

**Table S8.** Summary of genomic annotation for LD surrogates of rs12449931.

<b>FIELD</b>	<b>DESCRIPTION</b>
<b>chr</b>	Chromosome
<b>pos (hg38)</b>	Chromosome position on hg38 obtained from dbSNP build 141
<b>LD (<math>r^2</math>)</b>	Pairwise $r^2$ measure of LD with query SNP from 1000 Genomes Project EUR data
<b>LD (D')</b>	Pairwise D' measure of LD with query SNP from 1000 Genomes Project EUR data
<b>variant</b>	rsID of collected SNP
<b>Ref</b>	Reference nucleotide(s)
<b>Alt</b>	Alternate nucleotide(s)
<b>AFR freq</b>	Allele frequency for African population
<b>AMR freq</b>	Allele frequency for American population
<b>ASN freq</b>	Allele frequency for Asian population
<b>EUR freq</b>	Allele frequency for European population
<b>GERP cons</b>	Conserved regions by GERP (Blue: conserved)
<b>SiPhy cons</b>	Conserved regions by SiPhy (Purple: conserved)
<b>Promoter histone marks</b>	Summary of ChromHMM (core 15-state model) states corresponding to promoter elements from the Roadmap Epigenomics project
<b>Enhancer histone marks</b>	Summary of ChromHMM (core 15-state model) states corresponding to enhancer elements from the Roadmap Epigenomics project
<b>DNase</b>	Summary of DNase hypersensitivity from the Roadmap Epigenomics project
<b>Proteins bound</b>	Protein bound(s) by ChIP-Seq
<b>Motif changed</b>	Motif alteration(s) from TRANSFAC, JASPAR, and protein-binding microarray (PBM) experiments
<b>NHGRI/EBI GWAS hits</b>	SNP in NHGRI GWAS catalog (accessed October 31, 2015)
<b>GRASP QTL hits</b>	SNP in The GRASP Build 2.0.0.0 results and QTLs (non-GWAS)
<b>Selected eQTL hits</b>	SNP in eQTLs obtained from the GTEx analysis V6, the GEUVADIS analysis, and 10 other studies
<b>GENCODE genes</b>	Gene annotations by GENCODE version 13
<b>dbSNP func annot</b>	Functional annotations from dbSNP build 137
<b>RegulomeDB score</b>	RegulomeDB score ( <a href="http://regulomedb.org/help#score">http://regulomedb.org/help#score</a> ). 1 is most likely to be functional, to 7 = least likely.

chr	pos (hg38)	LD (r <sup>2</sup> )	LD (D')	variant	Ref	Alt	AFR freq	AMR freq	ASN freq	EUR freq	GERP cons	SiPhy cons	Promoter histone marks	Enhancer histone marks	DNase	Proteins bound	Motifs changed	NHGRI/EBI GWAS hits	GRASP QTL hits	Selected eQTL hits	GENCODE genes	dbSNP func annot	RegulomeDB score	
17	79278229	0.89	0.98	rs4789989	C	T	0.37	0.57	0.8	0.43				IPSC			CEBPB,Pax-4,Zfx					RBFOX3	intronic	5
17	79279996	1	1	rs12449931	T	C	0.38	0.57	0.8	0.42				MUS			Zic					RBFOX3	intronic	5
17	79280526	1	1	rs4465632	G	A	0.31	0.56	0.8	0.42				MUS	LNG		Pax-5					RBFOX3	intronic	2b