48751_SP107136
TCGA-DD-A1EF-01	DO48757_SP107146
TCGA-DD-AAEH-01	DO48759_SP107150
TCGA-2Y-A9H2-01	DO48760_SP107152
TCGA-2Y-A9GW-01	DO48761_SP107155
TCGA-ZS-A9CE-01	DO50774_SP112130
TCGA-DD-A4NQ-01	DO50776_SP112133
TCGA-5C-AAPD-01	DO50778_SP112138
TCGA-DD-AAVW-01	DO50783_SP112147
TCGA-EP-A2KC-01	DO50785_SP112152
TCGA-MI-A75E-01	DO50787_SP112156
TCGA-DD-A116-01	DO50789_SP112160
TCGA-GJ-A9DB-01	DO50791_SP112165

TCGA-CC-A7IL-01	DO50793_SP112168
TCGA-DD-AACC-01	DO50793_SP112170
TCGA-FV-A3R3-01	DO50798_SP112178
TCGA-HP-A5N0-01	DO50799_SP112180
TCGA-K7-A5RF-01	DO50800_SP112182
TCGA-ED-A7PZ-01	DO50802_SP112186
TCGA-YA-A8S7-01	DO50803_SP112188
TCGA-DD-A39X-01	DO50804_SP112190
TCGA-DD-AACF-01	DO50805_SP112192
TCGA-DD-A1EC-01	DO50806_SP112194
TCGA-DD-AAE0-01	DO50807_SP112196
TCGA-G3-AAV0-01	DO50808_SP112198
TCGA-XR-A8TD-01	DO50809_SP112201
TCGA-CC-A5UE-01	DO50811_SP112205
TCGA-DD-AACJ-01	DO50813_SP112208
TCGA-G3-AAV5-01	DO50814_SP112210
TCGA-DD-AAVS-01	DO50814_SP112211
TCGA-DD-A11B-01	DO50815_SP112213
TCGA-MI-A75C-01	DO50816_SP112215
TCGA-ED-A8O5-01	DO50817_SP112217
TCGA-BC-4072-01	DO50818_SP112219
TCGA-DD-AAW3-01	DO50819_SP112221
TCGA-G3-A5SK-01	DO50820_SP112224
TCGA-BC-A110-01	DO50822_SP112228
TCGA-DD-A3A7-01	DO50825_SP112234
TCGA-DD-AACN-01	DO50829_SP112241
TCGA-DD-AAD5-01	DO50832_SP112248
TCGA-CC-A3MC-01	DO50839_SP112261
TCGA-DD-A73A-01	DO50840_SP112265
TCGA-DD-AADI-01	DO50844_SP112273

TCGA-CC-A7IG-01	DO50850_SP112288
TCGA-G3-AAV3-01	DO50855_SP112300
TCGA-MI-A75H-01	DO50857_SP112304
TCGA-DD-A73E-01	DO50859_SP112310
TCGA-2Y-A9H7-01	
TCGA-CC-A8HV-01	
TCGA-DD-AADJ-01	
TCGA-DD-AAD6-01	
TCGA-BC-A10S-01	
TCGA-LG-A9QD-01	
TCGA-DD-A3A1-01	
TCGA-DD-AACZ-01	
TCGA-CC-A7IK-01	
TCGA-DD-AADO-01	
TCGA-CC-A7II-01	
TCGA-RC-A6M3-01	
TCGA-DD-AAW1-01	
TCGA-NI-A8LF-01	
TCGA-FV-A23B-01	
TCGA-DD-AADC-01	
TCGA-G3-A3CJ-01	
TCGA-ZP-A9D1-01	
TCGA-DD-A73C-01	
TCGA-CC-A9FU-01	
TCGA-G3-A25X-01	
TCGA-DD-AACP-01	
TCGA-UB-A7MB-01	
TCGA-DD-AADG-01	
TCGA-RC-A6M6-01	
TCGA-DD-A4NH-01	

TCGA-EP-A12J-01
TCGA-CC-5262-01
TCGA-ZS-A9CD-01
TCGA-DD-AAE9-01
TCGA-BD-A2L6-01
TCGA-DD-AAEI-01
TCGA-2Y-A9H3-01
TCGA-2Y-A9GV-01
TCGA-DD-AADS-01
TCGA-DD-A114-01
TCGA-DD-A39Z-01
TCGA-UB-A7MA-01
TCGA-EP-A2KB-01
TCGA-DD-AAEA-01
TCGA-UB-AA0V-01
TCGA-2Y-A9GY-01
TCGA-XR-A8TE-01
TCGA-ED-A4XI-01
TCGA-DD-AACG-01
TCGA-NI-A4U2-01
TCGA-DD-AAC9-01
TCGA-DD-AAE1-01
TCGA-DD-A11D-01
TCGA-DD-AADY-01
TCGA-ZP-A9D4-01
TCGA-DD-AAED-01
TCGA-DD-AACK-01
TCGA-DD-AAVQ-01
TCGA-BC-A112-01
TCGA-DD-A118-01

TCGA-DD-AACO-01
TCGA-DD-A1EB-01
TCGA-DD-A4NL-01
TCGA-EP-A3JL-01
TCGA-DD-AAD8-01
TCGA-5R-AA1C-01
TCGA-G3-A3CI-01
TCGA-G3-A3CK-01
TCGA-MI-A75G-01
TCGA-G3-A5SJ-01
TCGA-5R-AAAM-01
TCGA-BC-A3KG-01
TCGA-2Y-A9GS-01
TCGA-BD-A3ER-01
TCGA-BC-A10X-01
TCGA-MI-A75I-01
TCGA-CC-A7IF-01
TCGA-DD-AACE-01
TCGA-DD-AAVY-01
TCGA-DD-A1EG-01
TCGA-ED-A7PX-01
TCGA-DD-AAD1-01
TCGA-DD-AADN-01
TCGA-2Y-A9H9-01
TCGA-G3-A25Z-01
TCGA-BC-A217-01
TCGA-BC-A10R-01
TCGA-ED-A7XO-01
TCGA-G3-AAV7-01
TCGA-GJ-A3OU-01

TCGA-DD-AADB-01
TCGA-RC-A7SK-01
TCGA-DD-A4NE-01
TCGA-DD-AACT-01
TCGA-ZP-A9D0-01
TCGA-DD-AADF-01
TCGA-DD-A1EJ-01
TCGA-DD-AAVU-01
TCGA-G3-A3CG-01
TCGA-BC-A10W-01
TCGA-O8-A75V-01
TCGA-DD-A3A9-01
TCGA-DD-A73G-01
TCGA-DD-A1ED-01
TCGA-WX-AA47-01
TCGA-G3-A7M5-01
TCGA-DD-A4NI-01
TCGA-2Y-A9H8-01
TCGA-2Y-A9GT-01
TCGA-CC-5260-01
TCGA-DD-A119-01
TCGA-FV-A2QR-01
TCGA-G3-A25V-01
TCGA-CC-A8HT-01
TCGA-DD-AADL-01
TCGA-XR-A8TC-01
TCGA-CC-A7IJ-01
TCGA-5C-A9VH-01
TCGA-DD-AADR-01
TCGA-2Y-A9HB-01

TCGA-DD-AAE3-01
TCGA-DD-A4NA-01
TCGA-DD-AACI-01
TCGA-DD-AADU-01
TCGA-EP-A3RK-01
TCGA-CC-A5UD-01
TCGA-CC-A9FV-01
TCGA-DD-AAEE-01
TCGA-ZS-A9CF-01
TCGA-RC-A6M4-01
TCGA-G3-A7M8-01
TCGA-DD-AAVP-01
TCGA-UB-A7ME-01
TCGA-DD-A4NR-01
TCGA-G3-A25U-01
TCGA-DD-AAE6-01
TCGA-G3-AAV2-01
TCGA-ZP-A9CY-01
TCGA-DD-A39Y-01
TCGA-DD-A115-01

ICGC: International Cancer Genome Consortium; TCGA: The Cancer Genome Atlas.

Supplementary Table 2 Immune related genes

Immune Related Genes
A2M
ABAT
ABCA1
ABCB1
ABCC4
ABCD1

ABHD3

ABTB1

ACADM

ACAP1

ACKR1

ACKR2

ACKR3

ACKR4

ACO1

ACP5

ACSL4

ACTA1

ACTG1

ACTN4

ACTR3

ACVR1B

ACVR1C

ACVR2A

ACVR2B

ACVRL1

ADA2

ADAM12

ADAM28

ADAM8

ADAMTS12

ADAMTS3

ADAR

ADAT2

ADCY9

ADCYAP1R1

ADIPOQ

ADIPOR1

ADIPOR2

ADM

ADM2

ADORA2A

ADPRH

ADRB1

ADRB2

ADRM1

AEN

AGER

AGRP

AGT

AGTR1

AGTR2

AHCYL1

AHCYL2

AHNAK

AHR

AHSA1

AICDA

AIF1

AIM2

AIMP1

AKNA

AKR7A3

AKT1

AKT2

AKT3

ALB

ALCAM

ALDH1A2

ALDH3A2

ALDH9A1

ALOX15

AMBN

AMELX

AMH

AMHR2

AMPD2

AMT

ANGPT1

ANGPT4

ANGPTL1

ANGPTL2

ANGPTL3

ANGPTL4

ANGPTL5

ANGPTL6

ANGPTL7

ANK1

ANKRD10

ANKRD22

ANOS1

ANXA1

ANXA5

ANXA6

AP3B1

APLN

APLNR

APOBEC3A

APOBEC3C

APOBEC3F

APOBEC3G

APOBEC3H

APOD

APOH

APOL3

APOM

AQP3

AQP9

AR

ARAF

AREG

ARG2

ARHGAP10

ARHGAP15

ARHGAP25

ARHGAP30

ARHGAP9

ARL1

ARRB1

ARTN

ASB2

ASGR1

ASGR2

ATIC

ATM

ATP10D

ATP6V1A

ATP6V1B2

AVP

AVPR1A

AVPR1B

AVPR2

AXL

AZGP1

AZU1

B2M

B3GALNT1

B3GALT2

B3GAT1

BACH2

BANK1

BASP1

BATF

BBS12

BCL10

BCL11B

BCL2

BCL2L1

BCL3

BCL6

BDNF

BECN1

BID

BIRC3

BIRC5

BLK

BLNK

BMI1

BMP1

BMP10

BMP15

BMP2

BMP2K

BMP3

BMP4

BMP5

BMP6

BMP7

BMP8A

BMP8B

BMPER

BMPR1A

BMPR1B

BMPR2

BPHL

BPI

BPIFA1

BPIFA2

BPIFA3

BPIFB1

BPIFB2

BPIFB3

BPIFB4

BPIFB6

BPIFC

BRAF

BRD8

BRIP1

BST1

BST2

BTC

BTK

BTLA

BTN2A2

BTN3A2

BTNL2

BTNL8

BZW2

C11orf45

C1GALT1C1

C1orf162

C1orf54

C1QB

C1QC

C2CD4A

C2CD4B

C3

C3AR1

C5

C5AR1

C5AR2

C5orf15

C8G

CA2

CACYBP

CADM1

CALCA
CALCB
CALCR
CALCRL
CALD1
CALR
CAMP
CAMTA1
CANX
CAPG
CAPZA1
CARD11
CARD8
CASP1
CASP3
CASP5
CASQ1
CAT
CBL
CBLB
CBLC
CBX6
CCDC65
CCDC88A
CCK
CCL1
CCL11
CCL13
CCL14
CCL15

CCL15-CCL14

CCL16

CCL17

CCL18

CCL19

CCL2

CCL20

CCL21

CCL22

CCL23

CCL24

CCL25

CCL26

CCL27

CCL28

CCL3

CCL3L3

CCL4

CCL4L2

CCL5

CCL7

CCL8

CCN1

CCN2

CCN3

CCNA1

CCNA2

CCNB1

CCND1

CCR1

CCR10

CCR2

CCR3

CCR4

CCR5

CCR6

CCR7

CCR8

CCR9

CCRL2

CCT6B

CD101

CD109

CD14

CD151

CD160

CD177

CD180

CD19

CD1A

CD1B

CD1C

CD1D

CD1E

CD2

CD200

CD200R1

CD207

CD209

CD22

CD226

CD244

CD247

CD27

CD274

CD276

CD28

CD300E

CD300LB

CD300LF

CD302

CD320

CD33

CD36

CD37

CD38

CD3D

CD3E

CD3G

CD4

CD40

CD40LG

CD44

CD47

CD48

CD52

CD53

CD55

CD58

CD59

CD6

CD63

CD68

CD69

CD7

CD70

CD72

CD74

CD79A

CD79B

CD80

CD81

CD83

CD84

CD86

CD8A

CD8B

CD96

CDA

CDC25C

CDC42

CDC5L

CDC7

CDH1

CDH2

CDH3

CDHR1

CDK4

CDK5

CDK5R1

CDKN3
CDNF
CEACAM3
CEACAM8
CEBPA
CELA1
CENPF
CER1
CETN3
CETP
CFH
CFHR1
CFHR3
CFL1
CFLAR
CFP
CGA
CGB1
CGB2
CGB3
CGB5
CGB7
CGB8
CHGA
CHGB
CHIT1
CHP1
CHP2
CHRM3
CHRNA6

