

## Supplemental Table 3 - related to Figure 2

Term (translationally up in hESC vs NPC)	ID	N	p (Benjamini-corrected)
rRNA processing	GO:0006364	85	1.07E-45
translational initiation	GO:0006413	66	2.42E-41
viral transcription	GO:0019083	60	6.76E-41
translation	GO:0006412	85	1.20E-39
SRP-dependent cotranslational protein targeting to membrane	GO:0006614	54	7.65E-39
nuclear-transcribed mRNA catabolic process, nonsense-mediated decay	GO:0000184	58	9.49E-37
mitochondrial translational elongation	GO:0070125	37	1.96E-20
mitochondrial translational termination	GO:0070126	36	3.40E-19
mitochondrial translation	GO:0032543	16	9.60E-8
cytoplasmic translation	GO:0002181	11	0.000
negative regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle	GO:0051436	17	0.000
positive regulation of establishment of protein localization to telomere	GO:1904851	7	0.001
positive regulation of ubiquitin-protein ligase activity involved in regulation of mitotic cell cycle transition	GO:0051437	17	0.001
regulation of mRNA stability	GO:0043488	20	0.001
ribosomal small subunit assembly	GO:0000028	9	0.001
anaphase-promoting complex-dependent catabolic process	GO:0031145	17	0.001
positive regulation of telomerase RNA localization to Cajal body	GO:1904874	8	0.001
aerobic respiration	GO:0009060	11	0.001
protein folding	GO:0006457	27	0.001
ribosomal small subunit biogenesis	GO:0042274	8	0.002
mRNA splicing, via spliceosome	GO:0000398	30	0.003
cell-cell adhesion	GO:0098609	34	0.003
positive regulation of protein localization to Cajal body	GO:1904871	6	0.003
maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA)	GO:0000462	10	0.006
NIK/NF-kappaB signaling	GO:0038061	14	0.008
RNA processing	GO:0006396	17	0.011
mitochondrial electron transport, ubiquinol to cytochrome c	GO:0006122	7	0.011
oxidation-reduction process	GO:0055114	56	0.019
protein stabilization	GO:0050821	20	0.022
tRNA aminoacylation for protein translation	GO:0006418	10	0.029
mitochondrion organization	GO:0007005	14	0.031
ribosomal large subunit biogenesis	GO:0042273	8	0.030
regulation of cellular amino acid metabolic process	GO:0006521	11	0.040

Term (translationally up in NPC vs hESC)	ID	N	p (Benjamini-corrected)
positive regulation of transcription, DNA-templated	GO:0045893	46	0.0029
vascular endothelial growth factor receptor signaling pathway	GO:0048010	14	0.0077
cell migration	GO:0016477	21	0.020
axon guidance	GO:0007411	20	0.017