Table S1. DEGs identified in PDAC

Gene	logFC	P Value	FDR	regulated
LAMC2	2.650	1.51583E-33	2.28981E-29	Up-Regulated
S100P	4.297	3.48635E-33	2.63324E-29	Up-Regulated
KRT19	3.527	7.83878E-33	3.94709E-29	Up-Regulated
GPRC5A	2.936	2.42274E-32	7.59769E-29	Up-Regulated
ITGA2	2.048	2.51479E-32	7.59769E-29	Up-Regulated
SLPI	2.634	1.12073E-31	2.82161E-28	Up-Regulated
ANXA2	1.298	2.99506E-31	6.46334E-28	Up-Regulated
INHBA	3.142	2.69629E-30	5.09126E-27	Up-Regulated
GJB2	3.389	3.20932E-30	5.38667E-27	Up-Regulated
FN1	2.787	1.02154E-29	1.54314E-26	Up-Regulated
SLC6A14	3.817	1.86355E-29	2.55916E-26	Up-Regulated
KRT7	2.681	2.05178E-29	2.58285E-26	Up-Regulated
SULF1	3.126	3.60334E-29	4.18708E-26	Up-Regulated
SFN	2.944	6.54358E-29	7.06052E-26	Up-Regulated
AHNAK2	2.281	8.47941E-29	8.53934E-26	Up-Regulated
TNFRSF21	1.607	2.14461E-28	2.02478E-25	Up-Regulated
COL10A1	3.480	2.76465E-28	2.45664E-25	Up-Regulated
LAMB3	2.223	3.55549E-28	2.98384E-25	Up-Regulated
NQO1	2.573	6.26771E-28	4.98316E-25	Up-Regulated
ANO1	1.826	6.90453E-28	5.21499E-25	Up-Regulated
SERPINB5	2.598	1.64594E-27	1.18398E-24	Up-Regulated
S100A11	1.839	1.89543E-27	1.30147E-24	Up-Regulated
IGFBP3	2.459	2.09147E-27	1.37364E-24	Up-Regulated
S100A10	1.439	3.54929E-27	2.23398E-24	Up-Regulated
COL11A1	3.605	4.55117E-27	2.75E-24	Up-Regulated
SDR16C5	3.022	5.35834E-27	3.11319E-24	Up-Regulated
MBOAT2	1.350	5.73091E-27	3.20634E-24	Up-Regulated
TMPRSS4	2.301	7.61661E-27	4.10916E-24	Up-Regulated
S100A16	1.380	1.03867E-26	5.41041E-24	Up-Regulated
DCBLD1	1.237	1.46446E-26	7.37403E-24	Up-Regulated
ITGB1BP1	1.161	1.60406E-26	7.81644E-24	Up-Regulated
NHS	1.493	2.08194E-26	9.53022E-24	Up-Regulated
BIK	1.840	3.08514E-26	1.37071E-23	Up-Regulated
CTHRC1	3.221	3.35714E-26	1.44894E-23	Up-Regulated
S100A6	2.392	3.48733E-26	1.46332E-23	Up-Regulated
CAPG	1.813	7.40686E-26	3.024E-23	Up-Regulated
GJB3	1.206	7.8409E-26	3.11696E-23	Up-Regulated
SDC1	1.422	8.08522E-26	3.13167E-23	Up-Regulated
KDM5B	1.053	8.31294E-26	3.13938E-23	Up-Regulated
COL1A2	3.012	9.47339E-26	3.49037E-23	Up-Regulated
NOX4	1.997	1.15155E-25	4.14173E-23	Up-Regulated
HOXB7	1.497	2.20995E-25	7.76362E-23	Up-Regulated
TPBG	1.330	2.32188E-25	7.97144E-23	Up-Regulated
C15orf48	2.588	2.60955E-25	8.75998E-23	Up-Regulated
FHL2	1.802	3.28089E-25	1.07741E-22	Up-Regulated
ARNTL2	1.571	5.15371E-25	1.65642E-22	Up-Regulated
MXRA5	1.976	5.44454E-25	1.71344E-22	Up-Regulated
HOXB3	1.354	6.25057E-25	1.92696E-22	Up-Regulated
TSPAN1	2.076	7.43038E-25	2.24487E-22	Up-Regulated
COL5A2	2.580	8.67099E-25	2.54123E-22	Up-Regulated

MYOF	1.737	8.74778E-25	2.54123E-22	Up-Regulated
CTSE	3.136	1.22047E-24	3.47858E-22	Up-Regulated
ADAMTS12	1.508	1.38002E-24	3.86047E-22	Up-Regulated
SHISA2	2.153	1.94594E-24	5.34461E-22	Up-Regulated
THBS2	2.681	2.2053E-24	5.94881E-22	Up-Regulated
SOX4	1.139	2.48598E-24	6.5374E-22	Up-Regulated
EFNA5	1.332	2.51006E-24	6.5374E-22	Up-Regulated
RTP4	1.293	3.02265E-24	7.53528E-22	Up-Regulated
POSTN	3.309	3.04284E-24	7.53528E-22	Up-Regulated
IFI27	2.176	3.84702E-24	9.37307E-22	Up-Regulated
NET1	1.170	4.25854E-24	1.0211E-21	Up-Regulated
MSLN	2.889	4.34982E-24	1.02669E-21	Up-Regulated
AMIGO2	1.687	4.55706E-24	1.05906E-21	Up-Regulated
FXYD3	1.948	4.89832E-24	1.12112E-21	Up-Regulated
DKK1	2.605	6.63757E-24	1.49652E-21	Up-Regulated
LY6E	1.441	6.99354E-24	1.55359E-21	Up-Regulated
OSBPL3	1.600	7.66898E-24	1.67895E-21	Up-Regulated
KLK10	2.285	8.89584E-24	1.91972E-21	Up-Regulated
CEACAM6	3.786	9.25046E-24	1.96813E-21	Up-Regulated
CD9	1.272	1.16825E-23	2.44678E-21	Up-Regulated
STEAP1	1.770	1.18241E-23	2.44678E-21	Up-Regulated
LGALS3	1.412	1.35063E-23	2.75712E-21	Up-Regulated
ITGA3	1.502	1.63418E-23	3.29145E-21	Up-Regulated
NFE2L3	1.417	1.83919E-23	3.65563E-21	Up-Regulated
SMAGP	1.293	2.08687E-23	4.09407E-21	Up-Regulated
SESTD1	1.113	2.63383E-23	5.10084E-21	Up-Regulated
HN1	1.578	4.4819E-23	8.57008E-21	Up-Regulated
CKLF	1.335	6.04684E-23	1.1277E-20	Up-Regulated
PKM	1.358	7.1455E-23	1.31634E-20	Up-Regulated
FERMT1	1.786	7.94031E-23	1.44514E-20	Up-Regulated
TIMP1	2.013	1.02281E-22	1.83936E-20	Up-Regulated
CEACAM5	4.088	1.13206E-22	2.01187E-20	Up-Regulated
FGD6	1.354	1.37605E-22	2.41705E-20	Up-Regulated
MLPH	1.898	1.4598E-22	2.53468E-20	Up-Regulated
CST1	2.898	1.50379E-22	2.54506E-20	Up-Regulated
ACVR1	1.185	1.52125E-22	2.54506E-20	Up-Regulated
CSTB	1.250	1.52762E-22	2.54506E-20	Up-Regulated
NMU	2.293	1.53317E-22	2.54506E-20	Up-Regulated
CDH3	1.672	1.782E-22	2.89738E-20	Up-Regulated
KRT17	2.403	1.78377E-22	2.89738E-20	Up-Regulated
CD55	1.902	1.90417E-22	3.06005E-20	Up-Regulated
HK2	1.817	2.12681E-22	3.38186E-20	Up-Regulated
VCAN	2.583	2.62213E-22	4.12603E-20	Up-Regulated
PFKP	1.561	3.01228E-22	4.69108E-20	Up-Regulated
PPAPDC1A	1.987	3.18243E-22	4.90549E-20	Up-Regulated
COL5A1	2.057	3.74844E-22	5.71959E-20	Up-Regulated
CAPN8	2.587	4.6872E-22	7.01038E-20	Up-Regulated
ISG15	1.789	4.9303E-22	7.30167E-20	Up-Regulated
FAM19A5	1.674	5.60615E-22	8.22199E-20	Up-Regulated
LCN2	3.038	5.72284E-22	8.31242E-20	Up-Regulated
ANLN	1.890	6.21111E-22	8.93572E-20	Up-Regulated
FAT1	1.356	6.38669E-22	9.10163E-20	Up-Regulated

SDC4	1.179	6.95445E-22	9.81813E-20	Up-Regulated
LGALS3BP	1.471	9.72522E-22	1.33554E-19	Up-Regulated
SAMD9	1.562	9.8573E-22	1.34148E-19	Up-Regulated
KCNN4	1.514	1.09322E-21	1.47448E-19	Up-Regulated
MGLL	1.511	1.19484E-21	1.5695E-19	Up-Regulated
MARCKSL1	1.422	1.45721E-21	1.86548E-19	Up-Regulated
OSBPL10	1.299	1.50942E-21	1.91608E-19	Up-Regulated
SLC2A1	1.558	1.6045E-21	2.0198E-19	Up-Regulated
C19orf33	2.277	1.65881E-21	2.05393E-19	Up-Regulated
EFNB2	1.717	2.37555E-21	2.91748E-19	Up-Regulated
SMYD3	1.028	2.67288E-21	3.20448E-19	Up-Regulated
TMC5	2.298	3.15814E-21	3.7271E-19	Up-Regulated
KCNK1	1.745	4.20417E-21	4.92312E-19	Up-Regulated
ECT2	1.224	4.30037E-21	4.99703E-19	Up-Regulated
MAP4K4	1.029	5.36191E-21	6.13614E-19	Up-Regulated
AHR	1.388	5.47428E-21	6.18614E-19	Up-Regulated
TSPO	1.081	5.48751E-21	6.18614E-19	Up-Regulated
PMEPA1	1.536	5.77557E-21	6.45603E-19	Up-Regulated
TM4SF1	1.513	5.81239E-21	6.45603E-19	Up-Regulated
SYTL2	1.578	5.98494E-21	6.59917E-19	Up-Regulated
COL3A1	2.181	6.32843E-21	6.92733E-19	Up-Regulated
C1orf106	1.908	6.64896E-21	7.22584E-19	Up-Regulated
NBL1	1.346	8.69175E-21	9.34735E-19	Up-Regulated
MTMR11	1.381	8.72486E-21	9.34735E-19	Up-Regulated
FZD2	1.138	9.1288E-21	9.71124E-19	Up-Regulated
BPGM	1.144	1.14898E-20	1.197E-18	Up-Regulated
ABHD17C	1.880	1.40076E-20	1.43944E-18	Up-Regulated
HOXC6	2.015	1.69996E-20	1.73511E-18	Up-Regulated
NTM	1.360	2.01553E-20	2.01235E-18	Up-Regulated
SFTA2	2.327	2.40885E-20	2.3783E-18	Up-Regulated
SULF2	1.863	2.44863E-20	2.40188E-18	Up-Regulated
MPZL2	1.184	2.48877E-20	2.42551E-18	Up-Regulated
MST1R	1.477	2.56504E-20	2.48382E-18	Up-Regulated
SPON2	1.328	2.7176E-20	2.61478E-18	Up-Regulated
LEMD1	1.882	3.5026E-20	3.34875E-18	Up-Regulated
JUP	1.270	3.7489E-20	3.56169E-18	Up-Regulated
TMPRSS3	1.573	3.77929E-20	3.56812E-18	Up-Regulated
AGR2	2.754	3.91238E-20	3.67083E-18	Up-Regulated
INPP4B	1.572	4.11524E-20	3.81379E-18	Up-Regulated
APOL1	1.015	4.44019E-20	4.08985E-18	Up-Regulated
LTBP1	1.244	4.74966E-20	4.34839E-18	Up-Regulated
PCDH7	1.370	5.14774E-20	4.68444E-18	Up-Regulated
XAF1	1.794	6.10238E-20	5.39079E-18	Up-Regulated
PLAUR	1.502	6.62283E-20	5.81654E-18	Up-Regulated
KRT23	2.223	7.04892E-20	6.15497E-18	Up-Regulated
KLF5	2.085	7.29281E-20	6.33133E-18	Up-Regulated
CAP1	1.128	7.81989E-20	6.75013E-18	Up-Regulated
RAI14	1.204	8.56561E-20	7.35182E-18	Up-Regulated
SRPX2	1.435	9.36647E-20	7.94887E-18	Up-Regulated
PLAT	2.093	9.4624E-20	7.98542E-18	Up-Regulated
NPC1	1.184	9.79753E-20	8.2223E-18	Up-Regulated
EPHX4	1.131	1.02922E-19	8.54249E-18	Up-Regulated

TRIM59	1.357	1.03671E-19	8.55767E-18	Up-Regulated
RRAS	1.120	1.06038E-19	8.70553E-18	Up-Regulated
CST4	1.359	1.53495E-19	1.22682E-17	Up-Regulated
ANKRD22	1.468	1.70526E-19	1.35577E-17	Up-Regulated
ITPR3	1.044	1.74898E-19	1.38325E-17	Up-Regulated
GABRP	3.114	1.91682E-19	1.50809E-17	Up-Regulated
DKK3	1.346	1.94999E-19	1.52625E-17	Up-Regulated
SPARC	1.835	2.12078E-19	1.62573E-17	Up-Regulated
B4GALT5	1.059	2.21415E-19	1.68075E-17	Up-Regulated
ANXA3	1.651	2.34191E-19	1.76884E-17	Up-Regulated
FXYD5	1.535	2.47063E-19	1.84759E-17	Up-Regulated
RAB31	1.866	2.73711E-19	2.03678E-17	Up-Regulated
PLAU	1.695	2.75283E-19	2.03844E-17	Up-Regulated
BHLHE40	1.302	2.80005E-19	2.0633E-17	Up-Regulated
COL6A3	1.795	2.8611E-19	2.08791E-17	Up-Regulated
FOXQ1	2.130	3.01042E-19	2.18632E-17	Up-Regulated
MCU	1.158	3.13963E-19	2.26924E-17	Up-Regulated
KYNU	1.413	3.85769E-19	2.76181E-17	Up-Regulated
TNFSF4	1.336	4.01772E-19	2.86281E-17	Up-Regulated
OLFML2B	1.926	4.0393E-19	2.86468E-17	Up-Regulated
PRKCI	1.072	4.09814E-19	2.87937E-17	Up-Regulated
SPOCK1	1.585	4.15053E-19	2.90268E-17	Up-Regulated
RACGAP1	1.419	4.56045E-19	3.1601E-17	Up-Regulated
TMSB10	1.205	5.59327E-19	3.84054E-17	Up-Regulated
ENO2	1.475	6.4911E-19	4.43686E-17	Up-Regulated
NMI	1.158	7.3301E-19	4.98777E-17	Up-Regulated
GALNT5	1.265	7.44558E-19	5.04363E-17	Up-Regulated
FAP	2.128	7.56228E-19	5.09981E-17	Up-Regulated
GPX8	1.353	8.32964E-19	5.52453E-17	Up-Regulated
SGPP2	1.936	9.02938E-19	5.95624E-17	Up-Regulated
STYK1	1.455	1.03591E-18	6.80369E-17	Up-Regulated
DDX60	1.454	1.24758E-18	8.11378E-17	Up-Regulated
SGIP1	1.100	1.32494E-18	8.51685E-17	Up-Regulated
SLC24A3	1.224	1.33326E-18	8.53401E-17	Up-Regulated
EFNA1	1.186	1.56813E-18	9.78849E-17	Up-Regulated
BACE2	1.036	1.74271E-18	1.08335E-16	Up-Regulated
COL4A1	1.488	1.77377E-18	1.09814E-16	Up-Regulated
PALLD	1.644	1.92738E-18	1.18354E-16	Up-Regulated
VCL	1.026	1.94015E-18	1.18656E-16	Up-Regulated
MMP28	1.264	1.97516E-18	1.20262E-16	Up-Regulated
IFI44	1.484	1.98233E-18	1.20262E-16	Up-Regulated
PNMA1	1.363	2.0156E-18	1.21791E-16	Up-Regulated
SEMA3C	1.930	2.06285E-18	1.23656E-16	Up-Regulated
S100A4	1.891	2.18637E-18	1.30029E-16	Up-Regulated
STIL	1.006	2.22737E-18	1.31948E-16	Up-Regulated
PRC1	1.267	2.37343E-18	1.39506E-16	Up-Regulated
ACTN1	1.056	2.64075E-18	1.54617E-16	Up-Regulated
TPM4	1.102	2.73351E-18	1.58707E-16	Up-Regulated
ZNF532	1.159	2.74213E-18	1.58707E-16	Up-Regulated
AEBP1	1.840	3.13313E-18	1.80645E-16	Up-Regulated
OAS3	1.022	3.29969E-18	1.89525E-16	Up-Regulated
PLEK2	1.196	3.32845E-18	1.90261E-16	Up-Regulated

C1GALT1	1.198	3.55139E-18	2.00926E-16	Up-Regulated
KDELC1	1.285	4.06469E-18	2.27412E-16	Up-Regulated
ECM1	1.293	4.17247E-18	2.30877E-16	Up-Regulated
LIPH	1.393	4.28271E-18	2.36112E-16	Up-Regulated
NUAK1	1.308	4.40085E-18	2.39997E-16	Up-Regulated
LIMS1	1.056	4.94723E-18	2.6501E-16	Up-Regulated
EPS8	1.214	5.0295E-18	2.67995E-16	Up-Regulated
STEAP2	1.081	5.99628E-18	3.10845E-16	Up-Regulated
CEP55	1.535	6.00866E-18	3.10845E-16	Up-Regulated
COL12A1	1.991	6.12271E-18	3.14778E-16	Up-Regulated
TRIB2	1.280	6.12635E-18	3.14778E-16	Up-Regulated
FNDC1	2.137	6.18868E-18	3.16902E-16	Up-Regulated
PPL	1.259	6.2734E-18	3.20155E-16	Up-Regulated
WISP1	1.376	6.3148E-18	3.21183E-16	Up-Regulated
SLC16A4	1.625	7.102E-18	3.58806E-16	Up-Regulated
PI3	1.712	7.21087E-18	3.63091E-16	Up-Regulated
GPX2	2.203	7.74425E-18	3.87366E-16	Up-Regulated
SPAG1	1.290	8.67938E-18	4.29871E-16	Up-Regulated
COL4A2	1.442	8.86198E-18	4.37481E-16	Up-Regulated
NCEH1	1.420	9.50648E-18	4.64741E-16	Up-Regulated
CRIP1	1.967	9.68521E-18	4.71951E-16	Up-Regulated
SMS	1.119	1.02033E-17	4.95599E-16	Up-Regulated
LOXL1	1.559	1.03237E-17	4.96659E-16	Up-Regulated
AK4	1.202	1.20991E-17	5.75807E-16	Up-Regulated
OAS1	1.373	1.2353E-17	5.83603E-16	Up-Regulated
WNT5A	1.291	1.23628E-17	5.83603E-16	Up-Regulated
TGFBI	1.478	1.26796E-17	5.94838E-16	Up-Regulated
COMP	2.410	1.34936E-17	6.31068E-16	Up-Regulated
PON2	1.153	1.3991E-17	6.47403E-16	Up-Regulated
MELK	1.344	1.55736E-17	7.10741E-16	Up-Regulated
BGN	1.586	1.59439E-17	7.25449E-16	Up-Regulated
PRRG1	1.113	1.62923E-17	7.39075E-16	Up-Regulated
TMEM158	1.604	2.11202E-17	9.35939E-16	Up-Regulated
MMP7	2.582	2.11277E-17	9.35939E-16	Up-Regulated
MFAP2	1.436	2.25372E-17	9.9546E-16	Up-Regulated
MX1	1.383	2.36066E-17	1.03362E-15	Up-Regulated
LDHA	1.038	2.41231E-17	1.05015E-15	Up-Regulated
RSAD2	1.336	2.68468E-17	1.16203E-15	Up-Regulated
TCN1	2.807	2.69243E-17	1.16205E-15	Up-Regulated
EPPK1	1.470	2.78442E-17	1.19833E-15	Up-Regulated
TMEM200A	1.866	3.09337E-17	1.32375E-15	Up-Regulated
MICALL2	1.026	3.11866E-17	1.3308E-15	Up-Regulated
GCNT3	2.276	3.24691E-17	1.37775E-15	Up-Regulated
MAL2	1.980	3.71409E-17	1.56718E-15	Up-Regulated
SQLE	1.101	3.96162E-17	1.65316E-15	Up-Regulated
TIGD1	1.022	4.25751E-17	1.76202E-15	Up-Regulated
TOP2A	2.074	5.65143E-17	2.29491E-15	Up-Regulated
CORO1C	1.165	5.99609E-17	2.41539E-15	Up-Regulated
MXRA8	1.046	6.28608E-17	2.52E-15	Up-Regulated
THY1	1.339	6.28914E-17	2.52E-15	Up-Regulated
MMP11	1.411	6.40908E-17	2.5545E-15	Up-Regulated
CLIC1	1.023	6.58877E-17	2.61233E-15	Up-Regulated

CTSB	1.060	6.75911E-17	2.65894E-15	Up-Regulated
ZG16B	1.795	7.33611E-17	2.84152E-15	Up-Regulated
OLR1	2.105	8.03876E-17	3.07427E-15	Up-Regulated
SLC9B2	1.031	8.22732E-17	3.13843E-15	Up-Regulated
TFF1	3.213	8.83286E-17	3.32741E-15	Up-Regulated
MMP1	3.116	8.92279E-17	3.35293E-15	Up-Regulated
CDH11	1.338	1.03343E-16	3.81742E-15	Up-Regulated
CEP170	1.217	1.1912E-16	4.35695E-15	Up-Regulated
TGFB1I1	1.373	1.32404E-16	4.7849E-15	Up-Regulated
LY75	1.845	1.35219E-16	4.85183E-15	Up-Regulated
KIF14	1.181	1.48625E-16	5.30763E-15	Up-Regulated
GPR137B	1.372	1.5115E-16	5.3724E-15	Up-Regulated
KPNA2	1.169	1.53669E-16	5.44913E-15	Up-Regulated
ARL4C	1.320	1.60701E-16	5.67183E-15	Up-Regulated
OPN3	1.080	1.89396E-16	6.60744E-15	Up-Regulated
YWHAZ	1.015	1.9324E-16	6.72598E-15	Up-Regulated
SLC39A10	1.140	1.9613E-16	6.81089E-15	Up-Regulated
CMTM3	1.005	2.07359E-16	7.15152E-15	Up-Regulated
ATP2B4	1.122	2.09161E-16	7.18186E-15	Up-Regulated
CXCL5	2.714	2.22186E-16	7.57095E-15	Up-Regulated
SRGAP2B	1.127	2.25556E-16	7.65673E-15	Up-Regulated
MSMO1	1.215	2.28505E-16	7.72215E-15	Up-Regulated
HOXB2	1.124	2.31411E-16	7.80288E-15	Up-Regulated
NT5DC2	1.180	2.40667E-16	8.0216E-15	Up-Regulated
FKBP7	1.174	3.0456E-16	9.97977E-15	Up-Regulated
PMAIP1	1.513	3.05557E-16	9.99078E-15	Up-Regulated
CCL20	2.283	3.07064E-16	1.00184E-14	Up-Regulated
CKS2	1.816	3.2139E-16	1.04371E-14	Up-Regulated
CENPU	1.441	3.24358E-16	1.04618E-14	Up-Regulated
MALL	1.746	3.24811E-16	1.04618E-14	Up-Regulated
YWHAB	1.005	3.31212E-16	1.06227E-14	Up-Regulated
EDNRA	1.782	3.34831E-16	1.0716E-14	Up-Regulated
COL16A1	1.193	3.3594E-16	1.07288E-14	Up-Regulated
BEAN1	1.118	3.38959E-16	1.08024E-14	Up-Regulated
BAIAP2L1	1.167	3.46907E-16	1.09861E-14	Up-Regulated
PLXDC2	1.344	3.87247E-16	1.21364E-14	Up-Regulated
NDC80	1.431	4.33743E-16	1.34817E-14	Up-Regulated
LRRN1	1.442	4.37089E-16	1.35473E-14	Up-Regulated
CTSK	1.657	4.52339E-16	1.39166E-14	Up-Regulated
FAM83H	1.013	5.10153E-16	1.55593E-14	Up-Regulated
MX2	1.116	5.47241E-16	1.65664E-14	Up-Regulated
LGALS1	1.589	5.93138E-16	1.77777E-14	Up-Regulated
TRIM29	1.230	6.16585E-16	1.83727E-14	Up-Regulated
TXN	1.012	6.17749E-16	1.83727E-14	Up-Regulated
TNFAIP6	1.771	6.17858E-16	1.83727E-14	Up-Regulated
ANXA1	1.519	6.74158E-16	1.98129E-14	Up-Regulated
DACT1	1.484	6.99529E-16	2.04788E-14	Up-Regulated
CST2	1.255	7.16182E-16	2.08854E-14	Up-Regulated
HIST2H2BE	1.308	7.55608E-16	2.18663E-14	Up-Regulated
HK1	1.091	7.64906E-16	2.20509E-14	Up-Regulated
SLC44A4	1.777	9.6845E-16	2.72937E-14	Up-Regulated
F5	1.562	9.9096E-16	2.78242E-14	Up-Regulated

CD58	1.223	1.00986E-15	2.83022E-14	Up-Regulated
ADAM9	1.407	1.02266E-15	2.86081E-14	Up-Regulated
ERO1L	1.161	1.14599E-15	3.15325E-14	Up-Regulated
SH3KBP1	1.431	1.15764E-15	3.17951E-14	Up-Regulated
PANX1	1.020	1.18528E-15	3.24951E-14	Up-Regulated
GBP2	1.186	1.26479E-15	3.4425E-14	Up-Regulated
IFI6	1.684	1.34166E-15	3.6321E-14	Up-Regulated
PPFIBP1	1.043	1.38446E-15	3.72129E-14	Up-Regulated
VASP	1.011	1.48913E-15	3.95339E-14	Up-Regulated
FRMD6	1.312	1.65809E-15	4.37121E-14	Up-Regulated
SLC12A2	1.255	1.82547E-15	4.79574E-14	Up-Regulated
WNT2	1.150	1.86012E-15	4.84466E-14	Up-Regulated
SHROOM3	1.322	1.87381E-15	4.8719E-14	Up-Regulated
CXCL8	2.250	2.06172E-15	5.29666E-14	Up-Regulated
PCDHB10	1.085	2.13187E-15	5.4583E-14	Up-Regulated
BCL10	1.016	2.36054E-15	5.98897E-14	Up-Regulated
TNFAIP2	1.051	2.36292E-15	5.98897E-14	Up-Regulated
DPYSL3	1.416	2.3915E-15	6.04113E-14	Up-Regulated
GRHL1	1.044	2.77137E-15	6.89691E-14	Up-Regulated
DUOX2	2.509	2.8058E-15	6.94826E-14	Up-Regulated
KIF20A	1.135	2.87583E-15	7.11003E-14	Up-Regulated
IGF2BP2	1.138	3.10675E-15	7.59393E-14	Up-Regulated
SGK223	1.055	3.12857E-15	7.63493E-14	Up-Regulated
MIA	1.458	3.27425E-15	7.92641E-14	Up-Regulated
CORO2A	1.494	3.43756E-15	8.25561E-14	Up-Regulated
PXDN	1.352	3.93118E-15	9.39626E-14	Up-Regulated
HEPH	1.703	4.27913E-15	1.01001E-13	Up-Regulated
MDK	1.407	4.37578E-15	1.03121E-13	Up-Regulated
CAMK2N1	1.069	4.42386E-15	1.03447E-13	Up-Regulated
NUSAP1	1.264	4.86734E-15	1.13014E-13	Up-Regulated
TWIST1	1.532	4.87368E-15	1.13014E-13	Up-Regulated
ITGB6	1.716	5.35752E-15	1.23558E-13	Up-Regulated
MMP2	1.571	5.74944E-15	1.31393E-13	Up-Regulated
EPS8L1	1.096	5.78189E-15	1.31736E-13	Up-Regulated
SIPA1L2	1.028	6.21682E-15	1.4122E-13	Up-Regulated
EPHA2	1.110	7.12237E-15	1.60344E-13	Up-Regulated
EPSTI1	1.169	7.36535E-15	1.64344E-13	Up-Regulated
GOLM1	1.259	7.88583E-15	1.73903E-13	Up-Regulated
ZWINT	1.281	9.18079E-15	2.00412E-13	Up-Regulated
PCDHB14	1.128	9.9268E-15	2.14527E-13	Up-Regulated
PERP	1.298	9.99365E-15	2.15355E-13	Up-Regulated
ISLR	1.504	1.04452E-14	2.24126E-13	Up-Regulated
NPR3	1.491	1.05178E-14	2.25365E-13	Up-Regulated
PLOD2	1.068	1.07931E-14	2.30609E-13	Up-Regulated
DPCR1	2.320	1.13321E-14	2.41442E-13	Up-Regulated
SERPINH1	1.264	1.19385E-14	2.52228E-13	Up-Regulated
RARRES3	1.444	1.19768E-14	2.52453E-13	Up-Regulated
CENPW	1.121	1.21959E-14	2.5659E-13	Up-Regulated
DFNA5	1.012	1.31129E-14	2.73554E-13	Up-Regulated
HIST1H2BD	1.231	1.72907E-14	3.52964E-13	Up-Regulated
CENPK	1.466	1.8014E-14	3.67233E-13	Up-Regulated
S100A2	1.904	1.83378E-14	3.73331E-13	Up-Regulated

LAMB1	1.167	2.09315E-14	4.19908E-13	Up-Regulated
CCNB1	1.303	2.32886E-14	4.59657E-13	Up-Regulated
MN1	1.311	3.07782E-14	5.95407E-13	Up-Regulated
GREM1	2.467	3.09335E-14	5.96784E-13	Up-Regulated
RHPN2	1.428	3.12839E-14	6.02557E-13	Up-Regulated
ANXA10	2.381	3.2268E-14	6.1858E-13	Up-Regulated
CDCA7	1.553	3.34621E-14	6.3823E-13	Up-Regulated
F2R	1.090	3.49847E-14	6.64753E-13	Up-Regulated
MACC1	1.086	4.00144E-14	7.50878E-13	Up-Regulated
ITGB1	1.152	4.48617E-14	8.32531E-13	Up-Regulated
RARRES1	1.974	4.7124E-14	8.70238E-13	Up-Regulated
F3	1.054	4.80561E-14	8.84209E-13	Up-Regulated
EGLN3	1.353	4.87081E-14	8.91008E-13	Up-Regulated
TUFT1	1.089	5.38506E-14	9.67261E-13	Up-Regulated
PRR15	1.380	5.79512E-14	1.03232E-12	Up-Regulated
ARHGAP42	1.096	5.87083E-14	1.04458E-12	Up-Regulated
MATN3	1.764	5.94879E-14	1.05721E-12	Up-Regulated
VILL	1.380	6.14047E-14	1.08491E-12	Up-Regulated
PDGFRB	1.062	6.3265E-14	1.11255E-12	Up-Regulated
KIAA0101	1.130	6.56639E-14	1.15072E-12	Up-Regulated
BUB1B	1.243	6.57914E-14	1.15162E-12	Up-Regulated
FAM213B	1.012	7.32318E-14	1.26862E-12	Up-Regulated
SERPINA1	1.716	7.33583E-14	1.26936E-12	Up-Regulated
ZNF365	1.079	7.55467E-14	1.30424E-12	Up-Regulated
ASPN	1.422	8.02843E-14	1.37347E-12	Up-Regulated
GALNT4	1.152	8.29722E-14	1.41146E-12	Up-Regulated
S100A14	1.276	8.35303E-14	1.41936E-12	Up-Regulated
ASPHD2	1.013	8.36892E-14	1.42046E-12	Up-Regulated
IFI44L	1.567	8.58892E-14	1.45453E-12	Up-Regulated
LUM	1.234	8.7128E-14	1.47291E-12	Up-Regulated
IL18	1.261	8.87455E-14	1.49619E-12	Up-Regulated
C1orf116	1.277	8.89306E-14	1.49764E-12	Up-Regulated
DLGAP5	1.323	9.52373E-14	1.58792E-12	Up-Regulated
HIST1H2AC	1.115	9.75386E-14	1.62092E-12	Up-Regulated
NDNF	1.081	1.01828E-13	1.68664E-12	Up-Regulated
CLDN18	2.542	1.06104E-13	1.75554E-12	Up-Regulated
SUGCT	1.128	1.06298E-13	1.75683E-12	Up-Regulated
RAB34	1.109	1.09476E-13	1.80146E-12	Up-Regulated
LBH	1.101	1.1385E-13	1.86532E-12	Up-Regulated
COL1A1	1.345	1.15758E-13	1.89452E-12	Up-Regulated
KRT8	1.419	1.16049E-13	1.89723E-12	Up-Regulated
LIF	1.126	1.23973E-13	2.01585E-12	Up-Regulated
ARPC1B	1.233	1.60263E-13	2.535E-12	Up-Regulated
ST6GALNAC1	1.959	1.63561E-13	2.57638E-12	Up-Regulated
CLDN1	1.419	1.68431E-13	2.64207E-12	Up-Regulated
LRRC15	1.085	1.89821E-13	2.92305E-12	Up-Regulated
BCAS1	1.197	2.04639E-13	3.12249E-12	Up-Regulated
TIMP2	1.062	2.05992E-13	3.13998E-12	Up-Regulated
NEK2	1.128	2.21945E-13	3.36617E-12	Up-Regulated
GINS1	1.102	2.22607E-13	3.37281E-12	Up-Regulated
DTL	1.103	2.3368E-13	3.52644E-12	Up-Regulated
FBN1	1.455	2.46313E-13	3.70968E-12	Up-Regulated

