SNiPAcard

Block annotations

Block info

genomic range	chr7:23,272,144-23,332,280
block size	60,137 bp
variant count	21 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.333 [-2.465 – 1.258]	**gene(s) hit or close-by**	GPNMB
phastCons	μ = 0.058 [0 – 0.521]	**eQTL gene(s)**	AC005082.12, GPNMB, KLHL7, KLHL7-AS1, NUPL2
GERP++	μ = -0.903 [-9.76 – 2.64]	**potentially regulated gene(s)**	–
CADD score	μ = 3.494 [0.044 – 13.92]	**disease gene(s)**	KLHL7

Trait annotations

Disease gene annotation

gene	trait	source DB	source entry/link
KLHL7	RETINITIS PIGMENTOSA 42	OMIM	MIM:612943
KLHL7	Retinitis pigmentosa	OrphaNet	OrphaNet:791

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
NUPL2	?	ENSG00000136243	atrial appendage	8.06×10^{-19} (p-value)	GTEx Portal V6	21
KLHL7	?	ENSG00000122550	atrial appendage	1.73×10^{-8} (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	atrial appendage	2.53×10^{-18} (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	atrial appendage	1.80×10^{-11} (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	atrial appendage	2.25×10^{-11} (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	transformed fibroblasts	6.48×10^{-45} (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	transformed fibroblasts	6.10×10^{-9} (p-value)	GTEx Portal V6	7
KLHL7-AS1	?	ENSG00000230658	blood	3.10×10^{-15} (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	blood	1.06×10^{-6} (p-value)	GTEx Portal V6	17
AC005082.12	?	ENSG00000226816	blood	5.54×10^{-10} (p-value)	GTEx Portal V6	10
NUPL2	?	ENSG00000136243	breast	1.32×10^{-12} (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	breast	2.15×10^{-21} (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	breast	5.17×10^{-11} (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	skeletal muscle	2.51×10^{-12} (p-value)	GTEx Portal V6	21
KLHL7	?	ENSG00000122550	skeletal muscle	5.66×10^{-8} (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	skeletal muscle	3.06×10^{-28} (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	putamen	1.28×10^{-11} (p-value)	GTEx Portal V6	20

GPNMB	?	ENSG00000136235	putamen	2.39×10-11 (p-value)	GTEx Portal V6	19
KLHL7-AS1	?	ENSG00000230658	EBV lymphocytes	7.03×10-17 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	ovary	7.03×10-11 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	sun exposed skin	1.28×10-47 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	sun exposed skin	6.40×10-9 (p-value)	GTEx Portal V6	13
AC005082.12	?	ENSG00000226816	sun exposed skin	2.13×10-9 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	sun exposed skin	5.33×10-6 (p-value)	GTEx Portal V6	6
KLHL7-AS1	?	ENSG00000230658	unexposed skin	1.12×10-24 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	unexposed skin	6.75×10-9 (p-value)	GTEx Portal V6	20
NUPL2	?	ENSG00000136243	unexposed skin	9.48×10-6 (p-value)	GTEx Portal V6	1
NUPL2	?	ENSG00000136243	aorta	4.40×10-8 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	aorta	1.67×10-29 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	aorta	4.41×10-8 (p-value)	GTEx Portal V6	18
NUPL2	?	ENSG00000136243	left ventricle	3.04×10-21 (p-value)	GTEx Portal V6	21
KLHL7	?	ENSG00000122550	left ventricle	7.65×10-10 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	left ventricle	5.19×10-19 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	left ventricle	2.84×10-15 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	left ventricle	1.96×10-10 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	subcutaneous adipocytes	1.00×10-19 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	subcutaneous adipocytes	7.79×10-38 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	subcutaneous adipocytes	5.80×10-14 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	caudate basal ganglia	4.60×10-17 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	caudate basal ganglia	8.89×10-12 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	caudate basal ganglia	2.97×10-6 (p-value)	GTEx Portal V6	2
AC005082.12	?	ENSG00000226816	caudate basal ganglia	3.86×10-6 (p-value)	GTEx Portal V6	1
NUPL2	?	ENSG00000136243	visceral adipocytes	7.93×10-12 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	visceral adipocytes	4.09×10-19 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	visceral adipocytes	5.40×10-13 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	stomach	2.03×10-20 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	cortex	2.91×10-11 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	cortex	1.98×10-14 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	cortex	9.58×10-15 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	tibial nerve	5.80×10-19 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	tibial nerve	2.62×10-45 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	tibial nerve	2.35×10-6 (p-value)	GTEx Portal V6	4
KLHL7-AS1	?	ENSG00000230658	esophagus mucosa	4.36×10-26 (p-value)	GTEx Portal V6	21

