

# SNiPACard

## Block annotations

### Block info


genomic range	chr12:10,517,808-10,644,573 <i>e!</i>
block size	126,766 bp
variant count	73 variants

### Basic features


Conservation/deleteriousness		Linked genes	
phyloP	$\mu = -0.740$ [-4.39 – 0.939]	gene(s) hit or close-by	KLRC1 <i>e!</i> , KLRC2 <i>e!</i> , KLRC3 <i>e!</i> , KLRC4 <i>e!</i> , KLRC4-KLRK1 <i>e!</i> , KLRK1 <i>e!</i> , RP11-277P12.20 <i>e!</i> , RP11-277P12.6 <i>e!</i> , RP11-277P12.9 <i>e!</i>
phastCons	$\mu = 0.054$ [0 – 0.865]	eQTL gene(s)	GABARAPL1 <i>e!</i> , KLRC1 <i>e!</i> , KLRC2 <i>e!</i> , KLRC3 <i>e!</i> , KLRC4-KLRK1 <i>e!</i> , KLRD1 <i>e!</i> , KLRK1 <i>e!</i> , RP11-277P12.10 <i>e!</i> , RP11-277P12.20 <i>e!</i> , TAS2R10 <i>e!</i> , YBX3 <i>e!</i>
GERP++	$\mu = -0.537$ [-6.29 – 1.55]	potentially regulated gene(s)	CLEC1A <i>e!</i> , KLRC2 <i>e!</i> , KLRC3 <i>e!</i> , KLRD1 <i>e!</i> , KLRK1 <i>e!</i>
CADD score	$\mu = 3.036$ [0.042 – 10.47]	disease gene(s)	-

## Trait annotations

### Variant association

trait	min(p-value)	source DB	source entry/link	variant(s)
Obesity-related traits	<6.00×10 <sup>-6</sup>	GWAS Catalog	23251661 	1

### Variant annotation

trait	type	source DB	source entry/link	Variant(s)
?	HGMD curated	HGMD	CM099345 	1



## 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)
KLRC4-KLRK1 <i>e!</i>	missense variant	ENST00000616233 <i>e!</i>	NM_001199805.1	ENSP00000480609	T/A	Aca/Gca	tolerated	benign	1
KLRK1 <i>e!</i>	missense variant	ENST00000396451 <i>e!</i>	?	ENSP00000379726	T/A	Aca/Gca	tolerated	?	1
KLRK1 <i>e!</i>	missense variant	ENST00000240618 <i>e!</i>	NM_007360.3	ENSP00000240618	T/A	Aca/Gca	tolerated	benign	1
KLRK1 <i>e!</i>	missense variant	ENST00000540818 <i>e!</i>	?	ENSP00000446003	T/A	Aca/Gca	tolerated	benign	1




## Direct effect on regulation

### cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	pancreas	1.05×10 <sup>-6</sup> (p-value)	GTE Portal V6 	36
GABARAPL1 <i>e!</i>	ENST00000539170 <i>e!</i>	ILMN_2151281 <i>e!</i>	blood	8.21×10 <sup>-18</sup> (p-value)	MuTHER consortium 	18
GABARAPL1 <i>e!</i>	ENST00000541960 <i>e!</i>					
GABARAPL1 <i>e!</i>	ENST00000540424 <i>e!</i>					
GABARAPL1 <i>e!</i>	ENST00000266458 <i>e!</i>					