CHST12

CHST15

CHST2

CHST7

CHUK

CIITA

CKLF

CLCF1

CLCN5

CLDN4

CLEC10A

CLEC11A

CLEC17A

CLEC1A

CLEC2D

CLEC4A

CLEC4C

CLEC4M

CLEC5A

CLEC7A

CLEC9A

CLECL1

CLIC2

CLIC3

CLTB

CMA1

CMKLR1

CMTM1

CMTM2

CMTM3

CMTM4

CMTM5

CMTM6

CMTM7

CMTM8

CNPY3

CNPY4

CNR1

CNR2

CNTF

CNTFR

COL23A1

COL4A1

COL4A4

COL5A3

COLEC10

COLEC12

CORO1A

CORT

COX7A2L

CPA3

CPM

CR2

CRABP1

CRABP2

CREB1

CREB3L4

CREB5

CRH

CRHR1

CRHR2

CRIM1

CRLF1

CRLF2

CRLF3

CRP

CRTAM

CRTC2

CRTC3

CRYBB1

CSE1L

CSF1

CSF1R

CSF2

CSF2RA

CSF2RB

CSF3

CSF3R

CSH1

CSH2

CSHL1

CSK

CSNK2A2

CSPG5

CSRP1

CSRP2

CST4

CST7

CSTA

CSTB

CTBS

CTF1

CTLA4

CTSB

CTSC

CTSD

CTSE

CTSG

CTSL

CTSS

CTSZ

CX3CL1

CX3CR1

CXCL1

CXCL10

CXCL11

CXCL12

CXCL13

CXCL14

CXCL16

CXCL17

CXCL2

CXCL3

CXCL5

CXCL6

CXCL8

CXCL9

CXCR1

CXCR2

CXCR3

CXCR4

CXCR5

CXCR6

CYBB

CYLD

CYP27A1

CYP27B1

CYSLTR1

CYSLTR2

CYTH1

DAB1

DAB2

DACH1

DAPK1

DAPK2

DAPP1

DAXX

DAZAP2

DBNL

DCAF12

DCD

DCK

DDX17

DDX4

DDX55

DDX58

DEFA1

DEFA1B

DEFA3

DEFA4

DEFA5

DEFA6

DEFB1

DEFB103A

DEFB103B

DEFB104A

DEFB104B

DEFB105A

DEFB105B

DEFB106A

DEFB106B

DEFB107A

DEFB107B

DEFB108B

DEFB110

DEFB112

DEFB113

DEFB114

DEFB115

DEFB116

DEFB118

DEFB119

DEFB121

DEFB123

DEFB124

DEFB125

DEFB126

DEFB127

DEFB128

DEFB129

DEFB130A

DEFB130B

DEFB131A

DEFB131B

DEFB132

DEFB133

DEFB134

DEFB135

DEFB136

DEFB4A

DEFB4B

DEPDC5

DES

DGKH

DHFR

DHX58

DKK1

DLC1

DLEU7

DLL4

DMBT1

DNAJC12

DOC2B

DOCK11

DOCK2

DOCK9

DOK2

DPP4

DPYD

DUOX1

DUOX2

DUSP14

DUSP2

DUSP6

DYNLL1

DYRK2

EBI3

ECD

ECPAS

EDN1

EDN2

EDN3

EDNRA

EDNRB

EED

EGF

EGFR

EGR3

EIF1

EIF2A

EIF2AK1

EIF2AK2

EIF2AK3

EIF2AK4

EIF3M

EIF4A1

ELANE

ELAVL1

ELMO2

ELMOD3

ELN

EMP1

EMP3

ENC1

ENDOU

ENG

ENPP1

ENTPD1

ENTPD5

EPGN

EPO

EPOR

EPPIN

ERAP1

ERAP2

ERBB3

EREG

ERI1

ESCO2

ESM1

ESR1

ESR2

ESRRA

ESRRB

ESRRG

ETS1

ETV7

EVI2B

EVI5

EXO1

EXOC6

EXOSC9

EZH2

F11R

F12

F13A1

F2R

F2RL1

F5

FABP1

FABP12

FABP2

FABP3

FABP4

FABP5

FABP6

FABP7

FABP9

FADD

FAM3B

FAM3C

FAM3D

FAM49A

FAS

FASLG

FBXO30

FCAR

FCER1A

FCER1G

FCGR1A

FCGR2A

FCGR2B

FCGR3A

FCGR3B

FCGRT

FCN1

FCN2

FCRL1

FCRL2

FCRL3

FCRL4

FCRL5

FCRL6

FCRLA

FERMT3

FES

FFAR2

FGA

FGF1

FGF10

FGF11

FGF12

FGF13

FGF14

FGF16

FGF17

FGF18

FGF19

FGF2

FGF20

FGF21

FGF22

FGF23

FGF3

FGF4

FGF5

FGF6

FGF7

FGF8

FGF9

FGFR1

FGFR2

FGFR3

FGFR4

FGFRL1

FGR

FIGNL2

FKBP1A

FKBP4

FLT1

FLT3

FLT3LG

FLT4

FN1

FOS

FOSB

FOSL1

FOXP3

FPR1

FPR2

FRAT2

FRMD4A

FSHB

FSHR

FST

FSTL1

FTL

FUCA1

FURIN

FUT4

FUT5

FYN

FZD2

FZR1

GAB3

GABARAP

GAL

GALP

GALR2

GALR3

GAST

GATA2

GATA3

GATM

GBP2

GBP3

GCG

GCGR

GCNT1

GDE1

GDF1

GDF10

GDF11

GDF15

GDF2

GDF3

GDF5

GDF6

GDF7

GDF9

GDNF

GEMIN6

GFAP

GFPT2

GH1

GH2

GHR

GHRH

GHRHR

GHRL

GHSR

GIMAP4

GIMAP5

GIMAP6

GIMAP7

GIP

GIPR

GKN1

GLIPR1

GLP1R

GLP2R

GLS2

GLUD1

GLYR1

GM2A

GMFB

GMFG

GMPR

GNAI1

GNG7

GNLY

GNRH1

GNRH2

GNRHR

GPER1

GPHA2

GPHB5

GPI

GPNMB

GPR137B

GPR146

GPR17

GPR171

GPR18

GPR183

GPR25

GPR27

GPR32

GPR33

GPR65

GPRC5C

GPSM3

GPT2

GRAP2

GRB2

GREM1

GREM2

GRIN1

GRK2

GRN

GRP

GRSF1

GSK3B

GSS

GSTA4

GUCA2A

GUSB

GZMA

GZMB

GZMH

GZMK

GZMM

HAL

HAMP

HAPLN3

HAVCR1

HAVCR2

HBEGF

HCK

HCLS1

HCST

HDAC1

HDAC9

HDC

HDGF

HDGFL3

HELLS

HEY1

HFE

HGF

HHLA2

HIGD1A

HIVEP2

HJV

HK3

HLA-A

HLA-B

HLA-C

HLA-DMA

HLA-DMB

HLA-DOA

HLA-DOB

HLA-DPA1

HLA-DPB1

HLA-DQA1

HLA-DQA2

HLA-DQB1

HLA-DQB2

HLA-DRA

HLA-DRB1

HLA-DRB5

HLA-E

HLA-F

HLA-G

HMGB1

HMOX1

HNF4A

HNF4G

HNMT

HOXA1

HRAS

HRG

HRH1

HS2ST1

HS3ST1

HS3ST2

HS3ST3B1

HSD11B1

HSD17B11

HSDL2

HSP90AA1

HSP90AB1

HSPA1A

HSPA1B

HSPA1L

HSPA2

HSPA4

HSPA5

HSPA6

HSPA8

HSPB6

HTATIP2

HTN1

HTN3

HTR1A

HTR2B

HTR3A

HTR3B

HTR3C

HTR3D

HTR3E

HUNK

HVCN1

IAPP

ICAM1

ICAM2

ICAM3

ICOS

ICOSLG

IDH3A

IDO1

IDO2

IFFO1

IFI16

IFI30

IFIH1

IFIT1

IFIT2

IFIT3

IFITM1

IFITM2

IFITM3

IFNA1

IFNA10

IFNA13

IFNA14

IFNA16

IFNA17

IFNA2

IFNA21

IFNA4

IFNA5

IFNA6

IFNA7

IFNA8

IFNAR1

IFNAR2

IFNB1

IFNE

IFNG

IFNGR1

IFNGR2

IFNK

IFNL1

IFNL2

IFNL3

IFNLR1

IFNW1

IFT80

IGF1

IGF1R

IGF2

IGF2R

IGFBP5

IGSF6

IKBKB

IKBKE

IKBKG

IKZF1

IKZF2

IL10

IL10RA

IL10RB

IL11

IL11RA

IL12A

IL12B

IL12RB1

IL12RB2

IL13

IL13RA1

IL13RA2

IL15

IL15RA

IL16

IL17A

IL17B

IL17C

IL17D

IL17F

IL17RA

IL17RB

IL17RC

IL17RD

IL17RE

IL17REL

IL18

IL18BP

IL18R1

IL18RAP

IL19

IL1A

IL1B

IL1F10

IL1R1

IL1R2

IL1RAP

IL1RAPL1

IL1RAPL2

IL1RL1

IL1RL2

IL1RN

IL2

IL20

IL20RA

IL20RB

IL21

IL21R

IL22

IL22RA1

IL22RA2

IL23A

IL23R

IL24

IL25

IL26

IL27

IL27RA

IL2RA

IL2RB

IL2RG

IL3

IL31

IL31RA

IL32

IL33

IL34

IL36A

IL36B

IL36G

IL36RN

IL37

IL3RA

IL4

IL4I1

IL4R

IL5

IL5RA

IL6

IL6R

IL6ST

IL7

IL7R

IL9

IL9R

ILDR1

ILDR2

ILF2

ILF3

ILK

ILKAP

ILVBL

INHA

INHBA

INHBB

INHBC

INHBE

INPP5D

INPP5F

INS

INS-IGF2

INSL3

INSL4

INSL5

INSL6

INSR

IREB2

IRF1

IRF3

IRF4

IRF5

IRF7

IRF8

IRF9

ISG15

ISG20

ISG20L2

ISM2

ITGA2

ITGA2B

ITGA4

ITGA9

ITGAL

ITGAM

ITGAV

ITGB1

ITGB2

ITGB4

ITIH2

ITK

ITM2C

IVNS1ABP

JAG1

JAG2

JAK1

JAK2

JUN

JUND

KANK2

KCNH2

KDM4C

KDM6B

KDR

KIF11

KIR2DL1

KIR2DL3

KIR2DL4

KIR3DL1

KIR3DL2

KIR3DL3

KIRREL3

KITLG

KL

KLF5

KLHL21

KLHL6

KLHL7

KLKB1

KLRC1

KLRC2

KLRC3

KLRC4

KLRD1

KLRF1

KLRG1

KLRK1

KNG1

KNTC1

KRAS

KRT23

KRT80

KSR1

L1CAM

LACRT

LAG3

LAIR1

LAIR2

LALBA

LAMC1

LAMP2

LAMP3

LANCL1

LAPTM4B

LAT

LAX1

LAYN

LBP

LCK

LCN1

LCN10

LCN12

LCN15

LCN2

LCN6

LCN8

LCN9

LCNL1

LCORL

LCP2

LDB3

LEAP2

LECT2

LEFTY1

LEFTY2

LEP

LEPR

LEPROT

LGALS1

LGALS9

LGMN

LGR4

LGR5

LGR6

LHB

LHCGR

LIF

LIFR

LILRA4

LILRA5

LILRB1

LILRB3

LILRB5

LIMA1

LIME1

LIMS1

LIPA

LMBR1

LMBR1L

LMNB1

LONRF3

LPA

LPXN

LRMP

LRP1

LRRC32

LRRC42

LRSAM1

LSP1

LST1

LTA

LTB

LTB4R

LTB4R2

LTBP1

LTBP2

LTBP3

LTBP4

LTBR

LTC4S

LTF

LTK

LY75

LY9

LYN

LYZ

MAGED1

MAGEH1

MAK

MAL

MALT1

MAN1B1

MANF

MAP2K1

MAP2K2

MAP3K14

MAP3K8

MAPK1

MAPK14

MAPK3

MAPK7

MAPK8

MAPT

MARCKSL1

MARCO

MASP1

MASP2

MAVS

MBL2

MBP

MC1R

MC2R

MC3R

MC4R

MC5R

MCHR1

MCHR2

MDK

MEGF9

MET

METRNL

METTL7A

MFAP3L

MFNG

MGAM

MIA

MICA

MICAL3

MICB

MIF

MINPP1

MLN

MLNR

MLST8

MMD

MMP12

MMP15

MMP25

MMP7

MMP9

MNDA

MOCOS

MPEG1

MPL

MPO

MPZL1

MR1

MRC1

MS4A1

MS4A2

MS4A6A

MSR1

MSTN

MTNR1A

MTNR1B

MUC4

MUC5AC

MX1

MX2

MYC

MYDGF

MYL6B

MZB1

NAA16

NAB1

NAMPT

NCAM1

NCF1

NCF4

NCK1

NCK2

NCKAP1L

NCOA4

NCR1

NCR2

NCR3

NDFIP2

NDP

NDRG1

NDUFB9

NEDD4

NEFL

NENF

NEO1

NETO2

NFAT5

NFATC1

NFATC2

NFATC2IP

NFATC3

NFATC4

NFE2L3

NFKB1

NFKBIA

NFKBIB

NFKBIE

NFKBIZ

NFYA

NFYB

NFYC

NGF

NGFR

NKG7

NLRC3

NLRP12

NLRX1

NMB

NMBR

NOD1

NOD2

NODAL

NOL11

NOS1

NOS2

NOTCH3

NOX1

NOX3

NOX4

NOX5

NPFF

NPL

NPPA

NPPB

NPPC

NPR1

NPR3

NPTN

NPY

NR0B1

NR0B2

NR1D1

NR1D2

NR1H2

NR1H3

NR1H4

NR1I2

NR1I3

NR2C1

NR2C2

NR2E1

NR2E3

NR2F1

NR2F2

NR2F6

NR3C1

NR3C2

NR4A1

NR4A2

NR4A3

NR5A1

NR5A2

NR6A1

NRAS

NRG1

NRG2

NRG3

NRG4

NRP1

NRP2

NRTN

NTF3

NTF4

NTRK1

NTS

NUCB2

NUDT6

NUF2

OAS1

OAS2

OAS3

OASL

OBP2A

OBP2B

OFD1

OGFR

OGN

OGT

OLR1

OPRD1

OPRM1

ORM1

ORM2

OSBPL1A

OSGIN1

OSM

OSMR

OSTN

OXT

OXTR

P2RX5

P2RX7

P2RY10

P2RY14

P2RY2

P2RY8

PADI4

PAEP

PAG1

PAK1

PAK2

PAK3

PAK4

PAK5

PAK6

PANX1

PARVG

PAX5

PCSK1

PCSK2

PDCD1

PDCD1LG2

PDCD6

PDE4B

PDE6C

PDF

PDGFA

PDGFB

PDGFC

PDGFD

PDGFRA

PDGFRB

PDGFRL

PDIA2

PDIA3

PDIA4

PDK1

PDPN

PDYN

PELO

PENK

PF4

PF4V1

PGC

PGF

PGLYRP1

PGLYRP2

PGLYRP3

PGLYRP4

PGR

PGRMC2

PHEX

PHLDA1

PHRF1

PI15

PI3

PIK3CA

PIK3CB

PIK3CD

PIK3CG

PIK3IP1

PIK3R1

PIK3R2

PIK3R3

PIK3R5

PILRA

PKD2L2

PLA2G2A

PLA2G2D

PLA2G4A

PLAAT4

PLAC8

PLAT

PLAU

PLAUR

PLCG1

PLCG2

PLD4

PLEK

PLSCR1

PLTP

PLXNA1

PLXNA2

PLXNA3

PLXNA4

PLXNB1

PLXNB2

PLXNB3

PLXNC1

PLXND1

PMCH

PML

PMP2

PNOC

PNPLA6

POMC

PORCN

PPARA

PPARD

PPARG

PPBP

PPIA

PPP3CA

PPP3CB

PPP3CC

PPP3R1

PPP3R2

PPP4C

PPY

PQBP1

PRC1

PRDX1

PRDX2

PRF1

PRKCA

PRKCB

PRKCG

PRKCQ

PRL

PRLH

PRLHR

PRLR

PROC

PROCR

PROK1

PROK2

PRSS23

PRTN3

PSAP

PSAT1

PSMB8

PSMC1

PSMC2
PSMC3
PSMC4
PSMC5
PSMC6
PSMD1
PSMD10
PSMD11
PSMD13
PSMD14
PSMD2
PSMD3
PSMD4
PSMD5
PSMD6
PSMD7
PSMD8
PSME1
PSME2
PSME3
PSPN
PTAFR
PTCRA
PTGDR
PTGDR2
PTGDS
PTGER1
PTGER2
PTGER3
PTGER4

PTGES

PTGES2

PTGFR

PTGIR

PTGS1

PTGS2

PTH

PTH1R

PTH2

PTH2R

PTHLH

PTK2

PTK2B

PTN

PTPN11

PTPN6

PTPRC

PTPRCAP

PTPRJ

PTRH2

PTX3

PVRIG

PYY

QRFP

R3HDML

RAB1A

RAB27B

RAB38

RABEP1

RABEP2

RAC1

RAC2

RAC3

RAE1

RAET1E

RAET1G

RAET1L

RAF1

RALB

RALGPS2

RARA

RARB

RARG

RASGRP1

RASGRP3

RBMS3

RBP1

RBP2

RBP4

RBP5

RBP7

RCSD1

RDX

REG1A

REG3G

REL

RELA

RELB

REPS1

RETN

RETNLB

RFX5

RFXANK

RFXAP

RGS1

RGS16

RHOA

RLN1

RLN2

RLN3

RNASE2

RNASE3

RNASE7

RNASEL

RNF125

RNF128

RNF141

RNF145

ROBO1

ROBO2

ROBO3

RORA

RORB

RORC

RPL37A

RPS24

RPS7

RPS9

RRAGB

RRAGD

RRP12

RSAD2

RTKN2

RUNX2

RXFP1

RXFP2

RXFP3

RXRA

RXRB

RXRG

RYR1

S100A1

S100A10

S100A11

S100A12

S100A13

S100A14

S100A16

S100A2

S100A3

S100A4

S100A5

S100A6

S100A7

S100A7A

S100A7L2

S100A8

S100A9

S100B

S100G

S100P

S100Z

S1PR1

S1PR2

SAA1

SAA2

SAMSN1

SASH3

SAV1

SBDS

SCARB1

SCG2

SCGB3A1

SCT

SCTR

SDC1

SDC2

SDC3

SDC4

SDCBP

SEC14L1

SECTM1

SELE

SELL

SELP

SELPLG

SEM1

SEMA3A

SEMA3B

SEMA3C

SEMA3D

SEMA3E

SEMA3F

SEMA3G

SEMA4A

SEMA4B

SEMA4C

SEMA4D

SEMA4F

SEMA4G

SEMA5A

SEMA5B

SEMA6A

SEMA6B

SEMA6C

SEMA6D

SEMA7A

SEMG1

SEMG2

SEPTIN7

SERPINA3

SERPIND1

SERTAD2

SETD7

SFTPA1

SFTPA2

SFTPD

SFXN3

SH2D1A

SH2D1B

SH2D6

SH3BP2

SH3KBP1

SHC1

SHC2

SHC3

SHC4

SIGLEC1

SIGLEC10

SIGLEC14

SIGLEC5

SIGLEC6

SIGLEC7

SIGLEC8

SIGLEC9

SIK1

SIRPA

SIRPG

SIT1

SKAP1

SKIV2L

SLA

SLAMF1

SLAMF6

SLAMF9

SLC10A2

SLC11A1

SLC15A3

SLC18A2

SLC22A17

SLC25A37

SLC29A3

SLC35B3

SLC35F2

SLC40A1

SLC6A4

SLC7A7

SLIT1

SLIT2

SLPI

SLURP1

SMAD2

SMAD4

SNURF

SOCS1

SOCS2

SOCS3

SOD1

SORL1

SORT1

SOS1

SOS2

SOX5

SP1

SP100

SPAG11A

SPAG11B

SPCS3

SPIB

SPINK5

SPNS1

SPP1

SRA1

SRC

SSH1

SST

SSTR1

SSTR2

SSTR3

SSTR5

ST3GAL6

ST8SIA4

STAB1

STAB2

STAC

STAP1

STAT1

STAT3

STAT4

STAT5A

STAT5B

STC1

STC2

STEAP4

STING1

STK10

STX4

SYK

SYTL1

TAC1

TACR1

TACSTD2

TAFA1

TAFA2

TAFA3

TAFA4

TAFA5

TAGAP

TAL1

TANK

TAP1

TAP2

TAPBP

TAPBPL

TBC1D10C

TBK1

TBX21

TCF7L2

TCHHL1

TCL1A

TDGF1

TEC

TEK

TEX264

TFEC

TFR2

TFRC

TG

TGFA

TGFB1

TGFB1I1

TGFB2

TGFB3

TGFBI

TGFBR1

TGFBR2

TGFBR3

TGFBRAP1

THADA

THBD

THBS1

THEMIS2

THPO

THRA

THRB

THUMPD2

TIE1

TIGIT

TIMM13

TINAGL1

TIPIN

TIRAP

TK2

TKFC

TLR1

TLR2

TLR3

TLR4

TLR7

TLR8

TLR9

TM4SF19

TMBIM6

TMED2

TMEM184C

TMIGD2

TMPRSS3

TMPRSS6

TMSB10

TMSB15A

TMSB15B

TMSB15B

TMSB4X

TMSB4Y

TNC

TNF

TNFAIP1

TNFAIP2

TNFAIP3

TNFAIP6

TNFAIP8

TNFAIP8L1

TNFAIP8L2

TNFAIP8L3

TNFRSF10A

TNFRSF10B

TNFRSF10C

TNFRSF10D

TNFRSF11A

TNFRSF11B

TNFRSF12A

TNFRSF13B

TNFRSF13C

TNFRSF14

TNFRSF17

TNFRSF18

TNFRSF19

TNFRSF1A

TNFRSF1B

TNFRSF21

TNFRSF25

TNFRSF4

TNFRSF6B

TNFRSF8

TNFRSF9

TNFSF10

TNFSF11

TNFSF12

TNFSF12-TNFSF13

TNFSF13

TNFSF13B

TNFSF14

TNFSF15

TNFSF18

TNFSF4

TNFSF8

TNFSF9

TNIP2

TOR2A

TOX4

TPK1

TPM2

TPO

TPSAB1

TPT1

TRADD

TRAF1

TRAF3

TRAF3IP2

TRAF3IP3

TRANK1

TRAT1

TREM1

TREM2

TREML1

TREML4

TRH

TRHR

TRIB2

TRIM22

TRIM27

TRIM5

TRPC4AP

TSHB

TSHR

TSLP

TUBB3

TXK

TXLNA

TXNIP

TYK2

TYMP

TYRO3

TYROBP

UBA52

UBASH3A

UBD

UBR1

UBXN1

UCN

UCN2

UCN3

ULBP1

ULBP2

ULBP3

UMODL1

UNC93B1

UPK3A

UPP1

UQCRB

USP9Y

UTS2

UTS2B

VAMP5

VAV1

VAV2

VAV3

VCAM1

VEGFB

VEGFC

VEGFD

VGF

VIM

VIP

VIPR1

VIPR2

VNN1

VNN2

VNN3

VSIR

VTCN1

VTN

WFDC2

WFIKKN1

WIPF1

WNT5A

WNT5B

XCL1

XCL2

XCR1

XPO6

XRCC6

YBX2

ZAP70

ZBTB38

ZC3HAV1

ZC3HAV1L

ZCCHC2

ZCRB1

ZEB2

ZNF282
ZYX

Supplementary Table 3 ICPs related genes

Genes	Type
ADORA2A	Inhibitory
ARG1	Inhibitory
BTLA	Inhibitory
CD274	Inhibitory
CD276	Inhibitory
CTLA4	Inhibitory
EDNRB	Inhibitory
HAVCR2	Inhibitory
IDO1	Inhibitory
IL10	Inhibitory
IL13	Inhibitory
IL4	Inhibitory
KIR2DL1	Inhibitory
KIR2DL3	Inhibitory
LAG3	Inhibitory
PDCD1	Inhibitory
SLAMF7	Inhibitory
TGFB1	Inhibitory
TIGIT	Inhibitory
VEGFA	Inhibitory
VEGFB	Inhibitory
C10orf54	Inhibitory
VTCN1	Inhibitory
GZMA	Stimulaotry
BTN3A1	Stimulaotry

BTN3A2	Stimulaotry
CCL5	Stimulaotry
CD27	Stimulaotry
CD28	Stimulaotry
CD40	Stimulaotry
CD40LG	Stimulaotry
CD70	Stimulaotry
CD80	Stimulaotry
CX3CL1	Stimulaotry
CXCL10	Stimulaotry
CXCL9	Stimulaotry
ENTPD1	Stimulaotry
HMGB1	Stimulaotry
ICAM1	Stimulaotry
ICOS	Stimulaotry
ICOSLG	Stimulaotry
IFNA1	Stimulaotry
IFNA2	Stimulaotry
IFNG	Stimulaotry
IL1A	Stimulaotry
IL1B	Stimulaotry
IL2	Stimulaotry
IL2RA	Stimulaotry
ITGB2	Stimulaotry
PRF1	Stimulaotry
SELP	Stimulaotry
TLR4	Stimulaotry
TNF	Stimulaotry
TNFRSF14	Stimulaotry
TNFRSF18	Stimulaotry

TNFRSF4	Stimulaotry
TNFRSF9	Stimulaotry
TNFSF4	Stimulaotry
TNFSF9	Stimulaotry
IL12A	Inhibitory

ICP: Immune checkpoint.

Supplementary Table 4 ICDs related genes

ICDs related genes
ENTPD1
NT5E
CALR
HMGB1
HSP90AA1
ATG5
BAX
CASP8
PDIA3
EIF2AK3
PIK3CA
IFNB1
CXCR3
IFNA1
IL10
IL6
TNF
CASP1
IL1R1
IL1B
NLRP3

P2RX7
LY96
MYD88
TLR4
CD4
CD8A
FOXP3
CD8B
IFNG
IFNGR1
IL17A
IL17RA
PRF1

ICD: Immune cell death modulator.

Supplementary Table 5 Differentially expressed genes in HCC

Gene symbol	Median (tumor)	Median (normal)	Log$_2$ (fold change)	Adjp
AADAT	1.83	11.5	-2.143	8.81E-52
AASS	3.24	11.16	-1.52	9.03E-20
AATF	29.171	10.64	1.374	3.60E-73
ABCA8	3.33	13.07	-1.7	4.52E-35
ABCA9	0.63	3.27	-1.389	1.21E-33
ABCB6	39.371	18.615	1.041	8.28E-19
ABCC6P2	8.95	3.735	1.071	3.34E-29
ABCC9	2.25	6.825	-1.268	3.07E-26
ABHD12	35.671	12.07	1.488	3.60E-75
ABLIM3	12.69	37.135	-1.478	3.05E-29
AC004538.3	0.14	2.04	-1.415	9.74E-43
AC004540.4	0.17	1.654	-1.182	1.94E-25

AC005077.14	0.52	6.74	-2.348	2.36E-51
AC005255.3	3.45	0	2.154	6.77E-37
AC005943.2	1.38	0	1.251	8.76E-11
AC005943.6	2.24	0	1.696	5.01E-03
AC006128.2	1.15	7.035	-1.902	1.11E-20
AC007318.5	4.63	1.58	1.126	1.13E-24
AC009065.4	1.34	0	1.227	9.02E-31
AC009120.6	1.99	5.625	-1.148	4.51E-07
AC009963.3	12.75	43.499	-1.694	7.81E-18
AC012146.7	5.99	2.17	1.141	8.25E-30
AC016292.3	2.15	0.485	1.085	2.75E-23
AC016739.2	12.83	4.745	1.267	4.16E-35
AC016747.3	4.32	1.61	1.027	9.53E-37
AC068535.3	1.62	9.54	-2.008	3.12E-22
AC092171.4	2.23	0.56	1.05	2.10E-36
AC093673.5	5.26	2.085	1.021	1.12E-24
AC099668.5	2.33	10.819	-1.828	3.09E-21
AC104534.3	5.81	0.42	2.262	6.03E-12
AC104809.2	0.04	3.375	-2.073	1.11E-34
AC132217.4	21.11	365.062	-4.049	3.36E-12
AC138035.2	0.6	3.465	-1.481	7.14E-22
AC239868.2	22.92	4.91	2.017	4.33E-23
AC239868.3	22.92	4.91	2.017	4.33E-23
ACACB	8.47	23.61	-1.378	2.85E-25
ACAD11	12.74	40.844	-1.607	7.07E-44
ACADL	2.9	8.555	-1.293	3.27E-23
ACADS	39.17	97.48	-1.294	1.55E-37
ACADVL	359.313	861.913	-1.26	2.35E-22
ACAP3	7.86	17.3	-1.046	7.95E-04
ACBD6	24.71	9.845	1.245	2.08E-59

ACCS	6.22	14.189	-1.073	6.11E-12
ACLY	20.91	8.174	1.256	5.83E-28
ACOT12	13.96	29.518	-1.029	2.17E-12
ACP5	22.77	9.84	1.133	2.02E-08
ACP6	18.6	8.69	1.016	6.14E-32
ACSL1	129.984	406.58	-1.638	4.55E-31
ACSL4	33.02	2.355	3.342	4.63E-30
ACSM1	8.56	1.085	2.197	2.43E-16
ACSM3	18.45	58.215	-1.606	1.69E-24
ACSM5	28.829	79.263	-1.428	1.12E-22
ACTN4	102.749	47.2	1.106	1.82E-31
ADAM15	42.241	16.735	1.286	1.78E-44
ADAMTS1	3.15	7.81	-1.086	8.91E-16
ADAMTS13	2.32	14.475	-2.221	1.49E-97
ADAMTS2	1.37	4.445	-1.2	2.95E-16
ADAMTSL2	3.15	11.359	-1.574	3.48E-25
ADAT2	1.23	3.685	-1.071	1.97E-11
ADCK2	14.49	5.585	1.234	6.84E-62
ADCY1	0.4	4.115	-1.869	5.43E-29
ADGRA3	8.9	21.525	-1.186	8.54E-24
ADGRG7	0.72	4.425	-1.657	4.94E-46
ADH1B	360.135	884.396	-1.294	5.15E-11
ADH4	154.032	549.147	-1.827	2.35E-13
ADIPOR1	66.791	32.8	1.004	1.88E-43
ADM2	2.8	0.75	1.119	3.37E-20
ADRA1A	0.75	16.38	-3.312	2.62E-82
ADRA1B	1.21	3.855	-1.135	8.39E-31
ADRA2B	0.41	1.885	-1.033	4.15E-50
ADSL	31.91	14.58	1.079	1.69E-44
AF064858.6	0.81	3.285	-1.243	3.50E-13

