

SNiPAcad

Block annotations

Block info

genomic range	chr1:196,675,861-196,675,861 <i>e!</i>
block size	1 bp
variant count	1 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	0.57	gene(s) hit or close-by	CFH <i>e!</i>
phastCons	0.001	eQTL gene(s)	CFHR3 <i>e!</i>
GERP++	0.628	potentially regulated gene(s)	-
CADD score	2.058	disease gene(s)	CFHR3 <i>e!</i> , CFH <i>e!</i>

Trait annotations

Disease gene annotation

gene	trait	source DB	source entry/link
CFHR3 <i>e!</i>	Atypical hemolytic-uremic syndrome with anti-factor H antibodies	OrphaNet	OrphaNet:93581 orphanet
CFH <i>e!</i>	Immunodeficiency with factor H anomaly	OrphaNet	OrphaNet:200421 orphanet
CFH <i>e!</i>	Atypical hemolytic uremic syndrome with H factor anomaly	OrphaNet	OrphaNet:93579 orphanet
CFH <i>e!</i>	Dense deposit disease	OrphaNet	OrphaNet:93571 orphanet
CFH <i>e!</i>	Familial drusen	OrphaNet	OrphaNet:75376 orphanet
CFH <i>e!</i>	Immunoglobulin-mediated membranoproliferative glomerulonephritis	OrphaNet	OrphaNet:329903 orphanet

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
CFHR3 <i>e!</i>	?	ENSG00000116785 <i>e!</i>	atrial appendage	7.18×10 ⁻⁶ (p-value)	GTEx Portal V6 M	1
CFHR3 <i>e!</i>	?	ENSG00000116785 <i>e!</i>	tibial nerve	7.49×10 ⁻¹⁰ (p-value)	GTEx Portal V6 M	1
CFHR3 <i>e!</i>	?	ENSG00000116785 <i>e!</i>	aorta	6.75×10 ⁻⁷ (p-value)	GTEx Portal V6 M	1
CFHR3 <i>e!</i>	?	ENSG00000116785 <i>e!</i>	tibial artery	3.96×10 ⁻⁹ (p-value)	GTEx Portal V6 M	1
CFHR3 <i>e!</i>	?	ENSG00000116785 <i>e!</i>	subcutaneous adipocytes	2.39×10 ⁻⁷ (p-value)	GTEx Portal V6 M	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CFH <i>e!</i>	ENST00000466229 <i>e!</i>	?	?	1
CFH <i>e!</i>	ENST00000367429 <i>e!</i>	NM_000186.3	ENSP00000356399 <i>e!</i>	1

