Appendix:

Appendix 1: Top enriched KEGG pathways in treated WT enteroids in comparison to untreated (control) or treated with single agents at 6 and 24 hours.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
0.009245	3	22	18.04765	Proximal tubule bicarbonate reclamation	Atp1b1 Slc25a10 Slc4a4
0.001748	5	56	11.81691	Valine leucine and isoleucine degradation	Aldh6a1 Hadh Hsd17b10 Hibch Acaa2
0.007312	4	47	11.26378	Proteasome	Psmc3 Psma1 Psma6 Psmd8
0.001512	7	120	7.720382	Carbon metabolism	Aldh6a1 Fbp1 Got2 Hk2 Mdh2 Hibch Pgls
0.001748	7	131	7.072105	Spliceosome	Snrpd2 Srsf10 Srsf5 Snrpe Snu13 Thoc1 Prpf38b
4.39E-05	12	228	6.965758	Thermogenesis	Cox6b1 Gnas Hras mt-Nd4 Ndufa4 Prkag1 Smarca4 Sos1 Ndufs8 Cox20 Ndufa5 Smarcd2
0.001748	7	133	6.965758	Oxidative phosphorylation	Cox6b1 Atp6v1a mt-Nd4 Ndufa4 Ndufs8 Ppa1 Ndufa5
0.015484	5	104	6.362952	Glucagon signaling pathway	Fbp1 Gnas Prkag1 Ppp4c Calml4
6.47E-05	12	262	6.061804	Parkinson disease	Cox6b1 Gnas mt-Nd4 Ndufa4 Slc11a2 Psmc3 Ndufs8 Psma1 Psma6 Psmd8 Ndufa5 Calml4
0.009519	6	138	5.754322	Insulin signaling pathway	Fbp1 Hk2 Hras Prkag1 Sos1 Calml4
0.006352	7	173	5.355178	Hepatocellular carcinoma	Cdk4 Gsta4 Hras Smarca4 Sos1 Txnrd2 Smarcd2
0.014876	6	152	5.224318	Biosynthesis of cofactors	Ak4 Gss Alad Spr Cmpk1 Vkorc1l1
0.005371	8	220	4.812705	Chemical carcinogenesis-reactive oxygen species	Cox6b1 Gsta4 Hras mt-Nd4 Ndufa4 Sos1 Ndufs8 Ndufa5
0.000423	13	380	4.527743	Alzheimer disease	Cox6b1 Hsd17b10 Hras mt-Nd4 Ndufa4 Slc11a2 Psmc3 Ndufs8 Psma1 Psma6 Psmd8 Ndufa5 Calml4
0.004157	9	266	4.477987	Prion disease	Cox6b1 mt-Nd4 Ndufa4 Psmc3 Ndufs8 Psma1 Psma6 Psmd8 Ndufa5

0.002267	10	300	4.411647	Huntington disease	Cox6b1 mt-Nd4 Ndufa4 Psmc3 Ndufs8 Psma1 Psma6 Actr10 Psmd8 Ndufa5
0.001144	12	365	4.351213	Amyotrophic lateral sclerosis	Cox6b1 mt-Nd4 Ndufa4 Nup50 Psmc3 Ndufs8 Psma1 Psma6 Actr10 Psmd8 Ndufa5 Nup205
0.017681	7	219	4.230346	Reg. of actin cytoskeleton	Hras Itga2 Itga3 Arhgef1 Cyfip1 Sos1 Myh14
0.001748	13	469	3.668533	Pathways of neurodegeneration-multiple diseases	Cox6b1 Hsd17b10 Hras mt-Nd4 Ndufa4 Psmc3 Ndufs8 Psma1 Psma6 Actr10 Psmd8 Ndufa5 Calml4
5.02E-05	32	1611	2.628914	Metabolic pathways	Aldh6a1 Cox6b1 Ak4 Akr1b3 Atp6v1a Fbp1 Galnt4 Got2 Gss Gsta4 Hadh Hsd17b10 Hk2 Alad Man1a Mif Mdh2 mt-Nd4 Ndufa4 Pafah1b3 Spr Sephs2 Sqle Ndufs8 Hibch Acaa2 Smpd3 Pgls Cmpk1 Ndufa5 Vkorc1l1 Isyna1

Table 6.1: Top 20 enriched KEGG pathways in WT enteroids treated with 5-FU at 0.1 µM for 6 h vs. control healthy enteroids. KEGG pathway was selected by FDR, sorted by fold enrichment.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
0.005457	3	11	27.23554	Sulfur metabolism	Papss1 Papss2 Sqor
3.07E-05	9	88	10.21333	ECM-receptor interaction	Col4a1 Col4a2 Fn1 Hspg2 Itga2 Lama1 Lama5 Itgb4 Vtn
3.07E-05	10	115	8.683794	Nucleocytoplasmic transport	Tpr Ddx19a Kpna1 Ube2i Ahctf1 Nup188 Nup54 Thoc2 Srrm1 Acin1
0.001732	7	93	7.516618	Small cell lung cancer	Bax Col4a1 Col4a2 Fn1 Itga2 Lama1 Lama5
0.007818	6	92	6.512846	Drug metabolism-other enzymes	Ces1d Dut Gsta1 Gsta4 Gstm1 Umps
0.0001	11	170	6.461765	Protein processing in endoplasmic reticulum	Txndc5 Ssr1 Bax Hspa5 Hspa4l Prkcsh Ssr4 Ero1a Sec24d Pdia6 Rrbp1
0.02398	5	80	6.241477	Platinum drug resistance	Bax Casp8 Gsta1 Gsta4 Gstm1
0.015175	6	107	5.59983	Amoebiasis	Col4a1 Col4a2 Fn1 Lama1 Lama5 Prkaca

0.043393	5	101	4.943744	AGE-RAGE signaling pathway in diabetic complications	Bax Col4a1 Col4a2 Fn1 Hras
0.030395	6	131	4.573907	Spliceosome	Snrpe Snu13 Cherp Thoc2 Acin1 Snrpa1
0.006012	9	200	4.493864	Focal adhesion	Col4a1 Col4a2 Fn1 Hras Itga2 Lama1 Lama5 Itgb4 Vtn
0.000675	14	352	3.971849	Human papillomavirus infection	Bax Casp8 Col4a1 Col4a2 Fn1 Hras Itga2 Lama1 Lama5 Prkaca Itgb4 Vtn Tyk2 Ubr4
0.026977	8	220	3.631405	Chemical carcinogenesis-reactive oxygen species	Cox7c Gsta1 Gsta4 Gstm1 Hras Pld1 Uqcrq Ndufa6
0.02398	9	262	3.43043	Parkinson disease	Maob Bax Cox7c Hspa5 Prkaca Psma3 Uqcrq Psmd6 Ndufa6
0.024843	9	266	3.378845	Prion disease	Bax Cox7c Hspa5 Prkaca Psma3 Stip1 Uqcrq Psmd6 Ndufa6
0.000599	18	542	3.316505	Pathways in cancer	Tpr Bax Casp8 Col4a1 Col4a2 Ctbp2 Fn1 Gsta1 Gsta4 Gstm1 Hras Itga2 Kng1 Lama1 Lama5 Arhgef1 Prkaca Pld1
0.007818	12	365	3.283188	Amyotrophic lateral sclerosis	Tpr Bax Cox7c Gpx1 Hspa5 Matr3 Psma3 Uqcrq Nup188 Nup54 Psmd6 Ndufa6
0.043393	10	357	2.797301	PI3K-Akt signaling pathway	Col4a1 Col4a2 Eif4e Fn1 Hras Itga2 Lama1 Lama5 Itgb4 Vtn
0.039166	12	469	2.555146	Pathways of neurodegeneration-multiple diseases	Bax Casp8 Cox7c Gpx1 Hspa5 Hsd17b10 Hras Psma3 Uqcrq Psmd6 Ndufa6 Ppid
0.007818	31	1611	1.921647	Metabolic pathways	Acy1 Maob Dut Pygb Aldh1a1 Aldoa Cox7c Cyp51 Gpx1 Gsta1 Gsta4 Gstm1 Hsd17b10 Mif Pld1 Selenbp1 Ugdh Umps Uqcrq Hibch Uap1l1 Papss1 Papss2 Gnpda1 Coq5 Sqor Cndp2 Pgls Ndufa6 Isyna1 Cyp2s1

Table 6.2: Top 20 enriched KEGG pathways in WT enteroids treated with 5-FU at 0.1 µM for 24 h vs. control healthy enteroids. KEGG pathway was selected by FDR, sorted by fold enrichment.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
0.002862	6	115	10.61353	Nucleocytoplasmic transport	Nup155 Ube2i Thoc1 Ahctf1 Acin1 Nup35
0.032661	5	133	7.647591	Oxidative phosphorylation	Atp5k Cox7c Ndufb7 Ndufv2 Ppa2
0.070079	6	262	4.658609	Parkinson disease	Maob Cox7c Hspa5 Psmd14 Ndufb7 Ndufv2
0.070079	7	365	3.901319	Amyotrophic lateral sclerosis	Cox7c Hspa5 Nup155 Psmd14 Ndufb7 Nup35 Ndufv2
0.085573	4	131	6.211479	Spliceosome	Thoc1 Lsm2 Acin1 Puf60
0.085573	4	125	6.50963	Cell cycle	Bub3 Cdk4 Ywhaq Anapc5
0.086509	16	1611	2.020369	Metabolic pathways	Ndufb4 Acy1 Maob Atp5k Cox7c Hadh Me1 Aldh5a1 Pdxk Pmm2 Rdh7 Sqor Ndufb7 Ndufv2 Gale Cers2
0.086509	5	228	4.461095	Thermogenesis	Atp5k Cox7c Smarca4 Ndufb7 Ndufv2
0.11031	2	27	15.06859	Butanoate metabolism	Hadh Aldh5a1
0.130131	5	266	3.823796	Prion disease	Cox7c Hspa5 Psmd14 Ndufb7 Ndufv2
0.17454	2	38	10.70663	Biosynthesis of nucleotide sugars	Pmm2 Gale
0.195252	3	113	5.400688	Pancreatic secretion	Slc12a2 Clca3b Clca1

Table 6.3: The all enriched KEGG pathways in WT enteroids treated with TNF at 10 ng/mL for 24 h vs. control healthy enteroids. KEGG pathway was selected by FDR, sorted by fold enrichment.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
1.44E-10	11	47	24.14045	Proteasome	Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Psme3 Psma1 Psma6 Psma7 Psmd8 Psmd6
0.000343	5	36	14.32577	Fructose and mannose metabolism	Aldoc Akr1b3 Fbp1 Hk1 Khk
1.93E-10	15	131	11.81056	Spliceosome	Snrpd2 U2af1 Ddx5 Hnrnpc Hnrnpa1 Srsf2 Srsf5 Srsf7 Hnrnpa3 Lsm7 Ctnnbl1 Snrpd3 U2surp Srsf6 Lsm8
1.24E-06	11	130	8.7277	Ribosome	Rpl31 Rpsa Rpl22 Rps14 Rps15 Rps29 Rps3a1 Rpl17 Mrps10 Rpl38 Rps27a
5.28E-06	10	120	8.595462	Carbon metabolism	Aldh6a1 Acat2 Aldoc Dld Fbp1 Got1 Got2 Hk1 Pkm Sdsl
0.001393	6	78	7.934272	Biosynthesis of amino acids	Aldoc Got1 Got2 Pkm Mat2a Sdsl
0.005065	5	66	7.814056	Glycolysis/Gluconeogenesis	Aldoc Dld Fbp1 Hk1 Pkm
1.26E-05	10	133	7.755304	Oxidative phosphorylation	Atp6v1a mt-Nd4 Uqcrc1 Atp5l Atp5j2 Cyc1 Ndufb7 Ppa1 Ndufa5 Ndufb10
6.24E-10	19	262	7.48002	Parkinson disease	Eif2s1 mt-Nd4 Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Txn1 Uqcrc1 Psma1 Psma6 Psma7 Psmd8 Psmd6 Cyc1 Ndufb7 Ndufa5 Ndufb10 Rps27a
1.99E-05	10	141	7.315287	Spinocerebellar ataxia	Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Psma1 Psma6 Psma7 Psmd8 Psmd6
5.54E-09	18	266	6.979773	Prion disease	Csnk2a1 Eif2s1 mt-Nd4 Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Uqcrc1 Psma1 Psma6 Psma7 Psmd8 Psmd6 Cyc1 Ndufb7 Ndufa5 Ndufb10
1.44E-10	23	365	6.499582	Amyotrophic lateral sclerosis	Eif2s1 Hnrnpa1 mt-Nd4 Nup50 Psma2 Psmb4

					Psmb5 Psmb7 Psmc5 Uqcrc1 Srsf7 Hnrnpa3 Psma1 Psma6 Psma7 Actr1a Psmd8 Psmd6 Cyc1 Ndufb7 Ndufa5 Ndufb10 Nup205
1.59E-07	17	300	5.844914	Huntington disease	mt-Nd4 Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Uqcrc1 Psma1 Psma6 Psma7 Actr1a Psmd8 Psmd6 Cyc1 Ndufb7 Ndufa5 Ndufb10
1.59E-07	19	380	5.157277	Alzheimer disease	Ctnnb1 Csnk2a1 Eif2s1 mt-Nd4 Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Uqcrc1 Psma1 Psma6 Psma7 Psmd8 Psmd6 Cyc1 Ndufb7 Ndufa5 Ndufb10
0.002426	8	164	5.03149	Tight junction	Actn1 Cdk4 Cldn3 Myh11 Prkag1 Arpc3 Actn4 Arpc5l
0.0003	11	235	4.828089	Coronavirus disease-COVID-19	Rpl31 Rpsa Rpl22 Rps14 Rps15 Rps29 Rps3a1 Rpl17 Rpl38 Ace2 Rps27a
0.00767	7	152	4.750124	Biosynthesis of cofactors	Ak2 Dld Alad Nme1 Mat2a Cmpk1 Vkorc1l1
1.59E-07	21	469	4.618457	Pathways of neurodegeneration-multiple diseases	Ctnnb1 Csnk2a1 Eif2s1 mt-Nd4 Psma2 Psmb4 Psmb5 Psmb7 Psmc5 Uqcrc1 Psma1 Psma6 Psma7 Actr1a Psmd8 Psmd6 Cyc1 Ndufb7 Ndufa5 Ndufb10 Rps27a
0.001082	10	228	4.523927	Thermogenesis	mt-Nd4 Prkag1 Uqcrc1 Atp5l Actl6a Atp5j2 Cyc1 Ndufb7 Ndufa5 Ndufb10
1.14E-07	42	1611	2.689083	Metabolic pathways	Xylb Aldh6a1 Acaca Cbr3 Fdps Acat2 Ak2 Aldoc Akr1b3 Atp6v1a Cyp2c40 Pcbd1 Dld Fbp1 Got1 Got2 Hk1 Hprt Khk Alad Man1a mt-Nd4 Naga Nme1 Pkm Scp2 Uqcrc1 Mat2a Pfas Pgap1 Sdsl Gcdh Atp5l

					Atp5j2 Nudt2 Cyc1 Cmpk1 Ndufb7 Ndufa5 Ndufb10 Vkorc1l1 Mccc1

Table 6.4: Top 20 enriched KEGG pathways in WT enteroids treated with 5-FU (0.1 µM) +TNF (10 ng/mL) vs. 5-FU (0.1 µM) for 6 h. KEGG pathway was selected by FDR, sorted by fold enrichment.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
3.80E-08	13	130	11.0402	Ribosome	Rpl31 Rpl10a Rpl30 Rpl37a Rpl6 Rps29 Rps3a1 Rpl27a Rpl17 Rplp1 Mrpl1 Mrpl16 Mrpl27
0.017136	4	40	11.0402	Ferroptosis	Cp Gclc Vdac2 Acsl3
0.000668	8	115	7.68014	Nucleocytoplasmic transport	Ran Ahctf1 Nup188 Nup54 Nup98 Thoc2 Ddx39b Nup93
0.026692	5	88	6.272841	ECM-receptor interaction	Col4a1 Col4a2 Hspg2 Lama1 Lamc1
0.047801	4	73	6.049425	Metabolism of xenobiotics by cytochrome P450	Cbr3 Akr7a5 Gsta1 Gsto1
0.02821	5	93	5.935592	Small cell lung cancer	Bax Col4a1 Col4a2 Lama1 Lamc1
0.000165	12	235	5.637549	Coronavirus disease-COVID-19	Fgb Rpl31 Rpl10a Rpl30 Rpl37a Rpl6 Rps29 Rps3a1 Rpl27a Rpl17 Tyk2 Rplp1
0.039706	5	107	5.158972	Amoebiasis	Arg2 Col4a1 Col4a2 Lama1 Lamc1
0.026692	6	131	5.056581	Spliceosome	Eftud2 Prpf19 Thoc2 Ddx39b Snrpd3 Prpf31
0.026692	6	133	4.980542	Oxidative phosphorylation	Atp6v1e1 Uqcrq Atp5o Atp6v1g1 Uqcrb Ndufb10
0.046437	6	164	4.039098	Tight junction	Prkab1 Tuba4a Slc9a3r1 Cldn18 Ppp2r1b Arpc5l
0.046437	7	220	3.512791	Chemical carcinogenesis-reactive oxygen species	Gsta1 Gsto1 Uqcrq Vdac2 Atp5o Uqcrb Ndufb10
0.017136	11	352	3.450063	Human papillomavirus infection	Tubg1 Atp6v1e1 Bax Col4a1 Col4a2 Lama1 Lamc1 Slc9a3r1 Tyk2 Atp6v1g1 Ppp2r1b
0.039706	8	264	3.345515	Endocytosis	Epn1 Hgs Pdcd6ip Ap2s1 Snx3 Snx5 Arpc5l Rab35
0.017136	11	365	3.327184	Amyotrophic lateral sclerosis	Bax Tuba4a Uqcrq Nup188 Nup54 Nup98 Atp5o Vapb Uqcrb Ndufb10 Nup93

0.039706	8	266	3.320361	Prion disease	Bax Tuba4a Uqcrq Vdac2 Lamc1 Atp5o Uqcrb Ndufb10
0.02821	9	300	3.31206	Huntington disease	Bax Tgm2 Tuba4a Uqcrq Vdac2 Ap2s1 Atp5o Uqcrb Ndufb10
0.018837	28	1611	1.918843	Metabolic pathways	Pafah2 Cbr3 Pygb Arg2 Atp6v1e1 Dhfr Gclc Gls Gsta1 Gsto1 Mif Ppt1 Uqcrq Tkfc Pfas Aldh1a7 Atp5o Echdc1 Ptges3 Pgls Atp6v1g1 Cmpk1 Uqcrb Ndufb10 Pycr2 Acsl3 Fads1 Aoc1

Table 6.5: Top 18 enriched KEGG pathways in WT enteroids treated with 5-FU (0.1 µM) +TNF (10 ng/mL) vs. 5-FU (0.1 µM) for 24 h. KEGG pathway was selected by FDR, sorted by fold enrichment.

