Locus 167 (rs9469012)

SNiPAcard

Block annotations

Block info

genomic range	chr6:31,360,702-31,426,888
block size	66,187 bp
variant count	22 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.290 [-1.89 – 0.318]	**gene(s) hit or close-by**	HCP5, LINC01149, MICA, XXbac-BPG181B23.6, XXbac-BPG181B23.7, Y_RNA
phastCons	μ = 0.118 [0 – 0.47]	**eQTL gene(s)**	HCG22, HLA-B, LY6G5C, MICA, XXbac-BPG181B23.7
GERP++	μ = 0.053 [-0.718 – 0.641]	**potentially regulated gene(s)**	ABHD16A, ABHD16A, ABHD16A, ABHD16A, ABHD16A, ABHD16A, ABHD16A, AIF1, AIF1, AIF1, AIF1, AIF1, AIF1, BAG6, BAG6, BAG6, BAG6, BAG6, BAG6, BAG6, C2, C2, C2, C2, C2, C2, C2, C2, C2, C6orf48, C6orf48, C6orf48, C6orf48, C6orf48, C6orf48, CSNK2B, CSNK2B, CSNK2B, CSNK2B, CSNK2B, CSNK2B, CSNK2B, DDX39B, DDX39B, DDX39B, DDX39B, DDX39B, DDX39B, DDX39B, DDX39B, GPANK1, GPANK1, GPANK1, GPANK1, GPANK1, GPANK1, GPANK1, HCG22, HCG22, HCG22, HCG22, HCG22, HCG22, HCG22, HCG22, HCG22, HCG27, HCG27, HCG27, HCG27, HCG27, HCG27, HCG27, HCP5, HCP5, HCP5, HCP5, HLA-B, HLA-B, HLA-B, HLA-B, HLA-B, HLA-C, HLA-C, HLA-C, HLA-C, HLA-C, HLA-C, HLA-C, LST1, LST1, LST1, LST1, LST1, LST1, LST1, LST1, LTB, LTB, LTB, LTB, LTB, LTB, LTB, LTB, LY6G5C, LY6G5C, LY6G5C, LY6G5C, LY6G5C, LY6G5C, LY6G5C, MICA, MICA, MICA, MICA, MICA, MICB, MICB, MICB, MICB, MICB, MICB, MICB, MICB, PRRC2A, PRRC2A, PRRC2A, PRRC2A, PRRC2A, PRRC2A, PRRC2A, PRRC2A, TNF, TNF, TNF, TNF, TNF, TNF, TNF, TNF, TNF, UQCRHP1, UQCRHP1, UQCRHP1, UQCRHP1, UQCRHP1, UQCRHP1, VARS, VARS, VARS, VARS, VARS, VARS, VARS, XXbac-BPG299F13.16
CADD score	μ = 3.431 [0.17 – 8.268]	**disease gene(s)**	HLA-B, C2, TNF

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link		variant(s)
Behcet syndrome	1.25×10^{-6}	dbGaP	pha002888	dbGaP	1

Disease gene annotation

gene	trait	source DB	source entry/link	
HLA-B	Takayasu arteritis	OrphaNet	OrphaNet:3287	orphanet
HLA-B	Stevens-Johnson syndrome	OrphaNet	OrphaNet:36426	orphanet
HLA-B	Behcet disease	OrphaNet	OrphaNet:117	orphanet
C2	Immunodeficiency due to an early component of complement deficiency	OrphaNet	OrphaNet:169147	orphanet
	PSORIASIS 1, SUSCEPTIBILITY TO	OMIM	MIM:177900	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	PSORIASIS 1, SUSCEPTIBILITY TO	OMIM	MIM:177900	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	SEVERE CUTANEOUS ADVERSE REACTION, SUSCEPTIBILITY TOTOXIC EPIDERMAL [...]	OMIM	MIM:608579	OMIM
	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM

	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM
	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM
	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM
	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	PSORIASIS 1, SUSCEPTIBILITY TO	OMIM	MIM:177900	OMIM
C2	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
C2	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM
	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
TNF	HEPATITIS B VIRUS, SUSCEPTIBILITY TO	OMIM	MIM:610424	OMIM
TNF	MALARIA, SUSCEPTIBILITY TOMALARIA, RESISTANCE TO, INCLUDED	OMIM	MIM:611162	OMIM
TNF	PSORIATIC ARTHRITIS, SUSCEPTIBILITY TOPSORIATIC ARTHRITIS, SUSCEPTIBILITY [...]	OMIM	MIM:607507	OMIM
	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM
	COMPLEMENT COMPONENT 2 DEFICIENCY	OMIM	MIM:217000	OMIM
	MACULAR DEGENERATION, AGE-RELATED, 1	OMIM	MIM:603075	OMIM

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
MICA	?	ENSG00000204520	atrial appendage	2.93×10-8 (p-value)	GTEx Portal V6	13
XXbac-BPG181B23.7	?	ENSG00000272221	atrial appendage	1.51×10-7 (p-value)	GTEx Portal V6	21
MICA	?	ENSG00000204520	transformed fibroblasts	8.78×10-16 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	transformed fibroblasts	2.90×10-18 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	blood	4.17×10-14 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	blood	1.62×10-33 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	breast	2.51×10-10 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	breast	1.83×10-13 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	skeletal muscle	2.44×10-19 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	skeletal muscle	2.86×10-20 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	putamen	3.55×10-8 (p-value)	GTEx Portal V6	21
MICA	?	ENSG00000204520	putamen	4.08×10-7 (p-value)	GTEx Portal V6	11

XXbac-BPG181B23.7	?	ENSG00000272221	EBV lymphocytes	1.99×10-8 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	sun exposed skin	5.53×10-19 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	sun exposed skin	1.08×10-20 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	unexposed skin	1.60×10-12 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	unexposed skin	3.90×10-11 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	aorta	1.38×10-10 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	aorta	1.27×10-13 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	left ventricle	7.94×10-9 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	left ventricle	2.20×10-12 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	subcutaneous adipocytes	3.63×10-18 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	subcutaneous adipocytes	1.79×10-20 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	caudate basal ganglia	8.43×10-9 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	caudate basal ganglia	1.67×10-8 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	visceral adipocytes	2.35×10-12 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	visceral adipocytes	2.37×10-11 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	stomach	4.11×10-8 (p-value)	GTEx Portal V6	5
MICA	?	ENSG00000204520	cortex	9.16×10-12 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	cortex	2.89×10-9 (p-value)	GTEx Portal V6	21
MICA	?	ENSG00000204520	tibial nerve	3.93×10-13 (p-value)	GTEx Portal V6	22
HLA-B	?	ENSG00000234745	tibial nerve	1.12×10-7 (p-value)	GTEx Portal V6	12
XXbac-BPG181B23.7	?	ENSG00000272221	tibial nerve	7.42×10-17 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	esophagus mucosa	3.85×10-12 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	esophagus mucosa	1.01×10-11 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	pituitary	3.36×10-9 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	pituitary	1.09×10-9 (p-value)	GTEx Portal V6	12
MICA	?	ENSG00000204520	testis	3.08×10-10 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	testis	3.09×10-7 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	frontal cortex	4.84×10-9 (p-value)	GTEx Portal V6	13
XXbac-BPG181B23.7	?	ENSG00000272221	pancreas	3.99×10-10 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	pancreas	1.39×10-7 (p-value)	GTEx Portal V6	18
MICA	?	ENSG00000204520	muscularis mucosae	3.04×10-13 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	muscularis mucosae	2.96×10-12 (p-value)	GTEx Portal V6	22
HCG22	?	ENSG00000228789	muscularis mucosae	4.78×10-6 (p-value)	GTEx Portal V6	7
MICA	?	ENSG00000204520	lung	1.15×10-13 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	lung	3.96×10-21 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	tibial artery	1.35×10-16 (p-value)	GTEx Portal V6	22