GABARAPL1	e!	ENST00000542722	e!						
GABARAPL1	e!	ENST00000546017	e!						
GABARAPL1	e!	ENST00000535576	e!						
KLRD1	e!	ENST00000381908	e!	ILMN_1799134	e!	blood	1.75×10 <sup>-5</sup> (p-value)	MuTHER consortium	14
KLRD1	e!	ENST00000336164	e!						
KLRD1	e!	ENST00000344825	e!						
KLRD1	e!	ENST00000539374	e!						
KLRD1	e!	ENST00000544747	e!						
KLRD1	e!	ENST00000350274	e!						
KLRD1	e!	ENST00000543777	e!						
KLRD1	e!	ENST00000540271	e!						
KLRD1	e!	ENST00000539792	e!						
KLRC2	e!	?		ENSG00000205809	e!	muscularis mucosae	2.54×10 <sup>-10</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	lung	9.82×10 <sup>-20</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	transformed fibroblasts	1.20×10 <sup>-11</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	blood	3.58×10 <sup>-13</sup> (p-value)	GTEX Portal V6	68
KLRC3	e!	?		ENSG00000205810	e!	blood	2.21×10 <sup>-6</sup> (p-value)	GTEX Portal V6	15
KLRC2	e!	?		ENSG00000205809	e!	breast	1.41×10 <sup>-9</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	thyroid	1.32×10 <sup>-11</sup> (p-value)	GTEX Portal V6	68
RP11-277P12.20	e!	?		ENSG00000245648	e!	thyroid	3.93×10 <sup>-6</sup> (p-value)	GTEX Portal V6	1
KLRC2	e!	?		ENSG00000205809	e!	transverse colon	1.12×10 <sup>-8</sup> (p-value)	GTEX Portal V6	60
KLRK1	e!	?		ENSG00000213809	e!	blood	5.02×10 <sup>-3</sup> (q-value)	SeeQTL DB (HapMap)	5
RP11-277P12.10	e!	?		ENSG00000256288	e!	sun exposed skin	4.53×10 <sup>-7</sup> (p-value)	GTEX Portal V6	40
RP11-277P12.20	e!	?		ENSG00000245648	e!	sun exposed skin	3.53×10 <sup>-7</sup> (p-value)	GTEX Portal V6	44
RP11-277P12.20	e!	?		ENSG00000245648	e!	unexposed skin	4.51×10 <sup>-10</sup> (p-value)	GTEX Portal V6	67
KLRC2	e!	?		ENSG00000205809	e!	subcutaneous adipocytes	2.11×10 <sup>-8</sup> (p-value)	GTEX Portal V6	62
KLRC2	e!	?		ENSG00000205809	e!	terminal ileum	1.84×10 <sup>-8</sup> (p-value)	GTEX Portal V6	24
KLRC2	e!	?		ENSG00000205809	e!	stomach	1.10×10 <sup>-15</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	spleen	7.02×10 <sup>-11</sup> (p-value)	GTEX Portal V6	64
KLRC2	e!	?		ENSG00000205809	e!	nucleus accumbens	7.35×10 <sup>-9</sup> (p-value)	GTEX Portal V6	55
KLRC2	e!	?		ENSG00000205809	e!	vagina	1.21×10 <sup>-9</sup> (p-value)	GTEX Portal V6	60
KLRC2	e!	?		ENSG00000205809	e!	esophagus mucosa	3.88×10 <sup>-10</sup> (p-value)	GTEX Portal V6	68
RP11-277P12.20	e!	?		ENSG00000245648	e!	esophagus mucosa	1.10×10 <sup>-27</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	anterior cingulate cortex	2.84×10 <sup>-11</sup> (p-value)	GTEX Portal V6	68
RP11-277P12.20	e!	?		ENSG00000245648	e!	testis	2.48×10 <sup>-11</sup> (p-value)	GTEX Portal V6	68
KLRC2	e!	?		ENSG00000205809	e!	testis	1.63×10 <sup>-6</sup> (p-value)	GTEX Portal V6	19
KLRC2	e!	?		ENSG00000205809	e!	hypothalamus	4.78×10 <sup>-9</sup> (p-value)	GTEX Portal V6	56
KLRC2	e!	?		ENSG00000205809	e!	frontal cortex	1.07×10 <sup>-13</sup> (p-value)	GTEX Portal V6	68

