SNiPAcard

Block annotations

Block info

genomic range	chr6:30,080,036-30,194,873
block size	114,838 bp
variant count	30 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.388 [-2.652 – 1.382]	**gene(s) hit or close-by**	PAIP1P1, TRIM10, TRIM15, TRIM26, TRIM31, TRIM31-AS1, TRIM40
phastCons	μ = 0.053 [0 – 0.997]	**eQTL gene(s)**	HCG18, HLA-G, HLA-H, HLA-K, HLA-L, HLA-T, HLA-U, HLA-V, HLA-W, MICA, PPP1R11, TRIM10, TRIM15
GERP++	μ = -1.347 [-6.82 – 2.41]	**potentially regulated gene(s)**	PTMAP1, PTMAP1, PTMAP1, PTMAP1, PTMAP1, PTMAP1, PTMAP1, TRIM10, TRIM10, TRIM10, TRIM10, TRIM10, TRIM10, TRIM10, TRIM15, TRIM15, TRIM15, TRIM15, TRIM15, TRIM15, TRIM15, TRIM15, TRIM39, TRIM39, TRIM39, TRIM39, TRIM39, TRIM39, TRIM40, TRIM40, TRIM40, TRIM40, TRIM40, TRIM40, TRIM40
CADD score	μ = 3.632 [0.104 – 9.267]	**disease gene(s)**	–

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)
TRIM15	missense variant	ENST00000376688	?	ENSP00000365878	V/I	Gtt/Att	?	?	1
TRIM15	missense variant	ENST00000376694	NM_033229.2	ENSP00000365884	V/I	Gtt/Att	?	?	1

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
HLA-U	?	ENSG00000228078	atrial appendage	7.47×10^{-14} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	atrial appendage	5.23×10^{-9} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	atrial appendage	2.24×10^{-12} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	transformed fibroblasts	2.51×10^{-9} (p-value)	GTEx Portal V6	29
HCG18	?	ENSG00000231074	transformed fibroblasts	1.30×10^{-7} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	transformed fibroblasts	1.35×10^{-25} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	transformed fibroblasts	1.20×10^{-9} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	transformed fibroblasts	4.73×10^{-21} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	blood	9.09×10^{-13} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	blood	3.43×10^{-36} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	blood	7.62×10^{-12} (p-value)	GTEx Portal V6	29
HLA-T	?	ENSG00000231130	blood	6.27×10^{-13} (p-value)	GTEx Portal V6	29

HLA-H	?	ENSG00000206341	blood	3.90×10^{-15} (p-value)	GTEx Portal V6	29
TRIM15	?	ENSG00000204610	blood	1.28×10^{-7} (p-value)	GTEx Portal V6	12
HLA-W	?	ENSG00000235290	breast	4.28×10^{-7} (p-value)	GTEx Portal V6	26
HLA-U	?	ENSG00000228078	breast	1.16×10^{-19} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	breast	1.69×10^{-8} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	breast	1.60×10^{-12} (p-value)	GTEx Portal V6	29
MICA	ENST00000449934	ILMN_3241692	monocyte	4.23×10^{-5} (p-value)	Fairfax et al.	6
MICA	ENST00000616296					
MICA	ENST00000421350					
HLA-W	?	ENSG00000235290	skeletal muscle	6.79×10^{-6} (p-value)	GTEx Portal V6	23
HLA-U	?	ENSG00000228078	skeletal muscle	1.37×10^{-31} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	skeletal muscle	3.62×10^{-12} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	skeletal muscle	1.76×10^{-25} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	putamen	1.39×10^{-7} (p-value)	GTEx Portal V6	27
HLA-U	?	ENSG00000228078	putamen	1.37×10^{-6} (p-value)	GTEx Portal V6	3
HLA-U	?	ENSG00000228078	EBV lymphocytes	7.71×10^{-15} (p-value)	GTEx Portal V6	29
HLA-T	?	ENSG00000231130	EBV lymphocytes	8.40×10^{-8} (p-value)	GTEx Portal V6	27
HLA-H	?	ENSG00000206341	EBV lymphocytes	1.67×10^{-9} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	sun exposed skin	3.07×10^{-10} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	sun exposed skin	1.12×10^{-23} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	sun exposed skin	2.44×10^{-9} (p-value)	GTEx Portal V6	29
HLA-T	?	ENSG00000231130	sun exposed skin	8.52×10^{-9} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	sun exposed skin	5.20×10^{-15} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	unexposed skin	6.58×10^{-7} (p-value)	GTEx Portal V6	15
HLA-U	?	ENSG00000228078	unexposed skin	5.38×10^{-22} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	unexposed skin	6.77×10^{-10} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	unexposed skin	4.07×10^{-12} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	aorta	1.14×10^{-5} (p-value)	GTEx Portal V6	14
HLA-U	?	ENSG00000228078	aorta	5.14×10^{-17} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	aorta	4.69×10^{-8} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	aorta	6.58×10^{-17} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	left ventricle	3.72×10^{-17} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	left ventricle	1.11×10^{-6} (p-value)	GTEx Portal V6	16
HLA-H	?	ENSG00000206341	left ventricle	1.28×10^{-11} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	subcutaneous adipocytes	6.36×10^{-7} (p-value)	GTEx Portal V6	26
HLA-U	?	ENSG00000228078	subcutaneous adipocytes	3.17×10^{-24} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	subcutaneous adipocytes	2.05×10^{-6} (p-value)	GTEx Portal V6	16
HLA-T	?	ENSG00000231130	subcutaneous adipocytes	5.56×10^{-8} (p-value)	GTEx Portal V6	27

