

SNiPACard

Block annotations

Block info



genomic range	chr1:207,411,912-207,529,576 <i>e!</i>
block size	117,665 bp
variant count	79 variants

Basic features


Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.314$ [-2.969 – 1.497]	gene(s) hit or close-by	CD55 <i>e!</i> , RP11-6J21.2 <i>e!</i>
phastCons	$\mu = 0.070$ [0 – 0.985]	eQTL gene(s)	CD55 <i>e!</i> , CR1 <i>e!</i>
GERP++	$\mu = -0.380$ [-6.12 – 3.97]	potentially regulated gene(s)	C4BPAP2 <i>e!</i> , C4BPB <i>e!</i> , IL20 <i>e!</i> , PIGR <i>e!</i> , RP11-164O23.5 <i>e!</i>
CADD score	$\mu = 3.646$ [0.01 – 11.79]	disease gene(s)	CD55 <i>e!</i>

Trait annotations

Variant association






trait	min(p-value)	source DB	source entry/link	variant(s)
threonine	2.20×10 ⁻⁵	Metabolomics GWAS Server	24816252 	8
4-acetaminophen sulfate	8.26×10 ⁻⁵	Metabolomics GWAS Server	24816252 	1

Disease gene annotation

gene	trait	source DB	source entry/link
CD55 <i>e!</i>	BLOOD GROUP, CROMER SYSTEM	OMIM	MIM:613793 

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
CD55 <i>e!</i> ?		ENSG00000196352 <i>e!</i>	adrenal gland	3.70×10 ⁻⁸ (p-value)	GTEx Portal V6 	78
CD55 <i>e!</i> ?		ENSG00000196352 <i>e!</i>	tibial artery	1.85×10 ⁻⁸ (p-value)	GTEx Portal V6 	78
CD55 <i>e!</i> ?		ENSG00000196352 <i>e!</i>	transformed fibroblasts	6.82×10 ⁻⁶ (p-value)	GTEx Portal V6 	2
CR1 <i>e!</i>	ENST00000367051 <i>e!</i>	ILMN_1767193 <i>e!</i>	blood	2.76×10 ⁻⁵ (p-value)	MuTHER consortium 	16
CR1 <i>e!</i>	ENST00000367052 <i>e!</i>					
CR1 <i>e!</i>	ENST00000400960 <i>e!</i>					
CR1 <i>e!</i>	ENST00000367049 <i>e!</i>					
CR1 <i>e!</i>	ENST00000529814 <i>e!</i>					
CR1 <i>e!</i>	ENST00000367053 <i>e!</i>					
?	?	ILMN_1742601 <i>e!</i>	blood	3.62×10 ⁻⁵ (p-value)	MuTHER consortium 	9

Putative effect on regulation

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000053173 <i>e!</i>	1	ENCP00000006362	PIGR <i>e!</i>
		ENCP00000006355	IL20 <i>e!</i>

ENCE00000053309 <i>e!</i>	1	ENCP00000006375	RP11-164O23.5 <i>e!</i>
		ENCP00000006373	C4BPB <i>e!</i>
		ENCP00000006371	C4BPB <i>e!</i>
ENCE00000053321 <i>e!</i>	1	ENCP00000006373	C4BPB <i>e!</i>
ENCE00000053363 <i>e!</i>	1	ENCP00000006378	C4BPAP2 <i>e!</i>

