Locus 106 (rs867186)

SNiPAcard

Block annotations

Block info

genomic range	chr20:33,537,157-33,796,192
block size	259,036 bp
variant count	168 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.337 [-3.949 – 2.371]	gene(s) hit or close-by	EDEM2, GSS, MIR499A, MYH7B, PROCR, RNA5SP483, RNU6-407P, RP11-42O4.2, RP4-614O4.12, SNORD56, TRPC4AP
phastCons	μ = 0.091 [0 – 0.976]	eQTL gene(s)	ACSS2, CPNE1, EDEM2, EIF6, MAP1LC3A, MMP24, MMP24-AS1, PROCR, RBL1, RP4-614O4.11, TRPC4AP, UQCC1
GERP++	μ = -0.393 [-8.99 – 2.92]	potentially regulated gene(s)	ACSS2, C20orf173, CEP250, CPNE1, EDEM2, EIF6, ERGIC3, FER1L4, GDF5OS, GGT7, GSS, HMGB3P1, MMP24, MT1P3, MYH7B, NCOA6, NFS1, PIGU, RBM12, RP3-477O4.5, RPL37P1, SPAG4, TP53INP2, TRPC4AP
CADD score	μ = 4.335 [0.006 – 18.9]	disease gene(s)	GSS, MYH7B, NFS1

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link	variant(s)
Protein C levels	$<1.00\times10^{-64}$	GWAS Catalog	25376901	1
Amyotrophic lateral sclerosis (sporadic)	$<4.00\times10^{-6}$	GWAS Catalog	24529757	1
Prothrombin time	$<5.00\times10^{-13}$	GWAS Catalog	22703881	1
Hemostatic factors and hematological phenotypes	$<4.00\times10^{-34}$	GWAS Catalog	22443383	2
Anticoagulant levels	$<4.00\times10^{-9}$	GWAS Catalog	22216198	1
D-dimer levels	$<4.00\times10^{-6}$	GWAS Catalog	21502573	1
Protein C levels	$<2.00\times10^{-200}$	GWAS Catalog	20802025	1
Coagulation factor levels	$<6.00\times10^{-37}$	GWAS Catalog	20231535	1

Variant annotation

trait	type	source DB	source entry/link	Variant(s)
?	HGMD curated	HGMD	CM052909	1

Disease gene annotation

gene	trait	source DB	source entry/link
GSS	GLUTATHIONE SYNTHETASE DEFICIENCY OF ERYTHROCYTES, HEMOLYTIC [...]	OMIM	MIM:231900
GSS	GLUTATHIONE SYNTHETASE DEFICIENCY	OMIM	MIM:266130
GSS	Glutathione synthetase deficiency with 5-oxoprolinuria	OrphaNet	OrphaNet:289846
GSS	Glutathione synthetase deficiency without 5-oxoprolinuria	OrphaNet	OrphaNet:289849
MYH7B	Left ventricular noncompaction	OrphaNet	OrphaNet:54260
NFS1	Severe neonatal lactic acidosis due to NFS1-ISD11 complex deficiency	OrphaNet	OrphaNet:397593

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)
PROCR	missense variant	ENST00000216968	NM_006404.4	ENSP00000216968	G/S	Ggt/Agt	?	?	1