HLA-H	?	ENSG00000206341	subcutaneous adipocytes	5.09×10^{-17} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	caudate basal ganglia	3.57×10^{-10} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	caudate basal ganglia	4.13×10^{-7} (p-value)	GTEx Portal V6	22
HLA-H	?	ENSG00000206341	caudate basal ganglia	1.56×10^{-7} (p-value)	GTEx Portal V6	15
HLA-W	?	ENSG00000235290	visceral adipocytes	4.87×10^{-10} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	visceral adipocytes	2.42×10^{-17} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	visceral adipocytes	7.92×10^{-8} (p-value)	GTEx Portal V6	27
HLA-H	?	ENSG00000206341	visceral adipocytes	2.82×10^{-14} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	stomach	7.24×10^{-12} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	stomach	3.99×10^{-9} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	tibial nerve	1.22×10^{-20} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	tibial nerve	1.47×10^{-7} (p-value)	GTEx Portal V6	27
HLA-H	?	ENSG00000206341	tibial nerve	3.79×10^{-11} (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	esophagus mucosa	1.99×10^{-6} (p-value)	GTEx Portal V6	16
HLA-U	?	ENSG00000228078	esophagus mucosa	4.81×10^{-17} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	esophagus mucosa	4.58×10^{-7} (p-value)	GTEx Portal V6	28
HLA-H	?	ENSG00000206341	esophagus mucosa	6.18×10^{-13} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	pituitary	1.20×10^{-9} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	pituitary	6.01×10^{-9} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	testis	3.08×10^{-12} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	testis	9.27×10^{-9} (p-value)	GTEx Portal V6	29
HLA-K	?	ENSG00000230795	testis	3.36×10^{-6} (p-value)	GTEx Portal V6	24
HLA-W	?	ENSG00000235290	testis	1.25×10^{-5} (p-value)	GTEx Portal V6	8
HLA-U	?	ENSG00000228078	hypothalamus	7.20×10^{-9} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	hypothalamus	4.05×10^{-7} (p-value)	GTEx Portal V6	22
HLA-H	?	ENSG00000206341	hypothalamus	9.97×10^{-7} (p-value)	GTEx Portal V6	12
HLA-U	?	ENSG00000228078	frontal cortex	3.98×10^{-11} (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	frontal cortex	2.43×10^{-6} (p-value)	GTEx Portal V6	12
HLA-H	?	ENSG00000206341	frontal cortex	7.72×10^{-7} (p-value)	GTEx Portal V6	8
HLA-U	?	ENSG00000228078	pancreas	8.06×10^{-8} (p-value)	GTEx Portal V6	27
HLA-U	?	ENSG00000228078	muscularis mucosae	1.19×10^{-17} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	muscularis mucosae	6.55×10^{-18} (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	lung	8.11×10^{-19} (p-value)	GTEx Portal V6	29
HLA-V	?	ENSG00000181126	lung	2.79×10^{-6} (p-value)	GTEx Portal V6	27
HLA-W	?	ENSG00000235290	lung	2.23×10^{-10} (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	lung	3.29×10^{-26} (p-value)	GTEx Portal V6	29
HLA-T	?	ENSG00000231130	lung	9.14×10^{-14} (p-value)	GTEx Portal V6	29