AC005082.12	?	ENSG00000226816	esophagus mucosa	4.08×10-12 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	anterior cingulate cortex	8.00×10-9 (p-value)	GTEx Portal V6	16
KLHL7-AS1	?	ENSG00000230658	anterior cingulate cortex	2.23×10-7 (p-value)	GTEx Portal V6	15
KLHL7-AS1	?	ENSG00000230658	pituitary	6.13×10-16 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	pituitary	7.95×10-8 (p-value)	GTEx Portal V6	14
KLHL7-AS1	?	ENSG00000230658	testis	1.68×10-18 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	hypothalamus	3.37×10-12 (p-value)	GTEx Portal V6	20
GPNMB	?	ENSG00000136235	hypothalamus	5.24×10-10 (p-value)	GTEx Portal V6	12
KLHL7-AS1	?	ENSG00000230658	frontal cortex	1.62×10-14 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	frontal cortex	2.91×10-12 (p-value)	GTEx Portal V6	19
NUPL2	?	ENSG00000136243	frontal cortex	9.27×10-7 (p-value)	GTEx Portal V6	5
KLHL7-AS1	?	ENSG00000230658	uterus	4.92×10-12 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	pancreas	8.33×10-21 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	muscularis mucosae	1.24×10-7 (p-value)	GTEx Portal V6	18
KLHL7-AS1	?	ENSG00000230658	muscularis mucosae	1.90×10-32 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	muscularis mucosae	7.94×10-10 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	lung	4.43×10-13 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	lung	3.40×10-34 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	lung	1.57×10-8 (p-value)	GTEx Portal V6	18
NUPL2	?	ENSG00000136243	tibial artery	9.46×10-8 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	tibial artery	1.63×10-35 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	tibial artery	1.99×10-8 (p-value)	GTEx Portal V6	21
NUPL2	?	ENSG00000136243	thyroid	7.77×10-9 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	thyroid	1.16×10-38 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	thyroid	4.29×10-10 (p-value)	GTEx Portal V6	21
KLHL7	?	ENSG00000122550	thyroid	4.39×10-8 (p-value)	GTEx Portal V6	20
KLHL7-AS1	?	ENSG00000230658	prostate	1.25×10-11 (p-value)	GTEx Portal V6	18
GPNMB	?	ENSG00000136235	prostate	2.17×10-6 (p-value)	GTEx Portal V6	3
NUPL2	?	ENSG00000136243	transverse colon	7.39×10-11 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	transverse colon	10.00×10-20 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	liver	2.37×10-8 (p-value)	GTEx Portal V6	14
KLHL7-AS1	?	ENSG00000230658	terminal ileum	6.77×10-10 (p-value)	GTEx Portal V6	16
NUPL2	?	ENSG00000136243	spleen	5.25×10-8 (p-value)	GTEx Portal V6	15
KLHL7-AS1	?	ENSG00000230658	spleen	3.33×10-10 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	nucleus accumbens	3.92×10-13 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	nucleus accumbens	7.93×10-9 (p-value)	GTEx Portal V6	11

