Table S1. Signature genes

Name	Pvalue	logFC
AKR1B10	1.20E-05	4.81652036
MELK	0.000107427	2.17585373
ALDH3A1	0.00012336	1.33689212
MRAP2	0.000315078	1.48284567
PBK	0.000315078	2.16406466
GPC3	0.000369633	6.3568736
ISX	0.000408408	1.82938645
SLC7A11	0.000449106	1.82403631
TOP2A	0.000491725	2.69006218
FAM133A	0.000536263	1.11430925
KRT23	0.000606666	1.46834723
PEG10	0.000655997	2.77983435
GINS1	0.000760399	2.11815671
RACGAP1	0.000843718	2.3551255
PRC1	0.000872446	2.6182372
PITX1	0.00098477	1.17234783
HMMR	0.000992125	2.09374041
DLGAP5	0.000992125	1.77579121
NUF2	0.001023236	1.61330397
ANLN	0.001086886	1.94727453
NDC80	0.001152438	1.87978076
TTK	0.001219892	1.92741771
DTL	0.001289245	2.40790098
SULT1C2	0.001324634	2.29633446
ASPM	0.001360497	2.44801708
NQO1	0.00147093	3.09619283
COL15A1	0.001508689	2.23287033
RAP2A	0.001664455	1.18776818
HOXA10	0.00181809	1.05070495
SPINK1	0.002113222	4.87529958
LOC344887	0.002131769	1.08462864
SFN	0.002177079	2.22783069
KIF20A	0.002177079	2.19948109
AP1M2	0.002221492	1.28655243
PAGE4	0.002262118	1.46433101
KIF14	0.002315831	1.66585498
TSPAN8	0.002383232	1.14930774
UCHL1	0.002560728	1.72606951
FOXM1	0.00265602	1.99690727
ZWINT	0.00265602	2.40995412
GJA1	0.002917393	1.05477031
PRAME	0.002990753	1.13908221
BUB1B	0.003019166	2.02801192
PTTG1	0.003019166	2.74248254

SPP1	0.00318181	2.67840262
CAP2	0.003577637	2.05963377
MLLT11	0.003625596	1.15858006
TM4SF20	0.003777978	1.14612076
KIF4A	0.003874333	1.78142005
E2F8	0.003935066	1.44548528
CCNB2	0.004225957	2.28598014
SERPINE2	0.004475109	1.00851652
CENPF	0.004633722	1.54111944
REG3A	0.004803503	2.40145991
PRKAA2	0.004969792	1.06899394
LPL	0.00524695	1.3250612
CTHRC1	0.005897471	1.64312002
FGF13	0.006079314	1.46513016
RRM2	0.006198527	2.5339969
DKK1	0.006338202	1.97545053
HJURP	0.006338202	1.64384509
CCL20	0.006351804	2.67356803
NUSAP1	0.006429129	2.29152171
ACSL4	0.006506911	3.06088509
THBS4	0.006585151	1.65633629
CD109	0.006902678	1.33084641
GNG4	0.007346219	1.25876463
KIF15	0.007392655	1.25583455
E2F1	0.007583622	1.25636
MAP2	0.007716956	1.0647586
CEP55	0.007728413	1.45302355
CDK1	0.007899019	1.88402068
RAD51AP1	0.008158334	1.48156331
SMPX	0.00825941	1.09369066
LYPD1	0.008421731	1.26478403
SCGN	0.008505541	1.2409677
CCNA2	0.008689205	1.65570049
MAGEA12	0.008998818	1.62465754
ROBO1	0.00905217	2.75567607
CDKN3	0.009516038	2.30917058
UBE2C	0.00979977	2.28266676
FAM83D	0.009991176	1.49422177
ACACB	4.16E-05	-1.1127065
CLEC1B	4.93E-21	-4.5512457
VIPR1	5.99E-20	-2.8625484
FCN2	7.66E-19	-3.8746362
FCN3	9.51E-18	-4.8676078
CRHBP	1.49E-17	-3.9378051
ECM1	3.39E-17	-2.8418381
CLEC4M	8.77E-17	-3.1102605

CXCL14	1.41E-16	-3.5496167
DNASE1L3	3.70E-16	-3.5546821
MARCO	1.18E-15	-3.3659149
LCAT	2.07E-15	-2.1325359
GSTZ1	2.12E-15	-2.7374617
CLEC4G	2.75E-15	-2.9759173
APOF	3.50E-15	-3.8508131
TTC36	1.99E-14	-2.7092199
MT1F	4.29E-14	-4.6962524
NAT2	5.98E-14	-3.5913023
ACSM3	7.04E-14	-2.3281112
CFP	8.46E-14	-2.0426384
DBH	1.18E-13	-1.8198491
MT1X	1.21E-13	-4.5719731
STAB2	2.26E-13	-2.1042714
HAMP	3.02E-13	-6.3463563
LPA	4.43E-13	-2.7844426
OIT3	5.02E-13	-2.7269987
RDH16	5.05E-13	-3.5539957
ETFDH	1.26E-12	-1.9381399
SLC22A1	1.53E-12	-5.3300538
GYS2	1.75E-12	-3.3371203
MT1M	1.82E-12	-3.8516904
SLCO1B3	1.93E-12	-4.2717361
GCH1	2.22E-12	-2.1705258
CYP4A11	2.80E-12	-3.7953607
PBLD	2.97E-12	-2.1123802
IGFALS	3.10E-12	-2.6701795
CYP1A2	3.16E-12	-5.1317239
CETP	4.60E-12	-2.1283161
CPEB3	4.66E-12	-1.5952725
KLKB1	5.19E-12	-2.9494089
C9	5.64E-12	-4.5767069
F9	8.09E-12	-3.4433096
F11	8.64E-12	-2.6112713
PTH1R	8.81E-12	-1.9053592
C1RL	1.00E-11	-1.9433075
KBTBD11	1.05E-11	-2.0947582
NTF3	1.17E-11	-1.2945429
ASPA	2.26E-11	-2.1243444
EHD3	2.44E-11	-1.278375
HAO2	2.44E-11	-4.0328931
CYP2C8	2.59E-11	-3.3369435
ALDH8A1	2.66E-11	-2.6549763
CNDP1	2.68E-11	-3.5870817
ADRA1A	2.76E-11	-1.8622282

ACADS	3.07E-11	-1.2743707
COLEC10	3.25E-11	-1.8781191
FTCD	4.52E-11	-2.330476
C8A	5.61E-11	-3.2664216
STARD5	6.49E-11	-1.5209863
EGR1	7.75E-11	-3.5496919
CYP3A4	7.85E-11	-3.287012
GHR	7.87E-11	-2.7703362
MT1E	8.18E-11	-2.5151351
NGFR	1.02E-10	-1.4150838
MT1G	1.08E-10	-4.3373611
ESR1	1.11E-10	-1.3542346
ASS1	1.21E-10	-3.0357742
HGFAC	1.29E-10	-2.7881931
CYP2C9	1.63E-10	-2.4634006
SLC27A5	1.97E-10	-2.6494902
SORL1	2.05E-10	-1.8149001
ACADSB	2.26E-10	-1.8341283
GPD1	2.36E-10	-1.8175309
STEAP3	2.39E-10	-1.8284821
DCN	2.45E-10	-3.7027701
ADH6	2.51E-10	-2.2098024
GCDH	2.73E-10	-1.6883381
MTHFD1	2.78E-10	-1.9133417
MT2A	3.51E-10	-2.0810649
BCKDHB	3.96E-10	-1.3035277
TBXA2R	4.52E-10	-1.2073918
PDE2A	5.08E-10	-1.2503198
PROZ	5.42E-10	-2.2132835
SRPX	5.53E-10	-2.4066541
SLC4A4	5.72E-10	-1.4811441
GLYAT	6.09E-10	-2.9584388
PLAC8	6.31E-10	-2.3418135
HAAO	6.49E-10	-1.6128724
KMO	6.62E-10	-2.4951541
ID1	6.97E-10	-2.7191735
GCKR	7.46E-10	-1.7029752
CYP2B6	7.91E-10	-2.1776971
ANGPTL6	9.55E-10	-1.4640669
NDRG2	1.03E-09	-1.6878446
SKAP1	1.06E-09	-1.6904152
SLC10A1	1.09E-09	-3.2413654
ANXA10	1.16E-09	-2.6943748
GBA3	1.20E-09	-3.1293891
CXCL12	1.24E-09	-3.1877838
C1R	1.31E-09	-2.2637313

SLC35D1	1.36E-09	-1.1020779
GRAMD1C	1.48E-09	-1.9277351
RCL1	1.55E-09	-1.7989869
MAT1A	1.60E-09	-2.2497902
IVD	1.68E-09	-1.2532095
DCXR	1.83E-09	-2.1907139
DEPDC7	1.97E-09	-1.486951
FBP1	2.03E-09	-3.7486365
CD5L	2.06E-09	-2.8457106
ACSL1	2.09E-09	-2.1073727
HMGCL	2.34E-09	-1.119586
TDO2	2.46E-09	-2.881971
GNAO1	2.58E-09	-1.2600446
HGF	2.85E-09	-1.1419021
C8orf4	2.93E-09	-2.3437948
FYN	3.08E-09	-1.1896135
GNMT	3.62E-09	-3.4189183
PLSCR4	3.64E-09	-1.6395623
MPPED1	3.68E-09	-1.2180081
CXCL2	4.13E-09	-2.8670264
C6	4.18E-09	-3.193273
ZGPAT	4.18E-09	-1.8658265
CBR4	4.33E-09	-1.349716
ST3GAL6	4.41E-09	-1.6856118
AZGP1	4.51E-09	-2.6016253
NPY1R	4.52E-09	-1.9719778
SIGIRR	5.05E-09	-1.6040459
SRD5A2	5.17E-09	-2.1830969
GPM6A	5.86E-09	-1.5359787
EPHX2	6.51E-09	-2.2330617
SLC39A14	6.53E-09	-1.5077865
FOS	7.49E-09	-3.5825315
MT1H	7.54E-09	-2.7599557
NR1I2	7.62E-09	-1.7164043
BCO2	7.76E-09	-2.0728427
RCAN1	8.58E-09	-1.9276328
PRODH2	9.46E-09	-1.2985866
LYVE1	1.09E-08	-2.3616957
FAM134B	1.10E-08	-1.9292617
GNE	1.13E-08	-1.6960454
BMP5	1.30E-08	-1.0156141
AKR7A3	1.32E-08	-2.018007
ABCA8	1.34E-08	-1.9894174
CDC37L1	1.41E-08	-1.6514134
ACAA1	1.63E-08	-1.9631123
NAT1	1.75E-08	-1.3063045

MBL2	1.88E-08	-3.2950142
MASP1	1.96E-08	-1.1974506
ALDH2	2.09E-08	-1.2744569
CCBE1	2.15E-08	-1.2718249
EHHADH	2.56E-08	-1.6061288
MYOM2	2.65E-08	-1.4382596
MS4A6A	2.75E-08	-1.5283079
CD14	2.80E-08	-2.5966194
RHOB	2.80E-08	-1.5984537
CBFA2T3	2.90E-08	-1.0370873
IL1RAP	2.99E-08	-1.6950139
C1QTNF1	3.03E-08	-1.1353933
PCK1	3.21E-08	-3.2054814
ABAT	3.36E-08	-1.7374948
CYP2E1	3.44E-08	-4.5407316
EPB41L4B	3.45E-08	-1.1524938
SERPINF2	3.67E-08	-1.4969746
F8	3.84E-08	-1.2867453
IGF1	3.90E-08	-2.3507508
GRHPR	4.01E-08	-1.8113787
ECM2	4.14E-08	-1.3686747
RGN	4.24E-08	-1.7874237
CAT	4.31E-08	-1.5849977
OGDHL	4.32E-08	-1.9625111
AADAT	4.93E-08	-1.7576975
TMEM27	4.93E-08	-1.9688861
ACADL	4.94E-08	-1.9229193
MFSD2A	5.15E-08	-2.1976482
SPP2	5.33E-08	-3.3261448
PGM1	5.43E-08	-1.2158072
MASP2	5.51E-08	-1.6768941
C7	5.60E-08	-3.0091114
CD81	5.65E-08	-1.7063184
CYP2J2	5.65E-08	-1.6558509
KCNN2	5.75E-08	-2.686765
GPT	5.82E-08	-1.2745784
LIFR	6.00E-08	-1.6890516
ADH1B	6.21E-08	-2.5908598
BHMT	6.33E-08	-2.7567339
EDNRB	6.38E-08	-1.4649455
LHX2	6.40E-08	-1.2054954
ZFP36	6.49E-08	-2.0156627
AKR1D1	7.11E-08	-2.6665149
SLC17A2	7.23E-08	-1.7027201
XDH	7.82E-08	-1.7994657
FXYD1	7.87E-08	-2.2037549

SERPING1	8.02E-08	-1.7668557
DMD	9.45E-08	-1.0779863
ALDH6A1	9.90E-08	-1.5252914
IGFBP4	1.00E-07	-1.31535
PPAP2B	1.02E-07	-1.2178804
PEMT	1.09E-07	-1.6494415
AGL	1.15E-07	-1.2373592
PZP	1.19E-07	-2.3975001
MAN1C1	1.20E-07	-1.7361114
ADH1A	1.21E-07	-2.8695854
ACSM5	1.25E-07	-2.2152508
AFM	1.34E-07	-3.3454946
CYP39A1	1.36E-07	-2.2363366
SOCS2	1.40E-07	-1.9821345
C8B	1.42E-07	-2.5549706
LILRB5	1.44E-07	-1.1444426
CSAD	1.50E-07	-1.449243
TAT	1.52E-07	-3.120481
ADK	1.59E-07	-1.2329269
PON1	1.60E-07	-2.041208
CYP2C19	1.68E-07	-2.3233504
CHST4	1.73E-07	-1.3963063
ADAMTS13	1.76E-07	-1.3619455
TIMD4	1.78E-07	-1.3112105
GLS2	1.79E-07	-2.9407494
FAM65C	1.83E-07	-1.3621195
AR	1.95E-07	-1.7241458
SERPINA10	2.18E-07	-1.7388207
ANK3	2.21E-07	-1.0104334
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ACADM	2.39E-07	-1.1096075
DMGDH	2.43E-07	-1.6200659
AOX1	2.45E-07	-2.3324666
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GADD45G	2.52E-07	-1.5457619
CIDEB	2.60E-07	-1.4918566
SULT2A1	2.60E-07	-1.8370149
CYP4F2	2.66E-07	-2.1024806
SRD5A1	3.00E-07	-1.4809544
GPHN	3.02E-07	-1.080587
GADD45B	3.06E-07	-1.6279738
SLC6A12	3.09E-07	-1.6481543
DHRS1	3.19E-07	-1.6580649
APOA5	3.44E-07	-2.5645286
JUNB	3.49E-07	-1.2601859
PROC	3.49E-07	-1.139252

ACSL5	3.53E-07	-1.7993098
CYP2A7	3.56E-07	-2.2388899
CD4	3.72E-07	-1.1481491
FAM13A	3.81E-07	-1.5853135
CYP4F12	3.84E-07	-1.2216784
GPR182	3.96E-07	-1.4252061
RND3	4.22E-07	-2.3616756
ART4	4.37E-07	-1.2381551
DPT	4.62E-07	-2.0516098
PFKFB1	4.71E-07	-1.358037
GABARAPL1	5.04E-07	-1.5485624
PCK2	6.23E-07	-1.6178088
PAIP2B	6.26E-07	-1.2965425
KCND3	6.31E-07	-1.25193
ASPG	6.41E-07	-1.3057251
TPPP2	6.56E-07	-1.5294052
SLC25A47	6.86E-07	-2.2533929
PAMR1	6.97E-07	-1.2541654
ANGPTL1	7.11E-07	-1.0206683
DIRAS3	7.44E-07	-1.5122121
PLG	7.48E-07	-2.169892
SLC16A4	7.50E-07	-1.3080871
MSRA	7.71E-07	-1.1569271
SARDH	7.88E-07	-1.0617295
DUSP1	8.22E-07	-1.7762406
CYP2A13	8.84E-07	-1.6598643
LPAL2	9.02E-07	-1.017573
PPL	9.17E-07	-1.0727072
SCP2	9.33E-07	-1.1448559
TEK	9.79E-07	-1.0270728
MUT	1.02E-06	-1.1768603
CFI	1.05E-06	-1.6708026
DNAJC12	1.07E-06	-1.9077822
SERPINA4	1.07E-06	-1.6328837
BMPER	1.07E-06	-1.1750819
HRSP12	1.09E-06	-2.0883137
AQP3	1.13E-06	-1.3083148
SATB1	1.13E-06	-1.1286896
LDHD	1.16E-06	-1.1261787
BDH2	1.16E-06	-1.3297575
HHIP	1.26E-06	-1.3889573
NAAA	1.32E-06	-1.0199392
CYP2A6	1.34E-06	-2.5876751
RNF125	1.39E-06	-1.4651626
SLC28A1	1.48E-06	-1.5051442

CD1D	1.55E-06	-1.3278868
RBMS3	1.73E-06	-1.0368112
FCGR2B	1.78E-06	-1.5116862
AXL	1.87E-06	-1.0035269
ADH4	1.93E-06	-2.3620852
PXMP2	1.96E-06	-1.4116987
ALDOB	1.97E-06	-2.4929363
IDO2	2.00E-06	-2.083019
LECT2	2.01E-06	-3.1272799
PROS1	2.18E-06	-1.3452258
HPX	2.25E-06	-2.4296398
TIAM1	2.30E-06	-1.0892579
TGFBR3	2.36E-06	-1.0452917
OLFML3	2.36E-06	-1.6479978
PHYHD1	2.42E-06	-1.059328
IGFBP3	2.45E-06	-1.4163389
CP	2.60E-06	-1.7248123
HSD11B1	2.60E-06	-3.112447
SLC6A13	2.62E-06	-1.4312822
RDH5	2.65E-06	-1.1596392
KLHL2	2.69E-06	-1.1162846
ECHDC2	2.97E-06	-1.718431
BBOX1	3.06E-06	-2.456457
KCNK5	3.08E-06	-1.0548866
CLRN3	3.12E-06	-2.0462028
N4BP2L1	3.13E-06	-1.1323547
UROC1	3.19E-06	-1.3391814
ALAS1	3.21E-06	-1.3752293
NNMT	3.27E-06	-3.5136746
MOGAT2	3.27E-06	-1.5941718
FOLH1B	3.29E-06	-1.4800711
CTH	3.44E-06	-2.2553799
MRO	3.54E-06	-1.0618411
IL13RA2	3.60E-06	-1.6916207
FGA	3.88E-06	-1.5522685
CYP26A1	3.89E-06	-2.8631295
ADRB2	3.89E-06	-1.1276546
PON3	4.08E-06	-1.5524345
COLEC11	4.27E-06	-2.0903251
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NR1I3	4.56E-06	-1.5849316
FMO4	4.73E-06	-1.0819284
ASGR1	4.74E-06	-1.1880659
FOSB	4.98E-06	-2.2566663
ACADVL	5.00E-06	-1.2958758
SHBG	5.03E-06	-1.5071435

SLC38A4	5.31E-06	-1.9254105
OAT	5.33E-06	-2.1693477
ENO3	5.67E-06	-1.7925274
TUBE1	5.68E-06	-1.1683715
AGXT2	6.03E-06	-1.5534525
KHK	6.06E-06	-1.0255014
HPD	6.25E-06	-3.5060439
LY6E	6.34E-06	-1.6335249
CYP3A43	6.42E-06	-1.8652677
FMO3	6.50E-06	-2.0626914
ZG16	6.67E-06	-1.8749319
EXPH5	7.04E-06	-1.562592
ABCA6	7.65E-06	-1.4386179
P2RY13	7.67E-06	-1.1015402
ETS2	8.17E-06	-1.4549824
RBP5	8.25E-06	-1.5140043
DHODH	8.35E-06	-1.2245607
HBB	8.62E-06	-1.7149994
AGXT	9.28E-06	-1.9915725
CPN2	9.37E-06	-1.464027
CDH19	9.65E-06	-1.1414375
CYP8B1	9.87E-06	-2.5830588
CYB5A	1.03E-05	-1.0943156
C1S	1.05E-05	-1.6409663
LIPC	1.07E-05	-1.7601706
RSPO3	1.08E-05	-1.4598102
GPR128	1.09E-05	-1.237051
CTSO	1.09E-05	-1.335739
PIPOX	1.11E-05	-1.5390281
HAO1	1.12E-05	-2.0473897
SLC1A2	1.17E-05	-1.7939198
CYP2C18	1.18E-05	-1.848742
SEC14L2	1.21E-05	-1.4172308
FABP1	1.36E-05	-2.6030113
CAPN3	1.37E-05	-1.306311
SDPR	1.42E-05	-1.0013868
PRELP	1.45E-05	-1.1033983
ENPEP	1.51E-05	-1.0226632
KDM8	1.55E-05	-1.0227209
PDGFRA	1.55E-05	-1.3522976
SLCO1B1	1.67E-05	-2.0560127
ACAT1	1.71E-05	-1.1596309
PDK4	1.75E-05	-2.0277851
AASS	1.80E-05	-1.2677546
VSIG4	1.81E-05	-1.2847912
NTN4	1.83E-05	-1.0130808