HLA-T	?	ENSG00000231130	lung	9.14×10-14 (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	lung	1.36×10-11 (p-value)	GTEx Portal V6	29
HLA-K	?	ENSG00000230795	lung	1.04×10-6 (p-value)	GTEx Portal V6	27
HLA-W	?	ENSG00000235290	tibial artery	7.97×10-7 (p-value)	GTEx Portal V6	27
HLA-U	?	ENSG00000228078	tibial artery	6.96×10-25 (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	tibial artery	3.39×10-8 (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	tibial artery	3.22×10-19 (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	thyroid	9.36×10-8 (p-value)	GTEx Portal V6	27
HLA-U	?	ENSG00000228078	thyroid	1.25×10-21 (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	thyroid	9.21×10-11 (p-value)	GTEx Portal V6	29
HLA-T	?	ENSG00000231130	thyroid	7.54×10-6 (p-value)	GTEx Portal V6	23
HLA-H	?	ENSG00000206341	thyroid	9.90×10-19 (p-value)	GTEx Portal V6	29
HLA-L	?	ENSG00000243753	thyroid	6.64×10-7 (p-value)	GTEx Portal V6	12
HLA-U	?	ENSG00000228078	prostate	1.33×10-8 (p-value)	GTEx Portal V6	29
HLA-W	?	ENSG00000235290	transverse colon	3.42×10-7 (p-value)	GTEx Portal V6	27
HLA-U	?	ENSG00000228078	transverse colon	1.22×10-12 (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	transverse colon	2.41×10-6 (p-value)	GTEx Portal V6	15
HLA-H	?	ENSG00000206341	transverse colon	2.69×10-10 (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	terminal ileum	6.38×10-10 (p-value)	GTEx Portal V6	25
HLA-H	?	ENSG00000206341	terminal ileum	3.45×10-8 (p-value)	GTEx Portal V6	15
HLA-U	?	ENSG00000228078	nucleus accumbens	3.84×10-9 (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	nucleus accumbens	4.30×10-7 (p-value)	GTEx Portal V6	22
HLA-U	?	ENSG00000228078	spleen	1.32×10-7 (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	sigmoid colon	1.10×10-12 (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	sigmoid colon	3.91×10-10 (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	coronary artery	3.14×10-10 (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	coronary artery	9.05×10-9 (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	gastroesophageal junction	4.37×10-12 (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	gastroesophageal junction	6.45×10-11 (p-value)	GTEx Portal V6	29
PPP1R11	ENST00000376765	ILMN_1747598	blood	2.51×10-6 (p-value)	Westra et al.	9
PPP1R11	ENST00000376769					
PPP1R11	ENST00000376763					
PPP1R11	ENST00000376773					
PPP1R11	ENST00000376758					
PPP1R11	ENST00000376772					
HLA-L	ENST00000463348	ILMN_1675282	blood	5.75×10-7 (p-value)	Westra et al.	4
HLA-W	?	ENSG00000235290	adrenal gland	4.02×10-7 (p-value)	GTEx Portal V6	22
HLA-U	?	ENSG00000228078	adrenal gland	6.10×10-11 (p-value)	GTEx Portal V6	29
HLA-H	?	ENSG00000206341	adrenal gland	8.14×10-10 (p-value)	GTEx Portal V6	29