Enrichment FDR	nGenes	Pathway Genes	Fold Enrichment	Pathway	Genes
1.88E-06	7	31	20.49987	Glyoxylate and dicarboxylate metabolism	Shmt2 Acat2 Aco1 Aco2 Cat Shmt1 Pccb
0.000981	4	20	18.15702	2-Oxocarboxylic acid metabolism	Aco1 Aco2 Got2 Idh2
4.59E-09	12	78	13.96694	Biosynthesis of amino acids	Psat1 Shmt2 Aco1 Aco2 Arg2 Got2 Rpia Shmt1 Mat2a Phgdh Idh2 Eno1b
2.15E-05	7	47	13.52119	Proteasome	Psmb5 Psmb6 Psmc4 Psmd13 Psma1 Psmb2 Psmb3
4.98E-11	16	120	12.10468	Carbon metabolism	Psat1 Shmt2 Acat2 Aco1 Aco2 Adh5 Cat Glud1 Got2 Rpia Shmt1 Phgdh Idh2 Eno1b Pccb Sdha
4.48E-05	7	53	11.99049	Cysteine and methionine metabolism	Adi1 Psat1 Ahcyl Got2 Tst Mat2a Phgdh
0.003331	5	51	8.900502	Tryptophan metabolism	Acat2 Aldh2 Cat Aldh1b1 Aoc1
0.004137	5	54	8.40603	Arginine and proline metabolism	Aldh2 Arg2 Got2 Aldh1b1 Aoc1
0.004663	5	56	8.105815	Valine leucine and isoleucine degradation	Acat2 Aldh2 Pccb Mccc1 Aldh1b1
7.10E-06	11	130	7.681818	Ribosome	Rpl10a Rpl37a Rpl9 Rps3a1 Rps7 Rps27 Rpl23 Rpl36al Rpl14 Rpl38 Rpl22l1
7.10E-06	11	131	7.623178	Spliceosome	Snrpd2 Dhx15 Eftud2 Snrpd1 U2af2 Hnrnpu Snrnp40 Snrpd3 Srsf6 Prpf4 Hnrnpm
5.24E-06	12	152	7.167247	Biosynthesis of cofactors	Psat1 Shmt2 Aldh2 Cpox Shmt1 Cox15 Mat2a Gmppb Pmm2 Gmppa Cad Aldh1b1
0.002533	8	141	5.150929	Spinocerebellar ataxia	Itpr3 Psmb5 Psmb6 Psmc4 Psmd13 Psma1 Psmb2 Psmb3
2.88E-07	20	365	4.974527	Amyotrophic lateral sclerosis	Nup107 Sec13 Cat Itpr3 Kif5b Matr3 mt-Cytb Psmb5 Psmb6 Rac1 Psmc4 Psmd13 Psma1 Psmb2 Psmb3 Vcp Hnrnpa2b1 Ndufb7 Sdha Nup35
0.000166	13	262	4.504605	Parkinson disease	Itpr3 Kif5b mt-Cytb Psmb5 Psmb6 Psmc4 Psmd13 Psma1 Psmb2 Psmb3 Park7 Ndufb7 Sdha

0.000179	13	266	4.436867	Prion disease	Itpr3 Kif5b mt-Cytb Psmb5 Psmb6 Rac1 Psmc4 Psmd13 Psma1 Psmb2 Psmb3 Ndufb7 Sdha
0.000981	11	235	4.249516	Coronavirus disease-COVID-19	Rpl10a Rpl37a Rpl9 Rps3a1 Rps7 Rps27 Rpl23 Rpl36al Rpl14 Rpl38 Rpl22l1
0.000401	15	380	3.583623	Alzheimer disease	Ctnnb1 Ins1 Itpr3 Kif5b mt-Cytb Psmb5 Psmb6 Psmc4 Psmd13 Psma1 Psmb2 Psmb3 Ncstn Ndufb7 Sdha
0.000368	17	469	3.290719	Pathways of neurodegeneration-multiple diseases	Cat Ctnnb1 Itpr3 Kif5b mt-Cytb Psmb5 Psmb6 Rac1 Psmc4 Psmd13 Psma1 Psmb2 Psmb3 Vcp Park7 Ndufb7 Sdha
4.98E-11	53	1611	2.986724	Metabolic pathways	Rpn1 Adi1 Psat1 Shmt2 Fdps Acat2 Aco1 Aco2 Adh5 Ahcyl Aldh2 Arg2 Cat Cpox Fasn Glud1 Got2 Gsta1 Gstt1 Gstz1 mt-Cytb Naga Nsdhl Rpia Shmt1 Tst Cox15 Mat2a Cbr4 Phgdh Impdh2 Papss1 Cers6 Idh2 Gmppb Eno1b Pmm2 Rdh7 Impa1 Ptges3 Pccb Ndufb7 Sdha Gmppa Cad Mccc1 Aldh1b1 Gale Dhcr24 Grhpr Aoc1 Cers2 Lbr

Table 6.6: Top 20 enriched KEGG pathways in WT enteroids treated with 5-FU (0.1 µM) + TNF (10 ng/mL) vs. TNF (10 ng/mL) for 24 h. KEGG pathway was selected by FDR, sorted by fold enrichment.

Appendix 2: Significant proteomic changes in WT enteroids treated with 0.1 µM 5-FU in comparison to untreated enteroids at 6 hours.

Protein	Accession	Gene	p-value	Fold-Change
Rho guanine nucleotide exchange factor 1	Q61210	Arhgef1	0.0101771	5.66282
Serine/threonine-protein phosphatase 4 catalytic subunit	P97470	Ppp4c	0.0464549	4.29278
DNA-directed RNA polymerase I subunit RPA2	P70700	Polr1b	0.0382396	3.65091
SUMO-conjugating enzyme UBC9	P63280	Ube2i	0.00384959	3.57341
Negative elongation factor B	Q8C4Y3	Nelfb	0.0350092	3.56657
Sodium bicarbonate cotransporter 3	Q8BTY2	Slc4a7	0.0014679	3.46221
Transgelin-2	Q9WVA4	Tagln2	0.0309141	3.15415
Anterior gradient protein 2 homolog	O88312	Agr2	0.0103202	2.9957
Hexokinase-2	O08528	Hk2	0.0493485	2.96913
Gem (Nuclear organelle) associated protein 4	Q6P6L6	Gemin4	0.0304982	2.93366
Condensin complex subunit 1	Q8K2Z4	Ncapd2	0.0427576	2.91678
Cytochrome c oxidase subunit 6B1	P56391	Cox6b1	0.0229431	2.85224
Actin-related protein 10	Q9QZB7	Actr10	0.0283886	2.84361
Protein MIX23	Q8R3Q6	Mix23	0.0437168	2.83548
Unconventional myosin-Ic	Q9WTI7	Myo1c	0.0352663	2.76869
Ras-related GTP-binding protein A	Q80X95	Rraga	0.0321701	2.72122
Protein transport protein Sec61 subunit gamma	P60060	Sec61g	0.00694434	2.67176
Growth factor receptor-bound protein 7	Q03160	Grb7	0.00733685	2.6221
CCAAT/enhancer-binding protein zeta	P53569	Cebpz	0.0244518	2.61842
Serine/threonine-protein kinase 24	Q99KH8	Stk24	0.00186193	2.58837
Kinesin-like protein KIF23	E9Q5G3	Kif23	0.0360668	2.49175
39S ribosomal protein L17, mitochondrial	Q9D8P4	Mrpl17	0.0273964	2.41679
Transcription activator BRG1	Q3TKT4	Smarca4	0.0279573	2.38516
SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 2	Q99JR8	Smarcd2	0.00567948	2.35652
Adenylate kinase 4, mitochondrial	Q9WUR9	Ak4	0.0419455	2.33621
Normal mucosa of esophagus-specific gene 1 protein	Q810Q5	Nmes1	0.00792521	2.3277
Sorting nexin-3	O70492	Snx3	0.0160912	2.2887
Cytosolic endo-beta-N-acetylglucosaminidase	Q8BX80	Engase	0.0267257	2.27476
U3 small nucleolar RNA-associated protein 6 homolog	Q8VCY6	Utp6	0.0190546	2.26816
Charged multivesicular body protein 4b	Q9D8B3	Chmp4b	0.000933369	2.25984
2-5A-dependent ribonuclease	Q05921	Rnasel	0.0352989	2.24837
Hsc70-interacting protein	Q99L47	St13	0.0285357	2.22699

BUB3-interacting and GLEBS motif-containing protein ZNF207	Q9JMD0	Znf207	0.0276214	2.20715
NHP2-like protein 1	Q9D0T1	Snu13	0.00149258	2.20365
Dehydrogenase/reductase SDR family member 7B	Q99J47	Dhrs7b	0.0415358	2.20114
Calmodulin-like protein 4	Q91WQ9	Calml4	0.034675	2.19176
Son of sevenless homolog 1	Q62245	Sos1	0.0153407	2.18873
Macrophage migration inhibitory factor	P34884	Mif	0.0128507	2.18118
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	F2Z3U3	Raph1	0.0140958	2.13869
Electrogenic sodium bicarbonate cotransporter 1	O88343	Slc4a4	0.030329	2.12567
Hepatoma-derived growth factor	P51859	Hdgf	0.0260467	2.1199
5'-AMP-activated protein kinase subunit gamma-1	O54950	Prkag1	0.0176936	2.11943
EF-hand domain-containing protein D2	Q9D8Y0	Efhd2	0.0380275	2.10975
Eukaryotic translation initiation factor 1	P48024	Eif1	0.0412235	2.10047
Elongator complex protein 1	Q7TT37	Elp1	0.00709906	2.09946
Nuclear pore complex protein Nup50	Q9JIH2	Nup50	0.015232	2.09545
Mitochondrial dicarboxylate carrier	Q9QZD8	Slc25a10	0.00615933	2.09012
Guanine nucleotide-binding protein G(s) subunit alpha isoforms XLas	Q6R0H7	Gnas	0.0459328	2.07096
NADH dehydrogenase [ubiquinone] iron-sulfur protein 8, mitochondrial	Q8K3J1	Ndufs8	0.018388	2.02723
Cyclin-dependent kinase 4	P30285	Cdk4	0.00500004	2.00443
6-phosphogluconolactonase	Q9CQ60	Pgls	0.0120492	1.99756
NEDD8-conjugating enzyme Ubc12	P61082	Ube2m	0.00283627	1.99285
Thioredoxin reductase 2, mitochondrial	Q9JLT4	Txnrd2	0.0305265	1.97802
Dual specificity protein kinase CLK1	P22518	Clk1	0.0148837	1.97749
Muscleblind-like protein 1	Q9JKP5	Mbnl1	0.0343991	1.95639
Protein ELYS	Q8CJF7	Ahctf1	0.0369192	1.94702
THO complex subunit 1	Q8R3N6	Thoc1	0.0120395	1.94447
COP9 signalosome complex subunit 3	O88543	Cops3	0.0171426	1.93023
Galectin-2	Q9CQW5	Lgals2	0.024001	1.92947
Filamin-A	Q8BTM8	Flna	0.00942369	1.92805
Platelet-activating factor acetylhydrolase IB subunit alpha1	Q61205	Pafah1b3	0.048789	1.92327
UMP-CMP kinase	Q9DBP5	Cmpk1	0.0142822	1.92231
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	Q9JHS4	Clpx	0.0379239	1.9069
Aldo-keto reductase family 1 member B1	P45376	Akr1b1	0.0276786	1.89297
3-hydroxyacyl-CoA dehydrogenase type-2	O08756	Hsd17b10	0.027053	1.88774
X-ray repair cross-complementing protein 5	P27641	Xrcc5	0.0159222	1.85498
Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	P45700	Man1a1	0.00899353	1.82403

Sphingomyelin phosphodiesterase 3	Q9JJY3	Smpd3	0.00561751	1.82111
NADH-ubiquinone oxidoreductase chain 4	P03911	Mtnd4	0.0233675	1.80895
Membrane-associated progesterone receptor component 2	Q80UU9	Pgrmc2	0.000669116	1.80373
60S acidic ribosomal protein P1	P47955	Rplp1	0.0271128	1.78689
Ribosome biogenesis protein BRX1 homolog	Q9DCA5	Brix1	0.0228635	1.78332
Vitamin K epoxide reductase complex subunit 1-like protein 1	Q6TEK5	Vkorc1l1	0.0170761	1.77474
Structural maintenance of chromosomes protein 2	Q8CG48	Smc2	0.0162184	1.76862
Ribonuclease inhibitor	Q91VI7	Rnh1	0.0375308	1.76692
GTPase NRas	P08556	Hras	0.0144525	1.73262
Small integral membrane protein 24	Q0VG18	Smim24	0.0345298	1.7313
Peroxynitrite isomerase THAP4	Q6P3Z3	Thap4	0.0487388	1.69907
Inter-alpha-trypsin inhibitor heavy chain H3	Q61704	Itih3	0.00739484	1.69575
Signal recognition particle subunit SRP72	F8VQC1	Srp72	0.000186543	1.69033
Serine/threonine-protein kinase 38	Q91VJ4	Stk38	0.0129219	1.65888
Small nuclear ribonucleoprotein E	P62305	Snrpe	0.0462956	1.65112
Sulfotransferase family cytosolic 1B member 1	Q9QWG7	Sult1b1	0.0295558	1.62999
Hepatocyte nuclear factor 4-alpha	P49698	Hnf4a	0.0461941	1.60871
Ubiquitin-conjugating enzyme E2 N	P61089	Ube2n	0.00212388	1.59115
Pre-mRNA-splicing factor 38B	Q80SY5	Prpf38b	0.00777527	1.57146
Peptidyl-prolyl cis-trans isomerase FKBP5	Q64378	Fkbp5	0.0289875	1.56826
Pre-mRNA-splicing factor CWC22 homolog	Q8C5N3	Cwc22	0.0294472	1.56242
Nucleoporin 205	A0A0J9YUD5	Nup205	0.00123009	1.53898
Constitutive coactivator of PPAR-gamma-like protein 1	Q6A0A9	FAM120A	0.0477691	1.51335
DnaJ heat shock protein family (Hsp40) member C13	D4AFX7	Dnajc13	0.00853581	1.51258
Mitochondrial import inner membrane translocase subunit TIM50	Q9D880	Timm50	4.04E-06	1.50904
OCIA domain-containing protein 2	Q9D8W7	Ociad2	0.0292617	1.50263
Sorcin	Q6P069	Sri	0.0180091	1.48695
Inorganic pyrophosphatase	Q9D819	Ppa1	0.00897118	1.47735
Cytoplasmic FMR1-interacting protein 1	Q7TMB8	Cyfip1	0.0226813	1.46921
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Q9CPP6	Ndufa5	0.0475532	1.46563
26S proteasome regulatory subunit 6A	O88685	Psmc3	0.0363672	1.46476
Squalene monooxygenase	P52019	Sqle	0.00309592	1.44912
Protein odr-4 homolog	Q4PJX1	Odr4	0.000811542	1.44166
Cytochrome c oxidase subunit NDUFA4	Q62425	Ndufa4	0.0497791	1.41815
Exosome RNA helicase MTR4	Q9CZU3	Mtrex	0.0405829	1.40311
Phenylalanine--tRNA ligase, mitochondrial	Q99M01	Fars2	0.0242605	1.38652