SLC46A3	1.83E-05	-1.4857492
ASPDH	1.84E-05	-1.17733
ANGPTL3	1.87E-05	-1.6075464
SLC23A2	1.93E-05	-1.0008442
PPP1R1A	1.95E-05	-1.8483011
FETUB	2.00E-05	-2.023818
IL33	2.11E-05	-1.1234478
FERMT2	2.26E-05	-1.0088037
GADD45A	2.27E-05	-1.4641191
DAK	2.29E-05	-1.2411767
PANK1	2.33E-05	-1.3990975
CPN1	2.51E-05	-1.3116844
BCHE	2.65E-05	-2.0969587
HAND2	2.72E-05	-1.1307216
THRSP	3.10E-05	-2.1712677
FITM1	3.16E-05	-1.0834288
ADAMTSL2	3.28E-05	-1.1548567
CSRNP1	3.35E-05	-1.1421555
MPDZ	3.48E-05	-1.1509399
ACOX1	3.53E-05	-1.0152658
GLYATL1	3.62E-05	-1.6966682
SPTBN2	3.69E-05	-1.0399816
SLC17A3	3.80E-05	-1.0938556
ALPL	3.90E-05	-1.2802054
ANG	3.98E-05	-1.2373869
MGMT	4.12E-05	-1.0827213
ACOX2	4.31E-05	-1.2821118
CRYL1	4.36E-05	-1.114567
IRF8	4.64E-05	-1.1745495
FAH	4.84E-05	-1.2472107
MST1	4.92E-05	-1.0355509
ASGR2	4.96E-05	-1.3142555
APOC3	5.05E-05	-1.5465055
HMGCS2	5.37E-05	-1.6687435
CPT2	5.62E-05	-1.2464245
PRG4	5.69E-05	-1.1686338
AKR1C4	5.90E-05	-1.3125765
STEAP4	5.91E-05	-1.8021625
GOT2	6.01E-05	-1.0108088
ATOH8	6.04E-05	-1.0135364
GCGR	6.35E-05	-1.282817
BASP1	6.35E-05	-1.4305113
SAA4	6.48E-05	-2.3879469
FOLH1	6.53E-05	-1.0995657
CDHR2	6.72E-05	-1.7205634

CFHR4	6.77E-05	-2.1247856
AQP9	6.90E-05	-2.0016797
FAM149A	6.91E-05	-1.0659132
CD163	7.02E-05	-1.3588536
HSD17B6	7.02E-05	-2.0551356
TFR2	7.23E-05	-1.0582243
CBS	7.30E-05	-1.1218411
TSLP	7.65E-05	-1.1018582
FMO2	7.75E-05	-1.0422269
HP	7.87E-05	-1.1901597
ID2	8.21E-05	-1.5315926
CPS1	8.51E-05	-2.179981
SLC25A15	8.56E-05	-1.3820126
TM6SF2	8.70E-05	-1.1198199
FGB	9.27E-05	-1.4359463
MTTP	9.55E-05	-1.5119986
TFPI2	9.63E-05	-1.2230743
GPR125	9.78E-05	-1.1907802
SLC2A2	0.000101969	-1.3352046
C14orf180	0.000103563	-1.1449344
DPYS	0.000109575	-1.7073471
B3GAT1	0.000111003	-1.4937961
TMEM45A	0.000114721	-1.7305069
ADAMTS1	0.000116819	-1.2742087
HGD	0.000118264	-1.3693647
CLDN10	0.000122468	-1.1282272
APOA1	0.000123467	-2.0804865
HYAL1	0.000125267	-1.1251024
ARG1	0.000134112	-1.7396969
MXRA5	0.000145033	-1.2555809
CYP3A5	0.000145615	-1.166449
IFITM1	0.000147722	-1.3210762
FLJ22763	0.000152168	-1.0679601
SLCO2B1	0.000154221	-1.0318135
CA2	0.000155491	-2.2364687
CNGA1	0.00015806	-1.2275804
SLC7A2	0.000158282	-1.5504051
SLC1A1	0.000162037	-1.2989023
LINC01093	0.000164564	-1.2541159
QDPR	0.000171934	-1.0976519
CPB2	0.000174972	-1.2313178
ALB	0.000176961	-1.9201755
UPB1	0.000179226	-1.1428969
UGP2	0.000181881	-1.0390077
ABLIM3	0.000185965	-1.1648345
F12	0.000200223	-1.0071147

CDO1	0.000203719	-1.6763752
TRIM22	0.000203733	-1.2539243
SLC41A2	0.000211506	-1.2146323
HSD17B13	0.000221191	-2.3973133
GGT5	0.000221391	-1.1083722
HPR	0.000225829	-1.8008449
SLC27A2	0.000226942	-1.9737506
HSD17B2	0.000229041	-1.9572696
KCNJ8	0.00022925	-1.1674682
ABCG2	0.000233535	-1.1069897
ANO1	0.000234914	-1.2749304
ABCB4	0.000249352	-1.3510246
CDA	0.000264217	-1.0995867
DAO	0.000277798	-1.0363294
C4BPA	0.000280794	-1.5882554
TRIB1	0.000285336	-1.4093616
MFAP4	0.000297745	-1.2495703
CYP4V2	0.000298926	-1.1734598
HLF	0.000310915	-1.2313167
DUSP6	0.00032786	-1.050273
TPD52L1	0.000344125	-1.0221213
LEAP2	0.000368087	-1.4878807
HABP2	0.000374814	-1.2404175
ANGPTL4	0.000403571	-1.2940748
CTNNA3	0.000403577	-1.1543238
CD302	0.000405575	-1.0950159
ITLN1	0.000432122	-1.2378965
PALM3	0.000436375	-1.0726101
ADI1	0.000496713	-1.0648463
GLUD1	0.000503756	-1.093838
ADH1C	0.000510485	-1.2977988
LIPG	0.00051268	-1.1832198
PLIN1	0.000517586	-1.4305943
BGN	0.000530973	-1.0116124
CYP1A1	0.000536918	-1.6921774
OTC	0.000549114	-1.5379012
HOGA1	0.000557047	-1.1001015
PHGDH	0.000559799	-1.3876934
MOGAT1	0.000582719	-1.1156595
MFAP3L	0.000600771	-1.0150857
PSD3	0.000608824	-1.0017099
AADAC	0.00063187	-1.2934903
HAPLN4	0.000684126	-1.0141286
F2	0.000713905	-1.0746115
MT1HL1	0.000725717	-1.4676789
CYFIP2	0.0007352	-1.0576865

MME	0.000835829	-1.6447288
APOL1	0.000852927	-1.2010065
BDH1	0.00090988	-1.0485763
SLC22A7	0.000916685	-1.4958922
SDS	0.000929495	-2.5191715
ITIH1	0.000931685	-1.4477904
TTR	0.00093332	-1.4693121
SERPINA6	0.000980769	-1.0707458
FBLN5	0.001022876	-1.5423406
ERRFI1	0.001034065	-1.3451668
FREM2	0.001041551	-1.423358
RUNDC3B	0.001045787	-1.0784301
UGT2B7	0.001057836	-1.2165081
CES2	0.001078837	-1.3456564
GREM2	0.001080093	-1.5223523
C3P1	0.001087367	-1.9017435
GATM	0.001123091	-1.0128941
IGJ	0.001134094	-1.3557586
IYD	0.001260193	-1.1341978
ACMSD	0.001307629	-1.2130487
CCL21	0.001318174	-1.5507558
CNTN3	0.001324634	-1.1623865
ACOT12	0.001348643	-1.6220739
RNF165	0.001374245	-1.0723724
SLC39A5	0.001436058	-1.0479264
CHRNA4	0.001446628	-1.2816826
GPT2	0.001574891	-1.1803055
CUX2	0.001591344	-1.3141399
NR0B2	0.001640437	-1.0075627
AVPR1A	0.00177515	-1.2005762
DNMT3L	0.002001866	-1.1071631
SULT1E1	0.002032046	-1.3114032
PGLYRP2	0.002162559	-1.5232488
SLC13A5	0.002207227	-1.6020997
A1BG	0.002362581	-1.2642676
AGTR1	0.002449375	-1.7289914
BRP44L	0.002573973	-1.0586355
CYP4A22	0.002712234	-1.2000426
CFHR3	0.002758841	-1.4809904
CYR61	0.00291378	-1.4900366
A2M	0.002983048	-1.2490105
HRG	0.003298499	-2.2012928
CDH1	0.003435977	-1.0003448
CRISPLD2	0.003648226	-1.414394
GC	0.003686733	-1.0200428
RBP1	0.00446451	-1.2188022

GOT1	0.004872067	-1.1259044
AMDHD1	0.004885052	-1.2998797
FAM180A	0.005242057	-1.2806427
SERPINA7	0.005614088	-1.3074828
RNASE4	0.005796071	-1.0041055
SERPINC1	0.005844526	-1.3015281
CCL19	0.006030173	-1.0013918
ACSM2A	0.006417234	-1.1804805
CYP2B7P1	0.006822611	-1.0708784
PPARGC1A	0.007029251	-1.5357462
APOC4	0.007991636	-1.4533096
INMT	0.008071442	-1.4220324
C5orf27	0.008346364	-1.1966093
APCS	0.008416451	-1.7950957
MT1L	0.008599594	-1.2960215
DUSP5	0.008960751	-1.1094205
GK	0.009375324	-1.036319
PHLDA1	0.009418217	-1.148951
CD69	0.009895248	-1.0157878

Table S2. KEGG analysis of the most significant genes

Down genes					
ID	Description	GeneRatio	pvalue	geneID	Count
hsa00071	Fatty acid degradation	32/514	1.09E-22	ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/CPT2/CPT2/CYP4A11/EHHADH/ALDH2/ACSL1/ACSL1/GCDH/GCDH/CYP4A22/ACAA1/ACAA1/ACADL/ACADM/ACADM/ACADS/ACADS/ACADSB/ACADSB/ACADVL/ACAT1/ACAT1/ACOX1/ACSL5	32

hsa04610	Complement and coagulation cascades	37/514	1.81E-21	MASP2/VSIG4/CPB2/A2M/F2/F8/F9/F11/F12/F12/FGA/FGB/FGB/CFI/CFI/KLKB1/KLKB1/MBL2/SERPINC1/SERPINC1/PLG/SERPINF2/PROC/PROS1/PROS1/MASP1/SERPING1/SERPING1/C1R/C1S/C4BPA/C6/C7/C7/C8A/C8B/C9	37
hsa03320	PPAR signaling pathway	36/514	1.02E-18	SLC27A5/SLC27A2/APOA5/APOA5/CPT2/CPT2/CYP8B1/EHHADH/FABP1/FABP1/FABP1/ACSL1/ACSL1/GK/GK/ACAA1/ACAA1/HMGCS2/HMGCS2/ACADL/APOA1/APOA1/ACADM/ACADM/APOC3/APOC3/ACOX1/PCK1/PCK2/ANGPTL4/ACSL5/PLIN1/SCP2/SCP2/SCP2/ACOX2	36

hsa00830	Retinol metabolism	31/514	1.92E-18	ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/CYP1A1/CYP1A1/CYP1A2/CYP2A6/CYP2B6/CYP2C8/CYP2C9/CYP2C9/CYP2C18/CYP2C18/CYP3A4/CYP3A4/CYP3A5/CYP4A11/CYP26A1/AOX1/RDH5/RDH5/UGT2B7/RDH16/RDH16/HSD17B6/HSD17B6	31
hsa00280	Valine, leucine and isoleucine degradation	28/514	1.50E-17	ABAT/ABAT/EHHADH/ALDH2/ACAA1/ACAA1/HMGCL/HMGCS2/HMGCS2/AOX1/ACADM/ACADM/ACADS/ACADS/ACADSB/ACADSB/IVD/IVD/ACAT1/ACAT1/ALDH6A1/ALDH6A1/MUT/MUT/MUT/BCKDHB/BCKDHB/AGXT2	28
hsa00260	Glycine, serine and threonine metabolism	25/514	5.59E-16	SDS/SDS/CTH/DAO/DAO/SARDH/SARDH/AGXT/ALAS1/ALAS1/PHGDH/GATM/GATM/GNMT/GNMT/DMGDH/DMGDH/PIPOX/BHMT/BHMT/AGXT2/CBS/CBS/CBS/GRHPR	25

hsa05204	Chemical carcinogenesis	32/514	8.59E-15	NAT2/NAT2/ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/CYP1A1/CYP1A1/CYP1A2/CYP2A6/CYP2A13/CYP2C19/CYP2C8/CYP2C9/CYP2C9/CYP2C18/CYP2C18/CYP2E1/CYP3A4/CYP3A4/CYP3A5/HSD11B1/HSD11B1/CYP3A43/SULT2A1/SULT2A1/UGT2B7/NAT1	32
hsa00380	Tryptophan metabolism	21/514	1.59E-13	INMT/ACMSD/CYP1A1/CYP1A1/CYP1A2/IDO2/EHHADH/ALDH2/HAAO/GCDH/GCDH/AOX1/ACAT1/ACAT1/AADAT/AADAT/OGDHL/TDO2/CAT/KMO/KMO	21

hsa01200	Carbon metabolism	38/514	1.87E-13	SDS/SDS/CPS1/CPS1/CPS1/AGXT/EHHADH/ENO3/FBP1/ALDOB/ALDOB/PHGDH/GLUD1/GLUD1/GOT1/GOT1/GOT2/GPT/ACADM/ACADM/ACADS/ACADS/ACAT1/ACAT1/ALDH6A1/ALDH6A1/MUT/MUT/MUT/HAO2/HAO1/HAO1/OGDHL/CAT/GPT2/GPT2/RGN/RGN	38
hsa00250	Alanine, aspartate and glutamate metabolism	21/514	3.59E-13	CPS1/CPS1/CPS1/ABAT/ABAT/AGXT/FOLH1/GLS2/GLUD1/GLUD1/GOT1/GOT1/GOT2/GPT/ASPA/ASPA/ASS1/ASS1/AGXT2/GPT2/GPT2	21
hsa00350	Tyrosine metabolism	20/514	1.20E-12	ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/DBH/FAH/GOT1/GOT1/GOT2/GSTZ1/GSTZ1/HGD/AOX1/HPD/TAT/TAT	20
hsa00220	Arginine biosynthesis	16/514	3.37E-12	CPS1/CPS1/CPS1/GLS2/GLUD1/GLUD1/GOT1/GOT1/GOT2/GPT/ARG1/ASS1/ASS1/OTC/GPT2/GPT2	16

hsa00982	Drug metabolism - cytochrome P450	27/514	7.83E-12	ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/CYP1A2/CYP2A6/CYP2B6/CYP2C19/CYP2C8/CYP2C9/CYP2C9/CYP2E1/CYP3A4/CYP3A4/CYP3A5/FMO2/FMO2/FMO3/FMO3/FMO3/FMO4/AOX1/UGT2B7	27
hsa01230	Biosynthesis of amino acids	28/514	9.42E-12	SDS/SDS/CPS1/CPS1/CPS1/CTH/ENO3/ALDOB/ALDOB/PHGDH/GOT1/GOT1/GOT2/GPT/ARG1/MAT1A/ASS1/ASS1/OTC/AADAT/AADAT/TAT/TAT/GPT2/GPT2/CBS/CBS/CBS	28
hsa00980	Metabolism of xenobiotics by cytochrome P450	26/514	9.10E-11	ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/CYP1A1/CYP1A1/CYP1A2/CYP2A6/CYP2A13/CYP2B6/CYP2C9/CYP2C9/CYP2E1/CYP3A4/CYP3A4/CYP3A5/AKR7A3/HSD11B1/HSD11B1/SULT2A1/SULT2A1/UGT2B7	26

hsa00650	Butanoate metabolism	16/514	1.50E-10	ACSM2A/ABAT/ABAT/EHHADH/HMGCL/HMGCS2/HMGCS2/ACADS/ACADS/ACAT1/ACAT1/ACSM5/BDH2/BDH2/BDH1/ACSM3	16
hsa04976	Bile secretion	24/514	1.88E-09	SLCO1B1/SLCO1B1/SLCO1B1/SLC22A7/SLC27A5/CYP3A4/CYP3A4/SLCO1B3/SLCO1B3/AQP9/KCNN2/ABCB4/SLC10A1/SLC10A1/SLC22A1/SULT2A1/SULT2A1/CA2/CA2/NR0B2/SLC4A4/SLC4A4/ABCG2/ABCG2	24
hsa04146	Peroxisome	24/514	3.31E-09	SLC27A2/DAO/DAO/AGXT/EHHADH/EPHX2/ACSL1/ACSL1/ACAA1/ACAA1/HMGCL/ACOX1/HAO2/PIPOX/ACSL5/HAO1/HAO1/PXMP2/SCP2/SCP2/SCP2/XDH/ACOX2/CAT	24

hsa01212	Fatty acid metabolism	19/514	1.00E-08	CPT2/CPT2/EHHADH/ACSL1/ACSL1/ACAA1/ACAA1/ACADL/ACADM/ACADM/ACADS/ACADS/ACADSB/ACADSB/ACADVL/ACAT1/ACAT1/ACOX1/ACSL5	19
hsa00640	Propanoate metabolism	15/514	3.12E-08	ABAT/ABAT/EHHADH/ACACB/ACADM/ACADM/ACAT1/ACAT1/ALDH6A1/ALDH6A1/MUT/MUT/MUT/BCKDHB/BCKDHB	15
hsa00140	Steroid hormone biosynthesis	19/514	3.69E-08	AKR1C4/CYP1A1/CYP1A1/CYP1A2/CYP2E1/CYP3A4/CYP3A4/CYP3A5/HSD11B1/HSD11B1/HSD17B2/SRD5A1/SRD5A2/AKR1D1/SULT1E1/SULT1E1/UGT2B7/HSD17B6/HSD17B6	19
hsa00270	Cysteine and methionine metabolism	17/514	6.34E-08	CDO1/SDS/SDS/CTH/GOT1/GOT1/GOT2/MAT1A/ADI1/BHMT/BHMT/AGXT2/TAT/TAT/CBS/CBS/CBS	17

hsa00410	beta-Alanine metabolism	13/514	3.42E-07	ABAT/ABAT/DPYS/EHHADH/ALDH2/ACADM/ACADM/ALDH6A1/ALDH6A1/UPB1/UPB1/UPB1/CNDP1	13
hsa00072	Synthesis and degradation of ketone bodies	8/514	4.30E-07	HMGCL/HMGCS2/HMGCS2/ACAT1/ACAT1/BDH2/BDH2/BDH1	8
hsa00120	Primary bile acid biosynthesis	9/514	6.68E-07	SLC27A5/AKR1C4/CYP8B1/CYP39A1/SCP2/SCP2/SCP2/AKR1D1/ACOX2	9
hsa00630	Glyoxylate and dicarboxylate metabolism	12/514	1.48E-06	HOGA1/AGXT/ACAT1/ACAT1/MUT/MUT/MUT/HAO2/HAO1/HAO1/CAT/GRHPR	12
hsa00983	Drug metabolism - other enzymes	14/514	9.09E-06	NAT2/NAT2/CYP2A6/CYP3A4/CYP3A4/DPYS/UPB1/UPB1/UPB1/UGT2B7/XDH/CES2/NAT1/CDA	14
hsa00330	Arginine and proline metabolism	14/514	1.80E-05	HOGA1/DAO/DAO/ALDH2/GATM/GATM/GOT1/GOT1/GOT2/ARG1/OAT/OAT/PRODH2/CNDP1	14
hsa04964	Proximal tubule bicarbonate reclamation	9/514	3.11E-05	GLS2/GLUD1/GLUD1/PCK1/PCK2/CA2/CA2/SLC4A4/SLC4A4	9

hsa01210	2-Oxocarboxylic acid metabolism	8/514	4.48E-05	GOT1/GOT1/GOT2/GPT/AADAT/AADAT/GPT2/GPT2	8
hsa00591	Linoleic acid metabolism	9/514	5.19E-05	CYP1A2/CYP2C19/CYP2C8/CYP2C9/CYP2C9/CYP2E1/CYP2J2/CYP3A4/CYP3A4	9
hsa00010	Glycolysis / Gluconeogenesis	16/514	7.98E-05	ADH1A/ADH1B/ADH1B/ADH1C/ADH4/ADH4/ADH6/ADH6/ENO3/ALDH2/FBP1/ALDOB/ALDOB/PCK1/PCK2/PGM1	16
hsa00310	Lysine degradation	13/514	8.03E-05	AASS/AASS/EHHADH/ALDH2/GCDH/GCDH/ACAT1/ACAT1/AADAT/AADAT/PIPOX/OGDHL/BBOX1	13
hsa00790	Folate biosynthesis	7/514	0.000151737	GPHN/ALPL/ALPL/GCH1/GCH1/QDPR/QDPR	7
hsa00590	Arachidonic acid metabolism	13/514	0.000184867	CYP2B6/CYP2C19/CYP2C8/CYP2C9/CYP2C9/CYP2E1/CYP2J2/CYP4A11/EPHX2/GGT5/CYP4F3/CYP4F3/CYP4F2	13
hsa00340	Histidine metabolism	8/514	0.000212748	FTCD/UROC1/AMDHD1/AMDHD1/ALDH2/ASPA/ASPA/CNDP1	8
hsa00360	Phenylalanine metabolism	7/514	0.000433483	GLYAT/GOT1/GOT1/GOT2/HPD/TAT/TAT	7

hsa00910	Nitrogen metabolism	7/514	0.000546282	CPS1/CPS1/CPS1/GLUD1/GLUD1/CA2/CA2	7
hsa04978	Mineral absorption	11/514	0.001221249	MT1E/MT1F/MT1G/MT1H/MT1H/MT1M/MT1M/MT1X/MT1X/MT2A/MT1HL1	11
hsa05020	Prion diseases	9/514	0.002715674	EGR1/EGR1/FYN/C6/C7/C7/C8A/C8B/C9	9
hsa00430	Taurine and hypotaurine metabolism	5/514	0.002937681	CDO1/GGT5/CSAD/CSAD/CSAD	5
hsa00620	Pyruvate metabolism	9/514	0.00306143	ACOT12/LDHD/ALDH2/ACACB/ACAT1/ACAT1/PCK1/PCK2/GRHPR	9
hsa00770	Pantothenate and CoA biosynthesis	5/514	0.003694284	DPYS/UPB1/UPB1/UPB1/PANK1	5
hsa00500	Starch and sucrose metabolism	7/514	0.007775888	AGL/AGL/GYS2/PGM1/GBA3/GBA3/UGP2	7
hsa04975	Fat digestion and absorption	8/514	0.008538551	FABP1/FABP1/FABP1/GOT2/APOA1/APOA1/MTTP/MOGAT2	8
Up genes					
ID	Description	GeneRatio	pvalue	geneID	Count
hsa04110	Cell cycle	10/47	1.45E-08	E2F1/E2F1/SFN/BUB1B/TTK/CCNA2/CCNB2/PTTG1/PTTG1/CDK1	10
hsa04218	Cellular senescence	7/47	0.000248877	E2F1/E2F1/FOXM1/FOXM1/CCNA2/CCNB2/CDK1	7
hsa04115	p53 signaling pathway	4/47	0.001042149	SFN/RRM2/CCNB2/CDK1	4
hsa05218	Melanoma	4/47	0.001306003	E2F1/E2F1/FGF13/FGF13	4

