Locus 256 (rs805273)

SNiPAcard

Block annotations

Block info

genomic range	chr6:31,665,452-31,665,452
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	0.647	gene(s) hit or close-by	ABHD16A, MIR4646, XXbac-BPG32J3.20
phastCons	0.001	eQTL gene(s)	LY6G5C, OR10C1, OR10C1, XXbac-BPG181B23.7
GERP++	0.848	potentially regulated gene(s)	–
CADD score	7.531	disease gene(s)	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
XXbac-BPG181B23.7	?	ENSG00000272221	skeletal muscle	1.14×10^{-6} (p-value)	GTEx Portal V6	1
LY6G5C	?	ENSG00000204428	sun exposed skin	3.75×10^{-6} (p-value)	GTEx Portal V6	1
OR10C1	ENST00000623086	ILMN_1790706	monocyte	1.01×10^{-5} (p-value)	Fairfax et al.	1
OR10C1	ENST00000444197					
OR10C1	ENST00000622521					

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
ABHD16A	upstream gene variant	4619	ENST00000496579	?	?	1
MIR4646	downstream gene variant	3354	ENST00000580775	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
ABHD16A	ENST00000440843	NM_001177515.1	ENSP00000410347	1
ABHD16A	ENST00000482224	?	ENSP00000419742	1
ABHD16A	ENST00000395952	NM_021160.2	ENSP00000379282	1
ABHD16A	ENST00000498420	?	ENSP00000420628	1
ABHD16A	ENST00000477462	?	ENSP00000418331	1
ABHD16A	ENST00000492084	?	ENSP00000420585	1
ABHD16A	ENST00000468037	?	ENSP00000417566	1
ABHD16A	ENST00000495769	?	ENSP00000418170	1
XXbac-BPG32J3.20	ENST00000461287	?	ENSP00000475702	1

Locus 256 (sentinel SNP rs805273 + proxy variants in LD r2 > 0.8). SNiPA block annotation (www.snipa.org) based on 1000 Genomes Project phase 3 v5 (European population) variant set and Ensembl 82 annotations.