Cytoplasmic dynein 1 light intermediate chain 1	Q8R1Q8	Dync1li1	0.00782685	1.38522
Serine/threonine-protein phosphatase 6 regulatory subunit 3	Q922D4	Ppp6r3	0.0472141	1.37432
Methyltransferase-like 26	Q9DCS2	Mettl26	0.0414137	1.37377
Polypeptide N-acetylgalactosaminyltransferase 4	O08832	Galnt4	0.0355118	1.36841
Serine/threonine-protein kinase OSR1	Q6P9R2	Oxsr1	0.0302943	1.34212
Myosin-14	Q6URW6	Myh14	0.0312892	1.33601
Sepiapterin reductase	Q64105	Spr	0.0244162	1.3221
CDK5 regulatory subunit-associated protein 3	Q99LM2	Cdk5rap3	0.0350099	1.32064
Galectin-1	P16045	Lgals1	0.0217154	-1.33404
Serine/arginine-rich splicing factor 5	O35326	Srsf5	0.0480672	-1.34097
Glutathione synthetase	P51855	Gss	0.0265592	-1.34757
3-ketoacyl-CoA thiolase, mitochondrial	Q8BWT1	Acaa2	0.0299183	-1.38102
Proteasome subunit alpha type-1	Q9R1P4	Psma1	0.0204512	-1.38355
Glutathione S-transferase A4	P24472	Gsta4	0.0322167	-1.38412
Scaffold attachment factor B1	D3YXK2	Safb	0.0317372	-1.38803
26S proteasome non-ATPase regulatory subunit 8	Q9CX56	Psmd8	0.0435376	-1.38948
39S ribosomal protein L15, mitochondrial	Q9CPR5	Mrpl15	0.0105241	-1.39081
Band 4.1-like protein 3	Q9WV92	Epb41l3	0.045588	-1.40954
V-type proton ATPase catalytic subunit A	P50516	Atp6v1a	0.0163926	-1.42282
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	Q8QZS1	Hibch	0.0254557	-1.43542
Endoplasmic reticulum aminopeptidase 1	Q9EQH2	Erap1	0.0478247	-1.46809
Claudin-3	Q9Z0G9	Cldn3	0.0343786	-1.47336
Sodium/potassium-transporting ATPase subunit beta-1	P14094	Atp1b1	0.0452011	-1.47746
Aspartate aminotransferase, mitochondrial	P05202	Got2	0.0182057	-1.48363
Cytochrome c oxidase assembly protein COX20, mitochondrial	Q9D7J4	Cox20	0.00419686	-1.49236
Proteasome subunit alpha type-6	Q9QUM9	Psma6	0.00406423	-1.51985
Malectin	Q6ZQI3	Mlec	0.0494596	-1.52277
Basic leucine zipper and W2 domain-containing protein 2	Q91VK1	Bzw2	0.0477502	-1.533
Ras-related protein Rab-1B	Q9D1G1	Rab1b	0.0117469	-1.53649
Cation-dependent mannose-6-phosphate receptor	P24668	M6pr	0.008085	-1.5441
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	O35459	Ech1	0.0217602	-1.54611
Serine/arginine-rich splicing factor 10	Q9R0U0	Srsf10	0.0160477	-1.55218
Dipeptidyl peptidase 4	P28843	Dpp4	0.0188764	-1.55327
Malate dehydrogenase, mitochondrial	P08249	Mdh2	0.0145295	-1.57886

Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q61425	Hadh	0.0209796	-1.58694
Fibrinogen beta chain	Q8K0E8	Fgb	0.0411226	-1.59499
Protein cornichon homolog 4	Q9CX13	Cnih4	0.0142103	-1.60198
Selenide, water dikinase 2	P97364	Sephs2	0.0156923	-1.64319
Natural resistance-associated macrophage protein 2	P49282	Slc11a2	0.0292322	-1.65648
40S ribosomal protein S15	P62843	Rps15	0.030821	-1.71272
Inositol-3-phosphate synthase 1	Q9JHU9	Isyna1	0.00147694	-1.74296
Double-strand-break repair protein rad21 homolog	Q61550	Rad21	0.0110837	-1.74499
Collagen alpha-1(IV) chain	P02463	Col4a1	0.0137744	-1.76127
Small nuclear ribonucleoprotein Sm D2	P62317	Snrpd2	0.00834006	-1.76639
Integrin alpha-2	Q62469	Itga2	0.0482153	-1.79604
Integrin alpha-3	Q62470	Itga3	0.0192655	-1.80883
DNA repair protein XRCC1	Q60596	Xrcc1	0.00764261	-1.8138
Dehydrogenase/reductase SDR family member 11	Q3U0B3	Dhrs11	0.000555726	-1.83585
Delta-aminolevulinic acid dehydratase	P10518	Alad	0.00346868	-1.90017
Double-stranded RNA-specific adenosine deaminase	Q99MU3	Adar	0.010183	-1.92683
Probable ATP-dependent RNA helicase DDX56	Q9D0R4	Ddx56	0.0221285	-1.94091
Claudin-15	Q9Z0S5	Cldn15	0.00320192	-1.96619
Fucose mutarotase	Q8R2K1	Fuom	0.0391708	-2.04592
Fructose-1,6-bisphosphatase 1	Q9QXD6	Fbp1	0.0031157	-2.05985
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Q9EQ20	Aldh6a1	0.0402073	-2.08244
Transducin beta-like protein 2	Q9R099	Tbl2	0.000521867	-2.08871
Ubiquitin carboxyl-terminal hydrolase 4	P35123	Usp4	0.00296646	-2.11128
40S ribosomal protein S29	P62274	Rps29	0.0251288	-2.14182
Anaphase-promoting complex subunit 5	Q8BTZ4	Anapc5	0.0114708	-2.31065
4F2 cell-surface antigen heavy chain	P10852	Slc3a2	0.000314089	-2.37198
SEC14-like protein 2	Q99J08	Sec14l2	0.0259859	-2.56269
Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4	Q9CWW6	Pin4	0.0285603	-2.58056
Hemopexin	Q91X72	Hpx	0.0204999	-2.822
CD63 antigen	P41731	Cd63	0.0466652	-3.0372

Appendix 3: Significant proteomic changes in WT enteroids treated with 0.1 µM 5-FU in comparison to untreated enteroids at 24 hours.

Protein	Accession	Gene	p-value	Fold-Change
c-Myc-binding protein	Q9EQS3	Mycbp	0.000566817	5.2292
Negative elongation factor B	Q8C4Y3	Nelfb	0.0357996	4.91799
Proteasome assembly chaperone 3	Q9CZH3	Psmg3	7.29E-06	3.52986
Rho guanine nucleotide exchange factor 1	Q61210	Arhgef1	0.0166368	3.52395
Protein ELYS	Q8CJF7	Ahctf1	0.0188342	3.51473
SUMO-conjugating enzyme UBC9	P63280	Ube2i	0.0402676	3.33085
Anterior gradient protein 2 homolog	O88312	Agr2	0.00820107	3.28214
Small integral membrane protein 24	Q0VG18	Smim24	0.0259347	3.12062
Protein MIX23	Q8R3Q6	Mix23	0.0330559	3.0683
Enhancer of rudimentary homolog	P84089	Erh	0.026333	3.01875
Ubiquitin carboxyl-terminal hydrolase 15	Q8R5H1	Usp15	0.0225589	2.56727
Y-box-binding protein 3	Q9JKB3	Ybx3	0.0159666	2.56651
Serine/threonine-protein phosphatase 4 catalytic subunit	P97470	Ppp4c	0.0010519	2.54203
NHP2-like protein 1	Q9D0T1	Snu13	0.0170303	2.42729
Protein phosphatase 1 regulatory subunit 7	Q3UM45	Ppp1r7	0.01294	2.39159
Hsc70-interacting protein	Q99L47	St13	0.0467675	2.37626
U2 small nuclear ribonucleoprotein A'	P57784	Snrpa1	0.0371861	2.35407
Brain-specific angiogenesis inhibitor 1-associated protein 2-like protein 1	Q9DBJ3	Baiap2l1	0.0458347	2.30655
Coatomer subunit epsilon	O89079	Cope	0.0121841	2.26951
Zinc finger CCCH domain-containing protein 15	Q3TIV5	Zc3h15	0.00622139	2.25294
DNA-directed RNA polymerase I subunit RPA2	P70700	Polr1b	0.012653	2.19809
Macrophage migration inhibitory factor	P34884	Mif	0.0206731	2.14258
Splicing factor 1	Q64213	Sf1	0.018825	2.13495
Protein FAM162A	Q9D6U8	Fam162a	0.0191789	2.12133
Stromal cell-derived factor 2	Q9DCT5	Sdf2	0.000884063	2.11374
GTPase NRas	P08556	Hras	0.042086	2.11068
6-phosphogluconolactonase	Q9CQ60	Pgls	0.00321847	2.08579
Sodium bicarbonate cotransporter 3	Q8BTY2	Slc4a7	0.020307	2.0711
Small nuclear ribonucleoprotein E	P62305	Snrpe	0.0364853	2.07088
ERO1-like protein alpha	Q8R180	Ero1a	0.0147771	2.05537
Treacle protein	O08784	Tcof1	0.0268502	2.01628
MICOS complex subunit Mic19	Q9CRB9	Chchd3	0.0153473	1.99859
Transcription factor BTF3	Q64152	Btf3	0.0325075	1.99418
Structural maintenance of chromosomes protein 2	Q8CG48	Smc2	0.00235842	1.96097

Sorting nexin-3	O70492	Snx3	0.0194398	1.9235
Nucleolar complex protein 2 homolog	Q9WV70	Noc2l	0.0149857	1.92248
Gamma-glutamyl hydrolase	Q9Z0L8	Ggh	0.020836	1.87777
Chromobox protein homolog 3	P23198	Cbx3	0.0243553	1.87044
Putative RNA-binding protein Luc7-like 2	Q7TNC4	Luc7l2	0.037793	1.86344
Eukaryotic translation initiation factor 4E	P63073	Eif4e	0.00058914	1.85528
182 kDa tankyrase-1-binding protein	P58871	Tnks1bp1	0.0148927	1.8549
Conserved oligomeric Golgi complex subunit 4	Q8R1U1	Cog4	0.0244273	1.8537
CCA tRNA nucleotidyltransferase 1, mitochondrial	Q8K1J6	Trnt1	0.0308655	1.85319
Stress-induced-phosphoprotein 1	Q60864	Stip1	0.0242525	1.83967
Heterochromatin protein 1-binding protein 3	Q3TEA8	Hp1bp3	0.0366832	1.82409
Barrier-to-autointegration factor	O54962	Banf1	0.0455756	1.7891
Glucosidase 2 subunit beta	O08795	Prkcsh	0.00517031	1.78355
Translocon-associated protein subunit alpha	Q9CY50	Ssr1	0.0458365	1.78
Translationally-controlled tumor protein	P63028	Tpt1	0.0152862	1.77638
Chromogranin-A	P26339	Chga	0.0322486	1.75475
60S acidic ribosomal protein P1	P47955	Rplp1	0.00870547	1.7486
Pescadillo homolog	Q9EQ61	Pes1	0.0376383	1.7451
Serine/arginine repetitive matrix protein 1	Q52KI8	Srrm1	0.0482693	1.74289
Plasminogen activator inhibitor 1 RNA-binding protein	Q9CY58	Serbp1	0.0361811	1.7248
Thioredoxin domain-containing protein 5	Q91W90	Txndc5	0.0362734	1.72397
Mannose-P-dolichol utilization defect 1 protein	Q9R0Q9	Mpdu1	0.012781	1.71143
Membrane-associated progesterone receptor component 2	Q80UU9	Pgrmc2	0.0320246	1.70797
2-hydroxyacyl-CoA lyase 2	Q8BU33	Ilvbl	0.011569	1.70014
Nucleosome assembly protein 1-like 1	P28656	Nap1l1	0.0237058	1.69831
3-hydroxyacyl-CoA dehydrogenase type-2	O08756	Hsd17b10	0.0138474	1.69157
Nucleoprotein TPR	F6ZDS4	Tpr	0.0298457	1.68939
WD repeat-containing protein 3	Q8BHB4	Wdr3	0.00395326	1.68088
DBIRD complex subunit ZNF326	O88291	Znf326	0.00972462	1.67657
Ribonucleoprotein PTB-binding 1	Q9CW46	Raver1	0.0449846	1.67615
Replication factor C subunit 5	Q9D0F6	Rfc5	0.0420178	1.66677
Apoptotic chromatin condensation inducer in the nucleus	Q9JIX8	Acin1	0.0301074	1.66555
Sorcin	Q6P069	Sri	0.00713136	1.6626
Cytochrome c oxidase subunit 7C, mitochondrial	P17665	Cox7c	0.00554866	1.66176
Protein disulfide-isomerase A6	Q922R8	Pdia6	0.0354145	1.6598
Cytochrome P450 2S1	Q9DBX6	Cyp2s1	0.00529584	1.65513
Methanethiol oxidase	P17563	Selenbp1	0.0119622	1.63928

Mitochondrial dicarboxylate carrier	Q9QZD8	Slc25a10	0.000630617	1.63757
Peroxynitrite isomerase THAP4	Q6P3Z3	Thap4	0.0342348	1.63393
Unconventional myosin-Vb	P21271	Myo5b	0.0120447	1.63265
cAMP-dependent protein kinase catalytic subunit alpha	P05132	Prkaca	0.043252	1.62196
Elongation factor 1-delta	P57776	Eef1d	0.0477723	1.62192
DNA topoisomerase 1	Q04750	Top1	0.0496534	1.61792
Protein Red	Q9Z1M8	Ik	0.0350639	1.61691
Nucleophosmin	Q61937	Npm1	0.0351171	1.60858
Carboxylesterase 1D	Q8VCT4	Ces1d	0.0190777	1.60163
Ribosome-binding protein 1	Q99PL5	Rrbp1	0.0263483	1.6014
Normal mucosa of esophagus-specific gene 1 protein	Q810Q5	Nmes1	0.0378168	1.59585
ATP-dependent RNA helicase DDX19A	Q61655	Ddx19a	0.0435938	1.59413
SH3 domain-binding glutamic acid-rich-like protein 3	Q91VW3	Sh3bgrl3	0.0271429	1.58244
Calcium-binding mitochondrial carrier protein Aralar2	Q9QXX4	Slc25a13	0.0255365	1.57727
Claudin-18	P56857	Cldn18	0.00814801	1.5764
Cytochrome b-c1 complex subunit 8	Q9CQ69	Uqcrq	0.0333452	1.55498
Condensin complex subunit 1	Q8K2Z4	Ncapd2	0.0094308	1.5532
Calcium homeostasis endoplasmic reticulum protein	Q8CGZ0	Cherp	0.028593	1.55251
FACT complex subunit SSRP1	Q08943	Ssrp1	0.041344	1.53167
ATP-binding cassette sub-family F member 1	Q6P542	Abcf1	0.0469561	1.52823
Endoplasmic reticulum chaperone BiP	P20029	Hspa5	0.0448009	1.52782
Transmembrane protein 14C	Q9CQN6	Tmem14c	0.0477494	1.52743
Caspase-8	O89110	Casp8	0.0139371	1.52032
R3H and coiled-coil domain-containing protein 1	Q8BSI6	R3hcc1	0.0242368	1.51966
Nuclear pore complex protein Nup54	Q8BTS4	Nup54	0.0261398	1.51188
Fructose-bisphosphate aldolase A	P05064	Aldoa	0.0470299	1.50293
Histone H4	P62806	H4f16	0.000600167	1.4966
Vacuolar protein sorting-associated protein 4B	P46467	Vps4b	0.0156669	1.49419
Importin subunit alpha-7	O35345	Kpna1	0.0486609	1.48927
X-ray repair cross-complementing protein 5	P27641	Xrcc5	0.0063841	1.48862
THO complex subunit 2	B1AZI6	Thoc2	0.0348982	1.48021
Uridine 5'-monophosphate synthase	P13439	Umps	0.00948752	1.47737
Aprataxin and PNK-like factor	Q9D842	Aplf	0.0488669	1.47734
N-alpha-acetyltransferase 50	Q6PGB6	Naa50	0.0298159	1.47714
Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial	Q9D172	Gatd3a	0.039442	1.47621

