SNiPAcard

Block annotations

Block info

genomic range	chr19:55,392,646-55,392,646
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-2.068	**gene(s) hit or close-by**	FCAR
phastCons	0.09	**eQTL gene(s)**	–
GERP++	0	**potentially regulated gene(s)**	–
CADD score	2.603	**disease gene(s)**	–

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000348895 (CTCF binding site)	1	embryonic stem cell (H1ESC)	H3K27me3, Rad21, CTCF, DNase1
		Osteobl	CTCF
		blood (K562)	DNase1, H3K27me3, CTCF, Rad21
		cervix (HeLa-S3)	CTCF
		monocytes (Monocytes-CD14+)	H3K36me3, DNase1, CTCF, H4K20me1
		endothelium (HUVEC)	CTCF
		liver (HepG2)	CTCF, Rad21, DNase1
		blood (GM12878)	CTCF
		A549	H3K27me3, DNase1, CTCF

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
FCAR	ENST00000482092	?	?	1
FCAR	ENST00000355524	NM_002000.2	ENSP00000347714	1
FCAR	ENST00000472634	?	?	1
FCAR	ENST00000488066	?	ENSP00000474512	1
FCAR	ENST00000391726	NM_133273.2	ENSP00000375606	1
FCAR	ENST00000353758	NM_133277.2	ENSP00000338058	1
FCAR	ENST00000345937	NM_133271.2	ENSP00000338257	1
FCAR	ENST00000391724	NM_133278.2	ENSP00000375604	1
FCAR	ENST00000469767	NM_133279.2	ENSP00000473814	1
FCAR	ENST00000359272	NM_133272.2	ENSP00000352218	1
FCAR	ENST00000471750	?	?	1
FCAR	ENST00000391723	NM_133274.2	ENSP00000375603	1
FCAR	ENST00000391725	NM_133269.2	ENSP00000375605	1