HLA-B	?	ENSG00000234745	tibial artery	3.93×10-6 (p-value)	GTEx Portal V6	4
XXbac-BPG181B23.7	?	ENSG00000272221	tibial artery	1.76×10-19 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	thyroid	2.47×10-16 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	thyroid	3.66×10-17 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	transverse colon	1.21×10-8 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	transverse colon	1.07×10-11 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	liver	4.70×10-8 (p-value)	GTEx Portal V6	12
MICA	?	ENSG00000204520	nucleus accumbens	1.16×10-7 (p-value)	GTEx Portal V6	13
XXbac-BPG181B23.7	?	ENSG00000272221	coronary artery	3.81×10-7 (p-value)	GTEx Portal V6	4
MICA	?	ENSG00000204520	sigmoid colon	3.24×10-11 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	sigmoid colon	4.97×10-10 (p-value)	GTEx Portal V6	22
MICA	?	ENSG00000204520	gastroesophageal junction	1.08×10-10 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	gastroesophageal junction	8.57×10-12 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	adrenal gland	7.92×10-7 (p-value)	GTEx Portal V6	4
MICA	?	ENSG00000204520	hippocampus	1.98×10-8 (p-value)	GTEx Portal V6	22
XXbac-BPG181B23.7	?	ENSG00000272221	hippocampus	4.35×10-8 (p-value)	GTEx Portal V6	22
HCG22	ENST00000570223	ILMN_1667229	blood	4.45×10-7 (p-value)	MuTHER consortium	2
HCG22	ENST00000565192					
HCG22	ENST00000615046					
HCG22	ENST00000426185					
HCG22	ENST00000562344					
MICA	ENST00000449934	ILMN_3241692	monocyte	1.19×10-10 (p-value)	Fairfax et al.	2
MICA	ENST00000616296		b-cell	5.10×10-8 (p-value)	Fairfax et al.	2
MICA	ENST00000421350					
MICA	?	ENSG00000204520	vagina	5.53×10-7 (p-value)	GTEx Portal V6	10
LY6G5C	ENST00000383237	ILMN_1763467	blood	4.51×10-6 (p-value)	Westra et al.	1
LY6G5C	ENST00000474395					
LY6G5C	ENST00000375863					
LY6G5C	ENST00000474678					
LY6G5C	ENST00000467098					
LY6G5C	ENST00000460141					

Putative effect on regulation

ENCODE promoter-associated DHS

SNiPA promoter id	variant(s)	associated gene(s)
ENCP00000048013		MICA
		MICA
		HCP5
		MICA
		HCP5
		MICA

			MICA
			HCP5

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000444737	1	ENCP00000048058	BAG6 BAG6 BAG6 BAG6 BAG6 BAG6 BAG6
		ENCP00000048034	LTB LTB LTB LTB LTB LTB LTB
		ENCP00000048025	DDX39B DDX39B DDX39B DDX39B DDX39B DDX39B DDX39B DDX39B
		ENCP00000047992	HCG27 HCG27 HCG27 HCG27 HCG27 HCG27 HCG27
		ENCP00000048062	CSNK2B CSNK2B CSNK2B CSNK2B CSNK2B CSNK2B CSNK2B
		ENCP00000048036	LST1 LST1 LST1 LST1 LST1 LST1 LST1 LST1
		ENCP00000048043	AIF1 AIF1 AIF1 AIF1 AIF1 AIF1
		ENCP00000048007	HLA-B HLA-B HLA-B HLA-B HLA-B HLA-B
		ENCP00000048063	GPANK1 GPANK1 GPANK1 GPANK1 GPANK1 GPANK1 GPANK1

