

Table S9. Summary of genomic annotation for LD surrogates of rs17367673.

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

chr	pos (hg38)	LD (r ²)	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
19	46844195	0.7	0.87	rs112634057	G	A	0.05	0.21	0.06	0.18				6 tissues	7 tissues	13 bound proteins	16 altered motifs				AP2S1	intronic	4
19	46856603	0.72	0.9	rs71332952	CGTTT	C	0.04	0.21	0.05	0.19			22 tissues	9 tissues	35 tissues	5 bound proteins	19 altered motifs				5.7kb 5' of AP2S1		2a
19	46894238	1	1	rs17367673	C	T	0.04	0.2	0.05	0.17			STRM	10 tissues	8 tissues	CEBPB,JUND,TBP	RAR			2 hits	24kb 5' of ARHGAP35		4
19	46978425	0.75	0.87	rs73059314	G	A	0.04	0.21	0.05	0.17			MUS	22 tissues	5 tissues		PPAR				ARHGAP35	intronic	5