SNiPAcard

Block annotations

Block info

genomic range	chr1:169,490,772-169,510,475
block size	19,704 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = 0.045 [-0.268 – 0.251]	**gene(s) hit or close-by**	F5
phastCons	μ = 0.023 [0 – 0.069]	**eQTL gene(s)**	–
GERP++	μ = -0.358 [-1.42 – 0.198]	**potentially regulated gene(s)**	–
CADD score	μ = 1.928 [0.002 – 3.434]	**disease gene(s)**	F5

Trait annotations

Disease gene annotation

gene	trait	source DB	source entry/link
F5	STROKE, ISCHEMIC	OMIM	MIM:601367
F5	THROMBOPHILIA DUE TO ACTIVATED PROTEIN C RESISTANCE	OMIM	MIM:188055
F5	PREGNANCY LOSS, RECURRENT, SUSCEPTIBILITY TO, 1	OMIM	MIM:614389
F5	FACTOR V DEFICIENCY	OMIM	MIM:227400
F5	BUDD-CHIARI SYNDROME	OMIM	MIM:600880
F5	Congenital factor V deficiency	OrphaNet	OrphaNet:326
F5	Cerebral sinovenous thrombosis	OrphaNet	OrphaNet:329217
F5	BUDD-CHIARI SYNDROME	OrphaNet	OrphaNet:131
F5	East Texas bleeding disorder	OrphaNet	OrphaNet:391320

Direct effect on transcript

Amino acid sequence alteration

gene	effect type	affected transcript	RefSeq id	protein	exchanged AA's	exchanged codons	SIFT prediction	PolyPhen prediction	variant(s)
F5	missense variant	ENST00000367796	?	ENSP00000356770	I/L	Att/Ctt	?	?	1
F5	missense variant	ENST00000367797	NM_000130.4	ENSP00000356771	I/L	Att/Ctt	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
F5	ENST00000367796	?	ENSP00000356770	2
F5	ENST00000367797	NM_000130.4	ENSP00000356771	2