2-methoxy-6-polyprenyl-1,4-benzoquinol methylase, mitochondrial	Q9CXI0	Coq5	0.00333394	1.46388
C-terminal-binding protein 2	P56546	Ctbp2	0.00371339	1.46314
Histone H3.3C	P02301	H3-3b	0.00140997	1.45214
E3 ubiquitin-protein ligase LRSAM1	Q80ZI6	Lrsam1	0.00389835	1.42888
UDP-N-acetylhexosamine pyrophosphorylase-like protein 1	Q3TW96	Uap1l1	0.0429382	1.42828
Transcription elongation factor A protein 1	P10711	Tcea1	0.0440138	1.42415
Heterogeneous nuclear ribonucleoprotein U-like protein 1	Q8VDM6	Hnrnpul1	0.0300443	1.41572
Protein VAC14 homolog	Q80WQ2	Vac14	0.0441964	1.41517
Protein numb homolog	Q9QZS3	Numb	0.0188076	1.40835
Peptidyl-prolyl cis-trans isomerase D	Q9CR16	Ppid	0.00762947	1.3838
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 6	Q9CQZ5	Ndufa6	0.0311387	1.37554
Ras GTPase-activating protein-binding protein 1	P97855	G3bp1	0.0317966	1.36848
Protein flightless-1 homolog	Q9JJ28	Flii	0.0435508	1.35254
OCIA domain-containing protein 2	Q9D8W7	Ociad2	0.0453108	1.34772
Proteasome subunit alpha type-3	O70435	Psma3	0.0256275	1.34346
Cytosolic endo-beta-N-acetylglucosaminidase	Q8BX80	Engase	0.0250328	1.34003
Cytoplasmic dynein 1 light intermediate chain 1	Q8R1Q8	Dync1li1	0.00960253	1.30115
Stress-70 protein, mitochondrial	P38647	Hspa9	0.0218417	1.28432
Rho GTPase-activating protein 1	Q5FWK3	Arhgap1	0.0139371	1.27937
Activator of 90 kDa heat shock protein ATPase homolog 1	Q8BK64	Ahsa1	0.0414186	1.26702
Translocon-associated protein subunit delta	Q62186	Ssr4	0.0305065	1.25797
Matrin-3	Q8K310	Matr3	0.0301141	1.24875
Lanosterol 14-alpha demethylase	Q8K0C4	Cyp51a1	0.0247625	1.24561
MICOS complex subunit Mic60	Q8CAQ8	Immt	0.0415268	1.24305
26S proteasome non-ATPase regulatory subunit 6	Q99JI4	Psmd6	0.025314	1.22134
Programmed cell death 6-interacting protein	Q9WU78	Pdcd6ip	0.0491862	1.17423
Tubby-related protein 4	Q9JIL5	Tulp4	0.0186853	-1.18958
Glycogen phosphorylase, brain form	Q8CI94	Pygb	0.0169506	-1.29708
DNA repair protein XRCC1	Q60596	Xrcc1	0.0443792	-1.33355
Conserved oligomeric Golgi complex subunit 3	Q8CI04	Cog3	0.0421746	-1.34283
Glutathione S-transferase A4	P24472	Gsta4	0.00571754	-1.36147
Nucleoporin NUP188	Q6ZQH8	Nup188	0.0396973	-1.37026
Putative helicase MOV-10	P23249	Mov10	0.00138979	-1.39036
Band 4.1-like protein 3	Q9WV92	Epb41l3	0.0373356	-1.39217

WD40 repeat-containing protein SMU1	Q3UKJ7	Smu1	0.0258217	-1.40411
Inositol-3-phosphate synthase 1	Q9JHU9	Isyna1	0.0186957	-1.41877
Transmembrane 9 superfamily member 3	Q9ET30	Tm9sf3	0.0131055	-1.46152
Aminoacylase-1	Q99JW2	Acy1	0.044976	-1.46186
Nuclear cap-binding protein subunit 3	Q8BZR9	Ncbp3	0.0224287	-1.48217
UDP-glucose 6-dehydrogenase	O70475	Ugdh	0.0384841	-1.48299
Deoxyuridine 5'-triphosphate nucleotidohydrolase	Q8VCG1	Dut	0.0380121	-1.48387
28S ribosomal protein S27, mitochondrial	Q8BK72	Mrps27	0.0226395	-1.50807
Apoptosis regulator BAX	Q07813	Bax	0.0382824	-1.50813
cAMP-dependent protein kinase type II-alpha regulatory subunit	P12367	Prkar2a	0.0410673	-1.50892
HEAT repeat-containing protein 1	G3X9B1	Heatr1	0.0358513	-1.51974
Sulfide:quinone oxidoreductase, mitochondrial	Q9R112	Sqor	0.0271719	-1.5298
Vesicle-trafficking protein SEC22b	O08547	Sec22b	0.0184456	-1.60931
Amine oxidase [flavin-containing] B	Q8BW75	Maob	0.0158765	-1.62209
39S ribosomal protein L2, mitochondrial	Q9D773	Mrpl2	0.0258574	-1.62226
E3 ubiquitin-protein ligase UBR4	A2AN08	Ubr4	0.036475	-1.64132
Sec24-related gene family, member D (S. cerevisiae)	Q6NXL1	Sec24d	0.00118348	-1.65238
3-hydroxyisobutyryl-CoA hydrolase, mitochondrial	Q8QZS1	Hibch	0.00673031	-1.6656
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	Q60967	Papss1	0.0162426	-1.67909
Sterol O-acyltransferase 2	O88908	Soat2	0.0309392	-1.68332
Methionine aminopeptidase 2	O08663	Metap2	0.0243909	-1.68373
Unconventional myosin-IXb	Q9QY06	Myo9b	0.04447	-1.69161
Cytosolic non-specific dipeptidase	Q9D1A2	Cndp2	0.0185329	-1.69249
N-terminal kinase-like protein	Q9EQC5	Scyl1	0.00421748	-1.69837
Glutathione S-transferase A2	P10648	Gsta1	0.015944	-1.70296
Mucin-4	Q8JZM8	Muc4	0.0379369	-1.70429
Vitronectin	P29788	Vtn	0.0414337	-1.74054
Integrin alpha-2	Q62469	Itga2	0.0218304	-1.75357
Glutathione S-transferase Mu 1	P10649	Gstm1	0.0410603	-1.75681
Dehydrogenase/reductase SDR family member 11	Q3U0B3	Dhrs11	0.00442912	-1.76594
Coronin-7	Q9D2V7	Coro7	0.0208144	-1.77587
Fibronectin	P11276	Fn1	0.00297288	-1.82628
A-kinase anchor protein 9	Q70FJ1	Akap9	0.011255	-1.84836
Swi5-dependent recombination DNA repair protein 1 homolog	Q8BP27	Sfr1	0.000367872	-1.85438
Integrin beta-4	A2A863	Itgb4	0.00838198	-1.85703
40S ribosomal protein S29	P62274	Rps29	0.0375071	-1.85947

Glucosamine-6-phosphate isomerase 1	O88958	Gnpda1	0.0374535	-1.8648
Lysine-specific demethylase 9	Q80T69	Rsbn1	0.0342519	-1.8728
Kininogen-1	O08677	Kng1	0.00883257	-1.87887
Collagen alpha-1(XVIII) chain	P39061	Col18a1	0.00610847	-1.88385
Laminin subunit alpha-5	Q61001	Lama5	0.0165522	-1.88945
Fibulin-1	Q08879	Fbln1	0.000712789	-1.94632
Protein mono-ADP-ribosyltransferase PARP14	Q2EMV9	Parp14	0.0252474	-1.94732
Phospholipase D1	Q9Z280	Pld1	0.00830082	-1.95187
SPRY domain-containing protein 4	Q91WK1	Spryd4	0.0162131	-1.95626
Endonuclease G, mitochondrial	O08600	Endog	0.00671909	-1.97347
Lymphocyte-specific helicase	Q60848	Hells	0.0417262	-1.97838
Fibrinogen beta chain	Q8K0E8	Fgb	0.00459928	-1.9913
Pro-cathepsin H	P49935	Ctsh	0.00799918	-1.99438
Fibrinogen gamma chain	Q8VCM7	Fgg	0.0140291	-2.00088
[F-actin]-monooxygenase MICAL1	Q8VDP3	Mical1	0.0133273	-2.01849
Collagen alpha-2(IV) chain	P08122	Col4a2	0.00172993	-2.01969
Nidogen-2	O88322	Nid2	0.0211276	-2.03492
SWI/SNF complex subunit SMARCC2	Q6PDG5	Smarcc2	0.0122674	-2.06302
Double-stranded RNA-specific adenosine deaminase	Q99MU3	Adar	0.0071805	-2.07035
Murinoglobulin-1	P28665	Mug1	0.001267	-2.0969
Cadherin-like and PC-esterase domain-containing 1	B2RX70	Cped1	0.0476902	-2.11749
Serotransferrin	Q921I1	Tf	0.0245818	-2.12473
SPARC	P07214	Sparc	0.00249745	-2.13934
Laminin subunit alpha-1	P19137	Lama1	0.0210726	-2.1876
Tubulointerstitial nephritis antigen-like	Q99JR5	Tinagl1	0.00364143	-2.19603
Protein S100-G	P97816	S100g	0.00388215	-2.22288
Nidogen-1	P10493	Nid1	0.0172082	-2.22758
Basement membrane-specific heparan sulfate proteoglycan core protein	Q05793	Hspg2	0.00632381	-2.24125
Retinol-binding protein 2	Q08652	Rbp2	0.0212098	-2.24853
Activating signal cointegrator 1 complex subunit 3	E9PZJ8	Ascc3	0.0437636	-2.27064
Elongator complex protein 3	Q9CZX0	Elp3	0.0108854	-2.28638
Peroxidasin homolog	Q3UQ28	Pxdn	0.0171908	-2.32136
Ras-related protein Rab-35	Q6PHN9	Rab35	0.0384264	-2.36044
Collagen alpha-1(IV) chain	P02463	Col4a1	0.00125665	-2.36124
Retinal dehydrogenase 1	P24549	Aldh1a1	0.0248959	-2.45564
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 2	O88428	Papss2	0.0429087	-2.46737
Non-receptor tyrosine-protein kinase TYK2	Q9R117	Tyk2	0.0286284	-2.49149
Lysyl oxidase homolog 2	P58022	Loxl2	0.00441191	-2.51494

Probable E3 ubiquitin-protein ligase IRF2BPL	Q8K3X4	Irf2bpl	0.0384438	-2.66897
Glutathione peroxidase 1	P11352	Gpx1	0.0320656	-2.82186
Ceruloplasmin	Q61147	Cp	0.0115094	-2.83559
Transcription factor 20	Q9EPQ8	Tcf20	0.00152467	-2.87385
Potassium channel tetramerisation domain-containing 14	A0A0U1RNG7	Kctd14	0.00161383	-3.06309
Heat shock 70 kDa protein 4L	P48722	Hspa4l	0.0147076	-3.28959
Inner nuclear membrane protein Man1	Q9WU40	Lemd3	0.011474	-3.54765
Voltage-dependent T-type calcium channel subunit alpha	Q5SUF7	Cacna1g	0.0371174	-4.02135
WD repeat domain 86	D3Z757	Wdr86	0.0071819	-4.33965
39S ribosomal protein L11, mitochondrial	Q9CQF0	Mrpl11	0.00026434	-19.67

Appendix 4: Significant proteomic changes in WT enteroids treated with 10 ng/mL TNF in comparison to untreated enteroids at 24 hours.

Protein	Accession	Gene	p-value	Fold-Change
Chromogranin-A	P26339	Chga	0.0037249	4.319206648
Protein ELYS	Q8CJF7	Ahctf1	0.0103546	3.095304423
SUMO-conjugating enzyme UBC9	P63280	Ube2i	0.0402697	3.053565649
Coiled-coil-helix-coiled-coil-helix domain-containing protein 2	Q9D1L0	Chchd2	0.0288604	3.015490575
Clathrin interactor 1	Q99KN9	Clint1	0.0346615	2.959674436
Protein MIX23	Q8R3Q6	Mix23	0.0337355	2.736876676
Interferon-inducible double-stranded RNA-dependent protein kinase activator A	Q9WTX2	Prkra	8.38E-06	2.725627439
Endothelial differentiation-related factor 1	Q9JMG1	Edf1	0.0189783	2.690196922
Paraspeckle component 1	Q8R326	Pspc1	0.041731	2.663803965
EF-hand domain-containing protein D2	Q9D8Y0	Efhd2	0.0309867	2.470447274
BUB3-interacting and GLEBS motif-containing protein ZNF207	Q9JMD0	Znf207	0.0119766	2.434778374
Tropomyosin alpha-3 chain	P21107	Tpm3	0.0433695	2.39280245
Mitochondrial fission 1 protein	Q9CQ92	Fis1	0.0118354	2.369701939
Sodium bicarbonate cotransporter 3	Q8BTY2	Slc4a7	0.0219569	2.294162046
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 4	Q9CQC7	Ndufb4	0.000125748	2.264815859
Tubulin-specific chaperone A	P48428	Tbca	0.0218684	2.206205173
Translationally-controlled tumor protein	P63028	Tpt1	0.00456579	2.153914416
Stromal cell-derived factor 2	Q9DCT5	Sdf2	0.0213681	2.141754139
28S ribosomal protein S7, mitochondrial	Q80X85	Mrps7	0.000356106	2.131482638
NADH dehydrogenase [ubiquinone] flavoprotein 2, mitochondrial	Q9D6J6	Ndufv2	0.0104157	2.117733263

SH3 domain-binding glutamic acid-rich-like protein 3	Q91VW3	Sh3bgrl3	0.0390356	2.116850127
High mobility group protein B3	O54879	Hmgb3	0.00216728	2.111611328
RNA polymerase II-associated protein 1	Q80TE0	Rpap1	0.0264991	2.097099921
Protein phosphatase 1 regulatory subunit 7	Q3UM45	Ppp1r7	0.0228195	2.084458072
Chloride channel accessory 3B	E9PUL3	Clca3b	0.0481557	2.079853911
CDK5 regulatory subunit-associated protein 3	Q99LM2	Cdk5rap3	0.00364201	2.075692191
Dual specificity protein kinase CLK1	P22518	Clk1	0.00807307	1.983280942
THO complex subunit 1	Q8R3N6	Thoc1	0.0291732	1.980617675
Nucleoporin NUP35	Q8R4R6	Nup35	0.0314192	1.97315717
Ran-specific GTPase-activating protein	P34022	Ranbp1	0.0496064	1.912700523
Cyclin-dependent kinase 4	P30285	Cdk4	0.0330768	1.902873529
NEDD8-conjugating enzyme Ubc12	P61082	Ube2m	0.00946588	1.884289547
Coatomer subunit epsilon	O89079	Cope	0.0146895	1.830506117
Transcription activator BRG1	Q3TKT4	Smarca4	0.0361025	1.827171502
Conserved oligomeric Golgi complex subunit 4	Q8R1U1	Cog4	0.00111242	1.815649812
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	Q9CR61	Ndufb7	0.0239082	1.765864081
Structural maintenance of chromosomes protein 2	Q8CG48	Smc2	0.0269007	1.730364259
MYG1 exonuclease	Q9JK81	Myg1	0.00696524	1.702072614
Mitochondrial dicarboxylate carrier	Q9QZD8	Slc25a10	0.0118016	1.701435501
NHL repeat-containing protein 2	Q8BZW8	Nhlrc2	0.0444078	1.660655095
Inorganic pyrophosphatase 2, mitochondrial	Q91VM9	Ppa2	0.0296533	1.656989846
Probable 28S rRNA (cytosine-C(5))-methyltransferase	Q922K7	Nop2	0.000693525	1.648913366
Presequence protease, mitochondrial	Q8K411	Pitrm1	0.040621	1.642661901
Sorcin	Q6P069	Sri	1.61E-05	1.641642562
Mannose-P-dolichol utilization defect 1 protein	Q9R0Q9	Mpdu1	0.0473663	1.627000397
40S ribosomal protein S21	Q9CQR2	Rps21	0.0236721	1.615467128
Pescadillo homolog	Q9EQ61	Pes1	0.0312861	1.614212821
Apoptotic chromatin condensation inducer in the nucleus	Q9JIX8	Acin1	0.033523	1.612107573
Nuclear pore complex protein Nup155	Q99P88	Nup155	0.0114209	1.589117722
U6 snRNA-associated Sm-like protein LSm2	O35900	Lsm2	0.0336139	1.586314547
60S acidic ribosomal protein P1	P47955	Rplp1	0.0241463	1.571837698
Cytochrome c oxidase subunit 7C, mitochondrial	P17665	Cox7c	0.036215	1.548330358
Heterogeneous nuclear ribonucleoprotein U-like protein 1	Q8VDM6	Hnrnpul1	0.012499	1.542386318
Ras GTPase-activating protein-binding protein 1	P97855	G3bp1	0.0018541	1.538094762

