Locus 330 (rs35555795)

SNiPAcard

Block annotations

Block info

genomic range	chr6:26,454,363-26,949,672
block size	495,310 bp
variant count	57 variants

Basic features

Conservation/deleteriousness		Linked genes	
phyloP	μ = -0.372 [-9.929 – 5.311]	gene(s) hit or close-by	ABT1, BTN1A1, BTN2A1, BTN3A3, CTA-14H9.5, GUSBP2, HCG11, HMGN4, LINC00240, POM121L6P, RP11-457M11.6, RP11-457M11.7, ZNF322
phastCons	μ = 0.107 [0 – 1]	eQTL gene(s)	BTN2A2, BTN3A2, BTN3A3, HIST1H2BD, HIST1H4H, HIST1H4J, PRSS16, SCGN, TRIM38, ZNF391
GERP++	μ = -0.435 [-5.9 – 3.15]	potentially regulated gene(s)	ABT1, BTN1A1, BTN3A1, BTN3A2, BTN3A3, HCG11, HIST1H2AD, HIST1H2BD, HIST1H2BF, HIST1H3F, HIST1H4C, HIST1H4D, HIST1H4E, HMGN4, VN1R13P
CADD score	μ = 5.289 [0.005 – 24.6]	disease gene(s)	–

Trait annotations

Variant association

trait	min(p-value)	source DB	source entry/link		variant(s)
phenol sulfate	8.78×10^{-7}	Metabolomics GWAS Server	24816252		5
Lupus erythematosus, systemic	7.66×10^{-6}	dbGaP	pha002867	dbGaP	1
Lupus erythematosus, systemic	1.17×10^{-10}	dbGaP	pha002848	dbGaP	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)
BTN1A1	missense variant	ENST00000244513	NM_001732.2	ENSP00000244513	S/P	Tcc/Ccc	?	?	1
BTN1A1	missense variant	ENST00000613186	?	ENSP00000484707	S/P	Tcc/Ccc	?	?	1
BTN2A1	missense variant	ENST00000429381	NM_078476.3	ENSP00000416945	3	3			3
BTN2A1	missense variant	ENST00000541522	NM_001197233.2	ENSP00000443909	5	5			5
BTN2A1	missense variant	ENST00000312541	NM_007049.4	ENSP00000312158	5	5			5
BTN2A1	missense variant	ENST00000469185	NM_001197234.2	ENSP00000419043	3	3			3

Direct effect on regulation

cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
BTN3A2	?	ENSG00000186470	atrial appendage	1.06×10^{-18} (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	transformed fibroblasts	1.95×10^{-29} (p-value)	GTEx Portal V6	49

ZNF391	?	ENSG00000124613	transformed fibroblasts	1.19×10-5 (p-value)	GTEx Portal V6	19
BTN3A2	?	ENSG00000186470	breast	2.31×10-16 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	blood	3.20×10-54 (p-value)	GTEx Portal V6	49
TRIM38	?	ENSG00000112343	blood	5.60×10-6 (p-value)	GTEx Portal V6	2
BTN3A2	?	ENSG00000186470	skeletal muscle	3.00×10-43 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	EBV lymphocytes	1.45×10-9 (p-value)	GTEx Portal V6	28
BTN3A2	?	ENSG00000186470	unexposed skin	4.12×10-14 (p-value)	GTEx Portal V6	49
BTN2A2	?	ENSG00000124508	sun exposed skin	4.82×10-6 (p-value)	GTEx Portal V6	11
BTN3A2	?	ENSG00000186470	sun exposed skin	2.65×10-35 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	ovary	1.34×10-11 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	left ventricle	4.58×10-34 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	aorta	5.55×10-26 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	subcutaneous adipocytes	1.65×10-32 (p-value)	GTEx Portal V6	49
HIST1H4J	?	ENSG00000197238	subcutaneous adipocytes	1.69×10-6 (p-value)	GTEx Portal V6	4
BTN3A2	?	ENSG00000186470	caudate basal ganglia	5.23×10-6 (p-value)	GTEx Portal V6	28
BTN3A2	?	ENSG00000186470	visceral adipocytes	1.56×10-12 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	stomach	1.77×10-21 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	cortex	6.44×10-8 (p-value)	GTEx Portal V6	31
BTN3A2	?	ENSG00000186470	tibial nerve	4.81×10-36 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	pituitary	3.74×10-7 (p-value)	GTEx Portal V6	31
BTN3A2	?	ENSG00000186470	esophagus mucosa	1.14×10-33 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	testis	6.84×10-17 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	hypothalamus	6.80×10-8 (p-value)	GTEx Portal V6	31
BTN3A2	?	ENSG00000186470	frontal cortex	1.34×10-11 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	uterus	6.66×10-12 (p-value)	GTEx Portal V6	38
BTN3A2	?	ENSG00000186470	pancreas	5.39×10-18 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	muscularis mucosae	8.36×10-32 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	lung	1.27×10-42 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	tibial artery	2.40×10-39 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	thyroid	2.94×10-30 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	transverse colon	7.87×10-18 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	liver	5.30×10-9 (p-value)	GTEx Portal V6	47
BTN3A2	?	ENSG00000186470	nucleus accumbens	1.93×10-7 (p-value)	GTEx Portal V6	31
BTN3A2	?	ENSG00000186470	spleen	2.37×10-10 (p-value)	GTEx Portal V6	47