AFG3L1P	3.2	8.22	-1.134	2.33E-10
AFM	50.38	143.334	-1.49	1.15E-19
AFP	11.46	4.685	1.132	2.19E-11
AGAP4	2.28	5.63	-1.015	5.30E-08
AGAP5	1.11	3.235	-1.005	3.29E-11
AGAP6	3.38	12.338	-1.607	1.98E-13
AGAP9	2.16	10.75	-1.895	3.89E-19
AGBL5	8.21	3.445	1.051	2.57E-39
AGER	1.41	4.07	-1.073	5.63E-10
AGPAT1	46.821	21.794	1.069	7.90E-49
AGXT2	13.63	35.03	-1.3	1.27E-23
AIDA	24.519	10.875	1.104	1.27E-46
AIM1L	1.81	0.17	1.264	1.32E-33
AIMP2	27.651	13.26	1.007	1.33E-32
AKAP17A	10.16	25.474	-1.246	3.02E-09
AKIP1	12.78	5.335	1.121	7.69E-50
AKR1B10	177.158	3.015	5.472	9.84E-30
AKR1C1	481.068	212.636	1.174	9.13E-08
AKR1C2	299.123	125.148	1.25	8.98E-05
AKR1C3	351.236	89.588	1.959	3.03E-46
AKR1C8P	0.26	1.74	-1.121	2.75E-20
AKR1D1	10.96	40.685	-1.801	1.01E-11
AKR7L	4.43	14.072	-1.473	1.15E-28
AL158801.1	2.19	0.275	1.323	4.13E-33
AL161668.5	1.63	5.785	-1.367	3.53E-22
ALDH1A1	458.284	217.994	1.068	2.39E-10
ALDH3A1	2.17	0.46	1.119	7.82E-12
ALDH8A1	27.029	64.679	-1.229	3.10E-22
ALDOA	289.595	130.929	1.139	1.02E-26
ALG1	19.83	8.77	1.092	3.96E-57

ALG1L	7.27	0.325	2.642	9.46E-43
ALG3	57.289	26.005	1.11	3.84E-51
ALG8	45.711	19.841	1.164	3.48E-66
ALKBH2	25.259	11.915	1.024	4.09E-37
ALMS1	5	1.79	1.105	1.28E-57
ALOX12P2	1.39	6.128	-1.577	2.52E-25
ALPL	10.67	40.58	-1.833	1.71E-26
ALYREF	37.749	13.9	1.379	1.14E-52
AMDHD1	23.48	51.479	-1.1	6.39E-15
AMN	9.84	21.844	-1.075	1.73E-06
ANAPC11	192.35	76.061	1.327	1.35E-65
ANGPTL6	1.67	11.6	-2.238	1.35E-96
ANK3	1.01	3.435	-1.142	6.39E-15
ANKRD29	3.48	0.61	1.476	6.70E-29
ANKRD39	14.36	6.27	1.079	4.26E-64
ANLN	2.26	0.175	1.472	2.75E-40
ANO10	10.95	4.33	1.165	1.20E-42
ANXA10	10.59	34.34	-1.608	2.59E-18
ANXA11	86.99	38.454	1.157	3.81E-43
ANXA13	7.52	2.45	1.304	2.16E-08
ANXA2	254.866	63.065	1.998	1.96E-44
ANXA2P2	4.42	0.755	1.627	1.14E-37
AP000349.2	1.28	0.03	1.146	1.78E-25
AP000355.2	0.63	2.28	-1.009	1.62E-16
AP003391.1	2.06	0	1.614	1.08E-03
AP006285.6	0.47	2.525	-1.262	4.77E-13
AP006285.7	0.06	1.265	-1.095	2.02E-45
AP1M2	2.83	0.56	1.296	4.23E-15
AP1S1	45.54	17.135	1.36	4.79E-61
AP3B1	16.49	6.325	1.256	6.45E-72

APIP	18.439	8.705	1.002	1.29E-36
APLN	1.59	0.1	1.235	3.06E-34
APOA1BP	120.684	38.634	1.618	9.18E-90
APOA2	31278.852	10880.067	1.523	9.24E-04
APOA4	3.03	26.19	-2.754	1.79E-07
APOA5	97.267	211.834	-1.115	5.78E-13
APOBEC3B	2.34	0.22	1.453	2.35E-29
APOC2	2260.615	475.779	2.246	3.11E-13
APOE	5880.405	2771.689	1.085	8.27E-14
APOF	17.701	113.668	-2.616	2.62E-38
APOLD1	4.3	1.215	1.259	1.19E-25
AQP3	24.599	60.915	-1.274	4.29E-21
ARF1	269.025	132.775	1.013	3.51E-42
ARF3	30.759	14.79	1.008	1.65E-30
ARGLU1	17.771	38.953	-1.09	4.10E-06
ARHGAP10	1.86	5.19	-1.114	4.07E-22
ARHGEF39	1.81	0.4	1.005	1.83E-36
ARL2	24.729	8.94	1.372	6.90E-39
ARPC1A	87.772	39.045	1.148	8.56E-59
ARPC1B	99.181	38.33	1.349	1.13E-27
ARPC3	174.634	81.089	1.097	8.44E-55
ARPC5	86.762	29.82	1.51	3.85E-56
ARRDC2	15.5	7.085	1.029	1.11E-14
ARSE	49.9	23	1.085	9.66E-07
ARSEP1	2.5	0.09	1.683	1.24E-10
ARV1	17.67	8.02	1.049	3.26E-45
ASF1B	3.27	0.28	1.738	7.91E-48
ASMTL-AS1	3.23	11.1	-1.516	3.17E-06
ASNA1	43.761	17.964	1.239	1.73E-56
ASPDH	33.751	71.634	-1.064	4.55E-11

ASPG	7.77	75.475	-3.124	8.33E-41
ASPH	41.04	16.18	1.291	4.24E-21
ASPM	2.96	0.125	1.816	8.72E-54
ATAD2	6.91	1.855	1.47	1.16E-38
ATF3	14.94	36.796	-1.246	2.39E-11
ATF5	145.946	767.753	-2.387	6.51E-30
ATHL1	9.89	26.485	-1.336	7.22E-03
ATIC	66.201	32.119	1.021	1.34E-34
ATOH8	4.42	18.95	-1.88	2.47E-30
ATOX1	347.29	114.178	1.596	6.63E-63
ATP1A1	136.342	51.872	1.377	1.61E-31
ATP1B1	97.951	37.295	1.37	1.12E-29
ATP1B3	21.14	8.2	1.267	1.30E-18
ATP5E	77.471	33.549	1.184	5.86E-58
ATP5G1	239.967	89.216	1.417	2.90E-65
ATP5G2	428.751	189.499	1.174	3.40E-74
ATP5H	378.119	168.709	1.16	5.68E-70
ATP5J2	584.111	238.425	1.289	2.71E-73
ATP5J2-PTCD1	3.96	1.075	1.257	3.69E-31
ATP5L	304.183	126.381	1.261	4.57E-59
ATP6AP1	65.639	24.015	1.414	1.58E-72
ATP6V0B	142.339	68.669	1.041	8.52E-40
ATP6V0E1	207.691	99.105	1.06	2.92E-53
ATP6V1C1	16.8	6.985	1.157	5.23E-30
ATP6V1D	38.409	18.475	1.017	3.53E-39
ATP6V1E1	67.568	28.939	1.196	3.07E-53
ATP6V1F	102.047	36.464	1.46	5.33E-67
ATP6V1H	23.62	11.17	1.016	1.12E-44
ATRAID	74.109	34.835	1.068	2.28E-55
ATRN	27.481	10.28	1.336	3.10E-24

AURKA	7.35	0.99	2.069	2.38E-56
AURKB	5.25	0.53	2.03	3.98E-50
AUTS2	3.86	9.375	-1.094	2.28E-16
AVPR1A	0.47	5.405	-2.123	1.46E-24
AZGP1	569.518	1221.805	-1.1	5.97E-16
AZGP1P1	6.43	19.275	-1.448	8.77E-28
B3GAT1	0.11	1.63	-1.245	5.52E-11
B3GNT3	2.33	0.495	1.155	1.36E-10
B3GNT5	2.3	0.45	1.186	1.39E-19
B9D1	10.26	3.88	1.206	3.33E-37
BAG6	179.805	88.398	1.016	1.81E-55
BAMBI	13.81	6.22	1.036	1.44E-05
BANF1	152.165	69.61	1.117	1.06E-68
BAX	78.71	24.245	1.659	1.38E-59
BBOX1	2.69	11.375	-1.746	1.48E-11
BCAM	57.46	21.915	1.351	2.50E-22
BCAP31	202.657	70.416	1.512	1.98E-72
BCAS4	1.85	0.41	1.015	2.00E-31
BCHE	17.321	38.95	-1.125	8.65E-13
BCL2L12	19.401	8.03	1.176	9.33E-50
BCL3	31.12	75.011	-1.243	2.34E-15
BCL6	10.78	24.681	-1.124	5.88E-13
BCO2	2.42	31.444	-3.246	8.54E-76
BEX2	2.48	0.685	1.046	1.26E-11
BGN	56.79	133.176	-1.215	1.42E-13
BHMT	58.582	197.176	-1.734	1.51E-11
BIRC5	6.81	0.505	2.376	1.57E-54
BLOC1S1	213.441	94.87	1.161	2.56E-73
BLVRA	19.46	3.145	2.303	3.46E-46
BMPER	0.06	1.515	-1.246	1.97E-87

BMS1P8	1.92	0.11	1.395	1.45E-28
BOLA1	26.79	11.355	1.169	3.78E-58
BOLA2	10.8	2.74	1.658	3.31E-53
BOLA2B	84.67	20.26	2.011	1.17E-74
BOLA3	36.339	13.22	1.393	4.46E-65
BOP1	28.041	9.04	1.532	7.46E-50
BPGM	8.15	3.535	1.013	3.91E-40
BPNT1	13.67	6.01	1.065	1.24E-31
BRIX1	13	5.58	1.089	2.97E-39
BRMS1	30.751	11.85	1.305	3.54E-69
BROX	10.95	4.735	1.059	1.51E-45
BSG	301.329	101.335	1.563	1.20E-64
BTF3	338.66	168.376	1.004	8.92E-46
BTG3	8.55	3.095	1.222	8.12E-29
BUB1	1.72	0.11	1.293	3.44E-40
BUB1B	1.6	0.16	1.164	1.37E-34
BUD31	64.382	29.16	1.116	6.44E-52
BX842568.1	0.4	2.485	-1.316	3.16E-30
BYSL	12.53	4.635	1.264	2.49E-42
BZW2	15.3	6.63	1.095	3.77E-34
C10orf35	3.84	1.375	1.027	1.80E-18
C11orf96	6.79	26.472	-1.818	1.04E-24
C11orf98	63.592	30.65	1.029	1.59E-48
C12orf45	19.5	8.885	1.052	3.14E-58
C12orf73	7.32	2.955	1.073	9.38E-59
C12orf75	6.37	1.335	1.658	2.87E-18
C14orf105	5.67	19.307	-1.606	5.36E-20
C14orf166	107.94	52.815	1.017	2.38E-65
C14orf180	0.01	1.21	-1.13	2.10E-53
C15orf39	4.46	1.5	1.127	5.00E-32

C15orf40	15.5	7.065	1.033	4.08E-49
C15orf48	3.02	0.55	1.375	7.15E-16
C16orf59	2.19	0.37	1.219	1.35E-39
C17orf49	55.241	23.97	1.171	1.71E-42
C17orf58	10.87	4.22	1.185	4.39E-59
C17orf89	74.47	35.49	1.048	1.48E-45
C19orf48	26.67	11.515	1.145	7.86E-38
C19orf53	130.861	56.883	1.188	5.48E-67
C19orf66	42.679	100.513	-1.217	3.13E-30
C1orf106	1.81	0.26	1.157	1.60E-19
C1orf168	3.31	11.729	-1.562	6.25E-32
C1orf198	12.46	4.765	1.223	7.64E-27
C1orf228	1.79	6.188	-1.365	4.05E-27
C1orf35	12.7	5.775	1.016	1.91E-48
C1orf43	182.214	81.021	1.159	4.33E-62
C1orf54	7.23	2.655	1.171	3.55E-24
C1QA	81.492	39.245	1.035	1.34E-09
C1QTNF1	4.54	17.865	-1.768	5.91E-25
C1QTNF5	11.43	5.08	1.032	2.00E-19
C1R	414.692	877.009	-1.079	1.34E-22
C1RL-AS1	1.81	5.113	-1.121	6.51E-12
C20orf27	22.11	9.443	1.146	4.31E-49
C2orf54	6.44	2.305	1.171	4.81E-06
C3P1	11.36	51.089	-2.075	5.67E-42
C4A-AS1	2.72	10.738	-1.658	2.36E-24
C4B-AS1	2.72	10.738	-1.658	2.36E-24
C6	47.422	120.137	-1.323	5.41E-20
C6orf1	20.87	9.29	1.088	3.18E-43
C6orf47	10.63	4.24	1.15	4.29E-35
C6orf48	78.378	31.529	1.287	4.33E-40

C6orf89	20.281	9.085	1.077	1.24E-38
C7	5.88	49.485	-2.875	7.22E-31
C7orf50	47.619	20.535	1.175	3.79E-50
C8A	73.338	173.446	-1.231	4.02E-19
C8orf33	18.379	7.305	1.223	4.89E-48
C8orf4	12.81	58.63	-2.11	1.62E-36
C8orf46	1.62	5.51	-1.313	2.86E-14
C8orf59	87.069	34.17	1.324	3.10E-61
C8orf76	19.81	8.225	1.174	8.54E-53
C9	23.051	263.854	-3.461	3.80E-35
C9orf16	50.801	23.865	1.059	2.63E-38
CACNA1H	1.51	5.3	-1.328	2.70E-03
CACNB2	0.74	2.575	-1.039	1.27E-15
CACYBP	43.419	15.51	1.428	6.64E-39
CADM1	40.07	14.41	1.414	1.01E-20
CALM3	104.213	50.399	1.033	1.35E-34
CALR	813.782	337.302	1.268	2.50E-47
CAMK2B	0.24	2.31	-1.416	1.36E-26
CANT1	14.81	6.46	1.084	2.58E-39
CANX	179.83	85.843	1.058	6.23E-29
CAP2	8.86	1.345	2.072	3.05E-52
CAPG	26.6	3.725	2.546	7.53E-36
CAPN2	26.33	11.385	1.142	1.95E-25
CAPN3	3.25	13.15	-1.735	2.72E-26
CAPNS1	328.51	144.006	1.184	3.25E-61
CAPRIN1	35.17	17.019	1.005	9.85E-33
CASC5	3.48	1.025	1.146	7.01E-22
CASK	8.9	3.435	1.159	1.41E-26
CAV1	11.49	4.81	1.104	7.21E-21
CBFA2T3	0.57	2.535	-1.171	1.29E-39

CBR1	181.056	75.123	1.258	1.46E-21
CBS	4.02	13.905	-1.57	8.68E-05
CBX1	14.33	5.675	1.2	2.02E-35
CBX8	4.54	1.57	1.108	1.07E-43
CCBE1	0.06	1.185	-1.044	3.49E-54
CCDC107	40.179	15.745	1.298	1.88E-61
CCDC167	49.179	20.844	1.2	8.38E-48
CCDC28B	3.8	1.31	1.055	2.88E-26
CCDC34	5.74	1.22	1.602	1.03E-51
CCDC64	4.25	1.51	1.065	1.30E-13
CCDC80	4.3	1.31	1.198	5.83E-10
CCDC84	6.33	15.905	-1.206	2.85E-05
CCDC86	12.32	4.795	1.201	1.91E-38
CCHCR1	11.72	4.52	1.204	6.93E-41
CCL14	7.25	46.812	-2.535	1.04E-34
CCL15	29.421	9.305	1.562	1.09E-23
CCL18	2.04	0.51	1.01	1.72E-11
CCL19	2.7	8.89	-1.418	1.65E-06
CCL20	22.42	1.5	3.228	7.05E-19
CCL21	7.73	17.895	-1.114	1.21E-05
CCL23	0.22	2.155	-1.371	1.11E-67
CCNA2	2.96	0.455	1.445	1.85E-36
CCNB1	14.8	0.9	3.056	1.24E-71
CCNB2	4.81	0.27	2.194	3.46E-57
CCNE1	1.55	0.22	1.064	5.34E-30
CCNL1	21.84	60.633	-1.432	8.69E-22
CCNL2	33.029	101.006	-1.584	1.99E-10
CCT3	185.734	51.09	1.842	3.78E-87
CCT4	57.519	25.355	1.151	2.01E-54
CCT5	82.509	34.429	1.237	3.35E-42

CCT6A	83.169	34.536	1.244	1.14E-46
CCT7	105.829	49.213	1.089	1.59E-57
CD151	152.704	70.965	1.095	6.23E-29
CD163L1	2.63	0.49	1.285	1.64E-30
CD1D	1.31	5.54	-1.501	6.84E-32
CD24	50.85	6.745	2.743	5.43E-13
CD248	3.79	1.195	1.126	1.40E-25
CD2BP2	24.97	9.89	1.254	4.12E-56
CD320	20.33	9.475	1.026	1.42E-40
CD34	14.17	1.625	2.531	8.03E-94
CD36	16.32	7.178	1.083	7.68E-10
CD3D	4.12	1.295	1.158	2.24E-16
CD5L	1.35	3.725	-1.008	2.12E-11
CD63	685.588	273.832	1.321	1.84E-54
CD74	753.727	185.354	2.018	1.25E-25
CDA	15.42	32.819	-1.042	2.27E-14
CDC123	33.16	16.075	1	6.77E-45
CDC20	9.32	0.31	2.978	3.93E-63
CDC25C	1.84	0.055	1.429	3.83E-53
CDC45	3.07	0.32	1.624	7.92E-45
CDC6	2.44	0.365	1.334	8.64E-29
CDCA3	5.67	0.685	1.985	4.65E-50
CDCA5	3.89	0.275	1.939	6.90E-56
CDCA8	2.69	0.29	1.516	7.21E-44
CDH13	3.25	0.32	1.687	2.95E-66
CDHR2	1.82	16.165	-2.606	1.02E-28
CDK1	6.32	0.33	2.46	7.38E-61
CDK11A	11.85	26.269	-1.086	7.63E-07
CDK4	47.33	19.38	1.246	1.22E-41
CDK5	12.8	4.67	1.283	5.06E-63

CDKN2A	10.79	0.315	3.164	9.92E-63
CDKN2AIPNL	16.91	6.3	1.295	5.74E-71
CDKN2B	2.03	0.37	1.145	2.24E-30
CDKN2C	7.91	1.415	1.883	4.49E-54
CDKN3	10.96	0.45	3.044	4.14E-74
CDT1	3.68	0.265	1.887	1.30E-49
CENPA	2.09	0.12	1.464	6.70E-44
CENPF	6.14	0.295	2.463	1.12E-53
CENPH	3.04	0.59	1.345	7.84E-51
CENPK	1.51	0.24	1.017	2.37E-30
CENPL	1.82	0.34	1.073	8.02E-41
CENPM	5.97	0.33	2.39	8.75E-58
CENPN	6.1	2.08	1.205	4.90E-38
CENPU	4.69	0.885	1.594	4.48E-42
CENPW	8.1	1.1	2.115	3.78E-62
CEP131	5.98	2.185	1.132	3.42E-49
CES3	7.32	16.224	-1.05	1.23E-13
CES4A	1.93	10.081	-1.919	1.34E-22
CETN2	20.93	9.26	1.096	3.54E-44
CFHR3	33.541	174.664	-2.346	3.33E-15
CFL1	437.093	184.272	1.242	1.62E-54
CFP	2.32	8.934	-1.581	3.12E-36
CGREF1	9.8	4.105	1.081	7.12E-12
CH17-13I23.3	1.3	0.105	1.058	2.82E-10
CH17-340M24.3	9.38	4.11	1.022	8.62E-42
CHAF1A	5.12	1.39	1.357	4.33E-53
CHCHD3	24.45	10.515	1.144	7.26E-34
CHCHD6	8.61	3.59	1.066	5.59E-48
CHEK1	2.38	0.48	1.191	1.77E-38
CHMP2A	166.352	74.886	1.141	3.08E-69

CHMP4B	57.181	27.285	1.041	1.47E-42
CHRD	9.55	72.098	-2.793	1.16E-30
CHRNA4	0.33	12.095	-3.3	9.74E-29
CHST4	0.03	1.585	-1.327	1.28E-18
CIDEB	62.721	137.997	-1.125	1.22E-23
CITED2	16.549	36.75	-1.105	3.51E-15
CKAP2	3.09	0.855	1.141	2.09E-33
CKAP4	32.45	11.11	1.466	9.61E-39
CKB	26.379	10.115	1.301	4.73E-13
CKLF	29.829	9.115	1.608	2.26E-62
CKS1B	71.878	24.695	1.504	3.76E-61
CKS1BP3	5.44	0.475	2.126	1.92E-51
CKS2	31.349	8.62	1.75	3.56E-45
CLASRP	20.34	45.469	-1.123	2.99E-03
CLDN10	0.1	1.76	-1.327	6.13E-06
CLDN15	24.411	8.805	1.374	1.73E-16
CLDN2	5.48	16.855	-1.462	1.92E-05
CLDN7	35.24	14.474	1.228	2.16E-08
CLEC14A	7.72	3.055	1.105	1.10E-24
CLEC1B	0.03	8.658	-3.229	1.07E-97
CLEC4G	0.12	23.634	-4.459	5.34E-114
CLEC4M	0.02	18.949	-4.29	1.36E-146
CLGN	2.2	0.6	1	5.64E-11
CLIC1	143.867	43.331	1.708	1.91E-47
CLN6	19.69	9.18	1.023	2.95E-51
CLRN3	4	14.575	-1.639	1.60E-12
CLTA	122.402	57.029	1.089	1.99E-50
CMSS1	13.65	5.695	1.13	5.50E-47

