SNiPAcard

Block annotations

Block info

genomic range	chr10:52,017,680-52,029,901
block size	12,222 bp
variant count	22 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.701 [-3.248 – 2.176]	**gene(s) hit or close-by**	DYNC1I2P1
phastCons	μ = 0.113 [0 – 1]	**eQTL gene(s)**	FAM21A
GERP++	μ = -0.161 [-7.14 – 1.41]	**potentially regulated gene(s)**	–
CADD score	μ = 3.195 [0.039 – 11.92]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
FAM21A	?	ENSG00000099290	muscularis mucosae	4.66×10^{-6} (p-value)	GTEx Portal V6	14
FAM21A	?	ENSG00000099290	lung	9.80×10^{-11} (p-value)	GTEx Portal V6	18
FAM21A	?	ENSG00000099290	atrial appendage	1.18×10^{-8} (p-value)	GTEx Portal V6	17
FAM21A	?	ENSG00000099290	transformed fibroblasts	2.28×10^{-9} (p-value)	GTEx Portal V6	16
FAM21A	?	ENSG00000099290	breast	2.34×10^{-9} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	tibial artery	1.53×10^{-14} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	thyroid	1.61×10^{-12} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	skeletal muscle	3.93×10^{-19} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	liver	1.87×10^{-9} (p-value)	GTEx Portal V6	17
FAM21A	?	ENSG00000099290	sun exposed skin	1.22×10^{-15} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	unexposed skin	2.21×10^{-8} (p-value)	GTEx Portal V6	17
FAM21A	?	ENSG00000099290	left ventricle	6.73×10^{-8} (p-value)	GTEx Portal V6	16
FAM21A	?	ENSG00000099290	subcutaneous adipocytes	2.62×10^{-15} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	visceral adipocytes	5.71×10^{-13} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	sigmoid colon	3.70×10^{-7} (p-value)	GTEx Portal V6	17
FAM21A	?	ENSG00000099290	tibial nerve	4.95×10^{-10} (p-value)	GTEx Portal V6	18
FAM21A	?	ENSG00000099290	esophagus mucosa	5.48×10^{-12} (p-value)	GTEx Portal V6	19
FAM21A	?	ENSG00000099290	testis	7.29×10^{-9} (p-value)	GTEx Portal V6	17
FAM21A	?	ENSG00000099290	putamen	1.59×10^{-6} (p-value)	GTEx Portal V6	6
FAM21A	?	ENSG00000099290	gastroesophageal junction	7.79×10^{-7} (p-value)	GTEx Portal V6	8
FAM21A	?	ENSG00000099290	hippocampus	2.59×10^{-6} (p-value)	GTEx Portal V6	4

FAM21A	?	ENSG00000099290	frontal cortex	4.18×10^{-6} (p-value)	GTEx Portal V6	1
FAM21A	?	ENSG00000099290	anterior cingulate cortex	1.16×10^{-6} (p-value)	GTEx Portal V6	2

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001423388 (open chromatin region)	1	embryonic stem cell (H1ESC)	H3K36me3
		lung (IMR90)	H3K36me3, H3K27me3
		A549	H3K27me3
		blood (K562)	H3K27me3
		muscle (HSMM)	DNase1

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
DYNC1I2P1	upstream gene variant, downstream gene variant	77	ENST00000435916	?	?	16

Putative effect on transcript

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
DYNC1I2P1	ENST00000435916	?	3