Protein FAM162A	Q9D6U8	Fam162a	0.00261679	1.524929548
Filamin-B	Q80X90	Flnb	0.0305045	1.522132569
Histone H4	P62806	H4f16	0.0414677	1.491733558
ATP synthase subunit e, mitochondrial	Q06185	Atp5me	0.0136081	1.481841514
Solute carrier family 12 member 2	P55012	Slc12a2	0.0264564	1.473053434
DnaJ heat shock protein family (Hsp40) member C13	D4AFX7	Dnajc13	0.00313304	1.465497786
Toll-interacting protein	Q9QZ06	Tollip	0.0401653	1.430252997
Peflin	Q8BFY6	Pef1	0.00286483	1.423503755
Calcium-activated chloride channel regulator 1	Q9D7Z6	Clca1	0.0320606	1.358706729
Succinate-semialdehyde dehydrogenase, mitochondrial	Q8BWF0	Aldh5a1	0.049524	1.346908374
Eukaryotic translation initiation factor 4E	P63073	Eif4e	0.0140321	1.345809888
Poly(U)-binding-splicing factor PUF60	Q3UEB3	Puf60	0.0171598	1.342710826
14-3-3 protein theta	P68254	Ywhaq	0.0444218	1.337674533
Ketosamine-3-kinase	Q8K274	Fn3krp	0.0233697	1.332714954
26S proteasome non-ATPase regulatory subunit 14	O35593	Psmd14	0.00204921	1.329165072
Endoplasmic reticulum chaperone BiP	P20029	Hspa5	0.0409766	1.289236295
Hydroxyacyl-coenzyme A dehydrogenase, mitochondrial	Q61425	Hadh	0.0434	-1.33956
UDP-glucose 4-epimerase	Q8R059	Gale	0.0326406	-1.35752
Aldo-keto reductase family 1 member C13	Q8VC28	Akr1c13	0.0389713	-1.36241
Sulfide:quinone oxidoreductase, mitochondrial	Q9R112	Sqor	0.0387972	-1.38686
Mitotic checkpoint protein BUB3	Q9WVA3	Bub3	0.00645414	-1.39927
Perilipin-3	Q9DBG5	Plin3	0.0348883	-1.43456
Phosphatidylinositol transfer protein alpha isoform	P53810	Pitpna	0.0395551	-1.48907
Phosphomannomutase 2	Q9Z2M7	Pmm2	0.035563	-1.49992
Protein RER1	Q9CQU3	Rer1	0.0232194	-1.50314
Isochorismatase domain-containing protein 1	Q91V64	Isoc1	0.0112486	-1.50341
Band 4.1-like protein 3	Q9WV92	Epb41l3	0.0240391	-1.53721
Aldo-keto reductase a	Q9JLI0	Akr1c12	0.00597032	-1.59305
Ceramide synthase 2	Q924Z4	Cers2	0.0278237	-1.60422
RNA-binding protein 15	Q0VBL3	Rbm15	0.00681148	-1.62598
Huntingtin-interacting protein 1-related protein	Q9JKY5	Hip1r	0.00904336	-1.62723
High mobility group protein 20A	Q9DC33	Hmg20a	0.0133258	-1.62861
Methyltransferase-like 26	Q9DCS2	Mettl26	0.0270863	-1.65907
39S ribosomal protein L41, mitochondrial	Q9CQN7	Mrpl41	0.0488454	-1.71522
Carboxylic ester hydrolase	E9PV38	Ces2g	0.0452318	-1.71965

WD40 repeat-containing protein SMU1	Q3UKJ7	Smu1	0.0161029	-1.72101
NADP-dependent malic enzyme	P06801	Me1	0.0482729	-1.73505
Cysteine and histidine-rich domain-containing protein 1	Q9D1P4	Chordc1	0.0250951	-1.73797
Vesicle-trafficking protein SEC22b	O08547	Sec22b	0.00380838	-1.73893
Pyridoxal kinase	Q8K183	Pdxk	0.0191649	-1.79627
Apoptosis facilitator Bcl-2-like protein 14	Q9CPT0	Bcl2l14	0.0435274	-1.80812
Aminoacylase-1	Q99JW2	Acy1	0.0144731	-1.85937
Vacuole membrane protein 1	Q99KU0	Vmp1	0.0313683	-1.87168
Amine oxidase [flavin-containing] B	Q8BW75	Maob	0.00889969	-1.88817
Coronin-7	Q9D2V7	Coro7	0.0298519	-1.92436
Pro-cathepsin H	P49935	Ctsh	0.0195595	-1.9336
Heat shock 70 kDa protein 14	Q99M31	Hspa14	0.013457	-1.99663
ER membrane protein complex subunit 2	Q9CRD2	Emc2	0.0488132	-2.00846
3-alpha-hydroxysteroid dehydrogenase type 1	Q91WT7	Akr1c14	0.0433259	-2.1016
HEAT repeat-containing protein 1	G3X9B1	Heatr1	0.00455536	-2.11209
Pseudouridylate synthase 7 homolog	Q91VU7	Pus7	0.0413377	-2.31189
Fatty acid-binding protein, liver	P12710	Fabp1	0.0321483	-2.41053
Retinol dehydrogenase 7	O88451	Rdh7	0.0118972	-2.45887
Anaphase-promoting complex subunit 5	Q8BTZ4	Anapc5	0.0204977	-2.47539
Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	Usp7	0.0280752	-3.9029

Appendix 5: Significant proteomic changes in WT enteroids treated with 0.1 µM 5-FU + 10 ng/mL TNF in comparison to WT enteroids treated with 0.1 µM 5-FU alone at 6 hours.

Protein	Accession	Gene	p-value	Fold-Change
Angiotensin-converting enzyme 2	Q8R0I0	Ace2	0.00328198	3.91937
Serine dehydratase-like	Q8R238	Sdsl	0.0101495	3.23241
40S ribosomal protein S29	P62274	Rps29	0.0318747	3.07925
Hemopexin	Q91X72	Hpx	0.00613039	2.56914
RNA polymerase II subunit A C-terminal domain phosphatase SSU72	Q9CY97	Ssu72	0.00457534	2.51308
Anaphase-promoting complex subunit 5	Q8BTZ4	Anapc5	0.00289205	2.50542
28S ribosomal protein S10, mitochondrial	Q80ZK0	Mrps10	0.00187861	2.50388
CD63 antigen	P41731	Cd63	0.00316919	2.44088
Pterin-4-alpha-carbinolamine dehydratase	P61458	Pcbd1	0.00327687	2.39129
F-box-like/WD repeat-containing protein TBL1X	Q9QXE7	Tbl1x	0.00983768	2.30738
Beta-2-syntrophin	Q61235	Sntb2	0.0415514	2.26043
Methylmalonate-semialdehyde dehydrogenase [acylating], mitochondrial	Q9EQ20	Aldh6a1	0.0207006	2.08867

eIF-2-alpha kinase activator GCN1	E9PVA8	Gcn1	0.0289407	2.0519
Myosin-11	O08638	Myh11	0.00442145	2.03787
Fructose-1,6-bisphosphatase 1	Q9QXD6	Fbp1	0.0438718	2.00994
Fatty acid-binding protein 5	Q05816	Fabp5	0.0435646	1.96486
Ras-related protein Ral-B	Q9JIW9	Ralb	0.0257063	1.94751
Claudin-3	Q9Z0G9	Cldn3	0.00444524	1.93139
Serine/arginine-rich splicing factor 2	Q62093	Srsf2	0.0433708	1.90878
Glutaryl-CoA dehydrogenase, mitochondrial	Q60759	Gcdh	0.0465091	1.90309
U6 snRNA-associated Sm-like protein LSm8	Q6ZWM4	Lsm8	0.010844	1.88142
Serine/arginine-rich splicing factor 7	Q8BL97	Srsf7	0.0386847	1.85455
Protein kish-A	Q9CR64	Tmem167a	0.0370837	1.85209
Protein SGT1 homolog	Q9CX34	Sugt1	0.00388143	1.83053
Craniofacial development protein 1	O88271	Cfdp1	0.0357318	1.81929
Transducin beta-like protein 2	Q9R099	Tbl2	0.0459761	1.8076
Small nuclear ribonucleoprotein Sm D2	P62317	Snrpd2	0.0140427	1.79672
RNA pseudouridylate synthase domain-containing protein 2	Q149F1	Rpusd2	0.0460934	1.79271
Tetraspanin-8	Q8R3G9	Tspan8	0.00349677	1.78778
Tether containing UBX domain for GLUT4	Q8VBT9	Aspscr1	0.03965	1.78109
Delta-aminolevulinic acid dehydratase	P10518	Alad	0.0220686	1.77912
RNA-binding protein with serine-rich domain 1	Q99M28	Rnps1	0.0369227	1.77663
Ras GTPase-activating protein-binding protein 2	P97379	G3bp2	0.0224796	1.77015
Basic leucine zipper and W2 domain-containing protein 2	Q91VK1	Bzw2	0.012966	1.76733
40S ribosomal protein S15	P62843	Rps15	0.0186974	1.74466
Alpha-N-acetylgalactosaminidase	Q9QWR8	Naga	0.00107246	1.73094
Fructose-bisphosphate aldolase C	P05063	Aldoc	0.0213552	1.72606
Splicing factor U2AF 35 kDa subunit	Q9D883	U2af1	0.0133309	1.71373
Aspartate aminotransferase, cytoplasmic	P05201	Got1	0.037467	1.71017
Ras-related protein Rab-5C	P35278	Rab5c	0.0156585	1.70502
COP9 signalosome complex subunit 5	O35864	Cops5	0.0190964	1.70465
Calcyclin-binding protein	Q9CXW3	Cacybp	0.0193415	1.70001
Actin-like protein 6A	Q9Z2N8	Actl6a	0.0130817	1.69349
Beta-catenin-like protein 1	Q9CWL8	Ctnnbl1	0.0171585	1.69038
40S ribosomal protein S14	P62264	Rps14	0.00132187	1.67675
Integrin alpha-3	Q62470	Itga3	0.047635	1.67551
Proteasome subunit alpha type-6	Q9QUM9	Psma6	0.0127275	1.66689
RNA binding motif protein, X-linked-like-1	Q91VM5	Rbmxl1	0.020602	1.65801
Peptidyl-prolyl cis-trans isomerase B	P24369	Ppib	0.0153332	1.65412
Serine/arginine-rich splicing factor 6	Q3TWW8	Srsf6	0.00751312	1.63796
WD repeat domain 36	Q3TAQ9	Wdr36	0.0499458	1.63469

Hypoxanthine-guanine phosphoribosyltransferase	P00493	Hprt1	0.0163807	1.6246
Rho GDP-dissociation inhibitor 1	Q99PT1	Arhgdia	0.013899	1.6223
Phosphoribosylformylglycinamidine synthase	Q5SUR0	Pfas	0.0284903	1.61424
Delta(3,5)-Delta(2,4)-dienoyl-CoA isomerase, mitochondrial	O35459	Ech1	0.0369884	1.59359
Cold shock domain-containing protein E1	Q91W50	Csde1	0.0289739	1.59093
Bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]	P56380	Nudt2	0.0249138	1.58241
4F2 cell-surface antigen heavy chain	P10852	Slc3a2	0.00483829	1.58015
Serine/arginine-rich splicing factor 5	O35326	Srsf5	0.00248435	1.57738
Heterogeneous nuclear ribonucleoprotein A3	Q8BG05	Hnrnpa3	0.00522921	1.55481
DNA damage-binding protein 1	Q3U1J4	Ddb1	0.0463934	1.55212
Heterogeneous nuclear ribonucleoprotein A1	P49312	Hnrnpa1	0.0109867	1.54728
Malectin	Q6ZQI3	Mlec	0.0482676	1.54431
Proteasome activator complex subunit 3	P61290	Psme3	0.0319997	1.53211
Proteasome subunit beta type-7	P70195	Psmb7	0.0163251	1.52609
Thimet oligopeptidase	Q8C1A5	Thop1	0.0473003	1.5254
Heterogeneous nuclear ribonucleoprotein H	O35737	Hnrnph1	0.0499195	1.51584
Coronin-7	Q9D2V7	Coro7	0.0209642	1.51319
RNA-binding protein 28	Q8CGC6	Rbm28	0.044673	1.50516
Galectin-3-binding protein	Q07797	Lgals3bp	0.00244223	1.50248
Scaffold attachment factor B1	D3YXK2	Safb	0.0338818	1.50144
Transmembrane emp24 domain-containing protein 10	Q9D1D4	Tmed10	0.0323482	1.48626
Proteolipid protein 2	Q9R1Q7	Plp2	0.0446393	1.48486
Dihydropyrimidinase-related protein 2	O08553	Dpysl2	0.0199128	1.47965
Aspartate aminotransferase, mitochondrial	P05202	Got2	0.0115146	1.45856
Vacuolar protein sorting-associated protein 13C	Q8BX70	Vps13c	0.049153	1.44121
Alpha-adducin	Q9QYC0	Add1	0.0216258	1.44086
26S proteasome non-ATPase regulatory subunit 8	Q9CX56	Psmd8	0.0158997	1.43863
Splicing factor, proline- and glutamine-rich	Q8VIJ6	Sfpq	0.0220094	1.43585
Calreticulin	P14211	Calr	0.0149701	1.43268
Dihydrolipoyl dehydrogenase, mitochondrial	O08749	Dld	0.0261612	1.42223
Catenin beta-1	Q02248	Ctnnb1	0.0223288	1.42189
Proteasome subunit beta type-5	O55234	Psmb5	0.00495845	1.41675
Actin-related protein 2/3 complex subunit 3	Q9JM76	Arpc3	0.0170363	1.41633
Small nuclear ribonucleoprotein Sm D3	P62320	Snrpd3	0.0253455	1.41394
DNA topoisomerase 1	Q04750	Top1	0.0250654	1.41337

Proteasome subunit alpha type-2	P49722	Psma2	0.0171816	1.41289
Cytochrome P450 2C40	P56657	Cyp2c40	0.0180477	1.41135
60S ribosomal protein L22	P67984	Rpl22	0.00257496	1.41034
Xylulose kinase	Q3TNA1	Xylb	0.0368742	1.40958
Nucleoside diphosphate kinase A	P15532	Nme1	0.0375097	1.40604
60S ribosomal protein L31	P62900	Rpl31	0.0201257	1.4057
T-complex protein 1 subunit beta	P80314	Cct2	0.00466114	1.40306
V-type proton ATPase catalytic subunit A	P50516	Atp6v1a	0.0398881	1.40204
Ubiquitin carboxyl-terminal hydrolase 14	Q9JMA1	Usp14	0.0254222	1.40153
Acetyl-CoA acetyltransferase, cytosolic	Q8CAY6	Acat2	0.021025	1.38912
Proteasome subunit alpha type-7	Q9Z2U0	Psma7	0.0395232	1.38869
S-adenosylmethionine synthase isoform type-2	Q3THS6	Mat2a	0.0119297	1.38557
Heterogeneous nuclear ribonucleoproteins C1/C2	Q9Z204	Hnrnpc	0.0204942	1.37838
Septin-7	O55131	Septin7	0.0347553	1.37336
Ubiquitin-40S ribosomal protein S27a	P62983	Rps27a	0.0145219	1.36837
Ketohexokinase	P97328	Khk	0.0198052	1.36309
Elongation factor 1-gamma	Q9D8N0	Eef1g	0.0102412	1.36152
14-3-3 protein zeta/delta	P63101	Ywhaz	0.000528188	1.36015
Pyruvate kinase PKM	P52480	Pkm	0.034743	1.35879
[Pyruvate dehydrogenase (acetyl-transferring)] kinase isozyme 1, mitochondrial	Q8BFP9	Pdk1	0.0165942	1.35789
60S ribosomal protein L17	Q9CPR4	Rpl17	0.0243064	1.34978
Casein kinase II subunit alpha	Q60737	Csnk2a1	0.0279466	1.34052
Alpha-soluble NSF attachment protein	Q9DB05	Napa	0.0237932	1.33938
Alpha-actinin-1	Q7TPR4	Actn1	0.0233639	1.33621
26S proteasome regulatory subunit 8	P62196	Psmc5	0.042713	1.33044
Rab GDP dissociation inhibitor beta	Q61598	Gdi2	0.0102524	1.31869
Protein arginine N-methyltransferase 1	Q9JIF0	Prmt1	0.0374303	1.31777
Heat shock protein HSP 90-alpha	P07901	Hsp90aa1	0.0279289	1.31494
Proteasome subunit beta type-4	P99026	Psmb4	0.0468942	1.31477
Proteasome subunit alpha type-1	Q9R1P4	Psma1	0.0385325	1.31339
Endoplasmin	P08113	Hsp90b1	0.0149716	1.3111
Alpha-centractin	P61164	Actr1a	0.0275628	1.31108
Leucine-rich repeat-containing protein 59	Q922Q8	Lrrc59	0.00360268	1.30886
Glycine--tRNA ligase	Q9CZD3	Gars1	0.0472216	1.30266
ATP synthase subunit ATP5MJ, mitochondrial	P56379	Atp5mj	0.03767	1.30244
Farnesyl pyrophosphate synthase	Q920E5	Fdps	0.0181836	1.29988
Nodal modulator 1	Q6GQT9	Nomo1	0.00978538	1.2981
DNA mismatch repair protein Msh6	P54276	Msh6	0.0465651	1.2966