CMTM7	8.1	3.55	1	1.06E-15
CNDP1	0.49	17.989	-3.672	1.82E-56
CNIH4	32.81	10.014	1.618	1.20E-64
CNPY2	165.673	75.695	1.12	4.93E-71
CNTFR	0.49	3.555	-1.612	1.21E-06
CNTN3	0.08	2.035	-1.491	2.99E-40
COA3	130.119	62.989	1.035	3.77E-45
COA6	53.471	13.715	1.888	2.18E-88
COCH	1.42	0.18	1.036	1.03E-21
COL15A1	3.03	0.17	1.784	4.85E-52
COL1A1	28.3	10.504	1.349	2.14E-09
COL1A2	29.91	12.124	1.236	1.68E-09
COL27A1	6.03	16.685	-1.331	4.27E-10
COL4A1	26.299	4.465	2.321	3.62E-43
COL4A2	30.359	7.015	1.968	1.19E-37
COLEC10	0.39	12.865	-3.318	1.21E-96
COLEC11	18.71	53.509	-1.468	2.49E-20
COMMD4	110.17	35.546	1.605	1.73E-97
COMMD5	24.38	9.165	1.32	5.36E-65
COPA	47.009	19.744	1.211	6.92E-30
COPG2	6	2.18	1.138	8.90E-34
COPS6	83.707	38.084	1.116	9.69E-69
COPZ1	81.882	40.161	1.01	1.86E-49
CORO1B	47.55	23.209	1.004	1.49E-42
COX20	40.969	18.425	1.111	2.80E-44
COX4I2	3.1	0.33	1.624	4.93E-71
COX6A1	639.1	304.795	1.066	4.56E-61
COX6A2	2.46	6.19	-1.055	4.48E-09
COX6B1	407.285	148.543	1.449	4.41E-65
COX6B1P4	0	1.055	-1.039	8.51E-76

COX6C	582.17	237.502	1.29	3.06E-60
COX7A2	317.364	149.805	1.078	3.75E-45
COX7B	168.51	73.211	1.192	4.09E-56
COX7C	750.183	309.093	1.276	2.01E-63
COX7CP1	0	1.532	-1.34	6.12E-13
COX8A	396.56	187.065	1.08	2.35E-54
CPD	16.511	6.295	1.263	8.17E-23
CPE	15.74	4.685	1.558	2.12E-24
CPEB3	1.11	3.71	-1.158	7.09E-40
CPED1	3.01	7.33	-1.055	2.93E-23
CPQ	47.94	14.525	1.656	4.21E-58
CPSF3	13.29	5.94	1.042	1.43E-58
CPT1B	5.21	13.954	-1.268	5.88E-07
CPVL	14.5	2.755	2.045	3.69E-20
CRHBP	0.56	16.829	-3.515	3.43E-75
CRIP1	26.359	7.01	1.772	1.06E-23
CRNDE	4.62	0.5	1.906	2.52E-27
CRNKL1	13.85	5.9	1.106	4.78E-63
CROCCP2	2.91	7.045	-1.041	5.78E-21
CRP	251.671	2792.323	-3.467	1.62E-13
CRTAP	47.31	22.299	1.052	1.27E-22
CSAD	14.78	44.387	-1.524	5.27E-29
CSE1L	21.24	8.83	1.178	3.31E-55
CSF3R	1.43	6.905	-1.702	3.81E-27
CSNK2B	182.771	79.873	1.184	4.67E-67
CSRNP1	7.19	23.779	-1.597	3.50E-31
CSTB	62.012	30.3	1.009	3.64E-26
CSTF2	4.47	1.56	1.095	1.37E-34
CTB-25B13.12	9.2	3.654	1.132	2.22E-49
CTB-50L17.14	1.12	5.205	-1.549	6.55E-24

CTB-63M22.1	136.882	29.105	2.195	1.57E-20
CTB-79E8.3	0	2.14	-1.651	3.13E-21
CTB-89H12.4	1.4	3.94	-1.041	5.23E-13
CTC-246B18.10	5.76	1.865	1.238	2.29E-25
CTC-505O3.2	2.9	11.22	-1.648	1.94E-11
CTC-524C5.2	0.71	3.425	-1.372	4.47E-21
CTC-529I10.1	0.66	3.14	-1.318	2.44E-37
CTD-2240E14.4	0.3	2.59	-1.465	3.83E-54
CTD-2537I9.12	1.46	8.73	-1.984	1.04E-19
CTD-2540B15.11	125.4	57.014	1.124	2.20E-18
CTD-2619J13.27	1.41	6.11	-1.561	1.97E-20
CTD-2619J13.5	1.39	8.145	-1.936	1.05E-25
CTD-2619J13.8	1.95	6.439	-1.334	7.86E-19
CTD-3080P12.3	0.44	3.79	-1.734	1.40E-29
CTD-3092A11.2	2.47	9.255	-1.563	2.53E-27
CTHRC1	2.35	0.245	1.428	3.20E-24
CTNNA1	88.812	42.721	1.039	1.10E-43
CTNNBL1	45.379	20.99	1.077	2.39E-33
CTSA	181.974	53.563	1.746	1.71E-70
CTSC	35.961	14.13	1.289	1.43E-20
CTSD	769.138	382.084	1.007	1.02E-31
CTSH	163.46	77.63	1.065	5.46E-19
CTSS	37.281	13.98	1.354	5.87E-11
CUEDC1	7.88	3.19	1.084	6.86E-26
CUTA	288.894	108.548	1.404	1.34E-74
CXCL10	11.72	1.145	2.568	3.36E-23
CXCL12	11.66	60.325	-2.276	7.53E-40
CXCL14	0.19	14.215	-3.676	7.94E-78
CXCL2	18.181	119.784	-2.655	1.51E-45
CXCL9	4.18	0.765	1.553	5.77E-14

CXorf36	2.25	0.32	1.3	1.83E-66
CYB5R1	47.698	20.285	1.194	2.90E-52
CYC1	157.324	75.334	1.052	5.84E-48
CYP1A1	0.97	4.71	-1.535	1.72E-04
CYP1A2	0.48	44.13	-4.93	3.50E-37
CYP21A1P	2.25	6.15	-1.137	7.39E-04
CYP21A2	5.8	14.85	-1.221	6.93E-07
CYP26A1	0.28	4.96	-2.219	5.10E-42
CYP2A6	132.862	592.285	-2.148	3.83E-11
CYP2A7	1.97	29.83	-3.376	7.48E-14
CYP2B6	15.26	76.219	-2.248	3.21E-25
CYP2B7P	5.24	14.939	-1.353	1.85E-03
CYP2C19	0.33	6.81	-2.554	3.42E-45
CYP2C8	85.017	509.168	-2.568	5.79E-27
CYP2C9	134.596	470.368	-1.798	1.33E-17
CYP2D7	19.04	65.65	-1.734	1.53E-12
CYP2E1	500.525	2526.544	-2.333	3.98E-21
CYP39A1	3.25	17.415	-2.115	3.87E-28
CYP3A4	31.139	386.278	-3.591	1.22E-16
CYP3A43	0.75	2.875	-1.147	1.02E-13
CYP3A5	100.148	212.607	-1.078	1.23E-05
CYP4A11	108.217	299.559	-1.46	1.21E-15
CYP4A22	23.29	77.329	-1.689	1.47E-19
CYP7A1	10.65	1.939	1.987	7.80E-10
CYP8B1	34.489	127.326	-1.854	2.61E-21
CYR61	14.11	53.815	-1.859	8.70E-30
CYSTM1	72.781	21.57	1.709	6.22E-58
CYTH2	23.18	9.76	1.168	2.22E-48
DAD1	207.245	96.907	1.089	1.94E-61
DAP3	95.378	39.351	1.256	2.69E-68

DAPK2	4.37	1.105	1.351	2.77E-40
DARS2	10.48	3.105	1.484	3.52E-50
DAXX	23.62	10.495	1.099	5.71E-40
DBH	0.56	10.785	-2.917	5.04E-99
DBH-AS1	5.1	20.855	-1.841	1.48E-21
DBN1	4.76	1.49	1.21	5.55E-22
DBNDD1	11.41	2.12	1.992	7.68E-36
DBNDD2	8.35	3.465	1.066	1.79E-24
DBP	18.81	6.13	1.474	2.74E-34
DCAF13	17.179	6.265	1.323	4.36E-45
DCDC2	2.38	0.62	1.061	3.39E-11
DCK	3.95	1.415	1.035	8.38E-27
DCN	14.87	101.289	-2.688	1.21E-29
DCTN2	55.341	26.62	1.028	6.03E-34
DCTPP1	22.201	9.24	1.18	5.91E-53
DDAH2	45.041	19.78	1.148	3.31E-31
DDOST	104.22	48.816	1.079	1.42E-35
DDX3Y	3.68	8.605	-1.037	3.27E-10
DDX41	59.511	26.05	1.162	1.64E-69
DEFA1	0.09	2.755	-1.784	7.86E-44
DEFA1B	0	2.35	-1.744	8.92E-47
DEFA3	0	1.345	-1.23	2.14E-31
DEPTOR	9.3	3.985	1.047	4.12E-28
DERL1	56.191	26.628	1.05	5.19E-37
DES	0.19	2.725	-1.646	3.52E-34
DHFRP1	2.31	0.635	1.018	4.52E-10
DHODH	14.04	49.561	-1.749	3.99E-44
DHRS7	80.309	37.9	1.064	5.29E-22
DHX9	41.55	19.855	1.029	8.48E-40
DIO3OS	0.41	4.344	-1.922	2.75E-26

DIRAS3	0.25	2.305	-1.403	1.29E-38
DLGAP1-AS1	7.94	2.765	1.248	3.17E-30
DLGAP5	1.41	0.07	1.171	3.76E-38
DLL4	3.79	1.165	1.146	6.49E-35
DNAJB11	145.411	63.964	1.172	4.51E-58
DNAJC12	6.66	21.085	-1.528	1.18E-18
DNAJC19P9	2.02	0.425	1.084	5.55E-20
DNASE1L3	6.64	39.306	-2.399	3.21E-36
DNASE2	32.07	13.445	1.195	5.48E-27
DNHD1	1.45	6.529	-1.62	1.38E-17
DNPH1	125.6	57.579	1.112	3.92E-46
DOCK5	2.04	5.98	-1.199	5.82E-19
DOLK	10.08	4.42	1.032	8.50E-57
DPCD	7.67	3.15	1.063	3.19E-37
DPH1	10.36	22.265	-1.034	1.87E-17
DPM3	133.61	60.894	1.121	1.08E-40
DPP3	21.58	10.23	1.008	6.32E-37
DPP4	19.36	5.345	1.682	3.61E-16
DPT	0.55	6.09	-2.194	5.77E-25
DPY30	58.651	25.86	1.151	3.29E-71
DRAP1	101.391	38.361	1.379	4.29E-83
DRG1	40.159	18.46	1.081	7.30E-57
DSN1	7.32	2.66	1.185	1.72E-48
DTD1	10.72	4.72	1.035	4.28E-20
DTL	2.23	0.145	1.496	1.04E-41
DTNA	6.14	0.99	1.843	4.13E-27
DTNBP1	8.48	3.67	1.021	1.58E-32
DTX1	4.03	11.335	-1.294	1.17E-21
DTX4	3.77	8.57	-1.005	1.15E-10
DTYMK	19.68	7.14	1.345	3.89E-55

DUSP1	76.452	213.619	-1.47	6.33E-21
DUSP23	131.497	63.76	1.033	3.93E-33
DUSP9	2.14	0.27	1.306	1.47E-24
DUXAP8	1.89	0.225	1.238	1.59E-27
DYNC1H1	65.922	29.81	1.119	3.19E-53
DYNLL1	246.304	98.267	1.317	1.33E-55
DYNLRB1	145.139	51.949	1.465	1.38E-80
E2F1	5.49	0.28	2.342	2.90E-57
EBF4	2.55	6.54	-1.087	8.38E-07
ECHDC2	148.549	458.109	-1.618	1.73E-42
ECM1	2.51	17.755	-2.418	1.30E-63
ECT2	3	0.61	1.313	4.23E-34
EEF1A1P5	63.341	26.253	1.239	2.14E-14
EEF1A1P6	11.7	3.45	1.513	1.01E-30
EEF1A2	7.09	0.45	2.48	9.75E-14
EEF1D	621.107	280.43	1.144	2.20E-43
EEF1G	721.421	356.435	1.015	1.20E-44
EFCAB11	4.05	1.51	1.009	6.94E-49
EFHD1	5.26	17.155	-1.536	2.61E-09
EFNA4	8.27	2.885	1.255	2.00E-46
EFTUD2	32.139	14.38	1.107	2.23E-57
EGR1	18.64	44.085	-1.199	1.97E-11
EHD4	9.79	3.77	1.178	6.04E-22
EHMT2	23.36	8.135	1.415	1.27E-58
EIF2D	30.789	13.13	1.17	1.04E-57
EIF3CL	33.16	14.54	1.136	9.35E-38
EIF3D	84.829	35.248	1.244	9.48E-55
EIF3E	194.253	69.545	1.469	1.00E-45
EIF3H	142.754	54.924	1.362	7.81E-48
EIF3K	205.429	85.005	1.263	5.18E-70

EIF3M	133.963	61.922	1.101	2.64E-48
EIF4BP7	1.68	0.34	1	3.21E-40
EIF5AP4	3.95	0.16	2.093	9.78E-37
EIF6	180.305	77.275	1.212	5.07E-65
ELOVL1	37.6	17.105	1.092	1.59E-39
ELOVL2	17.6	4.335	1.802	7.73E-15
EMC2	31.99	14.01	1.136	6.04E-41
EMC3	74.279	28.66	1.344	1.83E-55
EMC4	77.299	36.715	1.054	5.22E-67
EMCN	3.89	1.22	1.139	2.32E-25
EMP1	7.72	3.295	1.022	2.12E-06
ENAH	10.65	2.805	1.614	2.54E-29
ENGASE	5.9	13.544	-1.076	1.47E-04
ENO3	11.36	58.1	-2.258	4.36E-29
ENPP2	14.99	3.555	1.812	3.56E-22
ENSA	109.949	44.47	1.287	1.18E-60
FUCA2	34.951	16.73	1.02	1.28E-29
SEMA3F	5.44	1.655	1.278	1.43E-50
LASP1	64.408	28.585	1.145	4.22E-38
SLC7A2	14.44	46.174	-1.611	3.88E-24
PLXND1	36.579	15.975	1.147	2.23E-29
LAMP2	125.756	60.959	1.033	4.88E-20
TMEM98	30.38	7.44	1.895	2.53E-21
TMEM132A	2.42	0.575	1.119	1.31E-17
TNFRSF12A	46.019	15.247	1.533	8.77E-15
GGCT	31.26	13.475	1.156	8.64E-56
GTF2IRD1	7.07	2.745	1.108	1.25E-33
IL32	748.417	295.25	1.339	1.34E-21
RPS20	1550.372	610.077	1.344	9.99E-54
TENM1	0.12	1.3	-1.038	5.58E-26

MLXIPL	98.7	263.982	-1.41	2.76E-10
METTL13	18	7.735	1.121	6.04E-57
SEMA3G	1.93	0.435	1.03	6.60E-27
SLC6A13	2.29	11.89	-1.97	1.19E-28
NME2	15.899	5.455	1.389	5.15E-22
SYT7	6.73	21.18	-1.521	2.42E-13
PSMC4	71.401	32.394	1.116	7.36E-60
SLC25A39	125.382	59.779	1.056	2.03E-60
TACC3	10.26	3.13	1.447	2.48E-40
POLA2	7.17	2.465	1.238	1.69E-50
NPC1L1	4.68	13.435	-1.346	1.66E-15
IGF1	4.77	12.475	-1.224	9.57E-14
RUFY3	6.88	14.95	-1.017	7.58E-15
SLC11A1	0.59	2.335	-1.069	5.08E-20
MARCO	0.39	19.3	-3.868	4.03E-61
HGF	0.79	6.615	-2.089	6.68E-35
SERPINB1	26.379	10.953	1.196	4.83E-24
RRAGD	8.76	3.255	1.198	1.36E-28
NCAPH2	23.71	10.6	1.091	1.53E-48
VIM	130.273	52.559	1.293	1.76E-19
RNASET2	42.86	17.46	1.248	9.02E-33
GRN	187.857	59.719	1.637	6.44E-71
TMSB10	859.646	208.556	2.038	1.53E-37
MYOM2	0.86	4.635	-1.599	2.62E-37
RPL26L1	43.989	19.929	1.104	1.27E-65
FAM65C	0.33	7.74	-2.716	8.69E-74
ZIC2	1.42	0.01	1.261	2.17E-31
TPR	20	9.455	1.006	7.29E-31
NEDD4L	25.941	11.405	1.119	1.58E-29
HEXB	156.096	62.003	1.318	5.25E-66

HOMER3	7.3	2.49	1.25	2.80E-23
RAD51	1.75	0.235	1.155	6.48E-39
THOC3	22.43	9.25	1.193	6.88E-48
PRSS8	3	10.11	-1.474	3.16E-09
LAMA3	3.81	0.88	1.355	1.87E-22
PHPT1	99.787	48.509	1.026	2.25E-41
TARBP1	14.1	5.62	1.19	5.14E-36
SPAG4	6.14	2.21	1.154	1.70E-20
POLD1	13.28	4.905	1.274	6.07E-49
SPA17	2.84	0.75	1.134	2.96E-32
NGFR	1.25	7.695	-1.95	2.04E-36
RFXANK	44.099	17.625	1.276	1.95E-58
OAT	9.78	26.915	-1.373	7.28E-09
ZNRD1	25.93	10.03	1.288	1.05E-59
PKM	38.791	13.675	1.439	7.36E-21
RRP15	4.32	1.655	1.003	5.88E-26
RHOA	154.396	75.585	1.021	1.12E-41
IFI35	35.901	15.2	1.188	3.78E-32
GPKOW	14.82	6.73	1.033	2.64E-56
PRR11	1.37	0.14	1.056	2.78E-35
UFD1L	57.039	23.485	1.245	3.98E-58
PABPC1	653.57	181.313	1.844	9.41E-59
RPL31	1529.028	743.015	1.04	2.85E-40
LMCD1	10.45	3.68	1.291	2.04E-21
WBSCR22	56.441	25.895	1.095	4.57E-64
TRIP13	1.55	0.21	1.075	3.15E-33
FAM50A	61.922	25.359	1.255	1.46E-43
HMMR	2.54	0.2	1.561	4.19E-43
P4HA2	15.899	5.81	1.311	1.88E-35
FCGR2B	1.64	9.1	-1.936	7.25E-22

XRCC1	13.98	4.955	1.331	6.31E-57
MCM2	6.75	0.735	2.159	1.21E-49
SMARCE1	49.05	20.464	1.221	1.03E-43
GSDMB	9.1	23.562	-1.282	5.33E-06
IGF2BP2	2.68	0.68	1.131	2.89E-15
NOTCH3	4.32	0.925	1.467	5.02E-30
TEAD2	7.46	3.145	1.029	1.47E-13
HACD3	47.261	19.23	1.254	2.71E-30
TUBE1	4.17	14.245	-1.56	2.56E-55
NUP37	10.3	3.445	1.346	1.67E-59
SEC31B	1.22	5.16	-1.472	4.60E-23
KIFAP3	9.63	3.71	1.174	1.70E-37
MCM6	7.88	1.485	1.837	2.31E-49
MCAM	14.76	3.97	1.665	3.84E-36
UBE2T	8.81	0.695	2.533	9.85E-75
IL4R	17.09	36.155	-1.038	2.59E-17
EXOSC5	22.461	8.788	1.261	1.15E-60
UBE2A	25.029	11.63	1.043	4.00E-40
FBLN1	8.62	3.655	1.047	4.88E-07
MAP2	3.05	0.965	1.043	8.47E-17
PMS2P1	5.08	2.01	1.014	4.84E-48
PAFAH1B3	14.81	3.225	1.904	2.54E-43
KCNN2	0.25	4.35	-2.098	1.91E-53
NDC80	2.91	0.18	1.728	3.06E-52
JMJD4	14.75	6.215	1.126	8.15E-59
HSPB11	21.91	10.425	1.004	5.79E-49
PLOD1	76.388	36.346	1.051	2.95E-32
SLC27A5	248.413	497.947	-1	5.86E-10
FAT1	33.42	11.8	1.427	3.61E-20
HAL	20.48	54.784	-1.377	3.89E-14

GCKR	22.119	98.499	-2.106	1.31E-37
IGSF9	1.64	7.91	-1.755	1.31E-18
TTC39A	2.76	0.555	1.274	3.15E-21
FTL	11550.758	5723.571	1.013	5.51E-19
GNAO1	0.68	7.76	-2.382	4.76E-52
PIR	23.02	9.2	1.236	1.28E-27
TPX2	6	0.765	1.988	5.60E-45
SMOX	4.76	1.82	1.03	1.40E-09
FKBP1A	88.56	40.05	1.125	5.76E-48
TESC	7.24	2.13	1.397	5.28E-16
RPL6	779.064	371.739	1.065	3.44E-53
RPLP0	1398.049	655.112	1.092	1.85E-44
IGBP1	20.49	8.45	1.185	2.05E-47
FXYD5	29.699	13.652	1.067	1.43E-14
GRAMD1A	18.69	8.595	1.037	7.23E-16
LYZ	81.413	9.505	2.972	1.14E-24
KIF4A	1.87	0.07	1.423	4.49E-43
ITGA6	10.25	2.74	1.589	1.72E-41
ESR1	0.53	4.47	-1.838	3.35E-35
TMEM101	23.46	9.185	1.264	7.51E-62
PSME1	221.797	100.384	1.136	5.05E-56
HAUS4	21.44	9.115	1.15	4.55E-25
WDR76	2.02	0.295	1.222	2.31E-41
TBX15	2.27	7.885	-1.442	1.26E-14
MYL6	1006.338	476.208	1.078	8.54E-53
UNC13D	1.63	5.01	-1.192	1.65E-13
SUCO	6.03	2.25	1.113	2.38E-32
MSH2	5.18	1.415	1.356	2.42E-46
HOOK2	8.22	22.89	-1.374	5.02E-07
TMEM38B	8.39	3.005	1.229	1.28E-35