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
EIF6	?	ENSG00000242372	skeletal muscle	2.24×10^{-7} (p-value)	GTEx Portal V6	99
RP4-614O4.11	?	ENSG00000261582	skeletal muscle	8.95×10^{-7} (p-value)	GTEx Portal V6	85
RP4-614O4.11	?	ENSG00000261582	lung	2.19×10^{-7} (p-value)	GTEx Portal V6	87
EIF6	?	ENSG00000242372	lung	6.41×10^{-8} (p-value)	GTEx Portal V6	111
PROCR	?	ENSG00000101000	transformed fibroblasts	1.38×10^{-13} (p-value)	GTEx Portal V6	165
TRPC4AP	?	ENSG00000100991	blood	2.31×10^{-10} (p-value)	GTEx Portal V6	135
EIF6	?	ENSG00000242372	blood	1.30×10^{-7} (p-value)	GTEx Portal V6	51
MAP1LC3A	?	ENSG00000101460	muscularis mucosae	3.42×10^{-5} (p-value)	GTEx Portal V6	5
PROCR	ENST00000216968	ILMN_1717262	skin	7.54×10^{-12} (p-value)	MuTHER consortium	28
			adipocyte	3.24×10^{-15} (p-value)	MuTHER consortium	28
ACSS2	ENST00000253382	ILMN_2336595	blood	1.24×10^{-5} (p-value)	Westra et al.	26
ACSS2	ENST00000481284					
ACSS2	ENST00000360596					
ACSS2	ENST00000494727					
ACSS2	ENST00000477932					
ACSS2	ENST00000476922					
ACSS2	ENST00000253382	ILMN_1714197	blood	1.30×10^{-6} (p-value)	Westra et al.	1
ACSS2	ENST00000481284					
ACSS2	ENST00000360596					
ACSS2	ENST00000494727					
ACSS2	ENST00000477932					
ACSS2	ENST00000476922					
EIF6	ENST00000447927	ILMN_1787410	monocyte	1.17×10^{-9} (p-value)	Fairfax et al.	8
EIF6	ENST00000621148					
EIF6	ENST00000374436					
EIF6	ENST00000440766					
EIF6	ENST00000462894					
EIF6	ENST00000374450					
EIF6	ENST00000374443					
?	?	ILMN_2387636	monocyte	3.21×10^{-11} (p-value)	Fairfax et al.	8
CPNE1	ENST00000397443	ILMN_2307025	monocyte	2.55×10^{-4} (p-value)	Fairfax et al.	6
CPNE1	ENST00000317677					
CPNE1	ENST00000498056					
CPNE1	ENST00000397445					
CPNE1	ENST00000415920					
CPNE1	ENST00000437340					
CPNE1	ENST00000462352					
CPNE1	ENST00000401607					

CPNE1	ENST00000430570					
CPNE1	ENST00000352393					
CPNE1	ENST00000483359					
CPNE1	ENST00000473373					
CPNE1	ENST00000483495					
UQCC1	ENST00000374384	ILMN_2381121	monocyte	1.44×10-4 (p-value)	Fairfax et al.	1
UQCC1	ENST00000359226					
UQCC1	ENST00000457259					
UQCC1	ENST00000482440					
UQCC1	ENST00000374380					
UQCC1	ENST00000472559					
UQCC1	ENST00000374394					
UQCC1	ENST00000453855					
UQCC1	ENST00000349714					
UQCC1	ENST00000496812					
UQCC1	ENST00000473982					
UQCC1	ENST00000424405					
UQCC1	ENST00000397556					
UQCC1	ENST00000374385					
RBL1	ENST00000373664	ILMN_1782745	monocyte	2.91×10-4 (p-value)	Fairfax et al.	2
EDEM2	?	ENSG00000088298	atrial appendage	1.23×10-8 (p-value)	GTEx Portal V6	28
PROCR	?	ENSG00000101000	EBV lymphocytes	3.94×10-9 (p-value)	GTEx Portal V6	66
RP4-614O4.11	?	ENSG00000261582	sun exposed skin	7.45×10-6 (p-value)	GTEx Portal V6	4
MMP24-AS1	?	ENSG00000126005	sun exposed skin	7.63×10-8 (p-value)	GTEx Portal V6	5
MMP24	?	ENSG00000125966	sun exposed skin	1.20×10-6 (p-value)	GTEx Portal V6	3
EIF6	ENST00000447927	ILMN_1787410	monocyte	1.97×10-24 (p-value)	Zeller et al.	12
EIF6	ENST00000440766					
EIF6	ENST00000374436					
EIF6	ENST00000621148					
EIF6	ENST00000462894					
EIF6	ENST00000374450					
EIF6	ENST00000374443					
?	?	ILMN_2387636	monocyte	1.83×10-26 (p-value)	Zeller et al.	12
TRPC4AP	ENST00000451813	ILMN_2402805	monocyte	3.59×10-17 (p-value)	Zeller et al.	12
TRPC4AP	ENST00000252015					
MMP24	?	ENSG00000125966	esophagus mucosa	4.69×10-6 (p-value)	GTEx Portal V6	2
EDEM2	?	ENSG00000088298	tibial artery	2.09×10-5 (p-value)	GTEx Portal V6	3
PROCR	?	ENSG00000101000	spleen	7.90×10-7 (p-value)	GTEx Portal V6	15
EDEM2	?	ENSG00000088298	left ventricle	1.93×10-5 (p-value)	GTEx Portal V6	5
PROCR	ENST00000216968	ILMN_1717262	liver	1.17×10-11 (p-value)	Innocenti et al.	1