hsa04512	ECM-receptor interaction	4/47	0.00252059	HMMR/SPP1/SPP1 /THBS4	4

Table S3. GO analysis of the most significant genes

GO_CC_up_sig_gene				
ID	Description	GeneRatio	pvalue	Count
GO:0005819	spindle	14/80	3.07E-11	14
GO:0030496	midbody	10/80	3.77E-10	10
GO:0005874	microtubule	11/80	1.34E-06	11
GO:0000777	condensed chromosome kinetochore	6/80	5.55E-06	6
GO:0000779	condensed chromosome, centromeric region	6/80	9.13E-06	6
GO:0000940	condensed chromosome outer kinetochore	3/80	1.82E-05	3
GO:0000776	kinetochore	6/80	2.39E-05	6
GO:0000793	condensed chromosome	7/80	3.28E-05	7
GO:0005876	spindle microtubule	4/80	9.78E-05	4
GO:0072686	mitotic spindle	4/80	0.000105141	4
GO:0005871	kinesin complex	4/80	0.000112847	4
GO:0000775	chromosome, centromeric	6/80	0.000171779	6
GO:0051233	spindle midzone	3/80	0.00023113	3
GO:0000922	spindle pole	5/80	0.000239828	5
GO:0005875	microtubule associated complex	5/80	0.000475339	5
GO:0098687	chromosomal region	7/80	0.000815289	7
GO:0000778	condensed nuclear chromosome kinetochore	2/80	0.000863253	2
GO:0070938	contractile ring	2/80	0.000863253	2
GO:0097431	mitotic spindle pole	2/80	0.000863253	2
GO:0005813	centrosome	8/80	0.001382832	8
GO:0045120	pronucleus	2/80	0.0017256	2
GO:0032153	cell division site	3/80	0.001797573	3
GO:0032155	cell division site part	3/80	0.001797573	3
GO:0000780	condensed nuclear chromosome, centromeric region	2/80	0.003196098	2
GO:0005680	anaphase-promoting complex	2/80	0.004280318	2
GO:0031225	anchored component of	4/80	0.005095593	4
GO_BP_up_sig_gene				
ID	Description	GeneRatio	pvalue	Count
GO:0007067	mitotic nuclear division	22/78	2.37E-17	22
GO:0007059	chromosome segregation	17/78	8.38E-14	17
GO:0098813	nuclear chromosome	16/78	1.07E-13	16
GO:0044770	cell cycle phase transition	19/78	4.67E-13	19
GO:0000819	sister chromatid segregation	14/78	1.00E-12	14
GO:0000070	mitotic sister chromatid	12/78	1.02E-12	12

GO:0044772	mitotic cell cycle phase	18/78	1.98E-12	18
GO:0007093	mitotic cell cycle checkpoint	10/78	2.04E-09	10
GO:1901987	regulation of cell cycle phase transition	13/78	2.24E-09	13
GO:0007346	regulation of mitotic cell cycle	15/78	3.35E-09	15
GO:0000075	cell cycle checkpoint	11/78	6.18E-09	11
GO:0000281	mitotic cytokinesis	6/78	8.64E-09	6
GO:1901990	regulation of mitotic cell cycle phase transition	12/78	1.11E-08	12
GO:0090068	positive regulation of cell cycle process	11/78	1.12E-08	11
GO:0000910	cytokinesis	9/78	1.30E-08	9
GO:0045786	negative regulation of cell cycle	14/78	1.73E-08	14
GO:0051304	chromosome separation	7/78	2.59E-08	7
GO:0061640	cytoskeleton-dependent	6/78	3.40E-08	6
GO:0045930	negative regulation of mitotic cell cycle	10/78	4.84E-08	10
GO:0030071	regulation of mitotic metaphase/anaphase transition	6/78	5.28E-08	6
GO:1902099	regulation of metaphase/anaphase transition	6/78	6.08E-08	6
GO:0007091	metaphase/anaphase transition of mitotic cell cycle	6/78	6.96E-08	6
GO:0010965	regulation of mitotic sister chromatid separation	6/78	6.96E-08	6
GO:0051983	regulation of chromosome segregation	7/78	7.55E-08	7
GO:0044784	metaphase/anaphase transition of cell cycle	6/78	7.95E-08	6
GO:0051306	mitotic sister chromatid	6/78	9.05E-08	6
GO:0033047	regulation of mitotic sister chromatid segregation	6/78	1.66E-07	6
GO:0007088	regulation of mitotic nuclear division	8/78	1.95E-07	8
GO:0045787	positive regulation of cell cycle	11/78	2.32E-07	11
GO:1901991	negative regulation of mitotic cell cycle phase transition	8/78	3.78E-07	8
GO:0033045	regulation of sister chromatid segregation	6/78	3.90E-07	6
GO:0051783	regulation of nuclear division	8/78	6.61E-07	8
GO:1901988	negative regulation of cell cycle phase transition	8/78	6.61E-07	8
GO:0010948	negative regulation of cell cycle process	9/78	8.21E-07	9
GO:0000086	G2/M transition of mitotic cell	8/78	2.39E-06	8

GO:0000226	microtubule cytoskeleton organization	11/78	2.87E-06	11
GO:0007052	mitotic spindle organization	5/78	2.88E-06	5
GO:0044839	cell cycle G2/M phase transition	8/78	3.40E-06	8
GO:0007094	mitotic spindle assembly	4/78	8.33E-06	4
GO:0071173	spindle assembly checkpoint	4/78	9.63E-06	4
GO:0045841	negative regulation of mitotic metaphase/anaphase transition	4/78	1.11E-05	4
GO:0071174	mitotic spindle checkpoint	4/78	1.11E-05	4
GO:2000816	negative regulation of mitotic sister chromatid separation	4/78	1.11E-05	4
GO:0051231	spindle elongation	3/78	1.15E-05	3
GO:0051303	establishment of chromosome localization	5/78	1.21E-05	5
GO:1902100	negative regulation of metaphase/anaphase transition of cell cycle	4/78	1.27E-05	4
GO:0050000	chromosome localization	5/78	1.31E-05	5
GO:0033048	negative regulation of mitotic sister chromatid segregation	4/78	1.44E-05	4
GO:1903035	negative regulation of response to wounding	5/78	1.63E-05	5
GO:0033046	negative regulation of sister chromatid segregation	4/78	1.85E-05	4
GO:0051985	negative regulation of chromosome segregation	4/78	2.08E-05	4
GO:0031577	spindle checkpoint	4/78	2.33E-05	4
GO:0033044	regulation of chromosome organization	6/78	3.54E-05	6
GO:0051302	regulation of cell division	6/78	3.54E-05	6
GO:0045839	negative regulation of mitotic nuclear division	4/78	3.94E-05	4
GO:1903034	regulation of response to	6/78	5.54E-05	6
GO:0051310	metaphase plate congression	4/78	6.79E-05	4
GO:0007018	microtubule-based movement	7/78	8.46E-05	7
GO:0031570	DNA integrity checkpoint	6/78	9.98E-05	6
GO:0010389	regulation of G2/M transition of mitotic cell cycle	4/78	0.000101204	4
GO:0007051	spindle organization	5/78	0.000104779	5
GO:0051784	negative regulation of nuclear division	4/78	0.000109079	4
GO:0044774	mitotic DNA integrity	5/78	0.000115078	5
GO:0044843	cell cycle G1/S phase transition	7/78	0.000120314	7
GO:2001251	negative regulation of chromosome organization	4/78	0.000165975	4

GO:0061045	negative regulation of wound healing	4/78	0.000177202	4
GO:1902749	regulation of cell cycle G2/M phase transition	4/78	0.000177202	4
GO:0032102	negative regulation of response to external stimulus	7/78	0.000198296	7
GO:0050680	negative regulation of epithelial cell proliferation	5/78	0.000202261	5
GO:0045931	positive regulation of mitotic cell cycle	5/78	0.00022808	5
GO:0000083	regulation of transcription involved in G1/S transition of mitotic cell cycle	3/78	0.000265754	3
GO:0042176	regulation of protein catabolic process	8/78	0.000274903	8
GO:0007062	sister chromatid cohesion	5/78	0.000287176	5
GO:0061041	regulation of wound healing	5/78	0.000287176	5
GO:0030326	embryonic limb morphogenesis	5/78	0.000309249	5
GO:0035113	embryonic appendage morphogenesis	5/78	0.000309249	5
GO:0061351	neural precursor cell	5/78	0.000320757	5
GO:0010837	regulation of keratinocyte proliferation	3/78	0.000329761	3
GO:0050678	regulation of epithelial cell proliferation	7/78	0.000341203	7
GO:0051640	organelle localization	9/78	0.000343962	9
GO:0009894	regulation of catabolic process	9/78	0.00048637	9
GO:0031145	anaphase-promoting complex-dependent catabolic process	4/78	0.000486401	4
GO:0045861	negative regulation of	7/78	0.000515122	7
GO:0030261	chromosome condensation	3/78	0.000531031	3
GO:1902806	regulation of cell cycle G1/S phase transition	5/78	0.000535375	5
GO:0035107	appendage morphogenesis	5/78	0.000607488	5
GO:0035108	limb morphogenesis	5/78	0.000607488	5
GO:0051656	establishment of organelle localization	8/78	0.000621045	8
GO:0031572	G2 DNA damage checkpoint	3/78	0.000629372	3
GO:0045926	negative regulation of growth	6/78	0.000661384	6
GO:0000077	DNA damage checkpoint	5/78	0.000666182	5
GO:0000082	G1/S transition of mitotic cell	6/78	0.000676843	6
GO:0043616	keratinocyte proliferation	3/78	0.000797501	3
GO:0051653	spindle localization	3/78	0.000797501	3
GO:0001523	retinoid metabolic process	4/78	0.000800879	4
GO:0007050	cell cycle arrest	6/78	0.000828944	6

GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class	4/78	0.000906869	4
GO:0010466	negative regulation of peptidase activity	6/78	0.000944167	6
GO:0051255	spindle midzone assembly	2/78	0.000949041	2
GO:0050673	epithelial cell proliferation	7/78	0.000984027	7
GO:0030308	negative regulation of cell	5/78	0.000997986	5
GO:0045840	positive regulation of mitotic nuclear division	3/78	0.001062553	3
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	4/78	0.00106308	4
GO:0016101	diterpenoid metabolic process	4/78	0.00106308	4
GO:0044773	mitotic DNA damage	4/78	0.00106308	4
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via	4/78	0.001104904	4
GO:0048736	appendage development	5/78	0.001142033	5
GO:0060173	limb development	5/78	0.001142033	5
GO:0030900	forebrain development	7/78	0.001225903	7
GO:0021987	cerebral cortex development	4/78	0.001237295	4
GO:0045604	regulation of epidermal cell differentiation	3/78	0.001377494	3
GO:0071156	regulation of cell cycle arrest	4/78	0.00138042	4
GO:0021681	cerebellar granular layer development	2/78	0.001383503	2
GO:0030330	DNA damage response, signal transduction by p53 class	4/78	0.001482022	4
GO:0006721	terpenoid metabolic process	4/78	0.001534729	4
GO:0010839	negative regulation of keratinocyte proliferation	2/78	0.001630096	2
GO:0032486	Rap protein signal transduction	2/78	0.001630096	2
GO:0034501	protein localization to	2/78	0.001630096	2
GO:0036445	neuronal stem cell division	2/78	0.001630096	2
GO:0055057	neuroblast division	2/78	0.001630096	2
GO:0043161	proteasome-mediated ubiquitin-dependent protein catabolic	7/78	0.001739321	7
GO:0016202	regulation of striated muscle tissue development	4/78	0.001817989	4
GO:0048634	regulation of muscle organ development	4/78	0.001940807	4
GO:0007405	neuroblast proliferation	3/78	0.001950464	3
GO:0051785	positive regulation of nuclear division	3/78	0.001950464	3

GO:0001933	negative regulation of protein phosphorylation	7/78	0.001962744	7
GO:1901861	regulation of muscle tissue development	4/78	0.002004321	4
GO:0001558	regulation of cell growth	7/78	0.002052049	7
GO:0052547	regulation of peptidase activity	7/78	0.002175997	7
GO:0007096	regulation of exit from mitosis	2/78	0.002181093	2
GO:0051782	negative regulation of cell	2/78	0.002181093	2
GO:0044708	single-organism behavior	7/78	0.002207872	7
GO:0006260	DNA replication	6/78	0.00224841	6
GO:0042770	signal transduction in response to DNA damage	4/78	0.002343594	4
GO:0007095	mitotic G2 DNA damage checkpoint	2/78	0.002485134	2
GO:0071459	protein localization to chromosome, centromeric	2/78	0.002485134	2
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	5/78	0.002619331	5
GO:1901989	positive regulation of cell cycle phase transition	3/78	0.002652896	3
GO:0010498	proteasomal protein catabolic process	7/78	0.002730853	7
GO:0006977	DNA damage response, signal transduction by p53 class mediator resulting in cell cycle	3/78	0.002783196	3
GO:0055024	regulation of cardiac muscle tissue development	3/78	0.002783196	3
GO:0000920	cell separation after cytokinesis	2/78	0.002807966	2
GO:0048670	regulation of collateral	2/78	0.002807966	2
GO:0072431	signal transduction involved in mitotic G1 DNA damage checkpoint	3/78	0.00291738	3
GO:1902400	intracellular signal transduction involved in G1 DNA damage checkpoint	3/78	0.00291738	3
GO:0006720	isoprenoid metabolic process	4/78	0.003050526	4
GO:0072413	signal transduction involved in mitotic cell cycle checkpoint	3/78	0.003055486	3
GO:1902402	signal transduction involved in mitotic DNA damage	3/78	0.003055486	3
GO:1902403	signal transduction involved in mitotic DNA integrity	3/78	0.003055486	3
GO:0008356	asymmetric cell division	2/78	0.003149409	2
GO:0042326	negative regulation of phosphorylation	7/78	0.003214064	7

GO:0072401	signal transduction involved in DNA integrity checkpoint	3/78	0.003343613	3
GO:0072422	signal transduction involved in DNA damage checkpoint	3/78	0.003343613	3
GO:2000045	regulation of G1/S transition of mitotic cell cycle	4/78	0.003406919	4
GO:0032465	regulation of cytokinesis	3/78	0.003493704	3
GO:0034103	regulation of tissue remodeling	3/78	0.003493704	3
GO:0045682	regulation of epidermis development	3/78	0.003493704	3
GO:0072395	signal transduction involved in cell cycle checkpoint	3/78	0.003493704	3
GO:0009896	positive regulation of catabolic process	6/78	0.003848206	6
GO:0055026	negative regulation of cardiac muscle tissue development	2/78	0.003887425	2
GO:0031571	mitotic G1 DNA damage checkpoint	3/78	0.004135062	3
GO:0044819	mitotic G1/S transition	3/78	0.004135062	3
GO:0048103	somatic stem cell division	2/78	0.004283648	2
GO:0033555	multicellular organismal response to stress	3/78	0.004305813	3
GO:0044783	G1 DNA damage checkpoint	3/78	0.004305813	3
GO:0048771	tissue remodeling	4/78	0.004419813	4
GO:0051436	negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3/78	0.004480792	3
GO:0010951	negative regulation of endopeptidase activity	5/78	0.004545082	5
GO:0051439	regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	3/78	0.00466003	3
GO:0044818	mitotic G2/M transition	2/78	0.004697783	2
GO:0048668	collateral sprouting	2/78	0.004697783	2
GO_MF_up_sig_gene				
ID	Description	GeneRatio	pvalue	Count
GO:0008017	microtubule binding	10/78	7.09E-08	10
GO:0015631	tubulin binding	11/78	1.17E-07	11
GO:0003777	microtubule motor activity	4/78	0.00050282	4
GO:0048487	beta-tubulin binding	3/78	0.00056597	3
GO_BP_down_sig_gene				
ID	Description	GeneRatio	pvalue	Count
GO:0016054	organic acid catabolic process	76/541	1.87E-57	76
GO:0044282	small molecule catabolic	87/541	2.78E-54	87
GO:0046395	carboxylic acid catabolic	65/541	4.04E-48	65

GO:1901565	organonitrogen compound catabolic process	73/541	2.05E-38	73
GO:1901605	alpha-amino acid metabolic	53/541	1.06E-34	53
GO:0044283	small molecule biosynthetic	76/541	2.10E-31	76
GO:0009063	cellular amino acid catabolic process	35/541	6.73E-31	35
GO:1901606	alpha-amino acid catabolic	33/541	3.02E-30	33
GO:0008202	steroid metabolic process	55/541	3.12E-28	55
GO:0016053	organic acid biosynthetic	54/541	9.81E-28	54
GO:0006631	fatty acid metabolic process	61/541	4.09E-27	61
GO:0006520	cellular amino acid metabolic process	54/541	4.85E-26	54
GO:0046394	carboxylic acid biosynthetic process	50/541	2.47E-25	50
GO:0072329	monocarboxylic acid catabolic process	32/541	1.31E-22	32
GO:0019373	epoxygenase P450 pathway	16/541	1.75E-22	16
GO:0072376	protein activation cascade	31/541	3.28E-21	31
GO:0016042	lipid catabolic process	46/541	2.68E-19	46
GO:0017144	drug metabolic process	18/541	7.96E-19	18
GO:0008652	cellular amino acid biosynthetic process	23/541	1.53E-18	23
GO:0051186	cofactor metabolic process	50/541	6.07E-18	50
GO:0044242	cellular lipid catabolic process	34/541	1.04E-16	34
GO:0010035	response to inorganic substance	54/541	1.17E-16	54
GO:0042493	response to drug	50/541	1.48E-16	50
GO:0006805	xenobiotic metabolic process	25/541	2.34E-16	25
GO:0019395	fatty acid oxidation	25/541	4.00E-16	25
GO:1901615	organic hydroxy compound metabolic process	50/541	5.06E-16	50
GO:0001676	long-chain fatty acid metabolic process	24/541	5.08E-16	24
GO:0034440	lipid oxidation	25/541	6.77E-16	25
GO:0071466	cellular response to xenobiotic stimulus	25/541	6.77E-16	25
GO:0006732	coenzyme metabolic process	42/541	9.20E-16	42
GO:0002526	acute inflammatory response	28/541	1.59E-15	28
GO:0043648	dicarboxylic acid metabolic	23/541	1.92E-15	23
GO:0009410	response to xenobiotic stimulus	25/541	4.86E-15	25
GO:0010038	response to metal ion	40/541	1.93E-14	40
GO:0006956	complement activation	22/541	2.18E-14	22
GO:0009064	glutamine family amino acid metabolic process	20/541	4.24E-14	20
GO:0009074	aromatic amino acid family catabolic process	11/541	4.61E-14	11
GO:0006635	fatty acid beta-oxidation	20/541	5.73E-14	20

GO:0009062	fatty acid catabolic process	22/541	6.15E-14	22
GO:0055088	lipid homeostasis	25/541	1.49E-13	25
GO:0030258	lipid modification	36/541	2.20E-13	36
GO:0006869	lipid transport	39/541	5.23E-13	39
GO:0030195	negative regulation of blood coagulation	16/541	7.20E-13	16
GO:1900047	negative regulation of	16/541	7.20E-13	16
GO:0010876	lipid localization	41/541	7.65E-13	41
GO:0009066	aspartate family amino acid metabolic process	17/541	8.33E-13	17
GO:0019369	arachidonic acid metabolic	16/541	1.05E-12	16
GO:0030193	regulation of blood coagulation	20/541	1.84E-12	20
GO:1900046	regulation of hemostasis	20/541	1.84E-12	20
GO:0050819	negative regulation of	16/541	2.15E-12	16
GO:0009072	aromatic amino acid family metabolic process	12/541	2.29E-12	12
GO:0042737	drug catabolic process	10/541	3.10E-12	10
GO:0015711	organic anion transport	38/541	3.49E-12	38
GO:0061045	negative regulation of wound healing	17/541	4.06E-12	17
GO:0050818	regulation of coagulation	20/541	4.67E-12	20
GO:0006066	alcohol metabolic process	35/541	9.46E-12	35
GO:0042730	fibrinolysis	12/541	1.35E-11	12
GO:0006790	sulfur compound metabolic	39/541	2.71E-11	39
GO:1903035	negative regulation of response to wounding	17/541	3.71E-11	17
GO:0006690	icosanoid metabolic process	20/541	3.85E-11	20
GO:0010043	response to zinc ion	15/541	5.69E-11	15
GO:0061041	regulation of wound healing	22/541	7.39E-11	22
GO:0033559	unsaturated fatty acid metabolic process	21/541	8.07E-11	21
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	10/541	8.47E-11	10
GO:0046942	carboxylic acid transport	32/541	1.03E-10	32
GO:2000257	regulation of protein activation cascade	12/541	1.51E-10	12
GO:0006953	acute-phase response	14/541	1.55E-10	14
GO:1901607	alpha-amino acid biosynthetic process	16/541	1.81E-10	16
GO:0072378	blood coagulation, fibrin clot formation	11/541	1.89E-10	11
GO:0034754	cellular hormone metabolic	20/541	2.05E-10	20
GO:0009991	response to extracellular	41/541	3.31E-10	41
GO:0051604	protein maturation	31/541	4.11E-10	31
GO:0042738	exogenous drug catabolic	8/541	5.16E-10	8
GO:0016485	protein processing	29/541	5.51E-10	29