KLRC4-KLRK1 <i>e!</i>	ENST00000591546 <i>e!</i>	1555691_a_at <i>e!</i>	blood	1.00×10 <sup>-9</sup> (p-value)	Dixon et al. 	2
KLRC4-KLRK1 <i>e!</i>	ENST00000586581 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000543572 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000590131 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000543812 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000585507 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000540818 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000539370 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000544449 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000240618 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000588263 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000539300 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000540267 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000616233 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000585711 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000591937 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000588447 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000396451 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000590323 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000591546 <i>e!</i>	205821_at <i>e!</i>	blood	1.90×10 <sup>-12</sup> (p-value)	Dixon et al. 	2
KLRC4-KLRK1 <i>e!</i>	ENST00000586581 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000543572 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000585711 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000590131 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000543812 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000544449 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000240618 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000539300 <i>e!</i>					
KLRK1 <i>e!</i>	ENST00000540267 <i>e!</i>					
KLRC4-KLRK1 <i>e!</i>	ENST00000616233 <i>e!</i>					
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	tibial nerve	2.43×10 <sup>-9</sup> (p-value)	GTEEx Portal V6 	57
YBX3 <i>e!</i>	ENST00000279550 <i>e!</i>	ILMN_1782788 <i>e!</i>	monocyte	1.40×10 <sup>-6</sup> (p-value)	Fairfax et al. 	2
YBX3 <i>e!</i>	ENST00000540447 <i>e!</i>					
YBX3 <i>e!</i>	ENST00000228251 <i>e!</i>					
YBX3 <i>e!</i>	ENST00000366286 <i>e!</i>					
YBX3 <i>e!</i>	ENST00000540975 <i>e!</i>					
YBX3 <i>e!</i>	ENST00000536823 <i>e!</i>					
YBX3 <i>e!</i>	ENST00000546164 <i>e!</i>					
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	cortex	1.77×10 <sup>-7</sup> (p-value)	GTEEx Portal V6 	8
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	cerebellar hemisphere	3.01×10 <sup>-6</sup> (p-value)	GTEEx Portal V6 	4
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	hippocampus	7.43×10 <sup>-8</sup> (p-value)	GTEEx Portal V6 	14
?	?	ILMN_1707328 <i>e!</i>	liver	9.23×10 <sup>-13</sup> (p-value)	Innocenti et al. 	1
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	cerebellum	2.71×10 <sup>-7</sup> (p-value)	GTEEx Portal V6 	29
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	putamen	7.07×10 <sup>-7</sup> (p-value)	GTEEx Portal V6 	3
KLRC1 <i>e!</i>	ENST00000347831 <i>e!</i>	ILMN_1752647 <i>e!</i>	blood	5.64×10 <sup>-5</sup> (p-value)	Westra et al. 	1
KLRC1 <i>e!</i>	ENST00000359151 <i>e!</i>					
KLRC1 <i>e!</i>	ENST00000544822 <i>e!</i>					
KLRC1 <i>e!</i>	ENST00000536188 <i>e!</i>					
KLRC1 <i>e!</i>	ENST00000408006 <i>e!</i>					

KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	visceral adipocytes	1.04×10 <sup>-6</sup> (p-value)	GTEx Portal V6 	23
TAS2R10 <i>e!</i>	?	ENSG00000121318 <i>e!</i>	EBV lymphocytes	1.55×10 <sup>-6</sup> (p-value)	GTEx Portal V6 	1
KLRC2 <i>e!</i>	?	ENSG00000205809 <i>e!</i>	caudate basal ganglia	3.48×10 <sup>-7</sup> (p-value)	GTEx Portal V6 	1

### Putative effect on regulation

#### ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000133909 <i>e!</i>	1	ENCP00000016103	CLEC1A <i>e!</i>
ENCE00000133997 <i>e!</i>	1	ENCP00000016122	KLRK1 <i>e!</i>
		ENCP00000016121	KLRK1 <i>e!</i>
		ENCP00000016129	KLRC2 <i>e!</i>
ENCE00000133946 <i>e!</i>	1	ENCP00000016116	KLRD1 <i>e!</i>
		ENCP00000016127	KLRC3 <i>e!</i>

#### Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000426296 <i>e!</i> (promoter)	3	embryonic stem cell (H1ESC) HSMMtube blood (K562) skin (NHDF-AD) muscle (HSMM) liver (HepG2) blood (GM12878) lung (IMR90) nervous (NH-A) skin (NHEK) NHLF Osteobl blood (DND-41) breast (HMEC) cervix (HeLa-S3) monocytes (Monocytes-CD14+) endothelium (HUVEC) A549	DNase1, H3K27ac, CTCF, Rad21, FOSL1, Yy1, TAF1, H3K4me2, SP1, H3K4me3 H3K4me2, H2AZ, DNase1 DNase1, H3K27ac, H3K9ac, H2AZ, PolII, H3K4me2, CTCF, H3K4me3 H3K4me2, H3K9ac, DNase1, H3K4me3, CTCF H2AZ, CTCF, H3K4me3, H3K27ac, H3K4me2, H3K9ac, DNase1 CTCF, H2AZ, H3K4me2, H3K9ac, H3K4me3, H3K27me3 H3K9ac, H3K4me2, H3K27ac, H3K4me3, IRF4, DNase1, H2AZ, BCLAF1, PolII, PU1, EBF1 CTCF, H3K9ac, H2BK120ac, H3K4me3, H4K5ac, H3K4me2, H3K18ac, H3K27ac, H4K8ac, DNase1 H3K9ac, H3K4me2, H3K4me3 CTCF, DNase1, H3K4me1, H3K27ac, H3K9ac, H3K4me2, H3K4me3 DNase1, H3K4me3, H3K27ac H2AZ, H3K27ac, H3K4me3, H3K4me2, CTCF H3K4me3, H3K9ac, H3K27ac, H3K4me2, H3K4me1 CTCF, H3K4me2, H3K9ac, H3K4me3, H3K27ac H3K9ac, DNase1, H3K4me2, H3K27ac, H3K4me3, CTCF, H3K36me3 DNase1, H3K27ac, H3K9ac, H3K4me3 PolII, H3K4me3, H3K4me2 H3K4me3, H3K4me2, H3K9ac, CTCF
ENSR00001609380 <i>e!</i> (CTCF binding site)	2	embryonic stem cell (H1ESC) HSMMtube blood (K562) skin (NHDF-AD) muscle (HSMM) liver (HepG2) lung (IMR90) blood (GM12878) nervous (NH-A) skin (NHEK) Osteobl blood (DND-41) breast (HMEC) cervix (HeLa-S3) endothelium (HUVEC) A549	CTCF, Rad21 H2AZ H3K27ac, H3K9ac, H2AZ, H3K4me3, H3K4me2, CTCF, DNase1 H3K4me2, H3K4me3, CTCF H2AZ, CTCF, H3K4me3, H3K4me2 CTCF, Rad21, H2AZ, H3K4me2, H3K4me3 CTCF, H4K5ac, H3K4me2, H3K18ac, H3K27ac, H4K8ac H2AZ, Rad21 H3K4me2 H3K27ac, H3K4me2, CTCF, H3K4me1 H2AZ, H3K4me2, CTCF H3K4me3, H3K9ac, H3K4me2, H3K4me1 CTCF, H3K4me2 DNase1, H3K4me2, H3K27ac, H3K4me3, CTCF, H3K36me3 H3K36me3, CTCF, H3K4me3, H3K4me2 CTCF
ENSR00001609383 <i>e!</i> (enhancer)	1	cervix (HeLa-S3) lung (IMR90)	H3K36me3 H3K36me3
ENSR00001461319 <i>e!</i> (promoter flanking region)	2	cervix (HeLa-S3) NHLF monocytes (Monocytes-CD14+)	DNase1, H3K4me2, H3K36me3 DNase1 H3K27me3