Putative effect on regulation

ENCODE promoter-associated distal DHS (Enhancer)

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

ENCE00000293121	1	ENCP00000031345	MYH7B
ENCE00000293052	1	ENCP00000031340	ACSS2
		ENCP00000031363	GDF5OS
		ENCP00000031370	CEP250
ENCE00000293009	1	ENCP00000031333	HMGB3P1
ENCE00000293100	1	ENCP00000031343	MYH7B
ENCE00000293101	1	ENCP00000031343	MYH7B
ENCE00000293304	1	ENCP00000031379	C20orf173
ENCE00000293169	1	ENCP00000031376	CEP250
		ENCP00000031354	MT1P3
ENCE00000293330	1	ENCP00000031391	RPL37P1
ENCE00000292949	1	ENCP00000031339	ACSS2
		ENCP00000031338	ACSS2
		ENCP00000031376	CEP250
		ENCP00000031371	CEP250
		ENCP00000031324	PIGU
ENCE00000292951	1	ENCP00000031339	ACSS2
		ENCP00000031324	PIGU
		ENCP00000031383	ERGIC3
ENCE00000293241	1	ENCP00000031369	CEP250
		ENCP00000031368	CEP250
ENCE00000292990	1	ENCP00000031386	ERGIC3
		ENCP00000031353	MT1P3
		ENCP00000031385	ERGIC3
		ENCP00000031328	TP53INP2
		ENCP00000031337	ACSS2
		ENCP00000031355	EIF6
		ENCP00000031393	FER1L4
		ENCP00000031367	CEP250
		ENCP00000031332	NCOA6
		ENCP00000031327	TP53INP2
		ENCP00000031380	ERGIC3
		ENCP00000031378	RP3-477O4.5
		ENCP00000031326	PIGU
		ENCP00000031346	MYH7B
		ENCP00000031406	NFS1
		ENCP00000031335	GGT7 ACSS2
		ENCP00000031387	FER1L4
		ENCP00000031398	SPAG4
		ENCP00000031342	GSS
		ENCP00000031389	FER1L4
		ENCP00000031336	ACSS2
		ENCP00000031334	GGT7
		ENCP00000031392	FER1L4
		ENCP00000031390	FER1L4
		ENCP00000031366	CEP250
		ENCP00000031348	EDEM2
		ENCP00000031351	MMP24
		ENCP00000031381	ERGIC3
		ENCP00000031405	CPNE1 RBM12

Locus 106 (sentinel SNP rs867186 + proxy variants in LD r2 > 0.8). SNiPA block annotation (www.snipa.org) based on 1000 Genomes Project phase 3 v5 (European population) variant set and Ensembl 82 annotations.