GO:0044262	cellular carbohydrate metabolic process	30/541	6.14E-10	30
GO:1903317	regulation of protein maturation	17/541	7.17E-10	17
GO:0006641	triglyceride metabolic process	19/541	7.37E-10	19
GO:0072330	monocarboxylic acid biosynthetic process	25/541	8.67E-10	25
GO:0006820	anion transport	42/541	1.04E-09	42
GO:0006536	glutamate metabolic process	11/541	1.19E-09	11
GO:0015850	organic hydroxy compound transport	26/541	1.22E-09	26
GO:0006639	acylglycerol metabolic process	20/541	1.26E-09	20
GO:1903034	regulation of response to	22/541	1.26E-09	22
GO:0002576	platelet degranulation	19/541	1.44E-09	19
GO:0006638	neutral lipid metabolic process	20/541	1.46E-09	20
GO:0030449	regulation of complement	11/541	1.78E-09	11
GO:0006959	humoral immune response	26/541	1.90E-09	26
GO:0016125	sterol metabolic process	21/541	2.45E-09	21
GO:0007597	blood coagulation, intrinsic	9/541	2.58E-09	9
GO:0051917	regulation of fibrinolysis	8/541	2.95E-09	8
GO:1990267	response to transition metal nanoparticle	20/541	3.08E-09	20
GO:0009065	glutamine family amino acid catabolic process	10/541	3.96E-09	10
GO:0044723	single-organism carbohydrate metabolic process	40/541	4.08E-09	40
GO:1902652	secondary alcohol metabolic process	20/541	4.11E-09	20
GO:0042445	hormone metabolic process	24/541	4.34E-09	24
GO:0006090	pyruvate metabolic process	18/541	4.34E-09	18
GO:0009068	aspartate family amino acid catabolic process	9/541	4.56E-09	9
GO:0070613	regulation of protein processing	16/541	4.79E-09	16
GO:0015849	organic acid transport	21/541	4.81E-09	21
GO:0010817	regulation of hormone levels	41/541	4.93E-09	41
GO:0002673	regulation of acute inflammatory response	15/541	5.34E-09	15
GO:0006006	glucose metabolic process	25/541	5.79E-09	25
GO:0019216	regulation of lipid metabolic	30/541	6.03E-09	30
GO:0008206	bile acid metabolic process	12/541	7.40E-09	12
GO:0006721	terpenoid metabolic process	18/541	8.20E-09	18
GO:0009636	response to toxic substance	25/541	9.70E-09	25
GO:0008203	cholesterol metabolic process	19/541	1.21E-08	19
GO:0007596	blood coagulation	34/541	1.27E-08	34
GO:0050817	coagulation	34/541	1.68E-08	34
GO:0015718	monocarboxylic acid transport	20/541	1.80E-08	20
GO:0007599	hemostasis	34/541	1.80E-08	34

GO:0006694	steroid biosynthetic process	21/541	1.91E-08	21
GO:0042402	cellular biogenic amine catabolic process	9/541	2.03E-08	9
GO:0006568	tryptophan metabolic process	7/541	2.51E-08	7
GO:0006720	isoprenoid metabolic process	19/541	3.10E-08	19
GO:0009310	amine catabolic process	9/541	3.16E-08	9
GO:0042180	cellular ketone metabolic	25/541	3.43E-08	25
GO:0071248	cellular response to metal ion	19/541	3.53E-08	19
GO:0050878	regulation of body fluid levels	41/541	3.95E-08	41
GO:0002920	regulation of humoral immune response	12/541	4.76E-08	12
GO:0019318	hexose metabolic process	26/541	5.08E-08	26
GO:0055090	acylglycerol homeostasis	10/541	5.63E-08	10
GO:0070328	triglyceride homeostasis	10/541	5.63E-08	10
GO:0031667	response to nutrient levels	35/541	5.73E-08	35
GO:0008015	blood circulation	40/541	6.18E-08	40
GO:0002455	humoral immune response mediated by circulating immunoglobulin	14/541	6.43E-08	14
GO:0006958	complement activation, classical pathway	13/541	7.42E-08	13
GO:0003013	circulatory system process	40/541	7.72E-08	40
GO:0045834	positive regulation of lipid metabolic process	18/541	7.86E-08	18
GO:0009069	serine family amino acid metabolic process	11/541	8.51E-08	11
GO:0008217	regulation of blood pressure	21/541	9.15E-08	21
GO:0051384	response to glucocorticoid	19/541	9.47E-08	19
GO:0008209	androgen metabolic process	9/541	1.04E-07	9
GO:0005996	monosaccharide metabolic	26/541	1.39E-07	26
GO:0043650	dicarboxylic acid biosynthetic process	7/541	1.87E-07	7
GO:0031638	zymogen activation	10/541	1.88E-07	10
GO:0072524	pyridine-containing compound metabolic process	18/541	2.11E-07	18
GO:0006898	receptor-mediated endocytosis	28/541	2.11E-07	28
GO:0006569	tryptophan catabolic process	6/541	2.13E-07	6
GO:0042436	indole-containing compound catabolic process	6/541	2.13E-07	6
GO:0046218	indolalkylamine catabolic	6/541	2.13E-07	6
GO:0046950	cellular ketone body metabolic process	6/541	2.13E-07	6
GO:1902224	ketone body metabolic process	6/541	2.13E-07	6
GO:0006094	gluconeogenesis	14/541	2.17E-07	14
GO:0006576	cellular biogenic amine metabolic process	11/541	2.89E-07	11

GO:0046686	response to cadmium ion	10/541	3.24E-07	10
GO:0051591	response to cAMP	15/541	3.36E-07	15
GO:0019319	hexose biosynthetic process	14/541	3.51E-07	14
GO:0071241	cellular response to inorganic substance	19/541	3.63E-07	19
GO:0006558	L-phenylalanine metabolic	6/541	4.57E-07	6
GO:0006559	L-phenylalanine catabolic	6/541	4.57E-07	6
GO:0034370	triglyceride-rich lipoprotein particle remodeling	6/541	4.57E-07	6
GO:0034372	very-low-density lipoprotein particle remodeling	6/541	4.57E-07	6
GO:0019362	pyridine nucleotide metabolic process	17/541	4.71E-07	17
GO:0046496	nicotinamide nucleotide metabolic process	17/541	4.71E-07	17
GO:0032496	response to lipopolysaccharide	28/541	4.91E-07	28
GO:0031960	response to corticosteroid	19/541	4.97E-07	19
GO:0006555	methionine metabolic process	7/541	5.34E-07	7
GO:0006586	indolalkylamine metabolic	7/541	5.34E-07	7
GO:0043691	reverse cholesterol transport	7/541	5.34E-07	7
GO:0034367	macromolecular complex remodeling	8/541	5.43E-07	8
GO:0034368	protein-lipid complex	8/541	5.43E-07	8
GO:0034369	plasma lipoprotein particle remodeling	8/541	5.43E-07	8
GO:1901361	organic cyclic compound catabolic process	35/541	5.72E-07	35
GO:0046364	monosaccharide biosynthetic process	14/541	6.43E-07	14
GO:0042430	indole-containing compound metabolic process	8/541	7.75E-07	8
GO:0071294	cellular response to zinc ion	7/541	8.50E-07	7
GO:0006069	ethanol oxidation	6/541	8.88E-07	6
GO:0014074	response to purine-containing compound	18/541	8.93E-07	18
GO:0071827	plasma lipoprotein particle organization	9/541	9.48E-07	9
GO:0002237	response to molecule of bacterial origin	28/541	1.16E-06	28
GO:0006525	arginine metabolic process	7/541	1.31E-06	7
GO:0031639	plasminogen activation	7/541	1.31E-06	7
GO:0006637	acyl-CoA metabolic process	14/541	1.49E-06	14
GO:0035383	thioester metabolic process	14/541	1.49E-06	14
GO:0015721	bile acid and bile salt transport	8/541	1.50E-06	8
GO:0071825	protein-lipid complex subunit organization	9/541	1.61E-06	9

GO:0072593	reactive oxygen species metabolic process	23/541	1.66E-06	23
GO:0001101	response to acid chemical	25/541	1.75E-06	25
GO:0007584	response to nutrient	19/541	1.93E-06	19
GO:0042537	benzene-containing compound metabolic process	7/541	1.96E-06	7
GO:0006733	oxidoreduction coenzyme metabolic process	17/541	1.98E-06	17
GO:0000096	sulfur amino acid metabolic	8/541	2.04E-06	8
GO:0006699	bile acid biosynthetic process	8/541	2.04E-06	8
GO:0046487	glyoxylate metabolic process	8/541	2.04E-06	8
GO:0010675	regulation of cellular carbohydrate metabolic process	16/541	2.32E-06	16
GO:0009108	coenzyme biosynthetic process	17/541	2.42E-06	17
GO:0006067	ethanol metabolic process	6/541	2.73E-06	6
GO:0006957	complement activation, alternative pathway	6/541	2.73E-06	6
GO:0019627	urea metabolic process	6/541	2.73E-06	6
GO:0050667	homocysteine metabolic process	6/541	2.73E-06	6
GO:0010906	regulation of glucose metabolic process	14/541	3.24E-06	14
GO:0010466	negative regulation of peptidase activity	23/541	4.25E-06	23
GO:0051289	protein homotetramerization	11/541	4.30E-06	11
GO:0046683	response to organophosphorus	16/541	4.37E-06	16
GO:0034375	high-density lipoprotein particle remodeling	6/541	4.43E-06	6
GO:0071276	cellular response to cadmium	6/541	4.43E-06	6
GO:0051188	cofactor biosynthetic process	19/541	5.02E-06	19
GO:0006109	regulation of carbohydrate metabolic process	17/541	5.27E-06	17
GO:0045861	negative regulation of	26/541	5.95E-06	26
GO:1901616	organic hydroxy compound catabolic process	10/541	6.61E-06	10
GO:0010951	negative regulation of endopeptidase activity	22/541	6.63E-06	22
GO:0071941	nitrogen cycle metabolic	6/541	6.89E-06	6
GO:0060191	regulation of lipase activity	12/541	7.45E-06	12
GO:0051918	negative regulation of	5/541	7.78E-06	5
GO:0070189	kynurenine metabolic process	5/541	7.78E-06	5
GO:0044272	sulfur compound biosynthetic process	20/541	9.03E-06	20
GO:0006084	acetyl-CoA metabolic process	8/541	1.01E-05	8
GO:0042304	regulation of fatty acid biosynthetic process	8/541	1.01E-05	8
GO:0006071	glycerol metabolic process	6/541	1.04E-05	6

GO:0009070	serine family amino acid biosynthetic process	6/541	1.04E-05	6
GO:0030194	positive regulation of blood coagulation	7/541	1.05E-05	7
GO:1900048	positive regulation of	7/541	1.05E-05	7
GO:0003018	vascular process in circulatory system	17/541	1.18E-05	17
GO:0050727	regulation of inflammatory response	25/541	1.25E-05	25
GO:0016051	carbohydrate biosynthetic	19/541	1.30E-05	19
GO:0019748	secondary metabolic process	10/541	1.30E-05	10
GO:0016101	diterpenoid metabolic process	13/541	1.32E-05	13
GO:0017187	peptidyl-glutamic acid	5/541	1.39E-05	5
GO:0018214	protein carboxylation	5/541	1.39E-05	5
GO:0050820	positive regulation of	7/541	1.40E-05	7
GO:0046890	regulation of lipid biosynthetic process	15/541	1.43E-05	15
GO:0006103	2-oxoglutarate metabolic	6/541	1.51E-05	6
GO:0031100	animal organ regeneration	11/541	1.67E-05	11
GO:0016064	immunoglobulin mediated immune response	15/541	1.90E-05	15
GO:0030301	cholesterol transport	11/541	2.18E-05	11
GO:0019724	B cell mediated immunity	15/541	2.29E-05	15
GO:0000050	urea cycle	5/541	2.32E-05	5
GO:0006107	oxaloacetate metabolic process	5/541	2.32E-05	5
GO:0032371	regulation of sterol transport	8/541	2.42E-05	8
GO:0032374	regulation of cholesterol	8/541	2.42E-05	8
GO:0015918	sterol transport	11/541	2.49E-05	11
GO:0050880	regulation of blood vessel size	15/541	2.51E-05	15
GO:0035150	regulation of tube size	15/541	2.74E-05	15
GO:0001523	retinoid metabolic process	12/541	2.94E-05	12
GO:0009084	glutamine family amino acid biosynthetic process	6/541	2.98E-05	6
GO:0019400	alditol metabolic process	6/541	2.98E-05	6
GO:0000038	very long-chain fatty acid metabolic process	7/541	3.05E-05	7
GO:0045471	response to ethanol	14/541	3.15E-05	14
GO:0032102	negative regulation of response to external stimulus	22/541	3.52E-05	22
GO:0051346	negative regulation of hydrolase activity	29/541	3.73E-05	29
GO:0018200	peptidyl-glutamic acid	7/541	3.87E-05	7
GO:0019835	cytolysis	7/541	3.87E-05	7
GO:0050673	epithelial cell proliferation	26/541	4.06E-05	26
GO:0006706	steroid catabolic process	6/541	4.06E-05	6

GO:0009067	aspartate family amino acid biosynthetic process	6/541	4.06E-05	6
GO:0000302	response to reactive oxygen species	19/541	4.07E-05	19
GO:0032368	regulation of lipid transport	12/541	4.12E-05	12
GO:0019217	regulation of fatty acid metabolic process	11/541	4.12E-05	11
GO:0001889	liver development	14/541	4.16E-05	14
GO:0009308	amine metabolic process	14/541	4.99E-05	14
GO:0009081	branched-chain amino acid metabolic process	6/541	5.44E-05	6
GO:0061008	hepaticobiliary system	14/541	5.46E-05	14
GO:0006096	glycolytic process	10/541	5.60E-05	10
GO:0052548	regulation of endopeptidase	27/541	5.75E-05	27
GO:0038066	p38MAPK cascade	7/541	6.05E-05	7
GO:0006757	ATP generation from ADP	10/541	6.38E-05	10
GO:0019439	aromatic compound catabolic process	29/541	6.39E-05	29
GO:0052547	regulation of peptidase activity	28/541	6.52E-05	28
GO:0007568	aging	22/541	6.62E-05	22
GO:1901654	response to ketone	16/541	7.12E-05	16
GO:0042632	cholesterol homeostasis	10/541	7.24E-05	10
GO:0055092	sterol homeostasis	10/541	7.24E-05	10
GO:0097006	regulation of plasma lipoprotein particle levels	9/541	7.26E-05	9
GO:0034308	primary alcohol metabolic	8/541	7.38E-05	8
GO:0046460	neutral lipid biosynthetic	8/541	7.38E-05	8
GO:0046463	acylglycerol biosynthetic	8/541	7.38E-05	8
GO:0019433	triglyceride catabolic process	7/541	7.47E-05	7
GO:0048545	response to steroid hormone	27/541	7.59E-05	27
GO:0051004	regulation of lipoprotein lipase activity	5/541	8.10E-05	5
GO:0070989	oxidative demethylation	5/541	8.10E-05	5
GO:0003073	regulation of systemic arterial blood pressure	11/541	8.26E-05	11
GO:0033273	response to vitamin	11/541	8.26E-05	11
GO:0051259	protein oligomerization	31/541	8.33E-05	31
GO:0006766	vitamin metabolic process	14/541	9.13E-05	14
GO:0045055	regulated exocytosis	22/541	9.17E-05	22
GO:0019674	NAD metabolic process	9/541	9.63E-05	9
GO:0006165	nucleoside diphosphate phosphorylation	11/541	0.00010265	11
GO:0006979	response to oxidative stress	27/541	0.000103938	27
GO:0051260	protein homooligomerization	21/541	0.000108698	21
GO:0042594	response to starvation	15/541	0.000110811	15
GO:0001659	temperature homeostasis	7/541	0.00011116	7

GO:1900745	positive regulation of p38MAPK cascade	5/541	0.00011462	5
GO:0015893	drug transport	6/541	0.000118775	6
GO:0090303	positive regulation of wound	8/541	0.00012023	8
GO:0097305	response to alcohol	15/541	0.000128644	15
GO:0033762	response to glucagon	8/541	0.000140229	8
GO:0044724	single-organism carbohydrate catabolic process	14/541	0.0001479	14
GO:0019218	regulation of steroid metabolic process	10/541	0.000148393	10
GO:1903825	organic acid transmembrane transport	10/541	0.000148393	10
GO:0050996	positive regulation of lipid catabolic process	6/541	0.000150204	6
GO:1900744	regulation of p38MAPK	6/541	0.000150204	6
GO:0006577	amino-acid betaine metabolic process	5/541	0.000158063	5
GO:0009112	nucleobase metabolic process	7/541	0.000160897	7
GO:0060193	positive regulation of lipase	9/541	0.000163558	9
GO:0046031	ADP metabolic process	10/541	0.000166001	10
GO:0097164	ammonium ion metabolic	11/541	0.000171642	11
GO:0002250	adaptive immune response	26/541	0.000187886	26
GO:0046939	nucleotide phosphorylation	11/541	0.000189355	11
GO:0006544	glycine metabolic process	5/541	0.000213044	5
GO:0046461	neutral lipid catabolic process	7/541	0.000227258	7
GO:0046464	acylglycerol catabolic process	7/541	0.000227258	7
GO:0031099	regeneration	15/541	0.000227299	15
GO:0046320	regulation of fatty acid	6/541	0.000232603	6
GO:0050994	regulation of lipid catabolic	8/541	0.000249608	8
GO:0098754	detoxification	11/541	0.000252064	11
GO:0044273	sulfur compound catabolic	7/541	0.000267851	7
GO:0006206	pyrimidine nucleobase metabolic process	5/541	0.00028146	5
GO:0006855	drug transmembrane transport	5/541	0.00028146	5
GO:0009083	branched-chain amino acid catabolic process	5/541	0.00028146	5
GO:1903036	positive regulation of response to wounding	8/541	0.000285755	8
GO:0016052	carbohydrate catabolic process	14/541	0.000288697	14
GO:0071222	cellular response to lipopolysaccharide	14/541	0.000288697	14
GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	19/541	0.000292045	19

GO:0015740	C4-dicarboxylate transport	4/541	0.000301687	4
GO:1900746	regulation of vascular endothelial growth factor	4/541	0.000301687	4
GO:1901568	fatty acid derivative metabolic process	4/541	0.000301687	4
GO:0055076	transition metal ion homeostasis	12/541	0.000303288	12
GO:1903510	mucopolysaccharide metabolic process	12/541	0.000303288	12
GO:1901652	response to peptide	28/541	0.000326825	28
GO:0045923	positive regulation of fatty acid metabolic process	6/541	0.000346959	6
GO:0044106	cellular amine metabolic	12/541	0.000356964	12
GO:0034377	plasma lipoprotein particle assembly	5/541	0.00036533	5
GO:1903319	positive regulation of protein maturation	5/541	0.00036533	5
GO:0006775	fat-soluble vitamin metabolic process	7/541	0.000366481	7
GO:0019432	triglyceride biosynthetic process	7/541	0.000366481	7
GO:0045907	positive regulation of vasoconstriction	6/541	0.000418554	6
GO:0071548	response to dexamethasone	6/541	0.000418554	6
GO:0090207	regulation of triglyceride metabolic process	6/541	0.000418554	6
GO:0015908	fatty acid transport	10/541	0.000419535	10
GO:0071219	cellular response to molecule of bacterial origin	14/541	0.000436384	14
GO:0006554	lysine catabolic process	4/541	0.000440954	4
GO:0007494	midgut development	4/541	0.000440954	4
GO:0009086	methionine biosynthetic process	4/541	0.000440954	4
GO:0010896	regulation of triglyceride catabolic process	4/541	0.000440954	4
GO:0043649	dicarboxylic acid catabolic	4/541	0.000440954	4
GO:1902547	regulation of cellular response to vascular endothelial growth factor stimulus	4/541	0.000440954	4
GO:0043434	response to peptide hormone	26/541	0.000442166	26
GO:0051262	protein tetramerization	13/541	0.000452085	13
GO:0008207	C21-steroid hormone metabolic process	6/541	0.000501174	6
GO:0090218	positive regulation of lipid kinase activity	6/541	0.000501174	6
GO:1905039	carboxylic acid transmembrane transport	9/541	0.000515188	9
GO:0065005	protein-lipid complex assembly	5/541	0.000588097	5

GO:0042558	pteridine-containing compound metabolic process	6/541	0.000595945	6
GO:0006633	fatty acid biosynthetic process	13/541	0.000598144	13
GO:0010517	regulation of phospholipase	8/541	0.000603109	8
GO:0098869	cellular oxidant detoxification	10/541	0.000607456	10
GO:0006531	aspartate metabolic process	4/541	0.000620659	4
GO:0006553	lysine metabolic process	4/541	0.000620659	4
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	4/541	0.000620659	4
GO:0036109	alpha-linolenic acid metabolic process	4/541	0.000620659	4
GO:0043568	positive regulation of insulin-like growth factor receptor signaling pathway	4/541	0.000620659	4
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	7/541	0.000650146	7
GO:0009135	purine nucleoside diphosphate metabolic process	10/541	0.00072475	10
GO:0009179	purine ribonucleoside diphosphate metabolic process	10/541	0.00072475	10
GO:1990748	cellular detoxification	10/541	0.00072475	10
GO:0007586	digestion	14/541	0.000729862	14
GO:0043567	regulation of insulin-like growth factor receptor signaling	5/541	0.000731583	5
GO:0048771	tissue remodeling	13/541	0.000732226	13
GO:0044057	regulation of system process	30/541	0.000733735	30
GO:0043410	positive regulation of MAPK cascade	29/541	0.000768495	29
GO:0005977	glycogen metabolic process	9/541	0.000769147	9
GO:0030168	platelet activation	14/541	0.000776198	14
GO:0048732	gland development	26/541	0.000804008	26
GO:0071320	cellular response to cAMP	7/541	0.000845773	7
GO:0006073	cellular glucan metabolic	9/541	0.000846416	9
GO:0044042	glucan metabolic process	9/541	0.000846416	9
GO:0009820	alkaloid metabolic process	4/541	0.000846744	4
GO:0034433	steroid esterification	4/541	0.000846744	4
GO:0034434	sterol esterification	4/541	0.000846744	4
GO:0034435	cholesterol esterification	4/541	0.000846744	4
GO:0045723	positive regulation of fatty acid biosynthetic process	4/541	0.000846744	4
GO:0009185	ribonucleoside diphosphate metabolic process	10/541	0.000860096	10
GO:0043200	response to amino acid	10/541	0.000860096	10
GO:0050678	regulation of epithelial cell proliferation	20/541	0.000888601	20

GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	5/541	0.000899684	5
GO:0038084	vascular endothelial growth factor signaling pathway	5/541	0.000899684	5
GO:0010518	positive regulation of phospholipase activity	7/541	0.000959586	7
GO:0032370	positive regulation of lipid	7/541	0.000959586	7
GO:0046503	glycerolipid catabolic process	7/541	0.000959586	7
GO:0051047	positive regulation of secretion	23/541	0.000964625	23
GO:0030212	hyaluronan metabolic process	6/541	0.000965225	6
GO:0048009	insulin-like growth factor receptor signaling pathway	6/541	0.000965225	6
GO:2000377	regulation of reactive oxygen species metabolic process	13/541	0.001011661	13
GO:0007588	excretion	8/541	0.001045096	8
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	8/541	0.001045096	8
GO:0006465	signal peptide processing	5/541	0.001094912	5
GO:0006000	fructose metabolic process	4/541	0.001125213	4
GO:0032354	response to follicle-stimulating hormone	4/541	0.001125213	4
GO:0043090	amino acid import	4/541	0.001125213	4
GO:0060192	negative regulation of lipase	4/541	0.001125213	4
GO:0009132	nucleoside diphosphate metabolic process	11/541	0.001196576	11
GO:0006091	generation of precursor metabolites and energy	23/541	0.001212331	23
GO:0010565	regulation of cellular ketone metabolic process	13/541	0.001294931	13
GO:0035924	cellular response to vascular endothelial growth factor	6/541	0.001295113	6
GO:0051193	regulation of cofactor metabolic process	7/541	0.001374621	7
GO:0051196	regulation of coenzyme metabolic process	7/541	0.001374621	7
GO:0009435	NAD biosynthetic process	4/541	0.001462078	4
GO:0010544	negative regulation of platelet activation	4/541	0.001462078	4
GO:0030540	female genitalia development	4/541	0.001462078	4
GO:0033189	response to vitamin A	4/541	0.001462078	4
GO:0071216	cellular response to biotic	14/541	0.001472398	14
GO:1901342	regulation of vasculature development	17/541	0.001543296	17

GO:0006760	folic acid-containing compound metabolic process	5/541	0.001577109	5
GO:1903524	positive regulation of blood circulation	9/541	0.001581891	9
GO:1904018	positive regulation of vasculature development	12/541	0.001591489	12
GO:0070542	response to fatty acid	6/541	0.001704813	6
GO:0046916	cellular transition metal ion homeostasis	9/541	0.001719539	9
GO:0032373	positive regulation of sterol transport	4/541	0.001863313	4
GO:0032376	positive regulation of cholesterol transport	4/541	0.001863313	4
GO:0090277	positive regulation of peptide hormone secretion	9/541	0.001866614	9
GO:0055072	iron ion homeostasis	8/541	0.002062008	8
GO:0006887	exocytosis	24/541	0.002068382	24
GO:0048806	genitalia development	6/541	0.002206016	6
GO:0042326	negative regulation of phosphorylation	25/541	0.002250667	25
GO:0009713	catechol-containing compound biosynthetic process	4/541	0.002334819	4
GO:0042423	catecholamine biosynthetic	4/541	0.002334819	4
GO:0006865	amino acid transport	9/541	0.002369015	9
GO:0030203	glycosaminoglycan metabolic process	13/541	0.00243099	13
GO:0002793	positive regulation of peptide secretion	9/541	0.002558465	9
GO:0006112	energy reserve metabolic	9/541	0.002558465	9
GO:1901617	organic hydroxy compound biosynthetic process	13/541	0.002565725	13
GO:0010543	regulation of platelet activation	5/541	0.002569899	5
GO:0031640	killing of cells of other	5/541	0.002569899	5
GO:0044364	disruption of cells of other	5/541	0.002569899	5
GO:0019229	regulation of vasoconstriction	7/541	0.00261474	7
GO:0045980	negative regulation of nucleotide metabolic process	7/541	0.00261474	7
GO:0003014	renal system process	10/541	0.00267916	10
GO:0034109	homotypic cell-cell adhesion	8/541	0.002684581	8
GO:0042310	vasoconstriction	8/541	0.002684581	8
GO:0002697	regulation of immune effector process	20/541	0.002851423	20
GO:0001935	endothelial cell proliferation	10/541	0.002866472	10
GO:0010954	positive regulation of protein processing	4/541	0.002882381	4

GO:0019359	nicotinamide nucleotide biosynthetic process	4/541	0.002882381	4
GO:0019363	pyridine nucleotide biosynthetic process	4/541	0.002882381	4
GO:0046653	tetrahydrofolate metabolic	4/541	0.002882381	4
GO:0090208	positive regulation of triglyceride metabolic process	4/541	0.002882381	4
GO:0070988	demethylation	7/541	0.002885537	7
GO:0046486	glycerolipid metabolic process	23/541	0.002920701	23
GO:0034637	cellular carbohydrate biosynthetic process	8/541	0.002921817	8
GO:0045926	negative regulation of growth	16/541	0.002958639	16
GO:0044264	cellular polysaccharide metabolic process	9/541	0.002973307	9
GO:0050714	positive regulation of protein secretion	15/541	0.003025163	15
GO:0046889	positive regulation of lipid biosynthetic process	7/541	0.0031773	7
GO:0044270	cellular nitrogen compound catabolic process	24/541	0.003259571	24
GO:0006875	cellular metal ion homeostasis	27/541	0.003355458	27
GO:0002921	negative regulation of humoral immune response	3/541	0.003438334	3
GO:0006527	arginine catabolic process	3/541	0.003438334	3
GO:0006560	proline metabolic process	3/541	0.003438334	3
GO:0008228	opsonization	3/541	0.003438334	3
GO:0010755	regulation of plasminogen	3/541	0.003438334	3
GO:0034380	high-density lipoprotein particle assembly	3/541	0.003438334	3
GO:0042178	xenobiotic catabolic process	3/541	0.003438334	3
GO:0006110	regulation of glycolytic process	5/541	0.003443332	5
GO:0010955	negative regulation of protein processing	5/541	0.003443332	5
GO:0050892	intestinal absorption	5/541	0.003443332	5
GO:0060421	positive regulation of heart	5/541	0.003443332	5
GO:1903318	negative regulation of protein maturation	5/541	0.003443332	5
GO:0006027	glycosaminoglycan catabolic process	7/541	0.00349106	7
GO:0015914	phospholipid transport	7/541	0.00349106	7
GO:0006022	aminoglycan metabolic process	13/541	0.003508455	13
GO:0070371	ERK1 and ERK2 cascade	17/541	0.003513033	17
GO:1901657	glycosyl compound metabolic process	24/541	0.003806062	24
GO:0098656	anion transmembrane transport	14/541	0.00386723	14

GO:1903532	positive regulation of secretion by cell	20/541	0.003937307	20
GO:0051180	vitamin transport	5/541	0.003951794	5
GO:0060416	response to growth hormone	5/541	0.003951794	5
GO:0046887	positive regulation of hormone secretion	10/541	0.003965758	10
GO:0015980	energy derivation by oxidation of organic compounds	17/541	0.004120696	17
GO:0042446	hormone biosynthetic process	7/541	0.004188761	7
GO:0042573	retinoic acid metabolic process	4/541	0.004228079	4
GO:0072525	pyridine-containing compound biosynthetic process	4/541	0.004228079	4
GO:0055078	sodium ion homeostasis	6/541	0.004382282	6
GO:0032355	response to estradiol	10/541	0.004489098	10
GO:0010863	positive regulation of phospholipase C activity	5/541	0.004511749	5
GO:0006081	cellular aldehyde metabolic	7/541	0.004574825	7
GO:0035384	thioester biosynthetic process	7/541	0.004574825	7
GO:0071616	acyl-CoA biosynthetic process	7/541	0.004574825	7
GO:0000185	activation of MAPKKK activity	3/541	0.004614577	3
GO:0006702	androgen biosynthetic process	3/541	0.004614577	3
GO:0010566	regulation of ketone biosynthetic process	3/541	0.004614577	3
GO:0010872	regulation of cholesterol esterification	3/541	0.004614577	3
GO:0016114	terpenoid biosynthetic process	3/541	0.004614577	3
GO:0019852	L-ascorbic acid metabolic	3/541	0.004614577	3
GO:0034374	low-density lipoprotein particle remodeling	3/541	0.004614577	3
GO:0045820	negative regulation of glycolytic process	3/541	0.004614577	3
GO:0051195	negative regulation of cofactor metabolic process	3/541	0.004614577	3
GO:0051198	negative regulation of coenzyme metabolic process	3/541	0.004614577	3
GO:0051955	regulation of amino acid	3/541	0.004614577	3
GO:0097286	iron ion import	3/541	0.004614577	3
GO:2000121	regulation of removal of superoxide radicals	3/541	0.004614577	3
GO:0070372	regulation of ERK1 and ERK2 cascade	16/541	0.004697372	16
GO:0015748	organophosphate ester transport	8/541	0.004707034	8
GO:0043550	regulation of lipid kinase	6/541	0.004859867	6
GO:0002449	lymphocyte mediated immunity	16/541	0.00488994	16
GO:1901136	carbohydrate derivative catabolic process	13/541	0.004944933	13

GO:0048514	blood vessel morphogenesis	27/541	0.00495281	27
GO:0042311	vasodilation	7/541	0.004987129	7
GO:0006700	C21-steroid hormone biosynthetic process	4/541	0.005036964	4
GO:0030539	male genitalia development	4/541	0.005036964	4
GO:0090181	regulation of cholesterol metabolic process	4/541	0.005036964	4
GO:0006730	one-carbon metabolic process	5/541	0.005125922	5
GO:0032103	positive regulation of response to external stimulus	17/541	0.005192193	17
GO:0042157	lipoprotein metabolic process	11/541	0.005352393	11
GO:0042542	response to hydrogen peroxide	10/541	0.005374422	10
GO:0060420	regulation of heart growth	6/541	0.005374606	6
GO:0006026	aminoglycan catabolic process	7/541	0.005426757	7
GO:2000379	positive regulation of reactive oxygen species metabolic	8/541	0.005457762	8
GO:0034284	response to monosaccharide	13/541	0.005689856	13
GO:0045766	positive regulation of	10/541	0.005698055	10
GO:0001990	regulation of systemic arterial blood pressure by hormone	5/541	0.005797002	5
GO:0006778	porphyrin-containing compound metabolic process	5/541	0.005797002	5
GO:0048662	negative regulation of smooth muscle cell proliferation	5/541	0.005797002	5
GO:1900274	regulation of phospholipase C activity	5/541	0.005797002	5
GO:1903409	reactive oxygen species biosynthetic process	8/541	0.005865749	8
GO:0046470	phosphatidylcholine metabolic process	7/541	0.005894797	7
GO:0046165	alcohol biosynthetic process	9/541	0.005904362	9
GO:0003081	regulation of systemic arterial blood pressure by renin-	4/541	0.00594336	4
GO:0043252	sodium-independent organic anion transport	4/541	0.00594336	4
GO:0045922	negative regulation of fatty acid metabolic process	4/541	0.00594336	4
GO:0045940	positive regulation of steroid metabolic process	4/541	0.00594336	4
GO:0009109	coenzyme catabolic process	3/541	0.006005785	3
GO:0009404	toxin metabolic process	3/541	0.006005785	3
GO:0019755	one-carbon compound transport	3/541	0.006005785	3
GO:0051818	disruption of cells of other organism involved in symbiotic	3/541	0.006005785	3
GO:0051883	killing of cells in other organism involved in symbiotic	3/541	0.006005785	3

GO:1901678	iron coordination entity	3/541	0.006005785	3
GO:1903522	regulation of blood circulation	18/541	0.006248375	18
GO:0001933	negative regulation of protein phosphorylation	22/541	0.00635613	22
GO:0046209	nitric oxide metabolic process	7/541	0.006392341	7
GO:0006734	NADH metabolic process	5/541	0.006527643	5
GO:0010677	negative regulation of cellular carbohydrate metabolic process	5/541	0.006527643	5
GO:0001655	urogenital system development	19/541	0.006619896	19
GO_CC_down_sig_gene				
ID	Description	GeneRatio	pvalue	Count
GO:0072562	blood microparticle	39/555	3.35E-26	39
GO:0060205	cytoplasmic membrane-bounded vesicle lumen	24/555	1.05E-14	24
GO:0031983	vesicle lumen	24/555	1.32E-14	24
GO:0034774	secretory granule lumen	20/555	1.26E-12	20
GO:0034358	plasma lipoprotein particle	14/555	3.05E-12	14
GO:1990777	lipoprotein particle	14/555	3.05E-12	14
GO:0034364	high-density lipoprotein particle	12/555	4.44E-12	12
GO:0032994	protein-lipid complex	14/555	6.91E-12	14
GO:0005759	mitochondrial matrix	41/555	4.15E-11	41
GO:0005782	peroxisomal matrix	13/555	3.23E-10	13
GO:0031907	microbody lumen	13/555	3.23E-10	13
GO:0031093	platelet alpha granule lumen	13/555	9.11E-09	13
GO:0044438	microbody part	16/555	1.47E-08	16
GO:0044439	peroxisomal part	16/555	1.47E-08	16
GO:0005777	peroxisome	19/555	1.47E-08	19
GO:0042579	microbody	19/555	1.47E-08	19
GO:0031091	platelet alpha granule	13/555	3.84E-07	13
GO:0031089	platelet dense granule lumen	5/555	4.42E-05	5
GO:0046930	pore complex	5/555	0.000126385	5
GO:0030141	secretory granule	24/555	0.000199035	24
GO:0034361	very-low-density lipoprotein	5/555	0.000293216	5
GO:0034385	triglyceride-rich lipoprotein	5/555	0.000293216	5
GO:0042827	platelet dense granule	5/555	0.000293216	5
GO:0016323	basolateral plasma membrane	16/555	0.000382646	16
GO:0005578	proteinaceous extracellular	23/555	0.0007534	23
GO:0005903	brush border	10/555	0.000768242	10
GO:0005788	endoplasmic reticulum lumen	15/555	0.001514781	15
GO:0071682	endocytic vesicle lumen	4/555	0.001563542	4
GO:0005581	collagen trimer	9/555	0.001585471	9
GO:0005796	Golgi lumen	9/555	0.002696985	9
GO:0042383	sarcolemma	10/555	0.003214003	10
GO:0099503	secretory vesicle	25/555	0.003943563	25
GO:0031526	brush border membrane	6/555	0.004269475	6
GO:0045177	apical part of cell	20/555	0.0052136	20

GO_MF_down_sig_gene

ID	Description	GeneRatio	pvalue	Count
GO:0048037	cofactor binding	56/537	6.40E-30	56
GO:0004497	monooxygenase activity	29/537	1.38E-20	29
GO:0019825	oxygen binding	21/537	2.84E-19	21
GO:0046906	tetrapyrrole binding	32/537	6.47E-19	32
GO:0020037	heme binding	31/537	7.18E-19	31
GO:0050662	coenzyme binding	36/537	1.10E-18	36
GO:0008391	arachidonic acid monooxygenase activity	13/537	4.59E-18	13
GO:0008392	arachidonic acid epoxygenase activity	13/537	4.59E-18	13
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	31/537	4.92E-18	31
GO:0016705	oxidoreductase activity, acting on paired donors, with incorporation or reduction of	31/537	8.68E-16	31
GO:0005506	iron ion binding	31/537	1.50E-15	31
GO:0016712	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one	14/537	1.00E-14	14
GO:0008395	steroid hydroxylase activity	15/537	2.87E-14	15
GO:0009055	electron carrier activity	24/537	2.77E-13	24
GO:0016709	oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, NAD(P)H as one donor, and incorporation of one atom of oxygen	15/537	2.08E-12	15
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	23/537	2.24E-12	23
GO:0030170	pyridoxal phosphate binding	16/537	1.39E-11	16
GO:1901681	sulfur compound binding	31/537	2.01E-11	31
GO:0043168	anion binding	33/537	3.66E-11	33
GO:0050660	flavin adenine dinucleotide	18/537	4.21E-11	18
GO:0016769	transferase activity, transferring nitrogenous groups	11/537	4.21E-11	11
GO:0070330	aromatase activity	11/537	4.21E-11	11
GO:0000062	fatty-acyl-CoA binding	12/537	7.24E-11	12
GO:0016627	oxidoreductase activity, acting on the CH-CH group of donors	15/537	2.94E-10	15
GO:0008483	transaminase activity	10/537	3.51E-10	10

GO:0052890	oxidoreductase activity, acting on the CH-CH group of donors, with a flavin as acceptor	9/537	3.96E-10	9
GO:0005319	lipid transporter activity	20/537	4.41E-10	20
GO:0003995	acyl-CoA dehydrogenase	9/537	8.18E-10	9
GO:0031406	carboxylic acid binding	22/537	3.64E-09	22
GO:0016725	oxidoreductase activity, acting on CH or CH2 groups	7/537	4.45E-09	7
GO:0005539	glycosaminoglycan binding	25/537	1.74E-08	25
GO:0005496	steroid binding	16/537	2.47E-08	16
GO:0017171	serine hydrolase activity	26/537	9.48E-08	26
GO:0004252	serine-type endopeptidase	24/537	1.28E-07	24
GO:0005342	organic acid transmembrane transporter activity	17/537	2.77E-07	17
GO:0008236	serine-type peptidase activity	25/537	2.79E-07	25
GO:0046943	carboxylic acid transmembrane transporter activity	16/537	1.00E-06	16
GO:0016702	oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two	8/537	1.21E-06	8
GO:0008028	monocarboxylic acid transmembrane transporter	9/537	1.40E-06	9
GO:0016645	oxidoreductase activity, acting on the CH-NH group of donors	8/537	1.67E-06	8
GO:0016701	oxidoreductase activity, acting on single donors with incorporation of molecular	8/537	1.67E-06	8
GO:0016903	oxidoreductase activity, acting on the aldehyde or oxo group of donors	10/537	1.93E-06	10
GO:0016829	lyase activity	19/537	3.40E-06	19
GO:0016830	carbon-carbon lyase activity	10/537	4.32E-06	10
GO:0008201	heparin binding	18/537	4.67E-06	18
GO:0019842	vitamin binding	12/537	1.13E-05	12
GO:0004866	endopeptidase inhibitor activity	18/537	1.20E-05	18
GO:0004867	serine-type endopeptidase inhibitor activity	13/537	1.37E-05	13
GO:0016878	acid-thiol ligase activity	7/537	1.54E-05	7
GO:0050661	NADP binding	9/537	1.58E-05	9
GO:0004745	retinol dehydrogenase activity	6/537	1.64E-05	6
GO:0061135	endopeptidase regulator activity	18/537	1.94E-05	18
GO:0030414	peptidase inhibitor activity	18/537	2.44E-05	18
GO:0051287	NAD binding	9/537	2.70E-05	9

GO:0015291	secondary active transmembrane transporter activity	21/537	2.86E-05	21
GO:1901618	organic hydroxy compound transmembrane transporter	8/537	3.98E-05	8
GO:0004175	endopeptidase activity	31/537	4.91E-05	31
GO:0005343	organic acid:sodium symporter activity	6/537	5.89E-05	6
GO:0016597	amino acid binding	9/537	6.03E-05	9
GO:0015296	anion:cation symporter activity	7/537	6.63E-05	7
GO:0015293	symporter activity	15/537	6.96E-05	15
GO:0015125	bile acid transmembrane transporter activity	5/537	8.67E-05	5
GO:0030246	carbohydrate binding	21/537	9.00E-05	21
GO:0008514	organic anion transmembrane transporter activity	11/537	9.39E-05	11
GO:0004857	enzyme inhibitor activity	27/537	0.000120428	27
GO:0015645	fatty acid ligase activity	5/537	0.000122739	5
GO:0043178	alcohol binding	10/537	0.000132668	10
GO:0022804	active transmembrane transporter activity	26/537	0.000152239	26
GO:0051213	dioxygenase activity	11/537	0.000159285	11
GO:0015370	solute:sodium symporter	8/537	0.000179865	8
GO:0016810	hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds	14/537	0.000232588	14
GO:0042562	hormone binding	9/537	0.000233449	9
GO:0016229	steroid dehydrogenase activity	6/537	0.000251566	6
GO:0061134	peptidase regulator activity	18/537	0.000278937	18
GO:0015485	cholesterol binding	7/537	0.00029254	7
GO:0016877	ligase activity, forming carbon-sulfur bonds	7/537	0.00029254	7
GO:0038024	cargo receptor activity	9/537	0.000296012	9
GO:0015294	solute:cation symporter activity	11/537	0.000342537	11
GO:0015248	sterol transporter activity	5/537	0.00039059	5
GO:0005283	sodium:amino acid symporter activity	4/537	0.000465987	4
GO:0032934	sterol binding	7/537	0.000617818	7
GO:0004467	long-chain fatty acid-CoA ligase activity	4/537	0.000655644	4
GO:0015245	fatty acid transporter activity	4/537	0.000655644	4
GO:0033218	amide binding	19/537	0.000740663	19
GO:0048029	monosaccharide binding	7/537	0.000809048	7
GO:0017046	peptide hormone binding	6/537	0.000891607	6
GO:0070402	NADPH binding	4/537	0.000894134	4