VSIG2	1.163	2.47333E-13	3.72133E-12	Up-Regulated
MXD1	1.308	2.61033E-13	3.90026E-12	Up-Regulated
IGFL2	1.096	2.72275E-13	4.04821E-12	Up-Regulated
CSGALNACT2	1.054	2.74257E-13	4.07368E-12	Up-Regulated
LIMA1	1.291	2.92145E-13	4.29712E-12	Up-Regulated
CXCL3	1.599	3.02208E-13	4.4279E-12	Up-Regulated
FA2H	1.100	3.08748E-13	4.51059E-12	Up-Regulated
PTPRR	1.226	3.68252E-13	5.27281E-12	Up-Regulated
TRNP1	1.066	3.68829E-13	5.27607E-12	Up-Regulated
LAMP5	1.428	4.08386E-13	5.74938E-12	Up-Regulated
AOC1	2.178	4.14177E-13	5.82547E-12	Up-Regulated
ANXA8L1	1.445	4.81922E-13	6.70959E-12	Up-Regulated
CDC20	1.255	4.87416E-13	6.77983E-12	Up-Regulated
FAM83D	1.515	5.12608E-13	7.0846E-12	Up-Regulated
FSCN1	1.005	5.74227E-13	7.84292E-12	Up-Regulated
GSDMB	1.077	6.62235E-13	8.90803E-12	Up-Regulated
RNF183	1.186	6.81454E-13	9.10171E-12	Up-Regulated
PTTG1	1.089	7.25558E-13	9.63118E-12	Up-Regulated
SERPINB2	1.831	7.51731E-13	9.93495E-12	Up-Regulated
C1QTNF3	1.038	8.28342E-13	1.08431E-11	Up-Regulated
CDC42EP5	1.369	8.56337E-13	1.1142E-11	Up-Regulated
NNMT	1.499	8.61793E-13	1.11937E-11	Up-Regulated
IL1R2	1.360	9.42321E-13	1.21138E-11	Up-Regulated
AURKA	1.088	9.48464E-13	1.21729E-11	Up-Regulated
FZD7	1.105	9.92186E-13	1.26695E-11	Up-Regulated
IFIT3	1.061	1.21111E-12	1.50452E-11	Up-Regulated
RAB25	1.549	1.22381E-12	1.51905E-11	Up-Regulated
CMPK2	1.011	1.22575E-12	1.52021E-11	Up-Regulated
ROBO1	1.270	1.30972E-12	1.60982E-11	Up-Regulated
FGF14	1.546	1.33946E-12	1.64236E-11	Up-Regulated
PELI1	1.022	1.39069E-12	1.69417E-11	Up-Regulated
CLEC5A	1.196	1.4365E-12	1.7392E-11	Up-Regulated
ABRACL	1.193	1.45235E-12	1.75514E-11	Up-Regulated
TNFRSF11B	1.205	1.73798E-12	2.06561E-11	Up-Regulated
PLAC8	2.011	1.85054E-12	2.19077E-11	Up-Regulated
TMEM154	1.049	1.88921E-12	2.22783E-11	Up-Regulated
CSTA	1.561	1.89723E-12	2.23554E-11	Up-Regulated
ACTA2	1.317	1.90984E-12	2.24864E-11	Up-Regulated
LIPG	1.119	2.08247E-12	2.43105E-11	Up-Regulated
CP	1.717	2.14414E-12	2.49032E-11	Up-Regulated
KIF11	1.211	2.16689E-12	2.51021E-11	Up-Regulated
TPX2	1.051	2.8211E-12	3.19452E-11	Up-Regulated
HILPDA	1.031	3.23456E-12	3.60068E-11	Up-Regulated
COTL1	1.188	3.28959E-12	3.65656E-11	Up-Regulated
PSCA	1.891	3.70686E-12	4.06061E-11	Up-Regulated
ZNF521	1.330	3.84208E-12	4.1905E-11	Up-Regulated
LXN	1.223	3.91008E-12	4.25852E-11	Up-Regulated
ADAM12	1.365	4.24067E-12	4.57242E-11	Up-Regulated
C5orf46	1.143	4.46416E-12	4.77928E-11	Up-Regulated
DHRS9	1.606	4.50451E-12	4.81906E-11	Up-Regulated
GBP1	1.458	4.50928E-12	4.82075E-11	Up-Regulated
IFIT1	1.170	4.55423E-12	4.86192E-11	Up-Regulated

DUSP6	1.077	4.93668E-12	5.22956E-11	Up-Regulated
ID1	1.385	5.06156E-12	5.34311E-11	Up-Regulated
SLC16A1	1.041	5.52143E-12	5.76014E-11	Up-Regulated
RAD51AP1	1.068	5.81156E-12	6.02122E-11	Up-Regulated
CCDC109B	1.240	6.18085E-12	6.33433E-11	Up-Regulated
EPS8L3	1.592	6.29704E-12	6.44465E-11	Up-Regulated
CEMIP	1.332	6.33802E-12	6.47782E-11	Up-Regulated
MUC20	1.023	6.76482E-12	6.86757E-11	Up-Regulated
RRM2	1.293	6.98133E-12	7.06836E-11	Up-Regulated
GBP3	1.490	7.04097E-12	7.10875E-11	Up-Regulated
NUF2	1.256	7.78147E-12	7.77426E-11	Up-Regulated
SLC16A3	1.163	9.07766E-12	8.93919E-11	Up-Regulated
ADAM28	1.061	9.40456E-12	9.21305E-11	Up-Regulated
PLS1	1.662	1.00685E-11	9.7622E-11	Up-Regulated
EZR	1.032	1.01101E-11	9.78996E-11	Up-Regulated
LGALS4	2.041	1.05443E-11	1.01196E-10	Up-Regulated
TTK	1.126	1.22197E-11	1.15514E-10	Up-Regulated
IFITM1	1.031	1.29914E-11	1.21893E-10	Up-Regulated
PDZK1IP1	1.466	1.42537E-11	1.31934E-10	Up-Regulated
MSN	1.045	1.44262E-11	1.33123E-10	Up-Regulated
CLIC3	1.289	1.48269E-11	1.35955E-10	Up-Regulated
HMCN1	1.263	1.62071E-11	1.46777E-10	Up-Regulated
AREG	1.699	1.63141E-11	1.47658E-10	Up-Regulated
IRF7	1.004	1.70301E-11	1.53038E-10	Up-Regulated
IFI16	1.176	1.74167E-11	1.5614E-10	Up-Regulated
GLT8D2	1.108	1.80352E-11	1.61111E-10	Up-Regulated
PPARG	1.023	1.81673E-11	1.62196E-10	Up-Regulated
NREP	1.109	1.99065E-11	1.7575E-10	Up-Regulated
VSIG1	1.814	2.01317E-11	1.77634E-10	Up-Regulated
COL8A1	1.204	2.05518E-11	1.80497E-10	Up-Regulated
KRT6B	1.279	2.38659E-11	2.06601E-10	Up-Regulated
SCEL	1.232	2.44237E-11	2.10946E-10	Up-Regulated
DSG2	1.184	2.7692E-11	2.36387E-10	Up-Regulated
PSMB8	1.040	3.25116E-11	2.7239E-10	Up-Regulated
FLRT3	1.135	3.29429E-11	2.75851E-10	Up-Regulated
SFRP2	1.815	3.43849E-11	2.86338E-10	Up-Regulated
PHACTR3	1.220	3.58874E-11	2.97539E-10	Up-Regulated
MMP12	2.147	4.71547E-11	3.81327E-10	Up-Regulated
GPR87	1.353	5.02891E-11	4.04078E-10	Up-Regulated
TOX3	1.534	5.56197E-11	4.43139E-10	Up-Regulated
LSR	1.191	6.25717E-11	4.89745E-10	Up-Regulated
SFRP4	1.914	6.42451E-11	5.02322E-10	Up-Regulated
RNF145	1.042	6.76187E-11	5.25436E-10	Up-Regulated
CDKN2B	1.077	6.79886E-11	5.27791E-10	Up-Regulated
PRRX1	1.203	6.87445E-11	5.32608E-10	Up-Regulated
ALOX5AP	1.383	7.00964E-11	5.41902E-10	Up-Regulated
ACSL5	1.352	7.19655E-11	5.55095E-10	Up-Regulated
KLK7	1.313	7.95897E-11	6.06907E-10	Up-Regulated
SYT13	1.205	8.08083E-11	6.15267E-10	Up-Regulated
MOXD1	1.287	8.32639E-11	6.3237E-10	Up-Regulated
C9orf152	1.432	9.24155E-11	6.92474E-10	Up-Regulated
TMEM45B	1.321	9.30149E-11	6.9643E-10	Up-Regulated

C1R	1.098	9.92438E-11	7.3489E-10	Up-Regulated
PCSK5	1.049	1.07449E-10	7.87543E-10	Up-Regulated
IRF6	1.078	1.2177E-10	8.81809E-10	Up-Regulated
SPP1	1.573	1.29766E-10	9.35231E-10	Up-Regulated
NCF2	1.244	1.44798E-10	1.0337E-09	Up-Regulated
GPNMB	1.310	1.45843E-10	1.03969E-09	Up-Regulated
MYL9	1.245	1.59559E-10	1.12525E-09	Up-Regulated
KRT18	1.122	1.69825E-10	1.19098E-09	Up-Regulated
TSPAN8	1.851	1.70566E-10	1.19563E-09	Up-Regulated
PLCB4	1.121	1.87122E-10	1.30081E-09	Up-Regulated
CLDN2	1.346	1.93792E-10	1.34409E-09	Up-Regulated
LOX	1.406	1.94504E-10	1.34655E-09	Up-Regulated
CTSC	1.133	2.22578E-10	1.53039E-09	Up-Regulated
TREM1	1.070	2.44615E-10	1.66449E-09	Up-Regulated
ARL14	1.887	2.46616E-10	1.67358E-09	Up-Regulated
COL6A2	1.104	2.69673E-10	1.81133E-09	Up-Regulated
TAGLN	1.202	2.75256E-10	1.84473E-09	Up-Regulated
COL17A1	1.003	3.72999E-10	2.42554E-09	Up-Regulated
PSMB9	1.156	4.07741E-10	2.62211E-09	Up-Regulated
PCOLCE	1.006	4.18709E-10	2.68123E-09	Up-Regulated
CRISPLD1	1.301	4.35228E-10	2.77313E-09	Up-Regulated
MUC16	1.409	4.47633E-10	2.84474E-09	Up-Regulated
GJA1	1.110	4.49878E-10	2.8566E-09	Up-Regulated
MUC5B	1.402	5.43885E-10	3.38104E-09	Up-Regulated
SERPINB3	1.566	6.17616E-10	3.7941E-09	Up-Regulated
CFH	1.021	7.14439E-10	4.33949E-09	Up-Regulated
PLEKHG1	1.031	7.15791E-10	4.34596E-09	Up-Regulated
THBS1	1.270	7.48846E-10	4.53026E-09	Up-Regulated
BIRC3	1.037	7.49465E-10	4.53219E-09	Up-Regulated
GEM	1.159	1.02838E-09	6.05405E-09	Up-Regulated
CHSY1	1.010	1.0327E-09	6.07713E-09	Up-Regulated
PLA2G10	1.041	1.05918E-09	6.22326E-09	Up-Regulated
GALNT3	1.049	1.07759E-09	6.32161E-09	Up-Regulated
HIST1H2BC	1.024	1.16447E-09	6.77337E-09	Up-Regulated
AGR3	1.959	1.16719E-09	6.78397E-09	Up-Regulated
PROM1	1.636	1.22819E-09	7.10029E-09	Up-Regulated
SOX9	1.133	1.36763E-09	7.82556E-09	Up-Regulated
SPON1	1.158	1.53745E-09	8.70166E-09	Up-Regulated
CYP3A5	1.519	1.69432E-09	9.51112E-09	Up-Regulated
CXCL14	1.494	1.73761E-09	9.72161E-09	Up-Regulated
SNAI2	1.096	1.88E-09	1.04179E-08	Up-Regulated
ELF3	1.138	2.12018E-09	1.16084E-08	Up-Regulated
RASEF	1.015	2.31281E-09	1.25764E-08	Up-Regulated
PBK	1.143	2.62141E-09	1.40821E-08	Up-Regulated
CGN	1.055	3.05972E-09	1.62062E-08	Up-Regulated
TRIM31	1.006	3.3439E-09	1.75331E-08	Up-Regulated
HLA-B	1.026	3.66143E-09	1.90591E-08	Up-Regulated
KLK6	1.078	4.11824E-09	2.11887E-08	Up-Regulated
SULT1C2	1.442	4.46631E-09	2.27548E-08	Up-Regulated
BASP1	1.004	4.70389E-09	2.38366E-08	Up-Regulated
HSD17B6	1.103	4.75381E-09	2.40654E-08	Up-Regulated
MUC1	1.410	5.01873E-09	2.53385E-08	Up-Regulated

PMP22	1.033	5.20828E-09	2.62429E-08	Up-Regulated
ODAM	1.256	5.26415E-09	2.65042E-08	Up-Regulated
MFAP5	1.455	6.06717E-09	3.01482E-08	Up-Regulated
APOC1	1.076	7.67199E-09	3.72048E-08	Up-Regulated
XDH	1.088	8.06859E-09	3.89406E-08	Up-Regulated
SLC26A9	1.361	8.7117E-09	4.1698E-08	Up-Regulated
EGR2	1.063	1.20023E-08	5.61368E-08	Up-Regulated
CYP4F3	1.191	1.26475E-08	5.89124E-08	Up-Regulated
AKR1C3	1.209	1.44312E-08	6.65218E-08	Up-Regulated
PLEKHA2	1.043	1.5081E-08	6.92441E-08	Up-Regulated
BCL2A1	1.427	1.69932E-08	7.73191E-08	Up-Regulated
PTPN12	1.076	1.85753E-08	8.36856E-08	Up-Regulated
CST6	1.077	2.12425E-08	9.43236E-08	Up-Regulated
OLFM4	2.251	2.14327E-08	9.51124E-08	Up-Regulated
IL7	1.036	2.25141E-08	9.93857E-08	Up-Regulated
DUSP5	1.005	2.32028E-08	1.02038E-07	Up-Regulated
CYP1B1	1.448	2.32558E-08	1.02212E-07	Up-Regulated
MUC13	1.198	3.38845E-08	1.44024E-07	Up-Regulated
HAS3	1.032	3.49404E-08	1.4797E-07	Up-Regulated
SPRR3	1.380	4.57081E-08	1.89117E-07	Up-Regulated
TFF2	1.942	4.61486E-08	1.90835E-07	Up-Regulated
PLA2G7	1.084	4.95178E-08	2.03045E-07	Up-Regulated
GIMAP2	1.173	5.75441E-08	2.33296E-07	Up-Regulated
EPYC	1.617	6.60456E-08	2.64849E-07	Up-Regulated
SLCO1B3	1.216	8.08402E-08	3.1926E-07	Up-Regulated
LY96	1.261	9.14146E-08	3.56548E-07	Up-Regulated
CCL18	1.263	9.68537E-08	3.75435E-07	Up-Regulated
RGS1	1.106	9.72708E-08	3.76859E-07	Up-Regulated
F2RL2	1.129	1.19647E-07	4.55033E-07	Up-Regulated
C3	1.154	1.62999E-07	6.08116E-07	Up-Regulated
CLEC2B	1.012	2.06775E-07	7.56854E-07	Up-Regulated
GDA	1.098	2.25459E-07	8.18752E-07	Up-Regulated
TYROBP	1.075	2.85602E-07	1.01462E-06	Up-Regulated
PTGS2	1.334	2.87499E-07	1.02043E-06	Up-Regulated
STMN2	1.103	3.30991E-07	1.16089E-06	Up-Regulated
LYZ	1.804	4.12868E-07	1.4236E-06	Up-Regulated
C5AR1	1.046	4.53852E-07	1.55357E-06	Up-Regulated
SUCNR1	1.012	4.61086E-07	1.57654E-06	Up-Regulated
REG4	2.122	5.30651E-07	1.79691E-06	Up-Regulated
CXCR4	1.169	5.3842E-07	1.8224E-06	Up-Regulated
MMP10	1.113	5.96684E-07	2.00078E-06	Up-Regulated
TFF3	1.248	7.11225E-07	2.3549E-06	Up-Regulated
LY6D	1.252	7.91683E-07	2.59812E-06	Up-Regulated
CHI3L1	1.135	8.01269E-07	2.62616E-06	Up-Regulated
AKR1B10	1.549	1.40075E-06	4.40461E-06	Up-Regulated
VNN1	1.201	1.41073E-06	4.43045E-06	Up-Regulated
CLRN3	1.370	1.63449E-06	5.07097E-06	Up-Regulated
RNF128	1.217	1.73336E-06	5.35135E-06	Up-Regulated
IGFBP1	1.032	2.41993E-06	7.2936E-06	Up-Regulated
FCER1G	1.014	3.6384E-06	1.06453E-05	Up-Regulated
DMBT1	1.282	5.95487E-06	1.68233E-05	Up-Regulated
HSD17B2	1.153	7.64269E-06	2.11254E-05	Up-Regulated

HPGD	1.069	9.79595E-06	2.64956E-05	Up-Regulated
EPCAM	1.121	1.09428E-05	2.93302E-05	Up-Regulated
CYP2C18	1.003	2.34638E-05	5.91529E-05	Up-Regulated
ACTG2	1.070	0.000247756	0.000515652	Up-Regulated
CDH17	1.044	0.0002552	0.000529546	Up-Regulated
FCGR3A	1.110	0.000476806	0.00094212	Up-Regulated
CRISP3	1.191	0.002721655	0.004742021	Up-Regulated
MYRIP	-1.482	8.40241E-22	1.17525E-19	Down-Regulated
CBFA2T3	-1.169	8.62691E-22	1.19558E-19	Down-Regulated
PDCD4	-1.060	2.46429E-19	1.84759E-17	Down-Regulated
BBIP1	-1.116	1.17597E-18	7.69011E-17	Down-Regulated
BTG2	-1.234	1.53958E-18	9.65015E-17	Down-Regulated
FAM46C	-1.363	2.14506E-18	1.28076E-16	Down-Regulated
ACAT1	-1.063	8.59424E-18	4.27055E-16	Down-Regulated
P2RX1	-1.575	2.33424E-17	1.02802E-15	Down-Regulated
PAIP2B	-1.700	3.15264E-17	1.34152E-15	Down-Regulated
FKBP11	-1.162	5.88817E-17	2.37825E-15	Down-Regulated
ECHDC3	-1.105	6.35463E-17	2.5395E-15	Down-Regulated
PTGER4	-1.088	2.19625E-16	7.50602E-15	Down-Regulated
KLB	-1.293	3.43929E-16	1.09377E-14	Down-Regulated
CA4	-1.128	3.88208E-16	1.21414E-14	Down-Regulated
BRSK2	-1.016	4.96551E-16	1.52148E-14	Down-Regulated
TPST2	-1.987	5.39493E-16	1.63646E-14	Down-Regulated
CCDC110	-1.689	9.47242E-16	2.67459E-14	Down-Regulated
GPHA2	-1.654	1.96692E-15	5.08771E-14	Down-Regulated
FAM129A	-1.181	2.00717E-15	5.1653E-14	Down-Regulated
MT1G	-1.387	2.55929E-15	6.43272E-14	Down-Regulated
SLC39A5	-1.462	3.3546E-15	8.08206E-14	Down-Regulated
GUCA1C	-1.778	3.71712E-15	8.89871E-14	Down-Regulated
AKAP7	-1.249	5.4876E-15	1.25981E-13	Down-Regulated
CTNND2	-1.372	7.14833E-15	1.6045E-13	Down-Regulated
MAT1A	-1.205	7.29331E-15	1.62977E-13	Down-Regulated
TRHDE	-1.871	7.37905E-15	1.64407E-13	Down-Regulated
SPX	-1.919	9.0344E-15	1.97788E-13	Down-Regulated
PSAT1	-1.776	9.54439E-15	2.0745E-13	Down-Regulated
LIFR	-1.129	1.14751E-14	2.44146E-13	Down-Regulated
LGALS2	-1.847	1.55359E-14	3.18866E-13	Down-Regulated
PM20D1	-1.984	1.58022E-14	3.23892E-13	Down-Regulated
CCKBR	-1.211	2.0991E-14	4.20545E-13	Down-Regulated
MT1F	-1.171	2.29597E-14	4.5456E-13	Down-Regulated
ECI2	-1.042	2.94533E-14	5.74093E-13	Down-Regulated
SLC16A10	-1.698	3.23866E-14	6.20066E-13	Down-Regulated
SEL1L	-1.494	3.59901E-14	6.81287E-13	Down-Regulated
MT1H	-1.128	3.65473E-14	6.90967E-13	Down-Regulated
C5	-1.451	4.49308E-14	8.3279E-13	Down-Regulated
SLC1A2	-1.176	5.12602E-14	9.30693E-13	Down-Regulated
ALB	-2.309	5.18738E-14	9.37512E-13	Down-Regulated
ERO1LB	-1.780	5.50567E-14	9.8775E-13	Down-Regulated
GNMT	-2.376	7.85779E-14	1.34886E-12	Down-Regulated
EPHX2	-1.174	1.06802E-13	1.76322E-12	Down-Regulated
SPACA3	-1.199	1.17106E-13	1.91243E-12	Down-Regulated
AQP12B	-1.489	1.71105E-13	2.67846E-12	Down-Regulated

SERPINI1	-1.302	3.62392E-13	5.19876E-12	Down-Regulated
PDK4	-1.768	5.31427E-13	7.30626E-12	Down-Regulated
NUCB2	-1.276	5.52708E-13	7.57642E-12	Down-Regulated
GLS2	-1.115	5.6076E-13	7.67981E-12	Down-Regulated
BACE1	-1.465	5.91272E-13	8.03939E-12	Down-Regulated
AOX1	-1.697	9.37851E-13	1.20778E-11	Down-Regulated
NRG4	-1.215	9.97368E-13	1.27249E-11	Down-Regulated
KIAA1324	-1.452	1.00066E-12	1.2755E-11	Down-Regulated
F8	-1.178	1.00765E-12	1.28127E-11	Down-Regulated
FAM150B	-1.863	1.0731E-12	1.35199E-11	Down-Regulated
TMEM52	-1.770	1.40472E-12	1.70989E-11	Down-Regulated
SLC30A2	-1.110	1.99525E-12	2.34372E-11	Down-Regulated
CTH	-1.137	2.07194E-12	2.4225E-11	Down-Regulated
BNIP3	-1.512	2.18662E-12	2.52918E-11	Down-Regulated
KCNK3	-1.176	4.35528E-12	4.68262E-11	Down-Regulated
TEX11	-2.158	6.38059E-12	6.5133E-11	Down-Regulated
RBPJL	-1.938	6.99278E-12	7.07522E-11	Down-Regulated
RGN	-1.284	7.45329E-12	7.47606E-11	Down-Regulated
SLC43A1	-1.398	9.76318E-12	9.52115E-11	Down-Regulated
MT1M	-1.488	9.81885E-12	9.56309E-11	Down-Regulated
EPHX1	-1.428	1.03011E-11	9.94046E-11	Down-Regulated
PRDX4	-1.117	1.13658E-11	1.07847E-10	Down-Regulated
AQP8	-2.859	1.3214E-11	1.2363E-10	Down-Regulated
EGF	-2.062	1.46148E-11	1.34371E-10	Down-Regulated
ZG16	-1.340	1.47795E-11	1.35637E-10	Down-Regulated
KIRREL2	-1.070	1.59822E-11	1.45002E-10	Down-Regulated
TMED6	-2.716	1.67971E-11	1.51214E-10	Down-Regulated
ACADL	-1.485	2.39616E-11	2.0731E-10	Down-Regulated
PLCE1	-1.272	2.8532E-11	2.42819E-10	Down-Regulated
GCAT	-1.021	2.99221E-11	2.52939E-10	Down-Regulated
RNF186	-1.488	3.21021E-11	2.69109E-10	Down-Regulated
PDIA2	-2.318	3.58459E-11	2.97358E-10	Down-Regulated
LMO3	-1.314	4.8459E-11	3.91037E-10	Down-Regulated
GAS2	-1.259	4.89485E-11	3.93956E-10	Down-Regulated
DPEP1	-1.261	9.81142E-11	7.28311E-10	Down-Regulated
ANPEP	-2.043	1.60954E-10	1.13351E-09	Down-Regulated
CXCL12	-1.111	2.186E-10	1.50509E-09	Down-Regulated
NR5A2	-1.683	3.26824E-10	2.15307E-09	Down-Regulated
SLC39A14	-1.132	3.79902E-10	2.46406E-09	Down-Regulated
TSPAN7	-1.059	5.02373E-10	3.15477E-09	Down-Regulated
ABAT	-1.126	7.637E-10	4.60537E-09	Down-Regulated
ERP27	-2.723	1.21515E-09	7.04108E-09	Down-Regulated
REEP1	-1.065	1.42719E-09	8.13549E-09	Down-Regulated
KLK1	-2.217	1.43191E-09	8.15322E-09	Down-Regulated
RNASE1	-1.188	1.47475E-09	8.38136E-09	Down-Regulated
HOMER2	-1.319	2.964E-09	1.57379E-08	Down-Regulated
SERPINI2	-3.170	3.17071E-09	1.67471E-08	Down-Regulated
SPAG4	-1.014	3.92013E-09	2.02522E-08	Down-Regulated
PAK3	-1.011	3.97762E-09	2.05211E-08	Down-Regulated
CTRL	-3.077	5.40512E-09	2.71488E-08	Down-Regulated
FGL1	-1.844	6.59196E-09	3.24465E-08	Down-Regulated
NRCAM	-1.102	6.90993E-09	3.38571E-08	Down-Regulated

BEX5	-1.033	7.49611E-09	3.64455E-08	Down-Regulated
PDZK1	-1.118	1.59658E-08	7.28861E-08	Down-Regulated
GSTA1	-1.704	3.50039E-08	1.48198E-07	Down-Regulated
NPY1R	-1.280	3.85082E-08	1.61316E-07	Down-Regulated
EPB41L4B	-1.091	3.95106E-08	1.65149E-07	Down-Regulated
DPT	-1.140	4.88095E-08	2.0063E-07	Down-Regulated
CELA2B	-2.910	7.96277E-08	3.15049E-07	Down-Regulated
IMPA2	-1.271	2.57283E-07	9.23381E-07	Down-Regulated
SYCN	-2.962	3.50146E-07	1.22324E-06	Down-Regulated
TMEM97	-1.307	3.63873E-07	1.26689E-06	Down-Regulated
PNLIPRP1	-2.740	4.21575E-07	1.45097E-06	Down-Regulated
SLC38A5	-1.031	4.52858E-07	1.55051E-06	Down-Regulated
SYBU	-1.169	4.89612E-07	1.66691E-06	Down-Regulated
KCNJ16	-1.465	6.22018E-07	2.07973E-06	Down-Regulated
IGFBP2	-1.565	1.31278E-06	4.14785E-06	Down-Regulated
SLC4A4	-1.317	1.59884E-06	4.96649E-06	Down-Regulated
CUZD1	-2.539	1.83578E-06	5.64345E-06	Down-Regulated
CPA2	-2.602	2.01216E-06	6.14675E-06	Down-Regulated
IL22RA1	-1.023	2.49217E-06	7.49188E-06	Down-Regulated
GP2	-2.474	2.93914E-06	8.72788E-06	Down-Regulated
ADH1B	-1.178	3.72565E-06	1.089E-05	Down-Regulated
HBB	-1.189	4.08678E-06	1.18607E-05	Down-Regulated
BEX1	-1.253	4.10013E-06	1.18949E-05	Down-Regulated
IAPP	-1.846	4.65086E-06	1.33516E-05	Down-Regulated
HBA2	-1.142	7.00797E-06	1.95246E-05	Down-Regulated
HBA1	-1.130	7.81029E-06	2.1555E-05	Down-Regulated
CLPS	-2.545	1.06328E-05	2.85799E-05	Down-Regulated
CTRC	-2.378	1.46022E-05	3.81496E-05	Down-Regulated
LYVE1	-1.014	1.83383E-05	4.70719E-05	Down-Regulated
PRSS3	-1.765	1.86821E-05	4.78974E-05	Down-Regulated
CELA2A	-2.554	3.81136E-05	9.19572E-05	Down-Regulated
AMY1B	-1.891	3.8715E-05	9.32592E-05	Down-Regulated
PLA2G1B	-2.451	7.56929E-05	0.000173219	Down-Regulated
CELA3B	-2.147	0.000105385	0.000234975	Down-Regulated
AZGP1	-1.267	0.000116793	0.00025854	Down-Regulated
CEL	-2.232	0.000126807	0.000278625	Down-Regulated
FAM3B	-1.154	0.00016175	0.000348669	Down-Regulated
CPA1	-2.353	0.00017442	0.000373955	Down-Regulated
CELA3A	-2.034	0.000322585	0.000657621	Down-Regulated
C6	-1.022	0.000326766	0.000665335	Down-Regulated
CTRB2	-1.893	0.000660523	0.001273336	Down-Regulated
PRSS1	-1.802	0.000969536	0.001814172	Down-Regulated
PNLIP	-1.942	0.001089736	0.002023298	Down-Regulated
REG1B	-1.863	0.00111134	0.002060371	Down-Regulated
REG1A	-1.512	0.001363792	0.002495027	Down-Regulated
CPB1	-1.805	0.001696906	0.003048698	Down-Regulated
REG3G	-1.111	0.007999744	0.012858495	Down-Regulated
REG3A	-1.015	0.031836087	0.045884547	Down-Regulated

Table S2. A list of 1791 MTGs with expression level >=0.5 TPM in PDAC derived from HCMDB

Genes
AAMP, ABCA2, ABCB1, ABCC5, ABCG2, ABI1, ABI2, ABL1, ABL2, ACE, ACE2, ACKR1, ACKR2, ACKR3, ACOT8, ACP5, ACTA2, ACTB, ACTL6A, ACTN4, ACTR2, ACTR3, ACVR1C, ADAM10, ADAM12, ADAM15, ADAM17, ADAM23, ADAM28, ADAM8, ADAM9, ADAMTS1, ADAMTS13, ADAMTS18, ADIPOQ, ADM, ADORA2B, ADRB2, AFAP1L1, AFAP1L2, AGER, AGO1, AGO2, AGO4, AGR2, AGR3, AGT, AGTR1, AHR, AIFM1, AJUBA, AKAP12, AKR1C2, AKR1C3, AKT1, AKT2, AKT3, ALCAM, ALDH1A1, ALDH1A3, ALDH3A1, ALDH7A1, ALDOA, ALK, ALOX5, ALPL, ALPP, ALYREF, AMACR, AMBP, AMFR, AMOT, ANGPT1, ANGPT2, ANGPTL2, ANGPTL4, ANGPTL6, ANKRD12, ANO1, ANO9, ANTXR1, ANXA1, ANXA2, ANXA2R, ANXA3, ANXA4, ANXA7, APAF1, APBA2, APC, APEX1, API5, APMAP, APOBEC3G, APOM, AQP1, AQP3, AQP5, AQP8, AR, ARF6, ARG1, ARHGAP35, ARHGAP5, ARHGDIA, ARHGDIB, ARHGEF1, ARHGEF2, ARHGEF39, ARID1A, ARID4A, ARID4B, ARL2BP, ARL6IP5, ARMC8, ARNT, ARNTL, ARRB1, ARTN, ASAP1, ASCL2, ASPN, ASS1, ATAD2, ATF3, ATF4, ATG10, ATM, ATP11A, ATP2A3, ATP5B, ATP6V1C1, ATPIF1, AURKA, AURKB, AUTS2, AXIN2, AXL, B2M, B3GAT1, B3GNT3, B3GNT7, B3GNT8, B4GALT1, B4GALT3, BAD, BAG1, BAG2, BAG3, BAIAP2, BAK1, BAP1, BAX, BAZ2A, BBC3, BCAM, BCAR1, BCAT1, BCL2, BCL2L1, BCL2L11, BCL2L12, BCL2L2, BCL9, BDKRB2, BDNF, BECN1, BGN, BIN1, BIRC2, BIRC3, BIRC5, BIRC7, BMI1, BMP1, BMP2, BMP4, BMP5, BMP6, BMP7, BNIP3, BRAF, BRCA1, BRCA2, BRD7, BRMS1, BRS3, BSG, BST2, BTG1, BVES, C14orf166, C1QA, C1QBP, C6orf106, CA2, CA9, CACUL1, CACYBP, CADM1, CALCA, CALR, CALU, CAMP, CANX, CAP1, CAPG, CAPNS1, CARD10, CARD9, CASP10, CASP3, CASP8, CASP9, CASS4, CAT, CAV1, CBL, CBLB, CBR1, CBR3, CBX4, CBX5, CBX7, CBX8, CCAR2, CCDC88A, CCDC88C, CCL14, CCL18, CCL19, CCL2, CCL21, CCL22, CCL3, CCL5, CCL7, CCL8, CCNA2, CCNB1, CCNB2, CCND1, CCND2, CCNG1, CCNG2, CCR1, CCR4, CCR5, CCR7, CCR9, CD109, CD14, CD151, CD164, CD200, CD22, CD24, CD274, CD276, CD34, CD4, CD40, CD44, CD47, CD55, CD63, CD74, CD80, CD81, CD82, CD9, CDC42, CDC73, CDCA8, CDCP1, CDH1, CDH11, CDH12, CDH13, CDH17, CDH2, CDH3, CDK1, CDK4, CDK5RAP3, CDK8, CDKN1A, CDKN1B, CDKN2A, CDX2, CEACAM1, CEACAM3, CEACAM5, CEACAM6, CEBPA, CEBPB, CEMIP, CENPW, CERS2, CERS6, CFL1, CFTR, CHAF1B, CHD1L, CHEK1, CHEK2, CHFR, CHGA, CHI3L1, CHRM3, CHRNA7, CHUK, CITED1, CITED2, CKS1B, CLCA1, CLCA2, CLCN3, CLDN1, CLDN11, CLDN16, CLDN18, CLDN3, CLDN4, CLDN5, CLDN7, CLEC4G, CLIC1, CLIC3, CLIC4, CLIP1, CLOCK, CLU, CMTM3, CNBP, CNR1, CNTN1, COL18A1, COL1A1, COL3A1, COL4A6, COPS3, CORO1C, CPE, CPEB2, CPEB4, CPNE3, CR1, CRABP2, CREB1, CREB3, CREB5, CREM, CRIM1, CRK, CRKL, CRMP1, CRP, CRTC2, CRYAB, CSE1L, CSF1, CSNK1A1, CSNK2A1, CSNK2B, CSPG4, CST3, CST6, CSTA, CTGF, CTHRC1, CTLA4, CTNNA1, CTNNAL1, CTNNB1, CTNND1, CTNND2, CTSB, CTSD, CTSH, CTSK, CTSL, CTSS, CTSZ, CTTN, CUL1, CUX1, CX3CR1, CXADR, CXCL1, CXCL10, CXCL12, CXCL14, CXCL2, CXCL3, CXCL6, CXCL8, CXCR1, CXCR2, CXCR3, CXCR4, CXCR6, CXXC4, CYB5R3, CYCS, CYLD, CYP1B1, CYP2J2, CYP3A4, CYP3A5, CYR61, DAB2, DAB2IP, DACH1, DACT2, DAG1, DAPK1, DDA1, DDB2, DDIT3, DDR1, DDR2, DEK, DEPDC1B, DEPTOR, DHFR, DIABLO, DIAPH1, DICER1, DIRAS1, DIRAS3, DIXDC1, DKK1, DKK3, DKK4, DLC1, DLEC1, DLL1, DLL4, DNAJA3, DNAJB4, DNAJB6, DNM2, DNMT3A, DNMT3B, DOCK1, DOCK4, DPEP1, DPP4, DPYD, DPYSL3, DRG1, DROSHA, DSC3, DSG3, DUSP1, DUSP6, DVL2, E2F1, E2F3, EBAG9, ECE1, ECE2, ECM1, ECT2, EDN1, EDNRA, EDNRB, EFEMP1, EFNB1, EFNB2, EGF, EGFL7, EGFR, EGLN3, EGR1, EGR3, EHD2, EHMT2, EIF1AX, EIF3I, EIF4B, EIF4E, EIF4EBP1, EIF5A2, EIF6, ELAVL1, ELAVL4, ELF1, ELF5, ELK3, ELMO1, EMP1, EMP3, ENAH, ENG, ENO1, ENO2, ENPP1, ENPP2, ENTPD1, EP300, EPAS1, EPB41L3, EPC1, EPCAM,