		nervous (NH-A)	DNase1
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1
ENSR00001609384 <i>e!</i>	1	cervix (HeLa-S3)	DNase1, H3K4me2, H3K36me3
(CTCF binding site)		monocytes (Monocytes-CD14+)	H3K27me3
		NHLF	DNase1
		nervous (NH-A)	DNase1
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1
ENSR00000653098 <i>e!</i>	2	NHLF	DNase1
(promoter flanking region)		embryonic stem cell (H1ESC)	DNase1
		HSMMtube	H3K27me3, DNase1
		Osteobl	H3K27ac, H3K4me2
		blood (DND-41)	H3K27me3
		skin (NHDF-AD)	DNase1
		muscle (HSMM)	DNase1
		breast (HMEC)	H3K4me2, H3K9ac, H3K27ac, DNase1
		cervix (HeLa-S3)	H3K36me3, PolII, H3K9ac, DNase1, Nrsf, H3K4me2, H3K27ac, H3K4me1, TAF1, H3K4me3, H3K79me2, Gabp
		monocytes (Monocytes-CD14+)	H3K27me3, H3K27ac, DNase1
		liver (HepG2)	FOXA1
		blood (GM12878)	BCL11A, DNase1, PU1
		A549	H3K4me3, H3K4me2, DNase1
		nervous (NH-A)	DNase1
		skin (NHEK)	DNase1, H3K4me1, H3K27ac, H3K4me2

### Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
KLRC1 <i>e!</i>	downstream gene variant, upstream gene variant	20	ENST00000544822 <i>e!</i>	NM_213658.2	ENSP00000438038 <i>e!</i>	10
KLRC1 <i>e!</i>	downstream gene variant, upstream gene variant	10	ENST00000347831 <i>e!</i>	NM_007328.3	ENSP00000256965 <i>e!</i>	10
KLRC1 <i>e!</i>	downstream gene variant, upstream gene variant	560	ENST00000543893 <i>e!</i>	?	ENSP00000442545 <i>e!</i>	10
KLRC1 <i>e!</i>	upstream gene variant	1137	ENST00000536188 <i>e!</i>	NM_001304448.1	ENSP00000441432 <i>e!</i>	4
KLRC1 <i>e!</i>	downstream gene variant, upstream gene variant	7	ENST00000359151 <i>e!</i>	NM_002259.4	ENSP00000352064 <i>e!</i>	10
KLRC1 <i>e!</i>	downstream gene variant, upstream gene variant	323	ENST00000537699 <i>e!</i>	?	?	11
KLRC1 <i>e!</i>	downstream gene variant, upstream gene variant	7	ENST00000408006 <i>e!</i>	NM_213657.2	ENSP00000385304 <i>e!</i>	10
KLRC2 <i>e!</i>	downstream gene variant	369	ENST00000535069 <i>e!</i>	?	ENSP00000438983 <i>e!</i>	1
KLRC2 <i>e!</i>	downstream gene variant	2105	ENST00000537017 <i>e!</i>	?	ENSP00000445240 <i>e!</i>	4
KLRC2 <i>e!</i>	downstream gene variant	1684	ENST00000381902 <i>e!</i>	NM_002260.3	ENSP00000371327 <i>e!</i>	4
KLRC2 <i>e!</i>	downstream gene variant, upstream gene variant	2065	ENST00000536833 <i>e!</i>	?	ENSP00000444754 <i>e!</i>	13
KLRC2 <i>e!</i>	downstream gene variant	1694	ENST00000619500 <i>e!</i>	?	ENSP00000479152 <i>e!</i>	4
KLRC2 <i>e!</i>	downstream gene variant	1694	ENST00000381901 <i>e!</i>	?	ENSP00000371326 <i>e!</i>	4
KLRC3 <i>e!</i>	downstream gene variant	2288	ENST00000396439 <i>e!</i>	NM_002261.2	ENSP00000379716 <i>e!</i>	2
KLRC4 <i>e!</i>	downstream gene variant, upstream gene variant	130	ENST00000309384 <i>e!</i>	NM_013431.2	ENSP00000310216 <i>e!</i>	4
KLRC4-KLRK1 <i>e!</i>	downstream gene variant	3563	ENST00000616233 <i>e!</i>	NM_001199805.1	ENSP00000480609 <i>e!</i>	5
KLRC4-KLRK1 <i>e!</i>	downstream gene variant	4201	ENST00000543812 <i>e!</i>	?	ENSP00000457500 <i>e!</i>	4
KLRC4-KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	2121	ENST00000543572 <i>e!</i>	?	ENSP00000456286 <i>e!</i>	7
KLRC4-KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	338	ENST00000586581 <i>e!</i>	?	ENSP00000467228 <i>e!</i>	5
KLRC4-KLRK1 <i>e!</i>	downstream gene variant	4269	ENST00000591546 <i>e!</i>	?	ENSP00000468432 <i>e!</i>	3
KLRC4-KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	338	ENST00000539300 <i>e!</i>	?	ENSP00000455951 <i>e!</i>	6
KLRC4-KLRK1 <i>e!</i>	downstream gene variant	188	ENST00000585507 <i>e!</i>	?	ENSP00000465434 <i>e!</i>	2