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001590164 <i>e!</i> (enhancer)	1	cervix (HeLa-S3) HSMMtube skin (NHEK)	DNase1, H3K27ac H3K27me3 H3K4me1
ENSR00000551826 <i>e!</i> (promoter flanking region)	10	embryonic stem cell (H1ESC) HSMMtube blood (DND-41) breast (HMEC) cervix (HeLa-S3) monocytes (Monocytes-CD14+) endothelium (HUVEC) liver (HepG2) A549 nervous (NH-A) skin (NHEK)	DNase1 H3K27me3 H3K27me3 H3K4me2, H3K27ac, DNase1 DNase1, Cjun, PolII, Jund, H3K4me2, H3K27ac, Max, Cmyc H3K27me3 H3K36me3 H3K4me1, FOXA1, H3K27ac, DNase1 H3K4me3 DNase1 DNase1, H3K4me1, H3K27ac, H3K4me2
ENSR00000551828 <i>e!</i> (CTCF binding site)	1	embryonic stem cell (H1ESC) blood (K562) skin (NHDF-AD) breast (HMEC) muscle (HSMM) cervix (HeLa-S3) endothelium (HUVEC) liver (HepG2) lung (IMR90) skin (NHEK)	Rad21, CTCF CTCF, Rad21 CTCF CTCF CTCF CTCF H3K36me3, DNase1, CTCF Rad21, CTCF CTCF CTCF
ENSR00000551831 <i>e!</i> (promoter flanking region)	4	cervix (HeLa-S3) embryonic stem cell (H1ESC) endothelium (HUVEC) nervous (NH-A) skin (NHDF-AD)	DNase1 DNase1 Cjun, DNase1, H3K4me2, H3K4me1, H3K27ac DNase1 DNase1
ENSR00001528072 <i>e!</i> (CTCF binding site)	1	Osteobl blood (DND-41) skin (NHDF-AD)	H3K27me3 H3K27me3 DNase1
ENSR00000551833 <i>e!</i> (enhancer)	1	cervix (HeLa-S3) HSMMtube blood (DND-41) skin (NHDF-AD)	H3K36me3 H3K27me3 H3K27me3 DNase1, H3K4me3
ENSR00000288774 <i>e!</i> (open chromatin region)	1	embryonic stem cell (H1ESC) blood (K562)	DNase1 H2AZ
ENSR00000288776 <i>e!</i> (promoter flanking region)	5	embryonic stem cell (H1ESC) HSMMtube blood (K562) skin (NHDF-AD) muscle (HSMM) liver (HepG2) blood (GM12878) nervous (NH-A) skin (NHEK) NHLF Osteobl blood (DND-41) breast (HMEC) cervix (HeLa-S3) monocytes (Monocytes-CD14+)	H3K36me3, DNase1 DNase1 Brg1, DNase1, H3K27ac, Max, Junb, PU1, MEF2A, Jund, Cmyc, H2AZ, Cjun DNase1 H2AZ, DNase1 H3K4me2 H2AZ, PU1 DNase1, H3K4me2 DNase1 DNase1 H3K27me3, H3K4me2 H3K27me3 DNase1, H3K27ac, H3K4me2 DNase1, Cjun, PolII, H3K9ac, Jund, H3K4me2, H3K27ac, TAF1, Max, Cfos H3K27ac, H3K4me1, DNase1

