

Supplementary Table 6. RegulomeDB annotation of the top *LOXL1* and *CACNA1A* SNPs (rs4886776 and rs4926244 respectively, marked with an *) and those in LD with them (1000 genomes Asians $r^2 > 0.8$).

Chr	Pos	r^2	D'	rsID	RefSeq gene name	dbSNP functional annotation	hits	RegulomeDB score
15	74219546	0.98	0.99	rs1048661	<i>LOXL1</i>	missense; intronic	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq CREBBP, Protein_Binding ChIP-seq IKZF1, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq MYC Motifs PWM Bach2, Motifs PWM AP-1, Motifs Footprinting AP-1,	4
15	74223500	0.99	1	rs150025731	<i>LOXL1</i>	intronic	Motifs Footprinting Bach2, Motifs PWM Fos, Motifs Footprinting Fos, Chromatin_Structure DNase-seq Motifs PWM HSF2, Motifs Footprinting HSF2,	5
15	74223767	0.99	1	rs1992314	<i>LOXL1</i>	intronic	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	5
15	74224996	1	1	rs4886776*	<i>LOXL1</i>	intronic	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	5
15	74226145	1	1	rs58270968	<i>LOXL1</i>	intronic	Chromatin_Structure DNase-seq	5
15	74227037	0.93	1	rs2028387	<i>LOXL1</i>	intronic	Motifs Footprinting Pax-6, Motifs PWM Pax-6, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq GATA2	2b
15	74228391	1	1	rs4077284	<i>LOXL1</i>	intronic	Chromatin_Structure DNase-seq	5
15	74228464	1	1	rs893816	<i>LOXL1</i>	intronic	Motifs PWM RUNX1, Motifs PWM AML, Motifs PWM PEBP, Motifs Footprinting AML, Motifs Footprinting RUNX1, Motifs Footprinting PEBP,	5
15	74229065	1	1	rs893817	<i>LOXL1</i>	intronic	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq SPI1	4
15	74229195	1	1	rs893818	<i>LOXL1</i>	intronic	Chromatin_Structure DNase-seq	5
15	74229477	1	1	rs67173550	<i>LOXL1</i>	intronic	Chromatin_Structure DNase-seq	5
15	74229791	1	1	rs4886785	<i>LOXL1</i>	intronic	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq	5
15	74230660	0.94	0.98	rs59755145	<i>LOXL1</i>	intronic	No data	7

19	13345526	0.73	0.95	rs11085837	CACNA1A	intronic	Motifs Footprinting Lmo2complex, Motifs PWM Lmo2complex, Motifs PWM Sp4, Motifs PWM Gcm1, Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq ZNF263, Protein_Binding ChIP-seq GABPA, Protein_Binding ChIP-seq EGR1, Protein_Binding ChIP-seq MYC, Protein_Binding ChIP-seq MAX, Protein_Binding ChIP-seq RAD21, Protein_Binding ChIP-seq ELF1, Protein_Binding ChIP-seq SMC3, Protein_Binding ChIP-seq STAT3, Protein_Binding ChIP-seq POLR2A, Protein_Binding ChIP-seq ZBTB7A, Protein_Binding ChIP-seq CTCF, Protein_Binding ChIP-seq CTCF	2b
19	13355068	0.79	0.98	rs12052059	CACNA1A	intronic	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq ZBTB7A, Protein_Binding ChIP-seq REST	4
19	13337966	0.70	0.95	rs3786935	CACNA1A	intronic	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq YY1	4
19	13351774	0.77	0.98	rs11881621	CACNA1A	intronic	Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq ETS1, Protein_Binding ChIP-seq CTCF	4
19	13351594	0.82	0.99	rs4926240	CACNA1A	intronic	Chromatin_Structure FAIRE, Chromatin_Structure DNase-seq, Protein_Binding ChIP-seq CTCF, Protein_Binding ChIP-seq REST	4
19	13368930	1	1	rs12151170	CACNA1A	intronic	Chromatin_Structure DNase-seq	5
19	13375287	1	1	rs4926246	CACNA1A	intronic	Motifs PWM Arnt, Motifs PWM Bhlhb2, Protein_Binding ChIP-seq STAT1	5

19	13339128	0.71	0.94	rs10405121	CACNA1A	intronic	Motifs PWM Zfp410, Chromatin_Structure DNase-seq	5
19	13371155	0.99	1	rs59384530	CACNA1A	intronic	Motifs PWM FOXP1, Motifs PWM FOXJ2, Motifs PWM Foxk1, Motifs PWM Zfp105, Motifs PWM Foxj1, Motifs PWM FAC1	6
19	13370986	1	1	rs62108599	CACNA1A	intronic	Motifs PWM FOXJ2, Motifs PWM MEF-2, Motifs Footprinting MEF-2	6
19	13357525	0.96	0.99	rs62111970	CACNA1A	intronic	Motifs PWM ZBRK1	6
19	13377081	0.94	1	rs61453777	CACNA1A	intronic	Motifs PWM Zbtb3	6
19	13357449	0.96	0.99	rs4926241	CACNA1A	intronic	Motifs PWM FOXP1, Motifs PWM Srf, Motifs Footprinting FOXD3, Motifs PWM FOXJ2, Motifs Footprinting Foxd3, Motifs PWM Foxd3, Motifs PWM Foxa2, Motifs PWM Zfp105, Motifs Footprinting HNF3alpha, Motifs PWM Tcfap2e, Motifs Footprinting FOXO1, Motifs PWM HNF3alpha, Motifs Footprinting HNF3, Motifs Footprinting FOXfactors, Motifs PWM FOXD3, Motifs PWM FOXfactors, Motifs PWM HNF3, Motifs PWM Elf3, Motifs PWM FOXO1	6
19	13374913	NA	NA	rs4926244	CACNA1A	intronic	No data	7
19	13371003	1	1	rs62108600	CACNA1A	intronic	No data	7
19	13329478	0.61	0.81	rs7256827	CACNA1A	intronic	No data	7
19	13353401	0.83	0.98	rs7247602	CACNA1A	intronic	No data	7
19	13354403	0.79	0.98	rs10412233	CACNA1A	intronic	No data	7

R² and D' values are measured between the SNP and the reported risk SNP* within the locus in 1000 genomes Cosmopolitan (HaploReg v2)

#RegulomeDB scores indicate the amount of supporting data for regulatory effects at a single coordinate. The lower the scores, the stronger the evidence, with 2b indicating overlapping evidence for transcription factor binding, any motif, DNase footprint and DNase peak at that location, 4 indicating evidence for both transcription factor binding and DNase peak at that location, 5 indicating data for either transcription factor binding or DNase peak, 6 indicating other evidence (e.g. motifs only) and 7 indicating no supporting data for that coordinate.