EPHA1, EPHA10, EPHA2, EPHA4, EPHA7, EPHB1, EPHB2, EPHB3, EPHB4, EPOR, EPS8, EPSTI1, ERAP1, ERBB2, ERBB3, ERCC1, EREG, ERG, ERP29, ESAM, ESM1, ESR1, ESRP1, ETS1, ETS2, ETV1, ETV4, ETV7, EVI5, EVL, EYA2, EZH2, EZR, F11R, F2R, F2RL1, F3, F7, FABP1, FABP3, FABP5, FADD, FAIM2, FAM120A, FAM134A, FAM3B, FANCD2, FAP, FAS, FASLG, FASN, FBLN5, FBN1, FBN2, FBXO11, FBXW7, FCGRT, FDFT1, FER, FERMT1, FERMT2, FERMT3, FGF1, FGF19, FGF2, FGFBP1, FGFR1, FGFR2, FGFR3, FGFR4, FGL2, FHIT, FHL2, FILIP1, FKBP5, FLI1, FLNA, FLOT1, FLOT2, FLT1, FLT4, FMNL2, FMNL3, FN1, FNDC3B, FOLH1, FOS, FOSB, FOSL1, FOXA2, FOXC1, FOXC2, FOXD3, FOXF2, FOXJ1, FOXJ2, FOXK1, FOXL1, FOXM1, FOXN3, FOXO1, FOXO3, FOXO4, FOXP3, FOXQ1, FPR2, FRAT1, FSCN1, FSCN2, FST, FSTL1, FUBP1, FURIN, FUS, FXR1, FXYD3, FXYD5, FYN, FZD2, FZD7, G3BP1, G3BP2, G6PD, GAB1, GAB2, GADD45A, GAL3ST2, GALNT3, GAS1, GAS6, GATA3, GATA4, GATA6, GBP2, GCNT1, GCNT2, GDF15, GDNF, GEMIN2, GFRA1, GGCT, GHITM, GHR, GHRL, GIT1, GJA1, GJB1, GJB2, GKN1, GKN2, GLG1, GLI1, GLI2, GLI3, GLRX3, GMNN, GNA12, GNA13, GNAI1, GNB3, GNPTG, GOLPH3, GPC3, GPC5, GPER1, GPI, GPNMB, GPR4, GPR68, GPR87, GPX1, GPX3, GRB2, GRB7, GRINA, GRM4, GRN, GSC, GSDMB, GSK3B, GSN, GSTM1, GSTM3, GSTP1, GUSB, GZMB, H2AFX, HAMP, HAS1, HAX1, HBEGF, HDAC1, HDAC10, HDAC2, HDAC4, HDGF, HES1, HEY1, HGF, HIC1, HIF1A, HIP1, HK1, HK2, HMGA1, HMGA2, HMGB1, HMMR, HMOX1, HNF1A, HNF4A, HNRNPA1, HNRNPAB, HNRNPD, HNRNPK, HNRNPM, HOMER1, HOPX, HOXA1, HOXA5, HOXA9, HOXB13, HOXB5, HOXB7, HOXB9, HOXC8, HOXD9, HP, HPN, HPSE, HRAS, HRC, HSF1, HSP90AA1, HSP90AB1, HSP90B1, HSPA4, HSPA5, HSPA9, HSPB1, HSPB2, HSPD1, HTATIP2, HTRA1, HTRA2, HTRA3, HTT, HVCN1, HYAL1, HYAL3, IBSP, ICAM1, ID1, ID2, ID3, IDH1, IDO1, IFIT2, IFITM1, IFNAR2, IGF1, IGF1R, IGF2BP1, IGF2BP3, IGFBP1, IGFBP2, IGFBP3, IGFBP4, IGFBP5, IGFBP7, IGSF8, IHH, IKBKB, IKBKE, IL10, IL11, IL12A, IL13RA1, IL13RA2, IL17RA, IL17RB, IL18, IL1A, IL1B, IL1RL1, IL23A, IL24, IL2RG, IL32, IL34, IL4R, IL6, IL7, IL7R, ILK, IMP3, ING1, ING4, ING5, INHBA, INPP4B, INPPL1, INS, IQGAP1, IQSEC1, IRAK1, IRF7, IRS1, IRS2, IRX1, IRX2, ISG15, ITGA2, ITGA3, ITGA4, ITGA5, ITGA6, ITGAM, ITGAV, ITGB1, ITGB2, ITGB3, ITGB3BP, ITGB4, ITGB5, ITGB6, ITGB8, ITIH1, ITIH3, IVNS1ABP, JAG1, JAG2, JAK1, JAK2, JAM3, JDP2, JUN, JUP, KARS, KAT5, KATNA1, KCNMA1, KCNN4, KDM1A, KDM3A, KDM4B, KDM4C, KDM5A, KDM6B, KDR, KEAP1, KHDRBS1, KIAA0100, KIAA1524, KIF14, KIF2C, KIF3C, KISS1, KISS1R, KIT, KITLG, KL, KLF2, KLF4, KLF5, KLF6, KLF8, KLK13, KLK3, KLK4, KLK6, KLK7, KLK8, KRAS, KRT14, KRT17, KRT18, KRT19, KRT20, KRT5, KRT6A, KRT7, KRT8, L1CAM, LAMA5, LAMB3, LAMC2, LAMP3, LAMTOR1, LAP3, LAPTM4B, LARP7, LASP1, LAT, LATS2, LCN2, LCP1, LDHA, LECT1, LEF1, LEP, LEPR, LGALS1, LGALS2, LGALS3, LGALS3BP, LGALS8, LGALS9, LGI4, LGR4, LGR5, LIF, LIFR, LIMA1, LIMK1, LIMK2, LIMS1, LIPH, LLGL1, LLGL2, LMCD1, LMNA, LOX, LOXL2, LOXL4, LPAR1, LPAR2, LRG1, LRP5, LRP6, LRRC26, LRRFIP1, LTB4R2, LTBP1, LYN, LYNX1, LYPD3, LYVE1, LZTS1, MACC1, MACROD1, MAEL, MAF, MAGEA3, MAGED1, MAL, MAML1, MAOA, MAP1LC3A, MAP1LC3B, MAP2, MAP2K4, MAP2K7, MAP3K1, MAP3K11, MAP3K7, MAP7D3, MAPK1, MAPK12, MAPK13, MAPK14, MAPK3, MAPK7, MAPK8, MAPK9, MAPKAP1, MARCKS, MARK2, MASP2, MBD1, MBD2, MBNL1, MCAM, MCL1, MCTS1, MDC1, MDK, MDM2, MECP2, MED19, MED23, MET, METAP2, MFAP3L, MGAT3, MGAT5, MGEA5, MGMT, MIA, MIA3, MICA, MIEN1, MIF, MITF, MKI67, MKL1, MLF2, MLH1, MME, MMP1, MMP10, MMP11, MMP12, MMP13, MMP14, MMP15, MMP16, MMP17, MMP2, MMP28, MMP3, MMP7, MMP9, MMS19, MOB1A, MPP3, MPZL1, MRC2, MRPL44, MSH2, MSI1, MSLN, MSN, MSR1, MSRA, MST1, MST1R, MTA1, MTA2, MTA3, MTAP, MTBP, MTDH, MTHFR, MTNR1A, MTOR, MTSS1, MUC1, MUC13, MUC16, MUC20, MUC4, MUC5AC, MUC6, MUCL1, MX1, MXD1, MYB, MYC, MYCN, MYD88, MYH9, MYO10, MYO1B, MYO5A, MYO9B, MZF1, NAA10, NAB2, NAMPT, NAT1, NBN, NCL, NCOA2, NCOA3, NCOA4,

NCOR2, NCR3LG1, NDC80, NDRG1, NDRG2, NDUFA13, NDUFB9, NEDD4, NEDD4L, NEDD9, NES, NET1, NEU1, NF2, NFATC1, NFATC2, NFE2L2, NFIB, NFKB1, NFKB2, NGF, NGFR, NISCH, NLRP1, NLRP3, NME1, NME2, NME3, NME9, NMU, NOB1, NOD2, NOG, NOL3, NOS2, NOS3, NOTCH1, NOTCH3, NOX1, NPEPPS, NPPA, NR1H4, NR2C2, NR2F2, NR4A1, NR4A2, NRAS, NRF1, NRG1, NRP1, NRP2, NT5E, NTN1, NTRK1, NTRK2, NUAK1, NUCB2, NUCKS1, NUDCD1, NUPR1, OCIAD1, OCLN, ODAM, ODC1, OGG1, OGT, OLR1, ONECUT1, OPCML, ORAI1, ORM2, OSBPL5, OSM, OTUB1, P2RY2, P4HA2, PAG1, PAK1, PAK4, PALLD, PAQR3, PARD3, PARD6A, PARK7, PARP1, PARVA, PARVB, PAX5, PAX8, PBX3, PBXIP1, PCBP1, PCDH10, PCDH9, PCMT1, PCNA, PCSK9, PDCD1, PDCD4, PDCD6IP, PDGFB, PDGFRA, PDGFRB, PDIA3, PDLIM1, PDLIM7, PDPN, PEAK1, PEBP1, PEBP4, PECAM1, PELP1, PER1, PFN1, PGF, PGK1, PGR, PHB, PIAS1, PIEZO1, PIGR, PIK3CA, PIK3CG, PIK3R1, PIM1, PIN1, PIP, PIP4K2A, PITPNM1, PITPNM3, PITX1, PIWIL1, PIWIL2, PIWIL4, PKD1, PKM, PKP3, PLA1A, PLA2G10, PLA2G16, PLA2G2A, PLA2G3, PLAGL1, PLAU, PLAUR, PLCE1, PLD1, PLD2, PLEC, PLK1, PLK4, PLOD2, PLS3, PLXDC1, PLXNB1, PLXND1, PMEL, PML, PMP22, PODXL, POMC, POSTN, POU5F1, PPA1, PPARD, PPARG, PPARGC1A, PPIA, PPM1D, PPP1R13L, PPP1R9B, PPP2CA, PPP3CA, PPT1, PRAF2, PRAME, PRDM2, PRDX1, PRDX2, PRDX4, PRDX6, PREP, PREX1, PREX2, PRKAA1, PRKCA, PRKCE, PRKCG, PRKCI, PRKCZ, PRKD1, PRKD2, PRKD3, PRKDC, PRLR, PRMT1, PRMT7, PRNP, PROC, PROM1, PROX1, PRRX1, PRSS3, PRSS8, PSAP, PSCA, PSMA7, PSMD10, PSME2, PSME3, PTAFR, PTCH1, PTEN, PTGER1, PTGER3, PTGES, PTGIS, PTGS1, PTGS2, PTH1R, PTHLH, PTK2, PTK2B, PTK6, PTK7, PTP4A1, PTP4A2, PTP4A3, PTPN1, PTPN11, PTPN13, PTPN2, PTPN3, PTPN6, PTPRD, PTPRR, PTTG1, PTX3, PXN, RAB11FIP4, RAB1A, RAB1B, RAB22A, RAB23, RAB25, RAB27B, RAB37, RAB3D, RAB40B, RAB5A, RABEP1, RABGEF1, RAC1, RAC2, RAC3, RACGAP1, RAD21, RAD51, RADIL, RAF1, RALA, RALB, RALBP1, RALGAPA2, RALGDS, RAN, RAP1A, RAP1B, RAPGEF3, RARB, RARG, RARRES3, RASA1, RASAL2, RASSF1, RASSF10, RASSF2, RASSF5, RB1, RBBP8, RBM5, RCN1, RDX, RECK, RECQL, REG4, RELA, RELB, RERG, RET, RETN, RETNLB, RFWD2, RGS16, RGS2, RGS5, RHOA, RHOB, RHOC, RICTOR, RIOK3, RLN2, RNASE1, RNF111, RNF180, RNF41, RNH1, ROBO1, ROCK1, ROCK2, ROR1, RPL39, RPS27, RPS6KA3, RPS6KB1, RPSA, RRAS2, RRM1, RRP1B, RSF1, RTKN, RUNX2, RUNX3, RXRA, S100A10, S100A11, S100A14, S100A2, S100A4, S100A6, S100A7, S100A8, S100A9, S100B, S100P, S1PR1, SAA1, SAE1, SALL4, SAMD9, SATB1, SATB2, SCARA3, SCARB2, SCGB2A1, SCGB2A2, SCGB3A1, SCGN, SCN1B, SCRN1, SCUBE2, SDC1, SDC2, SDC4, SDCBP, SDHB, SDPR, SELE, SELP, SELPLG, SEMA3E, SEMA3F, SEMA4B, SEMA4C, SEMA4D, SEMA5A, SEMA6B, SENP1, SENP3, SERBP1, SERPINA5, SERPINB3, SERPINB4, SERPINB5, SERPIND1, SERPINE1, SERPINE2, SERPINF1, SESN2, SET, SETD1A, SETD2, SETDB1, SFN, SFRP1, SFRP2, SFTPA1, SGK1, SH2B1, SHC1, SHH, SIAH1, SIK1, SIRT1, SIRT6, SIRT7, SIX1, SKIL, SKP2, SLC16A4, SLC1A5, SLC2A1, SLC2A3, SLC39A4, SLC39A6, SLC3A2, SLC9A1, SLIT2, SLITRK3, SLPI, SMAD1, SMAD2, SMAD3, SMAD4, SMAD6, SMAD7, SMARCA4, SMARCB1, SMARCC1, SMARCE1, SMO, SMPD3, SMURF1, SMURF2, SMYD3, SNAI1, SNAI2, SNCG, SND1, SOCS1, SOCS3, SOD2, SOD3, SOX12, SOX17, SOX2, SOX4, SOX8, SOX9, SP1, SP3, SPAG9, SPARC, SPDEF, SPHK1, SPINK1, SPINT1, SPINT2, SPN, SPOCK1, SPON2, SPP1, SQLE, SRA1, SRC, SRF, SRGN, SRPK1, SRR, SRXN1, SS18, SSR4, SSTR2, SSX2IP, ST14, ST3GAL1, ST6GAL1, ST6GALNAC2, ST8SIA1, STARD13, STAT1, STAT3, STAT5A, STAT5B, STAT6, STC1, STC2, STIM1, STK11, STMN1, STOML2, STUB1, STX2, STX6, STYK1, SULF2, SUV39H1, SUZ12, SYK, SYNJ2, SYNPO2, SYTL1, SYTL2, TAC1, TACC3, TACR1, TACSTD2, TAGLN, TAP1, TAZ, TBK1, TBL1XR1, TBX2, TBX21, TBX3, TBXAS1, TCF12, TCF3, TCF7L2, TEK, TES, TET1, TET2, TFAP4, TFCP2, TFF1, TFF2, TFF3, TFPI2, TG, TGFA, TGFB1, TGFB2, TGFBI, TGFBR1, TGFBR2,

TGFBR3, TGIF2, TGM2, THBS1, THBS2, THPO, THRB, THY1, TIAM1, TIMP1, TIMP2, TIMP3, TJP1, TLR2, TLR3, TLR4, TM4SF1, TM4SF5, TMBIM1, TMBIM4, TMBIM6, TMEM100, TMEM88, TMEM8B, TMEM97, TMPRSS2, TMPRSS4, TMSB15A, TMSB4X, TNC, TNF, TNFAIP1, TNFAIP2, TNFAIP3, TNFAIP8, TNFAIP8L2, TNFRSF10A, TNFRSF10B, TNFRSF11A, TNFRSF11B, TNFRSF12A, TNFRSF1A, TNFRSF1B, TNFRSF25, TNFRSF4, TNFSF11, TNFSF12, TNFSF13, TNK2, TNN, TNS1, TNS2, TNS3, TNS4, TOP2A, TP53, TP63, TP73, TPBG, TPD52, TPM1, TPM2, TPM3, TPP1, TPST1, TPX2, TRAF4, TRAF6, TRAP1, TRIM16, TRIM25, TRIM28, TRIM29, TRIM32, TRIM33, TRIP10, TRIT1, TRPC1, TRPM7, TRPS1, TRPV6, TSC2, TSG101, TSLP, TSPAN12, TSPAN2, TSPAN7, TSPAN8, TTC36, TTC9, TTF2, TUBB4B, TUSC3, TWIST1, TWIST2, TXN, TXNDC12, TXNIP, TYK2, TYMP, TYMS, TYRP1, UBA2, UBD, UBE2C, UBE2I, UBE2N, UBE2V1, UCHL1, UCP2, UGCG, UGT2B15, UGT2B17, UHRF1, UIMC1, ULK1, UMPS, UNC45A, UNC5B, UPF1, UPP1, USP14, USP22, USP28, UTRN, VANGL1, VASH1, VASP, VAV2, VAV3, VCAM1, VCAN, VCP, VDR, VEGFA, VEGFB, VEGFC, VEZT, VIM, VLDLR, VMP1, VSNL1, VTCN1, VWCE, WASF1, WASF2, WASF3, WASL, WFDC2, WIF1, WISP1, WISP2, WISP3, WLS, WNT11, WNT2B, WNT5A, WNT7B, WRAP53, WSB1, WT1, WWOX, WWP1, WWTR1, XCR1, XIAP, XRCC1, XRCC2, XRCC5, YAP1, YBX1, YES1, YWHAE, YWHAG, YWHAZ, YY1, ZBTB16, ZBTB20, ZBTB33, ZBTB7A, ZDHHC2, ZEB1, ZEB2, ZFHX3, ZFP36, ZFX, ZHX2, ZNF148, ZNF217, ZNF350, ZNF382, ZNF592, ZNF703.

Table S3. 246 DE-MTGs identified in PDAC

Gene	logFC	P Value	FDR	regulated
LAMC2	2.650	1.51583E-33	2.28981E-29	Up-Regulated
S100P	4.297	3.48635E-33	2.63324E-29	Up-Regulated
KRT19	3.527	7.83878E-33	3.94709E-29	Up-Regulated
ITGA2	2.048	2.51479E-32	7.59769E-29	Up-Regulated
SLPI	2.634	1.12073E-31	2.82161E-28	Up-Regulated
ANXA2	1.298	2.99506E-31	6.46334E-28	Up-Regulated
INHBA	3.142	2.69629E-30	5.09126E-27	Up-Regulated
GJB2	3.389	3.20932E-30	5.38667E-27	Up-Regulated
FN1	2.787	1.02154E-29	1.54314E-26	Up-Regulated
KRT7	2.681	2.05178E-29	2.58285E-26	Up-Regulated
SFN	2.944	6.54358E-29	7.06052E-26	Up-Regulated
LAMB3	2.223	3.55549E-28	2.98384E-25	Up-Regulated
ANO1	1.826	6.90453E-28	5.21499E-25	Up-Regulated
SERPINB5	2.598	1.64594E-27	1.18398E-24	Up-Regulated
S100A11	1.839	1.89543E-27	1.30147E-24	Up-Regulated
IGFBP3	2.459	2.09147E-27	1.37364E-24	Up-Regulated
S100A10	1.439	3.54929E-27	2.23398E-24	Up-Regulated
TMPRSS4	2.301	7.61661E-27	4.10916E-24	Up-Regulated
CTHRC1	3.221	3.35714E-26	1.44894E-23	Up-Regulated
S100A6	2.392	3.48733E-26	1.46332E-23	Up-Regulated
CAPG	1.813	7.40686E-26	3.024E-23	Up-Regulated
SDC1	1.422	8.08522E-26	3.13167E-23	Up-Regulated
HOXB7	1.497	2.20995E-25	7.76362E-23	Up-Regulated
TPBG	1.330	2.32188E-25	7.97144E-23	Up-Regulated
FHL2	1.802	3.28089E-25	1.07741E-22	Up-Regulated
THBS2	2.681	2.2053E-24	5.94881E-22	Up-Regulated
SOX4	1.139	2.48598E-24	6.5374E-22	Up-Regulated
POSTN	3.309	3.04284E-24	7.53528E-22	Up-Regulated
NET1	1.170	4.25854E-24	1.0211E-21	Up-Regulated
MSLN	2.889	4.34982E-24	1.02669E-21	Up-Regulated
FXYD3	1.948	4.89832E-24	1.12112E-21	Up-Regulated
DKK1	2.605	6.63757E-24	1.49652E-21	Up-Regulated
CEACAM6	3.786	9.25046E-24	1.96813E-21	Up-Regulated
CD9	1.272	1.16825E-23	2.44678E-21	Up-Regulated
LGALS3	1.412	1.35063E-23	2.75712E-21	Up-Regulated
ITGA3	1.502	1.63418E-23	3.29145E-21	Up-Regulated
PKM	1.358	7.1455E-23	1.31634E-20	Up-Regulated
FERMT1	1.786	7.94031E-23	1.44514E-20	Up-Regulated
TIMP1	2.013	1.02281E-22	1.83936E-20	Up-Regulated
CEACAM5	4.088	1.13206E-22	2.01187E-20	Up-Regulated
NMU	2.293	1.53317E-22	2.54506E-20	Up-Regulated
CDH3	1.672	1.782E-22	2.89738E-20	Up-Regulated
KRT17	2.403	1.78377E-22	2.89738E-20	Up-Regulated
CD55	1.902	1.90417E-22	3.06005E-20	Up-Regulated
HK2	1.817	2.12681E-22	3.38186E-20	Up-Regulated
VCAN	2.583	2.62213E-22	4.12603E-20	Up-Regulated
ISG15	1.789	4.9303E-22	7.30167E-20	Up-Regulated
LCN2	3.038	5.72284E-22	8.31242E-20	Up-Regulated
SDC4	1.179	6.95445E-22	9.81813E-20	Up-Regulated
LGALS3BP	1.471	9.72522E-22	1.33554E-19	Up-Regulated

SAMD9	1.562	9.8573E-22	1.34148E-19	Up-Regulated
KCNN4	1.514	1.09322E-21	1.47448E-19	Up-Regulated
SLC2A1	1.558	1.6045E-21	2.0198E-19	Up-Regulated
EFNB2	1.717	2.37555E-21	2.91748E-19	Up-Regulated
SMYD3	1.028	2.67288E-21	3.20448E-19	Up-Regulated
ECT2	1.224	4.30037E-21	4.99703E-19	Up-Regulated
AHR	1.388	5.47428E-21	6.18614E-19	Up-Regulated
TM4SF1	1.513	5.81239E-21	6.45603E-19	Up-Regulated
SYTL2	1.578	5.98494E-21	6.59917E-19	Up-Regulated
COL3A1	2.181	6.32843E-21	6.92733E-19	Up-Regulated
FZD2	1.138	9.1288E-21	9.71124E-19	Up-Regulated
SULF2	1.863	2.44863E-20	2.40188E-18	Up-Regulated
MST1R	1.477	2.56504E-20	2.48382E-18	Up-Regulated
SPON2	1.328	2.7176E-20	2.61478E-18	Up-Regulated
JUP	1.270	3.7489E-20	3.56169E-18	Up-Regulated
AGR2	2.754	3.91238E-20	3.67083E-18	Up-Regulated
INPP4B	1.572	4.11524E-20	3.81379E-18	Up-Regulated
LTBP1	1.244	4.74966E-20	4.34839E-18	Up-Regulated
PLAUR	1.502	6.62283E-20	5.81654E-18	Up-Regulated
KLF5	2.085	7.29281E-20	6.33133E-18	Up-Regulated
CAP1	1.128	7.81989E-20	6.75013E-18	Up-Regulated
DKK3	1.346	1.94999E-19	1.52625E-17	Up-Regulated
SPARC	1.835	2.12078E-19	1.62573E-17	Up-Regulated
ANXA3	1.651	2.34191E-19	1.76884E-17	Up-Regulated
FXYD5	1.535	2.47063E-19	1.84759E-17	Up-Regulated
PLAU	1.695	2.75283E-19	2.03844E-17	Up-Regulated
FOXQ1	2.130	3.01042E-19	2.18632E-17	Up-Regulated
PRKCI	1.072	4.09814E-19	2.87937E-17	Up-Regulated
SPOCK1	1.585	4.15053E-19	2.90268E-17	Up-Regulated
RACGAP1	1.419	4.56045E-19	3.1601E-17	Up-Regulated
ENO2	1.475	6.4911E-19	4.43686E-17	Up-Regulated
FAP	2.128	7.56228E-19	5.09981E-17	Up-Regulated
STYK1	1.455	1.03591E-18	6.80369E-17	Up-Regulated
PALLD	1.644	1.92738E-18	1.18354E-16	Up-Regulated
MMP28	1.264	1.97516E-18	1.20262E-16	Up-Regulated
S100A4	1.891	2.18637E-18	1.30029E-16	Up-Regulated
ECM1	1.293	4.17247E-18	2.30877E-16	Up-Regulated
LIPH	1.393	4.28271E-18	2.36112E-16	Up-Regulated
NUAK1	1.308	4.40085E-18	2.39997E-16	Up-Regulated
LIMS1	1.056	4.94723E-18	2.6501E-16	Up-Regulated
EPS8	1.214	5.0295E-18	2.67995E-16	Up-Regulated
WISP1	1.376	6.3148E-18	3.21183E-16	Up-Regulated
SLC16A4	1.625	7.102E-18	3.58806E-16	Up-Regulated
WNT5A	1.291	1.23628E-17	5.83603E-16	Up-Regulated
TGFBI	1.478	1.26796E-17	5.94838E-16	Up-Regulated
BGN	1.586	1.59439E-17	7.25449E-16	Up-Regulated
MMP7	2.582	2.11277E-17	9.35939E-16	Up-Regulated
MX1	1.383	2.36066E-17	1.03362E-15	Up-Regulated
LDHA	1.038	2.41231E-17	1.05015E-15	Up-Regulated
SQLE	1.101	3.96162E-17	1.65316E-15	Up-Regulated
TOP2A	2.074	5.65143E-17	2.29491E-15	Up-Regulated
CORO1C	1.165	5.99609E-17	2.41539E-15	Up-Regulated

THY1	1.339	6.28914E-17	2.52E-15	Up-Regulated
MMP11	1.411	6.40908E-17	2.5545E-15	Up-Regulated
CLIC1	1.023	6.58877E-17	2.61233E-15	Up-Regulated
CTSB	1.060	6.75911E-17	2.65894E-15	Up-Regulated
OLR1	2.105	8.03876E-17	3.07427E-15	Up-Regulated
TFF1	3.213	8.83286E-17	3.32741E-15	Up-Regulated
MMP1	3.116	8.92279E-17	3.35293E-15	Up-Regulated
CDH11	1.338	1.03343E-16	3.81742E-15	Up-Regulated
KIF14	1.181	1.48625E-16	5.30763E-15	Up-Regulated
YWHAZ	1.015	1.9324E-16	6.72598E-15	Up-Regulated
CMTM3	1.005	2.07359E-16	7.15152E-15	Up-Regulated
EDNRA	1.782	3.34831E-16	1.0716E-14	Up-Regulated
NDC80	1.431	4.33743E-16	1.34817E-14	Up-Regulated
CTSK	1.657	4.52339E-16	1.39166E-14	Up-Regulated
LGALS1	1.589	5.93138E-16	1.77777E-14	Up-Regulated
TRIM29	1.230	6.16585E-16	1.83727E-14	Up-Regulated
TXN	1.012	6.17749E-16	1.83727E-14	Up-Regulated
ANXA1	1.519	6.74158E-16	1.98129E-14	Up-Regulated
HK1	1.091	7.64906E-16	2.20509E-14	Up-Regulated
ADAM9	1.407	1.02266E-15	2.86081E-14	Up-Regulated
GBP2	1.186	1.26479E-15	3.4425E-14	Up-Regulated
VASP	1.011	1.48913E-15	3.95339E-14	Up-Regulated
CXCL8	2.250	2.06172E-15	5.29666E-14	Up-Regulated
TNFAIP2	1.051	2.36292E-15	5.98897E-14	Up-Regulated
DPYSL3	1.416	2.3915E-15	6.04113E-14	Up-Regulated
MIA	1.458	3.27425E-15	7.92641E-14	Up-Regulated
MDK	1.407	4.37578E-15	1.03121E-13	Up-Regulated
TWIST1	1.532	4.87368E-15	1.13014E-13	Up-Regulated
ITGB6	1.716	5.35752E-15	1.23558E-13	Up-Regulated
MMP2	1.571	5.74944E-15	1.31393E-13	Up-Regulated
EPHA2	1.110	7.12237E-15	1.60344E-13	Up-Regulated
EPSTI1	1.169	7.36535E-15	1.64344E-13	Up-Regulated
PLOD2	1.068	1.07931E-14	2.30609E-13	Up-Regulated
RARRES3	1.444	1.19768E-14	2.52453E-13	Up-Regulated
CENPW	1.121	1.21959E-14	2.5659E-13	Up-Regulated
S100A2	1.904	1.83378E-14	3.73331E-13	Up-Regulated
CCNB1	1.303	2.32886E-14	4.59657E-13	Up-Regulated
F2R	1.090	3.49847E-14	6.64753E-13	Up-Regulated
MACC1	1.086	4.00144E-14	7.50878E-13	Up-Regulated
ITGB1	1.152	4.48617E-14	8.32531E-13	Up-Regulated
F3	1.054	4.80561E-14	8.84209E-13	Up-Regulated
EGLN3	1.353	4.87081E-14	8.91008E-13	Up-Regulated
PDGFRB	1.062	6.3265E-14	1.11255E-12	Up-Regulated
ASPN	1.422	8.02843E-14	1.37347E-12	Up-Regulated
S100A14	1.276	8.35303E-14	1.41936E-12	Up-Regulated
IL18	1.261	8.87455E-14	1.49619E-12	Up-Regulated
CLDN18	2.542	1.06104E-13	1.75554E-12	Up-Regulated
COL1A1	1.345	1.15758E-13	1.89452E-12	Up-Regulated
KRT8	1.419	1.16049E-13	1.89723E-12	Up-Regulated
LIF	1.126	1.23973E-13	2.01585E-12	Up-Regulated
CLDN1	1.419	1.68431E-13	2.64207E-12	Up-Regulated
TIMP2	1.062	2.05992E-13	3.13998E-12	Up-Regulated

FBN1	1.455	2.46313E-13	3.70968E-12	Up-Regulated
MXD1	1.308	2.61033E-13	3.90026E-12	Up-Regulated
LIMA1	1.291	2.92145E-13	4.29712E-12	Up-Regulated
CXCL3	1.599	3.02208E-13	4.4279E-12	Up-Regulated
PTPRR	1.226	3.68252E-13	5.27281E-12	Up-Regulated
FSCN1	1.005	5.74227E-13	7.84292E-12	Up-Regulated
GSDMB	1.077	6.62235E-13	8.90803E-12	Up-Regulated
PTTG1	1.089	7.25558E-13	9.63118E-12	Up-Regulated
AURKA	1.088	9.48464E-13	1.21729E-11	Up-Regulated
FZD7	1.105	9.92186E-13	1.26695E-11	Up-Regulated
RAB25	1.549	1.22381E-12	1.51905E-11	Up-Regulated
ROBO1	1.270	1.30972E-12	1.60982E-11	Up-Regulated
TNFRSF11B	1.205	1.73798E-12	2.06561E-11	Up-Regulated
CSTA	1.561	1.89723E-12	2.23554E-11	Up-Regulated
ACTA2	1.317	1.90984E-12	2.24864E-11	Up-Regulated
TPX2	1.051	2.8211E-12	3.19452E-11	Up-Regulated
PSCA	1.891	3.70686E-12	4.06061E-11	Up-Regulated
ADAM12	1.365	4.24067E-12	4.57242E-11	Up-Regulated
DUSP6	1.077	4.93668E-12	5.22956E-11	Up-Regulated
ID1	1.385	5.06156E-12	5.34311E-11	Up-Regulated
CEMIP	1.332	6.33802E-12	6.47782E-11	Up-Regulated
MUC20	1.023	6.76482E-12	6.86757E-11	Up-Regulated
ADAM28	1.061	9.40456E-12	9.21305E-11	Up-Regulated
EZR	1.032	1.01101E-11	9.78996E-11	Up-Regulated
IFITM1	1.031	1.29914E-11	1.21893E-10	Up-Regulated
MSN	1.045	1.44262E-11	1.33123E-10	Up-Regulated
CLIC3	1.289	1.48269E-11	1.35955E-10	Up-Regulated
IRF7	1.004	1.70301E-11	1.53038E-10	Up-Regulated
PPARG	1.023	1.81673E-11	1.62196E-10	Up-Regulated
SFRP2	1.815	3.43849E-11	2.86338E-10	Up-Regulated
MMP12	2.147	4.71547E-11	3.81327E-10	Up-Regulated
GPR87	1.353	5.02891E-11	4.04078E-10	Up-Regulated
PRRX1	1.203	6.87445E-11	5.32608E-10	Up-Regulated
KLK7	1.313	7.95897E-11	6.06907E-10	Up-Regulated
SPP1	1.573	1.29766E-10	9.35231E-10	Up-Regulated
GPNMB	1.310	1.45843E-10	1.03969E-09	Up-Regulated
KRT18	1.122	1.69825E-10	1.19098E-09	Up-Regulated
TSPAN8	1.851	1.70566E-10	1.19563E-09	Up-Regulated
LOX	1.406	1.94504E-10	1.34655E-09	Up-Regulated
TAGLN	1.202	2.75256E-10	1.84473E-09	Up-Regulated
MUC16	1.409	4.47633E-10	2.84474E-09	Up-Regulated
GJA1	1.110	4.49878E-10	2.8566E-09	Up-Regulated
SERPINB3	1.566	6.17616E-10	3.7941E-09	Up-Regulated
THBS1	1.270	7.48846E-10	4.53026E-09	Up-Regulated
BIRC3	1.037	7.49465E-10	4.53219E-09	Up-Regulated
PLA2G10	1.041	1.05918E-09	6.22326E-09	Up-Regulated
GALNT3	1.049	1.07759E-09	6.32161E-09	Up-Regulated
AGR3	1.959	1.16719E-09	6.78397E-09	Up-Regulated
PROM1	1.636	1.22819E-09	7.10029E-09	Up-Regulated
SOX9	1.133	1.36763E-09	7.82556E-09	Up-Regulated
CYP3A5	1.519	1.69432E-09	9.51112E-09	Up-Regulated
CXCL14	1.494	1.73761E-09	9.72161E-09	Up-Regulated