GO:0016831	carboxy-lyase activity	6/537	0.001040572	6
GO:0017127	cholesterol transporter activity	4/537	0.001187738	4
GO:0034185	apolipoprotein binding	4/537	0.001187738	4
GO:0072341	modified amino acid binding	8/537	0.001405386	8
GO:0004033	aldo-keto reductase (NADP) activity	5/537	0.001407786	5
GO:0005416	cation:amino acid symporter activity	4/537	0.001542738	4
GO:0016722	oxidoreductase activity, oxidizing metal ions	4/537	0.001542738	4
GO:0048038	quinone binding	4/537	0.001965367	4
GO:0008238	exopeptidase activity	10/537	0.002416111	10
GO:0015238	drug transmembrane transporter activity	4/537	0.002461771	4
GO:0008509	anion transmembrane transporter activity	15/537	0.002875456	15
GO:0019838	growth factor binding	11/537	0.002983477	11
GO:0005537	mannose binding	4/537	0.003037966	4
GO:0005044	scavenger receptor activity	6/537	0.00339042	6
GO:0005548	phospholipid transporter activity	6/537	0.004229368	6
GO:0001871	pattern binding	4/537	0.004452972	4
GO:0015347	sodium-independent organic anion transmembrane	4/537	0.004452972	4
GO:0030247	polysaccharide binding	4/537	0.004452972	4
GO:0090484	drug transporter activity	4/537	0.004452972	4
GO:0015643	toxic substance binding	3/537	0.004807051	3
GO:0016836	hydro-lyase activity	6/537	0.005212424	6
GO:0015081	sodium ion transmembrane transporter activity	11/537	0.005637531	11
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	5/537	0.006159458	5
GO:0033293	monocarboxylic acid binding	6/537	0.006353227	6
GO:0052689	carboxylic ester hydrolase	11/537	0.006614989	11
GO:0016628	oxidoreductase activity, acting on the CH-CH group of donors, NAD or NADP as acceptor	4/537	0.007313728	4
GO:0071813	lipoprotein particle binding	4/537	0.007313728	4
GO:0071814	protein-lipid complex binding	4/537	0.007313728	4
GO:0016918	retinal binding	3/537	0.007933601	3
GO:0017017	MAP kinase tyrosine/serine/threonine phosphatase activity	3/537	0.007933601	3
GO:0019841	retinol binding	3/537	0.007933601	3
GO:0004181	metallocarboxypeptidase	4/537	0.008484281	4

GO:0033764	steroid dehydrogenase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	4/537	0.008484281	4

Annotation: 1.down_sig_gene: 577 down-regulated genes;2.up_sig_gene: 82 up-regulated genes; 3.BP: Biological Process; 4.CC: Cellular Component; 5.MF: Molecular Function

Table S4. KEGG analysis of the modules from WGCNA

brown					
ID	Description	GeneRatio	pvalue	geneID	Count
hsa04110	Cell cycle	4/5	3.88E-07	CCNA2/CCNB2/PTTG1/TTK	4
hsa04914	Progesterone-mediated oocyte maturation	2/5	0.001764807	CCNA2/CCNB2	2
hsa04114	Oocyte meiosis	2/5	0.002755317	CCNB2/PTTG1	2
hsa04218	Cellular senescence	2/5	0.00455036	CCNA2/CCNB2	2
hsa05166	HTLV-I infection	2/5	0.011283965	CCNB2/PTTG1	2
turquoise					
ID	Description	GeneRatio	pvalue	geneID	Count
hsa04610	Complement and coagulation cascades	26/311	5.27E-17	C1R/C1S/C4BPA/C6/C8A/C8B/C9/CFI/CPB2/F11/F12/F2/F8/F9/FGA/FGB/KLKB1/MASP1/MASP2/MBL2/PLG/PROC/PROS1/SERPINC1/SERPINF2/SERPING1	26
hsa00071	Fatty acid degradation	20/311	1.42E-16	ACAA1/ACADL/ACADM/ACADS/ACADSB/ACADVL/ACAT1/ACOX1/ACSL1/ACSL5/ADH1A/ADH1B/ADH4/ADH6/ALDH2/CPT2/CYP4A11/CYP4A22/EHHADH/GCDH	20

hsa03320	PPAR signaling pathway	22/311	8.36E-14	ACAA1/ACADL/ACADM/ACOX1/ACOX2/ACSL1/ACSL5/ANGPTL4/APOA1/APOA5/APOC3/CPT2/CYP8B1/EHHADH/FABP1/HMGCS2/PCK1/PCK2/PLIN1/SCP2/SLC27A2/SLC27A5	22
hsa00830	Retinol metabolism	20/311	1.01E-12	ADH1A/ADH1B/ADH4/ADH6/AOX1/CYP1A1/CYP1A2/CYP26A1/CYP2A6/CYP2B6/CYP2C18/CYP2C8/CYP2C9/CYP3A4/CYP3A5/CYP4A11/HSD17B6/RDH16/RDH5/UGT2B7	20
hsa00380	Tryptophan metabolism	15/311	2.94E-11	AADAT/ACAT1/ACMSD/ALDH2/AOX1/CAT/CYP1A1/CYP1A2/EHHADH/GCDH/HAAO/IDO2/KMO/OGDHL/TDO2	15
hsa00280	Valine, leucine and isoleucine degradation	16/311	5.08E-11	ABAT/ACAA1/ACADM/ACADS/ACADSB/ACAT1/AGXT2/ALDH2/ALDH6A1/AOX1/BCKDHB/EHHADH/HMGCL/HMGCS2/IVD/MUT	16

hsa05204	Chemical carcinogenesis	20/311	1.14E-10	ADH1A/ADH1B/ADH4/ADH6/CYP1A1/CYP1A2/CYP2A13/CYP2A6/CYP2C18/CYP2C19/CYP2C8/CYP2C9/CYP2E1/CYP3A4/CYP3A43/CYP3A5/NAT1/NAT2/SULT2A1/UGT2B7	20
hsa00260	Glycine, serine and threonine metabolism	14/311	4.01E-10	AGXT/AGXT2/ALAS1/BHMT/CBS/CTH/DAO/DMGDH/GATM/GNMT/GRHPR/PIPOX/SARDH/SDS	14
hsa00250	Alanine, aspartate and glutamate metabolism	13/311	7.32E-10	ABAT/AGXT/AGXT2/ASPA/ASS1/CPS1/FOLH1/GLS2/GLUD1/GOT1/GOT2/GPT/GPT2	13
hsa00350	Tyrosine metabolism	13/311	1.10E-09	ADH1A/ADH1B/ADH4/ADH6/AOX1/DBH/FAH/GOT1/GOT2/GSTZ1/HGD/HPD/TAT	13
hsa01200	Carbon metabolism	22/311	2.35E-09	ACADM/ACADS/ACAT1/AGXT/ALDH6A1/ALDOB/CAT/CPS1/EHHADH/ENO3/FBP1/GLUD1/GOT1/GOT2/GPT/GPT2/HAO1/HAO2/MUT/OGDHL/RGN/SDS	22

hsa00982	Drug metabolism - cytochrome P450	17/311	3.18E-09	ADH1A/ADH1B/ADH4/ADH6/AOX1/CYP1A2/CYP2A6/CYP2B6/CYP2C19/CYP2C8/CYP2C9/CYP2E1/CYP3A4/CYP3A5/FMO3/FMO4/UGT2B7	17
hsa00220	Arginine biosynthesis	10/311	3.88E-09	ARG1/ASS1/CPS1/GLS2/GLUD1/GOT1/GOT2/GPT/GPT2/OTC	10
hsa04146	Peroxisome	18/311	7.61E-09	ACAA1/ACOX1/ACOX2/ACSL1/ACSL5/AGXT/CAT/DAO/EHHADH/EPHX2/HAO1/HAO2/HMGCL/PIPOX/PXMP2/SCP2/SLC27A2/XDH	18
hsa00650	Butanoate metabolism	11/311	7.71E-09	ABAT/ACADS/ACAT1/ACSM2A/ACSM3/ACSM5/BDH1/BDH2/EHHADH/HMGCL/HMGCS2	11
hsa00980	Metabolism of xenobiotics by cytochrome P450	16/311	5.54E-08	ADH1A/ADH1B/ADH4/ADH6/AKR7A3/CYP1A1/CYP1A2/CYP2A13/CYP2A6/CYP2B6/CYP2C9/CYP2E1/CYP3A4/CYP3A5/SULT2A1/UGT2B7	16

hsa01230	Biosynthesis of amino acids	15/311	3.57E-07	ALDOB/ARG1/ASS1/CBS/CPS1/CTH/ENO3/GOT1/GOT2/GPT/GPT2/MAT1A/OTC/SDS/TAT	15
hsa01212	Fatty acid metabolism	12/311	4.94E-07	ACAA1/ACADL/ACADM/ACADS/ACADSB/ACADVL/ACAT1/ACOX1/ACSL1/ACSL5/CPT2/EHHADH	12
hsa04976	Bile secretion	14/311	1.26E-06	ABCB4/ABCG2/AQP9/CA2/CYP3A4/KCNN2/SLC10A1/SLC22A1/SLC22A7/SLC27A5/SLC4A4/SLCO1B1/SLCO1B3/SULT2A1	14
hsa00270	Cysteine and methionine metabolism	11/311	1.90E-06	ADI1/AGXT2/BHMT/CBS/CDO1/CTH/GOT1/GOT2/MAT1A/SDS/TAT	11
hsa00120	Primary bile acid biosynthesis	7/311	3.15E-06	ACOX2/AKR1C4/AKR1D1/CYP39A1/CYP8B1/SCP2/SLC27A5	7
hsa00630	Glyoxylate and dicarboxylate metabolism	8/311	1.44E-05	ACAT1/AGXT/CAT/GRHPR/HAO1/HAO2/HOGA1/MUT	8
hsa00072	Synthesis and degradation of ketone bodies	5/311	2.84E-05	ACAT1/BDH1/BDH2/HMGCL/HMGCS2	5
hsa00410	beta-Alanine metabolism	8/311	3.26E-05	ABAT/ACADM/ALDH2/ALDH6A1/CNDP1/DPYS/EHHADH/UPB1	8

hsa00330	Arginine and proline metabolism	10/311	3.76E-05	ALDH2/ARG1/CNDP1/DAO/GATM/GOT1/GOT2/HOGA1/OAT/PRODH2	10
hsa00640	Propanoate metabolism	8/311	4.19E-05	ABAT/ACACB/ACADM/ACAT1/ALDH6A1/BCKDHB/EHHADH/MUT	8
hsa00983	Drug metabolism - other enzymes	9/311	0.000110561	CES2/CYP2A6/CYP3A4/DPYS/NAT1/NAT2/UGT2B7/UPB1/XDH	9
hsa00010	Glycolysis / Gluconeogenesis	11/311	0.000119928	ADH1A/ADH1B/ADH4/ADH6/ALDH2/ALDOB/ENO3/FBP1/PCK1/PCK2/PGM1	11
hsa00591	Linoleic acid metabolism	7/311	0.00016286	CYP1A2/CYP2C19/CYP2C8/CYP2C9/CYP2E1/CYP2J2/CYP3A4	7
hsa00140	Steroid hormone biosynthesis	10/311	0.000163681	AKR1C4/AKR1D1/CYP1A1/CYP1A2/CYP2E1/CYP3A4/CYP3A5/HSD17B6/SRD5A1/UGT2B7	10
hsa00620	Pyruvate metabolism	8/311	0.000188896	ACACB/ACAT1/ACOT12/ALDH2/GRHPR/LDHD/PCK1/PCK2	8
hsa04979	Cholesterol metabolism	9/311	0.000216466	ANGPTL3/ANGPTL4/APOA1/APOC3/CETP/LCAT/LIPC/LIPG/LPA	9

hsa00590	Arachidonic acid metabolism	10/311	0.000250172	CYP2B6/CYP2C19/CYP2C8/CYP2C9/CYP2E1/CYP2J2/CYP4A11/CYP4F2/CYP4F3/EPHX2	10
hsa00340	Histidine metabolism	6/311	0.000306996	ALDH2/AMDHD1/ASPA/CNDP1/FTCD/UROC1	6
hsa04964	Proximal tubule bicarbonate reclamation	6/311	0.000306996	CA2/GLS2/GLUD1/PCK1/PCK2/SLC4A4	6
hsa00360	Phenylalanine metabolism	5/311	0.000544794	GLYAT/GOT1/GOT2/HPD/TAT	5
hsa01210	2-Oxocarboxylic acid metabolism	5/311	0.000728327	AADAT/GOT1/GOT2/GPT/GPT2	5
hsa00310	Lysine degradation	9/311	0.000775834	AADAT/AASS/ACAT1/ALDH2/BBOX1/EHHADH/GCDH/OGDHL/PIPOX	9
hsa04978	Mineral absorption	8/311	0.001254665	MT1E/MT1F/MT1G/MT1H/MT1HL1/MT1M/MT1X/MT2A	8
hsa05150	Staphylococcus aureus infection	8/311	0.002328527	C1R/C1S/CFI/FCGR2B/MASP1/MASP2/MBL2/PLG	8
blue					
ID	Description	GeneRatio	pvalue	geneID	Count
hsa04060	Cytokine-cytokine receptor interaction	5/15	0.000146024	CCL21/CXCL12/HGF/NGFR/PDGFRA	5
hsa04015	Rap1 signaling pathway	4/15	0.000701687	HGF/NGFR/PDGFRA/TEK	4

hsa04014	Ras signaling pathway	4/15	0.001087718	HGF/NGFR/PDGFRA/TEK	4
hsa04010	MAPK signaling pathway	4/15	0.002452679	HGF/NGFR/PDGFRA/TEK	4
hsa04151	PI3K-Akt signaling pathway	4/15	0.004661724	HGF/NGFR/PDGFRA/TEK	4

Table S5. KEGG and GO analysis of the sub-clusters from PPI network

KEGG-cluster1					
ID	Description	GeneRatio	pvalue	geneID	Count
hsa00071	Fatty acid degradation	16/37	9.90E-26	ACSL1/ACSL1/GCDH/GCDH/ACAA1/ACAA1/ACADL/ACADM/ACADM/ACADS/ACADS/ACADSB/ACADSB/ACAT1/ACAT1/ACSL5	16
hsa01212	Fatty acid metabolism	14/37	5.74E-21	ACSL1/ACSL1/ACAA1/ACAA1/ACADL/ACADM/ACADM/ACADS/ACADS/ACADSB/ACADSB/ACAT1/ACAT1/ACSL5	14
hsa00280	Valine, leucine and isoleucine degradation	13/37	2.44E-19	ACAA1/ACAA1/ACADM/ACADM/ACADS/ACADS/ACADSB/ACADSB/ACAT1/ACAT1/MUT/MUT/MUT	13

hsa04610	Complement and coagulation cascades	11/37	9.29E-14	F2/F8/FGA/FGB/FGB/PLG/SERPINF2/PROS1/PROS1/SERPING1/SERPING1	11
hsa00650	Butanoate metabolism	7/37	1.51E-10	ACSM2A/ACADS/ACADS/ACAT1/ACAT1/ACSM5/ACSM3	7
hsa00640	Propanoate metabolism	7/37	6.14E-10	ACADM/ACADM/ACAT1/ACAT1/MUT/MUT/MUT	7
hsa03320	PPAR signaling pathway	8/37	9.12E-09	ACSL1/ACSL1/ACAA1/ACAA1/ACADL/ACADM/ACADM/ACSL5	8
hsa01200	Carbon metabolism	9/37	1.90E-08	ACADM/ACADM/ACADS/ACADS/ACAT1/ACAT1/MUT/MUT/MUT	9
hsa00630	Glyoxylate and dicarboxylate metabolism	5/37	5.10E-07	ACAT1/ACAT1/MUT/MUT/MUT	5
hsa00380	Tryptophan metabolism	4/37	5.06E-05	GCDH/GCDH/ACAT1/ACAT1	4
hsa00061	Fatty acid biosynthesis	3/37	5.91E-05	ACSL1/ACSL1/ACSL5	3
hsa04146	Peroxisome	5/37	5.96E-05	ACSL1/ACSL1/ACAA1/ACAA1/ACSL5	5
hsa00310	Lysine degradation	4/37	0.000143368	GCDH/GCDH/ACAT1/ACAT1	4
hsa00072	Synthesis and degradation of ketone bodies	2/37	0.001544451	ACAT1/ACAT1	2
hsa04216	Ferroptosis	3/37	0.001893197	ACSL1/ACSL1/ACSL5	3
hsa00592	alpha-Linolenic acid metabolism	2/37	0.005419416	ACAA1/ACAA1	2

hsa00900	Terpenoid backbone biosynthesis	2/37	0.005779744	ACAT1/ACAT1	2
hsa01040	Biosynthesis of unsaturated fatty acids	2/37	0.006150777	ACAA1/ACAA1	2
hsa04920	Adipocytokine signaling pathway	3/37	0.008236355	ACSL1/ACSL1/ACSL5	3
hsa00040	Pentose and glucuronate interconversions	2/37	0.011409567	CRYL1/CRYL1	2
hsa00410	beta-Alanine metabolism	2/37	0.012425386	ACADM/ACADM	2

KEGG-cluster2

ID	Description	GeneRatio	pvalue	geneID	Count
hsa00830	Retinol metabolism	15/43	5.17E-21	CYP1A1/CYP1A1/CYP1A2/CYP2B6/CYP2C9/CYP2C9/CYP3A4/CYP3A4/CYP3A5/CYP4A11/CYP26A1/AOX1/UGT2B7/HSD17B6/HSD17B6	15
hsa00980	Metabolism of xenobiotics by cytochrome P450	11/43	1.09E-12	CYP1A1/CYP1A1/CYP1A2/CYP2B6/CYP2C9/CYP2C9/CYP2E1/CYP3A4/CYP3A4/CYP3A5/UGT2B7	11
hsa00140	Steroid hormone biosynthesis	10/43	1.73E-12	CYP1A1/CYP1A1/CYP1A2/CYP2E1/CYP3A4/CYP3A4/CYP3A5/UGT2B7/HSD17B6/HSD17B6	10
hsa00982	Drug metabolism - cytochrome P450	10/43	2.63E-11	CYP1A2/CYP2B6/CYP2C9/CYP2C9/CYP2E1/CYP3A4/CYP3A4/CYP3A5/AOX1/UGT2B7	10

hsa00590	Arachidonic acid metabolism	9/43	3.38E-11	CYP2B6/CYP2C9/CYP2C9/CYP2E1/CYP2J2/CYP4A11/CYP4F3/CYP4F3/CYP4F2	9
hsa05204	Chemical carcinogenesis	10/43	6.81E-11	CYP1A1/CYP1A1/CYP1A2/CYP2C9/CYP2C9/CYP2E1/CYP3A4/CYP3A4/CYP3A5/UGT2B7	10
hsa00380	Tryptophan metabolism	8/43	7.12E-11	CYP1A1/CYP1A1/CYP1A2/EHHADH/ALDH2/AOX1/KMO/KMO	8
hsa00591	Linoleic acid metabolism	7/43	9.96E-11	CYP1A2/CYP2C9/CYP2C9/CYP2E1/CYP2J2/CYP3A4/CYP3A4	7
hsa03320	PPAR signaling pathway	7/43	6.36E-07	EHHADH/APOA1/APOA1/APOC3/APOC3/ACOX1/ACOX2	7
hsa00071	Fatty acid degradation	5/43	1.30E-05	CYP4A11/EHHADH/ALDH2/ACADVL/ACOX1	5
hsa00280	Valine, leucine and isoleucine degradation	5/43	1.59E-05	EHHADH/ALDH2/AOX1/ALDH6A1/ALDH6A1	5
hsa00410	beta-Alanine metabolism	4/43	4.23E-05	EHHADH/ALDH2/ALDH6A1/ALDH6A1	4
hsa00640	Propanoate metabolism	4/43	6.88E-05	EHHADH/ACACB/ALDH6A1/ALDH6A1	4

hsa04976	Bile secretion	5/43	0.000110013	SLCO1B1/SLCO1B1/SLCO1B1/CYP3A4/CYP3A4	5
hsa00860	Porphyrin and chlorophyll metabolism	3/43	0.002234985	CP/CP/UGT2B7	3
hsa00983	Drug metabolism - other enzymes	3/43	0.003177045	CYP3A4/CYP3A4/UGT2B7	3
hsa01212	Fatty acid metabolism	3/43	0.004654575	EHHADH/ACADVL/ACOX1	3
hsa04913	Ovarian steroidogenesis	3/43	0.00516634	CYP1A1/CYP1A1/CYP2J2	3
hsa04977	Vitamin digestion and absorption	2/43	0.008240724	APOA1/APOA1	2
hsa00053	Ascorbate and aldarate metabolism	2/43	0.010354129	ALDH2/UGT2B7	2
hsa04146	Peroxisome	3/43	0.013060953	EHHADH/ACOX1/ACOX2	3
hsa04918	Thyroid hormone synthesis	3/43	0.013368099	SERPINA7/TTR/TTR	3
hsa05143	African trypanosomiasis	2/43	0.017245334	APOA1/APOA1	2
KEGG-cluster3					
ID	Description	BgRatio	pvalue	geneID	Count
hsa04978	Mineral absorption	73/10009	2.24E-22	MT1E/MT1F/MT1G/MT1H/MT1H/MT1M/MT1M/MT1X/MT1X/MT2A	10
GO_BP_cluster1					
ID	Description	GeneRatio	pvalue	geneID	Count
GO:0002576	platelet degranulation	16/32	1.42E-27	ITIH4/HRG/ALB/SERPINA4/IGF1/PROS1/SERPINF2/PLG/CDC37L1/FGB/F8/FGA/A1BG/SERPING1/SPP2/ECM1	16