HLA-U	?	ENSG00000228078	cerebellar hemisphere	4.61×10-8 (p-value)	GTEx Portal V6	29
HLA-G	?	ENSG00000204632	cerebellar hemisphere	6.29×10-7 (p-value)	GTEx Portal V6	27
HLA-U	?	ENSG00000228078	cerebellum	5.06×10-9 (p-value)	GTEx Portal V6	29
HLA-U	?	ENSG00000228078	hippocampus	1.99×10-8 (p-value)	GTEx Portal V6	26
HLA-H	?	ENSG00000206341	hippocampus	1.19×10-6 (p-value)	GTEx Portal V6	2
HLA-U	?	ENSG00000228078	cortex	5.39×10-7 (p-value)	GTEx Portal V6	12
?	?	240182_at	blood	8.00×10-10 (p-value)	Dixon et al.	1
HLA-U	?	ENSG00000228078	liver	1.35×10-6 (p-value)	GTEx Portal V6	2
TRIM10	ENST00000376704	ILMN_1746788	skin	2.24×10-5 (p-value)	MuTHER consortium	1
TRIM10	ENST00000449742					

Putative effect on regulation

FANTOM5 expressed promoter

SNiPA promoter id	variant(s)	associated transcript(s)	gene
FFCP00000735626	1	ENST00000376688, ENST00000376694	TRIM15
FFCP00000735631	1	ENST00000376688, ENST00000376694	TRIM15

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000444263	1	ENCP00000047883	TRIM10 TRIM10 TRIM10 TRIM10 TRIM10 TRIM10 TRIM10 TRIM10
		ENCP00000047882	TRIM40 TRIM40 TRIM40 TRIM40 TRIM40 TRIM40 TRIM40 TRIM40
		ENCP00000047922	PTMAP1 PTMAP1 PTMAP1 PTMAP1 PTMAP1 PTMAP1 PTMAP1
		ENCP00000047897	TRIM39 TRIM39 TRIM39 TRIM39 TRIM39 TRIM39 TRIM39
		ENCP00000047884	TRIM15 TRIM15 TRIM15 TRIM15 TRIM15

TRIM15
TRIM15
TRIM15

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001702952 (enhancer)	2	NHLF	H3K27me3
		HSMMtube	H3K27me3
		Osteobl	H3K27me3
		blood (K562)	H3K27me3
		blood (DND-41)	H3K27me3
		skin (NHDF-AD)	H3K27me3
		muscle (HSMM)	H3K27me3
		monocytes (Monocytes-CD14+)	H3K27me3
		endothelium (HUVEC)	H3K27me3
		liver (HepG2)	H3K4me1, H3K4me2
		lung (IMR90)	H3K27me3
		nervous (NH-A)	H3K27me3
		skin (NHEK)	H3K27me3
ENSR00000487613 (promoter)	6	embryonic stem cell (H1ESC)	DNase1, H3K27me3
		HSMMtube	H3K27me3
		Osteobl	H3K27me3
		blood (DND-41)	H3K4me1, H3K27me3
		blood (K562)	H3K27me3, Egr1
		cervix (HeLa-S3)	DNase1
		endothelium (HUVEC)	H3K36me3
		liver (HepG2)	DNase1, H3K27ac, Cmyc, H3K4me3, H3K27me3, Gabp, PolII, H3K79me2, TAF1, H2AZ, H3K4me2, HNF4A, H3K9ac
		lung (IMR90)	H3K27me3
		A549	H3K4me3
		nervous (NH-A)	DNase1
		skin (NHEK)	H3K27me3
ENSR00001032837 (open chromatin region)	1	embryonic stem cell (H1ESC)	DNase1, H3K36me3
		blood (K562)	H3K27me3, PU1
		muscle (HSMM)	H3K36me3
		breast (HMEC)	H3K36me3
		endothelium (HUVEC)	H3K36me3
		lung (IMR90)	H3K36me3
		blood (GM12878)	PU1, Max, IRF4, H3K79me2, H3K36me3
		A549	H3K36me3
		skin (NHEK)	H3K36me3
ENSR00001702964 (CTCF binding site)	1	blood (DND-41)	H3K36me3
		blood (K562)	H3K27me3
		skin (NHDF-AD)	H3K4me1, DNase1
		cervix (HeLa-S3)	H3K36me3
		monocytes (Monocytes-CD14+)	H4K20me1, H3K36me3
		endothelium (HUVEC)	H3K36me3
		liver (HepG2)	H3K36me3, H3K27ac, H3K9ac, H3K79me2, H3K4me1, H3K4me2
		blood (GM12878)	H3K79me2
		lung (IMR90)	H3K36me3
		A549	H3K36me3
		skin (NHEK)	H3K4me1, H3K36me3
ENSR00001494480 (promoter flanking region)	1	embryonic stem cell (H1ESC)	DNase1, H3K36me3, USF1
		blood (K562)	H3K27me3
		blood (DND-41)	H3K36me3
		skin (NHDF-AD)	H3K4me1, DNase1
		muscle (HSMM)	H3K79me2
		cervix (HeLa-S3)	H3K36me3
		monocytes (Monocytes-CD14+)	H4K20me1, H3K36me3
		endothelium (HUVEC)	H3K36me3
		liver (HepG2)	DNase1, HNF4G, H3K4me3, PolII, H3K79me2, USF1, H3K4me1, H3K4me2, HNF4A, FOXA1, H3K9ac, H3K27ac, Cmyc, H3K36me3
		lung (IMR90)	H3K36me3
		blood (GM12878)	H3K79me2, H3K4me2, H3K36me3
		A549	H3K36me3