SNAI2	1.096	1.88E-09	1.04179E-08	Up-Regulated
KLK6	1.078	4.11824E-09	2.11887E-08	Up-Regulated
MUC1	1.410	5.01873E-09	2.53385E-08	Up-Regulated
PMP22	1.033	5.20828E-09	2.62429E-08	Up-Regulated
ODAM	1.256	5.26415E-09	2.65042E-08	Up-Regulated
AKR1C3	1.209	1.44312E-08	6.65218E-08	Up-Regulated
CST6	1.077	2.12425E-08	9.43236E-08	Up-Regulated
IL7	1.036	2.25141E-08	9.93857E-08	Up-Regulated
CYP1B1	1.448	2.32558E-08	1.02212E-07	Up-Regulated
MUC13	1.198	3.38845E-08	1.44024E-07	Up-Regulated
TFF2	1.942	4.61486E-08	1.90835E-07	Up-Regulated
CCL18	1.263	9.68537E-08	3.75435E-07	Up-Regulated
PTGS2	1.334	2.87499E-07	1.02043E-06	Up-Regulated
REG4	2.122	5.30651E-07	1.79691E-06	Up-Regulated
CXCR4	1.169	5.3842E-07	1.8224E-06	Up-Regulated
MMP10	1.113	5.96684E-07	2.00078E-06	Up-Regulated
TFF3	1.248	7.11225E-07	2.3549E-06	Up-Regulated
CHI3L1	1.135	8.01269E-07	2.62616E-06	Up-Regulated
IGFBP1	1.032	2.41993E-06	7.2936E-06	Up-Regulated
EPCAM	1.121	1.09428E-05	2.93302E-05	Up-Regulated
CDH17	1.044	0.0002552	0.000529546	Up-Regulated
PDCD4	-1.060	2.46429E-19	1.84759E-17	Down-Regulated
CTNND2	-1.372	7.14833E-15	1.6045E-13	Down-Regulated
LIFR	-1.129	1.14751E-14	2.44146E-13	Down-Regulated
LGALS2	-1.847	1.55359E-14	3.18866E-13	Down-Regulated
NUCB2	-1.276	5.52708E-13	7.57642E-12	Down-Regulated
BNIP3	-1.512	2.18662E-12	2.52918E-11	Down-Regulated
PRDX4	-1.117	1.13658E-11	1.07847E-10	Down-Regulated
AQP8	-2.859	1.3214E-11	1.2363E-10	Down-Regulated
EGF	-2.062	1.46148E-11	1.34371E-10	Down-Regulated
PLCE1	-1.272	2.8532E-11	2.42819E-10	Down-Regulated
DPEP1	-1.261	9.81142E-11	7.28311E-10	Down-Regulated
CXCL12	-1.111	2.186E-10	1.50509E-09	Down-Regulated
TSPAN7	-1.059	5.02373E-10	3.15477E-09	Down-Regulated
RNASE1	-1.188	1.47475E-09	8.38136E-09	Down-Regulated
TMEM97	-1.307	3.63873E-07	1.26689E-06	Down-Regulated
IGFBP2	-1.565	1.31278E-06	4.14785E-06	Down-Regulated
LYVE1	-1.014	1.83383E-05	4.70719E-05	Down-Regulated
PRSS3	-1.765	1.86821E-05	4.78974E-05	Down-Regulated
FAM3B	-1.154	0.00016175	0.000348669	Down-Regulated

Table S4. Enrichment analysis

Category	Term	Count	%	PValue
GOTERM_BP_DIRECT	GO:0007155~cell adhesion	39	15.85365854	8.72103E-19
GOTERM_BP_DIRECT	GO:0022617~extracellular matrix disassembly	16	6.504065041	1.58595E-13
GOTERM_BP_DIRECT	GO:0030198~extracellular matrix organization	22	8.943089431	6.15769E-13
GOTERM_BP_DIRECT	GO:0042060~wound healing	13	5.284552846	1.28156E-09
GOTERM_BP_DIRECT	GO:0007165~signal transduction	45	18.29268293	1.68451E-09
GOTERM_BP_DIRECT	GO:0030574~collagen catabolic process	11	4.471544715	2.09882E-08
GOTERM_BP_DIRECT	GO:0042493~response to drug	20	8.130081301	7.09106E-08
GOTERM_BP_DIRECT	GO:0008284~positive regulation of cell proliferation	23	9.349593496	8.58517E-07
GOTERM_BP_DIRECT	GO:0001666~response to hypoxia	14	5.691056911	1.06001E-06
GOTERM_BP_DIRECT	GO:0016477~cell migration	14	5.691056911	1.06001E-06
GOTERM_BP_DIRECT	GO:0043066~negative regulation of apoptotic process	22	8.943089431	2.1985E-06
GOTERM_BP_DIRECT	GO:0043434~response to peptide hormone	8	3.25203252	2.57906E-06
GOTERM_BP_DIRECT	GO:0001525~angiogenesis	15	6.097560976	3.6781E-06
GOTERM_BP_DIRECT	GO:0006954~inflammatory response	19	7.723577236	8.06111E-06
GOTERM_BP_DIRECT	GO:0030199~collagen fibril organization	7	2.845528455	1.67874E-05
GOTERM_BP_DIRECT	GO:0001649~osteoblast differentiation	10	4.06504065	1.69349E-05
GOTERM_BP_DIRECT	GO:0001558~regulation of cell growth	9	3.658536585	1.74324E-05
GOTERM_BP_DIRECT	GO:0009612~response to mechanical stimulus	8	3.25203252	1.91681E-05
GOTERM_BP_DIRECT	GO:0006928~movement of cell or subcellular component	9	3.658536585	2.96656E-05
GOTERM_BP_DIRECT	GO:0098609~cell-cell adhesion	15	6.097560976	3.37603E-05
GOTERM_BP_DIRECT	GO:0045766~positive regulation of angiogenesis	10	4.06504065	3.78804E-05
GOTERM_BP_DIRECT	GO:0033627~cell adhesion mediated by integrin	5	2.032520325	4.75038E-05
GOTERM_BP_DIRECT	GO:0090004~positive regulation of establishment of protein localization to plasma membrane	6	2.43902439	5.85099E-05
GOTERM_BP_DIRECT	GO:0007507~heart development	12	4.87804878	6.11959E-05
GOTERM_BP_DIRECT	GO:0030335~positive regulation of cell migration	12	4.87804878	6.42846E-05
GOTERM_BP_DIRECT	GO:0010628~positive regulation of gene expression	14	5.691056911	9.70207E-05
GOTERM_BP_DIRECT	GO:0046718~viral entry into host cell	8	3.25203252	0.000138736
GOTERM_BP_DIRECT	GO:0001501~skeletal system development	10	4.06504065	0.000147454
GOTERM_BP_DIRECT	GO:0046697~decidualization	5	2.032520325	0.000159469
GOTERM_BP_DIRECT	GO:0008285~negative regulation of cell proliferation	17	6.910569106	0.000174741
GOTERM_BP_DIRECT	GO:0060070~canonical Wnt signaling pathway	8	3.25203252	0.000174929
GOTERM_BP_DIRECT	GO:0009611~response to wounding	7	2.845528455	0.000263354
GOTERM_BP_DIRECT	GO:0007160~cell-matrix adhesion	8	3.25203252	0.000289501
GOTERM_BP_DIRECT	GO:0051384~response to glucocorticoid	7	2.845528455	0.000312703
GOTERM_BP_DIRECT	GO:0048333~mesodermal cell differentiation	4	1.62601626	0.000426492
GOTERM_BP_DIRECT	GO:0071260~cellular response to mechanical stimulus	7	2.845528455	0.000505268
GOTERM_BP_DIRECT	GO:0007229~integrin-mediated signaling pathway	8	3.25203252	0.000518052
GOTERM_BP_DIRECT	GO:0071560~cellular response to transforming growth factor beta stimulus	6	2.43902439	0.000629074
GOTERM_BP_DIRECT	GO:0007584~response to nutrient	7	2.845528455	0.000630928
GOTERM_BP_DIRECT	GO:0002576~platelet degranulation	8	3.25203252	0.00065736
GOTERM_BP_DIRECT	GO:0043542~endothelial cell migration	5	2.032520325	0.00070732

GOTERM_BP_DIRECT	GO:0006508~proteolysis	18	7.317073171	0.000806691
GOTERM_BP_DIRECT	GO:0051017~actin filament bundle assembly	5	2.032520325	0.000807137
GOTERM_BP_DIRECT	GO:0010812~negative regulation of cell-substrate adhesion	4	1.62601626	0.00091172
GOTERM_BP_DIRECT	GO:0001503~ossification	7	2.845528455	0.000953886
GOTERM_BP_DIRECT	GO:0009615~response to virus	8	3.25203252	0.000971271
GOTERM_BP_DIRECT	GO:0048146~positive regulation of fibroblast proliferation	6	2.43902439	0.000985148
GOTERM_BP_DIRECT	GO:0007267~cell-cell signaling	12	4.87804878	0.001026738
GOTERM_BP_DIRECT	GO:0043065~positive regulation of apoptotic process	13	5.284552846	0.001225944
GOTERM_BP_DIRECT	GO:0051897~positive regulation of protein kinase B signaling	7	2.845528455	0.00123123
GOTERM_BP_DIRECT	GO:0070301~cellular response to hydrogen peroxide	6	2.43902439	0.001260256
GOTERM_BP_DIRECT	GO:0042127~regulation of cell proliferation	10	4.06504065	0.001299008
GOTERM_BP_DIRECT	GO:0001837~epithelial to mesenchymal transition	5	2.032520325	0.001306671
GOTERM_BP_DIRECT	GO:0051216~cartilage development	6	2.43902439	0.001472745
GOTERM_BP_DIRECT	GO:0010951~negative regulation of endopeptidase activity	8	3.25203252	0.001690816
GOTERM_BP_DIRECT	GO:0006935~chemotaxis	8	3.25203252	0.001772551
GOTERM_BP_DIRECT	GO:0050900~leukocyte migration	8	3.25203252	0.001772551
GOTERM_BP_DIRECT	GO:0032355~response to estradiol	7	2.845528455	0.001860252
GOTERM_BP_DIRECT	GO:0009653~anatomical structure morphogenesis	7	2.845528455	0.001966914
GOTERM_BP_DIRECT	GO:0043627~response to estrogen	6	2.43902439	0.002268786
GOTERM_BP_DIRECT	GO:0090090~negative regulation of canonical Wnt signaling pathway	9	3.658536585	0.002270892
GOTERM_BP_DIRECT	GO:0030336~negative regulation of cell migration	7	2.845528455	0.002314772
GOTERM_BP_DIRECT	GO:0045184~establishment of protein localization	5	2.032520325	0.002409752
GOTERM_BP_DIRECT	GO:0006952~defense response	6	2.43902439	0.002592844
GOTERM_BP_DIRECT	GO:0001957~intramembranous ossification	3	1.219512195	0.002890084
GOTERM_BP_DIRECT	GO:0045987~positive regulation of smooth muscle contraction	4	1.62601626	0.00309622
GOTERM_BP_DIRECT	GO:0030855~epithelial cell differentiation	6	2.43902439	0.003140075
GOTERM_BP_DIRECT	GO:0071300~cellular response to retinoic acid	6	2.43902439	0.003140075
GOTERM_BP_DIRECT	GO:0030155~regulation of cell adhesion	5	2.032520325	0.003148148
GOTERM_BP_DIRECT	GO:0070098~chemokine-mediated signaling pathway	6	2.43902439	0.003339681
GOTERM_BP_DIRECT	GO:0090103~cochlea morphogenesis	4	1.62601626	0.003547918
GOTERM_BP_DIRECT	GO:0043567~regulation of insulin-like growth factor receptor signaling pathway	3	1.219512195	0.004008375
GOTERM_BP_DIRECT	GO:0000187~activation of MAPK activity	7	2.845528455	0.004184996
GOTERM_BP_DIRECT	GO:0030216~keratinocyte differentiation	6	2.43902439	0.004476692
GOTERM_BP_DIRECT	GO:0071356~cellular response to tumor necrosis factor	7	2.845528455	0.004789709
GOTERM_BP_DIRECT	GO:0033629~negative regulation of cell adhesion mediated by integrin	3	1.219512195	0.005294705
GOTERM_BP_DIRECT	GO:0060054~positive regulation of epithelial cell proliferation involved in wound healing	3	1.219512195	0.005294705
GOTERM_BP_DIRECT	GO:0018149~peptide cross-linking	5	2.032520325	0.005439413
GOTERM_BP_DIRECT	GO:0061621~canonical glycolysis	4	1.62601626	0.005745781
GOTERM_BP_DIRECT	GO:0035025~positive regulation of Rho protein signal transduction	4	1.62601626	0.005745781
GOTERM_BP_DIRECT	GO:0042542~response to hydrogen peroxide	5	2.032520325	0.005837885
GOTERM_BP_DIRECT	GO:0034097~response to cytokine	5	2.032520325	0.006255344
GOTERM_BP_DIRECT	GO:0010800~positive regulation of peptidyl-threonine phosphorylation	4	1.62601626	0.006397206
GOTERM_BP_DIRECT	GO:0035987~endodermal cell differentiation	4	1.62601626	0.006397206
GOTERM_BP_DIRECT	GO:0044267~cellular protein metabolic process	7	2.845528455	0.006714821

GOTERM_BP_DIRECT	GO:0045198~establishment of epithelial cell apical/basal polarity	3	1.219512195	0.006744126
GOTERM_BP_DIRECT	GO:0006915~apoptotic process	17	6.910569106	0.007069602
GOTERM_BP_DIRECT	GO:0043388~positive regulation of DNA binding	4	1.62601626	0.007090884
GOTERM_BP_DIRECT	GO:0007411~axon guidance	8	3.25203252	0.007542748
GOTERM_BP_DIRECT	GO:0060548~negative regulation of cell death	5	2.032520325	0.007625391
GOTERM_BP_DIRECT	GO:0030203~glycosaminoglycan metabolic process	4	1.62601626	0.007827449
GOTERM_BP_DIRECT	GO:0040037~negative regulation of fibroblast growth factor receptor signaling pathway	3	1.219512195	0.008351794
GOTERM_BP_DIRECT	GO:0071803~positive regulation of podosome assembly	3	1.219512195	0.008351794
GOTERM_BP_DIRECT	GO:0044344~cellular response to fibroblast growth factor stimulus	4	1.62601626	0.008607483
GOTERM_BP_DIRECT	GO:0071407~cellular response to organic cyclic compound	5	2.032520325	0.009739928
GOTERM_BP_DIRECT	GO:0016266~O-glycan processing	5	2.032520325	0.010322184
GOTERM_BP_DIRECT	GO:0048661~positive regulation of smooth muscle cell proliferation	5	2.032520325	0.010322184
GOTERM_BP_DIRECT	GO:0045669~positive regulation of osteoblast differentiation	5	2.032520325	0.010322184
GOTERM_BP_DIRECT	GO:0008584~male gonad development	6	2.43902439	0.010845629
GOTERM_BP_DIRECT	GO:0015758~glucose transport	4	1.62601626	0.011213457
GOTERM_BP_DIRECT	GO:0010634~positive regulation of epithelial cell migration	4	1.62601626	0.011213457
GOTERM_BP_DIRECT	GO:0071364~cellular response to epidermal growth factor stimulus	4	1.62601626	0.011213457
GOTERM_BP_DIRECT	GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest	5	2.032520325	0.01155321
GOTERM_BP_DIRECT	GO:0090179~planar cell polarity pathway involved in neural tube closure	3	1.219512195	0.012023024
GOTERM_BP_DIRECT	GO:0035413~positive regulation of catenin import into nucleus	3	1.219512195	0.012023024
GOTERM_BP_DIRECT	GO:0006096~glycolytic process	4	1.62601626	0.012172178
GOTERM_BP_DIRECT	GO:0007586~digestion	5	2.032520325	0.012202562
GOTERM_BP_DIRECT	GO:0060337~type I interferon signaling pathway	5	2.032520325	0.012874845
GOTERM_BP_DIRECT	GO:0014032~neural crest cell development	3	1.219512195	0.01407741
GOTERM_BP_DIRECT	GO:0016337~single organismal cell-cell adhesion	6	2.43902439	0.014461836
GOTERM_BP_DIRECT	GO:0034332~adherens junction organization	4	1.62601626	0.015323296
GOTERM_BP_DIRECT	GO:0045893~positive regulation of transcription, DNA-templated	15	6.097560976	0.015324923
GOTERM_BP_DIRECT	GO:1902230~negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	3	1.219512195	0.016271691
GOTERM_BP_DIRECT	GO:0043508~negative regulation of JUN kinase activity	3	1.219512195	0.016271691
GOTERM_BP_DIRECT	GO:2000353~positive regulation of endothelial cell apoptotic process	3	1.219512195	0.016271691
GOTERM_BP_DIRECT	GO:0010839~negative regulation of keratinocyte proliferation	3	1.219512195	0.016271691
GOTERM_BP_DIRECT	GO:0033138~positive regulation of peptidyl-serine phosphorylation	5	2.032520325	0.017404267
GOTERM_BP_DIRECT	GO:0071347~cellular response to interleukin-1	5	2.032520325	0.018243944
GOTERM_BP_DIRECT	GO:0002042~cell migration involved in sprouting angiogenesis	3	1.219512195	0.018601525
GOTERM_BP_DIRECT	GO:0006821~chloride transport	4	1.62601626	0.018891761
GOTERM_BP_DIRECT	GO:0045071~negative regulation of viral genome replication	4	1.62601626	0.018891761
GOTERM_BP_DIRECT	GO:0032526~response to retinoic acid	4	1.62601626	0.020174719
GOTERM_BP_DIRECT	GO:0030334~regulation of cell migration	5	2.032520325	0.020912357
GOTERM_BP_DIRECT	GO:0090280~positive regulation of calcium ion import	3	1.219512195	0.021062661
GOTERM_BP_DIRECT	GO:0070848~response to growth factor	3	1.219512195	0.021062661
GOTERM_BP_DIRECT	GO:0007566~embryo implantation	4	1.62601626	0.021504548
GOTERM_BP_DIRECT	GO:0043086~negative regulation of catalytic activity	5	2.032520325	0.021852207
GOTERM_BP_DIRECT	GO:0060021~palate development	5	2.032520325	0.022817514
GOTERM_BP_DIRECT	GO:0030324~lung development	5	2.032520325	0.022817514

GOTERM_BP_DIRECT	GO:0031623~receptor internalization	4	1.62601626	0.022881278
GOTERM_BP_DIRECT	GO:2000811~negative regulation of anoikis	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0055093~response to hyperoxia	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0030033~microvillus assembly	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0050860~negative regulation of T cell receptor signaling pathway	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0048514~blood vessel morphogenesis	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0035567~non-canonical Wnt signaling pathway	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0010466~negative regulation of peptidase activity	3	1.219512195	0.023650941
GOTERM_BP_DIRECT	GO:0010977~negative regulation of neuron projection development	4	1.62601626	0.024304906
GOTERM_BP_DIRECT	GO:0036342~post-anal tail morphogenesis	3	1.219512195	0.0263623
GOTERM_BP_DIRECT	GO:0043123~positive regulation of I-kappaB kinase/NF-kappaB signaling	7	2.845528455	0.027022226
GOTERM_BP_DIRECT	GO:0051591~response to cAMP	4	1.62601626	0.027292695
GOTERM_BP_DIRECT	GO:0010595~positive regulation of endothelial cell migration	4	1.62601626	0.027292695
GOTERM_BP_DIRECT	GO:0043410~positive regulation of MAPK cascade	5	2.032520325	0.028030639
GOTERM_BP_DIRECT	GO:1905049~negative regulation of metallopeptidase activity	2	0.81300813	0.028146778
GOTERM_BP_DIRECT	GO:0097325~melanocyte proliferation	2	0.81300813	0.028146778
GOTERM_BP_DIRECT	GO:0071306~cellular response to vitamin E	2	0.81300813	0.028146778
GOTERM_BP_DIRECT	GO:0030825~positive regulation of cGMP metabolic process	2	0.81300813	0.028146778
GOTERM_BP_DIRECT	GO:0010710~regulation of collagen catabolic process	2	0.81300813	0.028146778
GOTERM_BP_DIRECT	GO:1900020~positive regulation of protein kinase C activity	2	0.81300813	0.028146778
GOTERM_BP_DIRECT	GO:0045600~positive regulation of fat cell differentiation	4	1.62601626	0.028856697
GOTERM_BP_DIRECT	GO:0032956~regulation of actin cytoskeleton organization	4	1.62601626	0.028856697
GOTERM_BP_DIRECT	GO:0031100~organ regeneration	4	1.62601626	0.028856697
GOTERM_BP_DIRECT	GO:0010975~regulation of neuron projection development	3	1.219512195	0.02919276
GOTERM_BP_DIRECT	GO:0042246~tissue regeneration	3	1.219512195	0.02919276
GOTERM_BP_DIRECT	GO:0032496~response to lipopolysaccharide	7	2.845528455	0.029213116
GOTERM_BP_DIRECT	GO:0006919~activation of cysteine-type endopeptidase activity involved in apoptotic process	5	2.032520325	0.030298421
GOTERM_BP_DIRECT	GO:0014911~positive regulation of smooth muscle cell migration	3	1.219512195	0.03213843
GOTERM_BP_DIRECT	GO:0008544~epidermis development	5	2.032520325	0.032671585
GOTERM_BP_DIRECT	GO:0051894~positive regulation of focal adhesion assembly	3	1.219512195	0.035195504
GOTERM_BP_DIRECT	GO:0042730~fibrinolysis	3	1.219512195	0.035195504
GOTERM_BP_DIRECT	GO:0071277~cellular response to calcium ion	4	1.62601626	0.035576961
GOTERM_BP_DIRECT	GO:0006955~immune response	12	4.87804878	0.037670245
GOTERM_BP_DIRECT	GO:0045727~positive regulation of translation	4	1.62601626	0.039212962
GOTERM_BP_DIRECT	GO:0045662~negative regulation of myoblast differentiation	3	1.219512195	0.041629067
GOTERM_BP_DIRECT	GO:0032967~positive regulation of collagen biosynthetic process	3	1.219512195	0.041629067
GOTERM_BP_DIRECT	GO:0042663~regulation of endodermal cell fate specification	2	0.81300813	0.041922899
GOTERM_BP_DIRECT	GO:0006725~cellular aromatic compound metabolic process	2	0.81300813	0.041922899
GOTERM_BP_DIRECT	GO:0035583~sequestering of TGFbeta in extracellular matrix	2	0.81300813	0.041922899
GOTERM_BP_DIRECT	GO:0032487~regulation of Rap protein signal transduction	2	0.81300813	0.041922899
GOTERM_BP_DIRECT	GO:0007204~positive regulation of cytosolic calcium ion concentration	6	2.43902439	0.042129182
GOTERM_BP_DIRECT	GO:0007173~epidermal growth factor receptor signaling pathway	4	1.62601626	0.045006179
GOTERM_BP_DIRECT	GO:0042733~embryonic digit morphogenesis	4	1.62601626	0.045006179
GOTERM_BP_DIRECT	GO:0030182~neuron differentiation	5	2.032520325	0.046130997

GOTERM_BP_DIRECT	GO:0042327~positive regulation of phosphorylation	3	1.219512195	0.048464657
GOTERM_BP_DIRECT	GO:0034612~response to tumor necrosis factor	3	1.219512195	0.048464657
GOTERM_BP_DIRECT	GO:0007159~leukocyte cell-cell adhesion	3	1.219512195	0.048464657
GOTERM_BP_DIRECT	GO:0031214~biomineral tissue development	3	1.219512195	0.048464657
GOTERM_BP_DIRECT	GO:0070373~negative regulation of ERK1 and ERK2 cascade	4	1.62601626	0.049090885
GOTERM_BP_DIRECT	GO:0051592~response to calcium ion	4	1.62601626	0.049090885
GOTERM_BP_DIRECT	GO:0001701~in utero embryonic development	7	2.845528455	0.049890899
GOTERM_CC_DIRECT	GO:0005615~extracellular space	92	37.39837398	2.4068E-41
GOTERM_CC_DIRECT	GO:0070062~extracellular exosome	103	41.8699187	7.81364E-24
GOTERM_CC_DIRECT	GO:0005578~proteinaceous extracellular matrix	30	12.19512195	2.39364E-18
GOTERM_CC_DIRECT	GO:0031012~extracellular matrix	29	11.78861789	3.19423E-16
GOTERM_CC_DIRECT	GO:0005576~extracellular region	65	26.42276423	5.24147E-16
GOTERM_CC_DIRECT	GO:0005925~focal adhesion	30	12.19512195	6.08752E-14
GOTERM_CC_DIRECT	GO:0009986~cell surface	31	12.60162602	3.83878E-11
GOTERM_CC_DIRECT	GO:0016324~apical plasma membrane	20	8.130081301	1.2905E-08
GOTERM_CC_DIRECT	GO:0005913~cell-cell adherens junction	20	8.130081301	6.83331E-08
GOTERM_CC_DIRECT	GO:0031982~vesicle	13	5.284552846	1.395E-07
GOTERM_CC_DIRECT	GO:0005886~plasma membrane	87	35.36585366	2.95405E-06
GOTERM_CC_DIRECT	GO:0031528~microvillus membrane	6	2.43902439	3.95721E-06
GOTERM_CC_DIRECT	GO:0005796~Golgi lumen	10	4.06504065	5.25678E-06
GOTERM_CC_DIRECT	GO:0071944~cell periphery	7	2.845528455	1.16493E-05
GOTERM_CC_DIRECT	GO:0048471~perinuclear region of cytoplasm	23	9.349593496	2.9934E-05
GOTERM_CC_DIRECT	GO:0071438~invadopodium membrane	4	1.62601626	4.49098E-05
GOTERM_CC_DIRECT	GO:0016328~lateral plasma membrane	7	2.845528455	7.01936E-05
GOTERM_CC_DIRECT	GO:0042470~melanosome	8	3.25203252	0.000398036
GOTERM_CC_DIRECT	GO:0016323~basolateral plasma membrane	10	4.06504065	0.000690812
GOTERM_CC_DIRECT	GO:0005737~cytoplasm	93	37.80487805	0.000979857
GOTERM_CC_DIRECT	GO:0005887~integral component of plasma membrane	34	13.82113821	0.001096818
GOTERM_CC_DIRECT	GO:0001726~ruffle	7	2.845528455	0.001266403
GOTERM_CC_DIRECT	GO:0030027~lamellipodium	9	3.658536585	0.00136351
GOTERM_CC_DIRECT	GO:0045121~membrane raft	10	4.06504065	0.001775488
GOTERM_CC_DIRECT	GO:0030175~filopodium	6	2.43902439	0.002529975
GOTERM_CC_DIRECT	GO:0005923~bicellular tight junction	7	2.845528455	0.003995982
GOTERM_CC_DIRECT	GO:0005882~intermediate filament	7	2.845528455	0.003995982
GOTERM_CC_DIRECT	GO:0031225~anchored component of membrane	7	2.845528455	0.003995982
GOTERM_CC_DIRECT	GO:0005604~basement membrane	6	2.43902439	0.004020885
GOTERM_CC_DIRECT	GO:0030426~growth cone	7	2.845528455	0.004541893
GOTERM_CC_DIRECT	GO:0032587~ruffle membrane	6	2.43902439	0.004714772
GOTERM_CC_DIRECT	GO:0008305~integrin complex	4	1.62601626	0.005345833
GOTERM_CC_DIRECT	GO:0042383~sarcolemma	6	2.43902439	0.005489782
GOTERM_CC_DIRECT	GO:0031093~platelet alpha granule lumen	5	2.032520325	0.006089339
GOTERM_CC_DIRECT	GO:0005581~collagen trimer	6	2.43902439	0.007640394
GOTERM_CC_DIRECT	GO:0009897~external side of plasma membrane	9	3.658536585	0.007728172
GOTERM_CC_DIRECT	GO:0015629~actin cytoskeleton	9	3.658536585	0.008834129

GOTERM_CC_DIRECT	GO:0031091~platelet alpha granule	3	1.219512195	0.014385346
GOTERM_CC_DIRECT	GO:0072686~mitotic spindle	4	1.62601626	0.017010652
GOTERM_CC_DIRECT	GO:0045177~apical part of cell	5	2.032520325	0.017685321
GOTERM_CC_DIRECT	GO:0019898~extrinsic component of membrane	5	2.032520325	0.023701701
GOTERM_CC_DIRECT	GO:0032154~cleavage furrow	4	1.62601626	0.024423122
GOTERM_CC_DIRECT	GO:0031258~lamellipodium membrane	3	1.219512195	0.025883019
GOTERM_CC_DIRECT	GO:0051233~spindle midzone	3	1.219512195	0.025883019
GOTERM_CC_DIRECT	GO:0043034~costamere	3	1.219512195	0.025883019
GOTERM_CC_DIRECT	GO:0034667~integrin alpha3-beta1 complex	2	0.81300813	0.026382767
GOTERM_CC_DIRECT	GO:0043202~lysosomal lumen	5	2.032520325	0.026616046
GOTERM_CC_DIRECT	GO:0034707~chloride channel complex	4	1.62601626	0.027222748
GOTERM_CC_DIRECT	GO:0043235~receptor complex	6	2.43902439	0.027305311
GOTERM_CC_DIRECT	GO:0005911~cell-cell junction	7	2.845528455	0.02748025
GOTERM_CC_DIRECT	GO:0030496~midbody	6	2.43902439	0.028948171
GOTERM_CC_DIRECT	GO:0015630~microtubule cytoskeleton	6	2.43902439	0.03613784
GOTERM_CC_DIRECT	GO:0031594~neuromuscular junction	4	1.62601626	0.036600944
GOTERM_CC_DIRECT	GO:0034666~integrin alpha2-beta1 complex	2	0.81300813	0.039313036
GOTERM_CC_DIRECT	GO:0097149~centralspindlin complex	2	0.81300813	0.039313036
GOTERM_CC_DIRECT	GO:0044393~microspike	2	0.81300813	0.039313036
GOTERM_CC_DIRECT	GO:0019897~extrinsic component of plasma membrane	3	1.219512195	0.043116912
GOTERM_CC_DIRECT	GO:0005623~cell	5	2.032520325	0.044303661
GOTERM_CC_DIRECT	GO:0005903~brush border	4	1.62601626	0.045519089
GOTERM_MF_DIRECT	GO:0005178~integrin binding	19	7.723577236	5.89619E-15
GOTERM_MF_DIRECT	GO:0005515~protein binding	175	71.13821138	5.26675E-12
GOTERM_MF_DIRECT	GO:0005509~calcium ion binding	34	13.82113821	1.6431E-09
GOTERM_MF_DIRECT	GO:0002020~protease binding	13	5.284552846	1.67672E-08
GOTERM_MF_DIRECT	GO:0098641~cadherin binding involved in cell-cell adhesion	20	8.130081301	2.70349E-08
GOTERM_MF_DIRECT	GO:0043236~laminin binding	8	3.25203252	3.70454E-08
GOTERM_MF_DIRECT	GO:0004222~metalloendopeptidase activity	12	4.87804878	5.24682E-07
GOTERM_MF_DIRECT	GO:0001968~fibronectin binding	7	2.845528455	1.27624E-06
GOTERM_MF_DIRECT	GO:0005518~collagen binding	9	3.658536585	1.77251E-06
GOTERM_MF_DIRECT	GO:0004252~serine-type endopeptidase activity	15	6.097560976	1.48661E-05
GOTERM_MF_DIRECT	GO:0008201~heparin binding	12	4.87804878	1.57453E-05
GOTERM_MF_DIRECT	GO:0001618~virus receptor activity	8	3.25203252	5.41413E-05
GOTERM_MF_DIRECT	GO:0008083~growth factor activity	11	4.471544715	9.53695E-05
GOTERM_MF_DIRECT	GO:0048306~calcium-dependent protein binding	7	2.845528455	0.000154472
GOTERM_MF_DIRECT	GO:0050840~extracellular matrix binding	5	2.032520325	0.00043709
GOTERM_MF_DIRECT	GO:0003779~actin binding	13	5.284552846	0.000562345
GOTERM_MF_DIRECT	GO:0044548~S100 protein binding	4	1.62601626	0.00069563
GOTERM_MF_DIRECT	GO:0005125~cytokine activity	10	4.06504065	0.000842758
GOTERM_MF_DIRECT	GO:0017147~Wnt-protein binding	5	2.032520325	0.00087095
GOTERM_MF_DIRECT	GO:0019834~phospholipase A2 inhibitor activity	3	1.219512195	0.001146305
GOTERM_MF_DIRECT	GO:0004869~cysteine-type endopeptidase inhibitor activity	5	2.032520325	0.001242298
GOTERM_MF_DIRECT	GO:0005201~extracellular matrix structural constituent	6	2.43902439	0.002443879

GOTERM_MF_DIRECT	GO:0019901~protein kinase binding	14	5.691056911	0.002525723
GOTERM_MF_DIRECT	GO:0005198~structural molecule activity	11	4.471544715	0.002558838
GOTERM_MF_DIRECT	GO:0042813~Wnt-activated receptor activity	4	1.62601626	0.003413753
GOTERM_MF_DIRECT	GO:0034235~GPI anchor binding	3	1.219512195	0.003902218
GOTERM_MF_DIRECT	GO:0008009~chemokine activity	5	2.032520325	0.004821112
GOTERM_MF_DIRECT	GO:0031995~insulin-like growth factor II binding	3	1.219512195	0.005155141
GOTERM_MF_DIRECT	GO:0019904~protein domain specific binding	9	3.658536585	0.009032837
GOTERM_MF_DIRECT	GO:0048407~platelet-derived growth factor binding	3	1.219512195	0.009850168
GOTERM_MF_DIRECT	GO:0004859~phospholipase inhibitor activity	3	1.219512195	0.009850168
GOTERM_MF_DIRECT	GO:0043394~proteoglycan binding	3	1.219512195	0.009850168
GOTERM_MF_DIRECT	GO:0050839~cell adhesion molecule binding	5	2.032520325	0.011029924
GOTERM_MF_DIRECT	GO:0005102~receptor binding	12	4.87804878	0.011106598
GOTERM_MF_DIRECT	GO:0031994~insulin-like growth factor I binding	3	1.219512195	0.011712069
GOTERM_MF_DIRECT	GO:0008191~metalloendopeptidase inhibitor activity	3	1.219512195	0.020528265
GOTERM_MF_DIRECT	GO:0005520~insulin-like growth factor binding	3	1.219512195	0.025699877
GOTERM_MF_DIRECT	GO:0017124~SH3 domain binding	6	2.43902439	0.02588126
GOTERM_MF_DIRECT	GO:0032403~protein complex binding	8	3.25203252	0.026009562
GOTERM_MF_DIRECT	GO:0008237~metallopeptidase activity	5	2.032520325	0.026834811
GOTERM_MF_DIRECT	GO:0042803~protein homodimerization activity	18	7.317073171	0.027876714
GOTERM_MF_DIRECT	GO:0042802~identical protein binding	18	7.317073171	0.034191453
GOTERM_MF_DIRECT	GO:0005254~chloride channel activity	4	1.62601626	0.039720521
GOTERM_MF_DIRECT	GO:0045296~cadherin binding	3	1.219512195	0.040608211
GOTERM_MF_DIRECT	GO:0005540~hyaluronic acid binding	3	1.219512195	0.040608211
GOTERM_MF_DIRECT	GO:0005544~calcium-dependent phospholipid binding	4	1.62601626	0.047469748
KEGG_PATHWAY	hsa04512:ECM-receptor interaction	14	5.691056911	5.85E-10
KEGG_PATHWAY	hsa05200:Pathways in cancer	24	9.756097561	2.26E-08
KEGG_PATHWAY	hsa05205:Proteoglycans in cancer	17	6.910569106	6.04E-08
KEGG_PATHWAY	hsa04510:Focal adhesion	16	6.504065041	0.000000556
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling pathway	18	7.317073171	0.0000201
KEGG_PATHWAY	hsa04670:Leukocyte transendothelial migration	10	4.06504065	0.0000678
KEGG_PATHWAY	hsa05222:Small cell lung cancer	8	3.25203252	0.00033
KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	12	4.87804878	0.001319575
KEGG_PATHWAY	hsa05219:Bladder cancer	5	2.032520325	0.003600229
KEGG_PATHWAY	hsa04066:HIF-1 signaling pathway	7	2.845528455	0.003676269
KEGG_PATHWAY	hsa05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	6	2.43902439	0.003725881
KEGG_PATHWAY	hsa04810:Regulation of actin cytoskeleton	10	4.06504065	0.005227546
KEGG_PATHWAY	hsa04015:Rap1 signaling pathway	10	4.06504065	0.005227546
KEGG_PATHWAY	hsa05146:Amoebiasis	7	2.845528455	0.00597232
KEGG_PATHWAY	hsa05144:Malaria	5	2.032520325	0.006850932
KEGG_PATHWAY	hsa04611:Platelet activation	7	2.845528455	0.015499847
KEGG_PATHWAY	hsa05230:Central carbon metabolism in cancer	5	2.032520325	0.017214857
KEGG_PATHWAY	hsa04115:p53 signaling pathway	5	2.032520325	0.020048517
KEGG_PATHWAY	hsa00010:Glycolysis / Gluconeogenesis	5	2.032520325	0.020048517
KEGG_PATHWAY	hsa04550:Signaling pathways regulating pluripotency of stem cells	7	2.845528455	0.021550131