	ENCP00000031347		TRPC4AP

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001665252 (CTCF binding site)	1	cervix (HeLa-S3)	CTCF
		Osteobl	CTCF
ENSR00000400200 (open chromatin region)	1	embryonic stem cell (H1ESC)	DNase1
		endothelium (HUVEC)	H3K27me3
		lung (IMR90)	H3K27me3
ENSR00000234246 (open chromatin region)	1	lung (IMR90)	H3K27me3
		blood (K562)	DNase1
ENSR00001665257 (CTCF binding site)	1	cervix (HeLa-S3)	CTCF
		embryonic stem cell (H1ESC)	H3K27me3
		endothelium (HUVEC)	PolII
		A549	H3K36me3
ENSR00000400209 (open chromatin region)	1	endothelium (HUVEC)	H3K36me3
		embryonic stem cell (H1ESC)	H3K36me3, DNase1
		lung (IMR90)	H3K36me3
		A549	H3K36me3
		muscle (HSMM)	H3K36me3
ENSR00001448520 (promoter flanking region)	1	embryonic stem cell (H1ESC)	H3K36me3
		blood (K562)	H3K36me3
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1, H3K36me3
		liver (HepG2)	H3K36me3
		lung (IMR90)	H3K36me3, DNase1
		blood (GM12878)	H3K36me3
		nervous (NH-A)	H3K36me3
		skin (NHEK)	H3K36me3
		NHLF	DNase1
		Osteobl	H3K36me3
		blood (DND-41)	H3K36me3
		cervix (HeLa-S3)	DNase1, H3K36me3
		monocytes (Monocytes-CD14+)	H3K36me3
		endothelium (HUVEC)	H3K36me3
		A549	H3K36me3
ENSR00001665259 (enhancer)	1	embryonic stem cell (H1ESC)	H3K36me3
		HSMMtube	H3K36me3
		blood (K562)	H3K36me3
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1, H3K36me3, H3K27ac
		liver (HepG2)	H3K36me3
		blood (GM12878)	H3K36me3
		lung (IMR90)	H3K36me3
		nervous (NH-A)	H3K36me3
		skin (NHEK)	H3K36me3
		NHLF	H3K36me3
		Osteobl	H3K36me3
		blood (DND-41)	H3K36me3
		breast (HMEC)	H3K36me3
		cervix (HeLa-S3)	H3K36me3
		monocytes (Monocytes-CD14+)	H3K36me3
		endothelium (HUVEC)	H3K36me3
		A549	H3K36me3
ENSR00001665262 (open chromatin region)	1	endothelium (HUVEC)	H3K36me3
		embryonic stem cell (H1ESC)	H3K36me3
		blood (GM12878)	H3K36me3
		lung (IMR90)	H3K36me3
		blood (K562)	H3K36me3
		A549	H3K36me3
		skin (NHEK)	H3K36me3
ENSR00001665263 (enhancer)	1	embryonic stem cell (H1ESC)	H3K36me3
		Osteobl	H3K36me3

		blood (K562)	H3K36me3
		blood (DND-41)	H3K36me3
		cervix (HeLa-S3)	H3K36me3
		monocytes (Monocytes-CD14+)	H3K36me3
		liver (HepG2)	H3K36me3
		nervous (NH-A)	H3K36me3
ENSR00000400218 (enhancer)	1	embryonic stem cell (H1ESC)	H3K36me3
		HSMMtube	H3K36me3
		Osteobl	H3K36me3
		blood (K562)	H3K79me2, H3K36me3
		blood (DND-41)	H3K36me3
		muscle (HSMM)	H3K36me3, H3K79me2
		cervix (HeLa-S3)	H3K36me3, H3K79me2
		monocytes (Monocytes-CD14+)	H4K20me1, H3K36me3
		endothelium (HUVEC)	H3K36me3
		liver (HepG2)	H3K79me2, H3K36me3
		lung (IMR90)	H3K79me2, H3K36me3
		blood (GM12878)	H3K79me2
		A549	H3K36me3
ENSR00001665264 (enhancer)	1	embryonic stem cell (H1ESC)	Rad21, CTCF
		Osteobl	CTCF
		blood (K562)	CTCF
		blood (DND-41)	CTCF
		skin (NHDF-AD)	CTCF
		breast (HMEC)	CTCF
		muscle (HSMM)	CTCF
		cervix (HeLa-S3)	CTCF
		monocytes (Monocytes-CD14+)	CTCF
		liver (HepG2)	H2AZ, CTCF
		lung (IMR90)	CTCF
		blood (GM12878)	CTCF
		nervous (NH-A)	CTCF
		A549	CTCF
		skin (NHEK)	CTCF
ENSR00001448525 (promoter flanking region)	2	cervix (HeLa-S3)	DNase1
		HSMMtube	H3K27me3
		Osteobl	H3K36me3
		A549	H3K36me3
		blood (K562)	H3K27me3
		skin (NHEK)	DNase1
		breast (HMEC)	DNase1
ENSR00001448526 (promoter flanking region)	2	NHLF	DNase1
		HSMMtube	H3K27ac, DNase1
		Osteobl	H3K27ac
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1, H3K27ac, H2AZ
		breast (HMEC)	H3K27ac
		cervix (HeLa-S3)	H3K36me3
		monocytes (Monocytes-CD14+)	H3K36me3
		endothelium (HUVEC)	Cjun
		lung (IMR90)	DNase1
		nervous (NH-A)	DNase1, H3K27ac
		A549	H3K36me3
ENSR00000400229 (promoter flanking region)	2	embryonic stem cell (H1ESC)	H3K36me3
		HSMMtube	H3K36me3
		blood (K562)	H3K36me3
		liver (HepG2)	H3K36me3
		blood (GM12878)	H3K36me3
		lung (IMR90)	H3K36me3
		nervous (NH-A)	H3K36me3
		skin (NHEK)	H3K36me3
		NHLF	DNase1, H3K36me3
		Osteobl	H3K36me3
		blood (DND-41)	H3K36me3

