SNiPAcard

Block annotations

Block info

genomic range	chr7:150,026,169-150,046,747
block size	20,579 bp
variant count	3 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.994 [-1.551 – -0.031]	**gene(s) hit or close-by**	LRRC61, ZBED6CL
phastCons	μ = 0.016 [0 – 0.025]	**eQTL gene(s)**	ACTR3C, LRRC61, RARRES2, REPIN1, RP4-584D14.5, RP4-584D14.7, ZBED6CL
GERP++	μ = -0.366 [-1.05 – 0.0465]	**potentially regulated gene(s)**	–
CADD score	μ = 5.794 [2.935 – 10.31]	**disease gene(s)**	–

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
LRRC61	?	ENSG00000127399	atrial appendage	2.53×10^{-9} (p-value)	GTEx Portal V6	3
RP4-584D14.7	?	ENSG00000261305	transformed fibroblasts	4.39×10^{-7} (p-value)	GTEx Portal V6	3
RARRES2	?	ENSG00000106538	transformed fibroblasts	3.72×10^{-15} (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	transformed fibroblasts	1.08×10^{-15} (p-value)	GTEx Portal V6	3
ACTR3C	?	ENSG00000106526	transformed fibroblasts	1.63×10^{-8} (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	breast	4.39×10^{-13} (p-value)	GTEx Portal V6	3
RP4-584D14.7	?	ENSG00000261305	breast	2.16×10^{-6} (p-value)	GTEx Portal V6	1
ZBED6CL	?	ENSG00000188707	blood	7.94×10^{-9} (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	blood	1.66×10^{-12} (p-value)	GTEx Portal V6	3
RARRES2	?	ENSG00000106538	skeletal muscle	3.14×10^{-10} (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	skeletal muscle	1.44×10^{-26} (p-value)	GTEx Portal V6	3
REPIN1	?	ENSG00000214022	skeletal muscle	1.12×10^{-35} (p-value)	GTEx Portal V6	3
ACTR3C	?	ENSG00000106526	skeletal muscle	2.01×10^{-14} (p-value)	GTEx Portal V6	3
RP4-584D14.5	?	ENSG00000240449	skeletal muscle	1.05×10^{-7} (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	putamen	1.51×10^{-7} (p-value)	GTEx Portal V6	1
LRRC61	?	ENSG00000127399	EBV lymphocytes	9.32×10^{-7} (p-value)	GTEx Portal V6	1
LRRC61	?	ENSG00000127399	unexposed skin	2.54×10^{-12} (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	unexposed skin	2.33×10^{-8} (p-value)	GTEx Portal V6	1
ZBED6CL	?	ENSG00000188707	sun exposed skin	1.15×10^{-7} (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	sun exposed skin	2.69×10^{-21} (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	ovary	2.48×10^{-10} (p-value)	GTEx Portal V6	3

ZBED6CL	?	ENSG00000188707	ovary	2.48×10-6 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	ovary	1.07×10-6 (p-value)	GTEx Portal V6	1
RP4-584D14.7	?	ENSG00000261305	left ventricle	1.55×10-10 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	left ventricle	4.88×10-11 (p-value)	GTEx Portal V6	3
REPIN1	?	ENSG00000214022	left ventricle	9.63×10-9 (p-value)	GTEx Portal V6	3
RP4-584D14.7	?	ENSG00000261305	aorta	6.33×10-8 (p-value)	GTEx Portal V6	3
RARRES2	?	ENSG00000106538	aorta	2.77×10-8 (p-value)	GTEx Portal V6	1
LRRC61	?	ENSG00000127399	aorta	9.45×10-15 (p-value)	GTEx Portal V6	3
ACTR3C	?	ENSG00000106526	aorta	3.56×10-6 (p-value)	GTEx Portal V6	1
RARRES2	?	ENSG00000106538	subcutaneous adipocytes	6.71×10-8 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	subcutaneous adipocytes	1.10×10-15 (p-value)	GTEx Portal V6	3
REPIN1	?	ENSG00000214022	subcutaneous adipocytes	1.51×10-7 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	caudate basal ganglia	4.68×10-13 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	visceral adipocytes	6.40×10-9 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	stomach	3.99×10-12 (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	stomach	4.15×10-8 (p-value)	GTEx Portal V6	2
LRRC61	?	ENSG00000127399	cortex	1.12×10-7 (p-value)	GTEx Portal V6	1
RP4-584D14.7	?	ENSG00000261305	tibial nerve	2.01×10-6 (p-value)	GTEx Portal V6	3
RARRES2	?	ENSG00000106538	tibial nerve	3.79×10-9 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	tibial nerve	1.74×10-17 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	pituitary	1.58×10-9 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	anterior cingulate cortex	8.22×10-8 (p-value)	GTEx Portal V6	1
RP4-584D14.7	?	ENSG00000261305	esophagus mucosa	2.08×10-9 (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	esophagus mucosa	3.59×10-20 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	esophagus mucosa	9.34×10-16 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	testis	2.79×10-20 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	hypothalamus	6.03×10-9 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	frontal cortex	8.28×10-10 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	pancreas	7.67×10-11 (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	pancreas	1.59×10-9 (p-value)	GTEx Portal V6	3
RARRES2	?	ENSG00000106538	pancreas	3.40×10-6 (p-value)	GTEx Portal V6	3
RP4-584D14.7	?	ENSG00000261305	muscularis mucosae	4.59×10-10 (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	muscularis mucosae	7.78×10-15 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	muscularis mucosae	6.56×10-10 (p-value)	GTEx Portal V6	3
REPIN1	?	ENSG00000214022	muscularis mucosae	1.12×10-6 (p-value)	GTEx Portal V6	2
ZBED6CL	?	ENSG00000188707	lung	5.61×10-9 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	lung	4.24×10-16 (p-value)	GTEx Portal V6	3