Major vault protein	Q9EQK5	Mvp	0.0146409	1.29528
Proliferation-associated protein 2G4	P50580	Pa2g4	0.0228212	1.28904
Poly(rC)-binding protein 2	Q61990	Pcbp2	0.0453241	1.28887
Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	Fkbp4	0.0157578	1.28874
ELAV-like protein 1	P70372	Elavl1	0.0231502	1.28041
40S ribosomal protein S3a	P97351	Rps3a	0.0327008	1.27795
Alpha-actinin-4	P57780	Actn4	0.0499516	1.27299
Eukaryotic translation initiation factor 2 subunit 1	Q6ZWX6	Eif2s1	0.00861924	1.26777
T-complex protein 1 subunit gamma	P80318	Cct3	0.0172108	1.26416
T-complex protein 1 subunit epsilon	P80316	Cct5	0.00607175	1.25705
60S ribosomal protein L38	Q9JJI8	Rpl38	0.0313725	1.25459
E3 ubiquitin-protein ligase MARCHF5	Q3KNM2	Marchf5	0.0242645	1.25076
Hypoxia up-regulated protein 1	Q9JKR6	Hyou1	0.0357252	1.23979
40S ribosomal protein SA	P14206	Rpsa	0.02444	1.23289
Elongation factor 2	P58252	Eef2	0.0354147	1.22471
ATP synthase subunit f, mitochondrial	P56135	Atp5mf	0.0207095	1.22398
Coatomer subunit delta	Q5XJY5	Arcn1	0.0157333	1.21976
Serine-threonine kinase receptor-associated protein	Q9Z1Z2	Strap	0.0214626	1.21944
26S proteasome non-ATPase regulatory subunit 6	Q99JI4	Psmd6	0.0159166	1.21034
Probable ATP-dependent RNA helicase DDX5	Q61656	Ddx5	0.0466963	1.20444
Cytochrome b-c1 complex subunit 1, mitochondrial	Q9CZ13	Uqcrc1	0.0329563	1.19923
Heat shock protein HSP 90-beta	P11499	Hsp90ab1	0.0346043	1.19683
Outer mitochondrial transmembrane helix translocase	Q9D5T0	Atad1	0.0430928	-1.19303
ATP synthase subunit g, mitochondrial	Q9CPQ8	Atp5mg	0.048806	-1.27861
Cytochrome c1, heme protein, mitochondrial	Q9D0M3	Cyc1	0.028258	-1.30993
Dynamin-1-like protein	Q8K1M6	Dnm1l	0.03561	-1.33776
MICOS complex subunit MIC13	Q8R404	Micos13	0.0416889	-1.33946
Catechol O-methyltransferase domain-containing protein 1	Q8BIG7	Comtd1	0.0418597	-1.3448
U2 snRNP-associated SURP motif-containing protein	Q6NV83	U2surp	0.0324272	-1.40247
Nucleoporin 205	A0A0J9YUD5	Nup205	0.0358448	-1.41852
CDGSH iron-sulfur domain-containing protein 3, mitochondrial	B1AR13	Cisd3	0.0272495	-1.47947
Inorganic pyrophosphatase	Q9D819	Ppa1	0.0187821	-1.48365
NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 5	Q9CPP6	Ndufa5	0.0395031	-1.51408
Aminoacyl tRNA synthase complex-interacting multifunctional protein 2	Q8R010	Aimp2	0.0055884	-1.54623

Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	Q99MR8	Mccc1	0.0412224	-1.56
Mannosyl-oligosaccharide 1,2-alpha-mannosidase IA	P45700	Man1a1	0.00207665	-1.57585
Cleavage and polyadenylation specificity factor subunit 1	Q9EPU4	Cpsf1	0.026114	-1.58696
Rho guanine nucleotide exchange factor 7	Q9ES28	Arhgef7	0.0347703	-1.62247
Exosome complex exonuclease RRP44	Q9CSH3	Dis3	0.0311782	-1.64006
Protein odr-4 homolog	Q4PJX1	Odr4	0.0147342	-1.65274
Gem-associated protein 5	Q8BX17	Gemin5	0.00824956	-1.68435
Cyclin-dependent kinase 4	P30285	Cdk4	0.0428029	-1.69116
Annexin A3	O35639	Anxa3	0.0240312	-1.71334
Sulfotransferase family cytosolic 1B member 1	Q9QWG7	Sult1b1	0.00947992	-1.72449
Ribosome biogenesis protein BRX1 homolog	Q9DCA5	Brix1	0.0483353	-1.74325
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Q9DCS9	Ndufb10	0.0348066	-1.74601
Cytochrome b5	P56395	Cyb5a	0.00182663	-1.74868
GPI inositol-deacylase	Q3UUQ7	Pgap1	0.010836	-1.76808
Nuclear pore complex protein Nup50	Q9JIH2	Nup50	0.0406299	-1.78332
Carbonyl reductase [NADPH] 3	Q8K354	Cbr3	0.0423588	-1.79115
Keratin, type I cytoskeletal 20	Q9D312	Krt20	0.0139646	-1.81723
NADH-ubiquinone oxidoreductase chain 4	P03911	Mtnd4	0.0428652	-1.81922
Aldo-keto reductase family 1 member B1	P45376	Akr1b1	0.0147062	-1.83912
Membrane-associated progesterone receptor component 2	Q80UU9	Pgrmc2	0.000235511	-1.85245
Torsin-1A-interacting protein 2	Q8BYU6	Tor1aip2	0.0344518	-1.85518
5'-AMP-activated protein kinase subunit gamma-1	O54950	Prkag1	0.0369221	-1.85705
Galectin-2	Q9CQW5	Lgals2	0.0330772	-1.85949
Methyltransferase-like 26	Q9DCS2	Mettl26	8.01E-05	-1.8602
UMP-CMP kinase	Q9DBP5	Cmpk1	0.0285472	-1.88083
Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	F2Z3U3	Raph1	0.0243174	-1.89802
AP-3 complex subunit mu-1	Q9JKC8	Ap3m1	0.00233324	-1.93969
Calpain-5	O08688	Capn5	0.0133276	-1.96219
Gelsolin	P13020	Gsn	0.0132046	-1.96682
Testin	P47226	Tes	0.0270619	-1.97373
Ester hydrolase C11orf54 homolog	Q91V76	C11orf54	0.0259059	-2.03769
Adenylate kinase 2, mitochondrial	Q9WTP6	Ak2	0.0419012	-2.0509
Sterol carrier protein 2	P32020	Scp2	0.047482	-2.07767
Actin-related protein 2/3 complex subunit 5-like protein	Q9D898	Arpc5l	0.0278166	-2.10257
General transcription factor IIF subunit 1	Q3THK3	Gtf2f1	0.000357104	-2.10631

DNA-directed RNA polymerase III subunit RPC2	P59470	Polr3b	0.0251387	-2.1287
COP9 signalosome complex subunit 3	O88543	Cops3	0.0130838	-2.14131
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	Q9CR61	Ndufb7	0.0312972	-2.1733
U6 snRNA-associated Sm-like protein LSm7	Q9CQQ8	Lsm7	0.0395001	-2.18014
Phosphoribosyl pyrophosphate synthase-associated protein 2	Q8R574	Prpsap2	0.014239	-2.22379
Acetyl-CoA carboxylase 1	Q5SWU9	Acaca	0.0229546	-2.31396
Thioredoxin	P10639	Txn	0.0333143	-2.33532
Hexokinase-1	P17710	Hk1	0.0317909	-2.43624
Mini-chromosome maintenance complex-binding protein	Q8R3C0	Mcmbp	0.00354193	-2.45734
Translation initiation factor eIF-2B subunit beta	Q99LD9	Eif2b2	0.0125885	-2.46215
Cullin-4B	A2A432	Cul4b	0.0334075	-2.51818
Vitamin K epoxide reductase complex subunit 1-like protein 1	Q6TEK5	Vkorc1l1	0.000814716	-2.52283
tRNA (guanine-N(7)-)-methyltransferase non-catalytic subunit WDR4	Q9EP82	Wdr4	0.0109923	-2.54384
Acyl-protein thioesterase 2	Q9WTL7	Lypla2	0.0145694	-2.81733
Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit	Q7TNL5	Ppp2r5d	0.0291574	-2.99388
Hepatoma-derived growth factor-related protein 2	Q3UMU9	Hdgfl2	0.00597513	-3.16401
Coiled-coil domain-containing protein 86	Q9JJ89	Ccdc86	0.00861573	-3.20562
SAGA-associated factor 29	Q9DA08	Sgf29	0.0273852	-3.46238
Cysteine-rich protein 1	P63254	Crip1	0.0275504	-3.76867
Growth factor receptor-bound protein 7	Q03160	Grb7	0.000807307	-4.13969
28S ribosomal protein S28, mitochondrial	Q9CY16	Mrps28	0.000169607	-23.9338

Appendix 6: Significant proteomic changes in WT enteroids treated with 0.1 µM 5-FU + 10 ng/mL TNF in comparison to WT enteroids treated with 0.1 µM 5-FU alone at 24 hours.

Protein	Accession	Gene	p-value	Fold-Change
Transcription factor BTF3 homolog 4	Q9CQH7	Btf3l4	0.037676	4.51967
LIM and senescent cell antigen-like-containing domain protein 1	Q99JW4	Lims1	0.0489155	3.05508
Chloride channel accessory 3B	E9PUL3	Clca3b	2.42E-05	2.98869
Inner nuclear membrane protein Man1	Q9WU40	Lemd3	0.0124452	2.54892
Serine/threonine-protein phosphatase 5	Q60676	Ppp5c	0.000551093	2.52322
Dual specificity protein kinase CLK1	P22518	Clk1	0.0487206	2.46742
Transcription factor 20	Q9EPQ8	Tcf20	7.71E-05	2.45312

Copine-1	Q8C166	Cpne1	0.0397107	2.44667
Ras-related protein Rab-35	Q6PHN9	Rab35	0.0467864	2.40749
Apoptosis regulator BAX	Q07813	Bax	0.0413052	2.37337
Peptidoglycan recognition protein 1	O88593	Pglyrp1	0.0224566	2.36321
AP-2 complex subunit sigma	P62743	Ap2s1	0.00759441	2.34096
Pleckstrin homology domain-containing, family A member 5	E9Q6H8	Plekha5	0.00564307	2.33474
Deaminated glutathione amidase	Q8VDK1	Nit1	0.0186566	2.27922
Brefeldin A-inhibited guanine nucleotide-exchange protein 2	A2A5R2	Arfgef2	0.0035717	2.24211
Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A beta isoform	Q7TNP2	Ppp2r1b	0.0260715	2.23273
40S ribosomal protein S29	P62274	Rps29	0.0222929	2.22402
Palmitoyl-protein thioesterase 1	O88531	Ppt1	0.0279843	2.12344
Hepatocyte growth factor-regulated tyrosine kinase substrate	Q99LI8	Hgs	0.00399088	2.12147
Fatty acid-binding protein 5	Q05816	Fabp5	0.0146782	2.09684
Ceruloplasmin	Q61147	Cp	0.000852091	2.09615
Potassium channel tetramerisation domain-containing 14	A0A0U1RNG7	Kctd14	0.0393392	2.09003
Pyrroline-5-carboxylate reductase 2	Q922Q4	Pycr2	0.0369127	2.08098
Elongin-C	P83940	Eloc	0.0133894	2.03172
Scaffold attachment factor B1	D3YXK2	Safb	0.0335484	1.98006
Elongator complex protein 3	Q9CZX0	Elp3	0.0419151	1.96965
Collagen alpha-1(IV) chain	P02463	Col4a1	0.0042198	1.93808
MICOS complex subunit Mic10	Q7TNS2	Micos10	0.00517431	1.9374
Thioredoxin reductase 2, mitochondrial	Q9JLT4	Txnrd2	0.0394906	1.83706
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	Q8C0L6	Paox	0.00585945	1.81367
Cellular nucleic acid-binding protein	P53996	Cnbp	0.0120435	1.78202
Tubulointerstitial nephritis antigen-like	Q99JR5	Tinagl1	0.0129983	1.76441
5'-AMP-activated protein kinase subunit beta-1	Q9R078	Prkab1	0.0262944	1.7487
Collagen alpha-2(IV) chain	P08122	Col4a2	0.00503318	1.72873
mRNA turnover protein 4 homolog	Q9D0I8	Mrto4	0.00111352	1.72766
60S ribosomal protein L37a	P61514	Rpl37a	0.0412873	1.72067
Olfactomedin-4	Q3UZZ4	Olfm4	0.00256596	1.70629
Hepatocyte nuclear factor 4-alpha	P49698	Hnf4a	0.0379993	1.70229
N-terminal kinase-like protein	Q9EQC5	Scyl1	0.00319256	1.69565
Amiloride-sensitive amine oxidase [copper-containing]	Q8JZQ5	Aoc1	0.0122084	1.65319
Murinoglobulin-1	P28665	Mug1	0.00322287	1.64437
SPARC	P07214	Sparc	0.00355876	1.62173

Phosphoribosylformylglycinamidine synthase	Q5SUR0	Pfas	0.0313852	1.61386
ER membrane protein complex subunit 1	Q8C7X2	Emc1	0.0326844	1.60335
Basement membrane-specific heparan sulfate proteoglycan core protein	Q05793	Hspg2	0.012358	1.59052
Spliceosome RNA helicase Ddx39b	Q9Z1N5	Ddx39b	0.00189506	1.57842
Tyrosine-protein kinase BAZ1B	Q9Z277	Baz1b	0.000842389	1.57075
Nuclear pore complex protein Nup98-Nup96	Q6PFD9	Nup98	0.0206793	1.56637
Non-receptor tyrosine-protein kinase TYK2	Q9R117	Tyk2	0.024361	1.56218
Coronin-7	Q9D2V7	Coro7	0.00196095	1.56132
Acyl-CoA (8-3)-desaturase	Q920L1	Fads1	0.0418633	1.56035
Solute carrier family 12 member 2	P55012	Slc12a2	0.00713993	1.55979
Probable ubiquitin carboxyl-terminal hydrolase FAF-X	P70398	Usp9x	0.0445755	1.54394
DnaJ homolog subfamily A member 3, mitochondrial	Q99M87	Dnaja3	0.0350842	1.54341
Tubulin gamma-1 chain	P83887	Tubg1	0.0256466	1.54208
BRCA2 and CDKN1A-interacting protein	Q9CWI3	Bccip	0.0244861	1.54086
Pentatricopeptide repeat domain-containing protein 3, mitochondrial	Q14C51	Ptcd3	0.0286118	1.53433
Cohesin subunit SA-1	Q9D3E6	Stag1	0.021586	1.51996
Hippocalcin-like protein 1	P62748	Hpcal1	0.00714861	1.51947
Ras GTPase-activating protein-binding protein 2	P97379	G3bp2	0.0359145	1.51614
Cation-dependent mannose-6-phosphate receptor	P24668	M6pr	0.0382909	1.50863
ER membrane protein complex subunit 7	Q9EP72	Emc7	0.0100063	1.49524
Tetraspanin-8	Q8R3G9	Tspan8	0.0252704	1.49203
Nidogen-2	O88322	Nid2	0.00814002	1.49008
Polyribonucleotide nucleotidyltransferase 1, mitochondrial	Q8K1R3	Pnpt1	0.0493058	1.48795
Translin-associated protein X	Q9QZE7	Tsnax	0.0397531	1.47863
28S ribosomal protein S27, mitochondrial	Q8BK72	Mrps27	0.0177907	1.46226
Nucleobindin-1	Q02819	Nucb1	0.038396	1.45895
Prosaposin	Q61207	Psap	0.023638	1.45136
Swi5-dependent recombination DNA repair protein 1 homolog	Q8BP27	Sfr1	0.000558581	1.44544
Prostaglandin E synthase 3	Q9R0Q7	Ptges3	0.0339281	1.42765
Nuclear transport factor 2	P61971	Nutf2	0.0358249	1.41695
Small nuclear ribonucleoprotein Sm D3	P62320	Snrpd3	0.0156495	1.41621
Fibrinogen beta chain	Q8K0E8	Fgb	0.0093528	1.40678
Eukaryotic translation initiation factor 3 subunit I	Q9QZD9	Eif3i	0.0284776	1.40591
Tubulin alpha-4A chain	P68368	Tuba4a	0.00155476	1.3996