		ENCP00000047991	HCG27 HCG27 HCG27 HCG27 HCG27 HCG27 HCG27
		ENCP00000047975	HCG22 HCG22 HCG22 HCG22 HCG22 HCG22 HCG22 HCG22
		ENCP00000047995	XXbac-BPG299F13.16
		ENCP00000048019	MICB MICB MICB MICB MICB MICB MICB MICB
		ENCP00000048078	ABHD16A ABHD16A ABHD16A ABHD16A ABHD16A ABHD16A ABHD16A
ENCE00000444880	1	ENCP00000048065	CSNK2B GPANK1 GPANK1 GPANK1 CSNK2B CSNK2B CSNK2B CSNK2B CSNK2B CSNK2B GPANK1 GPANK1 GPANK1 GPANK1
		ENCP00000048041	AIF1 AIF1 AIF1 AIF1 AIF1 AIF1
		ENCP00000048069	LY6G5C LY6G5C LY6G5C LY6G5C LY6G5C LY6G5C LY6G5C
		ENCP00000048050	PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A
		ENCP00000048017	HCP5 HCP5 HCP5 HCP5
		ENCP00000047997	HLA-C

	HLA-C HLA-C HLA-C HLA-C HLA-C HLA-C
ENCP00000048023	DDX39B DDX39B DDX39B DDX39B DDX39B DDX39B DDX39B DDX39B
ENCP00000048104	VARS VARS VARS VARS VARS VARS VARS
ENCP00000048052	PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A
ENCP00000048110	VARS VARS VARS VARS VARS VARS VARS
ENCP00000048109	VARS VARS VARS VARS VARS VARS VARS
ENCP00000048051	PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A
ENCP00000048033	TNF TNF TNF TNF TNF TNF TNF TNF
ENCP00000048035	LST1 LST1 LST1 LST1 LST1 LST1 LST1 LST1 LST1
ENCP00000047998	HLA-C HLA-C HLA-C HLA-C HLA-C HLA-C

		HLA-C
	ENCP00000048116	C6orf48 C6orf48 C6orf48 C6orf48 C6orf48
	ENCP00000048043	AIF1 AIF1 AIF1 AIF1 AIF1 AIF1
	ENCP00000048007	HLA-B HLA-B HLA-B HLA-B HLA-B HLA-B
	ENCP00000048048	PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A PRRC2A
	ENCP00000048020	MICB MICB MICB MICB MICB MICB MICB MICB
	ENCP00000048134	C2 C2 C2 C2 C2 C2 C2 C2
	ENCP00000048040	UQCRHP1 UQCRHP1 UQCRHP1 UQCRHP1 UQCRHP1 UQCRHP1
	ENCP00000048037	LST1 LST1 LST1 LST1 LST1 LST1 LST1 LST1

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000487835 (promoter)	1	embryonic stem cell (H1ESC)	DNase1, H3K9ac, H3K36me3, H3K27me3, PolII, Rad21, Egr1, CTCF, Yy1, Tcf12, TAF1, H3K4me2, SP1, USF1, H3K4me3
		HSMMtube	CTCF, H3K9ac, H3K36me3, H2AZ, H3K27ac, H3K4me2, DNase1
		blood (K562)	Ini1, Brg1, Egr1, H3K27ac, DNase1, H3K4me3, H3K36me3, H3K4me1, Max, Rad21, E2F6, H3K9ac, USF1, Cmyc, H3K79me2, HEY1, H2AZ, TAF1, Nrsf, Cfos, PolII, H3K4me2, CTCF
		skin (NHDF-AD)	H3K27ac, H3K4me2, H3K9ac, CTCF, H3K4me3, DNase1
		muscle (HSMM)	H3K36me3, DNase1, H3K9ac, H3K4me2, H2AZ, H3K79me2, CTCF, H3K4me3, H3K27ac
		liver (HepG2)	DNase1, H3K4me3, H3K27me3, Cmyc, CTCF, Gabp, PolII, H3K79me2, Rad21, TAF1, USF1, H3K4me1, H2AZ, H3K4me2, H3K9ac, H3K27ac
		lung (IMR90)	H3K4me3, H3K9ac, CTCF, H3K4me2, DNase1, H3K79me2
		blood (GM12878)	PolII, H2AZ, DNase1, Egr1, Yy1, Rad21, H3K79me2, H3K4me3, H3K27ac, H3K4me2, CTCF, H3K9ac