KLHL7	?	ENSG00000122550	nucleus accumbens	3.93×10-7 (p-value)	GTEx Portal V6	3
NUPL2	?	ENSG00000136243	nucleus accumbens	4.49×10-6 (p-value)	GTEx Portal V6	1
KLHL7-AS1	?	ENSG00000230658	sigmoid colon	1.85×10-17 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	sigmoid colon	2.51×10-8 (p-value)	GTEx Portal V6	18
KLHL7-AS1	?	ENSG00000230658	coronary artery	2.13×10-19 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	coronary artery	6.25×10-7 (p-value)	GTEx Portal V6	19
KLHL7-AS1	?	ENSG00000230658	vagina	8.80×10-9 (p-value)	GTEx Portal V6	15
NUPL2	?	ENSG00000136243	gastroesophageal junction	1.36×10-9 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	gastroesophageal junction	3.21×10-19 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	gastroesophageal junction	5.44×10-8 (p-value)	GTEx Portal V6	11
NUPL2	?	ENSG00000136243	adrenal gland	2.41×10-9 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	adrenal gland	1.71×10-15 (p-value)	GTEx Portal V6	21
AC005082.12	?	ENSG00000226816	adrenal gland	5.11×10-8 (p-value)	GTEx Portal V6	18
NUPL2	?	ENSG00000136243	cerebellar hemisphere	6.32×10-16 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	cerebellar hemisphere	5.96×10-9 (p-value)	GTEx Portal V6	20
GPNMB	?	ENSG00000136235	cerebellar hemisphere	6.64×10-11 (p-value)	GTEx Portal V6	19
NUPL2	?	ENSG00000136243	cerebellum	2.56×10-16 (p-value)	GTEx Portal V6	21
KLHL7-AS1	?	ENSG00000230658	cerebellum	2.05×10-9 (p-value)	GTEx Portal V6	21
GPNMB	?	ENSG00000136235	cerebellum	7.27×10-8 (p-value)	GTEx Portal V6	19
KLHL7-AS1	?	ENSG00000230658	hippocampus	1.16×10-8 (p-value)	GTEx Portal V6	20
NUPL2	?	ENSG00000136243	hippocampus	7.91×10-7 (p-value)	GTEx Portal V6	3
GPNMB	?	ENSG00000136235	hippocampus	3.46×10-7 (p-value)	GTEx Portal V6	5
NUPL2	ENST00000477844	ILMN_2115154	blood	1.42×10-6 (p-value)	MuTHER consortium	11
NUPL2	ENST00000489145		adipocyte	7.35×10-8 (p-value)	MuTHER consortium	11
NUPL2	ENST00000413919					
NUPL2	ENST00000437140					
NUPL2	ENST00000485250					
NUPL2	ENST00000438012					
NUPL2	ENST00000258742					
NUPL2	ENST00000477844	ILMN_1789616	adipocyte	1.21×10-6 (p-value)	MuTHER consortium	11
NUPL2	ENST00000489145					
NUPL2	ENST00000413919					
NUPL2	ENST00000437140					
NUPL2	ENST00000485250					
NUPL2	ENST00000438012					
NUPL2	ENST00000258742					
GPNMB	ENST00000478451	ILMN_1801205	blood	3.87×10-7 (p-value)	MuTHER consortium	11
GPNMB	ENST00000381990		skin	6.43×10-8 (p-value)	MuTHER consortium	11
GPNMB	ENST00000468723					
GPNMB	ENST00000463011					
GPNMB	ENST00000258733					
GPNMB	ENST00000470994					
GPNMB	ENST00000478451	ILMN_2407389	blood	2.81×10-5 (p-value)	MuTHER consortium	11

