

1 **Supplementary Table 3 The candidate functional variant lies on binding sites for multiple transcription factors.**

Position Weight Matrix ID	Strand	Match on:	
		Ref:	Alt:
		TATATACACTGGGAAACCAAAACATTTGTA	ATGACTCACTTTGTTGCAATATTTGTTTTA
		TATATACACTGGGAAACCAAAACATTTGTG	TGACTCACTTTGTTGCAATATTTGTTTTA
AP-1_disc3	-		DRTGASTCAY
AP-1_known3	+		VTGACTHA
AP-1_known4	+		MTGASTMAB
AP-2_disc1	-		VTGASTCABB
BAF155_disc1	-		GRTGASTCAS
BATF_disc1	+		KNDVTGASTCA
BCL_disc2	+		MTGASTCAKY
Bach1	+		RBSATGACTCAYSNE
Bach2	+		SRTGACKCAYS
Cdx	+	NAYWRHHARAKHRTAWA	
GATA_disc2	-		SHVTGAVTCA
GR_disc2	-		VTGASTCABN
Irf_disc2	-		DHTGASTCAD
KAP1_disc1	-		NDVTGASTCA
Mef2_disc3	+		AWGASTCAG
Myc_disc3	+		VTGASTCABB
PRDM1_disc2	-		RTGASTCAYH
RXRA_disc3	-		DTKASTMAHH
STAT_disc2	+		VTGANTCAYN
TCF4_disc1	+		VTGASTCABN
p300_disc1	+		VTGASTCABN

2 Ref. reference sequence, Alt., altered sequence.

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