BTN3A2	?	ENSG00000186470	coronary artery	6.37×10-16 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	vagina	3.81×10-15 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	gastroesophageal junction	1.27×10-20 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	adrenal gland	2.01×10-11 (p-value)	GTEx Portal V6	49
BTN3A2	?	ENSG00000186470	cerebellum	1.03×10-8 (p-value)	GTEx Portal V6	47
PRSS16	?	ENSG00000112812	cerebellum	2.12×10-7 (p-value)	GTEx Portal V6	18
SCGN	ENST00000334979	ILMN_1789648	adipocyte	9.10×10-6 (p-value)	MuTHER consortium	4
SCGN	ENST00000612225					
SCGN	ENST00000377961					
BTN2A2	ENST00000471116	ILMN_2256894	blood	5.64×10-5 (p-value)	Westra et al.	3
BTN2A2	ENST00000356709					
BTN2A2	ENST00000469230					
BTN2A2	ENST00000482636					
BTN2A2	ENST00000494184					
BTN2A2	ENST00000416795					
BTN2A2	ENST00000432533					
BTN2A2	ENST00000493275					
HIST1H4H	ENST00000377727	ILMN_1751120	blood	8.40×10-6 (p-value)	Westra et al.	3
BTN3A3	?	ENSG00000111801	blood	4.34×10-4 (q-value)	SeeQTL DB (HapMap)	2
BTN3A2	?	ENSG00000186470	blood	4.56×10-12 (q-value)	SeeQTL DB (HapMap)	2
HIST1H2BD	ENST00000289316	ILMN_1651496	monocyte	2.65×10-12 (p-value)	Zeller et al.	1
BTN3A2	ENST00000396934	ILMN_1676528	monocyte	8.02×10-83 (p-value)	Zeller et al.	2
BTN3A2	ENST00000508906					
BTN3A2	ENST00000356386					
?	?	ILMN_1820787	monocyte	2.91×10-58 (p-value)	Zeller et al.	2
?	?	ILMN_1883997	monocyte	5.68×10-16 (p-value)	Zeller et al.	2
BTN3A2	ENST00000524459	ILMN_1700067	monocyte	5.72×10-65 (p-value)	Zeller et al.	2
BTN3A2	ENST00000528541					
BTN3A3	ENST00000467524					
BTN3A3	ENST00000482451					
BTN3A3	ENST00000494393					
BTN3A2	ENST00000527417					
BTN3A3	ENST00000244519					
BTN3A2	ENST00000528222					
BTN3A3	ENST00000474790					
BTN3A2	ENST00000377708					
BTN3A3	ENST00000496719					
BTN3A2	ENST00000396948					
BTN3A2	ENST00000527422					
BTN3A2	ENST00000356386					
BTN3A2	ENST00000524682	209846_s_at	blood	7.30×10-22 (p-value)	Dixon et al.	1
BTN3A2	ENST00000604202					
BTN3A2	ENST00000396934					
BTN3A2	ENST00000532294					
BTN3A2	ENST00000508906					
BTN3A2	ENST00000377708					

BTN3A2	ENST00000527422					
BTN3A2	ENST00000531055					
BTN3A2	ENST00000396948					
BTN3A2	ENST00000356386					
BTN3A2	ENST00000396934	212613_at	blood	1.40×10-19 (p-value)	Dixon et al.	1
BTN3A2	ENST00000508906					
BTN3A2	ENST00000356386					
BTN3A3	ENST00000244519	204820_s_at	blood	3.50×10-21 (p-value)	Dixon et al.	1
BTN3A2	ENST00000396934					
BTN3A2	ENST00000508906					
BTN3A2	ENST00000356386					
BTN3A3	ENST00000480110					
BTN2A2	ENST00000471116	ILMN_2256894	b-cell	1.99×10-5 (p-value)	Fairfax et al.	1
BTN2A2	ENST00000356709					
BTN2A2	ENST00000494184					
BTN2A2	ENST00000482636					
BTN2A2	ENST00000469230					
BTN2A2	ENST00000416795					
BTN2A2	ENST00000432533					
BTN2A2	ENST00000493275					

trans-eQTL

gene	transcript	probe	chromosome	tissue	min(statistic) (type)	source	variant(s)
?	?	ILMN_1671054	chr6	monocyte	9.58×10-22 (p-value)	Zeller et al.	2
?	?	ILMN_1752592	chr6	monocyte	1.68×10-13 (p-value)	Zeller et al.	2