Nuclear pore complex protein Nup93	Q8BJ71	Nup93	0.0378357	1.39456
Ethylmalonyl-CoA decarboxylase	Q9D9V3	Echdc1	0.0305052	1.39442
60S ribosomal protein L30	P62889	Rpl30	0.0198357	1.3935
Collagen alpha-1(XVIII) chain	P39061	Col18a1	0.00848609	1.39123
Aflatoxin B1 aldehyde reductase member 2	Q8CG76	Akr7a2	0.0187949	1.37708
Nidogen-1	P10493	Nid1	0.00971653	1.37452
Nucleoporin NUP188	Q6ZQH8	Nup188	0.0437739	1.37267
Laminin subunit alpha-1	P19137	Lama1	0.0122758	1.36675
Fibulin-1	Q08879	Fbln1	0.0278847	1.3654
Eukaryotic translation initiation factor 3 subunit K	Q9DBZ5	Eif3k	0.046635	1.36498
AP-1 complex subunit mu-2	Q9WVP1	Ap1m2	0.0227465	1.36268
Pre-mRNA-processing factor 19	Q99KP6	Prpf19	0.0448004	1.36162
40S ribosomal protein S3a	P97351	Rps3a	0.00224136	1.34288
Receptor of activated protein C kinase 1	P68040	Rack1	0.0020092	1.34258
Laminin subunit gamma-1	P02468	Lamc1	0.0396628	1.34024
Kininogen-1	O08677	Kng1	0.0213288	1.3352
60S ribosomal protein L31	P62900	Rpl31	0.0317313	1.30685
Lymphocyte-specific helicase	Q60848	Hells	0.0304733	1.30541
Eukaryotic translation initiation factor 3 subunit B	Q8JZQ9	Eif3b	0.00420592	1.30489
Heterogeneous nuclear ribonucleoprotein L-like	Q921F4	Hnrnpll	0.0402405	1.30012
Glycogen phosphorylase, brain form	Q8CI94	Pygb	0.0411064	1.27707
Lupus La protein homolog	P32067	Ssb	0.0065691	1.26977
14-3-3 protein eta	P68510	Ywhah	0.00792491	1.2647
Protein arginine N-methyltransferase 1	Q9JIF0	Prmt1	0.00655043	1.25856
Core histone macro-H2A.1	Q9QZQ8	Macroh2a1	0.0244855	1.25377
60S ribosomal protein L17	Q9CPR4	Rpl17	0.0219838	1.23746
Proliferation-associated protein 2G4	P50580	Pa2g4	0.0203244	1.22399
116 kDa U5 small nuclear ribonucleoprotein component	O08810	Eftud2	0.037403	1.22212
60S ribosomal protein L10a	P53026	Rpl10a	0.0194096	1.19355
T-complex protein 1 subunit gamma	P80318	Cct3	0.00989745	1.18848
Elongation factor 2	P58252	Eef2	0.014419	1.17017
60S ribosomal protein L27a	P14115	Rpl27a	0.02199	1.16791
Valine--tRNA ligase	Q9Z1Q9	Vars1	0.00678225	1.16169
GTP-binding nuclear protein Ran	P62827	Ran	0.0465518	1.15135
Heat shock protein HSP 90-beta	P11499	Hsp90ab1	0.0290584	1.13896
60S ribosomal protein L6	P47911	Rpl6	0.028554	1.12792
Programmed cell death 6-interacting protein	Q9WU78	Pdcd6ip	0.0258467	-1.15274
Stress-70 protein, mitochondrial	P38647	Hspa9	0.0123242	-1.17804
Translocon-associated protein subunit delta	Q62186	Ssr4	0.035827	-1.22346

Electron transfer flavoprotein subunit beta	Q9DCW4	Etfb	0.0425205	-1.25624
U4/U6 small nuclear ribonucleoprotein Prp31	Q8CCF0	Prpf31	0.0346283	-1.25888
Perilipin-3	Q9DBG5	Plin3	0.0454114	-1.28777
Glutathione S-transferase omega-1	O09131	Gsto1	0.0375293	-1.2943
Twinfilin-1	Q91YR1	Twf1	0.0065459	-1.29498
Voltage-dependent anion-selective channel protein 2	Q60930	Vdac2	0.0482992	-1.29604
Transducin beta-like protein 2	Q9R099	Tbl2	0.0340337	-1.34566
Cytochrome P450 2D26	Q8CIM7	Cyp2d26	0.0443644	-1.36992
Glutamine amidotransferase-like class 1 domain-containing protein 3A, mitochondrial	Q9D172	Gatd3a	0.0341889	-1.37105
Fragile X mental retardation syndrome-related protein 1	Q61584	Fxr1	0.0136871	-1.37479
Ubiquitin-conjugating enzyme E2 K	P61087	Ube2k	0.0204788	-1.38989
Cytochrome b5 type B	Q9CQX2	Cyb5b	0.0359618	-1.39662
ATP synthase subunit O, mitochondrial	Q9DB20	Atp5po	0.0497261	-1.397
Glutathione S-transferase A2	P10648	Gsta1	0.0459525	-1.40711
F-box only protein 22	Q78JE5	Fbxo22	0.00135699	-1.41603
Membrane-associated progesterone receptor component 2	Q80UU9	Pgrmc2	0.048572	-1.41972
Platelet-activating factor acetylhydrolase 2, cytoplasmic	Q8VDG7	Pafah2	0.0202744	-1.43627
Claudin-18	P56857	Cldn18	0.0383415	-1.44305
NADH-cytochrome b5 reductase 3	Q9DCN2	Cyb5r3	0.0273885	-1.45103
Sorting nexin-5	Q9D8U8	Snx5	0.0478108	-1.47709
ATP-binding cassette sub-family F member 1	Q6P542	Abcf1	0.0394666	-1.48232
Coatomer subunit epsilon	O89079	Cope	0.00942219	-1.50987
Carbonyl reductase [NADPH] 3	Q8K354	Cbr3	0.0116859	-1.52986
Triokinase/FMN cyclase	Q8VC30	Tkfc	0.047971	-1.53078
THO complex subunit 2	B1AZI6	Thoc2	0.0129924	-1.55635
Structural maintenance of chromosomes protein 4	Q8CG47	Smc4	0.0103546	-1.56104
Glutaminase kidney isoform, mitochondrial	D3Z7P3	Gls	0.0238718	-1.56646
Aldehyde dehydrogenase, cytosolic 1	O35945	Aldh1a7	0.032106	-1.57173
Nuclear pore complex protein Nup54	Q8BTS4	Nup54	0.0093869	-1.58264
Protein-glutamine gamma-glutamyltransferase 2	P21981	Tgm2	0.0379256	-1.58309
Unconventional myosin-Vb	P21271	Myo5b	0.0168009	-1.58806
39S ribosomal protein L27, mitochondrial	Q99N92	Mrpl27	0.00227034	-1.61132
Trafficking protein particle complex subunit 11	B2RXC1	Trappc11	0.0390342	-1.61438
6-phosphogluconolactonase	Q9CQ60	Pgls	0.00112625	-1.61591

Cathepsin Z	Q9WUU7	Ctsz	0.0275466	-1.63556
39S ribosomal protein L16, mitochondrial	Q99N93	Mrpl16	0.00726656	-1.65736
von Willebrand factor A domain-containing protein 1	Q8R2Z5	Vwa1	0.0496506	-1.66096
V-type proton ATPase subunit G 1	Q9CR51	Atp6v1g1	0.0441703	-1.67448
Cytochrome b-c1 complex subunit 8	Q9CQ69	Uqcrq	0.00107127	-1.67744
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 10	Q9DCS9	Ndufb10	0.0474179	-1.67913
Erlin-2	Q8BFZ9	Erlin2	0.004252	-1.68007
Peroxiredoxin-like 2A	Q9CYH2	Prxl2a	0.0299278	-1.68716
Cytochrome b5	P56395	Cyb5a	0.0194582	-1.7021
39S ribosomal protein L38, mitochondrial	Q8K2M0	Mrpl38	0.0199744	-1.71353
39S ribosomal protein L1, mitochondrial	Q99N96	Mrpl1	0.0165044	-1.72996
Arginase-2, mitochondrial	O08691	Arg2	0.00696531	-1.73132
Adseverin	Q60604	Scin	0.0355654	-1.74161
UMP-CMP kinase	Q9DBP5	Cmpk1	0.00995084	-1.7537
Mitochondrial glutamate carrier 1	Q9D6M3	Slc25a22	0.0253778	-1.75466
Barrier-to-autointegration factor	O54962	Banf1	0.0382343	-1.77258
Dihydrofolate reductase	P00375	Dhfr	0.0336314	-1.79439
Sorting nexin-3	O70492	Snx3	0.02017	-1.79641
Vesicle-associated membrane protein-associated protein B	Q9QY76	Vapb	0.0445306	-1.82236
Long-chain-fatty-acid--CoA ligase 3	Q9CZW4	Acsl3	0.0192315	-1.86528
Cholinesterase	Q03311	Bche	0.0336165	-1.88152
Nuclear cap-binding protein subunit 3	Q8BZR9	Ncbp3	0.00270199	-1.88843
Family with sequence similarity 98, member C	E9PYD1	Fam98c	0.0199126	-1.91486
Protein ELYS	Q8CJF7	Ahctf1	0.0454868	-1.92347
60S acidic ribosomal protein P1	P47955	Rplp1	0.00137025	-1.94019
Hsp70-binding protein 1	Q99P31	Hspbp1	0.00119998	-1.97468
Vesicle-associated membrane protein-associated protein A	Q9WV55	Vapa	0.013163	-1.9999
Histidine triad nucleotide-binding protein 1	P70349	Hint1	0.00483843	-2.00164
PDZ and LIM domain protein 1	O70400	Pdlim1	0.0187427	-2.04589
Glutamate--cysteine ligase catalytic subunit	P97494	Gclc	0.00789472	-2.09128
Macrophage migration inhibitory factor	P34884	Mif	0.00297224	-2.09625
Gamma-glutamyl hydrolase	Q9Z0L8	Ggh	0.000902207	-2.15769
Oxidoreductase NAD-binding domain-containing protein 1	Q8VE38	Oxnad1	0.00478984	-2.17842
V-type proton ATPase subunit E 1	P50518	Atp6v1e1	0.0462674	-2.27771
Ubiquitin carboxyl-terminal hydrolase 4	P35123	Usp4	0.0113145	-2.28298
Enhancer of rudimentary homolog	P84089	Erh	0.0268425	-2.30902
Na(+)/H(+) exchange regulatory cofactor NHE-RF1	P70441	Slc9a3r1	0.0400259	-2.32003

Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	Usp7	0.033721	-2.32399
Lithostathine-1	P43137	Reg1	0.0291342	-2.33803
Ubiquitin carboxyl-terminal hydrolase 15	Q8R5H1	Usp15	0.0217781	-2.33949
Mth938 domain-containing protein	Q8R0P4	Aamdc	0.00639477	-2.55109
Histidine triad nucleotide-binding protein 2, mitochondrial	Q9D0S9	Hint2	0.00166356	-2.63136
Small integral membrane protein 24	Q0VG18	Smim24	0.0466144	-2.65396
Integrator complex subunit 14	Q8R3P6	Ints14	0.00699497	-2.71557
Cytochrome b-c1 complex subunit 7	Q9D855	Uqcrb	0.0105318	-2.72684
Epsin-1	Q80VP1	Epn1	0.0386085	-3.12566
Mitochondrial import inner membrane translocase subunit Tim9	Q9WV98	Timm9	0.0115844	-3.1784
Septin-11	Q8C1B7	Septin11	0.00101147	-4.71643
Actin-related protein 2/3 complex subunit 5-like protein	Q9D898	Arpc5l	0.00129527	-4.90136
Gamma-tubulin complex component 2	Q921G8	Tubgcp2	2.90E-05	-934.813

Appendix 7: Significant proteomic changes in WT enteroids treated with 0.1 µM 5-FU + 10 ng/mL TNF in comparison to WT enteroids treated with 10 ng/mL TNF alone at 24 hours.

Protein	Accession	Gene	p-value	Fold-Change
WD repeat domain 86	D3Z757	Wdr86	0.0449647	3.1468
Small glutamine-rich tetratricopeptide repeat-containing protein alpha	Q8BJU0	Sgta	0.0151149	3.11606
von Willebrand factor A domain-containing protein 1	Q8R2Z5	Vwa1	0.00955208	2.73369
Insulin-1	P01325	Ins1	0.0389884	2.5075
GDP-fucose protein O-fucosyltransferase 1	Q91ZW2	Pofut1	0.0179038	2.43337
Acyl-CoA-binding protein	P31786	Dbi	0.0382179	2.29538
A-kinase anchor protein 13	E9Q394	Akap13	0.0076537	2.27113
Activating signal cointegrator 1 complex subunit 3	E9PZJ8	Ascc3	0.00274324	2.16562
Polymerase delta-interacting protein 2	Q91VA6	Poldip2	0.000431119	2.03695
CCR4-NOT transcription complex subunit 10	Q8BH15	Cnot10	0.0268867	1.98822
Serine/threonine-protein kinase TAO3	Q8BYC6	Taok3	0.0449025	1.97908
Cullin-2	Q9D4H8	Cul2	0.00040176	1.93703
Tubulin-specific chaperone A	P48428	Tbca	0.0342826	1.9031
Probable E3 ubiquitin-protein ligase IRF2BPL	Q8K3X4	Irf2bpl	0.0136523	1.89681
Essential MCU regulator, mitochondrial	Q9DB10	Smdt1	0.0461908	1.89485
NADH dehydrogenase [ubiquinone] 1 beta subcomplex subunit 7	Q9CR61	Ndufb7	0.0189516	1.88819
Jupiter microtubule associated homolog 1	P97825	Jpt1	0.00428734	1.87433
Copine-1	Q8C166	Cpne1	0.00624505	1.85855

U4/U6 small nuclear ribonucleoprotein Prp4	Q9DAW6	Prpf4	0.0482403	1.84484
Small integral membrane protein 24	Q0VG18	Smim24	0.0422922	1.8218
Serotransferrin	Q921I1	Tf	0.0312988	1.79457
Apolipoprotein A-I	Q00623	Apoa1	0.0274075	1.76532
Glutathione S-transferase A2	P10648	Gsta1	0.0154407	1.697
Guanine nucleotide-binding protein subunit alpha-13	P27601	Gna13	0.0479527	1.68726
Histidine-rich glycoprotein	Q9ESB3	Hrg	0.0239377	1.67833
Prenylcysteine oxidase	Q9CQF9	Pcyox1	0.000570261	1.6542
Nucleoporin NUP35	Q8R4R6	Nup35	0.0118841	1.65212
Nicastrin	P57716	Ncstn	0.019633	1.64921
UDP-N-acetylglucosamine--peptide N-acetylglucosaminyltransferase 110 kDa subunit	Q8CGY8	Ogt	0.00349476	1.64315
Cathepsin Z	Q9WUU7	Ctsz	0.0341585	1.63344
Unconventional myosin-IXb	Q9QY06	Myo9b	0.0119483	1.61888
F-BAR and double SH3 domains protein 1	Q6PFY1	Fchsd1	0.0462958	1.60748
Methylcrotonoyl-CoA carboxylase subunit alpha, mitochondrial	Q99MR8	Mccc1	0.0336665	1.58687
Eukaryotic translation initiation factor 3 subunit J-A	Q3UGC7	Eif3j1	0.0301249	1.55051
Vitronectin	P29788	Vtn	0.0495386	1.54885
La-related protein 4B	Q6A0A2	Larp4b	0.0242719	1.54386
DNA topoisomerase 2-beta	Q64511	Top2b	0.0137463	1.53934
Vimentin	P20152	Vim	0.0388428	1.53655
Nidogen-1	P10493	Nid1	0.0474104	1.53633
Arginase-2, mitochondrial	O08691	Arg2	0.0129746	1.51889
La-related protein 1	Q6ZQ58	Larp1	0.0219302	1.50298
Albumin	P07724	Alb	0.0190836	1.49026
Synaptotagmin-like protein 4	Q9R0Q1	Sytl4	0.0496769	1.48228
Kininogen-1	O08677	Kng1	0.0457668	1.4739
mRNA turnover protein 4 homolog	Q9D0I8	Mrto4	0.0380204	1.457
Golgin subfamily A member 4	Q91VW5	Golga4	0.0495009	1.45214
Inorganic pyrophosphatase 2, mitochondrial	Q91VM9	Ppa2	0.0436746	1.42368
Bifunctional 3'-phosphoadenosine 5'-phosphosulfate synthase 1	Q60967	Papss1	0.0379717	1.41729
Thiosulfate sulfurtransferase	P52196	Tst	0.0212284	1.40973
GRIP1-associated protein 1	Q8VD04	Gripap1	0.004138	1.37853
Agrin	A2ASQ1	Agrn	0.035108	1.37561
DnaJ heat shock protein family (Hsp40) member C13	D4AFX7	Dnajc13	0.0352233	1.36957
Mitochondrial peptide methionine sulfoxide reductase	Q9D6Y7	Msra	0.00643368	1.36304