KEGG_PATHWAY	hsa04610:Complement and coagulation cascades	5	2.032520325	0.022088473
KEGG_PATHWAY	hsa04514:Cell adhesion molecules (CAMs)	7	2.845528455	0.022928144
KEGG_PATHWAY	hsa04390:Hippo signaling pathway	7	2.845528455	0.029864674
KEGG_PATHWAY	hsa05202:Transcriptional misregulation in cancer	7	2.845528455	0.045345963
KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	5	2.032520325	0.046105277
KEGG_PATHWAY	hsa04064:NF-kappa B signaling pathway	5	2.032520325	0.046105277
KEGG_PATHWAY	hsa04360:Axon guidance	6	2.43902439	0.04742403
KEGG_PATHWAY	hsa05323:Rheumatoid arthritis	5	2.032520325	0.047743658

Table S5. Reasons for exclusion from the evaluation of prognostic factors and establishment of nomogram

Case ID	Size	T	N	AJCC stage	Residual tumor	Surgical treatment	History of radiation therapy	History of targeted molecular therapy	Tobacco smoking history	Alocohol drinking history	History of chronic pancreatitis	History of diabetes
TCGA-IB-A7LX			NA									
TCGA-HZ-8637							NA		NA		NA	NA
TCGA-HZ-A77P							NA					
TCGA-XD-AAUI											NA	
TCGA-FB-A4P5							NA					
TCGA-IB-AAUT	NA											
TCGA-IB-A5SS						NA						
TCGA-PZ-A5RE					NA					NA	NA	NA
TCGA-HZ-A4BK							NA		NA		NA	NA
TCGA-2J-AAB6									NA			
TCGA-OE-A75W							NA					
TCGA-HZ-A49I							NA		NA		NA	NA
TCGA-HZ-8519							NA		NA		NA	NA
TCGA-FB-A78T							NA				NA	
TCGA-HZ-8002							NA		NA	NA	NA	NA
TCGA-3E-AAAZ					NA		NA			NA	NA	NA
TCGA-HV-A5A4	NA				NA							
TCGA-FB-A4P6					NA		NA					
TCGA-IB-A5ST							NA					
TCGA-HZ-7919							NA	NA	NA		NA	NA
TCGA-HZ-8003							NA		NA	NA	NA	NA
TCGA-HV-AA8V	NA											
TCGA-HZ-8001				NA			NA		NA	NA	NA	NA
TCGA-HZ-8317							NA		NA		NA	NA
TCGA-2L-AAQL					NA							
TCGA-Q3-A5QY								NA				
TCGA-HZ-A49G							NA		NA		NA	NA
TCGA-HV-A5A5	NA				NA							
TCGA-IB-A7M4	NA											
TCGA-2J-AABT							NA					
TCGA-HZ-7926					NA		NA	NA	NA		NA	NA
TCGA-2L-AAQI												NA
TCGA-FB-A545	NA				NA		NA				NA	
TCGA-2J-AABK									NA			
TCGA-2J-AAB8							NA		NA			
TCGA-HZ-A49H							NA		NA		NA	NA
TCGA-HZ-8315							NA		NA	NA	NA	NA
TCGA-HV-AA8X	NA											
TCGA-HZ-A77O							NA					
TCGA-HV-A7OL	NA											
TCGA-IB-7888									NA			
TCGA-YH-A8SY				NA	NA							
TCGA-IB-7652								NA				
TCGA-HZ-7925							NA		NA		NA	NA
TCGA-HV-A5A6	NA					NA				NA		
TCGA-Z5-AAPL	NA					NA				NA	NA	NA
TCGA-US-A779							NA	NA				
TCGA-HZ-A4BH							NA	NA	NA		NA	NA
TCGA-FB-AAPS								NA				
TCGA-3A-A9I7	NA							NA	NA			
TCGA-IB-8126							NA					
TCGA-3A-A9I5		NA		NA					NA			
TCGA-3E-AAAY					NA							
TCGA-FB-AAPY											NA	
TCGA-IB-8127										NA		
TCGA-IB-7645										NA		
TCGA-FB-A5VM							NA					
TCGA-LB-A8F3							NA				NA	
TCGA-HV-A5A3	NA		NA		NA				NA			
TCGA-Q3-AA2A	NA				NA						NA	
TCGA-H6-A45N					NA		NA					
TCGA-HZ-A77Q							NA	NA				
TCGA-HZ-8005									NA	NA	NA	NA
TCGA-2J-AABR									NA			

Table S6. Gene set enrichment analyses between high and low risk group in TCGA PAAD dataset

Terms enriched in high risk group

NAME	SIZE	ES	NES	NOM p-val	FDR q-val
C2 KEGG (19 terms)					
KEGG_NUCLEOTIDE_EXCISION_REPAIR	44	0.7201397	2.0976436	0	0.014243265
KEGG_DNA_REPLICATION	36	0.76967376	1.9800676	0.001984127	0.032056652
KEGG_CELL_CYCLE	124	0.6190967	1.9787879	0.002061856	0.02192012
KEGG_PENTOSE_PHOSPHATE_PATHWAY	26	0.6525248	1.9349254	0.004081633	0.031387735
KEGG_HOMOLOGOUS_RECOMBINATION	28	0.6866101	1.8651135	0	0.05900724
KEGG_P53_SIGNALING_PATHWAY	67	0.53078645	1.8600821	0	0.051003285
KEGG_MISMATCH_REPAIR	23	0.71814543	1.8482338	0.005988024	0.04848411
KEGG_PROTEASOME	44	0.72454447	1.8142364	0.001988072	0.057262708
KEGG_PYRIMIDINE_METABOLISM	96	0.52235556	1.8008125	0.005952381	0.059701934
KEGG_BASE_EXCISION_REPAIR	33	0.64210325	1.744873	0.002024292	0.09585684
KEGG_SPLICEOSOME	124	0.5726161	1.7331576	0.002004008	0.09630436
KEGG_ONE_CARBON_POOL_BY_FOLATE	17	0.6265623	1.7208614	0.004166667	0.09855121
KEGG_N_GLYCAN_BIOSYNTHESIS	46	0.5590183	1.7089907	0.012072435	0.10039359
KEGG_HUNTINGTONS_DISEASE	172	0.4956008	1.6758672	0.038934425	0.12364742
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	41	0.612716	1.6366665	0.016771488	0.15375604
KEGG_RNA_POLYMERASE	29	0.5731571	1.6191819	0.030425964	0.1654411
KEGG_RNA_DEGRADATION	57	0.54382604	1.6059408	0.024096385	0.17073308
KEGG_OOCYTE_MEIOSIS	111	0.45920682	1.5974178	0.025586354	0.17047107
KEGG_ALZHEIMERS_DISEASE	156	0.43739977	1.5367693	0.09306931	0.24166852
C5					
Biological process (646 terms)					
GO_CELL_CYCLE_G1_S_PHASE_TRANSITION	108	0.6594155	2.079041	0	0.17302747
GO_MITOTIC_CYTOKINESIS	31	0.77121973	2.0544686	0	0.12073248
GO_METAPHASE_PLATE_CONGRESSION	40	0.7632659	2.0319428	0	0.112749554
GO_CHROMOSOME_SEGREGATION	259	0.6232573	2.0318973	0	0.08456216
GO_MITOTIC_SISTER_CHROMATID_SEGREGATION	87	0.70989907	2.0139432	0	0.09089815
GO_DNA_PACKAGING	186	0.5678415	2.0118885	0	0.07762929
GO_SISTER_CHROMATID_SEGREGATION	169	0.67860454	2.009597	0	0.068468295
GO_NUCLEAR_CHROMOSOME_SEGREGATION	216	0.6231709	2.0071008	0	0.06222519
GO_MITOTIC_NUCLEAR_DIVISION	349	0.61095	2.006609	0	0.05602736
GO_MITOTIC_CELL_CYCLE	738	0.59008014	2.003901	0	0.053431753
GO_NEGATIVE_REGULATION_OF_CELL_DIVISION	58	0.6338843	2.0016801	0.002066116	0.050330997
GO_CELL_DIVISION	449	0.57844305	2.0005815	0	0.046962485
GO_POSITIVE_REGULATION_OF_CYTOKINESIS	35	0.6032073	1.9870645	0	0.053053077
GO_CHROMOSOME_LOCALIZATION	59	0.6648509	1.9844478	0	0.05093084
GO_ORGANELLE_FISSION	471	0.561181	1.9843669	0	0.04763153
GO_REGULATION_OF_CYTOKINESIS	63	0.5958506	1.9737135	0	0.05116467
GO_CHROMOSOME_CONDENSATION	29	0.7009857	1.9726745	0	0.048777815

GO_DNA_CONFORMATION_CHANGE	263	0.56042385	1.9689437	0.00204499	0.048354197
GO_TELOMERE_ORGANIZATION	103	0.60528266	1.9628264	0.002096436	0.049389604
GO_DNA_REPLICATION_INDEPENDENT_NUCLEOSOME_ORGANIZATION	51	0.66559476	1.9589338	0	0.04963587
GO_ATP_DEPENDENT_CHROMATIN_REMODELING	72	0.6025981	1.9567213	0	0.049041003
GO_SISTER_CHROMATID_COHESION	107	0.68042785	1.9516385	0	0.05041581
GO_HISTONE_EXCHANGE	51	0.6394713	1.9339594	0	0.061044134
GO_CELL_CYCLE_CHECKPOINT	185	0.5870263	1.9336329	0	0.05865187
GO_ANAPHASE_PROMOTING_COMPLEX_DEPENDENT_CATABOLIC_PROCESS	76	0.7079842	1.9265618	0.002012072	0.06160793
GO_CELL_CYCLE_PHASE_TRANSITION	249	0.5743212	1.924497	0	0.060587894
GO_REGULATION_OF_NUCLEAR_DIVISION	159	0.53920203	1.9222364	0	0.060322974
GO_POSITIVE_REGULATION_OF_LIGASE_ACTIVITY	108	0.6125599	1.9175805	0.001956947	0.062291212
GO_DNA_BIOSYNTHETIC_PROCESS	112	0.60502017	1.9162903	0	0.06116454
GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_INTERCONVERSION	21	0.71639425	1.9149318	0.002118644	0.06018737
GO_DNA_RECOMBINATION	199	0.57265526	1.9129227	0	0.059630796
GO_DNA_REPAIR	454	0.5581603	1.9126428	0	0.05802184
GO_PROTEIN_DNA_COMPLEX_SUBUNIT_ORGANIZATION	223	0.53689474	1.9116246	0	0.056921497
GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE_BY_P53_CLASS_MEDIATOR	14	0.7134073	1.9109195	0	0.05590264
GO_CHROMATIN_ASSEMBLY_OR_DISASSEMBLY	170	0.5439884	1.9093914	0	0.055217147
GO_MITOTIC_CELL_CYCLE_CHECKPOINT	133	0.58693933	1.9079821	0.002028398	0.05436471
GO_RECOMBINATIONAL_REPAIR	72	0.6230198	1.9062333	0	0.054252245
GO_REGULATION_OF_CELL_DIVISION	265	0.49105945	1.9006313	0	0.056953292
GO_CENTROMERE_COMPLEX_ASSEMBLY	46	0.6779127	1.8996428	0.002141328	0.056270037
GO_MACROMOLECULAR_COMPLEX_DISASSEMBLY	180	0.56804246	1.8982546	0	0.055735156
GO_DNA_STRAND_ELONGATION	30	0.754878	1.8978914	0.004081633	0.054624617
GO_TRANSCRIPTION_COUPLED_NUCLEOTIDE_EXCISION_REPAIR	72	0.6381792	1.8932533	0	0.056440137
GO_DNA_STRAND_ELONGATION_INVOLVED_IN_DNA_REPLICATION	25	0.772086	1.8922454	0.006048387	0.055737335
GO_NEGATIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	32	0.67065674	1.8917006	0.006122449	0.054746598
GO_NEGATIVE_REGULATION_OF_NUCLEAR_DIVISION	44	0.6242278	1.8906703	0.002070393	0.054341964
GO_CELL_CYCLE_PROCESS	1031	0.5272319	1.8901148	0	0.05352587
GO_CYTOSKELETON_DEPENDENT_CYTOKINESIS	39	0.67397314	1.8823988	0	0.057473022
GO_DOUBLE_STRAND_BREAK_REPAIR	158	0.5644916	1.8800385	0	0.057996474
GO_MITOTIC_RECOMBINATION	41	0.7160155	1.8800086	0.004106776	0.056845613
GO_REGULATION_OF_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	170	0.55327034	1.8796449	0	0.0559638
GO_CELL_DIFFERENTIATION_INVOLVED_IN_EMBRYONIC_PLACENTA_DEVELOPMENT	25	0.6224229	1.8785065	0	0.055537615
GO_DEOXYRIBONUCLEOTIDE_BIOSYNTHETIC_PROCESS	12	0.7682248	1.8755125	0	0.056754433
GO_REGULATION_OF_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	10	0.8647281	1.874774	0	0.056090236
GO_POSTREPLICATION_REPAIR	51	0.6270003	1.8745784	0	0.055233143
GO_REGULATION_OF_EXIT_FROM_MITOSIS	15	0.7092638	1.8734727	0.001984127	0.055012096
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	121	0.60866874	1.8680725	0.006024096	0.05695752
GO_NEGATIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	135	0.5763723	1.8665744	0.003984064	0.057070322
GO_RETROGRADE_VESICLE_MEDIATED_TRANSPORT_GOLGI_TO_ER	76	0.59436154	1.8658687	0.001926782	0.05659839
GO_MITOTIC_SPINDLE_ORGANIZATION	67	0.6308847	1.8642325	0	0.056519132

GO_NUCLEOTIDE_EXCISION_REPAIR	111	0.6047418	1.8637582	0	0.055921607
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_G1_S_TRANSITION_OF_MITOTIC_CELL_CYCLE	25	0.71017885	1.8603126	0	0.05764584
GO_CELL_CYCLE	1260	0.5062813	1.8590708	0.002024292	0.057687998
GO_DNA_REPLICATION_INITIATION	29	0.7229915	1.8582195	0.012195122	0.057261914
GO_REGULATION_OF_CHROMOSOME_SEGREGATION	82	0.6246313	1.8563925	0.001988072	0.057641525
GO_DNA_SYNTHESIS_INVOLVED_IN_DNA_REPAIR	72	0.600466	1.8559506	0.00610998	0.056985766
GO_GUANOSINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	14	0.72929907	1.8556812	0.006048387	0.056431606
GO_DNA_DAMAGE_RESPONSE_DETECTION_OF_DNA_DAMAGE	36	0.67355824	1.853649	0	0.057087526
GO_DNA_REPLICATION	199	0.58835423	1.8531232	0.004032258	0.056539003
GO_DNA_GEOMETRIC_CHANGE	79	0.64581376	1.8512492	0	0.056980796
GO_REGULATION_OF_MITOTIC_CELL_CYCLE	453	0.5071375	1.850487	0	0.05660831
GO_REGULATION_OF_CENTROSOME_CYCLE	38	0.6647558	1.8489791	0.002028398	0.056536384
GO_REGULATION_OF_LIGASE_ACTIVITY	128	0.57687914	1.8432896	0.002008032	0.059795626
GO_REGULATION_OF_TRANSLATION_IN_RESPONSE_TO_STRESS	19	0.7035845	1.8424728	0	0.059348173
GO_NUCLEOTIDE_PHOSPHORYLATION	57	0.5553161	1.842338	0.00631579	0.058638163
GO_DNA_METABOLIC_PROCESS	717	0.5147718	1.8394678	0	0.059833974
GO_DNA_INTEGRITY_CHECKPOINT	140	0.56185144	1.8364042	0.002020202	0.06106539
GO_REGULATION_OF_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	102	0.59517676	1.8353814	0	0.060981054
GO_CYTOKINESIS	84	0.57650286	1.8325056	0.004166667	0.06209914
GO_ADP_METABOLIC_PROCESS	45	0.5654191	1.8309293	0	0.062392663
GO_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	79	0.5514237	1.830807	0.006134969	0.06177915
GO_REGULATION_OF_CELL_CYCLE_PROCESS	542	0.4906111	1.8300204	0	0.061481383
GO_MITOTIC_DNA_INTEGRITY_CHECKPOINT	96	0.57074857	1.8278122	0.00204918	0.062323567
GO_CELL_SEPARATION_AFTER_CYTOKINESIS	17	0.7482304	1.8264953	0	0.06255374
GO_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	314	0.5196457	1.823072	0	0.064318925
GO_DNA_DEPENDENT_DNA_REPLICATION	93	0.6308172	1.8222849	0.006185567	0.064130776
GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	42	0.5442426	1.8202811	0	0.06478797
GO_POSITIVE_REGULATION_OF_MITOTIC_NUCLEAR_DIVISION	50	0.53670204	1.8185797	0.002079002	0.065406114
GO_MITOTIC_SPINDLE_ASSEMBLY	40	0.6259853	1.8131715	0.002040816	0.06872748
GO_CELL_CYCLE_DNA_REPLICATION	11	0.8093078	1.8111064	0.00204918	0.06932733
GO_ATTACHMENT_OF_SPINDLE_MICROTUBULES_TO_KINETOCHORE	14	0.7738783	1.8090951	0	0.07022309
GO_TELOMERE_MAINTENANCE_VIA_RECOMBINATION	32	0.71336704	1.8080405	0.012552301	0.07017772
GO_RNA_CAPPING	35	0.6500747	1.8052832	0.004048583	0.0715783
GO_ATP_GENERATION_FROM_ADP	37	0.5888407	1.8035351	0.004385965	0.07209955
GO_G1_DNA_DAMAGE_CHECKPOINT	70	0.56345177	1.8030847	0.001992032	0.071644515
GO_REGULATION_OF_SISTER_CHROMATID_SEGREGATION	65	0.6092445	1.802754	0.005952381	0.0711142
GO_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	208	0.50912297	1.801465	0	0.07115715
GO_REGULATION_OF_TRANSLATIONAL_INITIATION_IN_RESPONSE_TO_STRESS	13	0.7393982	1.8002415	0	0.07148471
GO_REGULATION_OF_DNA_REPAIR	72	0.5643014	1.7994635	0.00203252	0.07127585
GO_MULTI_ORGANISM_LOCALIZATION	66	0.60049486	1.7993892	0.001992032	0.07061423
GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME_CENTROMERIC_REGION	12	0.83075815	1.7988199	0	0.07028531
GO_NEGATIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	188	0.52133536	1.7979151	0.00409836	0.070325114
GO_KINETOCHORE_ORGANIZATION	11	0.80802447	1.7962064	0.002066116	0.07082972

GO_MEIOTIC_CELL_CYCLE	176	0.4838582	1.7961382	0.002222222	0.0701811
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE	25	0.56131184	1.7943506	0.00203666	0.07084026
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PROCESS	206	0.50823057	1.7938737	0.004032258	0.070462845
GO_TRANSLATIONAL_ELONGATION	110	0.629715	1.7927814	0.016460905	0.070737235
GO_REGULATION_OF_SPINDLE_ORGANIZATION	19	0.7267397	1.7925236	0.002028398	0.07014979
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	141	0.52799565	1.7925135	0.00407332	0.069550104
GO_POSITIVE_REGULATION_OF_VIRAL_PROCESS	86	0.548578	1.7916471	0.004024145	0.069623984
GO_TRANSLATIONAL_TERMINATION	92	0.66141635	1.7912972	0.012295082	0.069281995
GO_REGULATION_OF_MICROTUBULE_BASED_PROCESS	232	0.5188817	1.7911026	0	0.068790466
GO_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	33	0.6126696	1.7908406	0.004246285	0.0683846
GO_PURINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	14	0.69748753	1.7874415	0	0.070244305
GO_MICROTUBULE_DEPOLYMERIZATION	12	0.7090188	1.7863799	0.01417004	0.07037838
GO_INTERSTRAND_CROSS_LINK_REPAIR	43	0.6013596	1.7846135	0.002057613	0.070859075
GO_CELLULAR_RESPONSE_TO_DNA_DAMAGE_STIMULUS	683	0.50166297	1.7844547	0.004032258	0.07030248
GO_NEGATIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	163	0.5090511	1.7836775	0.002028398	0.070243925
GO_VIRION_ASSEMBLY	36	0.6286639	1.7814549	0.002	0.07128069
GO_REGULATION_OF_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	66	0.5912529	1.7800603	0.008368201	0.07176949
GO_MULTI_ORGANISM_ORGANELLE_ORGANIZATION	23	0.68883085	1.7789183	0.001996008	0.07195913
GO_TROPHOBLAST_GIANT_CELL_DIFFERENTIATION	12	0.69022644	1.7769783	0.010799136	0.07286079
GO_POSITIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	15	0.7426813	1.7744824	0.005758158	0.07419394
GO_NEGATIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	27	0.66377854	1.7719053	0.008032128	0.07558655
GO_NUCLEAR_ENVELOPE_REASSEMBLY	17	0.7206396	1.7717979	0	0.075102516
GO_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	20	0.64486015	1.7716019	0.001980198	0.07463592
GO_DEOXYRIBONUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	16	0.69725454	1.768188	0.008333334	0.076560736
GO_FOLIC_ACID_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	12	0.71220076	1.7679068	0.00409836	0.076205686
GO_REGULATION_OF_EXOSOMAL_SECRETION	17	0.6799501	1.767176	0.009940358	0.076118976
GO_PROTEIN_LOCALIZATION_TO_CHROMOSOME	42	0.6209102	1.7666308	0.012269938	0.075891905
GO_CELL_CYCLE_G2_M_PHASE_TRANSITION	135	0.539866	1.7662115	0.00204918	0.075547256
GO_MITOCHONDRIAL_TRANSLATION	105	0.6411833	1.7661473	0.018518519	0.0750145
GO_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	267	0.5174959	1.7644219	0.004048583	0.07577184
GO_POSITIVE_REGULATION_OF_MITOTIC_SISTER_CHROMATID_SEPARATION	14	0.73466486	1.7625535	0.004024145	0.07654687
GO_NIK_NF_KAPPAB_SIGNALING	83	0.58414763	1.7624601	0.006134969	0.07605178
GO_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	92	0.57401276	1.7610134	0.002008032	0.07656615
GO_G2_DNA_DAMAGE_CHECKPOINT	33	0.6117437	1.7604189	0.002074689	0.07645226
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_INCISION	39	0.616001	1.7570999	0.002040816	0.078350075
GO_NON_RECOMBINATIONAL_REPAIR	70	0.5445053	1.7564317	0.008350731	0.07827828
GO_NUCLEOSIDE_SALVAGE	17	0.6594303	1.7537136	0.004140787	0.07985341
GO_SIGNAL_TRANSDUCTION_IN_RESPONSE_TO_DNA_DAMAGE	93	0.52890885	1.7519087	0.001996008	0.080803335
GO_MEIOTIC_CELL_CYCLE_PROCESS	143	0.48117754	1.7515141	0.008849558	0.08058891
GO_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	77	0.57432973	1.7462572	0	0.08439547
GO_EXIT_FROM_MITOSIS	12	0.6857492	1.7448534	0.003960396	0.08524574
GO_TELOMERE_CAPPING	29	0.5822982	1.7446738	0.021008404	0.084795065
GO_APICAL_JUNCTION_ASSEMBLY	39	0.5617546	1.7444959	0.008298756	0.08436369

GO_SPINDLE_CHECKPOINT	24	0.6894951	1.7430066	0.014583333	0.08512426
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_ARREST	82	0.5195382	1.7426795	0.00203252	0.08480592
GO_PEPTIDYL_PROLINE_MODIFICATION	53	0.50628847	1.742659	0.010869565	0.08426755
GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	22	0.57435966	1.7398579	0.009784736	0.08606029
GO_MITOTIC_CHROMOSOME_CONDENSATION	14	0.75140095	1.7383711	0.007889546	0.086522676
GO_POSITIVE_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	192	0.50574815	1.7349168	0	0.08886197
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PROCESS	240	0.45668328	1.7347728	0.004149378	0.08845597
GO_DNA_REPLICATION_CHECKPOINT	14	0.7143572	1.7333574	0.004166667	0.08910595
GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	27	0.5420212	1.7315581	0.002262444	0.09013324
GO_SPLICEOSOMAL_SNRNP_ASSEMBLY	37	0.6423509	1.7309353	0.010121457	0.09010104
GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	27	0.568996	1.7298098	0.011904762	0.09053733
GO_NUCLEAR_ENVELOPE_ORGANIZATION	77	0.58041215	1.7294037	0.004024145	0.09026247
GO_NUCLEUS_ORGANIZATION	131	0.5249544	1.7291876	0	0.08989718
GO_PROTEIN_LOCALIZATION_TO_KINETOCHORE	10	0.8234618	1.7276508	0.00203252	0.090741135
GO_PURINE_NUCLEOSIDE_MONOPHOSPHATE_BIOSYNTHETIC_PROCESS	58	0.54420274	1.7263952	0.016597511	0.09123835
GO_NUCLEOBASE_METABOLIC_PROCESS	38	0.5366523	1.7263659	0.008298756	0.09069273
GO_CHROMOSOME_ORGANIZATION	970	0.4727875	1.7259496	0.00814664	0.09049012
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ORGANELLE	353	0.50328386	1.7258406	0.020491803	0.09003132
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE	46	0.59496236	1.72571	0.00408998	0.08962003
GO_REGULATION_OF_CENTROSOME_DUPLICATION	31	0.6211932	1.7253408	0.002028398	0.089393295
GO_GLYCOSYL_COMPOUND_BIOSYNTHETIC_PROCESS	113	0.48679727	1.7219335	0.004149378	0.09169525
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	54	0.4940323	1.7170415	0.010845987	0.095835604
GO_PYRIMIDINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	29	0.57662636	1.7162814	0.008368201	0.095952
GO_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	123	0.48191005	1.7117918	0.004032258	0.099519394
GO_RIBONUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	62	0.49100196	1.7112136	0.00617284	0.099623956
GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR	35	0.574451	1.710933	0.008247423	0.099326074
GO_MEIOSIS_I	81	0.48167685	1.7104652	0.004750594	0.0991738
GO_AMP_METABOLIC_PROCESS	13	0.6802312	1.7096415	0.003968254	0.09943079
GO_REGULATION_OF_TELOMERASE_RNA_LOCALIZATION_TO_CAJAL_BODY	15	0.7894643	1.7080733	0.014227643	0.100377515
GO_POSITIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	189	0.48823372	1.7070585	0.008016032	0.100768484
GO_TRANSLESION_SYNTHESIS	39	0.5749676	1.7067393	0.002061856	0.10053349
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_GAP_FILLING	24	0.64418495	1.7066292	0.010224949	0.10004112
GO_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	140	0.49218425	1.7065214	0.002053388	0.099613644
GO_DNA_TEMPLATED_TRANSCRIPTION_TERMINATION	98	0.57550466	1.7051836	0.007920792	0.100293
GO_AMIDE_BIOSYNTHETIC_PROCESS	490	0.4984211	1.705073	0.033755273	0.09980847
GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE	32	0.51905906	1.7044178	0.006036217	0.09975252
GO_REGULATION_OF_RNA_STABILITY	137	0.5245605	1.7044063	0.008097166	0.09921055
GO_MATURATION_OF_5_8S_RRNA	28	0.665308	1.7020051	0.016563147	0.10082497
GO_CELLULAR_COMPONENT_DISASSEMBLY	499	0.4264399	1.7010064	0	0.10127034
GO_NUCLEOSIDE_DIPHOSPHATE_METABOLIC_PROCESS	80	0.46829695	1.7008116	0.010309278	0.10089137
GO_BASE_EXCISION_REPAIR	39	0.5885106	1.7006632	0.014112903	0.10054234
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	49	0.52988714	1.7006015	0.008196721	0.10008834
GO_PROTEIN_TARGETING_TO_MITOCHONDRION	47	0.5936182	1.7004097	0.03869654	0.09972516

GO_SPINDLE_ASSEMBLY	69	0.5640803	1.6996964	0.010224949	0.099836
GO_RRNA_3_END_PROCESSING	13	0.76342064	1.6992583	0.014644352	0.099616945
GO_REGULATION_OF_ESTABLISHMENT_OF_PLANAR_POLARITY	110	0.501114	1.698461	0.016701462	0.09979157
GO_PYRUVATE_METABOLIC_PROCESS	62	0.48094097	1.6975366	0	0.10015196
GO_POSITIVE_REGULATION_OF_CHROMOSOME_SEGREGATION	25	0.6638723	1.6973723	0.012345679	0.099797376
GO_NCRNA_METABOLIC_PROCESS	509	0.532935	1.6961759	0.034907598	0.10051061
GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	88	0.4971241	1.6955172	0.016806724	0.100522935
GO_PENTOSE_PHOSPHATE_SHUNT	12	0.69673735	1.6938003	0.009881423	0.10167802
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_ASSEMBLY	29	0.6174684	1.6916432	0.003992016	0.10314338
GO_AMINO_ACID_ACTIVATION	51	0.61593795	1.6914419	0.016632017	0.10283297
GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	232	0.4728614	1.6911051	0.031185031	0.102691725
GO_REGULATION_OF_CELL_CYCLE_ARREST	103	0.4763836	1.6910665	0.004008016	0.10220632
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS	67	0.4943058	1.6900123	0.016427105	0.102614716
GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	77	0.5043767	1.6896877	0.019480519	0.102489196
GO_MONOSACCHARIDE_CATABOLIC_PROCESS	57	0.49460027	1.6875899	0.009009009	0.1037311
GO_NUCLEOBASE_BIOSYNTHETIC_PROCESS	18	0.6439601	1.6863327	0.021097047	0.10433999
GO_MATURATION_OF_SSU_RRNA	41	0.656936	1.6852481	0.027253669	0.10492139
GO_MULTIVESICULAR_BODY_ORGANIZATION	30	0.6336862	1.6851829	0.014056225	0.10445602
GO_GLOBAL_GENOME_NUCLEOTIDE_EXCISION_REPAIR	32	0.6082239	1.68373	0.008016032	0.10541214
GO_BICELLULAR_TIGHT_JUNCTION_ASSEMBLY	31	0.5562197	1.6834726	0.022774328	0.10513558
GO_CELLULAR_MACROMOLECULAR_COMPLEX_ASSEMBLY	687	0.44487453	1.682835	0.002083333	0.10522068
GO_POSITIVE_REGULATION_OF_DNA_REPAIR	37	0.5645221	1.6824293	0.012244898	0.10507682
GO_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	267	0.47290155	1.6824261	0.007984032	0.10458209
GO_PROTEASOME_ASSEMBLY	14	0.72373945	1.6820838	0.015686275	0.10443988
GO_BLASTOCYST_GROWTH	16	0.709049	1.6801829	0.012244898	0.10572605
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	90	0.5393969	1.6791266	0.031380754	0.10627534
GO_POSITIVE_REGULATION_OF_DNA_METABOLIC_PROCESS	182	0.45509538	1.6778299	0.008179959	0.10707712
GO_NADH_METABOLIC_PROCESS	34	0.5654207	1.677182	0.02079002	0.107167825
GO_RIBOSOME_BIOGENESIS	300	0.5818069	1.675016	0.055900622	0.10884301
GO_RECIPROCAL_DNA_RECOMBINATION	39	0.53736556	1.6745574	0.019823788	0.10875994
GO_PURINE_NUCLEOBASE_BIOSYNTHETIC_PROCESS	12	0.6861267	1.674366	0.02258727	0.10841905
GO_RIBONUCLEOPROTEIN_COMPLEX_BIOGENESIS	424	0.5539283	1.6738896	0.048780486	0.1083543
GO_REGULATION_OF_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	160	0.49074864	1.6728058	0.008130081	0.10882209
GO_REGULATION_OF_SPINDLE_ASSEMBLY	14	0.7212587	1.6718248	0.003960396	0.109294064
GO_PROTEIN_LOCALIZATION_TO_ORGANELLE	538	0.46319988	1.6710272	0.00408998	0.10957328
GO_ETHER_METABOLIC_PROCESS	12	0.6292144	1.6698705	0.018099548	0.11035504
GO_MITOTIC_G2_M_TRANSITION_CHECKPOINT	18	0.6400335	1.6696733	0.026970955	0.1100414
GO_CHROMOSOME_ORGANIZATION_INVOLVED_IN_MEIOTIC_CELL_CYCLE	47	0.49190363	1.6691711	0.016470589	0.1100737
GO_RRNA_METABOLIC_PROCESS	250	0.5796282	1.668882	0.062626265	0.10985583
GO_PEPTIDE_METABOLIC_PROCESS	548	0.46339744	1.6677742	0.036796536	0.11044193
GO_MISMATCH_REPAIR	27	0.6059561	1.6654557	0.016666668	0.11227384
GO_PURINE_NUCLEOSIDE_BIOSYNTHETIC_PROCESS	83	0.47392043	1.6642703	0.020876827	0.1130194
GO_MATURATION_OF_5_8S_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	19	0.6925778	1.6642603	0.016666668	0.11255172