GO:0045055	regulated exocytosis	16/32	8.68E-21	ITIH4/HRG/ALB/SERPINA4/IGF1/PROS1/SERPINF2/PLG/CDC37L1/FGB/F8/FGA/A1BG/SERPING1/SPP2/ECM1	16
GO:0006887	exocytosis	16/32	2.43E-18	ITIH4/HRG/ALB/SERPINA4/IGF1/PROS1/SERPINF2/PLG/CDC37L1/FGB/F8/FGA/A1BG/SERPING1/SPP2/ECM1	16
GO:0006631	fatty acid metabolic process	15/32	2.77E-17	ACADS/ECHDC2/ACSL5/CRYL1/ACADM/ACSM2A/ACSM5/MUT/ACAA1/ACSL1/ACSM3/ACAT1/GCDH/ACADL/ACADSB	15
GO:0042730	fibrinolysis	8/32	1.54E-16	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0072329	monocarboxylic acid catabolic process	10/32	4.01E-15	ACADS/ECHDC2/CRYL1/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	10
GO:0030195	negative regulation of blood coagulation	8/32	2.13E-14	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:1900047	negative regulation of hemostasis	8/32	2.13E-14	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8

GO:0050819	negative regulation of coagulation	8/32	3.62E-14	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0009062	fatty acid catabolic process	9/32	5.90E-14	ACADS/ECHDC2/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	9
GO:0061045	negative regulation of wound healing	8/32	1.70E-13	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:1903035	negative regulation of response to wounding	8/32	4.87E-13	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0006635	fatty acid beta-oxidation	8/32	6.98E-13	ACADS/ECHDC2/ACADM/ACAA1/ACAT1/GCDH/ACADL/ACADSB	8
GO:0046395	carboxylic acid catabolic process	10/32	1.96E-12	ACADS/ECHDC2/CRYL1/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	10
GO:0030193	regulation of blood coagulation	8/32	2.81E-12	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:1900046	regulation of hemostasis	8/32	2.81E-12	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0050818	regulation of coagulation	8/32	4.13E-12	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0016054	organic acid catabolic process	10/32	6.83E-12	ACADS/ECHDC2/CRYL1/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	10

GO:0019395	fatty acid oxidation	8/32	9.18E-12	ACADS/ECHDC2/ACADM/ACAA1/ACAT1/GCDH/ACADL/ACADSB	8
GO:0034440	lipid oxidation	8/32	1.08E-11	ACADS/ECHDC2/ACADM/ACAA1/ACAT1/GCDH/ACADL/ACADSB	8
GO:0044242	cellular lipid catabolic process	9/32	4.29E-11	ACADS/ECHDC2/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	9
GO:0061041	regulation of wound healing	8/32	6.75E-11	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:1903034	regulation of response to wounding	8/32	2.13E-10	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	5/32	2.14E-10	ACADS/ACADM/GCDH/ACADL/ACADSB	5
GO:0044282	small molecule catabolic process	10/32	4.09E-10	ACADS/ECHDC2/CRYL1/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	10
GO:0072378	blood coagulation, fibrin clot formation	5/32	1.20E-09	FGB/F8/FGA/SERPING1/F2	5
GO:0051918	negative regulation of fibrinolysis	4/32	2.33E-09	HRG/SERPINF2/PLG/F2	4
GO:0016042	lipid catabolic process	9/32	2.54E-09	ACADS/ECHDC2/ACADM/MUT/ACAA1/ACAT1/GCDH/ACADL/ACADSB	9

GO:0055088	lipid homeostasis	7/32	2.89E-09	ACADS/ACADM/ACSM2A/ACSM3/GCDH/ACADL/ACADSB	7
GO:0045861	negative regulation of proteolysis	9/32	3.52E-09	ITIH4/HRG/SERPINA4/PROS1/SERPINF2/SERPING1/F2/SPP2/ECM1	9
GO:0051917	regulation of fibrinolysis	4/32	1.10E-08	HRG/SERPINF2/PLG/F2	4
GO:0007596	blood coagulation	9/32	1.31E-08	HRG/PROS1/SERPINF2/PLG/FGB/F8/FGA/SERPING1/F2	9
GO:0010466	negative regulation of peptidase activity	8/32	1.37E-08	ITIH4/HRG/SERPINA4/PROS1/SERPINF2/SERPING1/SPP2/ECM1	8
GO:0050817	coagulation	9/32	1.45E-08	HRG/PROS1/SERPINF2/PLG/FGB/F8/FGA/SERPING1/F2	9
GO:0007599	hemostasis	9/32	1.48E-08	HRG/PROS1/SERPINF2/PLG/FGB/F8/FGA/SERPING1/F2	9
GO:0032102	negative regulation of response to external stimulus	8/32	2.18E-08	HRG/PROS1/SERPINF2/PLG/FGB/FGA/SERPING1/F2	8
GO:0030258	lipid modification	8/32	2.54E-08	ACADS/ECHDC2/ACADM/ACAA1/ACAT1/GCDH/ACADL/ACADSB	8
GO:0072376	protein activation cascade	6/32	5.08E-08	PROS1/FGB/F8/FGA/SERPING1/F2	6
GO:0030194	positive regulation of blood coagulation	4/32	1.37E-07	HRG/SERPINF2/PLG/F2	4

GO:1900048	positive regulation of hemostasis	4/32	1.37E-07	HRG/SERPINF2/PLG/F2	4
GO:0050820	positive regulation of coagulation	4/32	1.62E-07	HRG/SERPINF2/PLG/F2	4
GO:0002526	acute inflammatory response	6/32	1.68E-07	ITIH4/PROS1/SERPINF2/F8/SERPING1/F2	6
GO:0010951	negative regulation of endopeptidase activity	7/32	2.24E-07	ITIH4/HRG/SERPINA4/PROS1/SERPINF2/SERPING1/SPP2	7
GO:0050878	regulation of body fluid levels	9/32	2.54E-07	HRG/PROS1/SERPINF2/PLG/FGB/F8/FGA/SERPING1/F2	9
GO:0052547	regulation of peptidase activity	8/32	4.97E-07	ITIH4/HRG/SERPINA4/PROS1/SERPINF2/SERPING1/SPP2/ECM1	8
GO:0051346	negative regulation of hydrolase activity	8/32	5.80E-07	ITIH4/HRG/SERPINA4/PROS1/SERPINF2/SERPING1/SPP2/ECM1	8
GO:0006637	acyl-CoA metabolic process	5/32	8.21E-07	ACSL5/ACSM2A/ACSL1/ACAT1/GCDH	5
GO:0035383	thioester metabolic process	5/32	8.21E-07	ACSL5/ACSM2A/ACSL1/ACAT1/GCDH	5
GO:0006953	acute-phase response	4/32	1.88E-06	ITIH4/SERPINF2/F8/F2	4
GO:0090303	positive regulation of wound healing	4/32	1.88E-06	HRG/SERPINF2/PLG/F2	4
GO:0035337	fatty-acyl-CoA metabolic process	4/32	2.23E-06	ACSL5/ACSM2A/ACSL1/GCDH	4
GO:1903036	positive regulation of response to wounding	4/32	3.06E-06	HRG/SERPINF2/PLG/F2	4
GO:0052548	regulation of endopeptidase activity	7/32	4.61E-06	ITIH4/HRG/SERPINA4/PROS1/SERPINF2/SERPING1/SPP2	7

GO:0016485	protein processing	6/32	4.67E-06	PROS1/SERPINF2/FGB/FGA/SERPING1/F2	6
GO:0007597	blood coagulation, intrinsic pathway	3/32	6.10E-06	F8/SERPING1/F2	3
GO:0031639	plasminogen activation	3/32	6.10E-06	SERPINF2/FGB/FGA	3
GO:0035384	thioester biosynthetic process	4/32	6.55E-06	ACSL5/ACSL1/ACAT1/GCDH	4
GO:0071616	acyl-CoA biosynthetic process	4/32	6.55E-06	ACSL5/ACSL1/ACAT1/GCDH	4
GO:0051604	protein maturation	6/32	8.75E-06	PROS1/SERPINF2/FGB/FGA/SERPING1/F2	6
GO:0030168	platelet activation	5/32	1.29E-05	HRG/FGB/F8/FGA/F2	5
GO:0006732	coenzyme metabolic process	6/32	1.94E-05	ACSL5/ACSM2A/IGF1/ACSL1/ACAT1/GCDH	6
GO:0001676	long-chain fatty acid metabolic process	4/32	2.43E-05	ACSL5/ACAA1/ACSL1/ACADL	4
GO:0031638	zymogen activation	3/32	4.77E-05	SERPINF2/FGB/FGA	3
GO:0006790	sulfur compound metabolic process	6/32	5.07E-05	ACSL5/ACSM2A/MUT/ACSL1/ACAT1/GCDH	6
GO:0051186	cofactor metabolic process	6/32	6.19E-05	ACSL5/ACSM2A/IGF1/ACSL1/ACAT1/GCDH	6
GO:0046949	fatty-acyl-CoA biosynthetic process	3/32	7.52E-05	ACSL5/ACSL1/GCDH	3
GO:0009108	coenzyme biosynthetic process	4/32	0.000134981	ACSL5/ACSL1/ACAT1/GCDH	4
GO:0017187	peptidyl-glutamic acid	2/32	0.000194194	PROS1/F2	2
GO:0018214	protein carboxylation	2/32	0.000194194	PROS1/F2	2
GO:0034116	positive regulation of heterotypic cell-cell adhesion	2/32	0.000194194	FGB/FGA	2
GO:2000047	regulation of cell-cell adhesion mediated by cadherin	2/32	0.000194194	SERPINF2/PLG	2
GO:0009437	carnitine metabolic process	2/32	0.000274742	ACADM/ACADL	2
GO:0036109	alpha-linolenic acid metabolic process	2/32	0.000274742	ACAA1/ACSL1	2
GO:0046459	short-chain fatty acid metabolic process	2/32	0.000320148	ACADS/MUT	2

GO:0010810	regulation of cell-substrate adhesion	4/32	0.000328036	HRG/PLG/FGB/FGA	4
GO:0051188	cofactor biosynthetic process	4/32	0.000350046	ACSL5/ACSL1/ACAT1/GCDH	4
GO:0044331	cell-cell adhesion mediated by cadherin	2/32	0.000368959	SERPINF2/PLG	2
GO:0006577	amino-acid betaine metabolic process	2/32	0.000476745	ACADM/ACADL	2
GO:0070613	regulation of protein processing	3/32	0.000477323	PROS1/SERPINF2/SERPING1	3
GO:1903317	regulation of protein maturation	3/32	0.000495037	PROS1/SERPINF2/SERPING1	3
GO:0034114	regulation of heterotypic cell-cell adhesion	2/32	0.000535696	FGB/FGA	2
GO:0006959	humoral immune response	4/32	0.000565981	PROS1/FGB/FGA/SERPING1	4
GO:0044272	sulfur compound biosynthetic process	4/32	0.000565981	ACSL5/ACSL1/ACAT1/GCDH	4
GO:0009083	branched-chain amino acid catabolic process	2/32	0.000598002	ACAT1/ACADSB	2
GO:0045785	positive regulation of cell adhesion	5/32	0.000652073	HRG/IGF1/SERPINF2/FGB/FGA	5
GO:0022407	regulation of cell-cell adhesion	5/32	0.000684469	IGF1/SERPINF2/PLG/FGB/FGA	5
GO:0032967	positive regulation of collagen biosynthetic process	2/32	0.000732631	SERPINF2/F2	2
GO:0009081	branched-chain amino acid metabolic process	2/32	0.000804929	ACAT1/ACADSB	2
GO:0010714	positive regulation of collagen metabolic process	2/32	0.000804929	SERPINF2/F2	2
GO:0044253	positive regulation of multicellular organismal	2/32	0.000804929	SERPINF2/F2	2
GO:2001237	negative regulation of extrinsic apoptotic signaling pathway	3/32	0.000942089	IGF1/FGB/FGA	3
GO:0010811	positive regulation of cell-substrate adhesion	3/32	0.000969376	HRG/FGB/FGA	3
GO:0006465	signal peptide processing	2/32	0.001041613	PROS1/F2	2
GO:0022409	positive regulation of cell-cell adhesion	4/32	0.001080294	IGF1/SERPINF2/FGB/FGA	4
GO:2000352	negative regulation of endothelial cell apoptotic	2/32	0.001127063	FGB/FGA	2
GO:0070371	ERK1 and ERK2 cascade	4/32	0.001294729	IGF1/SERPINF2/FGB/FGA	4

GO:0032965	regulation of collagen biosynthetic process	2/32	0.001307726	SERPINF2/F2	2
GO:0032103	positive regulation of response to external stimulus	4/32	0.00149493	HRG/SERPINF2/PLG/F2	4
GO:0010543	regulation of platelet activation	2/32	0.001501324	HRG/F2	2
GO:0018200	peptidyl-glutamic acid	2/32	0.001501324	PROS1/F2	2
GO:0030449	regulation of complement activation	2/32	0.001602943	PROS1/SERPING1	2
GO:0045907	positive regulation of vasoconstriction	2/32	0.001602943	FGB/FGA	2
GO:0010955	negative regulation of protein processing	2/32	0.001707761	SERPINF2/SERPING1	2
GO:1900026	positive regulation of substrate adhesion-dependent cell	2/32	0.001707761	FGB/FGA	2
GO:1903318	negative regulation of protein maturation	2/32	0.001707761	SERPINF2/SERPING1	2
GO:2000257	regulation of protein activation cascade	2/32	0.001707761	PROS1/SERPING1	2
GO:0010712	regulation of collagen metabolic process	2/32	0.001815765	SERPINF2/F2	2
GO:0032964	collagen biosynthetic process	2/32	0.001926943	SERPINF2/F2	2
GO:0044246	regulation of multicellular organismal metabolic process	2/32	0.001926943	SERPINF2/F2	2
GO:1902042	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors	2/32	0.001926943	FGB/FGA	2
GO:0050880	regulation of blood vessel size	3/32	0.002034361	SERPINF2/FGB/FGA	3
GO:1904036	negative regulation of epithelial cell apoptotic process	2/32	0.002041284	FGB/FGA	2
GO:0035150	regulation of tube size	3/32	0.002078607	SERPINF2/FGB/FGA	3
GO:0008015	blood circulation	5/32	0.002127417	SERPINF2/FGB/FGA/ACSM3/SERPING1	5
GO:0003013	circulatory system process	5/32	0.002205172	SERPINF2/FGB/FGA/ACSM3/SERPING1	5
GO:0048771	tissue remodeling	3/32	0.002504011	HRG/PLG/SPP2	3
GO:0031589	cell-substrate adhesion	4/32	0.002513995	HRG/PLG/FGB/FGA	4
GO:2000351	regulation of endothelial cell apoptotic process	2/32	0.002530037	FGB/FGA	2
GO:0035338	long-chain fatty-acyl-CoA biosynthetic process	2/32	0.002929234	ACSL5/ACSL1	2

GO:2001236	regulation of extrinsic apoptotic signaling pathway	3/32	0.003149876	IGF1/FGB/FGA	3
GO:0003018	vascular process in circulatory system	3/32	0.00320788	SERPINF2/FGB/FGA	3
GO:0072577	endothelial cell apoptotic	2/32	0.003356054	FGB/FGA	2
GO:0030198	extracellular matrix organization	4/32	0.003499754	SERPINF2/PLG/FGB/FGA	4
GO:0034113	heterotypic cell-cell adhesion	2/32	0.003504411	FGB/FGA	2
GO:0035336	long-chain fatty-acyl-CoA metabolic process	2/32	0.003504411	ACSL5/ACSL1	2
GO:1900024	regulation of substrate adhesion-dependent cell spreading	2/32	0.003504411	FGB/FGA	2
GO:0043062	extracellular structure organization	4/32	0.003537819	SERPINF2/PLG/FGB/FGA	4
GO:0019731	antibacterial humoral response	2/32	0.003810185	FGB/FGA	2
GO:0002920	regulation of humoral immune response	2/32	0.00412796	PROS1/SERPING1	2
GO:0070374	positive regulation of ERK1 and ERK2 cascade	3/32	0.004157871	SERPINF2/FGB/FGA	3
GO:1901565	organonitrogen compound catabolic process	4/32	0.004315876	ACAT1/GCDH/ACADL/ACADSB	4
GO:0006888	ER to Golgi vesicle-mediated transport	3/32	0.004366242	PROS1/F8/F2	3
GO:0019730	antimicrobial humoral response	2/32	0.004799153	FGB/FGA	2
GO:1902041	regulation of extrinsic apoptotic signaling pathway via death domain receptors	2/32	0.004974312	FGB/FGA	2
GO:0070527	platelet aggregation	2/32	0.005152391	FGB/FGA	2
GO:0019229	regulation of vasoconstriction	2/32	0.005517271	FGB/FGA	2
GO:1901605	alpha-amino acid metabolic process	3/32	0.00574986	MUT/ACAT1/GCDH	3
GO:0007160	cell-matrix adhesion	3/32	0.005918008	HRG/FGB/FGA	3
GO:1904035	regulation of epithelial cell apoptotic process	2/32	0.006281602	FGB/FGA	2
GO:0014068	positive regulation of phosphatidylinositol 3-kinase signaling	2/32	0.006680876	IGF1/F2	2
GO:2001234	negative regulation of apoptotic signaling pathway	3/32	0.006895668	IGF1/FGB/FGA	3
GO:0050714	positive regulation of protein secretion	3/32	0.00708314	IGF1/FGB/FGA	3

GO_BP_clsuter2

ID	Description	GeneRatio	pvalue	geneID	Count

GO:0008202	steroid metabolic process	15/35	2.69E-18	GC/SLCO1B1/ACADVL/CYP2E1/HSD17B6/CYP1A1/ACOX2/CYP2C9/UGT2B7/CYP3A4/NR1I2/CYP1A2/APOA1/CYP2B6/CYP3A5	15
GO:0006631	fatty acid metabolic process	16/35	3.93E-18	CYP4F3/CYP2J2/ACADVL/CYP2E1/CYP1A1/ACOX2/CYP2C9/CYP4F2/APOC3/CYP1A2/APOA1/CYP4A11/CYP2B6/ACOX1/ACACB/EHHADH	16
GO:0019373	epoxygenase P450 pathway	8/35	6.87E-18	CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP4F2/CYP1A2/CYP4A11/CYP2B6	8
GO:0017144	drug metabolic process	9/35	9.62E-18	CYP2E1/CYP1A1/CYP2C9/CYP3A4/CYP4F2/NR1I2/CYP1A2/CYP2B6/CYP3A5	9
GO:0006805	xenobiotic metabolic process	10/35	3.62E-15	CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP3A4/NR1I2/CYP1A2/CYP26A1/CYP2B6/CYP3A5	10
GO:0006690	icosanoid metabolic process	10/35	5.00E-15	CYP4F3/CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP4F2/CYP1A2/CYP4A11/CYP2B6/ACOX1	10

GO:0071466	cellular response to xenobiotic stimulus	10/35	5.55E-15	CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP3A4/NR1I2/CYP1A2/CYP26A1/CYP2B6/CYP3A5	10
GO:0016042	lipid catabolic process	13/35	1.07E-14	CYP4F3/ACADVL/ACOX2/CYP3A4/CYP4F2/APOC3/CYP1A2/APOA1/CYP26A1/CYP4A11/ACOX1/ACACB/EHHADH	13
GO:0006721	terpenoid metabolic process	10/35	1.12E-14	CYP2E1/CYP1A1/CYP2C9/CYP3A4/TTR/APOC3/CYP1A2/APOA1/CYP26A1/ALDH8A1	10
GO:0009410	response to xenobiotic stimulus	10/35	1.24E-14	CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP3A4/NR1I2/CYP1A2/CYP26A1/CYP2B6/CYP3A5	10
GO:0033559	unsaturated fatty acid metabolic process	10/35	2.17E-14	CYP4F3/CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP4F2/CYP1A2/CYP4A11/CYP2B6/ACOX1	10
GO:0019369	arachidonic acid metabolic process	8/35	5.67E-14	CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP4F2/CYP1A2/CYP4A11/CYP2B6	8

GO:0044282	small molecule catabolic process	13/35	6.85E-14	CYP4F3/ACADVL/ALDH2/CYP1A1/ACOX2/CYP4F2/CYP26A1/CYP4A11/ACOX1/ACACB/KMO/EHHADH/ALDH6A1	13
GO:0006720	isoprenoid metabolic process	10/35	7.77E-14	CYP2E1/CYP1A1/CYP2C9/CYP3A4/TTR/APOC3/CYP1A2/APOA1/CYP26A1/ALDH8A1	10
GO:0001676	long-chain fatty acid metabolic process	9/35	1.47E-13	CYP2J2/CYP2E1/CYP1A1/CYP2C9/CYP4F2/CYP1A2/CYP4A11/CYP2B6/ACOX1	9
GO:0042737	drug catabolic process	6/35	2.69E-13	CYP2C9/CYP3A4/NR1I2/CYP1A2/CYP2B6/CYP3A5	6
GO:0016054	organic acid catabolic process	11/35	5.46E-13	CYP4F3/ACADVL/ACOX2/CYP4F2/CYP26A1/CYP4A11/ACOX1/ACACB/KMO/EHHADH/ALDH6A1	11
GO:0042738	exogenous drug catabolic process	5/35	2.37E-11	CYP2C9/CYP3A4/NR1I2/CYP1A2/CYP2B6	5
GO:0006766	vitamin metabolic process	8/35	2.31E-10	GC/CYP1A1/CYP3A4/CYP4F2/AOX1/CYP26A1/ACACB/CYB5A	8
GO:0030258	lipid modification	9/35	2.52E-09	ACADVL/CYP1A1/ACOX2/CYP3A4/APOA1/ACOX1/CYP3A5/ACACB/EHHADH	9

