Figure S10

A EC/ESC/iPSC co-hypomethylation module

DAVID Bioinformatics Resources 6.7 National Institute of Allergy and Infectious Diseases (NIAID), NIH									
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Current Background: Homo sapiens 75 DAVID IDs									
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Sublis		transcription regulation	⇔ RT Genes	Count % P-Value Benjamini 24 32.0 1.1E-7 1.8E-5					
	SP_PIR_KEYWORDS		RT	24 32.0 1.7E-7 1.4E-5					
	GOTERM_MF_FAT	transcription regulator activity	RT	19 25.3 6.5E-6 1.2E-3					
	GOTERM_BP_FAT	transcription	RT	23 30.7 7.2E-6 6.1E-3					
	SP_PIR_KEYWORDS	nucleus	RT	32 42.7 7.9E-6 4.2E-4					
	GOTERM_BP_FAT	negative regulation of transcription, DNA-dependent	<u>RT</u>	10 13.3 1.0E-5 4.4E-3					
	GOTERM_BP_FAT	negative regulation of cellular biosynthetic process	RT	12 16.0 1.1E-5 3.0E-3					
	GOTERM_BP_FAT	negative regulation of RNA metabolic process	RT	10 13.3 1.2E-5 2.5E-3					
	GOTERM_BP_FAT	negative regulation of biosynthetic process	RT	12 16.0 1.3E-5 2.2E-3					
	GOTERM_BP_FAT	regulation of transcription from RNA polymerase II promoter	RT	13 17.3 2.3E-5 3.2E-3					
	SP_PIR_KEYWORDS	dna-binding	RT	19 25.3 3.9E-5 1.6E-3					
	GOTERM_BP_FAT	regulation of RNA metabolic process	RT	20 26.7 4.1E-5 4.9E-3					
	GOTERM_BP_FAT	negative regulation of macromolecule biosynthetic process	<u>RT</u>	11 14.7 5.2E-5 5.5E-3					
	GOTERM_MF_FAT	transcription factor activity	<u>RT</u>	14 18.7 5.8E-5 5.3E-3					
	GOTERM_MF_FAT	DNA binding	RT	22 29.3 6.3E-5 3.9E-3					
	GOTERM_BP_FAT	negative regulation of transcription	<u>RT</u>	10 13.3 7.5E-5 7.1E-3					
	GOTERM_BP_FAT	negative regulation of transcription from RNA polymerase II promoter	RT	8 10.7 8.4E-5 7.2E-3					
	GOTERM_BP_FAT	regulation of transcription, DNA-dependent	<u>RT</u>	19 25.3 1.1E-4 8.3E-3					

B EC-unique hypomethylation module

Current Gene List: List_1 Current Background: Homo sapiens 103 DAVID IDs Options								
Rerun Using Options Create Sublist 35 chart records								
Sublist	Category :	<u>Term</u> ÷	RT Ge	nes <u>Count</u>	<u>%</u> ‡ <u>P-Value</u>	Benjamin‡		
	CGAP_SAGE_QUARTILE	toci or yolk sac tumor and teratoma seen. Size	<u>RT</u>	19	18.4 2.0E-6	6.7E-4		
	CGAP_SAGE_QUARTILE	testis. Embyronal Carcinoma, Mixed germ cell tumor consisting primarily of embryonal carcinoma with foci of yolk sac tumor and teratoma seen. Size	<u>RT</u>	19	18.4 7.9E-5	1.4E-2		

Supplemental Fig. S10. A: Functional annotation of the EC-ESC/iPSC co-hypomethylation module of 141 CpG targets mapped to 76 genes revealed significant association with homeobox and cell fate commitment genes (Table S2). B: Targets uniquely erased in EC relative to pluripotent references (161 targets mapped to 56 genes) are significantly enriched for genes with upregulated transcription in EC (Table S2).