Locus 37 (rs342706)

SNiPAcard

Block annotations

Block info

genomic range	chr13:92,414,715-92,453,051
block size	38,337 bp
variant count	76 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.632 [-5.445 – 1.165]	gene(s) hit or close-by	GPC5
phastCons	μ = 0.023 [0 – 0.991]	eQTL gene(s)	–
GERP++	μ = -0.480 [-5.75 – 2.7]	potentially regulated gene(s)	FABP5P4
CADD score	μ = 2.705 [0.015 – 13.41]	disease gene(s)	–

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link	variant(s)
LUNG CANCER	<6.00×10-6	GWAS Catalog	20304703	1

Putative effect on regulation

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000161614	2	ENCP00000018923	FABP5P4

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000518738 (CTCF binding site)	1	cervix (HeLa-S3)	CTCF
		embryonic stem cell (H1ESC)	Rad21, CTCF
		endothelium (HUVEC)	H3K36me3
		liver (HepG2)	Rad21, CTCF
		blood (K562)	CTCF

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
GPC5	ENST00000377067	NM_004466.4	ENSP00000366267	76