SMIM24	1.55	6.257	-1.509	9.69E-03
TREM2	3.51	0.245	1.857	9.01E-33
TMEM14A	50.499	22.89	1.108	1.53E-28
HSP90AB1	400.622	139.516	1.515	4.29E-45
SCD	205.457	85.176	1.26	1.12E-05
TSPAN15	5.6	2.11	1.086	1.23E-19
MZF1	4.09	11.175	-1.258	1.24E-10
IGFALS	2.83	40.84	-3.449	2.19E-47
GADD45B	66.472	152.783	-1.189	2.93E-20
SERPIND1	344.389	146.027	1.232	4.45E-04
MMP11	5.24	0.35	2.209	9.60E-39
GGT5	8.17	19.87	-1.186	5.36E-16
SNRPD3	99.401	46.269	1.087	1.58E-47
PES1	40.87	19.35	1.041	2.02E-45
LRP5L	2.81	7.535	-1.164	3.77E-13
PIK3IP1	7	2.74	1.097	1.30E-17
NHP2L1	81.379	35.463	1.176	1.60E-59
KDELR3	9.84	3.98	1.122	1.90E-13
TOMM22	38.84	17.85	1.08	5.91E-53
MCM5	21.45	4.025	2.16	2.99E-56
PDGFB	4.05	1.06	1.294	4.44E-36
ZMAT5	25.2	10.63	1.172	6.35E-63
SYNGR1	6.5	2.715	1.014	5.92E-08
SAMM50	30.89	14.73	1.02	2.94E-36
FOXRED2	6.45	2.045	1.291	1.30E-29
PVALB	0.11	1.22	-1	2.77E-41
KCTD17	4.51	1.625	1.07	2.73E-18
TIMM9	33.88	14.115	1.206	4.79E-61
GSTZ1	29.67	81.055	-1.42	1.10E-26
SLC10A1	33.819	69.567	-1.019	2.91E-07

VRK1	4.99	1.65	1.177	7.51E-52
PSMB5	103.421	47.67	1.101	6.32E-71
PSMA6	123.974	57.615	1.092	8.22E-62
PSME2	253.755	120.229	1.071	5.98E-45
REC8	2.28	7.14	-1.311	1.43E-14
PNN	14.91	32.62	-1.079	5.10E-11
MMP9	3.01	0.8	1.156	1.18E-15
PYGB	14.47	5.205	1.318	6.43E-36
GINS1	1.72	0.2	1.181	2.40E-37
IFT52	7.39	3.06	1.047	2.12E-37
MYBL2	4.07	0.19	2.091	3.56E-43
NDRG3	7.09	2.73	1.117	1.16E-41
PFDN4	21.78	8.525	1.258	3.44E-54
PRPF6	40.029	14.02	1.45	6.06E-85
SLC17A9	29.769	90.333	-1.57	4.91E-07
HM13	160.162	70.709	1.168	1.15E-45
MANBAL	32.901	15.21	1.064	1.33E-61
MAPRE1	14.98	6.11	1.168	5.40E-28
OXT	0.13	5.293	-2.477	6.22E-25
PXMP4	10.38	3.335	1.392	3.71E-58
FAM83D	4.5	0.855	1.568	1.65E-36
PIGU	16.75	4.875	1.595	1.06E-81
LIPG	8.01	21.904	-1.346	2.07E-20
PSMD10	20.941	8.67	1.182	5.29E-39
SRPX	0.84	5.53	-1.827	1.85E-35
F9	42.659	138.457	-1.675	2.08E-23
PLP2	24.319	8.734	1.379	1.90E-17
SMS	25.701	11.905	1.049	2.98E-37
HTATSF1	19.28	8.46	1.1	9.73E-37
MAGED2	63.711	22.045	1.49	1.27E-57

RBM3	79.539	36.115	1.118	1.99E-23
GLA	19.061	7.165	1.297	6.62E-36
RGCC	11.91	2.12	2.049	1.35E-36
MAPK3	24.54	9.99	1.217	2.16E-53
NUTF2	55.861	25.134	1.121	1.43E-51
HCFC1R1	44.622	21.699	1.007	2.88E-40
TAF1C	6.94	14.985	-1.01	1.46E-07
TCEB2	295.517	138.164	1.091	2.37E-51
PYCARD	16.68	4.764	1.617	1.09E-21
MAZ	114.332	43.406	1.377	1.78E-68
NOMO1	31.299	13.774	1.128	4.10E-47
OIP5	1.88	0.17	1.3	3.71E-42
RIPK2	6.29	2.515	1.052	6.24E-25
LAPTM4B	34.179	7.56	2.039	7.12E-31
NIPAL2	5.82	2.35	1.026	1.57E-22
SQLE	36.309	9.635	1.811	2.09E-25
SLC39A14	54.681	160.457	-1.536	6.14E-37
MCM4	11.24	2.725	1.716	1.41E-37
FGL1	714.652	1526.116	-1.093	5.42E-08
MAN2B1	55.591	17.704	1.597	1.74E-60
RELB	13.58	4.209	1.485	2.92E-31
RNASEH2A	16.151	2.735	2.199	4.56E-77
OLFM2	31.021	12.169	1.282	6.92E-10
PDCD5	85.241	41.33	1.027	2.56E-49
RPS16	1328.515	622.443	1.093	5.50E-47
FBL	123.391	47.738	1.352	7.33E-50
TBCB	58.351	26.444	1.113	4.50E-42
RPS19	1703.043	813.895	1.064	4.40E-40
PTPRS	0.58	2.84	-1.281	8.57E-09
LIG1	16.18	6.24	1.247	6.01E-44

PLA2G4C	16.41	5.25	1.478	3.54E-30
PPP2R1A	101.412	44.099	1.183	2.18E-57
LILRB5	1.45	4.175	-1.079	5.91E-27
TFPT	11.74	4.665	1.169	2.46E-54
PIK3R2	16.35	6.97	1.122	1.80E-33
TMEM147	69.05	28.196	1.263	1.04E-50
HAMP	6.75	669.968	-6.436	3.63E-66
NAMPT	38.001	86.288	-1.162	1.32E-14
H2AFV	78.302	31.871	1.271	2.69E-68
TAX1BP1	42.499	18.625	1.148	4.00E-42
GARS	59.231	24.455	1.243	2.68E-45
HSPB1	644.572	168.996	1.925	2.04E-43
PDAP1	72.978	35.554	1.017	1.75E-36
SNX8	17.73	5.43	1.542	3.64E-55
NUDT1	15.59	2.595	2.206	2.77E-77
SERPINE1	20.831	46.29	-1.115	3.42E-05
PLOD3	60.601	23.364	1.338	1.88E-53
EZH2	3.65	1.275	1.031	7.56E-30
LHX2	0.36	2.33	-1.292	3.44E-33
NPM3	17.14	5.595	1.46	2.79E-27
UBE2S	19.39	3.845	2.073	5.29E-67
RPL28	1238.089	565.741	1.129	5.32E-43
PBLD	29.59	69.384	-1.202	6.28E-19
KRT23	2.85	0.21	1.67	2.75E-10
RPL19	1450.263	637.353	1.185	4.15E-61
RAD51C	13.68	5.425	1.192	5.70E-52
TRIM16L	7.1	2.925	1.045	6.52E-17
RASD1	14.23	43.902	-1.56	8.63E-11
ICAM2	12.49	5.214	1.118	1.55E-25
SYNGR2	83.169	40.321	1.026	2.46E-38

LGALS3BP	160.385	54.264	1.546	2.76E-08
VAT1	49.37	16.41	1.533	1.56E-44
TMEM97	38.62	18.5	1.023	7.48E-16
SULT1E1	1.41	5.65	-1.464	1.08E-08
HGFAC	11.26	117.783	-3.276	5.22E-35
NCAPG	2.59	0.115	1.687	1.63E-46
HTATIP2	77.831	32.464	1.236	1.48E-26
FNBP4	9.22	20.065	-1.043	2.32E-05
SNX15	9.93	4.415	1.013	8.06E-43
HPX	1194.589	2403.131	-1.008	3.35E-11
MDK	132.339	3.805	4.794	7.57E-81
RPS13	649.415	322.018	1.01	6.76E-48
NDUFS8	131.06	64.625	1.009	9.08E-47
VWF	14.41	1.715	2.505	7.16E-57
PTGES3	137.758	65.443	1.062	8.02E-42
TNS2	24.931	67.367	-1.399	2.42E-23
MAGOHB	17.95	7.98	1.077	7.20E-53
TRPV4	0.77	2.83	-1.114	2.01E-14
FOXM1	5.72	0.91	1.815	2.70E-41
RAD51AP1	1.72	0.29	1.076	1.24E-31
MGP	34.7	15.225	1.138	2.51E-06
SPSB2	6.75	2.24	1.258	4.55E-54
SLCO1B3	1.89	30.546	-3.448	4.57E-31
GYS2	7.64	28.294	-1.761	1.57E-25
TMEM14C	101.159	43.904	1.186	2.44E-59
MCM3	20.53	5.435	1.742	9.00E-46
VNN1	17.96	39.013	-1.077	3.43E-09
GMNN	31.111	6.19	2.159	2.77E-59
SLC39A7	107.157	45.144	1.229	2.79E-43
VEGFA	53.05	116.073	-1.115	3.43E-07

SLC29A1	46.571	22.445	1.021	4.68E-19
LAMA4	4.83	1.38	1.293	2.58E-36
GHR	7.3	26.178	-1.711	1.09E-29
KIF20A	2.79	0.13	1.746	9.12E-45
SPARC	214.881	65.26	1.704	8.74E-29
IK	56.141	25.39	1.115	5.67E-66
THBS4	3.68	0.15	2.025	6.22E-40
LMNB1	7.73	2.21	1.443	2.22E-27
SUB1	184.144	73.124	1.321	2.45E-61
LIFR	0.71	3.515	-1.401	4.82E-49
H2AFY	56.539	24.299	1.185	1.46E-44
PDGFRB	10.1	4.26	1.077	1.10E-16
USP9Y	0.4	2.55	-1.342	1.78E-14
RPL24	884.733	404.767	1.126	5.84E-52
SLC41A3	18.379	6.215	1.425	5.16E-66
PLSCR4	5.39	13.155	-1.147	8.18E-31
RRP9	12.34	5.515	1.034	3.72E-45
VIPR1	0.56	11.848	-3.042	4.67E-92
SSR3	89.059	40.774	1.108	4.02E-38
NKTR	4.61	13.3	-1.35	1.96E-10
SPCS1	167.846	78.948	1.079	7.46E-50
STEAP3	19.849	62.63	-1.61	3.11E-40
TP53I3	20.09	5.15	1.778	2.13E-35
FNDC4	22.841	53.096	-1.182	9.26E-18
PSMD14	27.46	11.975	1.133	1.07E-37
PPM1G	39.769	17.025	1.177	6.71E-53
STAT1	38.62	17.54	1.096	1.35E-16
PDCL3	11.29	4.515	1.156	1.68E-53
IL1RL1	0.08	1.33	-1.109	2.80E-34
UXS1	15.49	5.405	1.364	1.89E-47

RND3	9.27	21.98	-1.162	3.53E-24
FAM20B	8.97	3.605	1.114	6.50E-49
ERRFI1	67.672	160.379	-1.233	7.82E-19
SCAMP3	85.793	25.355	1.72	5.81E-83
LAMTOR2	162.263	71.28	1.176	2.33E-64
UCHL5	15.85	7.27	1.027	2.61E-26
SRSF11	25.31	68.614	-1.404	8.39E-11
OLFML3	2.83	8.29	-1.278	3.70E-14
TMEM9	78.102	28.145	1.44	6.19E-64
HAO2	11.13	111.712	-3.216	4.03E-33
GNPAT	27.72	11.88	1.157	9.80E-51
TSNAX	14.6	6.555	1.046	5.62E-45
TBCE	16.95	7.4	1.096	1.50E-51
KMO	7.17	20.115	-1.37	7.00E-22
HSD11B1	76.531	189.827	-1.299	4.75E-11
IRF6	21.24	9.51	1.081	3.04E-07
RSRP1	16.95	36.53	-1.064	9.46E-03
STMN1	56.668	6.28	2.986	1.65E-75
MAN1C1	4.64	13.085	-1.32	1.14E-21
NEK2	3.21	0.11	1.923	2.38E-51
NENF	81.311	29.561	1.429	4.92E-71
NSL1	13.84	6.095	1.065	1.05E-34
TXNDC12	31.04	14.5	1.048	4.23E-55
MYL12B	310.295	142.938	1.113	5.47E-42
RPN2	201.829	74.294	1.43	1.68E-75
SPP1	75.378	8.524	3.004	2.34E-15
ITGB1BP1	32.839	12.855	1.288	1.65E-48
PHF19	6.2	1.995	1.265	3.53E-35
NDUFA8	57.432	27.36	1.043	3.50E-55
IFI27L2	12.91	4.625	1.306	1.37E-20

NPC2	121.456	52.019	1.208	5.03E-45
PPP1R3C	10.36	28.32	-1.368	1.33E-15
HELLS	1.83	0.405	1.01	1.27E-29
SFRP5	0.05	4.03	-2.26	1.01E-24
MTHFD1L	4.12	1.275	1.17	1.52E-27
LRP11	7.82	3.315	1.032	1.44E-31
PDZD11	30.37	11.065	1.379	4.14E-71
ENY2	127.009	62.88	1.003	1.36E-46
TGFBI	114.213	51.15	1.144	5.76E-22
EPHX2	47.891	106.244	-1.133	3.89E-18
ZNF706	102.992	38.45	1.398	4.72E-59
SCPEP1	25.849	11.89	1.059	5.18E-11
NCAPH	2.55	0.17	1.601	2.29E-45
MND1	2.58	0.17	1.613	4.58E-64
PILRB	7.6	26.129	-1.657	3.78E-11
RPL5	560.899	273.187	1.035	3.44E-40
FKBP9	17.64	8.315	1.001	5.14E-27
PLAU	2.82	0.77	1.11	1.07E-23
ZWINT	9.69	0.865	2.519	7.03E-58
PKN1	44.609	13.205	1.683	1.92E-45
ZC3H13	4.81	15.4	-1.497	1.80E-30
OPTN	50.569	22.641	1.125	2.32E-36
SPATS2	5.64	2.025	1.134	7.78E-35
ORMDL2	48.691	19.455	1.281	9.75E-68
NR4A1	8.57	25.707	-1.481	1.62E-17
TUBA1B	234.996	72.433	1.684	8.76E-30
HJURP	2.22	0.245	1.371	2.04E-40
G0S2	46.051	133.107	-1.511	9.21E-13
SLC12A5	2.37	0.515	1.153	6.52E-24
PIGT	65.05	22.78	1.474	1.20E-72

PTGIS	0.37	1.815	-1.039	1.91E-16
PCK1	84.799	405.426	-2.244	1.54E-23
SNRPC	118.742	39.239	1.573	4.96E-80
RPS10	973.069	427.846	1.184	1.26E-42
TBCC	11.02	4.93	1.019	3.26E-45
KLHDC3	61.12	29.215	1.04	5.23E-54
GNMT	30.38	90.336	-1.541	8.24E-10
MEA1	62.691	22.585	1.433	2.41E-84
SOX4	3.07	0.71	1.251	5.22E-16
SSR1	43.609	20.554	1.049	4.69E-23
RPP40	7.11	3.025	1.011	2.19E-36
MT1G	40.209	2587.601	-5.973	3.31E-51
MT2A	261.977	2324.572	-3.145	5.54E-41
RAP2A	5.38	1.86	1.158	1.82E-31
6-Sep	22.06	9.535	1.13	9.56E-18
NDUFA1	183.101	75.371	1.269	2.97E-71
SOX9	4.95	1	1.573	3.90E-17
MIF4GD	16.58	7.17	1.106	5.98E-40
PPDPF	190.982	72.223	1.391	1.61E-16
PLGLB2	65.348	195.78	-1.568	4.11E-23
RPL23	944.625	439.386	1.102	1.17E-46
TNFSF14	2.84	14.71	-2.032	5.52E-16
FOSB	1.62	4.38	-1.038	3.59E-11
SNRPD2	193.165	70.121	1.449	8.88E-60
RTN2	5.1	1.68	1.187	3.26E-19
TGM3	1.68	0.19	1.171	3.54E-22
SNRPB	126.473	35.895	1.789	1.23E-70
MKKS	22.899	10.375	1.071	4.69E-37
SNRPB2	28.699	12.59	1.128	1.39E-52
NECAB3	21.341	8.84	1.183	1.03E-53

ID1	15.63	47.12	-1.533	3.47E-20
RALY	63.039	26.163	1.237	1.08E-57
ERGIC3	192.324	94.039	1.024	4.39E-64
ROMO1	249.154	86.933	1.508	3.79E-69
PROZ	8.74	32.433	-1.779	3.48E-29
PDCD2L	6.35	2.57	1.042	1.95E-47
RBM42	52.83	21.78	1.241	5.56E-66
HCST	12.42	5.039	1.152	2.51E-17
PRDX5	278.165	128.23	1.111	2.65E-66
IFI6	95.742	36.279	1.376	2.97E-10
TIMM17B	46.659	22.065	1.047	2.67E-61
PZP	0.18	5.14	-2.379	1.20E-55
TRAF2	10.5	4.355	1.103	2.86E-43
TSPAN8	52.008	7.16	2.7	2.31E-22
PKMYT1	5.72	0.695	1.987	1.95E-56
SMARCA4	29.769	13.425	1.093	2.20E-50
VIL1	14.91	4.055	1.654	1.06E-07
SHFM1	305.07	97.133	1.641	1.47E-81
STYXL1	31.679	14.21	1.103	1.62E-37
STEAP4	0.77	4.24	-1.566	4.38E-36
ZFP36	53.742	127.304	-1.229	2.91E-21
SRD5A3	15.24	6.015	1.211	1.74E-50
GNAZ	2.38	0.15	1.555	1.68E-35
LSM8	21.201	8.135	1.281	6.01E-51
PODXL	5.7	1.355	1.508	8.20E-32
SMO	16.5	7.11	1.11	2.25E-16
KNSTRN	7.78	2.795	1.21	1.60E-38
RNASE1	56.531	18.8	1.539	4.55E-29
NEDD8	160.385	77.409	1.041	5.01E-71
INS-IGF2	0	4.03	-2.331	9.78E-65

PRKCSH	198.376	98.155	1.008	8.08E-72
THEM6	35.921	16.975	1.038	1.03E-27
TOMM40	36.99	16.13	1.149	8.57E-43
RPL36	739.803	336.869	1.133	1.54E-46
PLVAP	43.03	2.464	3.668	7.99E-127
NSUN5	17.259	7.33	1.132	4.49E-59
LSM7	71.848	34.91	1.021	2.95E-46
EPO	0.19	3.185	-1.814	6.95E-16
MAP1S	14.04	5.995	1.104	2.83E-44
GDF15	44.51	15.795	1.438	1.80E-15
LSM4	102.757	45.219	1.167	4.90E-61
PNPLA7	1.7	5.1	-1.176	7.03E-45
UBE2M	40.19	17.905	1.123	1.37E-56
TRIM28	143.419	66.495	1.097	4.58E-45
SLC6A8	3.29	1.05	1.065	4.62E-12
HIGD1B	2.2	0.19	1.427	6.54E-69
GINS2	2.4	0.41	1.27	1.15E-44
PPT1	19.291	7.325	1.285	1.05E-31
RAB11FIP4	5.22	1.225	1.483	3.08E-36
TUBG1	24.47	8.475	1.427	1.90E-43
RPL27	1270.164	553.58	1.197	2.01E-54
RAMP2	17.27	5.77	1.432	1.02E-32
NDUFA2	139.111	64.451	1.098	2.33E-63
EXOC4	11.34	5.17	1	6.07E-48
TOP2A	9.54	0.405	2.907	3.35E-65
PEX11B	23.079	10.54	1.061	3.73E-58
GCH1	11.76	29.19	-1.242	1.20E-26
LGALS3	30.231	6.845	1.993	1.84E-25
RAMP1	103.679	31.471	1.689	1.78E-15

RAN	208.441	81.905	1.337	2.40E-41
PNISR	11.81	31.325	-1.335	2.01E-08
SEC61G	167.195	79.423	1.064	8.75E-38
JCHAIN	2.83	8.089	-1.247	1.53E-07
ITGB4	5.13	1.67	1.199	9.14E-26
XAF1	7.13	29.705	-1.917	1.11E-22
PCNA	48.09	13.71	1.739	1.99E-57
NES	5.32	1.63	1.265	6.86E-33
LPIN3	4.75	13.924	-1.376	5.67E-11
PEMT	50.53	119.908	-1.23	5.18E-26
SPG20	1.55	5.41	-1.33	4.11E-21
RFC3	3.4	1.165	1.023	5.19E-32
GSTT2B	3.38	10.82	-1.432	6.07E-07
SEC14L4	2.04	5.92	-1.187	1.11E-14
SWAP70	5.09	1.985	1.029	7.00E-23
LYVE1	0.83	7.055	-2.138	1.12E-41
TTC9	2.24	0.43	1.18	1.69E-22
LOXL2	3.68	1.03	1.205	1.84E-25
GSTM1	1.28	70.601	-4.973	2.84E-03
SORT1	7.08	1.66	1.603	2.69E-34
PTGFRN	10.95	4.845	1.032	4.96E-18
FKBP11	70.438	29.725	1.217	5.20E-22
TMEM106C	44.05	11.765	1.819	6.54E-59
SAA2	105.36	2489.516	-4.549	4.99E-25
FST	51.929	24.758	1.039	7.56E-05
FOLH1B	0.43	4.13	-1.843	2.53E-28
TPGS2	20.93	8.2	1.253	2.54E-30
TIMM10	60.48	29.36	1.018	4.07E-50
TMEM258	160.841	73.84	1.113	4.55E-62
PDGFRA	0.92	3.855	-1.338	3.43E-19

