Locus 305 (rs6561333)

SNiPAcard

Block annotations

Block info

genomic range	chr13:47,420,312-47,423,291
block size	2,980 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.566 [-1.342 – -0.171]	gene(s) hit or close-by	HTR2A, HTR2A-AS1
phastCons	μ = 0.000 [0 – 0]	eQTL gene(s)	–
GERP++	μ = -0.212 [-0.764 – 0.108]	potentially regulated gene(s)	–
CADD score	μ = 2.501 [1.29 – 3.533]	disease gene(s)	–

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
HTR2A-AS1	upstream gene variant	2987	ENST00000455126	?	?	1
HTR2A-AS1	upstream gene variant	2996	ENST00000452352	?	?	1
HTR2A-AS1	upstream gene variant	2996	ENST00000430913	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
HTR2A	ENST00000378688	?	ENSP00000367959	3
HTR2A	ENST00000542664	NM_000621.4	ENSP00000437737	3
HTR2A	ENST00000543956	NM_001165947.2	ENSP00000441861	3