Locus 293 (rs6036478)

SNiPAcard

Block annotations

Block info

genomic range	chr20:23,569,186-23,622,880
block size	53,695 bp
variant count	118 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.764 [-5.092 – 1.089]	gene(s) hit or close-by	CST3, CST9, RP11-218C14.2, RP11-218C14.8
phastCons	μ = 0.020 [0 – 0.388]	eQTL gene(s)	CST3, CST9, NAPB, RP11-218C14.5, RP11-218C14.8
GERP++	μ = -0.828 [-5.85 – 1.96]	potentially regulated gene(s)	CST11, CST3, CST5, CST8, CSTL1, CSTP1, GGTLC1, GZF1, POM121L3P, RP11-218C14.2
CADD score	μ = 2.443 [0.013 – 10.32]	disease gene(s)	CST3

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link	variant(s)
Plasma cystastin c levels in acute coronary syndrome	$<1.00\times10^{-26}$	GWAS Catalog	24952865	1
Chronic kidney disease	$<2.00\times10^{-138}$	GWAS Catalog	20383146	1
Cystatin C	$<9.00\times10^{-9}$	GWAS Catalog	17903292	1
chiro-inositol	6.50×10^{-5}	Metabolomics GWAS Server	24816252	1
Blood pressure	7.50×10^{-5}	dbGaP	pha002898	1
Cystatins	8.45×10^{-9}	dbGaP	pha001330	1
Cystatins	1.19×10^{-7}	dbGaP	pha001328	1

Variant annotation

trait	type	source DB	source entry/link	Variant(s)
Age-related macular degeneration 11	pathogenic	ClinVar	RCV000005989.1	1
?	HGMD curated	HGMD	CR040863	1
?	HGMD curated	HGMD	CR040862	1
MACULAR DEGENERATION, AGE-RELATED, 11	OMIM curated	OMIM	MIM:604312	1

Disease gene annotation

gene	trait	source DB	source entry/link
CST3	CEREBRAL AMYLOID ANGIOPATHY, CST3-RELATED	OMIM	MIM:105150
CST3	MACULAR DEGENERATION, AGE-RELATED, 11	OMIM	MIM:611953
CST3	Hereditary cerebral hemorrhage with amyloidosis, Icelandic type	OrphaNet	OrphaNet:100008

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)
CST3	missense variant	ENST00000398411	NM_001288614.1	ENSP00000381448	T/A	Acc/Gcc	?	?	1

CST3	missense variant	ENST00000376925	NM_000099.3	ENSP00000366124	T/A	Acc/Gcc	?	?	1
CST3	missense variant, splice acceptor variant	ENST00000398409	?	ENSP00000381446	T/A	Acc/Gcc	?	?	2

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
CST3	ENST00000398411	ILMN_1800354	blood	1.17×10^{-26} (p-value)	MuTHER consortium	44
CST3	ENST00000376925					
CST3	ENST00000398409					
NAPB	?	ENSG00000125814	muscularis mucosae	5.77×10^{-7} (p-value)	GTEx Portal V6	26
CST9	?	ENSG00000173335	muscularis mucosae	1.39×10^{-5} (p-value)	GTEx Portal V6	5
CST3	?	ENSG00000101439	lung	1.52×10^{-8} (p-value)	GTEx Portal V6	108
CST3	?	ENSG00000101439	sigmoid colon	3.39×10^{-7} (p-value)	GTEx Portal V6	68
CST3	?	ENSG00000101439	blood	2.38×10^{-8} (p-value)	GTEx Portal V6	111
RP11-218C14.8	?	ENSG00000270001	cerebellar hemisphere	2.39×10^{-7} (p-value)	GTEx Portal V6	104
CST3	?	ENSG00000101439	testis	4.07×10^{-18} (p-value)	GTEx Portal V6	113
RP11-218C14.8	?	ENSG00000270001	testis	2.23×10^{-7} (p-value)	GTEx Portal V6	112
RP11-218C14.8	?	ENSG00000270001	aorta	1.58×10^{-7} (p-value)	GTEx Portal V6	108
CST3	?	ENSG00000101439	tibial nerve	3.46×10^{-10} (p-value)	GTEx Portal V6	110
CST3	ENST00000398411	ILMN_1800354	monocyte	1.81×10^{-25} (p-value)	Zeller et al.	13
CST3	ENST00000376925					
CST3	ENST00000398409					
CST3	ENST00000398411	ILMN_1800354	monocyte	1.49×10^{-14} (p-value)	Fairfax et al.	9
CST3	ENST00000376925					
CST3	ENST00000398409					
CST3	?	ENSG00000101439	atrial appendage	3.21×10^{-6} (p-value)	GTEx Portal V6	3
CST3	?	ENSG00000101439	skeletal muscle	2.70×10^{-6} (p-value)	GTEx Portal V6	9
RP11-218C14.5	?	ENSG00000225056	hypothalamus	7.71×10^{-7} (p-value)	GTEx Portal V6	17
RP11-218C14.8	?	ENSG00000270001	tibial artery	1.20×10^{-5} (p-value)	GTEx Portal V6	1

