Locus 302 (rs27303)

SNiPAcard

Block annotations

Block info

genomic range	chr5:96,374,150-96,374,150
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	-0.623	gene(s) hit or close-by	LNPEP
phastCons	0	eQTL gene(s)	ERAP2
GERP++	-3.9	potentially regulated gene(s)	–
CADD score	5.479	disease gene(s)	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
ERAP2	?	ENSG00000164308	pancreas	1.79×10^{-8} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	uterus	1.42×10^{-6} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	muscularis mucosae	9.10×10^{-9} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	lung	9.64×10^{-16} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	transformed fibroblasts	1.50×10^{-12} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	blood	3.15×10^{-10} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	breast	3.08×10^{-6} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	tibial artery	9.57×10^{-9} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	thyroid	1.23×10^{-16} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	skeletal muscle	1.79×10^{-13} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	EBV lymphocytes	2.53×10^{-6} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	transverse colon	2.06×10^{-8} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	liver	4.03×10^{-7} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	sun exposed skin	2.65×10^{-12} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	unexposed skin	2.61×10^{-9} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	left ventricle	8.70×10^{-7} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	aorta	7.76×10^{-8} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	subcutaneous adipocytes	1.29×10^{-15} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	stomach	2.16×10^{-8} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	visceral adipocytes	6.43×10^{-6} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	nucleus accumbens	5.66×10^{-8} (p-value)	GTEx Portal V6	1

ERAP2	?	ENSG00000164308	sigmoid colon	2.55×10^{-8} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	tibial nerve	1.36×10^{-11} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	esophagus mucosa	4.57×10^{-10} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	adrenal gland	3.22×10^{-11} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	cerebellar hemisphere	1.46×10^{-6} (p-value)	GTEx Portal V6	1
ERAP2	?	ENSG00000164308	testis	4.48×10^{-8} (p-value)	GTEx Portal V6	1

Putative effect on regulation

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
LNPEP	downstream gene variant	931	ENST00000231368	NM_005575.2	ENSP00000231368	1