		endothelium (HUVEC)	Cjun, Max, DNase1, H3K4me2, H3K27ac, PolII
		A549	H3K4me3, H3K4me2, DNase1
ENSR00001590170 <i>e!</i>	1	cervix (HeLa-S3)	DNase1, Junb, H3K4me2, H3K27ac
(CTCF binding site)		monocytes (Monocytes-CD14+)	DNase1, H3K4me1
		embryonic stem cell (H1ESC)	H3K36me3, DNase1
		nervous (NH-A)	DNase1
		blood (K562)	Brg1, DNase1, Junb, MEF2A, Junb, Cjun
ENSR00000551839 <i>e!</i>	2	embryonic stem cell (H1ESC)	PolII, Rad21, Junb, TAF7, Sin3Ak20, CTCF, H3K27ac, Yy1, TAF1, H3K4me2, USF1, H3K9ac, H3K4me3, DNase1, H3K27me3, H3K36me3
(promoter)		HSMMtube	H3K9ac, H3K4me2, H2AZ, H3K27me3, DNase1
		blood (K562)	H3K79me2, HEY1, H2AZ, TAF1, Cmyc, PolII, H3K4me2, CTCF, H3K36me3, DNase1, H3K4me3, H3K9ac, PU1, H3K27ac, Max
		skin (NHDF-AD)	H3K4me2, H3K9ac, DNase1, H3K4me3, CTCF, H3K27ac
		muscle (HSMM)	H2AZ, H3K4me3, H3K27ac, H3K4me2, H3K9ac, DNase1
		liver (HepG2)	DNase1, H3K27me3, H3K4me3, PolII, TAF1, H2AZ, H3K4me2, H3K9ac, Cmyc
		lung (IMR90)	DNase1, H3K4me2, H3K4me3
		blood (GM12878)	PolII, H2AZ, DNase1, CTCF, H3K4me3, H3K27ac, H3K4me2, H3K9ac
		nervous (NH-A)	H3K9ac, H3K4me2, H3K4me3, DNase1
		skin (NHEK)	CTCF, H3K27ac, H3K9ac, H3K4me2, H3K4me3, DNase1
		NHLF	H3K27ac, H3K9ac, H3K4me3, DNase1
		Osteobl	H3K27me3, H3K4me2, H3K4me3, H3K27ac, H2AZ
		blood (DND-41)	H3K27me3, H3K9ac, H3K4me2, H3K4me1
		breast (HMEC)	H3K4me2, H3K9ac, H3K4me3, H3K27ac, DNase1
		cervix (HeLa-S3)	H3K9ac, H3K4me2, H3K27ac, TAF1, Max, H3K4me3, H3K79me2, PolII, Cmyc, CTCF, H3K36me3, DNase1
		monocytes (Monocytes-CD14+)	DNase1, H3K4me1, CTCF, H3K4me2, H3K27ac, H3K9ac, H4K20me1, H3K36me3, H3K4me3
		endothelium (HUVEC)	H3K36me3, DNase1, Cmyc, PolII, H3K27ac, Cjun, Max, H3K4me2, H3K4me3, H3K9ac
		A549	DNase1, H3K27ac, H3K36me3, H3K9ac, H3K4me2, H3K4me3
ENSR00001590172 <i>e!</i>	1	embryonic stem cell (H1ESC)	H3K36me3, H3K27me3, PolII, Rad21, TAF7, Sin3Ak20, H3K27ac, Yy1, TAF1, H3K4me2, DNase1, H3K9ac, H3K4me3
(promoter)		HSMMtube	H3K9ac, H3K4me2, H2AZ
		blood (K562)	H3K27ac, Max, H3K9ac, Cmyc, H3K79me2, HEY1, H2AZ, PolII, H3K4me2, H3K36me3, H3K4me3
		skin (NHDF-AD)	H3K27ac, H3K4me2, H3K9ac, DNase1, H3K4me3, H3K36me3
		muscle (HSMM)	H3K4me2, H3K9ac, H3K36me3, H3K27ac, H2AZ, H3K4me3
		liver (HepG2)	H3K4me2, H3K9ac, H3K4me3, H3K27me3, DNase1
		lung (IMR90)	H3K4me2, H3K36me3, H3K4me3
		blood (GM12878)	PolII, H2AZ, DNase1, H3K4me3, H3K27ac, H3K4me2, H3K9ac, H3K36me3
		nervous (NH-A)	H3K9ac, H3K4me2, H3K4me3
		skin (NHEK)	H3K27ac, H3K9ac, H3K4me2, H3K4me3
		NHLF	H3K27ac, H3K9ac, H3K4me3
		Osteobl	H3K4me2, H3K4me3, H3K27ac, H2AZ
		blood (DND-41)	H3K4me1, H3K4me2, H3K9ac, H3K27me3
		breast (HMEC)	H3K4me2, H3K9ac, H3K4me3, H3K27ac, DNase1
		cervix (HeLa-S3)	H3K79me2, PolII, H3K36me3, H3K4me3, H3K27ac, H3K9ac, DNase1, H3K4me2
		monocytes (Monocytes-CD14+)	DNase1, H3K4me2, H3K27ac, H3K9ac, H4K20me1, H3K36me3, H3K4me3
		endothelium (HUVEC)	H3K4me2, H3K4me3, H3K9ac, H3K27ac, PolII, H3K36me3
		A549	H3K4me3, H3K4me2, H3K9ac, H3K27ac, H3K36me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
CD55 <i>e!</i>	upstream gene variant, downstream gene variant	457	ENST00000343420 <i>e!</i> ?		ENSP00000340631 <i>e!</i>	2
CD55 <i>e!</i>	upstream gene variant	174	ENST00000367064 <i>e!</i>	NM_000574.3	ENSP00000356031 <i>e!</i>	1
CD55 <i>e!</i>	upstream gene variant	399	ENST00000367067 <i>e!</i> ?		ENSP00000356034 <i>e!</i>	1
CD55 <i>e!</i>	upstream gene variant	1107	ENST00000465534 <i>e!</i> ?		?	3
CD55 <i>e!</i>	upstream gene variant, downstream gene variant	353	ENST00000488171 <i>e!</i> ?		?	3
CD55 <i>e!</i>	upstream gene variant	1107	ENST00000476590 <i>e!</i> ?		?	3
CD55 <i>e!</i>	upstream gene variant	309	ENST00000391921 <i>e!</i> ?		ENSP00000375788 <i>e!</i>	1
CD55 <i>e!</i>	upstream gene variant	367		NM_001114752.1	ENSP00000316333 <i>e!</i>	1
CD55 <i>e!</i>	upstream gene variant, downstream gene variant	198	ENST00000367063 <i>e!</i>	NM_001300902.1	ENSP00000356030 <i>e!</i>	3

Putative effect on transcript

Intron variant (splice region)

gene	affected transcript	RefSeq id	protein	variant(s)
RP11-6J21.2 <i>e!</i>	ENST00000417084 <i>e!</i>	?	?	1

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
CD55 <i>e!</i>	ENST00000343420 <i>e!</i>	?	ENSP00000340631 <i>e!</i>	3
CD55 <i>e!</i>	ENST00000314754 <i>e!</i>	NM_001114752.1	ENSP00000316333 <i>e!</i>	10
CD55 <i>e!</i>	ENST00000367064 <i>e!</i>	NM_000574.3	ENSP00000356031 <i>e!</i>	10
CD55 <i>e!</i>	ENST00000367067 <i>e!</i>	?	ENSP00000356034 <i>e!</i>	10
CD55 <i>e!</i>	ENST00000367063 <i>e!</i>	NM_001300902.1	ENSP00000356030 <i>e!</i>	3
CD55 <i>e!</i>	ENST00000488171 <i>e!</i>	?	?	3
CD55 <i>e!</i>	ENST00000391921 <i>e!</i>	?	ENSP00000375788 <i>e!</i>	10
CD55 <i>e!</i>	ENST00000465534 <i>e!</i>	?	?	8
CD55 <i>e!</i>	ENST00000476590 <i>e!</i>	?	?	8
RP11-6J21.2 <i>e!</i>	ENST00000417084 <i>e!</i>	?	?	48