GO_PROTEIN_HETEROTETRAMERIZATION	38	0.55923903	1.663671	0.03267974	0.11261031
GO_DNA_LIGATION	16	0.6472004	1.6635885	0.012448133	0.11219521
GO_GLUCOSE_CATABOLIC_PROCESS	28	0.5748583	1.6634889	0.025531914	0.11179181
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_EXONUCLEOLYTIC	30	0.6257131	1.663338	0.015936255	0.111445874
GO_REGULATION_OF_CELL_CYCLE	916	0.42964968	1.6619779	0.004140787	0.11218119
GO_STRAND_DISPLACEMENT	26	0.66460353	1.6617657	0.027659575	0.11195323
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_BY_P53_CLASS_MEDIATOR	18	0.5776873	1.660324	0.008064516	0.11282457
GO_MATURATION_OF_SSU_RRNA_FROM_TRICISTRONIC_RRNA_TRANSCRIPT_SSU_RRNA_5_8S_RRNA_LSU_RRNA_	33	0.6593365	1.6602219	0.027484143	0.1124324
GO_REGULATION_OF_DOUBLE_STRAND_BREAK_REPAIR_VIA_HOMOLOGOUS_RECOMBINATION	16	0.62631017	1.6599126	0.012552301	0.112225205
GO_NEGATIVE_REGULATION_OF_CYTOSKELETON_ORGANIZATION	212	0.45684937	1.659608	0.00621118	0.11206614
GO_CYTOPLASMIC_TRANSLATION	40	0.674575	1.6594002	0.05	0.11182244
GO_NCRNA_PROCESSING	371	0.55377424	1.6589243	0.046121594	0.11179535
GO_POSITIVE_REGULATION_OF_CELL_DIVISION	129	0.41216528	1.6579272	0.004464286	0.11228066
GO_TRNA_METABOLIC_PROCESS	168	0.5328607	1.6576976	0.04453441	0.11209809
GO_GENE_SILENCING_BY_RNA	132	0.4748704	1.6576579	0.012605042	0.11166818
GO_MITOCHONDRION_ORGANIZATION	554	0.45329762	1.6568488	0.030674847	0.11190521
GO_REGULATION_OF_TRANSLATIONAL_FIDELITY	14	0.66256046	1.6560736	0.022222223	0.112191744
GO_PROTEIN_SUMOYLATION	114	0.53670955	1.6559697	0.020366598	0.11185084
GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	17	0.6455646	1.6542842	0.02244898	0.1129871
GO_CENTROSOME_CYCLE	45	0.5848687	1.6542404	0.022044089	0.1125969
GO_HEMIDESMOSOME_ASSEMBLY	12	0.7616932	1.6532965	0.031380754	0.113046475
GO_PROTEIN_FOLDING	213	0.45727825	1.6531543	0.0385439	0.1127647
GO_POSITIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	33	0.59140277	1.6509857	0.024242423	0.11453892
GO_CYTOPLASMIC_SEQUESTERING_OF_PROTEIN	40	0.5050585	1.6493893	0.022633744	0.11540048
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I	65	0.58247536	1.6493425	0.037815128	0.114988394
GO_INNER_CELL_MASS_CELL_PROLIFERATION	10	0.74379396	1.6480967	0.004056795	0.11565598
GO_FORMATION_OF_TRANSLATION_PREINITIATION_COMPLEX	20	0.7011439	1.6479492	0.022540983	0.11534986
GO_PROTEIN_NEDDYLATION	13	0.66709745	1.6473082	0.021186441	0.11552463
GO_REGULATION_OF_PROTEIN_MODIFICATION_BY_SMALL_PROTEIN_CONJUGATION_OR_REMOVAL	273	0.464782	1.6467485	0.00814664	0.11564379
GO_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	28	0.55277413	1.6463332	0.012711864	0.115595415
GO_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	31	0.59295875	1.6463189	0.013916501	0.115165494
GO_REGULATION_BY_VIRUS_OF_VIRAL_PROTEIN_LEVELS_IN_HOST_CELL	11	0.7313822	1.6461384	0.008179959	0.11488493
GO_HISTONE_MRNA_METABOLIC_PROCESS	28	0.6104358	1.6438702	0.020408163	0.1167043
GO_PYRIMIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	39	0.5239098	1.6433322	0.006651885	0.116701595
GO_POSITIVE_REGULATION_OF_DNA_REPLICATION	86	0.46408218	1.6417035	0.012631579	0.117811665
GO_REGULATION_OF_DNA_REPLICATION	157	0.46481165	1.6413407	0.01446281	0.11775781
GO_LAGGING_STRAND_ELONGATION	11	0.7205379	1.6412145	0.018255578	0.117417365
GO_EPIDERMIS_DEVELOPMENT	251	0.40702897	1.6406761	0.011848342	0.11760686
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_DEADENYLATION_DEPENDENT_DECAY	55	0.5646253	1.639923	0.008064516	0.11803533
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS_EXONUCLEOLYTIC	34	0.5772202	1.6398538	0.014	0.11765547
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_DNA_DAMAGE_STIMULUS	62	0.5005591	1.6389098	0.008438818	0.11819216

GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME_TELOMERIC_REGION	14	0.71783954	1.6386812	0.029239766	0.117948964
GO_MITOCHONDRIAL_TRANSPORT	164	0.46030748	1.6375666	0.03469388	0.11859662
GO_CHAPERONE_MEDIATED_PROTEIN_FOLDING	46	0.5198293	1.6370066	0.036480688	0.118789576
GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_CATABOLIC_PROCESS	60	0.5202055	1.6367737	0.006276151	0.11858529
GO_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	35	0.5784832	1.6346914	0.016260162	0.120059446
GO_DNA_REPLICATION_DEPENDENT_NUCLEOSOME_ORGANIZATION	32	0.594156	1.6328253	0.05458515	0.121492095
GO_TRANSLATIONAL_INITIATION	143	0.6316149	1.6323658	0.084886126	0.1215511
GO_SPONGIOTROPHOBLAST_LAYER_DEVELOPMENT	13	0.6083587	1.632331	0.02826087	0.12114935
GO_PROTEIN_LOCALIZATION_TO_CYTOSKELETON	28	0.5787906	1.6322637	0.010204081	0.1207968
GO_CLEAVAGE_INVOLVED_IN_RRNA_PROCESSING	19	0.67891294	1.6319609	0.030737706	0.12066312
GO_GENE_SILENCING	198	0.4489919	1.6313207	0.014705882	0.120854415
GO_FOLIC_ACID_METABOLIC_PROCESS	17	0.5700676	1.630616	0.02244898	0.121070765
GO_HISTONE_PHOSPHORYLATION	25	0.59341866	1.6303482	0.013015185	0.120930165
GO_ACTIVATION_OF_ANAPHASE_PROMOTING_COMPLEX_ACTIVITY	14	0.66654783	1.6300902	0.022403259	0.12071544
GO_POSITIVE_REGULATION_OF_CELL_CYCLE	321	0.4178142	1.6296318	0.00617284	0.120778345
GO_MEIOTIC_CHROMOSOME_SEGREGATION	59	0.46690586	1.6283472	0.027149322	0.121669434
GO_NEGATIVE_REGULATION_OF_ORGANELLE_ORGANIZATION	373	0.43668905	1.6274787	0.008163265	0.122104004
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	23	0.62186843	1.6274781	0.019880716	0.12168296
GO_CENTRIOLE_ASSEMBLY	19	0.6235702	1.6272955	0.036885247	0.121420175
GO_EPHRIN_RECEPTOR_SIGNALING_PATHWAY	84	0.46086365	1.6263669	0.019313306	0.12191179
GO__DE_NOVO_PROTEIN_FOLDING	19	0.6387575	1.6258576	0.037190083	0.12205555
GO_RESPONSE_TO_X_RAY	30	0.55028033	1.6240091	0.012552301	0.12345899
GO_PROTEIN_LOCALIZATION_TO_CHROMATIN	13	0.6629752	1.6239226	0.023762377	0.12314838
GO_RNA_3_END_PROCESSING	96	0.5354875	1.6234496	0.025948104	0.12318276
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	217	0.46043256	1.6225238	0.049792532	0.12376629
GO_POSITIVE_REGULATION_OF_NUCLEAR_DIVISION	61	0.4481835	1.622456	0.012793177	0.123424254
GO_POSITIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	117	0.45392507	1.6224071	0.014583333	0.12306769
GO_REGULATION_OF_TELOMERE_MAINTENANCE	65	0.54234195	1.620608	0.022357723	0.12441463
GO_MEMBRANE_DISASSEMBLY	45	0.5983302	1.6203101	0.012145749	0.1242771
GO_PYRIMIDINE_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	28	0.5435781	1.6186004	0.018907564	0.12564668
GO_NEGATIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	17	0.5736048	1.617386	0.017621145	0.12645203
GO_FEMALE_MEIOTIC_DIVISION	24	0.5519421	1.6165161	0.021786492	0.12698773
GO_ORGANONITROGEN_COMPOUND_BIOSYNTHETIC_PROCESS	990	0.39255878	1.6154091	0.033826638	0.12777627
GO_CHROMATIN_REMODELING	145	0.4551741	1.6117985	0.025210084	0.13104786
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNE_RECEPTORS_VIA_SOMATIC_MUTATION	12	0.66634965	1.611468	0.025052192	0.13099684
GO_ENDOPLASMIC_RETICULUM_CALCIUM_ION_HOMEOSTASIS	20	0.5683146	1.6114258	0.03909465	0.13060898
GO_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	49	0.5492812	1.6104445	0.027833002	0.13109685
GO_VIRAL_LIFE_CYCLE	283	0.47923476	1.6103368	0.05625	0.13078111
GO_PURINE_NUCLEOBASE_METABOLIC_PROCESS	20	0.5457782	1.6083285	0.034764826	0.1325733
GO_CELLULAR_RESPONSE_TO_EXOGENOUS_DSRNA	12	0.6279286	1.6082007	0.01898734	0.13228145
GO_KERATINOCYTE_DIFFERENTIATION	100	0.46730345	1.6079144	0.040358745	0.13210614
GO_RNA_PROCESSING	804	0.4871173	1.6044775	0.037924152	0.13527974
GO_PROTEIN_FOLDING_IN_ENDOPLASMIC_RETICULUM	8	0.7624372	1.6040546	0.039130434	0.13528039
GO_CHROMATIN_SILENCING_AT_RDNA	37	0.53959227	1.6036577	0.05869565	0.13528517

GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME	10	0.7669568	1.6025994	0.029296875	0.13602458
GO_RIBOSOMAL_SMALL_SUBUNIT_BIOGENESIS	56	0.61942846	1.6018542	0.05376344	0.13634804
GO_TRNA_TRANSPORT	33	0.6363494	1.6008004	0.024340771	0.13708006
GO_CYTOPLASMIC_TRANSLATIONAL_INITIATION	14	0.7204476	1.6001648	0.025157232	0.13722196
GO_NEGATIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	12	0.64454997	1.6001253	0.03846154	0.13684778
GO_NEGATIVE_REGULATION_OF_BINDING	130	0.42551756	1.6000961	0.022727273	0.13645495
GO_POSITIVE_REGULATION_OF_VIRAL_TRANSCRIPTION	35	0.5302324	1.5996712	0.02734375	0.13639127
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	94	0.46996018	1.5983187	0.02414487	0.13745455
GO_PROTEIN_TARGETING	398	0.44846377	1.5976114	0.045360826	0.13782918
GO_CHROMATIN_SILENCING	89	0.46880132	1.5972772	0.042643923	0.13778754
GO_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	177	0.46515867	1.5959437	0.020242915	0.13883571
GO_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	42	0.50944906	1.5957978	0.029761905	0.13855402
GO_TERMINATION_OF_RNA_POLYMERASE_II_TRANSCRIPTION	61	0.56394786	1.5956404	0.021956088	0.13827363
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	65	0.5114081	1.5952528	0.052525252	0.13820371
GO_TRNA_PROCESSING	108	0.51782244	1.5951381	0.05894309	0.13789539
GO_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONSE	27	0.5559191	1.5937105	0.03125	0.13896428
GO_POSITIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	258	0.4348542	1.5933176	0.016260162	0.13892047
GO_PYRIMIDINE_NUCLEOTIDE_METABOLIC_PROCESS	43	0.5001171	1.5929148	0.03258656	0.13890141
GO_ORGANELLE_INHERITANCE	10	0.7226244	1.5925819	0.027613413	0.13885458
GO_RNA_DEPENDENT_DNA_BIOSYNTHETIC_PROCESS	20	0.61242217	1.5921737	0.022821577	0.13886362
GO_BLASTOCYST_DEVELOPMENT	60	0.4743266	1.5919619	0.020618556	0.13867922
GO_REGULATION_OF_MITOPHAGY	42	0.51737005	1.5904069	0.017892644	0.1399737
GO_REGULATION_OF_CELL_AGING	33	0.5077976	1.5899751	0.029106028	0.14006491
GO_HEPATOCYTE_APOPTOTIC_PROCESS	13	0.6284453	1.5893102	0.025896415	0.14025025
GO_RESPONSE_TO_GAMMA_RADIATION	50	0.47149116	1.5890555	0.031380754	0.14007652
GO_CELLULAR_RESPONSE_TO_GAMMA_RADIATION	19	0.5660698	1.5883001	0.030120483	0.14047687
GO_CYTOKINETIC_PROCESS	14	0.6248528	1.58805	0.016096579	0.14036182
GO_NEGATIVE_REGULATION_OF_PROTEIN_BINDING	78	0.4521903	1.5868472	0.026748972	0.14122596
GO_PROTEIN_DEPOLYMERIZATION	24	0.5136619	1.5866829	0.022774328	0.14099534
GO_NEGATIVE_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	13	0.622219	1.5866578	0.035416666	0.14062527
GO_NAD_METABOLIC_PROCESS	50	0.47350103	1.5859405	0.03821656	0.14101388
GO_REGULATION_OF_PROTEIN_PHOSPHATASE_TYPE_2A_ACTIVITY	24	0.5866307	1.5857997	0.023904383	0.14074191
GO_CELLULAR_AMIDE_METABOLIC_PROCESS	700	0.40960628	1.5854009	0.053418804	0.14071782
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	22	0.58831346	1.5849158	0.024048096	0.1408914
GO_RNA_CATABOLIC_PROCESS	220	0.5371845	1.5844659	0.07966457	0.14102334
GO_VIRAL_LATENCY	11	0.62504584	1.5840694	0.033333335	0.14097312
GO_REGULATION_OF_TRANSLATIONAL_INITIATION	80	0.506341	1.5838306	0.026262626	0.14081226
GO_RNA_SURVEILLANCE	13	0.692264	1.5836991	0.030800821	0.14057864
GO_SNRNA_METABOLIC_PROCESS	75	0.5207528	1.5828741	0.031128405	0.14098318
GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	30	0.5617273	1.5828017	0.03773585	0.14065894
GO_ENDOSOME_ORGANIZATION	59	0.5256305	1.5824311	0.04016064	0.1406737
GO_POSITIVE_REGULATION_OF_MITOTIC_CELL_CYCLE	122	0.44230005	1.5811651	0.026748972	0.14158994

GO_REGULATION_OF_TRANSLATIONAL_ELONGATION	22	0.5712228	1.5802245	0.028397566	0.14221674
GO_TELOMERE_MAINTENANCE_VIA_TELOMERASE	16	0.62255204	1.5768968	0.038306452	0.14551127
GO_EMBRYONIC_PLACENTA_MORPHOGENESIS	22	0.5112771	1.5762943	0.024948025	0.1457848
GO_POSITIVE_REGULATION_OF_CELL_CYCLE_PHASE_TRANSITION	67	0.49255556	1.5761569	0.027253669	0.1455381
GO_MITOCHONDRION_MORPHOGENESIS	19	0.5927601	1.5761557	0.04016064	0.14513718
GO_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	57	0.4899331	1.5761284	0.057082452	0.14475194
GO_NUCLEAR_IMPORT	129	0.45581442	1.574707	0.022357723	0.14588198
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	17	0.58119744	1.5745853	0.031847134	0.14565429
GO_RESPONSE_TO_INTERFERON_BETA	22	0.5781779	1.574044	0.056338027	0.1458214
GO_MICROTUBULE_ORGANIZING_CENTER_ORGANIZATION	82	0.5133101	1.5730438	0.028571429	0.14641729
GO_PSEUDOURIDINE_SYNTHESIS	17	0.6395971	1.5726429	0.04048583	0.14642988
GO_EPIDERMAL_CELL_DIFFERENTIATION	141	0.4144382	1.5724658	0.025581395	0.14619198
GO_MEMBRANE_BUDDING	112	0.4724145	1.5715499	0.03992016	0.14678794
GO_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	25	0.57518685	1.5698383	0.036511157	0.14826018
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN	172	0.45528126	1.569804	0.04526749	0.14790924
GO_RNA_SPLICING_VIA_TRANSESTERIFICATION_REACTIONS	261	0.51012	1.5690255	0.030181086	0.14841086
GO_RIBONUCLEOPROTEIN_COMPLEX_LOCALIZATION	116	0.52188843	1.5679911	0.04715128	0.14922139
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_BIPOLAR_CELL_POLARITY	35	0.46850136	1.567368	0.026258206	0.14952666
GO_POSITIVE_REGULATION_OF_MITOCHONDRIAL_OUTER_MEMBRANE_PERMEABILIZATION_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	36	0.52516276	1.5652249	0.031936128	0.1515109
GO_NEGATIVE_REGULATION_OF_NECROTIC_CELL_DEATH	10	0.6354812	1.5651423	0.031512607	0.15120251
GO_IMP_BIOSYNTHETIC_PROCESS	11	0.6579039	1.5648502	0.043032788	0.15117213
GO_MICROTUBULE_CYTOSKELETON_ORGANIZATION	324	0.43703225	1.564712	0.03131524	0.15096769
GO_HEXOSE_CATABOLIC_PROCESS	48	0.46404567	1.5639964	0.022371365	0.15133919
GO_AEROBIC_RESPIRATION	50	0.5302928	1.563956	0.07942974	0.15098658
GO_MACROMOLECULE_CATABOLIC_PROCESS	888	0.41344407	1.5636342	0.016494846	0.15096347
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE	413	0.4108412	1.56357	0.010224949	0.15064198
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	63	0.5802417	1.5628382	0.104627766	0.15108581
GO_CELLULAR_PROTEIN_COMPLEX_LOCALIZATION	22	0.5339042	1.5625414	0.025531914	0.15095669
GO_EPITHELIAL_CELL_APOPTOTIC_PROCESS	25	0.5139568	1.5615313	0.018595042	0.15154304
GO_PENTOSE_METABOLIC_PROCESS	12	0.6390608	1.5604236	0.046875	0.15235753
GO_PROTEIN_IMPORT_INTO_MITOCHONDRIAL_MATRIX	13	0.6604067	1.560142	0.062240664	0.15226544
GO_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	90	0.46126264	1.560042	0.04526749	0.15198179
GO_NCRNA_3_END_PROCESSING	20	0.6232819	1.5592606	0.06369427	0.15247053
GO_GOLGI_LOCALIZATION	11	0.64478964	1.5590006	0.044806518	0.15238899
GO_CELLULAR_RESPONSE_TO_STRESS	1505	0.39090124	1.5584394	0.012658228	0.15266372
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN	16	0.6677399	1.5579678	0.09445585	0.15278412
GO_ERROR_PRONE_TRANSLESION_SYNTHESIS	19	0.61055756	1.5566612	0.034623217	0.15391776
GO_REGULATION_OF_PROTEASOMAL_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	144	0.4616643	1.5556101	0.028282829	0.1547059
GO_PYRIMIDINE_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	19	0.5683157	1.5554326	0.047311828	0.15452549
GO_TRNA_MODIFICATION	55	0.53642595	1.5552013	0.070564516	0.15436977
GO_CELLULAR_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	14	0.5889746	1.5545489	0.052192066	0.15467556
GO_PROTEIN_UBIQUITINATION_INVOLVED_IN_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	130	0.47086424	1.554432	0.032786883	0.15445262
GO_PROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	1472	0.3757891	1.5540224	0.013215859	0.15449212

GO_REGULATION_OF_DNA_DEPENDENT_DNA_REPLICATION	40	0.5456863	1.5534828	0.051759835	0.15469943
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	50	0.48659703	1.5519848	0.06198347	0.1559742
GO_RESPONSE_TO_UV	121	0.4420489	1.5516354	0.028169014	0.15596138
GO_ER_NUCLEUS_SIGNALING_PATHWAY	32	0.5530536	1.5516127	0.069767445	0.15560655
GO_POSTTRANSCRIPTIONAL_REGULATION_OF_GENE_EXPRESSION	431	0.43722954	1.550897	0.027196653	0.1560048
GO_CELL_AGING	67	0.44464937	1.5501338	0.023255814	0.15646519
GO_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	383	0.40868995	1.549618	0.02385686	0.15668575
GO_RETROGRADE_TRANSPORT_ENDOSOME_TO_PLASMA_MEMBRANE	14	0.6091372	1.5493841	0.02970297	0.1566431
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_HEAT	74	0.52601004	1.5486622	0.04761905	0.15710159
GO_OXIDATIVE_PHOSPHORYLATION	81	0.58444434	1.5473527	0.13253012	0.15830076
GO_RIBONUCLEOPROTEIN_COMPLEX_SUBUNIT_ORGANIZATION	188	0.49146363	1.5466876	0.064	0.15863594
GO_NEGATIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	94	0.48971176	1.5462658	0.058232933	0.158704
GO_NEGATIVE_REGULATION_OF_MEGAKARYOCYTE_DIFFERENTIATION	18	0.5954302	1.5462632	0.06753813	0.15832974
GO_INTERSPECIES_INTERACTION_BETWEEN_ORGANISMS	646	0.42536652	1.5455391	0.021052632	0.15873803
GO_CELLULAR_RESPIRATION	138	0.5058192	1.545427	0.10229645	0.1584965
GO_MRNA_METABOLIC_PROCESS	590	0.47116327	1.5440335	0.0583501	0.15977114
GO_CELLULAR_RESPONSE_TO_IONIZING_RADIATION	50	0.48978946	1.5438718	0.05042017	0.1595537
GO_REGULATION_OF_SISTER_CHROMATID_COHESION	17	0.6117025	1.5435853	0.04233871	0.15950096
GO_GLYCERALDEHYDE_3_PHOSPHATE_METABOLIC_PROCESS	17	0.5725192	1.5435529	0.049356222	0.15915067
GO_NUCLEAR_PORE_ORGANIZATION	14	0.7047688	1.5428927	0.022357723	0.15952346
GO_REGULATION_OF_CELL_CYCLE_G1_S_PHASE_TRANSITION	142	0.4407111	1.5422535	0.018480493	0.15994358
GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	19	0.5484239	1.5415641	0.029288704	0.1602636
GO_POSITIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	27	0.49841425	1.5395498	0.043568466	0.16220939
GO_RESPONSE_TO_IONIZING_RADIATION	139	0.43480495	1.5387628	0.035416666	0.16276686
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STARVATION	25	0.52588487	1.5368571	0.032719836	0.16464622
GO_PROTEIN_POLYUBIQUITINATION	241	0.4554047	1.5351281	0.03	0.16622384
GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	31	0.49813926	1.5348908	0.04883227	0.16607612
GO_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	139	0.39194217	1.5341789	0.024590164	0.16653709
GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_RESPONSE_TO_DNA_DAMAGE_BY_P53_CLASS_MEDIATOR	29	0.5153681	1.5337777	0.0372807	0.16661108
GO_REGULATION_OF_CENTRIOLE_REPLICATION	13	0.6356969	1.533775	0.04225352	0.16623415
GO_MUSCLE_CELL_MIGRATION	18	0.5630288	1.5336554	0.05970149	0.16599831
GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	25	0.4835207	1.5334377	0.059196617	0.16585717
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_STRESS	23	0.538537	1.5329794	0.07592191	0.16597195
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	51	0.5931561	1.5315089	0.13017751	0.1673122
GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	18	0.5742912	1.5313616	0.04742268	0.1671008
GO_NEGATIVE_REGULATION_OF_RECEPTOR_BINDING	12	0.5855992	1.5302474	0.06430155	0.16804732
GO_HETEROCHROMATIN_ORGANIZATION	11	0.59971744	1.5295434	0.064449064	0.16852069
GO_MRNA_3_END_PROCESSING	71	0.5349652	1.5295151	0.04828974	0.16815786
GO_MITOTIC_G2_DNA_DAMAGE_CHECKPOINT	13	0.62313336	1.5286505	0.05353319	0.16874343
GO_NEGATIVE_REGULATION_OF_DNA_REPAIR	13	0.6194612	1.5284623	0.039175257	0.16858019
GO_REGULATION_OF_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	93	0.4231957	1.5284573	0.020920502	0.16821282

GO_POSITIVE_REGULATION_OF_PROTEOLYSIS	359	0.3930322	1.5283394	0.02834008	0.16795316
GO_ESTABLISHMENT_OF_MITOTIC_SPINDLE_LOCALIZATION	23	0.57097465	1.5270542	0.03805497	0.16902728
GO_MULTI_ORGANISM_METABOLIC_PROCESS	137	0.5849009	1.5248636	0.13333334	0.17129175
GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	38	0.5100401	1.5235986	0.054435484	0.17244771
GO_DNA_LIGATION_INVOLVED_IN_DNA_REPAIR	12	0.6199461	1.5219305	0.04158004	0.17403997
GO_MAINTENANCE_OF_LOCATION_IN_CELL	94	0.41798985	1.5212244	0.038383838	0.17455986
GO_OOCYTE_MATURATION	18	0.5282279	1.5204601	0.044871796	0.17521882
GO_NON_CANONICAL_WNT_SIGNALING_PATHWAY	136	0.4259627	1.5199434	0.039215688	0.17552137
GO_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	123	0.5859238	1.5198927	0.1446541	0.17516784
GO_NUCLEOSIDE_PHOSPHATE_BIOSYNTHETIC_PROCESS	176	0.3935531	1.5194492	0.033259425	0.17531246
GO_NEGATIVE_REGULATION_OF_KERATINOCYTE_PROLIFERATION	11	0.63567877	1.5194094	0.06889353	0.17498218
GO_NUCLEAR_TRANSCRIBED_MRNA_CATABOLIC_PROCESS_NONSENSE_MEDIATED_DECAY	118	0.6110302	1.5186458	0.12394958	0.17551385
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	53	0.51150393	1.5181314	0.09090909	0.17582342
GO_REGULATION_OF_NUCLEASE_ACTIVITY	23	0.5285359	1.5179935	0.055785123	0.17559029
GO_NUCLEAR_TRANSCRIBED_MRNA_POLY_A_TAIL_SHORTENING	24	0.59765035	1.5173901	0.042424243	0.1759111
GO_RRNA_MODIFICATION	26	0.5619706	1.515691	0.085020244	0.17768057
GO_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	58	0.47179985	1.5156221	0.047210302	0.1773969
GO_CELL_ADHESION_MEDIATED_BY_INTEGRIN	12	0.6202394	1.515035	0.08387097	0.17766862
GO_CENTROSOME_LOCALIZATION	17	0.57272005	1.5141715	0.041753653	0.17831294
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_CHROMOSOME	12	0.645052	1.5135477	0.06483301	0.17864473
GO_MACROMOLECULAR_COMPLEX_ASSEMBLY	1344	0.37074906	1.5134256	0.017167382	0.17841312
GO_MATURATION_OF_LSU_RRNA	13	0.6626204	1.513074	0.07660455	0.17846975
GO_CELLULAR_RESPONSE_TO_INTERFERON_BETA	15	0.56751174	1.5128471	0.060728744	0.17838947
GO_INTRA_S_DNA_DAMAGE_CHECKPOINT	12	0.6365468	1.5124797	0.0373444	0.17844746
GO_NEGATIVE_REGULATION_OF_DNA_BINDING	46	0.43709004	1.512281	0.031982943	0.17833325
GO_MOLTING_CYCLE	82	0.39085853	1.510801	0.047727272	0.17973287
GO_POSITIVE_REGULATION_OF_DNA_BIOSYNTHETIC_PROCESS	58	0.46895972	1.5098438	0.05102041	0.180545
GO_REGULATION_OF_DNA_METABOLIC_PROCESS	329	0.40646434	1.5085998	0.045738045	0.18170743
GO_REGULATION_OF_CELLULAR_SENESCENCE	26	0.5117104	1.5085652	0.047311828	0.18136767
GO_NUCLEIC_ACID_PHOSPHODIESTER_BOND_HYDROLYSIS	237	0.4335418	1.5078535	0.06584362	0.18185654
GO_REGULATION_OF_CHROMOSOME_ORGANIZATION	270	0.4302104	1.5078403	0.054766733	0.18148182
GO_IMP_METABOLIC_PROCESS	14	0.6106762	1.5074241	0.06584362	0.18160848
GO_SEMAPHORIN_PLEXIN_SIGNALING_PATHWAY_INVOLVED_IN_NEURON_PROJECTION_GUIDANCE	13	0.62460417	1.5070964	0.057494868	0.18161672
GO_ERROR_FREE_TRANSLESION_SYNTHESIS	18	0.6109432	1.5069528	0.05338809	0.18140732
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	355	0.37844005	1.5063379	0.06355932	0.18174796
GO_SKIN_DEVELOPMENT	209	0.37679955	1.5057054	0.04195804	0.18225016
GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	14	0.5270898	1.5054826	0.036247335	0.18214546
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_ENDOPLASMIC_RETICULUM	104	0.62269175	1.503305	0.15843621	0.18454817
GO_NEGATIVE_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	106	0.43300185	1.5026797	0.060085837	0.18491058
GO_POST_TRANSLATIONAL_PROTEIN_MODIFICATION	34	0.45841885	1.5026714	0.06638116	0.1845344
GO_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	33	0.48168427	1.5022527	0.0546875	0.18459988
GO_NCRNA_TRANSCRIPTION	81	0.4867627	1.5022146	0.05367793	0.18425298
GO_POSITIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	151	0.39292046	1.5012039	0.029045643	0.18512414
GO_NEGATIVE_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	159	0.4011032	1.5000222	0.050438598	0.18608472

GO_REGULATION_OF_DNA_BINDING	92	0.38619563	1.4980425	0.017699115	0.18819477
GO_CELLULAR_RESPONSE_TO_UV	65	0.44896537	1.4976366	0.04106776	0.1883516
GO_RIBONUCLEOSIDE_TRIPHOSPHATE_BIOSYNTHETIC_PROCESS	45	0.47853106	1.4973111	0.082474224	0.18828984
GO_RNA_SPLICING_VIA_ENDONUCLEOLYTIC_CLEAVAGE_AND_LIGATION	15	0.58370966	1.4968566	0.07883818	0.18848501
GO_RRNA_CATABOLIC_PROCESS	17	0.57743335	1.4950815	0.08835341	0.1902312
GO_ALDITOL_METABOLIC_PROCESS	20	0.5028575	1.4937595	0.057268724	0.19142371
GO_RIBOSOMAL_LARGE_SUBUNIT_BIOGENESIS	48	0.5669852	1.4929674	0.15113872	0.19198897
GO_ELECTRON_TRANSPORT_CHAIN	92	0.53031886	1.4927338	0.14285715	0.19193782
GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	40	0.4952055	1.4926171	0.07048458	0.1917013
GO_INNATE_IMMUNE_RESPONSE_ACTIVATING_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY	106	0.46091464	1.4920572	0.056565657	0.19205773
GO_CELLULAR_SENESCENCE	33	0.4568801	1.491538	0.0491453	0.1923158
GO_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	354	0.36081424	1.4915352	0.028688524	0.19193213
GO_NUCLEAR_PORE_COMPLEX_ASSEMBLY	10	0.70784354	1.4912796	0.04918033	0.1918406
GO_KERATINIZATION	50	0.52368057	1.4912466	0.0995671	0.19149546
GO_REGULATION_OF_CHROMATIN_SILENCING	21	0.543905	1.4909911	0.09465021	0.19144797
GO_LUNG_EPITHELIUM_DEVELOPMENT	34	0.4672559	1.4901252	0.057446808	0.1921905
GO_MITOCHONDRIAL_RNA_PROCESSING	12	0.63876474	1.489744	0.07862903	0.19229023
GO_MICROTUBULE_POLYMERIZATION_OR_DEPOLYMERIZATION	40	0.4849424	1.4892792	0.06517312	0.19249447
GO_SOMATIC_DIVERSIFICATION_OF_IMMUNOGLOBULINS	26	0.54636294	1.48913	0.08649789	0.19230746
GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_UNFOLDED_PROTEIN_RESPONSE	10	0.6652538	1.4890409	0.05533597	0.19206189
GO_PROTEIN_IMPORT	153	0.41852522	1.488504	0.024948025	0.19233322
GO_FOLIC_ACID_CONTAINING_COMPOUND_METABOLIC_PROCESS	28	0.47451204	1.488491	0.06666667	0.19198042
GO_RNA_SPLICING	355	0.46885148	1.4876264	0.07692308	0.19274046
GO_IRON_ION_IMPORT	12	0.574514	1.4874718	0.059957173	0.19254595
GO_REGULATION_OF_MEMBRANE_PERMEABILITY	69	0.44457835	1.4862523	0.06762295	0.19366565
GO_REGULATION_OF_PROTEOLYSIS	694	0.33735624	1.4858111	0.01746725	0.19388075
GO_RNA_LOCALIZATION	178	0.4730566	1.484771	0.067073174	0.19484966
GO_HOMOLOGOUS_CHROMOSOME_SEGREGATION	43	0.4375008	1.4846144	0.062052507	0.1946737
GO_RRNA_CONTAINING_RIBONUCLEOPROTEIN_COMPLEX_EXPORT_FROM_NUCLEUS	11	0.6575775	1.4842494	0.070393376	0.19474292
GO_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	192	0.38099268	1.483885	0.051948052	0.19482088
GO_RNA_PHOSPHODIESTER_BOND_HYDROLYSIS	110	0.44614342	1.4834741	0.083333336	0.19496189
GO_EARLY_ENDOSOME_TO_GOLGI_TRANSPORT	11	0.62660444	1.4829842	0.06451613	0.1951682
GO_SYNAPSIS	34	0.4589449	1.4824505	0.056650247	0.19535756
GO_REGULATION_OF_GENE_EXPRESSION_EPIGENETIC	217	0.40698326	1.4811561	0.051172707	0.19654217
GO_ESTABLISHMENT_OF_SPINDLE_ORIENTATION	25	0.5218277	1.4808928	0.05327869	0.19648266
GO_PROTEIN_TETRAMERIZATION	133	0.37001997	1.4806575	0.037647057	0.19641604
GO_VENTRICULAR_SYSTEM_DEVELOPMENT	26	0.4945192	1.4800029	0.06852248	0.19683646
GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	20	0.5024933	1.4778327	0.08351178	0.1992829
GO_REGULATION_OF_ORGAN_MORPHOGENESIS	241	0.36304462	1.4767836	0.044345897	0.20021512
GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	16	0.5830128	1.4756051	0.0951417	0.20122449
GO_NEURON_APOPTOTIC_PROCESS	34	0.4694683	1.4748383	0.057026476	0.20184852
GO_PROTEIN_EXPORT_FROM_NUCLEUS	29	0.5255518	1.4739771	0.047325104	0.20260467
GO_PROTEIN_HETEROOLIGOMERIZATION	112	0.3709261	1.4736912	0.038636364	0.2026625
GO_POSITIVE_REGULATION_OF_TELOMERASE_ACTIVITY	28	0.51299244	1.4733267	0.057142857	0.20273837