STT3A	76.882	32.829	1.203	1.44E-42
NREP	17.25	7.315	1.134	3.45E-19
GOLM1	22.4	5.695	1.805	7.37E-18
SDS	58.318	343.496	-2.538	1.03E-11
GLS2	7.55	64.115	-2.929	2.16E-23
TROAP	6.69	0.325	2.537	3.39E-57
PAN2	13.25	46.264	-1.73	5.37E-17
HNRNPA1	363.698	146.569	1.305	6.58E-44
GNS	30.759	13.59	1.122	3.96E-38
NTPCR	54.161	16.505	1.656	2.67E-68
GLUL	323.024	144.037	1.16	5.79E-11
PIGC	22.07	6.605	1.601	1.92E-71
LAMC1	26.829	5.775	2.038	2.21E-43
STAB2	0.08	3.505	-2.06	1.98E-103
GPNMB	12.74	3.525	1.602	4.77E-17
RAC1	116.994	54.913	1.077	8.53E-51
RTP4	5.18	1.725	1.181	3.68E-22
MRPL47	30.3	14.075	1.054	8.16E-49
EPRS	37.111	13.56	1.388	2.11E-61
UGGT1	14.17	5.615	1.197	1.62E-43
TXN	347.458	121.873	1.504	1.17E-50
RPS6	1117.066	553.925	1.011	2.75E-32
YIPF3	100.002	47.349	1.063	3.77E-55
TMEM14B	75.572	32.725	1.183	2.85E-60
TUBB2A	60.17	28.979	1.029	8.62E-16
LRRC1	2.35	0.34	1.322	2.45E-27
UQCC2	98.373	32.169	1.583	7.45E-74
HMGA1	36.319	6.9	2.24	8.96E-51
TCF19	4.27	0.44	1.872	6.76E-47

NRM	8.47	2.63	1.383	1.91E-38
MYO7A	4.79	10.68	-1.012	2.15E-13
MRPL15	50.699	24.155	1.039	2.07E-40
GGH	121.852	51.186	1.235	1.99E-17
SORL1	6.55	15	-1.084	1.74E-23
NUSAP1	8.31	1.675	1.799	2.72E-40
KIF23	1.48	0.19	1.059	7.83E-31
RPLP1	1491.242	599.659	1.313	5.50E-68
ITPKA	3.46	0.555	1.52	3.00E-30
RPL7P9	28.391	9.16	1.533	1.79E-48
SLC3A1	0.66	2.48	-1.068	4.67E-03
LOXL4	3.58	0.72	1.413	6.30E-08
OIT3	2.66	15.075	-2.135	1.80E-52
RPS24	1646.514	799.358	1.042	1.33E-38
METTL5	34.82	15.849	1.088	4.15E-61
OLA1	40.941	16.146	1.291	2.43E-44
UBL7	29.531	12.445	1.183	4.75E-68
FAM13A	3.1	15.24	-1.986	1.03E-33
RASGEF1B	4.63	11.45	-1.145	8.14E-25
LEF1	2.67	0.29	1.508	8.05E-29
PAPSS1	6.5	2.495	1.102	1.33E-25
MAPK8IP3	5.62	18.72	-1.575	5.30E-08
ZCRB1	33.481	15.205	1.089	1.97E-48
RPL14P1	9.55	3.85	1.121	3.84E-40
SNRPF	27.971	13.225	1.026	4.38E-44
FAM222A	4.25	1.125	1.305	9.68E-36
SLC46A3	11.35	23.705	-1	1.20E-15
SLC39A5	52.399	108.891	-1.041	3.77E-11
RDH16	39.609	193.762	-2.262	4.68E-32
NABP2	19.38	7.77	1.217	5.42E-57

N4BP2L1	12.22	28.05	-1.136	5.56E-34
VPS33A	7.39	3.075	1.042	3.20E-40
SLAIN1	0.63	2.575	-1.133	7.08E-22
FITM1	1.31	7.18	-1.824	3.99E-55
SLC38A6	6.79	2.24	1.266	5.55E-61
SLC25A47	13.85	213.567	-3.853	3.91E-45
GTF2A2	61.158	26.395	1.182	1.28E-61
SRP14	253.474	113.165	1.156	1.94E-66
UBE2Q2	5.68	2.01	1.15	1.86E-21
NEIL1	8.76	20.924	-1.168	1.85E-11
FANCI	3.08	0.565	1.382	1.22E-44
OSGIN1	89.492	40.993	1.108	1.48E-08
SKAP1	7.37	17.729	-1.162	9.64E-12
PTRH2	27.851	13.168	1.026	6.31E-49
SLC13A5	60.4	161.954	-1.408	6.58E-20
SECTM1	5.34	2.085	1.039	4.35E-19
RNF157	3.3	0.58	1.444	5.21E-26
RNF165	0.16	1.53	-1.125	1.29E-60
P3H4	3.91	1.29	1.1	3.48E-29
SAMD1	17.89	7.82	1.099	1.55E-40
SLC39A3	29.3	11.91	1.231	6.69E-58
SIK1	1.57	4.18	-1.011	6.29E-07
SAE1	33.261	12.505	1.343	1.26E-52
TM4SF5	200.31	92.641	1.104	3.90E-09
RPS11	1591.31	734.489	1.114	3.62E-54
SH3BGRL3	70.629	32.565	1.094	7.00E-26
FCN3	2.32	67.3	-4.363	1.37E-68
HSPG2	22.611	8.685	1.286	9.63E-24
ITGB3BP	8.56	3.155	1.202	6.97E-46
KIF2C	2.21	0.17	1.456	6.33E-43

SLC44A3	6.79	1.63	1.567	4.44E-26
TIPRL	13.95	6.325	1.029	5.64E-42
MPC2	279.053	110.929	1.323	4.12E-61
UCK2	18.22	6	1.457	5.06E-48
TMCO1	124.94	41.106	1.581	1.55E-60
RFWD2	30.789	12.06	1.283	9.26E-68
UFC1	97.497	33.145	1.528	7.85E-76
NUF2	2.48	0.13	1.623	8.54E-46
RGS5	18.01	4.01	1.924	2.20E-34
PFDN2	104.959	42.964	1.269	3.23E-57
PRCC	41.28	15.355	1.37	7.36E-76
MRPL24	161.735	54.922	1.541	2.07E-75
LYPLAL1	36.221	14.405	1.273	2.19E-48
SF3B4	35.839	10.79	1.644	1.44E-68
ZNF687	11.88	4.36	1.265	3.11E-45
RFX5	10.55	3.49	1.363	4.80E-36
MRPL9	49.261	19.215	1.314	1.94E-66
GOLPH3L	9.31	3.605	1.163	6.65E-38
SMYD2	30.199	12.82	1.175	1.71E-33
SUSD4	3.92	1.295	1.1	1.23E-08
TP53BP2	12.89	4.945	1.224	1.25E-22
S100A8	3.42	29.025	-2.764	1.36E-39
TPM3	124.154	46.16	1.408	3.43E-50
SNAPIN	32.479	15.445	1.026	1.25E-54
SLC39A1	72.098	29.34	1.269	8.80E-45
HAX1	107.328	46.864	1.178	6.03E-70
ILF2	80.991	27.02	1.549	3.65E-67
SRP9	168.685	79.5	1.076	2.63E-44
PARP1	36.99	15.685	1.187	1.12E-34
PSEN2	14.1	6.11	1.087	1.08E-31

PYCR2	40.649	18.06	1.128	1.26E-48
EPHX1	1532.848	505.37	1.599	2.23E-17
PDIA6	159.155	77.753	1.024	3.64E-27
FBLN7	6.2	2.045	1.242	1.89E-27
TRPM8	4.06	10.085	-1.131	5.06E-12
FANCD2	2.68	0.595	1.206	8.55E-35
FAM198A	0.36	3.95	-1.864	4.73E-34
RPL32	1338.312	560.083	1.255	1.99E-50
RP11-977G19.10	1.01	0	1.007	1.70E-11
NFKBIZ	3.85	18.334	-1.995	1.07E-34
NR1I2	9.26	30.295	-1.609	2.22E-27
PLAC8	1.03	5.975	-1.781	4.43E-28
NDUFS6	89.12	35.605	1.3	6.13E-68
RPL37	1566.576	594.465	1.396	2.08E-66
TSLP	0.33	2.1	-1.221	2.45E-42
NHP2	99.332	37.635	1.377	6.68E-71
TBC1D7	15.92	6.43	1.187	8.27E-60
ZMAT2	48.509	23.279	1.028	1.50E-47
HIGD2A	145.804	67.002	1.11	1.48E-68
FAM193B	17.13	46.951	-1.403	3.06E-04
TNFRSF21	5.45	2.02	1.095	5.04E-13
PRIM2	4.04	1.06	1.291	2.40E-57
NFKBIE	11.85	4.04	1.35	4.40E-28
RSPO3	0.06	1.57	-1.278	2.81E-43
IGFBP3	49.428	164.471	-1.714	1.52E-24
PSPH	8.69	2.705	1.387	2.07E-35
TMEM209	5.27	2.015	1.056	2.42E-34
NCAPG2	2.93	0.895	1.052	3.71E-28
TMEM27	1.03	7.24	-2.021	5.51E-33
GPC3	148.158	0.92	6.28	6.38E-59

SLC25A37	4.4	12.924	-1.367	8.04E-34
RPL7	1178.47	467.589	1.332	4.79E-43
POLR2K	55.819	19.015	1.505	8.99E-80
NDUFB9	377.752	144.862	1.377	2.15E-64
TATDN1	22.869	8.72	1.296	7.80E-54
RP11-35N6.1	3.71	1.305	1.031	1.27E-21
GSN	85.882	37.655	1.168	6.32E-15
LCN2	38.101	5.525	2.583	1.58E-13
MKI67	2.9	0.17	1.737	6.18E-46
RGS10	7.6	1.915	1.561	4.08E-31
SAA4	251.479	770.846	-1.612	7.75E-21
PAMR1	0.7	2.855	-1.181	6.04E-24
GLYAT	35.37	138.764	-1.942	3.66E-18
SERPINH1	37.121	15.61	1.199	5.16E-20
ST14	8.05	2.715	1.285	2.33E-11
PLCH2	0.57	2.5	-1.157	6.00E-03
TMEM25	2.85	7.29	-1.107	1.37E-21
FAU	796.206	363.206	1.13	2.00E-62
TM7SF2	103.407	41.026	1.313	3.57E-16
TMCO3	15.33	5.335	1.366	1.16E-24
LYPD1	2.34	0.225	1.447	3.30E-24
GPM6A	0.16	1.64	-1.186	9.84E-45
PRSS53	0.23	4.55	-2.174	2.46E-52
MAT1A	220.907	484.649	-1.13	7.57E-19
THRSP	6.27	72.531	-3.338	4.00E-20
NDUFC2	323.853	140.872	1.195	2.15E-56
ITIH2	623.739	212.342	1.55	1.81E-09
TMEM45B	29.9	8.1	1.764	7.97E-11
TDO2	76.478	213.996	-1.472	1.71E-17
GEMIN6	11.22	5.08	1.007	7.82E-55

HAUS1	8.63	3.675	1.043	4.37E-37
SPC25	2.11	0.16	1.423	3.18E-47
SPARCL1	19.1	4.845	1.782	1.87E-22
GJA1	4.23	1.415	1.115	3.08E-18
GGPS1	12.93	5.865	1.021	4.77E-50
RASSF3	6.27	2.21	1.179	1.48E-21
SLC25A27	2.23	11.03	-1.897	7.15E-23
FAM49B	17.579	7.295	1.163	1.50E-28
LINC00467	10.37	4.585	1.026	1.15E-42
THY1	20.42	1.995	2.838	1.97E-62
FAM134B	2.32	9.124	-1.609	1.44E-17
TCEB1	67.911	26.575	1.321	2.54E-55
LY96	8.45	3.375	1.111	7.04E-14
SKA1	1.33	0.04	1.164	7.50E-40
ZCCHC10	18.15	8.21	1.056	1.41E-57
RHOC	174.755	63.284	1.451	4.75E-51
KDM8	5.66	45.724	-2.811	9.08E-45
VBP1	18.29	8.53	1.017	3.50E-39
NAT2	2.28	27.324	-3.11	1.07E-60
SLC28A1	8.97	30.939	-1.68	7.70E-22
UQCRB	349.269	129.912	1.42	4.17E-69
RPL30	1964.708	654.091	1.585	1.70E-64
HKDC1	8.11	1.01	2.18	3.33E-23
UTP14A	7.05	2.75	1.102	2.94E-44
WDYHV1	8.96	3.605	1.113	2.23E-42
FBXO32	4.23	1.22	1.236	3.93E-29
NSMCE2	20.92	5.565	1.739	4.91E-85
PDE6D	11.73	5.08	1.066	9.55E-46
NRG1	0.45	2.87	-1.416	1.20E-10
MMP14	15	5	1.415	6.88E-21

SLC35B2	32.739	13.99	1.17	4.34E-43
TMEM164	2.59	0.78	1.012	5.00E-28
PSMG3	31.519	11.92	1.332	7.20E-62
KRTCAP3	1.41	6.48	-1.634	1.47E-04
MRPL17	33.91	14.065	1.212	5.09E-61
FANCC	2.86	7.004	-1.052	1.14E-24
TAGLN2	252.545	76.164	1.716	3.34E-43
SLAMF8	2.05	0.415	1.108	2.94E-20
OR10J6P	0.62	5.62	-2.031	6.99E-38
FAM160B2	9.28	22.195	-1.174	1.12E-07
MIS18A	4.36	1.595	1.047	1.36E-38
STC1	2.25	0.325	1.294	2.19E-22
RCAN1	17.179	48.371	-1.441	5.50E-43
SNF8	88.101	39.81	1.127	1.69E-58
PSMD4	242.576	78.784	1.61	2.53E-79
PSMB4	347.073	134.526	1.361	3.11E-83
UROC1	3.89	38.638	-3.019	9.88E-33
SPON2	94.851	45.069	1.057	1.97E-17
TPPP3	4.09	1.46	1.049	3.36E-13
G6PD	9.9	2.875	1.492	1.33E-28
SPATC1L	3.81	0.41	1.77	3.21E-38
FCN2	0.28	30.658	-4.628	2.54E-103
GPSM1	3.67	1.165	1.109	1.63E-18
TLCD1	16.11	4.87	1.543	4.12E-47
FLAD1	34.291	12.85	1.349	4.75E-73
SHC1	58.189	27.29	1.065	5.31E-27
UBE2Q1	39.719	15.774	1.279	3.97E-40
FDPS	291.63	108.698	1.416	2.85E-38
RUSC1	10.76	4.85	1.007	2.44E-33

FAM189B	12.53	4.445	1.313	1.79E-47
PMF1	61.158	26.235	1.191	2.11E-61
LMNA	175.52	45.859	1.913	4.12E-85
PTH1R	1.32	23.575	-3.405	1.44E-102
GPATCH4	18.181	7.33	1.203	2.74E-34
HK3	1.21	4.105	-1.208	1.17E-20
LY6E	54.53	259.294	-2.229	6.44E-29
VPS28	192.071	76.699	1.313	3.18E-66
RECQL4	8.65	1.435	1.987	6.01E-51
SQSTM1	460.225	152.9	1.583	1.68E-40
RPL8	1876.722	569.775	1.718	6.14E-59
RACGAP1	4.61	0.705	1.718	1.73E-50
SPC24	5.15	0.33	2.209	5.18E-66
IP6K3	0.36	2.394	-1.319	3.14E-09
PAQR4	3.82	0.8	1.421	7.08E-32
FLYWCH2	14.31	4.85	1.388	1.74E-39
UBXN1	75.378	36.076	1.043	4.46E-62
RPL29	1049.145	487.919	1.103	1.66E-49
PDZK1IP1	15.74	1.505	2.74	1.12E-16
FAM151A	0.45	2.274	-1.175	1.09E-05
RBP7	17.259	2.635	2.329	3.32E-59
TMEM82	5.08	21.11	-1.863	2.33E-21
LAPTM5	28.489	13.69	1.005	3.00E-11
RBBP4	30.969	14.58	1.037	1.25E-12
KIAA1522	11.99	3.85	1.421	4.79E-36
GBP2	45.972	15.32	1.525	3.30E-36
IGSF8	46.529	21.859	1.056	1.58E-26
PEA15	45.819	12.42	1.803	3.81E-58
NCSTN	62.552	26.736	1.196	1.96E-34

OLFML2B	2.78	0.275	1.568	3.12E-45
FLVCR1	3.43	0.705	1.378	3.91E-51
MT2P1	0	7.11	-3.02	1.10E-64
MRPL55	113.739	49.114	1.195	2.74E-56
H3F3A	397.496	139.034	1.509	9.56E-73
INHBB	10.18	4.304	1.076	1.55E-09
SCNM1	33.21	10.825	1.533	9.85E-72
VPS72	28.489	8.295	1.666	7.94E-78
S100A11	77.321	36.376	1.067	7.15E-13
SPRR3	0	1.315	-1.211	5.13E-29
S100A9	11.29	46.889	-1.962	1.32E-14
S100A12	0.19	3.425	-1.895	2.35E-62
PMVK	77.262	35.51	1.1	2.50E-58
PBXIP1	38.369	13.51	1.44	5.51E-53
PYGO2	15.31	6.875	1.05	1.25E-47
TMEM183A	27.02	12.51	1.052	5.56E-52
KRTCAP2	342.651	102.454	1.732	1.10E-93
SSR2	259.267	82.939	1.633	6.01E-67
HDAC11	8.49	2.1	1.614	4.48E-54
SERPINI1	3.56	0.94	1.233	6.41E-31
RPL22L1	61.469	28.814	1.067	3.95E-20
THOC7	41.271	19.789	1.024	1.66E-54
GMPS	19.41	6.88	1.373	9.06E-52
MTHFD2L	3.57	9.69	-1.226	7.44E-37
RPN1	160.362	76.362	1.061	9.65E-46
RFC4	12.42	3.89	1.457	1.42E-48
RPL39L	5.42	1.46	1.384	1.23E-15
TKT	113.921	35.77	1.644	3.14E-33
LRPAP1	95.259	43.646	1.108	2.91E-40
S100P	6.05	2.36	1.069	1.30E-08

H2AFZ	99.808	32.785	1.577	4.21E-53
PLXNB1	30.89	67.29	-1.099	9.51E-09
TEX264	62.651	29.615	1.056	3.68E-67
POC1A	4.81	1.72	1.095	4.36E-44
HMGB2	34.871	11.52	1.519	1.95E-43
HAND2	0.4	5.02	-2.104	1.16E-45
MAD2L1	3.9	0.535	1.675	1.61E-47
HPGD	14.55	40.456	-1.415	6.59E-12
NPY1R	0.4	2.24	-1.211	1.79E-37
HHIP	0.06	1.475	-1.223	2.21E-43
NDUFAF2	25.06	11.515	1.058	6.33E-43
NDUFS4	82.081	38.374	1.077	4.28E-45
SPINK1	187.155	23.855	2.92	1.47E-06
ESM1	3.22	0.09	1.953	1.59E-52
NSA2	56.629	26.857	1.049	7.30E-45
RPS14	955.822	419.331	1.187	1.83E-54
PTTG1	20.589	0.87	3.529	5.59E-80
KCNK5	1.67	4.375	-1.009	3.47E-14
FABP5	16.66	2.88	2.186	1.76E-44
RAD21	33.499	14.025	1.199	1.17E-29
TMEM184A	5.88	13.27	-1.052	3.29E-07
YWHAZ	107.38	40.699	1.378	1.29E-36
KIAA1429	32.019	13.155	1.222	4.60E-66
KIAA0196	15.47	6.095	1.215	2.18E-52
NUDT2	20.569	9.42	1.05	1.35E-43
FBP1	116.403	296.902	-1.343	4.11E-20
WBSCR27	3.28	0.965	1.123	2.17E-25
NDUFB6	61.601	29.35	1.044	8.17E-52
MELK	2.23	0.1	1.554	1.08E-44
SPTSSA	24.609	11.13	1.078	1.28E-21

FOLR2	10.76	4.165	1.187	2.82E-09
MBL2	12.81	37.715	-1.487	4.36E-18
HEPACAM	0.07	1.355	-1.138	2.67E-04
SKA3	1.16	0.07	1.013	1.35E-39
KIAA1462	3.31	0.52	1.504	9.40E-51
NDRG2	83.239	176.349	-1.074	4.03E-23
PRAP1	676.102	259.618	1.377	4.48E-05
PSMC3	107.507	52.736	1.014	1.17E-59
IFI27L1	14.55	4.515	1.495	1.39E-60
IFI27	145.209	26.64	2.403	3.73E-19
TPP1	67.568	32.47	1.035	2.90E-23
MOGAT2	5.55	49.036	-2.933	1.71E-41
RIC3	0.07	1.775	-1.375	1.08E-35
WDR72	1.77	8.21	-1.733	1.72E-23
TRIM66	0.84	3.18	-1.184	1.30E-17
RPL27A	1599.05	693.57	1.204	5.94E-51
MFAP4	3.46	14.005	-1.75	2.29E-16
MCM7	32.919	12.145	1.368	6.89E-41
TMED3	20.71	6.7	1.495	1.13E-09
SEC11C	180.33	89.39	1.004	4.71E-25
NGFRAP1	82.928	34.27	1.251	1.48E-06
NNMT	269.342	1779.553	-2.719	8.31E-23
PPIB	710.208	316.299	1.164	2.58E-57
KIAA0101	9.86	1.51	2.113	9.70E-50
PLIN1	1.84	8.99	-1.815	7.43E-29
MESP1	3.86	0.96	1.31	6.00E-48
GLYATL1	44.609	140.035	-1.629	8.95E-25
PLK1	3.77	0.765	1.434	6.79E-36
PDIA3	370.671	173.452	1.091	2.37E-44
PHB	120.25	54.451	1.129	2.57E-52

