

TF Motif	Z-value of Motif Activity	PCC	Pattern	Status in the Comparison
IRF2_STAT2_IRF8_IRF1	7,68	IRF2	AAGGAAAGC GAAACCGAA AC	Up-regulated in hiPSCs-derived LSECs
MEIS2	6,33	MEIS2	TTGACAG	Up-regulated in hiPSCs-derived LSECs
ERG	4,66	ERG	ACAGGAAGT G	Up-regulated in hiPSCs-derived LSECs
SPI1	4,60	SPI1	AGGAAGT	Up-regulated in hiPSCs-derived LSECs
IRF7	4,45	IRF7	GAAAGTGAA A	Up-regulated in hiPSCs-derived LSECs
WRNIP1	3,96	WRNIP1	GGGAAGAGG GAG	Up-regulated in hiPSCs-derived LSECs
HIC2	3,74	HIC2	ATGCCACC	Up-regulated in hiPSCs-derived LSECs
NFIX_NFIB	3,42		CTTGGCA	Up-regulated in hiPSCs-derived LSECs
BATF	3,2	BATF	ATGAGTCATA	Up-regulated in hiPSCs-derived LSECs
PATZ1_KL4	3,11	PATZ1	GGGGGAGG GGCCG	Up-regulated in hiPSCs-derived LSECs
MYCN_MYC_MXI1	8,41	MYCN	CCACGTG	Up-regulated in hiPSCs
YBX1_FOS_NFYC_NFYA_NFYB_CEBPZ	7,00	CEBPZ	GGGGATTGG CC	Up-regulated in hiPSCs
ETV5_ELK4_ELK1_ELK3_ELF4	6,43	ETV5	GCCGGAAGT G	Up-regulated in hiPSCs
E2F7_E2F1	5,86	E2F7	CTTTTCCCG CCA	Up-regulated in hiPSCs
ZEB1	5,59	ZEB1	CTCACCTG	Up-regulated in hiPSCs
RCOR1_MTA3	4,90	MTA3	GGAGGCGG GG	Up-regulated in hiPSCs
TAF1	3,94	TAF1	GCCGCCATC TT	Up-regulated in hiPSCs

KLF16_SP2	3,30	KLF16_SP2	GCCACGCCC CC	Up-regulated in hiPSCs
PBX3	3,19	PBX3	CCTGTCAAT CA	Up-regulated in hiPSCs
E2F2_E2F5	3,13	E2F5	TTTGGCGC	Up-regulated in hiPSCs

Table 1: Top 10 Transcription Factor (TF) motifs extracted in the comparison between hiPSCs-derived LSECs and hiPSCs by ISAMARA analysis, sorting by highest Z-value. “TF motif” represents a set of Transcription Factors with similar target nucleotide sequence pattern identified by CAGE. “PCC” is the gene with the strongest Pearson correlation coefficient for the TF Motif identified. “Pattern” describes the nucleotide sequence pattern of the motif for the PCC selected genes.