GPNMB	ENST00000478451	ILMN_2407389	blood	2.81×10-5 (p-value)	MuTHER consortium	11
GPNMB	ENST00000381990		skin	1.34×10-8 (p-value)	MuTHER consortium	11
GPNMB	ENST00000468723					
GPNMB	ENST00000463011					
GPNMB	ENST00000258733					
GPNMB	ENST00000470994					
NUPL2	ENST00000477844	ILMN_2115154	monocyte	4.52×10-19 (p-value)	Fairfax et al.	5
NUPL2	ENST00000489145		b-cell	1.25×10-10 (p-value)	Fairfax et al.	5
NUPL2	ENST00000413919					
NUPL2	ENST00000485250					
NUPL2	ENST00000437140					
NUPL2	ENST00000438012					
NUPL2	ENST00000258742					
NUPL2	ENST00000477844	ILMN_1789616	monocyte	8.72×10-14 (p-value)	Fairfax et al.	5
NUPL2	ENST00000489145		b-cell	3.25×10-7 (p-value)	Fairfax et al.	5
NUPL2	ENST00000413919					
NUPL2	ENST00000485250					
NUPL2	ENST00000437140					
NUPL2	ENST00000438012					
NUPL2	ENST00000258742					
GPNMB	ENST00000478451	ILMN_1801205	monocyte	1.93×10-20 (p-value)	Fairfax et al.	5
GPNMB	ENST00000381990					
GPNMB	ENST00000463011					
GPNMB	ENST00000468723					
GPNMB	ENST00000258733					
GPNMB	ENST00000470994					
GPNMB	ENST00000478451	ILMN_2407389	monocyte	1.34×10-5 (p-value)	Fairfax et al.	5
GPNMB	ENST00000381990					
GPNMB	ENST00000463011					
GPNMB	ENST00000468723					
GPNMB	ENST00000258733					
GPNMB	ENST00000470994					
GPNMB	?	ENSG00000136235	blood	1.10×10-2 (q-value)	SeeQTL DB (HapMap)	4
KLHL7	ENST00000409689	ILMN_1760792	blood	2.13×10-6 (p-value)	Westra et al.	11
KLHL7	ENST00000469845					
KLHL7	ENST00000339077					
KLHL7	ENST00000521082					
KLHL7	ENST00000409689	ILMN_1674458	blood	8.65×10-5 (p-value)	Westra et al.	4
KLHL7	ENST00000339077					
KLHL7	ENST00000521082					
NUPL2	ENST00000477844	ILMN_2115154	monocyte	6.98×10-47 (p-value)	Zeller et al.	3
NUPL2	ENST00000489145					
NUPL2	ENST00000413919					
NUPL2	ENST00000437140					
NUPL2	ENST00000485250					
NUPL2	ENST00000438012					
NUPL2	ENST00000258742					
NUPL2	ENST00000477844	ILMN_1789616	monocyte	7.00×10-24 (p-value)	Zeller et al.	3
NUPL2	ENST00000489145					
NUPL2	ENST00000413919					
NUPL2	ENST00000437140					
NUPL2	ENST00000485250					

NUPL2	ENST00000438012					
NUPL2	ENST00000258742					
GPNMB	ENST00000478451	ILMN_2407389	monocyte	2.73×10-19 (p-value)	Zeller et al.	3
GPNMB	ENST00000381990					
GPNMB	ENST00000468723					
GPNMB	ENST00000463011					
GPNMB	ENST00000258733					
GPNMB	ENST00000470994					
GPNMB	ENST00000478451	ILMN_1801205	monocyte	3.67×10-44 (p-value)	Zeller et al.	3
GPNMB	ENST00000381990					
GPNMB	ENST00000468723					
GPNMB	ENST00000463011					
GPNMB	ENST00000258733					
GPNMB	ENST00000470994					

Putative effect on regulation

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000623151 (promoter flanking region)	1	Osteobl	H3K4me2
		blood (K562)	H2AZ
		blood (DND-41)	H3K27me3
		breast (HMEC)	DNase1
		cervix (HeLa-S3)	DNase1
		endothelium (HUVEC)	H3K36me3, H3K27me3
		liver (HepG2)	USF1, H3K27me3
		blood (GM12878)	DNase1, H2AZ, CTCF, H3K27ac, H3K4me2
		nervous (NH-A)	DNase1
		skin (NHEK)	H3K4me2, DNase1
ENSR00000065472 (promoter)	1	embryonic stem cell (H1ESC)	DNase1, H3K27me3, Rad21, CTCF
		HSMMtube	DNase1, H3K27me3, CTCF
		blood (K562)	PolII, Ini1, Egr1, Nfe2, Rad21, CTCF, DNase1, H3K27me3
		skin (NHDF-AD)	CTCF
		muscle (HSMM)	CTCF
		liver (HepG2)	Rad21, DNase1, H3K4me2, CTCF
		lung (IMR90)	CTCF, H3K27me3, DNase1
		blood (GM12878)	Rad21, H3K4me3, H3K27ac, H3K4me2, CTCF, H3K9ac, DNase1, H2AZ, PolII
		nervous (NH-A)	DNase1, CTCF, H3K27me3
		skin (NHEK)	CTCF
		NHLF	DNase1, CTCF
		Osteobl	CTCF, H3K36me3, H3K27me3
		blood (DND-41)	H3K4me1, CTCF, H3K27me3
		breast (HMEC)	CTCF
		cervix (HeLa-S3)	Jund, H3K4me2, TAF1, Max, Cmyc, CTCF, DNase1
		monocytes (Monocytes-CD14+)	CTCF
		endothelium (HUVEC)	H3K36me3, CTCF, DNase1
		A549	H3K4me3, H3K4me2, CTCF, DNase1, H3K27ac
ENSR00000065473 (CTCF binding site)	2	embryonic stem cell (H1ESC)	Rad21, CTCF, DNase1
		HSMMtube	CTCF
		blood (K562)	DNase1, Rad21, CTCF
		skin (NHDF-AD)	CTCF
		muscle (HSMM)	CTCF
		liver (HepG2)	CTCF, Rad21
		lung (IMR90)	CTCF
		blood (GM12878)	Rad21, CTCF
		nervous (NH-A)	CTCF
		skin (NHEK)	H3K36me3, CTCF
		NHLF	CTCF
		Osteobl	CTCF