SNRPD1	42.22	14.7	1.461	1.13E-60
UGT1A6	70.37	21.275	1.68	2.54E-05
IGF2	10.29	89.75	-3.007	3.53E-10
TBC1D16	5.07	1.81	1.111	6.32E-26
RRM1	13.68	4.735	1.356	1.14E-46
FN3K	54.059	25.804	1.039	7.59E-25
TRAPPC2L	54.651	23.875	1.162	1.09E-53
TUBA1A	15.45	6.205	1.191	8.89E-18
TUBA1C	72.028	27.1	1.378	5.52E-19
GPD1	15.39	46.359	-1.531	1.03E-17
LENG8	19.07	47.91	-1.285	1.03E-05
YIF1B	47.891	22.32	1.068	4.91E-35
HDGFRP2	27.739	12.485	1.092	3.29E-62
PLIN4	4.27	22.554	-2.16	1.51E-25
SLC43A2	4.48	1.57	1.092	9.52E-20
TK1	17.25	2.335	2.452	2.99E-58
SRRM2	123.442	265.349	-1.098	9.48E-06
FTH1	3615.3	1496.627	1.272	3.64E-49
POLR2G	53.772	23.625	1.153	1.79E-62
RPSA	680.38	312.941	1.118	2.42E-39
SAC3D1	13.78	4.47	1.434	1.33E-70
SCARA3	3.69	1.065	1.183	2.01E-20
PBK	2.1	0.1	1.495	8.04E-41
RAB4A	37.219	17.995	1.009	1.56E-41
RNF187	55.749	23.695	1.2	3.40E-56
NT5DC2	11.39	3.31	1.523	4.62E-26
SMIM4	34.9	9.335	1.796	1.83E-59
MFSD2A	3.81	77.691	-4.032	5.52E-45
TAP1	22.079	9.69	1.11	1.05E-22
STIP1	52.57	22.525	1.187	2.85E-33

FEN1	12.59	2.9	1.801	7.26E-62
RNF181	192.417	83.178	1.2	5.57E-67
VAMP5	90.88	33.767	1.402	1.87E-43
PPIC	23.64	11.08	1.028	2.60E-31
STXBP6	6.17	1.34	1.615	9.91E-40
LGALS9	20.79	8.12	1.257	1.77E-17
SLC25A6	110.063	52.654	1.05	5.00E-32
NSMCE1	51.61	24.375	1.052	2.32E-56
RP11-231C14.4	6.94	27.937	-1.866	3.68E-16
LMAN2	226.866	97.544	1.209	4.84E-65
SLC50A1	65.289	24.135	1.399	1.38E-50
NPIPB3	8.82	24.769	-1.392	1.05E-07
PTK2	22.721	9.61	1.161	3.37E-38
SDC2	176.557	68.859	1.346	1.43E-24
FAM103A1	15.7	7.285	1.011	9.60E-51
SPNS1	31.6	13.335	1.185	4.26E-64
FASN	217.896	108.112	1.004	2.11E-08
MT1E	86.228	797.532	-3.194	1.59E-32
RAC3	14.47	6.25	1.093	3.17E-22
ROBO1	9.19	1.07	2.299	1.09E-32
MUC3A	1.62	5.13	-1.226	5.18E-04
TM4SF4	430.001	95.683	2.156	2.86E-18
TM4SF1	41.469	14.024	1.499	5.03E-16
HNRNPA3	124.077	57.412	1.098	4.79E-50
GLB1	33.079	15.252	1.068	3.66E-39
FABP4	7.47	2.645	1.216	2.62E-10
FOS	15.56	80.208	-2.294	5.31E-30
HSD17B13	6.73	74.827	-3.294	2.68E-16
PA2G4	52.57	23.56	1.125	6.70E-46
NUDCD2	15.3	6.895	1.046	8.99E-32

HSPA4	68.029	27.19	1.292	1.13E-52
SYT9	0.01	1.26	-1.162	8.39E-44
GSTA4	18.01	6.855	1.275	2.86E-28
TPT1-AS1	3.42	8.05	-1.034	1.23E-12
ZNF160	1.91	4.945	-1.031	1.05E-15
FPR1	0.53	2.29	-1.105	7.81E-18
LRG1	121.229	339.166	-1.477	1.29E-15
KCND3	0.84	3.235	-1.203	7.35E-28
KRT13	0	2.74	-1.903	6.91E-36
ZNF581	9.69	4.23	1.031	1.32E-44
MCC	1.22	3.825	-1.12	2.64E-38
ETFDH	27.81	58.846	-1.055	2.86E-33
FGB	3258.516	6850.767	-1.072	1.51E-09
RP11-443P15.2	1.78	0.02	1.447	1.02E-27
LGALS4	224.27	46.12	2.257	2.48E-06
RHNO1	6.63	1.77	1.462	2.76E-52
RRM2	9.26	0.595	2.685	1.36E-50
RPS21	1270.692	486.517	1.383	9.69E-56
RPS7	895.903	394.121	1.183	1.42E-54
PPIH	16.36	6.63	1.186	8.15E-51
QARS	101.447	45.099	1.152	6.28E-61
MRPL13	47.431	19.64	1.23	8.48E-57
ISG20	19.96	9.17	1.043	7.63E-16
STARD5	6.45	19.359	-1.45	3.13E-42
TTC36	4	63.26	-3.684	2.66E-42
MYEOV2	94.693	41.148	1.183	1.77E-53
FIBP	36.801	17.76	1.011	8.92E-57
RPL38	1230.73	457.934	1.424	8.63E-66
MIR4435-2HG	33.1	4.45	2.645	4.40E-53
TRMT112	215.358	83.786	1.352	3.43E-75

MTX1	58.838	20.895	1.45	1.55E-82
SNCG	6.78	1.72	1.516	1.21E-23
PPP1R3B	10.71	24.785	-1.139	9.18E-19
NAA20	71.858	29.014	1.279	1.48E-58
SAA1	287.157	4468.423	-3.955	3.44E-23
MST1	205.486	472.132	-1.196	7.93E-24
SULT1B1	1.05	3.175	-1.026	2.81E-14
UQCRH	217.594	83.829	1.366	1.14E-57
MUC13	5.82	0.22	2.483	6.99E-25
TOMM20	65.871	21.944	1.543	3.13E-69
SPTBN2	8.04	18.735	-1.126	2.26E-16
PHLDA3	6.77	2.53	1.138	4.69E-10
PODN	1.39	3.865	-1.025	7.70E-11
EXO1	1.81	0.1	1.353	1.41E-45
RPL4	1141.566	557.933	1.032	2.02E-40
RPL15	755.139	377.046	1	1.90E-44
HRAS	32.271	15.19	1.039	3.00E-48
SEZ6L2	2.88	0.205	1.687	3.02E-23
SLC22A1	56.102	495.588	-3.12	2.77E-29
UBE2C	13.24	0.6	3.154	1.56E-68
MARCKSL1	29.07	13.709	1.032	3.51E-18
PSMD2	81.48	38.55	1.06	4.01E-29
PHYHD1	14.71	34.515	-1.177	9.58E-19
PHYKPL	20.569	47.765	-1.177	1.10E-27
UCP2	14.85	5.555	1.274	9.18E-13
RMI2	3.39	0.47	1.578	1.38E-41
RUVBL1	17.349	7.765	1.066	1.18E-37
SFN	9.74	0.605	2.742	1.61E-31
ETV4	3.97	0.46	1.767	9.97E-26
KBTBD11	0.26	2.645	-1.532	7.57E-57

RNF152	2.87	7.37	-1.113	7.43E-30
TTTY14	0.41	2.95	-1.486	2.34E-05
TYMS	16.4	3.05	2.103	2.21E-48
TYMSOS	2.58	0.44	1.314	1.16E-36
TALDO1	149.955	65.534	1.182	8.91E-51
ZFAS1	81.002	27.78	1.511	7.16E-40
ERICH5	18.92	3.41	2.175	1.43E-14
RPLP2	879.597	343.329	1.355	2.02E-51
GBA	73.48	12.61	2.452	2.46E-103
POLR2L	155.448	74.78	1.046	6.25E-51
SOX12	4.26	1.51	1.067	6.01E-28
MAMDC4	2.66	11.405	-1.761	4.27E-16
RPS27	3269.149	1428.86	1.193	1.73E-47
IMPDH2	67.662	29.13	1.188	2.28E-39
GRAMD1C	2.24	5.925	-1.096	1.36E-19
STAP2	66.68	31.891	1.041	2.07E-21
EXOSC4	41.63	15.195	1.396	1.23E-55
RRS1	16	4.47	1.636	1.32E-34
MAGED1	64.44	31.6	1.005	1.20E-12
HLA-DQB1	22.92	5.189	1.95	3.59E-16
LINC00174	1.05	3.635	-1.177	4.56E-19
SHARPIN	59.272	24.24	1.256	4.45E-61
MAF1	56.469	23.51	1.229	1.43E-55
TPPP2	0.76	3.525	-1.362	1.01E-29
PUF60	112.259	47.77	1.216	3.24E-54
TMEM150B	6.44	0.645	2.177	3.44E-36
GREM2	0.93	6.41	-1.941	4.38E-16
FAM83H	14.96	5.055	1.398	1.52E-39
MRPL14	79.71	35.33	1.152	9.91E-59

LSMEM1	0.64	3.055	-1.306	5.49E-22
NQO1	11.72	1.285	2.477	2.02E-29
NPM1	485.355	170.378	1.505	2.36E-47
TMEM45A	11.38	32.179	-1.422	4.51E-14
RPL24P4	9.02	3.245	1.239	7.20E-36
MRPS23	28.859	9.985	1.443	1.07E-47
PHLDA2	4.54	1.015	1.459	2.33E-12
SNRPE	137.548	38.494	1.811	5.11E-83
RP11-69E11.4	0.83	3.935	-1.431	4.93E-20
TDRKH	4.09	1.165	1.233	1.56E-35
MRPS16	81.452	35.44	1.178	4.09E-69
YBEY	17.97	8.19	1.046	9.18E-35
KPNA2	28.43	6.31	2.009	1.03E-62
MFSD5	14.31	5.98	1.133	6.51E-58
SATB1	1.65	4.965	-1.17	2.49E-22
SKA2	14.76	6.375	1.096	2.07E-41
RPL35A	803.914	353.091	1.185	3.04E-53
SLC25A18	21.47	46.775	-1.088	1.48E-13
HMGN4	13.39	5.36	1.178	1.88E-18
PYCR1	6.32	2.035	1.27	4.77E-11
RABIF	6.21	2.225	1.161	5.55E-69
RUVBL2	50.822	22.285	1.154	9.46E-65
PLGLB1	29.8	74.586	-1.295	1.09E-20
TMEM50A	50.779	20.175	1.29	2.01E-54
TRAIP	1.87	0.385	1.051	1.16E-40
NUDT14	19.94	9.41	1.008	7.68E-22
FAM3B	2.72	0.6	1.217	4.04E-11
IQGAP3	2.35	0.12	1.581	4.48E-45
UQCR10	135.532	66.201	1.023	7.94E-53
NR2C2AP	14.33	4.33	1.524	1.09E-71

IRAK1	36.75	13.79	1.352	1.22E-39
RPL23AP82	9.59	4.1	1.054	1.44E-41
WDR27	2.94	8.715	-1.302	8.39E-10
PTP4A3	8.63	2.31	1.541	1.56E-32
SOCS3	6.84	20.916	-1.483	7.50E-13
NDUFA12	82.681	39.89	1.033	1.74E-63
TMED9	183.304	91.034	1.002	6.92E-43
IMMP2L	17.52	8.165	1.015	8.77E-32
LCN12	6.83	17.9	-1.271	7.33E-14
MUC6	0.02	1.58	-1.339	2.73E-09
MANEAL	9.16	3.035	1.332	1.01E-29
NOMO2	83.609	35.69	1.205	5.96E-48
WBP5	20.89	9.55	1.053	1.10E-06
UBALD2	27.02	12.254	1.08	6.24E-33
IL3RA	2.95	0.6	1.304	7.64E-59
SMYD3	13.12	3.06	1.798	2.36E-59
PARPBP	1.5	0.19	1.071	4.70E-39
OLFML2A	1.48	0.175	1.078	1.57E-41
NDUFA4L2	14.62	3.17	1.905	4.81E-41
NTF3	0.23	2.445	-1.486	1.37E-78
SLC52A2	14.78	5.38	1.307	2.94E-44
NPIPB4	4.31	16.34	-1.707	4.23E-13
NDUFA13	306.702	131.338	1.217	6.06E-60
POLR3C	10.38	4.26	1.113	5.62E-43
SLC51B	3.87	0.415	1.783	6.74E-27
TOR3A	17.179	7.93	1.026	1.02E-27
MST1P2	9.95	74.23	-2.78	5.13E-30
RPS23	1376.605	648.044	1.086	5.30E-45
MST1L	10.36	64.444	-2.526	5.43E-21
MPPED1	1.34	5.769	-1.532	5.30E-26

TNFRSF4	2.97	0.32	1.589	4.05E-65
NAP1L1	87.462	40.215	1.102	1.73E-30
MT1X	145.29	1597.997	-3.45	8.62E-43
EPOR	2.57	7.27	-1.212	1.33E-17
PTMA	508.498	243.57	1.059	1.61E-41
ISG15	71.55	30.819	1.189	9.07E-13
HAPLN4	0.31	1.81	-1.101	1.90E-25
GABRD	1.66	0.06	1.327	1.49E-62
HIST1H1C	128.818	48.314	1.396	2.82E-24
PALM3	7.61	18.025	-1.144	2.18E-17
TPRG1	1.7	4.69	-1.075	2.30E-23
MORN2	12.46	5.615	1.025	9.02E-40
LAMTOR4	128.079	55.479	1.192	3.09E-57
PLA2G2A	23.811	207.166	-3.069	5.77E-07
ZP3	2.71	0.66	1.16	1.18E-29
H2AFX	14.94	4.97	1.417	8.39E-40
HBA2	22.15	162.612	-2.821	4.20E-38
CLN3	58.809	19.355	1.555	2.78E-68
SUMO2	146.859	49.28	1.556	7.57E-57
IDO2	0.11	2.54	-1.673	3.37E-33
PARVB	16.31	6.394	1.227	3.72E-13
RBM34	44.711	15.919	1.434	4.00E-70
PRELP	1.25	4.32	-1.241	4.30E-16
RPL14	706.917	314.714	1.165	1.55E-49
NDUFA4	120.508	59.309	1.011	1.15E-48
FAM111B	1.57	0.09	1.237	5.95E-33
H1F0	142.438	60.62	1.219	4.46E-28
HN1	64.208	19.065	1.7	8.00E-54
S100A13	75.29	27.839	1.403	6.17E-19
FHIT	11.09	4.22	1.212	4.78E-39

FAM150B	0.13	1.28	-1.013	5.92E-11
FAM180A	0.22	3.43	-1.86	4.66E-57
KAZN	0.34	1.91	-1.119	1.53E-33
IL1RAP	6.41	25.615	-1.845	5.13E-43
KIAA0895L	2.04	7.16	-1.424	1.66E-10
HLA-DRB1	66.431	27.555	1.24	4.58E-10
SERPINA3	370.748	888.913	-1.259	9.53E-13
S100A4	29.25	13.083	1.103	9.94E-12
HRCT1	4.34	0.48	1.851	2.27E-36
TUBB	207.015	88.763	1.212	3.10E-32
PPIA	1363.405	530.68	1.36	1.65E-75
EVL	25.86	54.749	-1.054	8.84E-15
XRCC6	110.598	53.725	1.028	4.22E-48
ZNF775	8.49	3.35	1.125	1.01E-34
MYL6B	27.219	9.079	1.485	1.42E-52
NACA	953.903	425.79	1.162	3.21E-62
MME	0.91	7.135	-2.091	2.01E-06
LINC00238	0.19	3.295	-1.852	2.37E-34
TOMM7	327.397	128.181	1.346	3.43E-57
PDXDC2P	2.91	11.375	-1.662	3.44E-20
HLA-DQA1	12.49	3.505	1.582	1.17E-09
GM2A	16	4.965	1.511	1.23E-64
ZNF585A	5.72	2.155	1.091	7.45E-34
LAGE3	36.59	11.005	1.647	2.33E-67
FAM163B	0.09	2.415	-1.648	2.16E-47
SRC	8.85	3.365	1.174	1.05E-12
SND1	82.521	38.05	1.097	2.44E-57
MRPL21	61.23	29.245	1.041	5.43E-45
OGDHL	18.45	41.286	-1.12	1.77E-17
PDGFA	9.08	1.965	1.765	1.02E-27

NMB	3.43	0.835	1.272	8.27E-32
S100A10	241.168	54.345	2.129	2.01E-41
RPL37A	2021.064	985.047	1.036	9.48E-37
GPAA1	115.511	39.639	1.52	7.85E-66
UGT2B17	0.75	3.04	-1.207	1.79E-03
HIST1H2BK	106.042	36.82	1.501	4.03E-23
S100A6	69.07	28.38	1.254	2.49E-12
RPL12	922.752	451.379	1.03	9.95E-36
MPZL1	21.41	8.445	1.247	1.17E-30
RPS4X	486.365	194.576	1.317	6.51E-48
GRK6	10.62	4.71	1.025	1.04E-47
PRIM1	5.97	1.56	1.445	1.73E-42
RP11-347C12.1	0.37	1.89	-1.077	4.93E-25
ZNF544	9.53	3.565	1.206	2.66E-35
SULT1C2	4.09	0.35	1.915	3.66E-19
RPL23A	690.213	342.33	1.01	5.01E-38
UBL5	409.522	183.329	1.155	1.28E-70
MT1F	7	191.386	-4.588	6.81E-49
TXNRD1	30.751	11.718	1.32	1.14E-22
FLVCR1-AS1	2.93	0.71	1.201	1.73E-32
HLA-DRB5	14.2	5.88	1.144	1.50E-05
ZNF28	3.54	0.65	1.46	1.30E-20
PPIAP22	165.466	34.006	2.25	9.13E-79
STK39	2.72	0.525	1.286	7.44E-24
TAT	98.25	345.525	-1.804	4.06E-16
LPA	1.21	8.365	-2.083	6.63E-44
MT-CO2	13276.616	27014.567	-1.025	1.28E-24
GLMP	123.023	36.071	1.742	4.49E-67
MT-CYB	6751.535	15334.037	-1.183	2.38E-28
F5	206.614	92.446	1.152	8.08E-13

EPS8L3	4.76	0.13	2.35	2.06E-30
MT-ND2	6531.958	14680.362	-1.168	2.13E-23
MT-ND5	1410.997	3065.91	-1.119	9.28E-17
SCAMP5	3.87	0.69	1.527	2.60E-24
HMGN2	225.736	103.877	1.112	3.38E-42
SELM	33.981	12.185	1.408	9.10E-14
MT-ND3	9254.247	19245.719	-1.056	5.56E-24
TSEN15	11.54	5.17	1.023	1.19E-41
MT-ND4	9684.084	23104.719	-1.254	1.08E-34
MT-ND1	5574.782	11534.356	-1.049	3.52E-24
SHISA4	11.06	3.83	1.32	1.95E-21
MT-ATP6	11214.673	31942.729	-1.51	1.16E-41
PRC1	10.68	1.12	2.462	3.32E-64
RPL39	1924.809	846.93	1.183	1.93E-44
SOWAHA	2.79	0.565	1.276	1.14E-34
MFAP3L	1.98	7.005	-1.426	9.41E-28
TGM2	49.931	107.727	-1.094	3.91E-12
RNU4-2	13.67	5.598	1.153	5.34E-06
TATDN3	7.83	3.265	1.05	3.12E-45
SAMD5	0.48	2.47	-1.229	5.79E-26
SOX18	4.61	1.78	1.013	5.70E-29
FAM127B	33.109	15.435	1.053	8.59E-12
NEU4	9.57	24.385	-1.264	4.71E-12
GGTA1P	3.88	1.105	1.213	7.57E-28
PFDN6	118.569	41.236	1.501	1.97E-73
HNRNPCP2	7.96	0.895	2.241	1.00E-63
HLA-DMA	37.32	12.255	1.532	1.92E-20
TAP2	17.289	7.24	1.15	1.36E-20
HLA-DRA	171.468	42.669	1.982	3.47E-16
FKBPL	5.26	2.025	1.049	4.76E-60

NELFE	58.618	14.75	1.92	4.92E-73
NEU1	55.299	15.57	1.765	3.02E-68
LSM2	38.869	13.895	1.42	2.80E-64
VARS	36.521	13.985	1.324	3.20E-47
GPANK1	16.02	6.145	1.252	4.25E-59
NFKBIL1	18.87	8.68	1.038	1.09E-51
HLA-C	499.658	223.828	1.155	7.73E-16
LRCOL1	1.04	7.855	-2.118	2.13E-29
TRIM31	2.55	0.295	1.455	7.90E-21
PPP1R11	42.579	19.67	1.076	8.00E-46
GNB2L1	891.937	427.994	1.058	4.11E-47
HLA-F	95.709	30.939	1.598	5.53E-21
GABBR1	0.68	2.665	-1.125	3.18E-12
ST8SIA6-AS1	3.81	0	2.266	2.87E-27
FAM83A-AS1	0.45	4.95	-2.037	2.15E-08
PRSS1	0	1.17	-1.118	6.84E-25
PSENEN	80.968	34.785	1.196	1.95E-59
PSMB10	59.112	28.645	1.02	1.14E-29
KRT17P4	0.05	1.34	-1.156	1.80E-35
MT1H	2.16	332.67	-6.722	2.39E-61
MT1DP	0.59	4.235	-1.719	2.76E-18
MT1A	15.19	81.693	-2.353	1.74E-18
MT1M	1.78	112.018	-5.345	8.93E-60
EXOC3L4	17.59	43.365	-1.255	2.97E-16
SERF1B	18.65	6.19	1.45	1.62E-60
HMGN1	69.42	32.281	1.081	3.30E-36
LCMT1	12.62	5.335	1.104	5.15E-53
SMIM11	4.77	1.32	1.314	3.18E-14
FAM99B	0.23	3.835	-1.975	1.97E-44
FAM99A	1.1	37.31	-4.189	1.13E-52