Integrin-linked kinase-associated serine/threonine phosphatase 2C	Q8R0F6	Ilkap	0.0162015	1.3268
Cleavage and polyadenylation specificity factor subunit 1	Q9EPU4	Cpsf1	0.0387611	1.30582
Dynamin-1-like protein	Q8K1M6	Dnm1l	0.0248423	1.28168
Coatomer subunit gamma-1	Q9QZE5	Copg1	0.0280187	1.19589
Alcohol dehydrogenase class-3	P28474	Adh5	0.0271003	-1.13131
Farnesyl pyrophosphate synthase	Q920E5	Fdps	0.00708008	-1.1529
Receptor of activated protein C kinase 1	P68040	Rack1	0.0105876	-1.15411
Aconitate hydratase, mitochondrial	Q99KI0	Aco2	0.0117815	-1.16929
RNA-splicing ligase RtcB homolog	Q99LF4	Rtcb	0.0391042	-1.18747
Cytoplasmic aconitate hydratase	P28271	Aco1	0.0484323	-1.18977
Elongation factor 2	P58252	Eef2	0.0264637	-1.19547
GTP-binding nuclear protein Ran	P62827	Ran	0.049229	-1.19593
Importin subunit beta-1	P70168	Kpnb1	0.0412073	-1.19773
Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1	Q91YQ5	Rpn1	0.00430234	-1.20679
26S proteasome non-ATPase regulatory subunit 13	Q9WVJ2	Psmd13	0.049766	-1.21184
116 kDa U5 small nuclear ribonucleoprotein component	O08810	Eftud2	0.0197825	-1.21192
Lysine--tRNA ligase	Q99MN1	Kars1	0.0422829	-1.21716
Transitional endoplasmic reticulum ATPase	Q01853	Vcp	0.0319479	-1.22439
Heterogeneous nuclear ribonucleoprotein A0	Q9CX86	Hnrnpa0	0.0479042	-1.23043
Heat shock 70 kDa protein 4	Q61316	Hspa4	0.00553739	-1.23059
Nucleolar protein 58	Q6DFW4	Nop58	0.0402829	-1.23235
Valine--tRNA ligase	Q9Z1Q9	Vars1	0.0181334	-1.23565
Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial	Q8K2B3	Sdha	0.0468408	-1.23813
Proteasome subunit beta type-5	O55234	Psmb5	0.0200855	-1.23858
Catalase	P24270	Cat	0.0165932	-1.23924
Proliferation-associated protein 2G4	P50580	Pa2g4	0.0398316	-1.24335
14-3-3 protein epsilon	P62259	Ywhae	0.0063882	-1.24449
T-complex protein 1 subunit zeta	P80317	Cct6a	0.00188278	-1.24599
Heat shock protein HSP 90-alpha	P07901	Hsp90aa1	0.0295524	-1.24951
T-complex protein 1 subunit gamma	P80318	Cct3	0.0106829	-1.25083
Eukaryotic translation initiation factor 3 subunit B	Q8JZQ9	Eif3b	0.0376081	-1.25175
Proteasome subunit alpha type-1	Q9R1P4	Psma1	0.0142239	-1.25203
Heterogeneous nuclear ribonucleoprotein M	Q9D0E1	Hnrnpm	0.0198728	-1.25533
ATP-dependent RNA helicase A	O70133	Dhx9	0.0076749	-1.25767
60S ribosomal protein L36a	P83882	Rpl36a	0.0149991	-1.26951
Adenylyl cyclase-associated protein 1	P40124	Cap1	0.0390878	-1.27015

Alpha-enolase	P17182	Eno1	0.0286709	-1.27111
Inositol monophosphatase 1	O55023	Impa1	0.00551661	-1.27252
Fatty acid synthase	P19096	Fasn	0.0198845	-1.27318
Parkinson disease protein 7 homolog	Q99LX0	Park7	0.044032	-1.27366
40S ribosomal protein S3a	P97351	Rps3a	0.0244023	-1.27595
Eukaryotic translation initiation factor 3 subunit C	Q8R1B4	Eif3c	0.00790998	-1.27606
Isocitrate dehydrogenase [NADP], mitochondrial	P54071	Idh2	0.0498106	-1.2824
Aldehyde dehydrogenase, mitochondrial	P47738	Aldh2	0.00847868	-1.28561
T-complex protein 1 subunit beta	P80314	Cct2	0.00139197	-1.28613
T-complex protein 1 subunit epsilon	P80316	Cct5	0.0236392	-1.28933
40S ribosomal protein S7	P62082	Rps7	0.0305459	-1.29028
Catenin beta-1	Q02248	Ctnnb1	0.040835	-1.29977
60S ribosomal protein L38	Q9JJI8	Rpl38	0.0176873	-1.30151
Pre-mRNA-splicing factor ATP-dependent RNA helicase DHX15	O35286	Dhx15	0.0224276	-1.30186
Acetyl-CoA acetyltransferase, cytosolic	Q8CAY6	Acat2	0.0117216	-1.30382
Matrin-3	Q8K310	Matr3	0.0190763	-1.30458
Beta-1,4 N-acetylgalactosaminyltransferase 2	Q09199	B4galnt2	0.0141105	-1.30531
Aldehyde dehydrogenase X, mitochondrial	Q9CZS1	Aldh1b1	0.00391143	-1.30591
Ras-related protein Rab-7a	P51150	Rab7a	0.0108672	-1.30688
Vigilin	Q8VDJ3	Hdlbp	0.0452594	-1.30957
Nodal modulator 1	Q6GQT9	Nomo1	0.0275883	-1.30982
Glutamate dehydrogenase 1, mitochondrial	P26443	Glud1	0.00104421	-1.31165
60S ribosomal protein L14	Q9CR57	Rpl14	0.0432978	-1.31269
Proteasome subunit beta type-2	Q9R1P3	Psmb2	0.00423911	-1.31519
T-complex protein 1 subunit alpha	P11983	Tcp1	0.00632247	-1.31674
Delta(14)-sterol reductase LBR	Q3U9G9	Lbr	0.0480337	-1.32124
Aflatoxin B1 aldehyde reductase member 2	Q8CG76	Akr7a2	0.0358432	-1.32267
Desmoplakin	E9Q557	Dsp	0.00912865	-1.32563
Adenosylhomocysteinase	P50247	Ahcy	0.0150737	-1.32677
Heterogeneous nuclear ribonucleoprotein L	Q8R081	Hnrnpl	0.0137332	-1.32802
Cathepsin B	P10605	Ctsb	0.00461334	-1.32869
Aspartate aminotransferase, mitochondrial	P05202	Got2	0.0311783	-1.32894
Elongation factor 1-gamma	Q9D8N0	Eef1g	0.0463909	-1.33305
Phosphoserine aminotransferase	Q99K85	Psat1	0.0443263	-1.33694
Ras-related C3 botulinum toxin substrate 1	P63001	Rac1	0.0362942	-1.33913
Sterol-4-alpha-carboxylate 3-dehydrogenase, decarboxylating	Q9R1J0	Nsdhl	0.0226094	-1.33949
Puromycin-sensitive aminopeptidase	Q11011	Npepps	0.00871299	-1.3455
ELAV-like protein 1	P70372	Elavl1	0.00221525	-1.34801
Polyadenylate-binding protein 1	P29341	Pabpc1	0.0352886	-1.34865

Peptidyl-prolyl cis-trans isomerase FKBP4	P30416	Fkbp4	0.0108761	-1.35778
Endoplasmic reticulum aminopeptidase 1	Q9EQH2	Erap1	0.0127989	-1.35881
Ubiquitin carboxyl-terminal hydrolase 14	Q9JMA1	Usp14	0.0055005	-1.3638
ATP-dependent RNA helicase DDX1	Q91VR5	Ddx1	0.00496685	-1.3645
Nucleolar RNA helicase 2	Q9JIK5	Ddx21	0.00397101	-1.36926
Heterogeneous nuclear ribonucleoproteins A2/B1	O88569	Hnrnpa2b1	0.0221473	-1.37182
SUMO-activating enzyme subunit 2	Q9Z1F9	Uba2	0.0379511	-1.37991
UDP-glucose 4-epimerase	Q8R059	Gale	0.0270249	-1.38607
Splicing factor U2AF 65 kDa subunit	P26369	U2af2	0.045913	-1.38691
Heterogeneous nuclear ribonucleoprotein U	Q8VEK3	Hnrnpu	0.00616367	-1.39206
DNA-directed RNA polymerase I subunit RPA1	O35134	Polr1a	0.0490071	-1.39301
Valacyclovir hydrolase	Q8R164	Bphl	0.0238189	-1.39308
60S ribosomal protein L10a	P53026	Rpl10a	0.0047942	-1.39382
Actin-like protein 6A	Q9Z2N8	Actl6a	0.0414599	-1.39448
Eukaryotic translation initiation factor 3 subunit I	Q9QZD9	Eif3i	0.000580364	-1.39843
Small nuclear ribonucleoprotein Sm D1	P62315	Snrpd1	0.00398858	-1.39907
Core histone macro-H2A.1	Q9QZQ8	Macroh2a1	0.00605453	-1.40408
Glyoxylate reductase/hydroxypyruvate reductase	Q91Z53	Grhpr	0.028243	-1.40414
60S ribosomal protein L37a	P61514	Rpl37a	0.0161072	-1.4056
Annexin A4	P97429	Anxa4	0.00293928	-1.40867
Transcription intermediary factor 1-beta	Q62318	Trim28	0.00848251	-1.41414
Proteasome subunit beta type-3	Q9R1P1	Psmb3	0.00898304	-1.41427
D-3-phosphoglycerate dehydrogenase	Q61753	Phgdh	0.0144469	-1.41455
Obg-like ATPase 1	Q9CZ30	Ola1	0.0375397	-1.4222
Histone-binding protein RBBP7	Q60973	Rbbp7	0.0182634	-1.42263
DNA replication licensing factor MCM4	P49717	Mcm4	0.0378096	-1.42578
Protein NDRG1	Q62433	Ndrg1	0.010631	-1.42809
Tetraspanin-8	Q8R3G9	Tspan8	0.0149608	-1.42848
Serine hydroxymethyltransferase, cytosolic	P50431	Shmt1	0.00722215	-1.43808
Plastin-2	Q61233	Lcp1	0.00255472	-1.43948
40S ribosomal protein S27	Q6ZWU9	Rps27	0.00818909	-1.44998
S-adenosylmethionine synthase isoform type-2	Q3THS6	Mat2a	0.00115119	-1.45903
60S ribosomal protein L9	P51410	Rpl9	0.0103871	-1.45924
Protein SEC13 homolog	Q9D1M0	Sec13	0.00944086	-1.46762
Proliferating cell nuclear antigen	P17918	Pcna	0.0471504	-1.46822
Prostaglandin E synthase 3	Q9R0Q7	Ptges3	0.000100988	-1.48141
Proteasome subunit beta type-6	Q60692	Psmb6	0.0301791	-1.48305
Heterogeneous nuclear ribonucleoprotein F	Q9Z2X1	Hnrnpf	0.0283662	-1.48415
DnaJ homolog subfamily C member 11	Q5U458	Dnajc11	0.0359074	-1.48718

Cytosolic endo-beta-N-acetylglucosaminidase	Q8BX80	Engase	0.0493502	-1.4874
Desmoglein-2	O55111	Dsg2	0.00775753	-1.49206
Staphylococcal nuclease domain-containing protein 1	Q78PY7	Snd1	0.00712094	-1.49283
Small nuclear ribonucleoprotein Sm D2	P62317	Snrpd2	0.00443181	-1.50085
H/ACA ribonucleoprotein complex subunit DKC1	Q9ESX5	Dkc1	0.00671855	-1.50085
Phosphomannomutase 2	Q9Z2M7	Pmm2	0.0297552	-1.50264
DNA topoisomerase 1	Q04750	Top1	0.017892	-1.50416
Oxygen-dependent coproporphyrinogen-III oxidase, mitochondrial	P36552	Cpox	0.00941842	-1.50477
Small nuclear ribonucleoprotein Sm D3	P62320	Snrpd3	0.0335863	-1.50484
Serine hydroxymethyltransferase, mitochondrial	Q9CZN7	Shmt2	0.012219	-1.5088
26S proteasome regulatory subunit 6B	P54775	Psmc4	0.0145451	-1.51022
Kinesin-1 heavy chain	Q61768	Kif5b	0.0105321	-1.51722
Cholinesterase	Q03311	Bche	0.0459089	-1.52263
Vesicle-trafficking protein SEC22b	O08547	Sec22b	0.0446852	-1.54219
Signal peptidase complex catalytic subunit SEC11A	Q9R0P6	Sec11a	0.0132921	-1.55507
Lupus La protein homolog	P32067	Ssb	0.00624525	-1.55728
60S ribosomal protein L23	P62830	Rpl23	0.00270508	-1.55778
Cysteine--tRNA ligase, cytoplasmic	Q9ER72	Cars1	0.0100425	-1.56255
Phosphatidylinositol-binding clathrin assembly protein	Q7M6Y3	Picalm	0.00894481	-1.56817
Mannose-1-phosphate guanyltransferase alpha	Q922H4	Gmppa	0.0142013	-1.59519
CAD protein	B2RQC6	Cad	0.0387325	-1.59605
Nucleolar and coiled-body phosphoprotein 1	E9Q5C9	Nolc1	0.0288491	-1.59964
CDGSH iron-sulfur domain-containing protein 1	Q91WS0	Cisd1	0.00235763	-1.61842
Inosine-5'-monophosphate dehydrogenase 2	P24547	Impdh2	0.000698707	-1.62009
28S ribosomal protein S29, mitochondrial	Q9ER88	Dap3	0.0147241	-1.62085
Dynamin-2	P39054	Dnm2	0.0133389	-1.62513
Chloride channel accessory 3B	E9PUL3	Clca3b	0.0384246	-1.63603
U5 small nuclear ribonucleoprotein 40 kDa protein	Q6PE01	Snrnp40	0.0296814	-1.64023
Ceramide synthase 2	Q924Z4	Cers2	0.048418	-1.64363
Ceramide synthase 6	Q8C172	Cers6	0.0377368	-1.64405
Calcyclin-binding protein	Q9CXW3	Cacybp	0.0298452	-1.64694
DNA replication licensing factor MCM5	P49718	Mcm5	0.0147009	-1.65149
Mitotic checkpoint protein BUB3	Q9WVA3	Bub3	0.0207535	-1.65181
ATP-binding cassette sub-family F member 2	Q99LE6	Abcf2	0.0142797	-1.65896

Fibroblast growth factor-binding protein 1	O70514	Fgfbp1	0.0125384	-1.68141
Mannose-1-phosphate guanyltransferase beta	Q8BTZ7	Gmppb	0.0337112	-1.68174
Magnesium transporter protein 1	Q9CQY5	Magt1	0.00641997	-1.71773
Chloride intracellular channel protein 6	Q8BHB9	Clic6	0.0184281	-1.72012
Serine/arginine repetitive matrix protein 1	Q52KI8	Srrm1	0.00662666	-1.7204
RNA-binding protein Raly	Q64012	Raly	0.0121874	-1.72303
Eukaryotic translation initiation factor 2A	Q8BJW6	Eif2a	0.00879062	-1.74326
Serine/arginine-rich splicing factor 6	Q3TWW8	Srsf6	0.0138025	-1.74561
Nuclear pore complex protein Nup107	Q8BH74	Nup107	0.0360176	-1.75058
Glutathione S-transferase theta-1	Q64471	Gstt1	0.0179791	-1.75119
Ribose-5-phosphate isomerase	P47968	Rpia	0.00488524	-1.80223
Phosphatidylinositol transfer protein alpha isoform	P53810	Pitpna	0.0316517	-1.8241
Claudin-7	Q9Z261	Cldn7	0.0295111	-1.83554
Serine/threonine-protein kinase VRK1	Q80X41	Vrk1	0.00935366	-1.84281
Cytochrome b	P00158	Mt-Cyb	0.021942	-1.86057
Peroxisomal N(1)-acetyl-spermine/spermidine oxidase	Q8C0L6	Paox	0.0154336	-1.863
60S ribosomal protein L22-like 1	Q9D7S7	Rpl22l1	0.00354493	-1.86577
DnaJ homolog subfamily A member 3, mitochondrial	Q99M87	Dnaja3	0.0146869	-1.88659
Retinol dehydrogenase 7	O88451	Rdh7	0.0367426	-1.89973
HEAT repeat-containing protein 1	G3X9B1	Heatr1	0.0184464	-1.90434
Centromere protein V	Q9CXS4	Cenpv	0.00304734	-1.90451
Cytochrome c oxidase assembly protein COX15 homolog	Q8BJ03	Cox15	0.0235424	-1.91536
GTP-binding protein SAR1a	P36536	Sar1a	0.0140443	-1.91826
Syntaxin-binding protein 3	Q60770	Stxbp3	0.0448002	-1.92851
Amiloride-sensitive amine oxidase [copper-containing]	Q8JZQ5	Aoc1	0.00357096	-1.95043
3-oxoacyl-[acyl-carrier-protein] reductase	Q91VT4	Cbr4	0.0178414	-1.96415
28S ribosomal protein S30, mitochondrial	Q9D0G0	Mrps30	0.0346967	-1.96871
1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase	Q99JT9	Adi1	0.0424975	-1.97588
Inositol 1,4,5-trisphosphate receptor type 3	P70227	Itpr3	0.00582775	-1.98802
Alpha-N-acetylgalactosaminidase	Q9QWR8	Naga	0.016173	-1.98886
Alpha-adducin	Q9QYC0	Add1	0.0116151	-2.01264
Maleylacetoacetate isomerase	Q9WVL0	Gstz1	0.03876	-2.0195
Propionyl-CoA carboxylase beta chain, mitochondrial	Q99MN9	Pccb	0.0202237	-2.03247
Thioredoxin-related transmembrane protein 1	Q8VBT0	Tmx1	0.0373236	-2.05773

Mitochondrial-processing peptidase subunit beta	Q9CXT8	Pmpcb	0.0134664	-2.0818
Delta(24)-sterol reductase	Q8VCH6	Dhcr24	0.00473783	-2.15554
ATP-dependent Clp protease ATP-binding subunit clpX-like, mitochondrial	Q9JHS4	Clpx	0.0410246	-2.35373
Heterochromatin protein 1-binding protein 3	Q3TEA8	Hp1bp3	0.001143	-2.426
Sigma intracellular receptor 2	Q8VD00	Tmem97	0.00113353	-2.43607
Ubiquitin carboxyl-terminal hydrolase 7	Q6A4J8	Usp7	0.0286038	-2.93179
Zinc finger ZZ-type and EF-hand domain-containing protein 1	Q5SSH7	Zzef1	0.0398786	-3.8346