

Table S13. De novo motifs enriched in predicted enhancer regions.

Name	Consensus	Known Match (score)	Enhancer over-conservation Z-score (stdev)	Enhancer enrichment Z-score (stdev)	Promoter over-conservation Z-score (stdev)	Promoter enrichment Z-score (stdev)	Promoter depletion Z-score (stdev)
M01	VTGABTCRC	AP-1 (80%)	36.0	37.1	15.7		
M02	TAATTGM	NKX2-5 (88%)	36.0	4.2	14.8		
M03	MAAKGTCR	SF-1 (80%)	35.7	20.4	11.7		
M04	CTTTGAW	TCF-4 (97%)	32.2	8.4	12.9		
M05	YGANTYRGC		31.1	26.8	13.1		4.6
M06	GGAARTGA	STAT1 (88%)	29.5	13.1	21.4	8.3	
M07	TAATTAC	CHX10 (80%)	27.2	4.3	11.0		
M08	YTGCCNNNNNKYCMR	NF-1 (82%)	25.5	30.2	11.3		13.7
M09	YCATTAGY		25.4	5.0	9.2		3.8
M10	ATYWGTCR		23.8	14.0	6.5		
M11	RCATTCCA	TEF-1 (79%)	20.9	21.5	8.2		
M12	RACAGMTGK	TAL-1ALPHA/E47 (86%)	20.3		8.8		9.3
M13	CNTRGCAAC		18.9	5.6	21.7		
M14	AAACCACA	AML1 (86%)	18.6	13.1	5.8		3.7
M15	TGASGTCR	CREB (85%)	18.4	12.7	18.6	15.7	
M16	TAAWTTA	POU6F1 (78%)	15.7				3.3
M17	GCCARGAA		15.7	7.9	5.3		13.9
M18	CACNAGNGGG		15.5		8.3		
M19	GCTAWWWWTAG	MEF-2 (83%)	15.3	8.6	9.0	4.2	
M20	CATNANTAAT		15.1	5.2	5.8		
M21	TGTYKACR		14.6	3.3	6.8		
M22	GCCARNNNAACA		12.0	15.1			
M23	TATTNNNNYYGGC		12.0	3.7			
M24	YGTCNRRACA		11.8	4.3			
M25	TAATGAGC	CHX10 (83%)	11.6		5.5		
M26	TAATTGGC	CHX10 (83%)	11.5		4.2		
M27	AGGTTAAT		11.5	3.7			
M28	ATTANNNYGACR		10.5				
M29	GTCAGAC		10.3	4.4	4.1		
M30	YGTCRNNNNNATTA		10.3				
M31	CANYAGVTGGC		10.1		7.3		3.6
M32	YGCRRTCA		9.8		9.7		
M33	SATCAATCR	PBX-1 (84%)	9.5				
M34	YGATTNNTGC		9.5	4.1	7.8	4.7	
M35	AGGCNNNNGCCAR		8.3	9.9	3.8		18.7
M36	GCCRRNNNNNATTA		7.5				8.6
M37	GGAAWTNCCC	P65 (94%)	7.4	5.5	4.5		
M38	CAKCTGGA	RP58 (85%)	7.3	4.9	4.4		12.9
M39	AGCAGCTGC	AP-4 (90%)	6.5		4.2		
M40	RCCATATGGY		4.7				8.4
M41	GTYNCCANRGNRAC		3.7		4.1		