Putative effect on regulation

ENCODE promoter-associated distal DHS (Enhancer)

SNiPA enhancer id	variant(s)	associated SNiPA promoter id	associated gene(s)
ENCE00000442938	1	ENCP00000047667	BTN3A2
		ENCP00000047679	BTN1A1
ENCE00000442976	1	ENCP00000047676	BTN3A3
ENCE00000442878	1	ENCP00000047649	HIST1H2AD HIST1H2BF
		ENCP00000047646	HIST1H4D
		ENCP00000047671	BTN3A1
		ENCP00000047680	HCG11
		ENCP00000047665	BTN3A2
		ENCP00000047640	HIST1H4C
		ENCP00000047644	HIST1H2BD
		ENCP00000047681	HMGN4
		ENCP00000047658	HIST1H3F
		ENCP00000047682	ABT1
		ENCP00000047674	BTN3A3
		ENCP00000047651	HIST1H4E
ENCE00000443031	1	ENCP00000047691	VN1R13P

Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00001494264	2	monocytes (Monocytes-CD14+)	H3K36me3

(enhancer)		blood (DND-41)	H3K36me3
		skin (NHDF-AD)	H3K4me1, DNase1
ENSR00001214106 (enhancer)	1	monocytes (Monocytes-CD14+)	DNase1, H3K4me1, H3K27ac
		endothelium (HUVEC)	H3K27me3
		liver (HepG2)	H3K4me1
		blood (K562)	PolII, Ini1, DNase1, PU1, H2AZ, H3K4me1
ENSR00001214131 (promoter flanking region)	1	embryonic stem cell (H1ESC)	DNase1, H3K27ac, PolII, Rad21, TAF7, Yy1, TAF1, H3K4me2, H3K4me3
		HSMMtube	H3K4me2, DNase1, H2AZ
		blood (K562)	PolII, Ini1, Brg1, DNase1, PolIII, THAP1, H3K27ac, Max, H3K9ac, Cmyc, H2AZ, Nrsf, H3K4me2, H3K4me3
		skin (NHDF-AD)	H3K4me3, DNase1, H3K4me2
		muscle (HSMM)	DNase1, H3K4me2
		liver (HepG2)	Gabp, PolII, H2AZ, H3K4me2, H3K9ac, Cmyc, H3K4me3, H3K27me3, DNase1
		lung (IMR90)	H3K4me2, H3K4me3, DNase1
		blood (GM12878)	PolII, MEF2A, H2AZ, DNase1, Yy1, PolIII, H3K4me3, H3K27ac, H3K4me2, H3K9ac
		nervous (NH-A)	DNase1, H3K4me2, H3K9ac
		skin (NHEK)	DNase1, H3K4me2
		NHLF	H3K4me3, DNase1
		Osteobl	H3K4me2, H3K4me3, H3K27ac, H2AZ
		blood (DND-41)	H3K4me1, H3K4me2, H3K27ac, H3K9ac, H3K4me3
		breast (HMEC)	DNase1, H3K4me3, H3K4me2
		cervix (HeLa-S3)	DNase1, Max, H3K4me3, Gabp, H3K27ac, H3K4me2, H3K9ac, Jund
		monocytes (Monocytes-CD14+)	DNase1, H3K27me3, H3K4me3
		endothelium (HUVEC)	Cjun, H3K4me2, PolII, DNase1
		A549	H3K9ac, H3K4me2, H3K4me3, DNase1
ENSR00001494272 (promoter flanking region)	1	embryonic stem cell (H1ESC)	Rad21, CTCF, H3K4me2, H3K4me3, DNase1
		HSMMtube	DNase1, H3K27me3, H2AZ, H3K4me2, CTCF
		blood (K562)	PolII, Ini1, DNase1, PolIII, Egr1, H3K27ac, Max, Rad21, H3K9ac, H2AZ, H3K4me2, CTCF, H3K4me3
		skin (NHDF-AD)	DNase1, H3K9ac, H3K4me2, H3K4me3, CTCF
		muscle (HSMM)	H2AZ, CTCF, H3K4me3, H3K4me2, DNase1
		liver (HepG2)	DNase1, H3K27me3, Rad21, H2AZ, H3K4me2, FOXA1, H3K9ac, H3K27ac, CTCF, Cmyc, H3K4me3
		lung (IMR90)	DNase1, H3K4me3, CTCF
		blood (GM12878)	H2AZ, DNase1, Yy1, Rad21, H3K4me3, H3K27ac, H3K4me2, CTCF, H3K9ac
		nervous (NH-A)	DNase1, H3K4me3, H3K4me2, CTCF, H3K9ac
		skin (NHEK)	CTCF, H3K4me3, DNase1, H3K9ac, H3K4me2
		NHLF	DNase1, H3K4me3, CTCF
		Osteobl	CTCF, H3K4me2, H3K4me3, H3K27ac, H2AZ
		blood (DND-41)	H3K4me1, CTCF, H3K4me3
		breast (HMEC)	CTCF, H3K4me3, DNase1
		cervix (HeLa-S3)	PolII, H3K9ac, H3K4me2, H3K27ac, H3K4me3, CTCF, DNase1
		monocytes (Monocytes-CD14+)	DNase1, CTCF, H3K4me2, H3K4me3
		endothelium (HUVEC)	H3K36me3, H3K4me2, H3K4me3, CTCF, DNase1, Cmyc
		A549	DNase1, CTCF, H3K9ac, H3K4me2, H3K4me3
ENSR00001214144 (CTCF binding site)	2	HSMMtube	H3K27me3
		Osteobl	H3K27me3
		blood (DND-41)	H3K27me3
		blood (K562)	CTCF, H2AZ
		cervix (HeLa-S3)	CTCF
		monocytes (Monocytes-CD14+)	H3K27me3
		endothelium (HUVEC)	H3K27me3
		lung (IMR90)	H3K27me3
		nervous (NH-A)	H3K27me3
ENSR00001702766 (CTCF binding site)	1	embryonic stem cell (H1ESC)	TAF1, H3K4me2, SP1, H3K4me3, DNase1, HDAC2, CTCF, H3K27ac, PolII, Rad21, Gabp, TAF7, H3K9ac
		HSMMtube	CTCF, H2AZ, DNase1
		blood (K562)	ELF1, Cfos, CTCFL, PolII, H3K4me2, CTCF, DNase1, H3K4me3, TAF1, H2AZ, H3K27ac, Max, Rad21, H3K9ac, Gabp, Cmyc, HEY1
		skin (NHDF-AD)	CTCF, H3K4me3, DNase1, H3K9ac, H3K4me2
		muscle (HSMM)	H2AZ, CTCF, H3K4me3
		liver (HepG2)	DNase1, Gabp, H3K4me3, PolII, TAF1, ELF1, H3K4me2, H3K9ac, H3K27ac, CTCF
		lung (IMR90)	CTCF, DNase1, H3K4me2, H3K4me3
		blood (GM12878)	DNase1, Gabp, ELF1, Rad21, H3K4me3, H3K27ac, Cfos, CTCF, H3K9ac, PolII, H2AZ
		nervous (NH-A)	DNase1
		skin (NHEK)	DNase1, H3K9ac, H3K4me3, CTCF

