

KEGG_Pathway

Term	Count	p-Value	Genes
hsa04080:Neuroactive ligand-receptor interaction	60	4.48E-12	
hsa04020:Calcium signaling pathway	47	1.28E-11	
hsa04340:Hedgehog signaling pathway	23	8.56E-10	
hsa05217:Basal cell carcinoma	22	3.86E-09	
hsa05200:Pathways in cancer	63	7.48E-09	
hsa04916:Melanogenesis	25	5.20E-06	
hsa04310:Wnt signaling pathway	30	6.86E-05	WNT5A, CER1, WNT16, NKD1, WNT5B, APC2, WNT3A, PPP2R5C, WNT2, WNT1, WNT3, FRAT1, CAMK2B, WNT6, NFATC1, WNT10A, WNT10B, FZD1, LEF1, FZD2, WNT2B, SFRP5, DKK2, FZD10, DKK1, PRICKLE1, SFRP4, WNT9B, WNT11, WNT7A
hsa04950:Maturity onset diabetes of the young	10	2.12E-04	
hsa05414:Dilated cardiomyopathy	19	0.001305	

Supplemental Figure S5: DAVID-KEGG (<http://david.abcc.ncifcrf.gov>) signaling pathway analysis with the overlapped H3K27me3-marked genes in human ESCs from two independent reports (Pan et al. 2007; Zhao et al. 2007). Only the pathways with $p < 0.001$ are listed. Genes of the WNT signaling pathway with H3K27me3 enrichment in human ESCs are listed.

Supplemental References

Pan G, Tian S, Nie J, Yang C, Ruotti V, Wei H, Jonsdottir GA, Stewart R, Thomson JA. 2007. Whole-genome analysis of histone H3 lysine 4 and lysine 27 methylation in human embryonic stem cells. *Cell stem cell* 1: 299-312.

Zhao XD, Han X, Chew JL, Liu J, Chiu KP, Choo A, Orlov YL, Sung WK, Shahab A, Kuznetsov VA *et al.* 2007. Whole-genome mapping of histone H3 Lys4 and 27 trimethylations reveals distinct genomic compartments in human embryonic stem cells. *Cell stem cell* 1: 286-298.