GO:0044242	cellular lipid catabolic process	8/35	3.30E-09	ACADVL/ACOX2/APOC3/APOA1/CYP26A1/ACOX1/ACACB/EHHADH	8
GO:1901615	organic hydroxy compound metabolic process	10/35	7.51E-09	GC/CYP4F3/ACADVL/ALDH2/CYP1A1/CYP3A4/TTR/CYP4F2/APOA1/CYP4A11	10
GO:0070989	oxidative demethylation	4/35	2.18E-08	CYP2C9/CYP3A4/CYP1A2/CYP3A5	4
GO:0006775	fat-soluble vitamin metabolic process	5/35	2.44E-08	GC/CYP1A1/CYP3A4/CYP4F2/CYP26A1	5
GO:0001523	retinoid metabolic process	6/35	2.80E-08	CYP1A1/TTR/APOC3/APOA1/CYP26A1/ALDH8A1	6
GO:0016101	diterpenoid metabolic process	6/35	4.41E-08	CYP1A1/TTR/APOC3/APOA1/CYP26A1/ALDH8A1	6
GO:0016053	organic acid biosynthetic process	8/35	6.49E-08	ACADVL/CYP1A1/ACOX2/APOC3/APOA1/ACACB/KMO/ALDH8A1	8
GO:0072329	monocarboxylic acid catabolic process	6/35	8.00E-08	ACADVL/ACOX2/CYP26A1/ACOX1/ACACB/EHHADH	6
GO:0034754	cellular hormone metabolic process	6/35	8.47E-08	HSD17B6/UGT2B7/CYP3A4/TTR/CYP26A1/ALDH8A1	6
GO:0042493	response to drug	9/35	9.18E-08	CYP2E1/CYP1A1/CYP2C9/CYP3A4/NR1I2/CYP1A2/APOA1/CYP2B6/ACACB	9

GO:0046395	carboxylic acid catabolic process	7/35	1.37E-07	ACADVL/ACOX2/CYP26A1/ACOX1/ACACB/EHHADH/ALDH6A1	7
GO:0070988	demethylation	5/35	1.40E-07	CYP1A1/CYP2C9/CYP3A4/CYP1A2/CYP3A5	5
GO:0042180	cellular ketone metabolic process	7/35	2.66E-07	ACADVL/CYP4F2/APOC3/APOA1/CYP2B6/ACACB/KMO	7
GO:0006635	fatty acid beta-oxidation	5/35	3.57E-07	ACADVL/ACOX2/ACOX1/ACACB/EHHADH	5
GO:0044283	small molecule biosynthetic process	9/35	4.57E-07	ACADVL/CYP1A1/ACOX2/CYP3A4/APOC3/APOA1/ACACB/KMO/ALDH8A1	9
GO:0009062	fatty acid catabolic process	5/35	1.11E-06	ACADVL/ACOX2/ACOX1/ACACB/EHHADH	5
GO:1901568	fatty acid derivative metabolic process	3/35	1.38E-06	CYP4F3/CYP4F2/CYP4A11	3
GO:0019395	fatty acid oxidation	5/35	1.70E-06	ACADVL/ACOX2/ACOX1/ACACB/EHHADH	5
GO:0042445	hormone metabolic process	6/35	1.82E-06	HSD17B6/UGT2B7/CYP3A4/TTR/CYP26A1/ALDH8A1	6
GO:0034440	lipid oxidation	5/35	1.88E-06	ACADVL/ACOX2/ACOX1/ACACB/EHHADH	5
GO:0009820	alkaloid metabolic process	3/35	3.04E-06	CYP3A4/CYP1A2/CYP3A5	3

GO:0010817	regulation of hormone levels	8/35	3.86E-06	SLCO1B1/HSD17B6/UGT2B7/CYP3A4/TTR/CYP26A1/SERPINA7/ALDH8A1	8
GO:1901616	organic hydroxy compound catabolic process	4/35	4.43E-06	CYP4F3/ALDH2/CYP4F2/CYP4A11	4
GO:0033539	fatty acid beta-oxidation using acyl-CoA dehydrogenase	3/35	8.03E-06	ACADVL/ACOX2/ACOX1	3
GO:0042359	vitamin D metabolic process	3/35	9.43E-06	GC/CYP1A1/CYP3A4	3
GO:0046394	carboxylic acid biosynthetic process	6/35	1.29E-05	ACADVL/ACOX2/APOC3/APOA1/ACACB/KMO	6
GO:0045922	negative regulation of fatty acid metabolic process	3/35	1.46E-05	ACADVL/APOC3/ACACB	3
GO:0019217	regulation of fatty acid metabolic process	4/35	2.08E-05	ACADVL/APOC3/APOA1/ACACB	4
GO:0008209	androgen metabolic process	3/35	2.39E-05	HSD17B6/UGT2B7/CYP3A4	3
GO:0000038	very long-chain fatty acid metabolic process	3/35	2.98E-05	ACADVL/CYP4F2/ACOX1	3
GO:0006691	leukotriene metabolic process	3/35	2.98E-05	CYP4F3/CYP4F2/CYP4A11	3
GO:0072330	monocarboxylic acid biosynthetic process	5/35	3.46E-05	ACADVL/ACOX2/APOC3/APOA1/ACACB	5
GO:0032368	regulation of lipid transport	4/35	3.99E-05	CYP4F2/APOC3/APOA1/CYP4A11	4
GO:0006869	lipid transport	6/35	4.28E-05	SLCO1B1/CYP4F2/APOC3/APOA1/CYP4A11/ACACB	6
GO:0042304	regulation of fatty acid biosynthetic process	3/35	4.85E-05	ACADVL/APOC3/APOA1	3
GO:0006778	porphyrin-containing compound metabolic process	3/35	5.77E-05	CYP1A1/HPX/CYP1A2	3
GO:0010876	lipid localization	6/35	7.59E-05	SLCO1B1/CYP4F2/APOC3/APOA1/CYP4A11/ACACB	6

GO:0051186	cofactor metabolic process	6/35	0.000104863	CYP1A1/HPX/CYP4F2/CYP1A2/ACACB/KMO	6
GO:0055088	lipid homeostasis	4/35	0.00012375	ACADVL/ACOX2/APOC3/APOA1	4
GO:0050994	regulation of lipid catabolic process	3/35	0.000174559	APOC3/APOA1/ACACB	3
GO:0015718	monocarboxylic acid transport	4/35	0.000187488	SLCO1B1/CYP4F2/CYP4A11/ACACB	4
GO:0009111	vitamin catabolic process	2/35	0.000190644	CYP4F2/CYP26A1	2
GO:0006633	fatty acid biosynthetic process	4/35	0.000198216	ACADVL/APOC3/APOA1/ACACB	4
GO:0019748	secondary metabolic process	3/35	0.000229458	CYP1A1/CYP1A2/KMO	3
GO:0033013	tetrapyrrole metabolic process	3/35	0.000229458	CYP1A1/HPX/CYP1A2	3
GO:0016114	terpenoid biosynthetic process	2/35	0.000232702	CYP1A1/ALDH8A1	2
GO:0034370	triglyceride-rich lipoprotein particle remodeling	2/35	0.000232702	APOC3/APOA1	2
GO:0034372	very-low-density lipoprotein particle remodeling	2/35	0.000232702	APOC3/APOA1	2
GO:0050665	hydrogen peroxide biosynthetic process	2/35	0.000232702	CYP1A1/CYP1A2	2
GO:1901361	organic cyclic compound catabolic process	6/35	0.000241537	CYP1A1/CYP3A4/CYP1A2/AOX1/KMO/ALDH6A1	6
GO:0010565	regulation of cellular ketone metabolic process	4/35	0.000272118	ACADVL/APOC3/APOA1/ACACB	4
GO:0009404	toxin metabolic process	2/35	0.000278875	CYP1A1/CYP1A2	2
GO:0010896	regulation of triglyceride catabolic process	2/35	0.000278875	APOC3/APOA1	2
GO:0006066	alcohol metabolic process	5/35	0.000286239	ACADVL/ALDH2/CYP3A4/TTR/APOA1	5
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	2/35	0.000329145	ACOX2/ACOX1	2

GO:0033700	phospholipid efflux	2/35	0.000383496	APOC3/APOA1	2
GO:0045717	negative regulation of fatty acid biosynthetic process	2/35	0.000383496	ACADVL/APOC3	2
GO:0032305	positive regulation of icosanoid secretion	2/35	0.000441913	CYP4F2/CYP4A11	2
GO:0034375	high-density lipoprotein particle remodeling	2/35	0.000441913	APOC3/APOA1	2
GO:0051004	regulation of lipoprotein lipase activity	2/35	0.000441913	APOC3/APOA1	2
GO:0060192	negative regulation of lipase activity	2/35	0.000441913	APOC3/APOA1	2
GO:2000193	positive regulation of fatty acid transport	2/35	0.000504377	CYP4F2/CYP4A11	2
GO:0045833	negative regulation of lipid metabolic process	3/35	0.000516019	ACADVL/APOC3/ACACB	3
GO:0001977	renal system process involved in regulation of blood volume	2/35	0.000570875	CYP4F2/CYP4A11	2
GO:0032303	regulation of icosanoid secretion	2/35	0.000570875	CYP4F2/CYP4A11	2
GO:0043691	reverse cholesterol transport	2/35	0.000570875	APOC3/APOA1	2
GO:0015908	fatty acid transport	3/35	0.000744034	CYP4F2/CYP4A11/ACACB	3
GO:1901565	organonitrogen compound catabolic process	5/35	0.000766373	CYP3A4/AOX1/CYP3A5/KMO/ALDH6A1	5
GO:0034377	plasma lipoprotein particle assembly	2/35	0.000794398	APOC3/APOA1	2
GO:0042537	benzene-containing compound metabolic process	2/35	0.000794398	CYP2E1/KMO	2
GO:0006767	water-soluble vitamin metabolic process	3/35	0.00082309	AOX1/ACACB/CYB5A	3
GO:0006706	steroid catabolic process	2/35	0.000876863	CYP3A4/CYP1A2	2
GO:0042573	retinoic acid metabolic process	2/35	0.000876863	CYP26A1/ALDH8A1	2
GO:0035902	response to immobilization stress	2/35	0.000963279	CYP1A1/CYP1A2	2
GO:0050995	negative regulation of lipid catabolic process	2/35	0.000963279	APOC3/ACACB	2
GO:0065005	protein-lipid complex assembly	2/35	0.000963279	APOC3/APOA1	2
GO:0072337	modified amino acid transport	2/35	0.001053631	SLCO1B1/SERPINA7	2

GO:0003071	renal system process involved in regulation of systemic arterial blood pressure	2/35		0.001147902	CYP4F2/CYP4A11	2
GO:0032369	negative regulation of lipid transport	2/35		0.001147902	CYP4F2/APOC3	2
GO:0034367	macromolecular complex remodeling	2/35		0.001147902	APOC3/APOA1	2
GO:0034368	protein-lipid complex remodeling	2/35		0.001147902	APOC3/APOA1	2
GO:0034369	plasma lipoprotein particle remodeling	2/35		0.001147902	APOC3/APOA1	2
GO:2000191	regulation of fatty acid transport	2/35		0.001147902	CYP4F2/CYP4A11	2
GO:0044550	secondary metabolite biosynthetic process	2/35		0.001246078	CYP1A2/KMO	2
GO:0006641	triglyceride metabolic process	3/35		0.001298264	CYP2E1/APOC3/APOA1	3
GO:0044270	cellular nitrogen compound catabolic process	5/35		0.001437668	CYP3A4/AOX1/CYP3A5/KMO/ALDH6A1	5
GO:0008299	isoprenoid biosynthetic process	2/35		0.001454076	CYP1A1/ALDH8A1	2
GO:0009812	flavonoid metabolic process	2/35		0.001454076	CYP1A1/UGT2B7	2
GO:0046320	regulation of fatty acid oxidation	2/35		0.001563868	ACADVL/ACACB	2
GO:1903793	positive regulation of anion transport	2/35		0.001794958	CYP4F2/CYP4A11	2
GO:0090207	regulation of triglyceride metabolic process	2/35		0.001916224	APOC3/APOA1	2
GO:0006639	acylglycerol metabolic process	3/35		0.001917763	CYP2E1/APOC3/APOA1	3
GO:0006638	neutral lipid metabolic process	3/35		0.001964544	CYP2E1/APOC3/APOA1	3
GO:0034381	plasma lipoprotein particle clearance	2/35		0.002041284	APOC3/APOA1	2
GO:0046942	carboxylic acid transport	4/35		0.002098273	SLCO1B1/CYP4F2/CYP4A11/ACACB	4
GO:0019433	triglyceride catabolic process	2/35		0.002170123	APOC3/APOA1	2
GO:0051180	vitamin transport	2/35		0.002170123	GC/APOA1	2
GO:0055090	acylglycerol homeostasis	2/35		0.002170123	APOC3/APOA1	2
GO:0070328	triglyceride homeostasis	2/35		0.002170123	APOC3/APOA1	2

GO:0003091	renal water homeostasis	2/35	0.002302724	CYP4F2/CYP4A11	2
GO:0071827	plasma lipoprotein particle organization	2/35	0.002302724	APOC3/APOA1	2
GO:0046890	regulation of lipid biosynthetic process	3/35	0.002312042	ACADVL/APOC3/APOA1	3
GO:1902652	secondary alcohol metabolic process	3/35	0.002312042	ACADVL/CYP3A4/APOA1	3
GO:0019216	regulation of lipid metabolic process	4/35	0.002502704	ACADVL/APOC3/APOA1/ACACB	4
GO:0071825	protein-lipid complex subunit organization	2/35	0.002579152	APOC3/APOA1	2
GO:0009112	nucleobase metabolic process	2/35	0.002722949	AOX1/ALDH6A1	2
GO:0032371	regulation of sterol transport	2/35	0.002870447	APOC3/APOA1	2
GO:0032374	regulation of cholesterol transport	2/35	0.002870447	APOC3/APOA1	2
GO:0046461	neutral lipid catabolic process	2/35	0.003021631	APOC3/APOA1	2
GO:0046464	acylglycerol catabolic process	2/35	0.003021631	APOC3/APOA1	2
GO:0046686	response to cadmium ion	2/35	0.003021631	CYP1A2/CYB5A	2
GO:0033344	cholesterol efflux	2/35	0.003334995	APOC3/APOA1	2
GO:0008206	bile acid metabolic process	2/35	0.003662921	SLCO1B1/ACOX2	2
GO:0032309	icosanoid secretion	2/35	0.003662921	CYP4F2/CYP4A11	2
GO:0042743	hydrogen peroxide metabolic process	2/35	0.003662921	CYP1A1/CYP1A2	2
GO:0034308	primary alcohol metabolic	2/35	0.003832307	ALDH2/TTR	2
GO:0006694	steroid biosynthetic process	3/35	0.0038549	ACOX2/CYP3A4/APOA1	3
GO:0051055	negative regulation of lipid biosynthetic process	2/35	0.004005288	ACADVL/APOC3	2
GO:0071715	icosanoid transport	2/35	0.004181849	CYP4F2/CYP4A11	2
GO:0015711	organic anion transport	4/35	0.004219629	SLCO1B1/CYP4F2/CYP4A11/ACACB	4
GO:0006879	cellular iron ion homeostasis	2/35	0.004545653	HPX/CP	2
GO:0055078	sodium ion homeostasis	2/35	0.004545653	CYP4F2/CYP4A11	2

GO:0048871	multicellular organismal homeostasis	4/35	0.004659594	ACADVL/CYP4F2/CYP4A11/ACACB	4
GO:0032370	positive regulation of lipid transport	2/35	0.004732866	CYP4F2/CYP4A11	2
GO:0046503	glycerolipid catabolic process	2/35	0.004732866	APOC3/APOA1	2
GO:0097006	regulation of plasma lipoprotein particle levels	2/35	0.006141117	APOC3/APOA1	2
GO:0050891	multicellular organismal water homeostasis	2/35	0.00657446	CYP4F2/CYP4A11	2
GO:0015914	phospholipid transport	2/35	0.007249862	APOC3/APOA1	2
GO:0019915	lipid storage	2/35	0.007955385	APOA1/ACACB	2
GO:0015850	organic hydroxy compound transport	3/35	0.008053573	SLCO1B1/APOC3/APOA1	3
GO:0043270	positive regulation of ion transport	3/35	0.008858799	CYP4F2/CYP4A11/DMD	3
GO:0046700	heterocycle catabolic process	4/35	0.009177063	CYP1A1/AOX1/KMO/ALDH6A1	4
GO:0030104	water homeostasis	2/35	0.009197156	CYP4F2/CYP4A11	2
GO:0042632	cholesterol homeostasis	2/35	0.009197156	APOC3/APOA1	2
GO:0055092	sterol homeostasis	2/35	0.009197156	APOC3/APOA1	2
GO:0055072	iron ion homeostasis	2/35	0.009716601	HPX/CP	2
GO:0030301	cholesterol transport	2/35	0.010248872	APOC3/APOA1	2
GO:0015918	sterol transport	2/35	0.010519783	APOC3/APOA1	2
GO_BP_cluster3					
ID	Description	BgRatio	pvalue	geneID	Count
GO:0071294	cellular response to zinc ion	18/16672	4.49E-22	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0010043	response to zinc ion	52/16672	1.89E-18	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7

GO:1990267	response to transition metal nanoparticle	124/16672	1.06E-15	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0071248	cellular response to metal ion	129/16672	1.41E-15	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0071241	cellular response to inorganic substance	149/16672	3.95E-15	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0071276	cellular response to cadmium ion	15/16672	5.87E-15	MT1F/MT1G/MT1X/MT1E/MT1H	5
GO:0045926	negative regulation of growth	226/16672	7.67E-14	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0010038	response to metal ion	297/16672	5.31E-13	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0046686	response to cadmium ion	39/16672	1.12E-12	MT1F/MT1G/MT1X/MT1E/MT1H	5
GO:0010035	response to inorganic substance	455/16672	1.08E-11	MT1F/MT1M/MT1G/MT1X/MT1E/MT1H/MT2A	7
GO:0046688	response to copper ion	21/16672	3.16E-05	MT1G/MT1X	2
GO:0046916	cellular transition metal ion homeostasis	85/16672	0.000530583	MT1X/MT2A	2
GO:0055076	transition metal ion homeostasis	113/16672	0.000935224	MT1X/MT2A	2

Table S6.Univariate cox analyses and Kaplan-Meier survival analysis of the Cluster 1 gene(N=212)

gene symbol	Univariate Analysis		KM survival
	HR (95% CI)	p value	log-rank test P
FGB	0.96(0.787-1.172)	0.689	0.5729
F2	0.954(0.79-1.153)	0.626	0.0546
ECM1	0.897(0.629-1.28)	0.55	0.1642
ALB	0.928(0.746-1.154)	0.5	0.0522
PROS1	0.901(0.734-1.106)	0.318	0.0893
ACADSB	0.897(0.743-1.082)	0.256	0.2355
ITIH4	0.905(0.767-1.067)	0.235	0.1741
ACSL5	0.911(0.786-1.056)	0.218	0.4363

ACADL	0.849(0.666-1.081)	0.184	0.0784
FGA	0.89(0.757-1.047)	0.16	0.5018
ACADS	0.749(0.515-1.089)	0.13	0.2192
ACAA1	0.825(0.655-1.038)	0.1	0.0454
PLG	0.902(0.799-1.019)	0.096	0.0605
IGF1	0.853(0.708-1.028)	0.095	0.1137
SERPINA4	0.886(0.779-1.009)	0.068	0.0568
ACSL1	0.867(0.744-1.011)	0.068	0.4589
SERPINF2	0.842(0.706-1.004)	0.055	0.1173
SERPING1	0.837(0.71-0.985)	0.032^{*}	0.0833
F8	0.772(0.614-0.97)	0.026^{*}	0.0238^{*}
ACSM3	0.751(0.602-0.937)	0.011^{*}	0.0042^{***}
ACAT1	0.743(0.601-0.917)	0.006^{**}	0.1827
HRG	0.867(0.785-0.958)	0.005^{**}	0.0126^{*}
GCDH	0.71(0.56-0.899)	0.0044^{***}	0.003^{***}
MUT	0.686(0.543-0.866)	0.0015^{***}	0.0002^{***}
CRYL1	0.733(0.614-0.876)	0.0006^{***}	0.0262^{*}
CDC37L1	0.564(0.417-0.762)	0.0002^{***}	0.0007^{***}
SPP2	0.826(0.749-0.911)	0.0001^{***}	$<0.0001^{***}$
ACADM	0.599(0.468-0.767)	$<0.0001^{***}$	0.0003^{***}
ECHDC2	0.624(0.495-0.786)	$<0.0001^{***}$	0.0006^{***}

HR Hazard ratio,CI confdence interval,*Signifcant P value,*** P<0.005,** P<0.01,* P<0.05

Table S7.Cox proportional hazards models in discovery cohort and internal testing cohort

	discovery cohort (N=106)					internal testing cohort (N=106)			
Factor	Univariate Analysis		Multivariate Analysis			Univariate Analysis		Multivariate Analysis	
	HR (95% CI)	*p* value	HR (95% CI)	*p* value		HR (95% CI)	*p* value	HR (95% CI)	*p* value
Sex, male v	1.13(0.44-2.9)	0.8	1.2(0.47-3.08)	0.699		2.67(0.82-8.64)	0.102	2.12(0.64-6.96)	0.217
Age	1.01(0.98-1.04)	0.7	1.01(0.98-1.04)	0.643		0.98(0.95-1.00)	0.082	0.98(0.96-1.01)	0.273
Risk Score	2.72(1.84-4.02)	<0.001***	2.72(1.84-4.01)	<0.001***		1.51(1.12-2.04)	0.007**	1.42(1.04-1.94)	0.026*

HR Hazard ratio,CI confdence interval,*Signifcant P value,*** P<0.005,** P<0.01,* P<0.05