Locus 275 (rs7325116)

SNiPAcard

Block annotations

Block info

genomic range	chr13:92,554,173-92,604,445
block size	50,273 bp
variant count	13 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.557 [-2.987 – 0.88]	**gene(s) hit or close-by**	GPC5
phastCons	μ = 0.073 [0 – 0.849]	**eQTL gene(s)**	GPC5
GERP++	μ = -1.026 [-5.52 – 1.62]	**potentially regulated gene(s)**	–
CADD score	μ = 2.599 [0.117 – 5.609]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
GPC5	?	ENSG00000179399	subcutaneous adipocytes	1.66×10^{-5} (p-value)	GTEx Portal V6	3
GPC5	ENST00000377067	ILMN_1688886	adipocyte	3.94×10^{-7} (p-value)	MuTHER consortium	5

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
GPC5	ENST00000377067	NM_004466.4	ENSP00000366267	13