		breast (HMEC)	H3K36me3
		cervix (HeLa-S3)	DNase1, H3K36me3, H3K27ac
		monocytes (Monocytes-CD14+)	H3K36me3
		endothelium (HUVEC)	Cjun, H3K4me1, H3K27ac, PolII, DNase1
		A549	H3K36me3
ENSR00001665267 (enhancer)	1	skin (NHDF-AD)	DNase1
ENSR00000234264 (enhancer)	1	embryonic stem cell (H1ESC)	H3K4me1, H3K4me2
		endothelium (HUVEC)	Cmyc, DNase1, PolII, Max, Cjun
		blood (K562)	DNase1
ENSR00001448528 (CTCF binding site)	1	endothelium (HUVEC)	H3K36me3
		blood (DND-41)	H3K27me3
		A549	H3K36me3
ENSR00001665271 (promoter flanking region)	1	embryonic stem cell (H1ESC)	Rad21, CTCF, DNase1
		HSMMtube	CTCF, DNase1
		blood (K562)	H3K27me3, DNase1, Rad21, CTCF
		skin (NHDF-AD)	H3K4me3, CTCF, DNase1, H3K4me2
		muscle (HSMM)	CTCF
		liver (HepG2)	CTCF, DNase1, Rad21, H3K4me1, H3K4me2, FOXA1
		lung (IMR90)	CTCF
		blood (GM12878)	CTCF, Rad21
		nervous (NH-A)	CTCF
		skin (NHEK)	CTCF
		NHLF	CTCF
		Osteobl	H3K4me2, CTCF, H3K36me3
		blood (DND-41)	CTCF
		breast (HMEC)	CTCF, H3K4me2
		cervix (HeLa-S3)	CTCF, DNase1
		monocytes (Monocytes-CD14+)	DNase1, CTCF
		endothelium (HUVEC)	H3K36me3, CTCF, DNase1
		A549	CTCF, DNase1, H3K27ac, H3K4me2, H3K4me3
ENSR00000009183 (CTCF binding site)	1	embryonic stem cell (H1ESC)	DNase1, Rad21, CTCF
		HSMMtube	CTCF, DNase1
		blood (K562)	H3K27me3, DNase1, Rad21, CTCF
		skin (NHDF-AD)	H3K4me2, DNase1, H3K4me3, CTCF
		muscle (HSMM)	CTCF
		liver (HepG2)	Rad21, H3K4me1, H3K4me2, FOXA1, CTCF, DNase1
		lung (IMR90)	CTCF
		blood (GM12878)	CTCF, Rad21
		nervous (NH-A)	CTCF
		skin (NHEK)	CTCF
		NHLF	CTCF
		Osteobl	CTCF, H3K4me2
		blood (DND-41)	CTCF
		breast (HMEC)	H3K4me2, CTCF
		cervix (HeLa-S3)	DNase1, CTCF
		monocytes (Monocytes-CD14+)	DNase1, CTCF
		endothelium (HUVEC)	H3K36me3, CTCF, DNase1
		A549	H3K27ac, H3K4me3, H3K4me2, CTCF, DNase1