Putative effect on regulation

Transcription factor binding site variation

transcription factor	binding motif	motif position	highly informative position	score change	variant(s)
CTCF	MA0139.1	14	no	0.000	1

ENCODE promoter-associated DHS

SNiPA promoter id	variant(s)	associated gene(s)
ENCP00000031087		

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000290793	1	ENCP00000031085	RP11-218C14.2
ENCE00000290764	1	ENCP00000031095	CST5
ENCE00000290765	1	ENCP00000031095	CST5
ENCE00000290698	1	ENCP00000031098	GGTLC1
		ENCP00000031079	CST11
		ENCP00000031078	CSTL1
		ENCP00000031081	CST8
		ENCP00000031096	CSTP1
ENCE00000290858	1	ENCP00000031097	POM121L3P GGTLC1
ENCE00000290678	1	ENCP00000031087	CST3
		ENCP00000031074	GZF1

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001021906 (enhancer)	3	embryonic stem cell (H1ESC)	H3K27me3, DNase1
		HSMMtube	H3K27me3
		liver (HepG2)	H3K4me1, DNase1
		blood (K562)	PU1, H2AZ
		A549	H3K27me3
ENSR00001664573 (open chromatin region)	2	endothelium (HUVEC)	H3K27me3
		lung (IMR90)	H3K27me3
		blood (GM12878)	H3K27me3
		A549	H3K27me3
ENSR00000649134 (CTCF binding site)	3	embryonic stem cell (H1ESC)	CTCF, Yy1, DNase1, Rad21
		HSMMtube	CTCF, H3K27me3, DNase1
		blood (K562)	CTCF, Rad21, H3K27me3
		skin (NHDF-AD)	CTCF
		muscle (HSMM)	DNase1, CTCF
		liver (HepG2)	Rad21, CTCF, H3K27me3, DNase1
		blood (GM12878)	CTCF, Rad21, DNase1
		lung (IMR90)	H3K27me3, CTCF
		nervous (NH-A)	CTCF
		skin (NHEK)	DNase1, CTCF
		NHLF	CTCF
		Osteobl	CTCF
		blood (DND-41)	CTCF
		breast (HMEC)	CTCF
		cervix (HeLa-S3)	DNase1, CTCF
		monocytes (Monocytes-CD14+)	DNase1, CTCF, H3K27me3
		endothelium (HUVEC)	H3K36me3, CTCF
		A549	CTCF
ENSR00001664575 (open chromatin region)	2	endothelium (HUVEC)	H3K27me3
		lung (IMR90)	H3K27me3
ENSR00001448098 (promoter flanking region)	12	embryonic stem cell (H1ESC)	DNase1
		HSMMtube	H3K9ac, H3K4me2, H3K27ac, H3K27me3, DNase1
		blood (K562)	H3K27me3
		skin (NHDF-AD)	H3K27ac, H3K4me2, H3K9ac, DNase1, H3K4me3
		muscle (HSMM)	H3K27ac, H3K4me2, DNase1, H3K9ac
		liver (HepG2)	FOSL2, Jund, H3K4me3, H3K4me1, H3K4me2, H3K27me3, DNase1
		lung (IMR90)	H3K4me2
		blood (GM12878)	EBF1
		nervous (NH-A)	DNase1, H3K4me2, H3K9ac
		skin (NHEK)	H3K4me2, H3K9ac, H3K27ac, DNase1
		NHLF	H3K27ac, DNase1
		Osteobl	H3K4me2, H3K27ac