HBA1	10	98.975	-3.184	2.99E-47
HLA-H	36.931	6.175	2.402	1.66E-34
HLA-A	714.504	165.214	2.106	3.22E-46
IGKC	145.713	295.005	-1.013	2.58E-03
IGLV1-51	1.47	5.9	-1.482	1.29E-04
IGLV1-40	1.33	6.649	-1.715	1.26E-03
IGLV3-25	0.84	3.975	-1.435	9.68E-04
IGLV2-14	2.14	11.483	-1.991	2.77E-06
IGLV2-11	1.12	4.605	-1.403	9.43E-05
IGLC2	39.769	93.769	-1.217	5.45E-03
IGLC3	24.69	52.18	-1.05	1.49E-03
TRBC2	11.13	5.035	1.007	3.92E-09
IGHA2	2.83	10.167	-1.544	5.71E-12
IGHG4	4.9	13.65	-1.312	2.88E-03
IGHG2	10.09	28.674	-1.42	3.72E-04
IGHA1	21.08	103.5	-2.243	3.01E-16
IGHM	8.76	27.634	-1.553	1.81E-10
IGHV2-5	0.23	1.725	-1.148	3.21E-04
IGHV3-15	0.45	1.995	-1.046	6.26E-03
IGHV3-33	0.74	2.745	-1.106	4.21E-03
IGHV5-51	0.64	2.455	-1.075	1.92E-03
RPL15P3	8.69	3.015	1.271	6.17E-38
MT-ND4L	5341.391	15483.027	-1.535	6.04E-27
LPAL2	1.31	6.39	-1.678	4.47E-39
RP11-641D5.1	174.126	60.058	1.52	2.02E-49
SUPT4H1	66.192	30.304	1.102	4.01E-58
GSTM2	4.74	20.76	-1.923	4.67E-22
LCAT	32.421	153.649	-2.21	2.18E-42
GBP7	6.71	14.798	-1.035	7.89E-07
RPLP0P6	13.89	4.415	1.459	7.08E-44

SLX1A-SULT1A3	2.04	6.45	-1.293	6.72E-12
HEXA	76.68	33.93	1.153	2.55E-44
SLC35F6	16.66	7.18	1.11	4.73E-44
UGT2B11	3.8	0.615	1.572	4.59E-20
UBD	334.949	7.468	5.31	1.60E-66
LTB4R	2.01	5.365	-1.08	3.40E-08
TAX1BP3	26.981	11.99	1.107	2.37E-17
TSPAN4	40.52	18.425	1.096	2.62E-21
LYRM4	16	6.435	1.193	1.35E-52
PTMAP5	2.79	0.765	1.103	9.23E-26
PLIN5	18.75	68.379	-1.813	8.12E-20
RPL7P1	20.549	5	1.845	1.49E-45
MEG3	2.21	22.203	-2.854	6.21E-17
TOMM6	230.017	86.413	1.402	1.25E-72
RP11-480I12.5	3.39	0.955	1.167	3.16E-25
GOLGA8B	7.7	19.393	-1.229	3.83E-03
GCGR	4.47	57.661	-3.423	2.38E-39
TSTD1	79.181	35.715	1.127	6.37E-20
IFI30	140.769	51.639	1.429	1.31E-30
RPS2P55	2.26	0.33	1.293	2.92E-51
RP11-475C16.1	15.42	7.145	1.011	2.34E-28
FTH1P8	9.88	1.33	2.223	4.15E-60
RP11-40C6.2	389.91	0	8.611	3.30E-78
TRIM16	6.27	2.35	1.118	7.03E-22
HEPN1	0.21	5.295	-2.379	5.40E-09
UBA52	852.821	414.275	1.04	8.44E-57
TIAF1	0.48	2.72	-1.33	2.07E-39
LINC00152	35.26	4.54	2.711	1.71E-59
RP11-632K20.7	1.68	5.815	-1.346	2.31E-26
HLA-DPB1	59.821	17.4	1.725	2.74E-14

UBE2SP2	3.54	0.085	2.065	3.79E-71
SNRPGP15	0.25	1.765	-1.145	4.66E-19
HNRNPA1P48	7.86	3.015	1.142	1.06E-33
RP11-51O6.1	21.64	8.325	1.28	1.06E-44
SH3BP5-AS1	0.9	3.05	-1.092	1.24E-18
RP11-228B15.4	0.38	2.354	-1.281	1.39E-25
RP11-415J8.3	0.74	3.8	-1.464	3.31E-31
RP11-390F4.3	1.26	4.439	-1.267	5.45E-28
RPL35P5	5.17	1.38	1.374	7.81E-45
MTND2P28	211.541	441.922	-1.059	2.46E-12
FAM195B	68.721	30.14	1.163	3.78E-40
FAM229A	1.52	4.93	-1.235	6.43E-12
RP11-384K6.2	1.46	4.205	-1.081	2.87E-23
NOL7	38.55	15.44	1.266	1.50E-59
RP4-706A16.3	22.42	9.355	1.177	2.60E-30
RP11-419C5.2	2.46	11.16	-1.813	2.07E-18
RP11-61N20.3	6.12	1.49	1.516	1.21E-19
FTH1P20	13.07	1.48	2.504	1.81E-84
RP11-128M1.1	1.61	0.24	1.074	4.26E-37
TBCAP1	1.64	0.26	1.067	8.15E-27
RP3-417G15.1	2.94	0.94	1.022	5.27E-29
LINC00511	1.86	0.105	1.372	2.19E-23
RPS28P7	722.222	182.518	1.979	1.96E-74
WASH7P	1.2	4.41	-1.298	1.11E-15
HPN-AS1	0.59	3.69	-1.561	1.59E-26
LTB	7.99	2.18	1.499	1.25E-15
SPAG5-AS1	0.5	2.125	-1.059	1.73E-24
RP11-452F19.3	11.78	4.12	1.32	1.81E-47
MT-ATP8	11020.483	37358.527	-1.761	1.62E-29
LINC01320	0.46	2.05	-1.063	1.73E-09

ORM2	1430.198	3502.573	-1.292	8.12E-14
OST4	273.879	129.4	1.076	7.70E-69
RP3-342P20.2	0.1	3.96	-2.173	5.87E-47
RP1-241P17.4	3.77	0.74	1.455	9.14E-15
SPCS2P4	30.96	12.14	1.282	2.97E-41
RP11-556E13.1	1.14	0	1.098	1.21E-22
LINC00659	1.39	4.703	-1.255	2.20E-14
PGA4	0.05	1.7	-1.362	3.57E-43
MT1P3	0	1.41	-1.269	1.22E-09
HMGN1P37	1.59	0	1.373	5.96E-38
ORM1	4575.773	15121.356	-1.724	3.35E-19
HLA-DRB6	4.28	0.965	1.426	1.57E-14
PET100	68.322	29.18	1.2	8.36E-63
PGA3	0.06	2.469	-1.71	8.52E-49
GOLGA6L5P	0.93	3.465	-1.21	1.80E-18
RP4-631H13.6	0	1.5	-1.322	1.76E-07
HLA-DPA1	49.969	17.045	1.498	2.45E-11
RPS18	2144.461	874.278	1.293	5.72E-48
FTH1P7	25.5	2.38	2.971	2.02E-72
GOLGA8N	1.07	3.665	-1.172	2.69E-20
LINC00665	2.16	0.485	1.089	3.09E-18
GTF2IP4	23.86	8.225	1.43	1.57E-28
MTND4P20	4	25.358	-2.398	3.83E-27
RP11-295G20.2	20.34	5.555	1.703	9.96E-37
MT1XP1	0	2.03	-1.599	2.90E-28
RP11-250B2.3	0.5	2.48	-1.214	3.11E-40
H2BFS	7.35	2.365	1.311	1.07E-27
MAGI2-AS3	1.53	8.76	-1.948	1.65E-24
HMGN2P5	42.659	13.404	1.6	2.32E-34
RP11-465N4.4	4.77	1.63	1.134	3.17E-22

RP11-166B2.1	0.87	3.453	-1.252	1.57E-17
GAS5	169.388	80.573	1.063	1.93E-27
HLA-B	788.298	281.004	1.485	1.15E-16
RPS3AP6	12.82	5.885	1.005	1.09E-27
RPL23AP42	644.751	238.359	1.432	1.41E-52
SOX9-AS1	2.87	0.72	1.17	9.13E-19
FABP5P7	8.22	1.645	1.801	1.41E-32
TECRP1	6.04	1.785	1.338	4.63E-39
HGH1	22.409	10.215	1.062	1.99E-38
RPL39P3	319.151	110.798	1.518	2.15E-18
RP4-763G1.2	5.4	19.574	-1.685	9.76E-20
SUMO2P1	1.16	0	1.111	1.18E-06
FAM103A2P	6.95	2.265	1.284	2.92E-28
RP11-575L7.8	0.44	2.52	-1.289	9.72E-23
SNRPGP10	1.81	5.694	-1.252	3.22E-15
TOPORS-AS1	9.65	3.685	1.185	1.22E-48
RPL6P27	12.27	4.93	1.162	9.28E-36
H3F3AP4	144.256	34.374	2.038	4.70E-16
PNMA6A	9.82	4.305	1.028	2.33E-07
RP11-215A21.2	2.32	0.17	1.505	1.69E-56
HSPB1P1	5.31	0	2.658	1.66E-49
RP11-175B9.3	1.41	4.86	-1.282	6.52E-12
RPL13AP5	68.802	31.064	1.122	1.31E-37
PITPNA-AS1	8.52	3.245	1.165	5.67E-37
LINC00106	0.56	2.26	-1.063	1.09E-12
LINC01554	1.42	69.249	-4.859	4.99E-26
NDUFA6-AS1	5.28	12.819	-1.138	9.18E-15
RP4-669L17.10	3.09	8.316	-1.188	1.19E-09
HAND2-AS1	0.12	2.285	-1.552	3.44E-58
HLA-DQA2	2.19	0.425	1.163	1.62E-08

UBE2Q2P6	655.975	307.128	1.092	1.39E-15
KIFC1	4.37	0.205	2.156	2.31E-55
LINC01370	0.53	6.555	-2.304	1.99E-14
LINC00844	5.59	37.984	-2.565	5.09E-17
PTENP1	1.98	0.39	1.1	5.57E-32
OR2I1P	25.71	1.305	3.535	2.25E-34
SCARNA12	0.37	1.865	-1.064	5.67E-19
RP11-464D20.2	2.61	0.35	1.419	1.55E-43
RP11-295P9.3	3.58	10.585	-1.339	6.20E-08
NME1	100.099	29.344	1.736	3.98E-60
MRPS17	16.48	7.29	1.076	5.73E-45
ITIH4-AS1	0.58	3.97	-1.653	4.22E-33
IGKV3-20	6.35	17.302	-1.316	2.63E-03
LY6G5B	1.49	4.07	-1.026	3.60E-05
PSMB9	50.011	17.194	1.487	6.35E-29
RP11-499P20.2	2.1	7.765	-1.499	3.20E-16
PLGLA	4.32	22.95	-2.171	6.68E-46
FLJ22763	0.76	6.25	-2.042	3.65E-27
IGKV2-24	0.37	2.074	-1.166	5.29E-08
RPL36A	883.691	296.337	1.573	5.82E-59
IGKV3-11	8.89	19.145	-1.026	2.15E-03
RPP21	44.901	18.17	1.26	2.39E-62
RPL37P6	2.03	0	1.599	8.18E-40
PSMC1P1	13.25	5.405	1.154	3.47E-19
INMT	1.57	7.73	-1.764	6.84E-36
IGKV1-9	0.57	2.357	-1.097	1.74E-03
HOGA1	7.79	21.02	-1.325	6.56E-23
PRR34-AS1	7.78	3.39	1	3.51E-24
IGKV1-33	1.17	5.51	-1.585	1.25E-03
LINC00969	15.97	33.294	-1.015	1.63E-03

PEG10	5.21	0.71	1.861	3.12E-13
STAG3L5P	5.22	13.125	-1.183	5.08E-08
UGT1A10	1.21	0.1	1.007	4.13E-17
HLA-DMB	14.22	4.74	1.407	5.56E-17
MBL1P	0.22	3.06	-1.735	3.31E-49
FTH1P23	2.4	0.63	1.061	2.57E-49
IGKV1-5	1.45	5.679	-1.447	3.65E-03
NME1-NME2	398.434	162.714	1.287	1.52E-54
RP11-274B21.3	4.96	12.679	-1.199	4.58E-10
RP11-6B4.1	0.17	4.765	-2.301	2.21E-48
RP5-966M1.6	6.86	66.16	-3.095	4.32E-35
PLA2G4B	1.46	4.7	-1.212	7.46E-13
NPIPB5	9.71	48.205	-2.2	8.53E-16
RPS12P21	0.07	1.17	-1.02	2.74E-46
RPL23AP65	2.83	0.525	1.329	2.76E-26
RP11-404G16.2	0.35	2.57	-1.403	1.16E-22
IGKV2-28	2.52	8.89	-1.49	2.38E-04
IFITM10	1.82	8.635	-1.773	3.62E-14
XXbac-BPG116M5.17	5.75	1.324	1.538	9.66E-05
LINC01296	2.28	0.15	1.512	2.92E-34
RP11-10G12.1	2.99	0	1.996	3.34E-66
IGKV1-27	0.4	1.94	-1.07	5.39E-03
HBB	15.86	167.277	-3.319	2.55E-49
NEAT1	124.507	481.719	-1.943	1.13E-11
SNHG6	110.921	47.349	1.211	2.29E-36
H2AFJ	110.208	42.105	1.367	5.74E-43
UBAP1L	0.45	1.93	-1.015	5.99E-24
TWF2	30.83	12.465	1.241	1.10E-36
MTND4P12	39.65	0.81	4.489	5.49E-17
RRN3P1	1.24	5.655	-1.571	1.25E-33

TRIM52-AS1	9.2	3.35	1.229	7.07E-50
MTATP6P1	1387.526	3715.008	-1.42	1.04E-23
RP11-328K4.1	3.02	13.645	-1.865	2.86E-17
RP11-510N19.5	0.27	1.56	-1.011	8.48E-13
RP11-290F5.1	3.19	20.87	-2.384	1.44E-36
LINC01093	0.55	23.3	-3.971	3.78E-87
NPM1P27	5.95	1.935	1.244	5.04E-35
RP11-434D9.1	1.32	11.964	-2.482	2.64E-30
RP11-423H2.3	0.19	1.485	-1.062	2.96E-15
ECSCR	6.8	2.27	1.254	1.22E-32
PVT1	6.01	1.035	1.784	7.25E-20
GBA3	8.22	31.277	-1.808	1.37E-18
LINC01018	5.58	19.171	-1.616	8.20E-12
YJEFN3	0.55	2.535	-1.189	4.56E-10
RP11-622A1.2	5.56	23.667	-1.911	1.49E-28
HULC	307.319	57.466	2.399	1.54E-20
F11-AS1	2.75	8.87	-1.396	2.92E-32
IGKV1D-39	3.94	11.967	-1.392	4.79E-03
MALAT1	13.79	31.885	-1.153	4.83E-04
RP11-119D9.1	4.61	10.829	-1.076	2.11E-05
RNA5SP216	0	7.302	-3.054	1.59E-19
TRNP1	5.14	1.415	1.346	8.41E-12
LINC01604	8.22	3.345	1.085	3.98E-34
PRKDC	22.389	9.685	1.13	4.97E-16
RP11-115J16.1	0.56	3.09	-1.391	1.34E-09
RP11-115C10.1	1.93	7.789	-1.585	9.26E-04
RP11-496I9.1	0.65	2.6	-1.125	9.34E-08
RNF185-AS1	3.09	0.212	1.755	6.30E-05
RP11-326C3.2	0.96	7.133	-2.053	1.31E-07
SAA2-SAA4	2.75	17.052	-2.267	1.56E-11

PIGY	8.94	0.005	3.306	6.41E-13
RP11-111M22.3	4.52	1.645	1.061	4.45E-37
RP11-196G11.1	0.57	2.975	-1.34	2.77E-47
MT1JP	0.05	4.62	-2.42	1.61E-49
TRAPPC2B	10.94	3.775	1.322	5.49E-35
RPL41P2	37.139	17.225	1.065	2.90E-18
RP1-102E24.8	0.27	2.495	-1.46	2.12E-46
RP11-73M18.2	1.31	0	1.208	1.45E-21
RP11-680F8.1	3.77	1.305	1.049	1.13E-16
SNRPEP2	7.97	1.61	1.781	2.82E-64
HP	8497.954	26421.961	-1.636	2.98E-17
RP11-203J24.9	1.67	4.945	-1.155	4.29E-11
RP11-579D7.2	1.95	0.33	1.149	5.42E-28
RP11-620J15.3	5.08	1.055	1.565	8.54E-53
RP11-1143G9.4	17.64	3.005	2.219	4.02E-19
RP11-256L6.3	0.83	3.32	-1.239	5.22E-20
RP11-386G11.10	69.622	32.095	1.094	7.95E-18
RP11-161H23.5	58.602	23.37	1.29	4.29E-30
RP11-164J13.1	0.77	2.985	-1.171	1.98E-22
RP11-66N24.3	1.31	5.55	-1.504	6.60E-14
LINC01595	0.99	6.505	-1.915	1.21E-14
RP11-316M1.12	78.699	24.778	1.628	2.61E-19
RP11-830F9.5	0.04	1.39	-1.2	2.41E-51
SLX1B-SULT1A4	0.99	3.245	-1.093	4.32E-11
MRC1	1.92	5.135	-1.071	2.95E-07
RP11-345J4.6	2.12	0	1.642	1.56E-04
MT1L	5.34	45.263	-2.867	1.56E-33
PECAM1	11.39	3.285	1.532	2.92E-39
SMG1P7	1.05	4.145	-1.328	1.69E-23
RP11-345J4.5	18.04	5.385	1.576	5.76E-58

RP11-676J12.7	0.11	1.625	-1.242	6.65E-29
RP11-667K14.4	6.33	0.655	2.147	5.25E-22
GDF2	0	4.84	-2.546	1.40E-115
RP11-334E6.12	6.87	0.46	2.43	1.24E-44
RP11-159D12.2	1	3.94	-1.305	8.45E-12
SNRPGP2	9.32	2.87	1.415	5.66E-38
GJA5	2.24	0.385	1.226	1.02E-31
RBM8A	83.152	34.049	1.264	3.29E-57
RP11-138I1.4	198.074	98.4	1.002	6.64E-21
RP11-524F11.1	0.37	2.685	-1.427	1.64E-41
RP11-452I5.2	7.38	2.75	1.16	3.59E-14
RP5-890E16.4	4.32	0	2.411	2.20E-14
MRPS21	63.999	22.47	1.47	1.96E-74
FXYD1	79.34	237.14	-1.568	2.63E-12
RP11-49K24.6	3.59	1.135	1.104	3.04E-08
SMUG1P1	0	1.055	-1.039	1.88E-58
POLR2J2	5.5	2.205	1.02	1.64E-14
NDUFA7	96.837	42.579	1.167	9.36E-70
RP3-461F17.3	7.65	1.78	1.638	3.70E-34
ZSCAN16-AS1	8.45	3.54	1.058	4.19E-41
PTOV1-AS2	2.39	6.895	-1.22	4.51E-08
RP11-394O4.5	0.48	2.335	-1.172	1.21E-17
RP5-940J5.9	20.359	2.015	2.825	1.22E-06
RP11-34P13.16	0.85	2.82	-1.046	5.09E-08
RP1-232P20.1	0.06	1.595	-1.292	1.26E-34
NBPF8	2.65	12.719	-1.91	1.69E-33
HIST2H4A	8.54	3.165	1.196	6.77E-22
RP11-238F2.1	0.14	2.04	-1.415	1.53E-04
SRXN1	30.141	10.395	1.45	1.06E-28

RP11-1259L22.2	0.32	2.325	-1.333	1.81E-26
SNX29P2	0.59	3.925	-1.631	4.19E-40
RP11-42O15.3	4.66	11.395	-1.131	6.70E-13
HIST2H2AA4	29.59	9.48	1.545	1.62E-12
RP11-284F21.10	1.99	0.06	1.496	3.11E-29
RP11-713M15.2	10.17	3.25	1.394	3.38E-32
STAG3L5P-PVRIG2P-PILRB	14.78	42.15	-1.451	4.67E-08
LL22NC03-N14H11.1	1.96	0.29	1.198	1.07E-26
RP3-508I15.20	0	1.745	-1.457	4.80E-18
RP11-458F8.4	1.31	3.715	-1.029	1.74E-12
RP4-583P15.15	2.09	7.12	-1.394	1.02E-32
RP11-756A22.7	2.13	0	1.646	2.60E-20
TAF9	33.171	15.97	1.01	1.93E-35
Metazoa_SRP	343.769	129.247	1.404	1.20E-14
uc_338	0	1.365	-1.242	4.08E-27
RP4-568C11.4	1.02	3.25	-1.073	3.07E-10
RP4-564F22.6	0.54	5.865	-2.156	5.41E-43
RP13-516M14.10	0.38	1.96	-1.101	1.50E-25
PRSS2	0.03	1.25	-1.127	1.60E-22
HULC	127.221	34.625	1.848	6.45E-12
UHRF1	1.79	0.115	1.323	6.25E-35
HERC2P2	4.35	13.429	-1.431	8.98E-06
MARCKS	15.05	5.1	1.396	5.08E-28
TRAC	7.94	2.665	1.286	3.38E-12
PSMB3	225.627	100.068	1.165	7.70E-57
SRD5A2	1.17	6.605	-1.809	1.59E-20
RP11-452N17.1	37.569	5.96	2.47	9.36E-52
IGLV2-8	0.55	2.785	-1.288	3.27E-06
RP11-132A1.6	1.1	6.998	-1.929	2.20E-45

RP11-609D21.3	1.08	3.6	-1.145	9.69E-08
RP11-369J21.12	1.73	0.33	1.038	8.97E-05
RP11-258F1.2	0.23	1.655	-1.11	9.13E-37
RP11-715H19.2	0	1.02	-1.014	1.02E-18
RPL41	2353.512	831.227	1.5	7.63E-52
RP11-394B2.1	0.23	1.495	-1.02	2.61E-32
RP11-43N16.4	0.69	3.215	-1.318	1.67E-22
RP11-286N22.16	0.06	1.165	-1.03	5.25E-29
RP11-361L15.3	20.53	65.36	-1.624	1.61E-03
LINC01348	1.2	8.645	-2.132	5.14E-42
U91328.1	1.96	0	1.566	1.88E-03
RP11-817J15.3	0.04	1.375	-1.191	3.70E-21
WASH5P	5.2	12.53	-1.126	3.52E-05
LINC01002	3.89	14.567	-1.671	1.84E-11

HCC: Hepatocellular carcinoma.