blood (DND-41)	CTCF
breast (HMEC)	CTCF
cervix (HeLa-S3)	CTCF
monocytes (Monocytes-CD14+)	CTCF
endothelium (HUVEC)	H3K36me3, CTCF
A549	CTCF

Variation in RISC binding site

gene	variant(s)	affected transcript(s)	targeting miRNA(s)
GPNMB	1	ENST00000258733 ENST00000381990	hsa-miR-103a-3p hsa-miR-107 hsa-miR-503-5p hsa-miR-508-3p hsa-miR-876-5p

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
GPNMB	upstream gene variant, downstream gene variant	863	ENST00000492858	?	?	3
GPNMB	upstream gene variant, downstream gene variant	213	ENST00000463011	?	?	9
GPNMB	upstream gene variant, downstream gene variant	822	ENST00000465673	?	?	3
GPNMB	upstream gene variant, downstream gene variant	543	ENST00000470994	?	?	7
GPNMB	downstream gene variant	4001	ENST00000474157	?	?	1
GPNMB	downstream gene variant	913	ENST00000381990	NM_001005340.1	ENSP00000371420	4
GPNMB	downstream gene variant	1886	ENST00000459927	?	?	1
GPNMB	upstream gene variant, downstream gene variant	387	ENST00000479625	?	?	6
GPNMB	downstream gene variant	941	ENST00000492512	?	?	2
GPNMB	upstream gene variant, downstream gene variant	199	ENST00000478451	?	?	9
GPNMB	downstream gene variant	1886	ENST00000487890	?	?	1
GPNMB	upstream gene variant, downstream gene variant	378	ENST00000468723	?	?	9
GPNMB	downstream gene variant	748	ENST00000409458	?	ENSP00000386476	1
GPNMB	downstream gene variant	912	ENST00000258733	NM_002510.2	ENSP00000258733	4

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
GPNMB	ENST00000258733	NM_002510.2	ENSP00000258733	11
GPNMB	ENST00000381990	NM_001005340.1	ENSP00000371420	11
GPNMB	ENST00000468723	?	?	1
GPNMB	ENST00000409458	?	ENSP00000386476	3
GPNMB	ENST00000470994	?	?	4
GPNMB	ENST00000465673	?	?	4
GPNMB	ENST00000492858	?	?	3
GPNMB	ENST00000487890	?	?	3
GPNMB	ENST00000479625	?	?	2
GPNMB	ENST00000459927	?	?	2
GPNMB	ENST00000478451	?	?	1

GPNMB	ENST00000492512	?	?	2
GPNMB	ENST00000463011	?	?	1

3'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
GPNMB	ENST00000258733	NM_002510.2	ENSP00000258733	1
GPNMB	ENST00000381990	NM_001005340.1	ENSP00000371420	1

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
GPNMB	ENST00000470994	?	1
GPNMB	ENST00000479625	?	1