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
EDEM2	downstream gene variant, upstream gene variant	33	ENST00000374491	NM_001145025.1	ENSP00000363615	12
EDEM2	downstream gene variant, upstream gene variant	26	ENST00000374492	NM_018217.2	ENSP00000363616	12
GSS	upstream gene variant	657	ENST00000216951	NM_000178.2	ENSP00000216951	3
GSS	upstream gene variant	4622	ENST00000451957	?	ENSP00000407517	1
MIR499A	upstream gene variant, downstream gene variant	1528	ENST00000384903	?	?	4
MYH7B	upstream gene variant, downstream gene variant	1387	ENST00000446156	?	ENSP00000395858	6
MYH7B	upstream gene variant, downstream gene variant	579	ENST00000618182	?	ENSP00000483640	9
MYH7B	upstream gene variant, downstream gene variant	1387	ENST00000435272	?	ENSP00000391939	6

MYH7B	upstream gene variant, downstream gene variant	1387	ENST00000435272	?	ENSP00000391939	6
MYH7B	upstream gene variant, downstream gene variant	437	ENST00000481922	?	?	7
MYH7B	upstream gene variant, downstream gene variant	1387	ENST00000453028	?	ENSP00000409103	6
MYH7B	upstream gene variant, downstream gene variant	730	ENST00000262873	NM_020884.3	ENSP00000262873	8
MYH7B	upstream gene variant, downstream gene variant	179	ENST00000470929	?	?	7
MYH7B	upstream gene variant, downstream gene variant	1387	ENST00000433934	?	ENSP00000412594	6
MYH7B	upstream gene variant, downstream gene variant	1387	ENST00000456649	?	ENSP00000396368	6
PROCR	upstream gene variant, downstream gene variant	604	ENST00000216968	NM_006404.4	ENSP00000216968	4
RNA5SP483	upstream gene variant, downstream gene variant	579	ENST00000363431	?	?	4
RNU6-407P	downstream gene variant, upstream gene variant	249	ENST00000365280	?	?	5
RP11-42O4.2	downstream gene variant, upstream gene variant	1832	ENST00000615962	?	?	2
RP4-614O4.12	downstream gene variant	2873	ENST00000594413	?	?	1
SNORD56	downstream gene variant, upstream gene variant	1805	ENST00000364281	?	?	9
TRPC4AP	downstream gene variant, upstream gene variant	1960	ENST00000451813	NM_199368.1	ENSP00000400614	7
TRPC4AP	downstream gene variant, upstream gene variant	1896	ENST00000252015	NM_015638.2	ENSP00000252015	7

Putative effect on transcript

Synonymous coding variant

gene	affected transcript	RefSeq id	protein	AA's	exchanged codons	variant(s)
MYH7B	ENST00000618182	?	ENSP00000483640	2	2	2
MYH7B	ENST00000262873	NM_020884.3	ENSP00000262873	2	2	2

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
EDEM2	ENST00000374491	NM_001145025.1	ENSP00000363615	27
EDEM2	ENST00000374492	NM_018217.2	ENSP00000363616	27
GSS	ENST00000216951	NM_000178.2	ENSP00000216951	2
GSS	ENST00000451957	?	ENSP00000407517	2
MYH7B	ENST00000618182	?	ENSP00000483640	8
MYH7B	ENST00000262873	NM_020884.3	ENSP00000262873	11
MYH7B	ENST00000470929	?	?	3
TRPC4AP	ENST00000252015	NM_015638.2	ENSP00000252015	62
TRPC4AP	ENST00000451813	NM_199368.1	ENSP00000400614	62

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
MYH7B	ENST00000470929	?	2