

Supplemental table 3

Gene_Symbol	Up/down	Estimate1	NegLog10pEstimate1	Pathways
COL3A1	?	1,147	29,553	cell communication, ECM receptor interaction
THBS4	?	1,086	15,115	cell communication, ECM receptor interaction
SNAI2	?	0,795	9,243	adherens junction
ARF4	?	0,731	11,957	cholera infection
CDKN1B/p27	?	0,700	8,055	cell cycle
RPS19	?	0,616	8,872	ribosome
RPL15	?	0,610	10,369	ribosome
YES1	?	0,597	7,279	adherens junction
COL6A3	?	0,590	7,599	cell communication, ECM receptor interaction
ITGB5	?	0,574	8,079	ECM Receptor interaction
THBS2	?	0,556	11,919	cell communication, ECM receptor interaction
COX7A2L	?	0,545	6,188	oxidative phosphorylation
C15ORF15	?	0,532	7,405	ribosome
SKP1A	?	0,498	5,366	cell cycle, ubiquitin mediated proteolysis
SEC61G	?	0,487	10,001	cholera infection
SDHD	?	0,486	3,593	oxidative phosphorylation
FNDC1	?	0,472	7,287	ECM Receptor interaction
FAU	?	0,462	5,989	Ribosome
UBE2E1	?	0,456	4,094	ubiquitin mediated proteolysis
RPL8	?	0,455	4,877	ribosome
COX7A2	?	0,441	7,586	oxidative phosphorylation
ATP5C1	?	0,437	6,180	ATP synthesis, oxidative phosphorylation
HDAC1	?	0,435	5,908	cell cycle
ALG5	?	0,422	5,202	N glycan biosynthesis
KRT10	?	0,413	19,105	cell communication
RPL30	?	0,412	4,799	ribosome
DPM1	?	0,408	7,389	N glycan biosynthesis
RPL13	?	0,405	5,998	ribosome
PCNA	?	0,402	5,418	cell cycle
PSMB4	?	0,394	13,849	proteasome
RPS21	?	0,393	11,285	ribosome
RPN1	?	0,390	6,714	N glycan biosynthesis
PSMB3	?	0,374	4,336	proteasome
PSMD14	?	0,358	8,103	proteasome
SDC1	?	0,353	7,830	ECM Receptor interaction
SDC2	?	0,347	8,460	ECM Receptor interaction
ITGA6	?	0,337	6,817	cell communication, ECM receptor interaction
DSG1	?	0,332	4,518	cell communication
NDUFA8	?	0,317	3,953	oxidative phosphorylation
HEXB	?	0,315	4,233	Aminosugars metabolism
CDC7	?	0,313	4,697	cell cycle
ATP5E	?	0,312	11,176	ATP synthesis, oxidative phosphorylation
ATP5O	?	0,301	5,640	ATP synthesis, oxidative phosphorylation
PSMD12	?	0,274	7,981	proteasome
PSMB5	?	0,255	4,659	proteasome
HDAC2	?	0,253	4,076	cell cycle
MTMR6	?	0,249	7,175	aminosugars metabolism
CMAS	?	0,245	3,351	aminosugars metabolism
MAP3K7	?	0,238	5,709	adherens junction
MGAT2	?	0,238	6,694	N glycan biosynthesis
ATP6V0B	?	0,230	3,152	ATP synthesis, cholera infection, oxidative phosphorylation
ATP5I	?	0,224	6,363	ATP synthesis, oxidative phosphorylation
CDC23	?	0,218	4,461	cell cycle, ubiquitin mediated proteolysis
ATP6V0E	?	0,216	10,230	ATP synthesis, cholera infection, oxidative phosphorylation
BUB3	?	0,215	11,122	cell cycle
COX5B	?	0,214	5,167	oxidative phosphorylation
NANS	?	0,213	4,514	aminosugars metabolism
CSNK2A2	?	0,208	4,132	adherens junction
PSMD13	?	0,207	3,834	proteasome
PSMA1	?	0,206	3,179	proteasome
NDUFC2	?	0,206	3,742	oxidative phosphorylation

PSMD2	?	0,206	3,322	proteasome
RHOA	?	0,203	4,355	adherens junction
ATP6V0D2	?	0,198	8,047	ATP synthesis, cholera infection, oxidative phosphorylation
ATP6V1A	?	0,198	4,788	ATP synthesis, cholera infection, oxidative phosphorylation
UQCRB	?	0,195	4,917	oxidative phosphorylation
ARF6	?	0,193	3,055	cholera infection
ATP6V1G1	?	0,192	3,799	ATP synthesis, cholera infection, oxidative phosphorylation
EP300	?	0,192	3,190	adherens junction, cell cycle
NDUFA6	?	0,189	4,347	oxidative phosphorylation
UBE2D2	?	0,189	5,498	ubiquitin mediated proteolysis
NDUFS3	?	0,185	3,084	oxidative phosphorylation
CDC2	?	0,184	3,272	cell cycle
BECN1	?	0,179	3,129	regulation of autophagy
COX7C	?	0,176	4,078	oxidative phosphorylation
ACTG1	?	0,176	4,890	adherens junction, cell communication, cholera infection
PVRL3	?	0,175	5,142	adherens junction
CTNND1	?	0,172	7,974	adherens junction
CDKN1C/p57	?	0,165	5,653	cell cycle
UQCRC2	?	0,158	3,580	oxidative phosphorylation
MGAT4A	?	0,152	4,194	N glycan biosynthesis
ST6GAL1	?	0,150	4,218	N glycan biosynthesis
PSMB1	?	0,137	4,594	proteasome
RPL5	?	0,131	3,523	ribosome
TRIM23	?	0,120	3,146	cholera infection
PRKAA1	?	0,109	4,113	regulation of autophagy
ATG5	?	0,108	3,147	regulation of autophagy
ULK2	?	0,096	3,111	regulation of autophagy
PIK3C3	?	0,081	3,040	regulation of autophagy
MLLT4	?	-0,087	3,255	adherens junction
FNTB	?	-0,122	3,841	N glycan biosynthesis
PRKDC	?	-0,138	3,349	cell cycle
MGAT5	?	-0,179	5,151	N glycan biosynthesis
CTNNB1	?	-0,181	4,284	adherens junction
TGFB2	?	-0,199	5,106	cell cycle
FARP2	?	-0,233	5,445	adherens junction
RPN2	?	-0,235	12,761	N glycan biosynthesis
LMNB2	?	-0,237	3,504	cell communication
IGF1R	?	-0,265	7,351	adherens junction
WWP2	?	-0,275	4,102	ubiquitin mediated proteolysis
ANAPC4	?	-0,295	3,535	cell cycle, ubiquitin mediated proteolysis
THBS3	?	-0,297	3,372	cell communication, ECM receptor interaction
LAMB2	?	-0,300	5,859	cell communication, ECM receptor interaction
ANAPC5	?	-0,307	17,809	cell cycle, ubiquitin mediated proteolysis
TCF7L2	?	-0,314	8,916	adherens junction
ATG12	?	-0,328	3,276	regulation of autophagy
COL1A2	?	-0,337	4,193	cell communication, ECM receptor interaction
SPP1	?	-0,347	4,472	cell communication, ECM receptor interaction
GFPT2	?	-0,404	5,410	aminosugars metabolism
GNE	?	-0,470	8,216	aminosugars metabolism
SDC4	?	-0,519	3,341	ECM Receptor interaction