		blood (DND-41)	H3K27me3
		breast (HMEC)	H3K4me2, H3K9ac, H3K27ac
		cervix (HeLa-S3)	DNase1, H3K4me2, Jund
		monocytes (Monocytes-CD14+)	H3K27ac, H3K4me3
		endothelium (HUVEC)	H3K36me3, DNase1, Cjun, H3K4me2, PolII
		A549	H3K4me3, H3K4me2, H3K9ac, DNase1
ENSR00000399197 (promoter flanking region)	4	embryonic stem cell (H1ESC)	DNase1
		HSMMtube	H3K27me3, DNase1
		blood (DND-41)	H3K27me3
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1
		cervix (HeLa-S3)	DNase1
		liver (HepG2)	H3K4me1
		skin (NHEK)	DNase1
ENSR00001448099 (open chromatin region)	1	muscle (HSMM)	DNase1
ENSR00000399198 (promoter flanking region)	5	NHLF	DNase1
		embryonic stem cell (H1ESC)	DNase1
		HSMMtube	H3K27me3
		blood (DND-41)	H3K27me3
		muscle (HSMM)	DNase1
		breast (HMEC)	H3K27ac
		cervix (HeLa-S3)	DNase1
		monocytes (Monocytes-CD14+)	H3K4me1
		endothelium (HUVEC)	H3K36me3, Cjun, Max, DNase1, Cmyc
		liver (HepG2)	H3K4me1, H3K4me2, HNF4A, H3K9ac, H3K27ac, Cmyc, DNase1, USF1, PolII
		nervous (NH-A)	DNase1
		A549	H3K36me3
		skin (NHEK)	H3K36me3
ENSR00001664576 (CTCF binding site)	1	NHLF	DNase1
		embryonic stem cell (H1ESC)	DNase1
		blood (DND-41)	H3K27me3
		muscle (HSMM)	DNase1
		breast (HMEC)	H3K27ac
		cervix (HeLa-S3)	DNase1
		monocytes (Monocytes-CD14+)	H3K4me1
		endothelium (HUVEC)	Max, DNase1, Cmyc, Cjun
		liver (HepG2)	PolII, USF1, H3K4me1, H3K4me2, HNF4A, H3K9ac, H3K27ac, Cmyc, DNase1
		nervous (NH-A)	DNase1
ENSR00000399203 (promoter)	4	embryonic stem cell (H1ESC)	H3K36me3, H3K27me3, Egr1, Yy1, H3K4me2, H3K4me3, DNase1
		HSMMtube	DNase1, H2AZ, H3K9ac, H3K4me2, H3K4me3
		blood (K562)	Egr1, H3K9ac, H3K79me2, HEY1, PolII, H3K4me2, DNase1, H3K4me3
		skin (NHDF-AD)	H3K4me2, H3K9ac, DNase1, H3K4me3
		muscle (HSMM)	DNase1, H3K36me3, H3K9ac, H3K4me2, H3K27ac, H3K4me3
		liver (HepG2)	H3K4me2, H3K9ac, H3K27ac, Cmyc, H3K4me3, H3K27me3, H3K36me3, Gabp, PolII, H3K79me2, TAF1, ELF1, H3K4me1, DNase1
		lung (IMR90)	H3K9ac, DNase1, H3K27ac, H3K4me2, H3K36me3, H3K4me3
		blood (GM12878)	PolII, H2AZ, ELF1, H3K4me3, H3K4me2, H3K9ac, DNase1
		nervous (NH-A)	H3K4me3, H3K4me2, H3K9ac, H3K36me3, DNase1
		skin (NHEK)	H3K4me2, H3K9ac, H3K4me1, H3K4me3, H3K36me3, DNase1
		NHLF	H3K27ac, H3K9ac, H3K4me3, DNase1
		Osteobl	H3K36me3, H3K4me2, H3K4me3, H3K27ac
		blood (DND-41)	H3K27me3
		breast (HMEC)	H3K4me2, H3K9ac, H3K4me3, H3K27ac, DNase1, H3K36me3
		cervix (HeLa-S3)	DNase1, PolII, H3K4me3, H3K27ac, H3K4me2, H3K9ac
		monocytes (Monocytes-CD14+)	H3K4me2, H3K27ac, H3K9ac, H4K20me1, H3K36me3, H3K4me3
		endothelium (HUVEC)	H3K36me3, Cmyc, DNase1, H3K4me3, H3K4me2, H3K9ac, H3K4me1, H3K27ac, PolII
		A549	H3K36me3, DNase1, H3K9ac, H3K4me2, H3K4me3
ENSR00000649136 (promoter flanking region)	12	embryonic stem cell (H1ESC)	CTCF, Rad21, DNase1
		HSMMtube	H3K27me3, DNase1
		blood (DND-41)	H3K27me3
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1
		monocytes (Monocytes-CD14+)	DNase1, H3K4me1

		endothelium (HUVEC)	H3K36me3
		liver (HepG2)	H3K4me3, PolII, USF1, H3K4me1, H2AZ, H3K4me2, CTCF, DNase1
		lung (IMR90)	DNase1
ENSR00001664577 (CTCF binding site)	2	monocytes (Monocytes-CD14+)	H3K4me1
		embryonic stem cell (H1ESC)	CTCF, Rad21
		liver (HepG2)	H3K4me1, H3K4me2
		HSMMtube	DNase1
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CST3	downstream gene variant, upstream gene variant	70	ENST00000398411	NM_001288614.1	ENSP00000381448	32
CST3	downstream gene variant, upstream gene variant	24	ENST00000376925	NM_000099.3	ENSP00000366124	25
CST3	downstream gene variant, upstream gene variant	33	ENST00000398409	?	ENSP00000381446	23
CST9	downstream gene variant, upstream gene variant	171	ENST00000376971	NM_001008693.2	ENSP00000366170	21
RP11-218C14.2	downstream gene variant	2039	ENST00000437612	?	?	5
RP11-218C14.8	downstream gene variant, upstream gene variant	158	ENST00000602977	?	?	16

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CST3	ENST00000398409	?	ENSP00000381446	8
CST3	ENST00000398411	NM_001288614.1	ENSP00000381448	14
CST3	ENST00000376925	NM_000099.3	ENSP00000366124	7
CST9	ENST00000376971	NM_001008693.2	ENSP00000366170	1

3'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
CST3	ENST00000398411	NM_001288614.1	ENSP00000381448	4
CST9	ENST00000376971	NM_001008693.2	ENSP00000366170	2

5'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
CST3	ENST00000398409	?	ENSP00000381446	3
CST3	ENST00000398411	NM_001288614.1	ENSP00000381448	1
CST3	ENST00000376925	NM_000099.3	ENSP00000366124	3

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
RP11-218C14.8	ENST00000602977	?	2