KLRC4-KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	69	ENST00000539370 <i>e!</i> ?	?	3
KLRC4-KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	2128	ENST00000585711 <i>e!</i> ?	ENSP00000467316 <i>e!</i>	5
KLRC4-KLRK1 <i>e!</i>	downstream gene variant	4292	ENST00000590131 <i>e!</i> ?	ENSP00000467152 <i>e!</i>	3
KLRC4-KLRK1 <i>e!</i>	downstream gene variant	39	ENST00000591937 <i>e!</i> ?	ENSP00000466326 <i>e!</i>	3
KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	1452	ENST00000396451 <i>e!</i> ?	ENSP00000379726 <i>e!</i>	5
KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	715	ENST00000544449 <i>e!</i> ?	?	7
KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	170	ENST00000540818 <i>e!</i> ?	ENSP00000446003 <i>e!</i>	9
KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	722	ENST00000240618 <i>e!</i> NM_007360.3	ENSP00000240618 <i>e!</i>	8
KLRK1 <i>e!</i>	downstream gene variant, upstream gene variant	97	ENST00000540267 <i>e!</i> ?	?	11
RP11-277P12.20 <i>e!</i>	downstream gene variant	3880	ENST00000500682 <i>e!</i> ?	?	1
RP11-277P12.6 <i>e!</i>	downstream gene variant	2288	ENST00000539033 <i>e!</i> ?	ENSP00000437563 <i>e!</i>	2
RP11-277P12.9 <i>e!</i>	upstream gene variant	4164	ENST00000535911 <i>e!</i> ?	?	3

### Putative effect on transcript

#### Non-coding exon variant (splice region)

gene	affected transcript	RefSeq id	variant(s)
RP11-277P12.20 <i>e!</i>	ENST00000500682 <i>e!</i>	?	1

#### Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
KLRC1 <i>e!</i>	ENST00000544822 <i>e!</i>	NM_213658.2	ENSP00000438038 <i>e!</i>	6
KLRC1 <i>e!</i>	ENST00000359151 <i>e!</i>	NM_002259.4	ENSP00000352064 <i>e!</i>	6
KLRC1 <i>e!</i>	ENST00000536188 <i>e!</i>	NM_001304448.1	ENSP00000441432 <i>e!</i>	12
KLRC1 <i>e!</i>	ENST00000543893 <i>e!</i>	?	ENSP00000442545 <i>e!</i>	2
KLRC1 <i>e!</i>	ENST00000347831 <i>e!</i>	NM_007328.3	ENSP00000256965 <i>e!</i>	6
KLRC1 <i>e!</i>	ENST00000408006 <i>e!</i>	NM_213657.2	ENSP00000385304 <i>e!</i>	6
KLRC2 <i>e!</i>	ENST00000535069 <i>e!</i>	?	ENSP00000438983 <i>e!</i>	3
KLRC4-KLRK1 <i>e!</i>	ENST00000588447 <i>e!</i>	?	ENSP00000465254 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000585507 <i>e!</i>	?	ENSP00000465434 <i>e!</i>	23
KLRC4-KLRK1 <i>e!</i>	ENST00000543812 <i>e!</i>	?	ENSP00000457500 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000591546 <i>e!</i>	?	ENSP00000468432 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000590323 <i>e!</i>	?	ENSP00000467880 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000539300 <i>e!</i>	?	ENSP00000455951 <i>e!</i>	23
KLRC4-KLRK1 <i>e!</i>	ENST00000543572 <i>e!</i>	?	ENSP00000456286 <i>e!</i>	23
KLRC4-KLRK1 <i>e!</i>	ENST00000590131 <i>e!</i>	?	ENSP00000467152 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000586581 <i>e!</i>	?	ENSP00000467228 <i>e!</i>	23
KLRC4-KLRK1 <i>e!</i>	ENST00000616233 <i>e!</i>	NM_001199805.1	ENSP00000480609 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000539370 <i>e!</i>	?	?	22
KLRC4-KLRK1 <i>e!</i>	ENST00000588263 <i>e!</i>	?	ENSP00000468074 <i>e!</i>	25
KLRC4-KLRK1 <i>e!</i>	ENST00000591937 <i>e!</i>	?	ENSP00000466326 <i>e!</i>	23
KLRC4-KLRK1 <i>e!</i>	ENST00000585711 <i>e!</i>	?	ENSP00000467316 <i>e!</i>	23