GO_SINGLE_ORGANISM_MEMBRANE_BUDDING	71	0.46066266	1.473266	0.08266129	0.20244548
GO_NEGATIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	10	0.61814266	1.4728879	0.0782241	0.2026123
GO_PLACENTA_DEVELOPMENT	136	0.3719189	1.472862	0.04077253	0.20226535
GO_NUCLEOTIDE_EXCISION_REPAIR_PREINCISION_COMPLEX_STABILIZATION	21	0.5603863	1.4720036	0.047034767	0.2030191
GO_NUCLEAR_EXPORT	143	0.4790644	1.4716072	0.09218437	0.20314384
GO_PROTEIN_CATABOLIC_PROCESS	552	0.39969206	1.4711798	0.059917357	0.20330524
GO_REGULATION_OF_IRE1_MEDIATED_UNFOLDED_PROTEIN_RESPONSE	13	0.6109477	1.4710661	0.08436214	0.20307177
GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	43	0.44566274	1.4701965	0.07053942	0.20392127
GO_RNA_MODIFICATION	112	0.46641412	1.468932	0.10887097	0.20522493
GO_NEGATIVE_REGULATION_OF_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	84	0.3942602	1.4685829	0.04375	0.20535375
GO_RNA_POLYADENYLATION	29	0.54238045	1.4684963	0.070393376	0.20508876
GO_SNRNA_PROCESSING	21	0.5797777	1.4679121	0.09147609	0.20549107
GO_CELLULAR_RESPONSE_TO_RADIATION	134	0.4012889	1.4676086	0.04680851	0.20551635
GO_PYRIMIDINE_CONTAINING_COMPOUND_SALVAGE	12	0.5575156	1.4673659	0.06530612	0.20540048
GO_REGULATION_OF_PROTEIN_INSERTION_INTO_MITOCHONDRIAL_MEMBRANE_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	29	0.50916857	1.4651835	0.06122449	0.2079532
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_IN_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	12	0.5878166	1.4651124	0.085653104	0.20766713
GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS	99	0.3975	1.4629766	0.06889353	0.21020266
GO_UTP_METABOLIC_PROCESS	10	0.57772774	1.4616547	0.06680162	0.21148053
GO_TRNA_THREONYLCARBAMOYLADENOSINE_METABOLIC_PROCESS	10	0.6488712	1.4593706	0.08179959	0.21417874
GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	210	0.35909238	1.4585828	0.032608695	0.21483399
GO_PROTEIN_COMPLEX_BIOGENESIS	1090	0.34844548	1.4574643	0.01978022	0.2159715
GO_ER_ASSOCIATED_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	60	0.45484906	1.4571611	0.09330629	0.215973
GO_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	150	0.37742627	1.4571247	0.036511157	0.21563792
GO_POSITIVE_REGULATION_OF_APOPTOTIC_SIGNALING_PATHWAY	169	0.38517627	1.4571152	0.047717843	0.21525581
GO_GLUCOSE_6_PHOSPHATE_METABOLIC_PROCESS	21	0.49969208	1.456996	0.075	0.21502712
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERASE	11	0.6402931	1.4560418	0.07258064	0.21586408
GO_RETROGRADE_PROTEIN_TRANSPORT_ER_TO_CYTOSOL	15	0.5572315	1.4559267	0.10663984	0.21563052
GO_REGULATION_OF_UBIQUITIN_PROTEIN_LIGASE_ACTIVITY	17	0.5713142	1.4555545	0.059670784	0.21573532
GO_NUCLEAR_TRANSPORT	348	0.40952337	1.4550376	0.057142857	0.21605115
GO_DNA_DEPENDENT_DNA_REPLICATION_MAINTENANCE_OF_FIDELITY	21	0.5674606	1.4536737	0.09504132	0.21750094
GO_DNA_DOUBLE_STRAND_BREAK_PROCESSING	20	0.5471035	1.4527555	0.08418891	0.21832769
GO_NEGATIVE_REGULATION_OF_CELL_CYCLE_G2_M_PHASE_TRANSITION	24	0.51811874	1.4516387	0.08074534	0.21944042
GO_REGULATION_OF_CYTOSKELETON_ORGANIZATION	483	0.3616694	1.4514031	0.04192872	0.21938741
GO_GUANOSINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	44	0.42632088	1.4510466	0.058467742	0.219484
GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESS	27	0.46947467	1.4504627	0.0824295	0.2198553
GO_MULTIVESICULAR_BODY_SORTING_PATHWAY	12	0.60667384	1.4482514	0.08213552	0.22245868
GO_TUMOR_NECROSIS_FACTOR_MEDIATED_SIGNALING_PATHWAY	117	0.41685018	1.4472725	0.09148936	0.22347729
GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	37	0.45077518	1.4471354	0.075203255	0.22329395
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	38	0.43080264	1.4470136	0.056112226	0.22305422
GO_CARBOHYDRATE_CATABOLIC_PROCESS	109	0.37255985	1.4464288	0.04587156	0.22342595
GO_PROTEIN_K63_LINKED_UBIQUITINATION	35	0.49382013	1.4460695	0.09406953	0.22357745
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	35	0.44051778	1.4453897	0.087248325	0.22409159

GO_UV_PROTECTION	12	0.5691848	1.4438189	0.06458333	0.2257971
GO_NEGATIVE_REGULATION_OF_CELLULAR_COMPONENT_ORGANIZATION	664	0.3575015	1.4437197	0.042918455	0.22553395
GO_NEGATIVE_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	24	0.5132615	1.4435034	0.10643016	0.22542474
GO_RNA_SECONDARY_STRUCTURE_UNWINDING	40	0.50787556	1.4423504	0.098121084	0.22657688
GO_MICROTUBULE_BASED_PROCESS	486	0.38647392	1.4421577	0.067653276	0.22640604
GO_POSITIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	150	0.38947695	1.441331	0.07112971	0.22717477
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	281	0.3831179	1.4404978	0.10537634	0.22795004
GO_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	21	0.5538261	1.4403216	0.07272727	0.2278075
GO_REGULATION_OF_ORGANELLE_ORGANIZATION	1131	0.36017844	1.4402056	0.05394191	0.22756171
GO_NEURAL_TUBE_FORMATION	94	0.41673422	1.4397032	0.08955224	0.22786528
GO_NEGATIVE_REGULATION_OF_PROTEIN_CATABOLIC_PROCESS	104	0.39640492	1.4392163	0.06854839	0.22813666
GO_EMBRYONIC_PLACENTA_DEVELOPMENT	83	0.39085948	1.43858	0.05764967	0.2286164
GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DEVELOPMENT	13	0.50955546	1.4384964	0.07692308	0.22835054
GO_PROTEIN_HYDROXYLATION	15	0.5507586	1.4380302	0.10262009	0.2285407
GO_RESPONSE_TO_INTERFERON_ALPHA	20	0.5538519	1.4379902	0.14107884	0.22818534
GO_SNORNA_METABOLIC_PROCESS	11	0.62633044	1.4378388	0.10878661	0.2279992
GO_REGULATION_OF_VIRAL_INDUCED_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	15	0.53910124	1.4377257	0.09453782	0.22775784
GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	19	0.54391444	1.4375317	0.10973085	0.22761299
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_I_PROMOTER	23	0.5013259	1.4373362	0.085365854	0.22751053
GO_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	22	0.4873981	1.437061	0.12896407	0.22747451
GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	23	0.45457274	1.4367915	0.0809628	0.22747615
GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_ELONGATION	22	0.5418124	1.4359347	0.086	0.22826068
GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY_INVOLVED_IN_APOPTOTIC_SIGNALING_PATHWAY	22	0.5082441	1.4350964	0.11089109	0.22899482
GO_PHARYNGEAL_SYSTEM_DEVELOPMENT	17	0.4973697	1.4350053	0.09799554	0.22875942
GO_SPINDLE_LOCALIZATION	37	0.49652103	1.4341915	0.07484408	0.22948314
GO_RESPONSE_TO_TYPE_I_INTERFERON	67	0.4771617	1.4333689	0.1411043	0.23015103
GO_POSITIVE_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	51	0.42312166	1.433278	0.07933194	0.22987813
GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	307	0.36661145	1.4327234	0.06485356	0.23022531
GO_PYRIMIDINE_NUCLEOSIDE_METABOLIC_PROCESS	47	0.41960624	1.4321733	0.05172414	0.23053145
GO_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	158	0.3997333	1.4309685	0.13502109	0.23181802
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	120	0.3617729	1.4309012	0.05032823	0.23152944
GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	33	0.4780291	1.4298053	0.116228074	0.23259605
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_ELONGATION_FROM_RNA_POLYMERASE_II_PROMOTER	13	0.5997665	1.4280106	0.08678501	0.23462704
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_UBIQUINOL_TO_CYTOCHROME_C	13	0.6326901	1.427622	0.14693877	0.2347817
GO_POSITIVE_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	15	0.5307552	1.4276093	0.10548523	0.23441756
GO_POSITIVE_REGULATION_OF_PROTEASOMAL_PROTEIN_CATABOLIC_PROCESS	98	0.41793364	1.4266988	0.09475806	0.23531146
GO_REGULATION_OF_SYMBIOSIS_ENCOMPASSING_MUTUALISM_THROUGH_PARASITISM	197	0.3803984	1.4260347	0.07942974	0.23579445
GO_NEGATIVE_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	87	0.36800772	1.4245623	0.05668934	0.23739609
GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	136	0.36185429	1.4245013	0.057569295	0.23707862
GO_GLYCOPROTEIN_CATABOLIC_PROCESS	15	0.5134987	1.4240898	0.09151786	0.23729669
GO_VESICLE_MEDIATED_TRANSPORT_BETWEEN_ENDOSOMAL_COMPARTMENTS	19	0.48755735	1.4238993	0.08074534	0.23717298

GO_POSITIVE_REGULATION_OF_VIRAL_GENOME_REPLICATION	30	0.48889267	1.4229779	0.107942976	0.23808959
GO_PYRIMIDINE_DEOXYRIBONUCLEOTIDE_METABOLIC_PROCESS	16	0.539462	1.4225523	0.09484536	0.23831993
GO__DE_NOVO_POSTTRANSLATIONAL_PROTEIN_FOLDING	14	0.59737015	1.422233	0.12288135	0.23835641
GO_VESICLE_TARGETING	76	0.44035625	1.4214916	0.0995935	0.23895232
GO_RESPONSE_TO_COPPER_ION	27	0.42024258	1.4207448	0.06966292	0.23958413
GO_ORGAN_REGENERATION	82	0.3648199	1.4196901	0.062222224	0.24064414
GO_XENOPHAGY	102	0.36214796	1.4183961	0.049327355	0.24206313
GO_CELL_JUNCTION_ASSEMBLY	127	0.4021139	1.4183797	0.10089686	0.24169518
GO_ESTABLISHMENT_OR_MAINTENANCE_OF_MONOPOLAR_CELL_POLARITY	14	0.5201075	1.4183027	0.09110629	0.24141425
GO_RIBOSOME_ASSEMBLY	51	0.5295766	1.418097	0.17547569	0.24131612
GO_CYTOPLASMIC_PATTERN_RECOGNITION_RECEPTOR_SIGNALING_PATHWAY	32	0.49847338	1.4180194	0.108606555	0.2410393
GO_ANTIGEN_PROCESSING_AND_PRESENTATION	208	0.39964935	1.4174423	0.12215321	0.2414706
GO_NEGATIVE_REGULATION_OF_TRANSFERASE_ACTIVITY	344	0.35006714	1.4170276	0.049484536	0.2416179
GO_POSITIVE_REGULATION_OF_CHROMOSOME_ORGANIZATION	146	0.41882142	1.4169807	0.10483871	0.24130231
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_MEMBRANE	262	0.4132945	1.4163158	0.14437367	0.24186458
GO_REGULATION_OF_MEIOTIC_CELL_CYCLE	40	0.38980982	1.415836	0.073913045	0.24209775
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	209	0.40071943	1.4155234	0.1368421	0.24216908
GO_REGULATION_OF_LAMELLIPODIUM_ASSEMBLY	25	0.47570863	1.4149483	0.08955224	0.24251461
GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	50	0.4084888	1.4149425	0.06320542	0.24214344
GO_NEGATIVE_REGULATION_OF_DNA_REPLICATION	54	0.44962394	1.4137537	0.11632653	0.24332906
GO_FC_EPSILON_RECEPTOR_SIGNALING_PATHWAY	124	0.43849242	1.4136603	0.11155379	0.24310654
GO_REGULATION_OF_CANONICAL_WNT_SIGNALING_PATHWAY	231	0.35564774	1.412885	0.06113537	0.24383551
GO_SOMATIC_RECOMBINATION_OF_IMMUNOGLOBULIN_GENE_SEGMENTS	21	0.5353969	1.4124781	0.11578947	0.24400632
GO_CELLULAR_PROTEIN_COMPLEX_ASSEMBLY	322	0.36791855	1.4111583	0.064935066	0.24545921
GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	51	0.3933611	1.4106404	0.09544469	0.24579279
GO_NUCLEOBASE_CONTAINING_COMPOUND_TRANSPORT	192	0.42502254	1.4099041	0.126294	0.24653637
GO_REGULATION_OF_MITOCHONDRION_ORGANIZATION	205	0.36713192	1.4093359	0.07515658	0.24690057
GO_INTRACELLULAR_PROTEIN_TRANSPORT	760	0.37135062	1.4093143	0.07157464	0.24653347
GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	29	0.45176756	1.4092094	0.093495935	0.24628109
GO_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	28	0.42844018	1.4091908	0.08908686	0.24591477
GO_MITOCHONDRIAL_RNA_METABOLIC_PROCESS	24	0.553498	1.4091585	0.13195877	0.24558549
GO_REGULATION_OF_GENE_SILENCING	51	0.43264243	1.408258	0.10606061	0.24644935
GO_NEGATIVE_REGULATION_OF_TELOMERE_MAINTENANCE_VIA_TELOMERE_LENGTHENING	16	0.5693925	1.4056624	0.115234375	0.24963623
Cellular component (203 terms)					
GO_SPINDLE_MIDZONE	26	0.84104335	2.3260758	0	0
GO_CONDENSED_CHROMOSOME	184	0.625094	2.0458548	0	0.01949567
GO_NUCLEOTIDE_EXCISION_REPAIR_COMPLEX	14	0.7983497	2.0102675	0	0.038233623
GO_CONDENSED_CHROMOSOME_CENTROMERIC_REGION	94	0.6848244	1.9877609	0	0.038488626
GO_KINETOCHORE	112	0.657697	1.9568988	0	0.04419017
GO_CONDENSED_NUCLEAR_CHROMOSOME	80	0.584971	1.9561487	0	0.036825143
GO_MITOTIC_SPINDLE	51	0.6454512	1.9554551	0	0.03201563
GO_REPLICATION_FORK	62	0.6866982	1.9434314	0.001972387	0.03494824
GO_CHROMOSOMAL_REGION	319	0.59015507	1.9427758	0	0.031548277
GO_CONDENSED_NUCLEAR_CHROMOSOME_CENTROMERIC_REGION	16	0.8323831	1.9366175	0	0.030137176

GO_PROTEASOME_COMPLEX	76	0.66312754	1.9265217	0.007858546	0.030978143
GO_CHROMOCENTER	13	0.7435613	1.9160497	0.002123142	0.032441642
GO_ORGANELLE_ENVELOPE_LUMEN	76	0.5594049	1.9022834	0.004040404	0.036134213
GO_CHROMOSOME_CENTROMERIC_REGION	166	0.6220622	1.9008061	0	0.034466125
GO_SPINDLE_MICROTUBULE	57	0.6339331	1.9004064	0	0.032366376
GO_REPLISOME	29	0.69838977	1.892537	0.001941748	0.033068
GO_METHYLOSOME	12	0.89705026	1.8873161	0	0.033075836
GO_MIDBODY	129	0.5590375	1.8792971	0	0.03451685
GO_SPINDLE	275	0.54570806	1.8760564	0	0.03406348
GO_CHROMOSOME	849	0.51045597	1.85601	0	0.041126177
GO_NUCLEAR_CHROMOSOME	506	0.49960688	1.8502165	0.00203666	0.0412078
GO_CHROMOSOME_TELOMERIC_REGION	158	0.54874	1.8380488	0.002057613	0.046140872
GO_XY_BODY	15	0.71142715	1.8375856	0.002004008	0.04421172
GO_NUCLEAR_REPLICATION_FORK	39	0.66956687	1.8347232	0.002016129	0.043765962
GO_NUCLEAR_CHROMOSOME_TELOMERIC_REGION	128	0.5549181	1.8295096	0.004115226	0.04469737
GO_PROTEIN_DNA_COMPLEX	171	0.5284183	1.8286493	0.006237006	0.043512262
GO_SMN_SM_PROTEIN_COMPLEX	17	0.75621843	1.8266293	0.004115226	0.04252426
GO_PROTEASOME_ACCESSORY_COMPLEX	24	0.7513342	1.8184818	0.00204499	0.045735843
GO_SPINDLE_POLE	116	0.5731225	1.8079107	0.002	0.051044542
GO_U1_SNRNP	17	0.7229952	1.7972847	0.008130081	0.055034705
GO_CONDENSED_CHROMOSOME_OUTER_KINETOCHORE	11	0.9060836	1.7920536	0.004016064	0.056582082
GO_COPI_COATED_VESICLE_MEMBRANE	16	0.7472838	1.783408	0.003944773	0.059525277
GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT_MEMBRANE	58	0.5610592	1.7821074	0.010351967	0.058385517
GO_DNA_PACKAGING_COMPLEX	104	0.5660737	1.7751032	0.02244898	0.060003523
GO_PRECATALYTIC_SPLICEOSOME	21	0.7182518	1.7679787	0.009881423	0.062912434
GO_ORGANELLAR_RIBOSOME	69	0.6611375	1.7659861	0.024340771	0.062298488
GO_NUCLEAR_PORE	74	0.59543335	1.7587587	0.00984252	0.06515336
GO_PRONUCLEUS	15	0.7300796	1.7550066	0.00203252	0.065573655
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	31	0.6932568	1.7451748	0.028	0.07033719
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	25	0.69598883	1.7440757	0.03	0.06922811
GO_PRERIBOSOME	59	0.6383732	1.7440171	0.018518519	0.067539625
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	17	0.6711382	1.7391809	0.009784736	0.06890651
GO_TELOMERASE_HOLOENZYME_COMPLEX	19	0.6935331	1.7383791	0.014198783	0.06787225
GO_SPLICEOSOMAL_TRI_SNRNP_COMPLEX	26	0.6877061	1.7232084	0.033009708	0.076120496
GO_COPI_VESICLE_COAT	12	0.745048	1.7228241	0.006012024	0.07458845
GO_RIBONUCLEOPROTEIN_COMPLEX	693	0.5154228	1.7174256	0.020120725	0.076408155
GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT	97	0.501618	1.7138463	0.008048289	0.076830775
GO_DNA_REPAIR_COMPLEX	38	0.5748586	1.7115395	0.008032128	0.07716386
GO_FILAMENTOUS_ACTIN	20	0.599922	1.6987783	0.016771488	0.08463159
GO_NUCLEOID	40	0.59771866	1.6982188	0.021956088	0.08314815
GO_ESCRT_COMPLEX	24	0.6488868	1.6947006	0.012170386	0.08428198
GO_ESCRT_III_COMPLEX	11	0.74569863	1.686286	0.010080645	0.08892367
GO_KINESIN_COMPLEX	54	0.5088976	1.6823125	0.014112903	0.090632655
GO_SMALL_NUCLEAR_RIBONUCLEOPROTEIN_COMPLEX	59	0.578973	1.6813229	0.027613413	0.089919195

GO_NUCLEOLAR_PART	61	0.590519	1.6805143	0.020833334	0.08898666
GO_SITE_OF_DOUBLE_STRAND_BREAK	31	0.5890624	1.6788667	0.023483366	0.08832552
GO_DESMOSOME	26	0.5904874	1.6775085	0.01754386	0.08793189
GO_CYTOPLASMIC_EXOSOME_RNASE_COMPLEX_	15	0.68985546	1.6749554	0.00811359	0.08796088
GO_CUL4_RING_E3_UBIQUITIN_LIGASE_COMPLEX	25	0.6250275	1.674746	0.00984252	0.08664821
GO_RIBOSOME	217	0.60081834	1.6742573	0.074152544	0.08562632
GO_NUCLEOLUS	820	0.469929	1.6734222	0.02008032	0.08486685
GO_U12_TYPE_SPLICEOSOMAL_COMPLEX	25	0.641022	1.664671	0.027944112	0.089238115
GO_METHYLTRANSFERASE_COMPLEX	83	0.55210423	1.6615765	0.010060363	0.090183884
GO_DNA_DIRECTED_RNA_POLYMERASE_I_COMPLEX	13	0.678317	1.6611584	0.018595042	0.08910698
GO_90S_PRERIBOSOME	23	0.65391266	1.649779	0.018789144	0.096765004
GO_HOLO_TFIIH_COMPLEX	12	0.7022134	1.6420639	0.028225806	0.10165976
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	130	0.5698359	1.6396762	0.070393376	0.10252093
GO_CATALYTIC_STEP_2_SPLICEOSOME	86	0.57532	1.6386323	0.031189084	0.10166273
GO_ORGANELLE_INNER_MEMBRANE	498	0.45414358	1.635548	0.03773585	0.102840886
GO_NUCLEAR_NUCLEOSOME	40	0.5954632	1.6316879	0.048117153	0.10475935
GO_DNA_DIRECTED_RNA_POLYMERASE_II_HOLOENZYME	95	0.5098183	1.6307847	0.012	0.10408149
GO_SEX_CHROMOSOME	27	0.59284085	1.6248122	0.015936255	0.107553735
GO_NUCLEAR_PERIPHERY	118	0.4930427	1.61825	0.018367346	0.11191613
GO_DNA_DIRECTED_RNA_POLYMERASE_III_COMPLEX	18	0.6140867	1.6176693	0.023952097	0.11102001
GO_RIBOSOMAL_SUBUNIT	158	0.6377086	1.6158568	0.0968421	0.11104481
GO_FANCONI_ANAEMIA_NUCLEAR_COMPLEX	13	0.67521495	1.6158319	0.016359918	0.1095837
GO_NUCLEAR_EXOSOME_RNASE_COMPLEX_	15	0.6742558	1.6134888	0.02258727	0.11010733
GO_EXOSOME_RNASE_COMPLEX_	21	0.6221308	1.6128706	0.022177419	0.10920379
GO_CHROMATIN	430	0.4313483	1.6126702	0.01048218	0.10792079
GO_CARBOXY_TERMINAL_DOMAIN_PROTEIN_KINASE_COMPLEX	22	0.6263262	1.6096051	0.014492754	0.10906407
GO_NUCLEAR_CHROMATIN	285	0.42781344	1.6067563	0.008281574	0.110226825
GO_RNA_POLYMERASE_COMPLEX	120	0.49278396	1.6023597	0.027722772	0.11247446
GO_PERICENTRIC_HETEROCHROMATIN	14	0.67543846	1.602022	0.023904383	0.111368574
GO_EUKARYOTIC_TRANSLATION_INITIATION_FACTOR_3_COMPLEX	16	0.6755767	1.6000555	0.031936128	0.11198203
GO_U2_SNRNP	18	0.6504549	1.6000228	0.040650405	0.11066459
GO_ANAPHASE_PROMOTING_COMPLEX	20	0.6247281	1.5992827	0.015936255	0.110066384
GO_SMALL_SUBUNIT_PROCESSOME	33	0.60705775	1.597637	0.04192872	0.11036505
GO_NUCLEAR_UBIQUITIN_LIGASE_COMPLEX	40	0.52782065	1.5963944	0.02918288	0.11022969
GO_MITOCHONDRIAL_MATRIX	397	0.44345337	1.5951979	0.045360826	0.11008649
GO_NUCLEAR_HETEROCHROMATIN	32	0.5408817	1.5940279	0.024390243	0.109908015
GO_MITOCHONDRIAL_PART	900	0.41722912	1.5907418	0.052738335	0.11160001
GO_EXTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	25	0.5463017	1.590667	0.017274473	0.11041337
GO_ARP2_3_PROTEIN_COMPLEX	11	0.6767838	1.5901756	0.037401576	0.109803736
GO_DNA_DIRECTED_RNA_POLYMERASE_II_CORE_COMPLEX	16	0.5928018	1.5896355	0.025742574	0.108954884
GO_SMALL_RIBOSOMAL_SUBUNIT	67	0.63669467	1.588632	0.10782241	0.10863769
GO_ENVELOPE	1034	0.39451194	1.5882437	0.01778656	0.10787465
GO_U4_U6_X_U5_TRI_SNRNP_COMPLEX	21	0.6486582	1.5877584	0.061023623	0.10709463
GO_MITOCHONDRIAL_ENVELOPE	651	0.4246095	1.5872039	0.049586777	0.10661438

GO_TRANSCRIPTION_FACTOR_TFTC_COMPLEX	14	0.6385319	1.5843153	0.020449897	0.10783634
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	44	0.5077217	1.5821255	0.059760958	0.108412735
GO_COHESIN_COMPLEX	11	0.6819116	1.5775199	0.04112554	0.11088169
GO_DNA_POLYMERASE_COMPLEX	13	0.6344448	1.5756717	0.03846154	0.11123737
GO_MLL1_2_COMPLEX	26	0.5921828	1.5754778	0.018255578	0.11033714
GO_CELL_SUBSTRATE_JUNCTION	393	0.43214065	1.574573	0.04592902	0.110123545
GO_LATERAL_ELEMENT	10	0.64834774	1.572871	0.05605381	0.11041852
GO_PROTEASOME_REGULATORY_PARTICLE_BASE_SUBCOMPLEX	12	0.7154797	1.5725623	0.026156941	0.10965078
GO_COPI_COATED_VESICLE	22	0.5840315	1.5723255	0.046692606	0.10884525
GO_CYTOSOLIC_PROTEASOME_COMPLEX	11	0.7212852	1.5721248	0.026209677	0.10805043
GO_SPLICEOSOMAL_COMPLEX	165	0.51497704	1.5676765	0.05882353	0.11020962
GO_HETEROCHROMATIN	66	0.48235494	1.5633675	0.018556701	0.11293165
GO_PRERIBOSOME_LARGE_SUBUNIT_PRECURSOR	20	0.67208725	1.5618517	0.04621849	0.11303397
GO_CELL_DIVISION_SITE	52	0.478522	1.5618477	0.026584867	0.112032674
GO_LARGE_RIBOSOMAL_SUBUNIT	91	0.6388327	1.5562295	0.10683761	0.11507954
GO_EUCHROMATIN	30	0.5025108	1.5548385	0.030864198	0.11530045
GO_PIGMENT_GRANULE	101	0.45336327	1.5444121	0.055785123	0.12283112
GO_SMN_COMPLEX	12	0.6385872	1.541536	0.053497944	0.124197826
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	101	0.5738572	1.5405756	0.10973085	0.123900265
GO_NUCLEAR_MATRIX	95	0.47337177	1.5404632	0.024793388	0.12290171
GO_ANCHORING_JUNCTION	483	0.39881375	1.535496	0.04761905	0.12622277
GO_MITOCHONDRIAL_MEMBRANE_PART	161	0.49835575	1.5349631	0.10580913	0.12542067
GO_DNA_HELICASE_COMPLEX	14	0.64322674	1.5339364	0.036217302	0.12520336
GO_CYTOCHROME_COMPLEX	20	0.5842063	1.5322926	0.088607594	0.12542772
GO_MICROTUBULE_END	21	0.5945179	1.5303905	0.0513347	0.12607974
GO_ORGANELLE_MEMBRANE_CONTACT_SITE	11	0.6966256	1.5293269	0.027079303	0.1259721
GO_INVADOPODIUM	12	0.59802914	1.5277249	0.060344826	0.12614769
GO_CAJAL_BODY	49	0.51509035	1.5222515	0.062626265	0.1298703
GO_RESPIRATORY_CHAIN	78	0.5824595	1.5213636	0.11958763	0.12955233
GO_TRANSLATION_PREINITIATION_COMPLEX	16	0.64571077	1.5183176	0.0734127	0.13123667
GO_NUCLEAR_EUCHROMATIN	23	0.5188934	1.5174655	0.033195022	0.13102703
GO_BETA_CATENIN_DESTRUCTION_COMPLEX	14	0.5651986	1.5098767	0.033126295	0.13640216
GO_MITOCHONDRION	1546	0.37719896	1.5048269	0.059063137	0.14022863
GO_INTERCELLULAR_BRIDGE	40	0.48296908	1.503907	0.043824703	0.14003058
GO_GERM_CELL_NUCLEUS	18	0.50249916	1.5007719	0.055201698	0.1417771
GO_PROTEIN_PHOSPHATASE_TYPE_2A_COMPLEX	20	0.55312675	1.5004094	0.044806518	0.14105962
GO_VESICLE_COAT	44	0.49916184	1.5000247	0.06420233	0.14043976
GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	30	0.52727294	1.4953043	0.050314464	0.14352527
GO_INO80_TYPE_COMPLEX	21	0.5713214	1.4863981	0.058704454	0.15045401
GO_PRP19_COMPLEX	13	0.6547913	1.4801719	0.06990291	0.15514763
GO_PRESPLICEOSOME	21	0.54631174	1.4782227	0.08863199	0.15592083
GO_CLATHRIN_COAT_OF_ENDOCYTIC_VESICLE	12	0.58347094	1.4724025	0.06097561	0.16057241
GO_OXIDOREDUCTASE_COMPLEX	92	0.46642926	1.4689081	0.126294	0.16312899
GO_SMALL_NUCLEOLAR_RIBONUCLEOPROTEIN_COMPLEX	19	0.5963133	1.4648672	0.09876543	0.16626109

GO_DNA_REPLICATION_FACTOR_A_COMPLEX	15	0.5857178	1.4594969	0.06187625	0.17042628
GO_CORNIFIED_ENVELOPE	45	0.5670365	1.4584446	0.09567198	0.17036583
GO_GOLGI_ASSOCIATED_VESICLE_MEMBRANE	48	0.43847212	1.455886	0.057312254	0.17188369
GO_COMPACT_MYELIN	14	0.5562161	1.4535052	0.07505071	0.17300765
GO_MICROTUBULE_ORGANIZING_CENTER_PART	138	0.41464427	1.4502409	0.068136275	0.17500137
GO_CENTROSOME	467	0.39898914	1.4440563	0.074	0.17991252
GO_SYNAPTONEMAL_COMPLEX	33	0.44054693	1.4431202	0.058139537	0.17960514
GO_MICROTUBULE_ORGANIZING_CENTER	589	0.3896266	1.4401463	0.06288032	0.1814978
GO_TOR_COMPLEX	13	0.5768153	1.4379207	0.072265625	0.18276168
GO_MICROTUBULE_CYTOSKELETON	1012	0.37152585	1.4359473	0.05858586	0.1836914
GO_ENDOPLASMIC_RETICULUM_QUALITY_CONTROL_COMPARTMENT	13	0.603353	1.4357442	0.10958904	0.18267743
GO_ENDOPLASMIC_RETICULUM_CHAPERONE_COMPLEX	11	0.6550231	1.4351535	0.09856263	0.18209048
GO_MRNA_CLEAVAGE_AND_POLYADENYLATION_SPECIFICITY_FACTOR_COMPLEX	12	0.60519123	1.4257753	0.108606555	0.19079481
GO_MICROTUBULE_PLUS_END	16	0.5741014	1.424729	0.09343936	0.190661
GO_MYELIN_SHEATH	165	0.39438027	1.4230833	0.1	0.19094916
GO_NUCLEAR_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	15	0.5912651	1.4204445	0.10204082	0.19279106
GO_PHOSPHATASE_COMPLEX	44	0.48636755	1.4184752	0.134	0.19343357
GO_CYTOSOLIC_PART	213	0.44941416	1.4160222	0.1695279	0.19505422
GO_CLATHRIN_COAT_OF_COATED_PIT	16	0.5293268	1.4157741	0.112	0.19418441
GO_CYTOPLASMIC_STRESS_GRANULE	31	0.50593203	1.4157735	0.12273642	0.19298574
GO_SCHMIDT_LANTERMAN_INCISURE	10	0.5664076	1.4141964	0.08782435	0.19345312
GO_NADH_DEHYDROGENASE_COMPLEX	42	0.587203	1.4137212	0.18609408	0.19280127
GO_INTRINSIC_COMPONENT_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	120	0.39054215	1.4105048	0.08382066	0.19528994
GO_MCM_COMPLEX	11	0.6448941	1.4092671	0.1252485	0.19549616
GO_N_TERMINAL_PROTEIN_ACETYLTRANSFERASE_COMPLEX	9	0.60607094	1.4059713	0.077731095	0.19751412
GO_LATERAL_PLASMA_MEMBRANE	49	0.4071368	1.4014344	0.11214953	0.20105983
GO_CYTOPLASMIC_UBIQUITIN_LIGASE_COMPLEX	13	0.5510336	1.390843	0.08565737	0.21121041
GO_CYTOSOLIC_RIBOSOME	109	0.58284867	1.387264	0.24472573	0.21404941
GO_CYTOSOLIC_SMALL_RIBOSOMAL_SUBUNIT	43	0.62217426	1.3870012	0.20940171	0.21305254
GO_MRNA_CLEAVAGE_FACTOR_COMPLEX	17	0.560563	1.3845685	0.118609406	0.21439931
GO_CYTOSOLIC_LARGE_RIBOSOMAL_SUBUNIT	58	0.61769307	1.3824157	0.23868313	0.21563461
GO_SIN3_TYPE_COMPLEX	16	0.54448086	1.3814529	0.115234375	0.21535446
GO_RIBONUCLEOPROTEIN_GRANULE	142	0.39726046	1.3798908	0.12298387	0.2159885
GO_CYTOSKELETAL_PART	1375	0.32888514	1.3790755	0.04831933	0.21564575
GO_SEMAPHORIN_RECEPTOR_COMPLEX	11	0.5403336	1.376138	0.13821138	0.217876
GO_U5_SNRNP	16	0.5630189	1.3748124	0.15445544	0.21816726
GO_IKAPPAB_KINASE_COMPLEX	11	0.5401259	1.3737681	0.12394958	0.2180395
GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_COMPLEX	101	0.38475907	1.3713241	0.116564415	0.21951196
GO_TRANSFERASE_COMPLEX	671	0.38780746	1.3692687	0.14457831	0.22069615
GO_STAGA_COMPLEX	14	0.54380524	1.3684026	0.107421875	0.22051162
GO_HISTONE_METHYLTRANSFERASE_COMPLEX	64	0.4613078	1.366467	0.16071428	0.2213981
GO_CATALYTIC_COMPLEX	995	0.36449766	1.3624283	0.13572854	0.22445054
GO_CENTRIOLE	96	0.40761477	1.3590596	0.13114753	0.22682957
GO_GAMMA_TUBULIN_COMPLEX	19	0.48909497	1.3567177	0.13095239	0.2280362

