

Supplementary Table SIII Enriched Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways (false discovery rate (FDR) < 0.05) from gene set enrichment analysis (positive normalized enrichment score (NES), pathway upregulated; negative NES, pathway downregulated) of 9728 genes differentially expressed upon trophoblast stem cell (TSC) differentiation to syncytiotrophoblast (STB) ($P < 0.01$, TSC $n = 4$, STB $n = 4$; [Okae et al., 2018](#)).

Gene set	Description	Size	NES	FDR
hsa05322	Systemic lupus erythematosus	47	3.031	<1.00E–04
hsa05034	Alcoholism	87	2.150	3.10E–03
hsa04913	Ovarian steroidogenesis	21	2.080	3.62E–03
hsa04080	Neuroactive ligand-receptor interaction	56	1.941	1.28E–02
hsa04060	Cytokine–cytokine receptor interaction	79	1.841	1.99E–02
hsa04630	JAK-STAT signalling pathway	77	1.785	2.51E–02
hsa04610	Complement and coagulation cascades	28	1.733	2.99E–02
hsa04978	Mineral absorption	23	1.720	2.89E–02
hsa05222	Small cell lung cancer	69	–1.677	4.89E–02
hsa05219	Bladder cancer	31	–1.691	4.57E–02
hsa03460	Fanconi anaemia pathway	36	–1.693	4.97E–02
hsa05217	Basal cell carcinoma	39	–1.719	3.93E–02
hsa04310	Wnt signalling pathway	90	–1.737	3.68E–02
hsa04974	Protein digestion and absorption	32	–1.748	3.68E–02
hsa04390	Hippo signalling pathway	98	–1.754	4.08E–02
hsa03030	DNA replication	35	–1.793	2.93E–02
hsa04218	Cellular senescence	114	–1.808	3.08E–02
hsa03440	Homologous recombination	31	–1.854	2.08E–02
hsa04110	Cell cycle	110	–2.115	<1.00E–04