KLRK1 <i>e!</i>	ENST00000396451 <i>e!</i>	?	ENSP00000379726 <i>e!</i>	19
KLRK1 <i>e!</i>	ENST00000540267 <i>e!</i>	?	?	9
KLRK1 <i>e!</i>	ENST00000240618 <i>e!</i>	NM_007360.3	ENSP00000240618 <i>e!</i>	18
KLRK1 <i>e!</i>	ENST00000544449 <i>e!</i>	?	?	18
KLRK1 <i>e!</i>	ENST00000540818 <i>e!</i>	?	ENSP00000446003 <i>e!</i>	16
RP11-277P12.20 <i>e!</i>	ENST00000500682 <i>e!</i>	?	?	32
RP11-277P12.6 <i>e!</i>	ENST00000539033 <i>e!</i>	?	ENSP00000437563 <i>e!</i>	4

### 3'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
KLRC1 <i>e!</i>	ENST00000544822 <i>e!</i>	NM_213658.2	ENSP00000438038 <i>e!</i>	2
KLRC1 <i>e!</i>	ENST00000359151 <i>e!</i>	NM_002259.4	ENSP00000352064 <i>e!</i>	2
KLRC1 <i>e!</i>	ENST00000347831 <i>e!</i>	NM_007328.3	ENSP00000256965 <i>e!</i>	2
KLRC1 <i>e!</i>	ENST00000408006 <i>e!</i>	NM_213657.2	ENSP00000385304 <i>e!</i>	2
KLRC4-KLRK1 <i>e!</i>	ENST00000588447 <i>e!</i>	?	ENSP00000465254 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000585507 <i>e!</i>	?	ENSP00000465434 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000543812 <i>e!</i>	?	ENSP00000457500 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000591546 <i>e!</i>	?	ENSP00000468432 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000590323 <i>e!</i>	?	ENSP00000467880 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000539300 <i>e!</i>	?	ENSP00000455951 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000543572 <i>e!</i>	?	ENSP00000456286 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000590131 <i>e!</i>	?	ENSP00000467152 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000586581 <i>e!</i>	?	ENSP00000467228 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000588263 <i>e!</i>	?	ENSP00000468074 <i>e!</i>	1
KLRC4-KLRK1 <i>e!</i>	ENST00000585711 <i>e!</i>	?	ENSP00000467316 <i>e!</i>	1

### Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
KLRC4-KLRK1 <i>e!</i>	ENST00000539370 <i>e!</i>	?	2
KLRK1 <i>e!</i>	ENST00000540267 <i>e!</i>	?	3
KLRK1 <i>e!</i>	ENST00000544449 <i>e!</i>	?	3
RP11-277P12.20 <i>e!</i>	ENST00000500682 <i>e!</i>	?	3