		nervous (NH-A)	DNase1, H3K9ac, H4K20me1, CTCF, H3K4me2, H3K4me3, H3K27ac, H3K36me3
		skin (NHEK)	H3K36me3, DNase1, CTCF, H3K4me3, H3K4me2, H3K9ac
		NHLF	DNase1, H3K4me3, CTCF, H3K9ac, H3K27ac
		Osteobl	H3K36me3, CTCF, H3K4me2, H3K4me3, H3K27ac, H2AZ
		blood (DND-41)	H3K4me1, CTCF, H3K27ac, H4K20me1, H3K9ac, H3K4me3, H3K36me3
		breast (HMEC)	DNase1, H3K27ac, H3K4me3, H3K9ac, H3K4me2, H3K36me3, CTCF
		cervix (HeLa-S3)	DNase1, PolII, CTCF, Gabp, H3K79me2, H3K9ac, H3K4me2, H3K27ac, TAF1, H3K4me3
		monocytes (Monocytes-CD14+)	DNase1, H3K4me1, CTCF, H3K4me2, H3K27ac, H3K9ac, H4K20me1, H3K36me3, H3K4me3
		endothelium (HUVEC)	H3K36me3, Cjun, H3K4me2, H3K4me3, PolII, CTCF, DNase1
		A549	H3K4me3, H3K36me3, H3K27ac, DNase1, CTCF, H3K9ac, H3K4me2
ENSR00001703045 (CTCF binding site)	1	monocytes (Monocytes-CD14+)	H3K27me3
		endothelium (HUVEC)	H3K27me3
		HSMMtube	H3K27me3
		blood (DND-41)	H3K27me3
ENSR00001703047 (open chromatin region)	2	endothelium (HUVEC)	H3K27me3
		embryonic stem cell (H1ESC)	H3K36me3
		A549	H3K27me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
HCP5	upstream gene variant	4071	ENST00000541196	?	?	1
HCP5	upstream gene variant	28	ENST00000414046	?	?	1
HCP5	upstream gene variant	4074	ENST00000460889	?	?	1
HCP5	upstream gene variant	4074	ENST00000467369	?	?	1
LINC01149	downstream gene variant	2	ENST00000430364	?	?	7
MICA	upstream gene variant, downstream gene variant	278	ENST00000421350	?	ENSP00000402410	2
MICA	upstream gene variant, downstream gene variant	278	ENST00000449934	NM_001177519.2	ENSP00000413079	2
MICA	downstream gene variant	280	ENST00000616296	NM_001289152.1, NM_001289153.1, NM_001289154.1	ENSP00000482382	1
XXbac-BPG181B23.6	downstream gene variant	3617	ENST00000440087	?	?	2
XXbac-BPG181B23.7	downstream gene variant	983	ENST00000606743	?	?	2
Y_RNA	downstream gene variant	1478	ENST00000362462	?	?	1

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
HCP5	ENST00000414046	?	?	19
LINC01149	ENST00000430364	?	?	3
MICA	ENST00000616296	NM_001289152.1, NM_001289153.1, NM_001289154.1	ENSP00000482382	1
MICA	ENST00000421350	?	ENSP00000402410	1
MICA	ENST00000449934	NM_001177519.2	ENSP00000413079	1

5'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
MICA	ENST00000616296	NM_001289152.1, NM_001289153.1, NM_001289154.1	ENSP00000482382	1

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
LINC01149	ENST00000430364	?	2

Locus 167 (sentinel SNP rs9469012 + 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.