GO_MALE_GERM_CELL_NUCLEUS	14	0.47775525	1.3541172	0.12298387	0.23000774
GO_MICROTUBULE_ASSOCIATED_COMPLEX	143	0.37958485	1.3536754	0.11554622	0.22930379
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_CATALYTIC_DOMAIN	17	0.49567354	1.3482997	0.16227181	0.23439552
GO_CYTOPLASMIC_MICROTUBULE	52	0.402194	1.3462011	0.15913978	0.23570903
GO_PROTEIN_PHOSPHATASE_TYPE_1_COMPLEX	10	0.60121113	1.34456	0.15662651	0.2362129
GO_TRANSFERASE_COMPLEX_TRANSFERRING_PHOSPHORUS_CONTAINING_GROUPS	233	0.38622758	1.3428963	0.15587045	0.23687142
GO_ENDOPLASMIC_RETICULUM_SUBCOMPARTMENT	16	0.5017041	1.3425262	0.13778706	0.23611408
GO_ENDORIBONUCLEASE_COMPLEX	17	0.51173073	1.3410311	0.15800416	0.23668586
GO_PROTEIN_KINASE_COMPLEX	89	0.3974052	1.3408469	0.13292433	0.23562504
GO_GEMINI_OF_COILED_BODIES	10	0.5861722	1.3382926	0.1680498	0.23715729
GO_EXON_EXON_JUNCTION_COMPLEX	21	0.52045196	1.3318206	0.14910537	0.24316098
GO_NUCLEAR_ENVELOPE	400	0.34301764	1.3304824	0.14663951	0.24342686
GO_CLATHRIN_VESICLE_COAT	23	0.45778513	1.3296793	0.138833	0.24322869
GO_OUTER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	12	0.5612569	1.3252932	0.16221766	0.24678905
GO_SUPRAMOLECULAR_FIBER	646	0.3024545	1.3243201	0.081196584	0.24669227
GO_CENTRIOLAR_SATELLITE	24	0.45929345	1.3214265	0.12830958	0.24896678
GO_TRANSCRIPTIONALLY_ACTIVE_CHROMATIN	19	0.4687087	1.3193872	0.15062761	0.24999443
Molecular function (57 terms)					
GO_CYCLIN_DEPENDENT_PROTEIN_KINASE_ACTIVITY	34	0.59596914	1.772709	0.002004008	0.2264464
GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	31	0.5639808	1.7726935	0.004	0.20380178
GO_UNFOLDED_PROTEIN_BINDING	93	0.5652977	1.7709087	0.013861386	0.1883973
GO_DNA_SECONDARY_STRUCTURE_BINDING	24	0.6747988	1.7625717	0.005964215	0.18935034
GO_DEOXYRIBONUCLEASE_ACTIVITY	65	0.54601496	1.7546927	0.003838772	0.19224492
GO_FOUR_WAY_JUNCTION_DNA_BINDING	15	0.73733616	1.7443064	0.003992016	0.19441648
GO_TELOMERASE_RNA_BINDING	13	0.73477966	1.7424701	0.005780347	0.18500839
GO_DNA_APURINIC_OR_APYRIMIDINIC_SITE_LYASE_ACTIVITY	14	0.67090636	1.7395418	0.005736138	0.1779046
GO_TRANSLATION_FACTOR_ACTIVITY_RNA_BINDING	85	0.5673898	1.7317507	0.01417004	0.18196087
GO_SNORNA_BINDING	26	0.66639566	1.7308675	0.0227704	0.17317854
GO_ENDODEOXYRIBONUCLEASE_ACTIVITY	49	0.5563542	1.730388	0.003875969	0.16459635
GO_RNA_POLYMERASE_ACTIVITY	43	0.5890996	1.7267307	0.009633912	0.16133244
GO_EXODEOXYRIBONUCLEASE_ACTIVITY	15	0.6851024	1.724979	0.007633588	0.15597253
GO_DNA_POLYMERASE_BINDING	12	0.7362106	1.7079195	0.011952192	0.17373806
GO_RNA_DNA_HYBRID_RIBONUCLEASE_ACTIVITY	7	0.85012937	1.702509	0.007797271	0.1755684
GO_POLY_A_RNA_BINDING	1136	0.5163767	1.7017269	0.006085193	0.16976267
GO_EXONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	42	0.6049815	1.7005074	0.003921569	0.16501117
GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	18	0.59686893	1.6979871	0.015968064	0.16195983
GO_RIBONUCLEOPROTEIN_COMPLEX_BINDING	94	0.5515675	1.6961001	0.01004016	0.15839937
GO_DNA_HELICASE_ACTIVITY	52	0.6337112	1.6949878	0.011904762	0.15478322
GO_ATP_DEPENDENT_MICROTUBULE_MOTOR_ACTIVITY	18	0.620893	1.6936761	0.002079002	0.15116644
GO_LIGASE_ACTIVITY_FORMING_CARBON_OXYGEN_BONDS	44	0.61798465	1.6883807	0.020283977	0.15364894
GO_NUCLEOTIDYLTRANSFERASE_ACTIVITY	123	0.5028087	1.67752	0.0078125	0.16441652
GO_HISTONE_KINASE_ACTIVITY	19	0.645991	1.6714854	0.02631579	0.16863915
GO_RNA_BINDING	1538	0.4852454	1.6673499	0.014112903	0.17003563

GO_AMINOACYL_TRNA_EDITING_ACTIVITY	9	0.7373682	1.6592922	0.01417004	0.17785034
GO_PHOSPHATASE_ACTIVATOR_ACTIVITY	11	0.6918341	1.6559213	0.013182675	0.17761366
GO_L_ASCORBIC_ACID_BINDING	17	0.6026333	1.6534616	0.014403292	0.17594169
GO_MACROLIDE_BINDING	18	0.568697	1.6533175	0.033663366	0.17139137
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	27	0.57158434	1.6518219	0.012219959	0.16927741
GO_RNA_POLYMERASE_II_CARBOXY_TERMINAL_DOMAIN_KINASE_ACTIVITY	16	0.6771608	1.6509368	0.005964215	0.16651683
GO_STRUCTURE_SPECIFIC_DNA_BINDING	118	0.4839008	1.6368496	0.010245902	0.18350117
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	48	0.48290274	1.6363481	0.018255578	0.1798862
GO_ATP_DEPENDENT_DNA_HELICASE_ACTIVITY	33	0.62332255	1.6339344	0.01192843	0.17932701
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_ACTIVITY	29	0.59377337	1.6145074	0.025145067	0.20471442
GO_ENDODEOXYRIBONUCLEASE_ACTIVITY_PRODUCING_5_PHOSPHOMONOESTERS	11	0.63884395	1.6143475	0.021653544	0.20025939
GO_METAL_CLUSTER_BINDING	61	0.48897392	1.6123128	0.01968504	0.19880192
GO_CIS_TRANS_ISOMERASE_ACTIVITY	45	0.49063978	1.6090858	0.024096385	0.20019035
GO_ISOMERASE_ACTIVITY	156	0.40923655	1.6086198	0.012345679	0.19650543
GO_STRUCTURAL_CONSTITUENT_OF_NUCLEAR_PORE	13	0.7319034	1.5983399	0.010183299	0.20838094
GO_NUCLEOSIDE_KINASE_ACTIVITY	13	0.62519777	1.5966307	0.019157087	0.20682418
GO_NF_KAPPAB_BINDING	30	0.5529674	1.5868734	0.031936128	0.21856599
GO_RIBOSOMAL_SMALL_SUBUNIT_BINDING	12	0.6759848	1.5858672	0.024742268	0.2159485
GO_EXONUCLEASE_ACTIVITY	73	0.51389986	1.5818905	0.028846154	0.21884224
GO_ENDONUCLEASE_ACTIVITY_ACTIVE_WITH_EITHER_RIBO_OR_DEOXYRIBONUCLEIC_ACIDS_AND_PRODUCING_5_PHOSPHOMONOESTERS	34	0.5370378	1.5810101	0.035019454	0.2161074
GO_3_5_EXONUCLEASE_ACTIVITY	47	0.5491874	1.570972	0.031558186	0.23034796
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	202	0.5533821	1.5599234	0.10515873	0.24592353
GO_METHYL_CPG_BINDING	20	0.573909	1.5590467	0.03041825	0.24335279
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_INTERCONVERTING_ALDOSES_AND_KETOSES	11	0.6543069	1.5538702	0.021912351	0.24854536
C6 Oncological signature (28 terms)					
BIOCARTA_PTC1_PATHWAY	11	0.8459149	1.945383	0.002118644	0.06398674
BIOCARTA_P27_PATHWAY	13	0.7969798	1.9289968	0	0.038441528
BIOCARTA_G2_PATHWAY	24	0.6917375	1.9036189	0.006160164	0.03788111
BIOCARTA_CELLCYCLE_PATHWAY	23	0.65959394	1.8606957	0.00408998	0.045502532
BIOCARTA_PROTEASOME_PATHWAY	28	0.77732474	1.8319854	0.007936508	0.04707304
BIOCARTA_GLYCOLYSIS_PATHWAY	10	0.79025996	1.7912003	0.010351967	0.06358903
BIOCARTA_MCM_PATHWAY	18	0.71597147	1.7694954	0.018556701	0.06876878
BIOCARTA_HIF_PATHWAY	15	0.6840519	1.7625527	0.004366812	0.065344326
BIOCARTA_SRCRPTP_PATHWAY	11	0.71615475	1.7487165	0.010615711	0.06870219
BIOCARTA_RB_PATHWAY	13	0.6846301	1.7439233	0	0.06439214
BIOCARTA_RANMS_PATHWAY	10	0.82737935	1.7220055	0.016	0.073742755
BIOCARTA_SKP2E2F_PATHWAY	10	0.702789	1.7103677	0.005928854	0.075584196
BIOCARTA_SALMONELLA_PATHWAY	13	0.7176766	1.7035477	0.007968128	0.07478445
BIOCARTA_EIF2_PATHWAY	11	0.76882476	1.7004058	0.002024292	0.07195907
BIOCARTA_RAB_PATHWAY	12	0.70288587	1.6705955	0.021868788	0.08710322
BIOCARTA_EIF_PATHWAY	16	0.6816011	1.6425833	0.021868788	0.10431794
BIOCARTA_ATRBRCA_PATHWAY	21	0.63465095	1.6402888	0.017716536	0.10076495
BIOCARTA_RACCYCD_PATHWAY	26	0.5962543	1.6380337	0.02008032	0.096681274

BIOCARTA_FREE_PATHWAY	9	0.6763291	1.5989605	0.023861172	0.12729096
BIOCARTA_UCALPAIN_PATHWAY	18	0.60840744	1.580332	0.031578947	0.14142391
BIOCARTA_CDC42RAC_PATHWAY	16	0.65308535	1.5594262	0.033864543	0.15784384
BIOCARTA_G1_PATHWAY	28	0.5214182	1.5509028	0.046938777	0.1612215
BIOCARTA_MTA3_PATHWAY	18	0.538474	1.5497025	0.039130434	0.15579833
BIOCARTA_P35ALZHEIMERS_PATHWAY	11	0.60613376	1.4991324	0.03976143	0.21654968
BIOCARTA_DNAFRAGMENT_PATHWAY	10	0.628387	1.4850376	0.072434604	0.22850932
BIOCARTA_ATM_PATHWAY	20	0.5571135	1.4751178	0.064449064	0.23431115
BIOCARTA_ACTINY_PATHWAY	20	0.54589474	1.4745562	0.07185629	0.22656365
BIOCARTA_PTDINS_PATHWAY	23	0.5363502	1.45985	0.071428575	0.23828006
Terms enriched in low risk group					
C2 KEGG (1 terms)					
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERACTION	270	-0.5301249	-1.9103235	0	0.09315833
C5					
Biological process (0 terms)					
Cellular component (3 terms)					
GO_MAIN_AXON	57	-0.6137751	-1.9344873	0	0.13338119
GO_APICAL_DENDRITE	13	-0.68443125	-1.8339114	0.001848429	0.20765187
GO_NEURON_PROJECTION_MEMBRANE	34	-0.5705935	-1.6494124	0.012433393	0.24696921
Molecular function (30 terms)					
GO_POTASSIUM_CHANNEL_ACTIVITY	119	-0.5401616	-1.881483	0	0.18842526
GO_SIGNALING_RECEPTOR_ACTIVITY	1321	-0.40520954	-1.8378897	0	0.22552337
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	817	-0.38562855	-1.8358582	0	0.17340446
GO_PEPTIDE_RECEPTOR_ACTIVITY	127	-0.54304916	-1.8121959	0.003584229	0.18765643
GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	36	-0.6197212	-1.8067665	0.003478261	0.16693386
GO_PHOSPHORIC_DIESTER_HYDROLASE_ACTIVITY	90	-0.4992297	-1.7794026	0	0.19396083
GO_RECEPTOR_ACTIVITY	1563	-0.39239866	-1.777063	0.001838235	0.17344797
GO_ADRENERGIC_RECEPTOR_BINDING	19	-0.6341564	-1.7739949	0.006036217	0.15868044
GO_CARBOXYPEPTIDASE_ACTIVITY	38	-0.53562874	-1.7690663	0.001703578	0.15114729
GO_VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	133	-0.49740162	-1.7464465	0.004926108	0.17381446
GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	18	-0.6049076	-1.7460067	0.003745318	0.16047662
GO_GATED_CHANNEL_ACTIVITY	319	-0.454151	-1.7320489	0.001652893	0.1702009
GO_CATION_CHANNEL_ACTIVITY	290	-0.4486865	-1.7271901	0.00331675	0.16735497
GO_LIGAND_GATED_CHANNEL_ACTIVITY	138	-0.46703282	-1.7210503	0.001636661	0.16623475
GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	22	-0.7278793	-1.7166375	0.020183487	0.16316581
GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	25	-0.6101103	-1.7129616	0.005736138	0.15961972
GO_PHOSPHOLIPASE_C_ACTIVITY	31	-0.5476513	-1.7128425	0.007518797	0.15093626
GO_EXTRACELLULAR_LIGAND_GATED_ION_CHANNEL_ACTIVITY	75	-0.51395744	-1.7126123	0.006568145	0.14321831
GO_3_5_CYCLIC_GMP_PHOSPHODIESTERASE_ACTIVITY	14	-0.67524856	-1.7057961	0.015296367	0.145294
GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	20	-0.65179735	-1.6942664	0.014159292	0.15501155
GO_VOLTAGE_GATED_ION_CHANNEL_ACTIVITY	188	-0.4572963	-1.677874	0.006644518	0.17324595
GO_CYTOKINE_RECEPTOR_ACTIVITY	85	-0.5309697	-1.6516032	0.030797102	0.21209529
GO_PEPTIDE_HORMONE_BINDING	36	-0.5490085	-1.645897	0.009345794	0.2134605
GO_CYCLASE_ACTIVITY	21	-0.57964176	-1.644735	0.018656716	0.20693746

GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	15	-0.6743193	-1.6427832	0.0227704	0.20302416
GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	22	-0.5571651	-1.6124709	0.021558871	0.24808282
GO_SIGNAL_TRANSDUCER_ACTIVITY	1652	-0.34759322	-1.5912715	0.007590133	0.24472035
GO_SERINE_TYPE_CARBOXYPEPTIDASE_ACTIVITY	14	-0.5939026	-1.5881804	0.03564728	0.24348828
GO_IMMUNOGLOBULIN_RECEPTOR_BINDING	7	-0.8023157	-1.5816555	0.020522388	0.24862528
GO_CAMP_BINDING	22	-0.553671	-1.5807339	0.021778584	0.24358347
C6 Oncological signature (terms)					
BIOCARTA_GRANULOCYTES_PATHWAY	13	-0.8286528	-1.8326796	0.001858736	0.14008604
BIOCARTA_THELPER_PATHWAY	12	-0.8545251	-1.545204	0.029126214	0.23535249
BIOCARTA_TCYTOTOXIC_PATHWAY	12	-0.8540751	-1.5399984	0.034951456	0.23010892

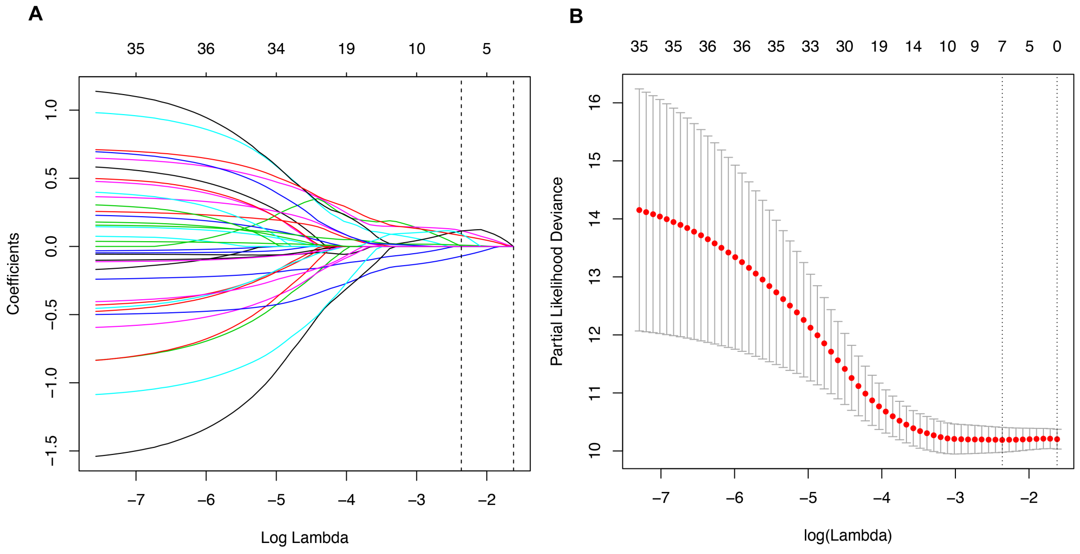
Supplementary figure legends

Figure S1 LASSO analysis of the 36 prognostic DE-MTGs in PDAC. (A) LASSO coefficient profiles of the 36 prognostic DE-MTGs in PDAC. (B) Lasso deviance profiles of the 36 prognostic DE-MTGs in PDAC.

Figure S2 (A–C) ROC curves for 1-, 2-, and 3-year overall survival predictions for the MTG-based gene signature compared with those of the AJCC staging system and three previously defined gene signatures in the TCGA-PAAD datasets. (D–F) ROC curves for 1-, 2-, and 3-year overall survival predictions for the MTG-based gene signature compared with those of the AJCC staging system and three previously defined gene signatures in the external validation dataset GSE62452. (G–I) ROC curves for 1-, 2-, and 3-year overall survival predictions for the MTG-based gene signature compared with those of the three previously defined gene signatures in the external validation dataset ICGC.

Figure S3 (A–C) ROC curves for 1-, 2-, and 3-year overall survival predictions of the nomogram compared with those of the AJCC staging system in TCGA-PAAD dataset. (D–F) ROC curves for 1-, 2-, and 3-year overall survival predictions of the nomogram compared with those of the gene signature proposed by Zhou C et al. in TCGA-PAAD dataset. (G–I) ROC curves for 1-, 2-, and 3-year overall survival predictions of the nomogram compared with those of the gene signature proposed by Chen H et al. in TCGA-PAAD dataset. (J–L) ROC curves for 1-, 2-, and 3-year overall survival predictions of the nomogram compared with those of the gene signature proposed by Liao X et al. in TCGA-PAAD dataset.

Figure S1



LASSO coefficent profiles

LASSO deviance profiles

Figure S2

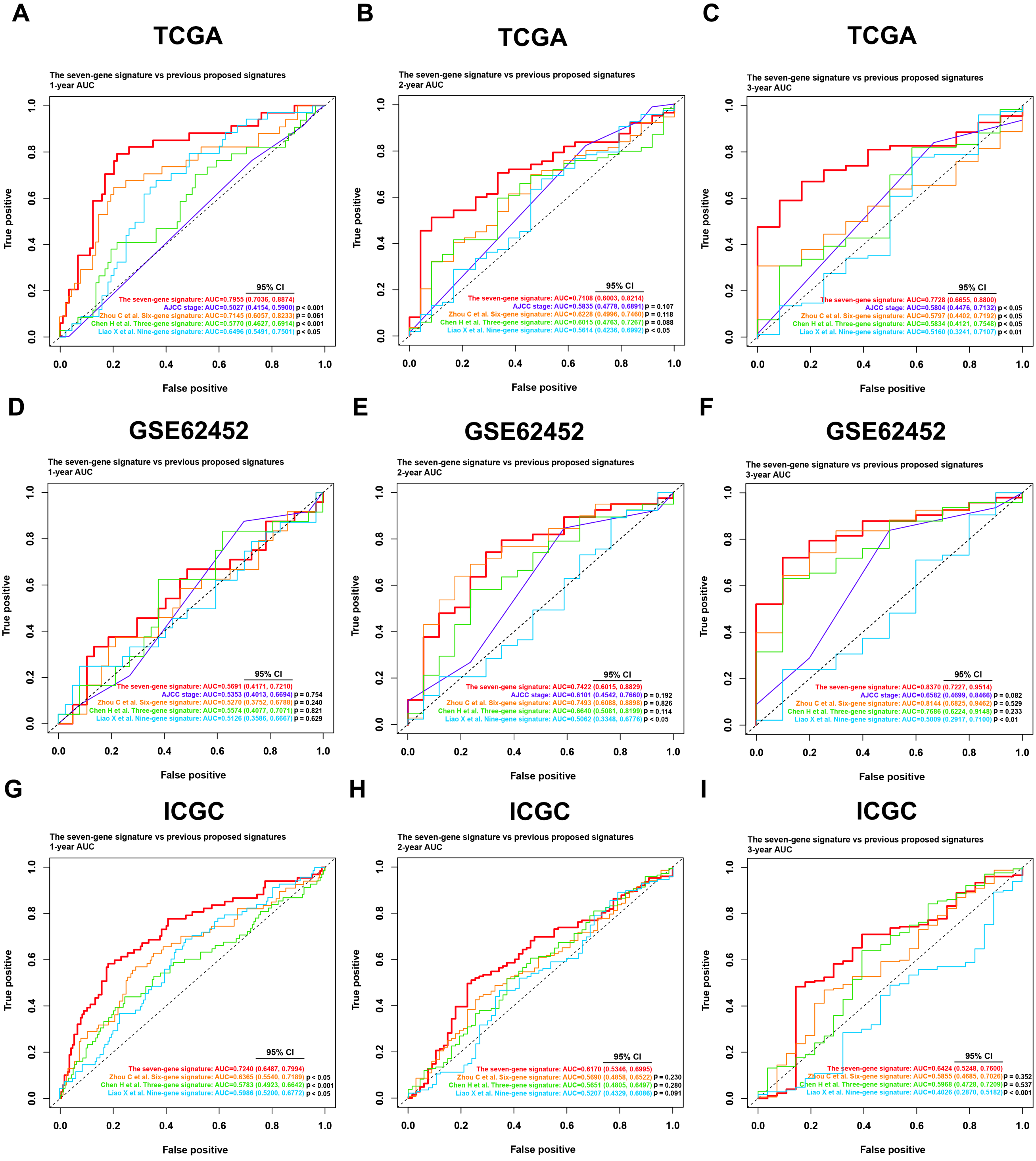
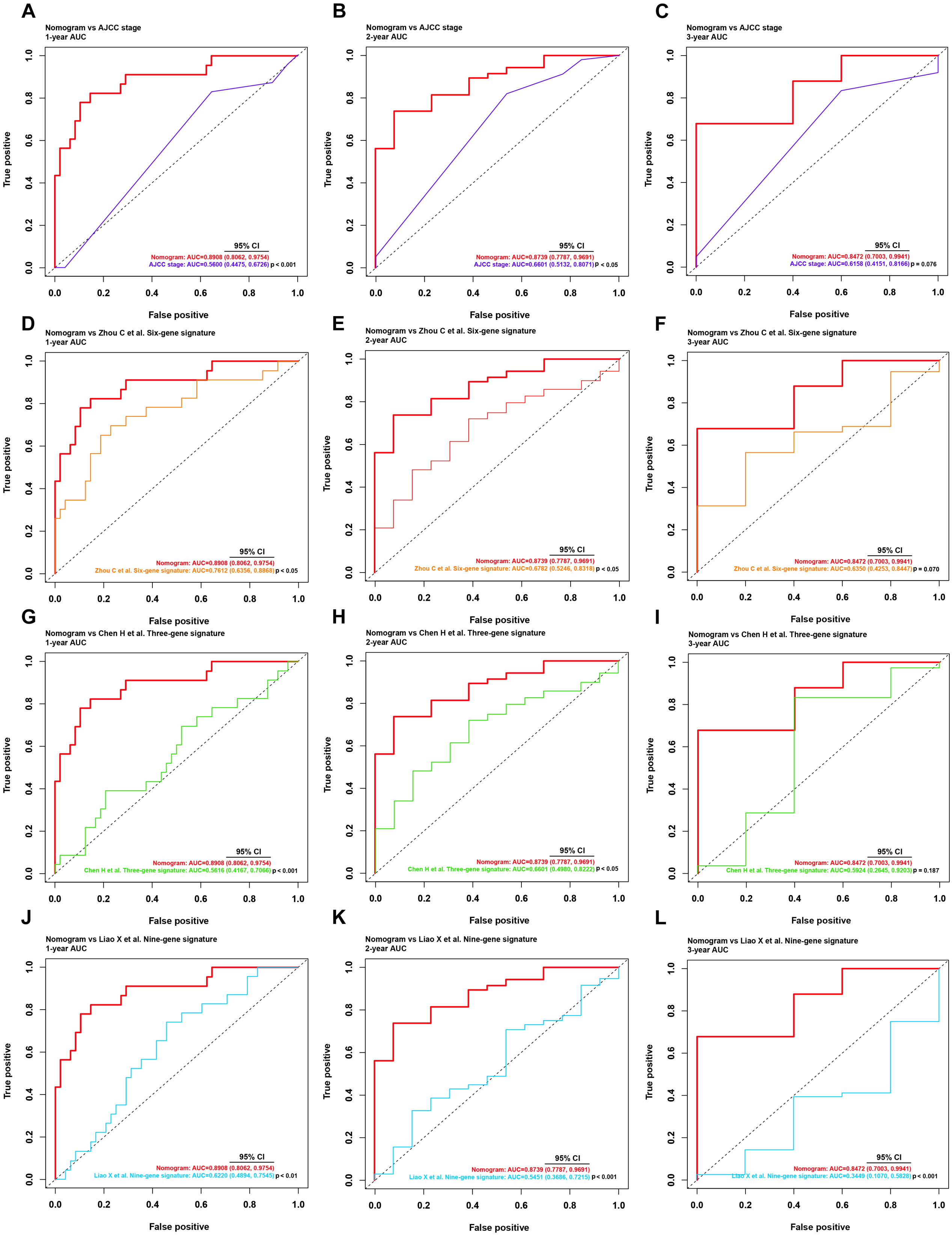

A
TCGA
The seven-gene signature vs previous proposed signatures
1-year AUC
True positive
False positive
0.0
0.2
0.4
0.6
0.8
1.0
95% CI
The seven-gene signature: AUC=0.7955 (0.7036, 0.8874)
AJCC stage: AUC=0.5027 (0.4154, 0.5900) p < 0.001
Zhou C et al. Six-gene signature: AUC=0.7145 (0.6057, 0.8233) p = 0.061
Chen H et al. Three-gene signature: AUC=0.5770 (0.4627, 0.6914) p < 0.001
Liao X et al. Nine-gene signature: AUC=0.6496 (0.5491, 0.7501) p < 0.05
B
TCGA
The seven-gene signature vs previous proposed signatures
2-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.7108 (0.6003, 0.8214)
AJCC stage: AUC=0.5835 (0.4778, 0.6891) p = 0.107
Zhou C et al. Six-gene signature: AUC=0.6228 (0.4996, 0.7460) p = 0.118
Chen H et al. Three-gene signature: AUC=0.6015 (0.4763, 0.7267) p = 0.088
Liao X et al. Nine-gene signature: AUC=0.5614 (0.4236, 0.6992) p < 0.05
C
TCGA
The seven-gene signature vs previous proposed signatures
3-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.7728 (0.6655, 0.8800)
AJCC stage: AUC=0.5804 (0.4476, 0.7132) p < 0.05
Zhou C et al. Six-gene signature: AUC=0.5797 (0.4402, 0.7192) p < 0.05
Chen H et al. Three-gene signature: AUC=0.5834 (0.4121, 0.7548) p < 0.05
Liao X et al. Nine-gene signature: AUC=0.5160 (0.3241, 0.7107) p < 0.01
D
GSE62452
The seven-gene signature vs previous proposed signatures
1-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.5691 (0.4171, 0.7210)
AJCC stage: AUC=0.5353 (0.4013, 0.6694) p = 0.754
Zhou C et al. Six-gene signature: AUC=0.5270 (0.3752, 0.6788) p = 0.240
Chen H et al. Three-gene signature: AUC=0.5574 (0.4077, 0.7071) p = 0.821
Liao X et al. Nine-gene signature: AUC=0.5126 (0.3586, 0.6667) p = 0.629
E
GSE62452
The seven-gene signature vs previous proposed signatures
2-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.7422 (0.6015, 0.8829)
AJCC stage: AUC=0.6101 (0.4542, 0.7660) p = 0.192
Zhou C et al. Six-gene signature: AUC=0.7493 (0.6088, 0.8898) p = 0.826
Chen H et al. Three-gene signature: AUC=0.6640 (0.5081, 0.8199) p = 0.114
Liao X et al. Nine-gene signature: AUC=0.5062 (0.3348, 0.6776) p < 0.05
F
GSE62452
The seven-gene signature vs previous proposed signatures
3-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.8370 (0.7227, 0.9514)
AJCC stage: AUC=0.6582 (0.4699, 0.8466) p = 0.082
Zhou C et al. Six-gene signature: AUC=0.8144 (0.6825, 0.9462) p = 0.529
Chen H et al. Three-gene signature: AUC=0.7686 (0.6224, 0.9148) p = 0.233
Liao X et al. Nine-gene signature: AUC=0.5009 (0.2917, 0.7100) p < 0.01
G
ICGC
The seven-gene signature vs previous proposed signatures
1-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.7240 (0.6487, 0.7994)
Zhou C et al. Six-gene signature: AUC=0.6365 (0.5540, 0.7189) p < 0.05
Chen H et al. Three-gene signature: AUC=0.5783 (0.4923, 0.6642) p < 0.001
Liao X et al. Nine-gene signature: AUC=0.5986 (0.5200, 0.6772) p < 0.05
H
ICGC
The seven-gene signature vs previous proposed signatures
2-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.6170 (0.5346, 0.6995)
Zhou C et al. Six-gene signature: AUC=0.5690 (0.4858, 0.6522) p = 0.230
Chen H et al. Three-gene signature: AUC=0.5651 (0.4805, 0.6497) p = 0.280
Liao X et al. Nine-gene signature: AUC=0.5207 (0.4329, 0.6086) p = 0.091
I
ICGC
The seven-gene signature vs previous proposed signatures
3-year AUC
True positive
False positive
95% CI
The seven-gene signature: AUC=0.6424 (0.5248, 0.7600)
Zhou C et al. Six-gene signature: AUC=0.5855 (0.4685, 0.7026) p = 0.352
Chen H et al. Three-gene signature: AUC=0.5968 (0.4728, 0.7209) p = 0.537
Liao X et al. Nine-gene signature: AUC=0.4026 (0.2870, 0.5182) p < 0.001

Figure S3


A
Nomogram vs AJCC stage
1-year AUC
95% CI
Nomogram: AUC=0.8908 (0.8062, 0.9754)
AJCC stage: AUC=0.5600 (0.4475, 0.6726) p < 0.001
B
Nomogram vs AJCC stage
2-year AUC
95% CI
Nomogram: AUC=0.8739 (0.7787, 0.9691)
AJCC stage: AUC=0.6601 (0.5132, 0.8071) p < 0.05
C
Nomogram vs AJCC stage
3-year AUC
95% CI
Nomogram: AUC=0.8472 (0.7003, 0.9941)
AJCC stage: AUC=0.6158 (0.4151, 0.8166) p = 0.076
D
Nomogram vs Zhou C et al. Six-gene signature
1-year AUC
95% CI
Nomogram: AUC=0.8908 (0.8062, 0.9754)
Zhou C et al. Six-gene signature: AUC=0.7612 (0.6356, 0.8868) p < 0.05
E
Nomogram vs Zhou C et al. Six-gene signature
2-year AUC
95% CI
Nomogram: AUC=0.8739 (0.7787, 0.9691)
Zhou C et al. Six-gene signature: AUC=0.6782 (0.5246, 0.8318) p < 0.05
F
Nomogram vs Zhou C et al. Six-gene signature
3-year AUC
95% CI
Nomogram: AUC=0.8472 (0.7003, 0.9941)
Zhou C et al. Six-gene signature: AUC=0.6350 (0.4253, 0.8447) p = 0.070
G
Nomogram vs Chen H et al. Three-gene signature
1-year AUC
95% CI
Nomogram: AUC=0.8908 (0.8062, 0.9754)
Chen H et al. Three-gene signature: AUC=0.5616 (0.4167, 0.7066) p < 0.001
H
Nomogram vs Chen H et al. Three-gene signature
2-year AUC
95% CI
Nomogram: AUC=0.8739 (0.7787, 0.9691)
Chen H et al. Three-gene signature: AUC=0.6601 (0.4980, 0.8222) p < 0.05
I
Nomogram vs Chen H et al. Three-gene signature
3-year AUC
95% CI
Nomogram: AUC=0.8472 (0.7003, 0.9941)
Chen H et al. Three-gene signature: AUC=0.5924 (0.2645, 0.9203) p = 0.187
J
Nomogram vs Liao X et al. Nine-gene signature
1-year AUC
95% CI
Nomogram: AUC=0.8908 (0.8062, 0.9754)
Liao X et al. Nine-gene signature: AUC=0.6220 (0.4894, 0.7545) p < 0.01
K
Nomogram vs Liao X et al. Nine-gene signature
2-year AUC
95% CI
Nomogram: AUC=0.8739 (0.7787, 0.9691)
Liao X et al. Nine-gene signature: AUC=0.5451 (0.3686, 0.7215) p < 0.001
L
Nomogram vs Liao X et al. Nine-gene signature
3-year AUC
95% CI
Nomogram: AUC=0.8472 (0.7003, 0.9941)
Liao X et al. Nine-gene signature: AUC=0.3449 (0.1070, 0.5828) p < 0.001
True positive
0.0 0.2 0.4 0.6 0.8 1.0
False positive
0.0 0.2 0.4 0.6 0.8 1.0