		skin (NHEK)	H3K4me1, H3K4me2, H3K36me3
ENSR00000487623 (promoter)	1	embryonic stem cell (H1ESC)	H3K36me3, H3K27me3, PolII, TAF7, H3K27ac, TAF1, H3K4me2, SP1, H3K9ac, H3K4me3, DNase1
		HSMMtube	H2AZ, H3K4me3, H3K4me2, DNase1, H3K9ac, H3K79me2
		blood (K562)	H3K27me3, H3K9ac, DNase1, H3K4me3
		skin (NHDF-AD)	H3K4me3, DNase1, H3K9ac, H3K4me2, H3K27ac
		muscle (HSMM)	DNase1, H2AZ, H3K79me2, H3K4me3, H3K27ac, H3K4me2, H3K9ac, H3K36me3
		liver (HepG2)	Gabp, PolII, H3K79me2, TAF1, ELF1, H3K4me1, H2AZ, H3K4me2, H3K9ac, H3K27ac, H3K4me3, H3K27me3, DNase1
		lung (IMR90)	H3K9ac, H3K4me3, H3K4me2, DNase1
		blood (GM12878)	H3K79me2, H3K4me3, H3K27ac, H3K4me2, H3K9ac, ELF1, DNase1, PolII, H2AZ
		nervous (NH-A)	H3K4me2, H3K9ac, H3K4me3, DNase1
		skin (NHEK)	DNase1, H3K36me3, H3K4me3, H3K4me2, H3K27ac, H3K9ac
		NHLF	DNase1, H3K4me3, H3K9ac, H3K27ac
		Osteobl	H3K4me2, H3K4me3, H3K27ac, H2AZ
		blood (DND-41)	H3K4me1, H3K4me2, H3K27ac, H3K9ac, H3K4me3, H3K27me3, H3K36me3
		breast (HMEC)	DNase1, H3K27ac, H3K4me3, H3K9ac, H3K4me2
		cervix (HeLa-S3)	Ini1, H3K9ac, H3K4me2, H3K27ac, TAF1, H3K4me3, H3K79me2, Gabp, PolII, DNase1
		monocytes (Monocytes-CD14+)	H3K36me3, H3K4me3, H3K9ac, H3K27ac, DNase1, H3K4me2
		endothelium (HUVEC)	H3K4me2, H3K4me3, H3K9ac, PolII, DNase1, Max
		A549	H3K36me3, DNase1, H3K9ac, H3K4me2, H3K4me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
PAIP1P1	downstream gene variant	224	ENST00000446875	?	?	2
TRIM10	downstream gene variant, upstream gene variant	2412	ENST00000376704	NM_052828.2	ENSP00000365894	8
TRIM10	downstream gene variant, upstream gene variant	2412	ENST00000449742	NM_006778.3	ENSP00000397073	8
TRIM15	upstream gene variant, downstream gene variant	113	ENST00000433744	?	ENSP00000398285	9
TRIM15	downstream gene variant	576	ENST00000619857	?	ENSP00000484001	1
TRIM15	downstream gene variant	569	ENST00000376694	NM_033229.2	ENSP00000365884	1
TRIM15	upstream gene variant, downstream gene variant	2113	ENST00000477944	?	?	3
TRIM15	upstream gene variant, downstream gene variant	137	ENST00000376688	?	ENSP00000365878	3
TRIM26	upstream gene variant	672	ENST00000418026	?	ENSP00000387530	1
TRIM26	upstream gene variant	692	ENST00000487829	?	?	1
TRIM26	upstream gene variant	638	ENST00000416596	?	ENSP00000413673	1