LRRC61	?	ENSG00000127399	lung	4.84×10-16 (p-value)	GTEx Portal V6	3
RP4-584D14.7	?	ENSG00000261305	tibial artery	2.30×10-8 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	tibial artery	2.26×10-11 (p-value)	GTEx Portal V6	3
ACTR3C	?	ENSG00000106526	tibial artery	2.30×10-7 (p-value)	GTEx Portal V6	1
RP4-584D14.7	?	ENSG00000261305	thyroid	2.83×10-6 (p-value)	GTEx Portal V6	1
ZBED6CL	?	ENSG00000188707	thyroid	3.87×10-10 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	thyroid	2.87×10-26 (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	prostate	1.20×10-7 (p-value)	GTEx Portal V6	1
LRRC61	?	ENSG00000127399	transverse colon	6.53×10-10 (p-value)	GTEx Portal V6	3
ZBED6CL	?	ENSG00000188707	transverse colon	5.01×10-12 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	liver	2.51×10-9 (p-value)	GTEx Portal V6	1
LRRC61	?	ENSG00000127399	terminal ileum	3.56×10-9 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	nucleus accumbens	2.92×10-11 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	spleen	6.82×10-11 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	coronary artery	5.43×10-8 (p-value)	GTEx Portal V6	1
ZBED6CL	?	ENSG00000188707	sigmoid colon	3.21×10-7 (p-value)	GTEx Portal V6	1
ZBED6CL	?	ENSG00000188707	gastroesophageal junction	9.67×10-10 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	cerebellar hemisphere	1.14×10-11 (p-value)	GTEx Portal V6	3
LRRC61	?	ENSG00000127399	cerebellum	2.66×10-8 (p-value)	GTEx Portal V6	2
LRRC61	?	ENSG00000127399	hippocampus	6.31×10-10 (p-value)	GTEx Portal V6	3
RARRES2	ENST00000466675	ILMN_1810844	skin	3.55×10-9 (p-value)	MuTHER consortium	1
RARRES2	ENST00000482669		blood	1.56×10-12 (p-value)	MuTHER consortium	1
RARRES2	ENST00000223271		adipocyte	5.22×10-13 (p-value)	MuTHER consortium	1
RARRES2	ENST00000478771					
REPIN1	ENST00000425389	ILMN_2404385	adipocyte	1.31×10-19 (p-value)	MuTHER consortium	1
REPIN1	ENST00000397281					
REPIN1	ENST00000489432					
REPIN1	ENST00000444957					
REPIN1	ENST00000479668					
LRRC61	ENST00000359623	ILMN_1669722	blood	5.28×10-25 (p-value)	MuTHER consortium	1
LRRC61	ENST00000323078					
ZBED6CL	ENST00000343855	ILMN_1678863	blood	8.46×10-13 (p-value)	MuTHER consortium	1

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001564976	1	embryonic stem cell (H1ESC)	DNase1, H3K36me3, H3K27me3, CTCF, Rad21, H3K4me1, Tcf12, H3K4me2, H3K27ac
(promoter flanking region)		HSMMtube	DNase1
		blood (K562)	PolII, H3K36me3
		blood (DND-41)	H3K36me3

muscle (HSMM)	DNase1
cervix (HeLa-S3)	PolII, H3K36me3
monocytes (Monocytes-CD14+)	H3K36me3
liver (HepG2)	H3K36me3
blood (GM12878)	PolII, H3K36me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
LRRC61	downstream gene variant	294	ENST00000463441	?	?	1
LRRC61	downstream gene variant	3161	ENST00000471872	?	?	1
ZBED6CL	upstream gene variant	709	ENST00000343855	NM_138434.2	ENSP00000343242	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
LRRC61	ENST00000493307	?	ENSP00000420560	1
LRRC61	ENST00000359623	NM_001142928.1	ENSP00000352642	1
LRRC61	ENST00000323078	NM_023942.2	ENSP00000339047	1