TRIM26	downstream gene variant, upstream gene variant	199	ENST00000437089	?	ENSP00000395491	3
TRIM26	upstream gene variant	691	ENST00000434785	?	ENSP00000400920	1
TRIM26	downstream gene variant	199	ENST00000480999	?	?	1
TRIM26	downstream gene variant, upstream gene variant	199	ENST00000454678	NM_003449.4	ENSP00000410446	2
TRIM26	downstream gene variant, upstream gene variant	199	ENST00000453195	NM_001242783.1	ENSP00000391879	2
TRIM31	upstream gene variant	4060	ENST00000468264	?	?	1
TRIM31	upstream gene variant	553	ENST00000480808	?	?	3
TRIM31	upstream gene variant	73	ENST00000485864	?	?	3
TRIM31	upstream gene variant	1378	ENST00000493404	?	?	2
TRIM31	upstream gene variant	747	ENST00000376734	NM_007028.3	ENSP00000365924	2
TRIM40	downstream gene variant	259	ENST00000307859	NM_138700.4	ENSP00000308310	1
TRIM40	downstream gene variant	259	ENST00000376724	?	ENSP00000365914	1
TRIM40	downstream gene variant	259	ENST00000396581	NM_001286633.1	ENSP00000379826	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
TRIM15	ENST00000433744	?	ENSP00000398285	1
TRIM15	ENST00000619857	?	ENSP00000484001	6
TRIM15	ENST00000376688	?	ENSP00000365878	6
TRIM15	ENST00000376694	NM_033229.2	ENSP00000365884	6
TRIM26	ENST00000480999	?	?	2
TRIM26	ENST00000453195	NM_001242783.1	ENSP00000391879	7
TRIM26	ENST00000454678	NM_003449.4	ENSP00000410446	7
TRIM26	ENST00000434785	?	ENSP00000400920	5
TRIM26	ENST00000418026	?	ENSP00000387530	5
TRIM26	ENST00000437089	?	ENSP00000395491	5
TRIM26	ENST00000487829	?	?	5
TRIM26	ENST00000416596	?	ENSP00000413673	5
TRIM31	ENST00000376734	NM_007028.3	ENSP00000365924	1
TRIM31	ENST00000493404	?	?	1
TRIM31-AS1	ENST00000440874	?	?	3
TRIM40	ENST00000396581	NM_001286633.1	ENSP00000379826	2
TRIM40	ENST00000376724	?	ENSP00000365914	2
TRIM40	ENST00000307859	NM_138700.4	ENSP00000308310	2

5'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
TRIM15	ENST00000619857	?	ENSP00000484001	3
TRIM15	ENST00000376694	NM_033229.2	ENSP00000365884	2
TRIM26	ENST00000453195	NM_001242783.1	ENSP00000391879	1
TRIM26	ENST00000454678	NM_003449.4	ENSP00000410446	1
TRIM26	ENST00000437089	?	ENSP00000395491	1
TRIM26	ENST00000416596	?	ENSP00000413673	1

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
PAIP1P1	ENST00000446875	?	1
TRIM15	ENST00000477944	?	1
TRIM26	ENST00000487829	?	1