		NHLF	H3K9ac, H3K27ac, CTCF, H3K4me3, DNase1
		Osteobl	CTCF, H3K4me2, H3K4me3
		blood (DND-41)	CTCF, H3K27ac, H3K9ac
		breast (HMEC)	H3K27ac, H3K4me3, H3K4me2, CTCF
		cervix (HeLa-S3)	H3K9ac, H3K4me2, H3K27ac, TAF1, H3K4me3, Gabp, PolII, CTCF, DNase1
		monocytes (Monocytes-CD14+)	CTCF, H3K9ac, H3K4me3
		endothelium (HUVEC)	H3K4me3, PolII, CTCF, DNase1
		A549	H3K27ac, DNase1, CTCF, H3K4me2, H3K4me3
ENSR00001214204 (promoter)	1	embryonic stem cell (H1ESC)	DNase1, H3K4me3, H3K27ac, PolII, Rad21, Gabp, TAF7, H3K9ac, CTCF, HDAC2, TAF1, H3K4me2, SP1
		HSMMtube	H2AZ, CTCF, DNase1
		blood (K562)	H3K27ac, Max, Rad21, H3K9ac, Gabp, Cmyc, HEY1, H2AZ, TAF1, ELF1, Cfos, CTCFL, PolII, H3K4me2, CTCF, DNase1, H3K4me3
		skin (NHDF-AD)	H3K4me2, H3K9ac, DNase1, CTCF, H3K4me3
		muscle (HSMM)	H2AZ, CTCF, H3K4me3
		liver (HepG2)	DNase1, Gabp, H3K4me3, FOXA2, PolII, TAF1, ELF1, H3K4me2, FOXA1, H3K9ac, H3K27ac, CTCF
		blood (GM12878)	CTCF, H3K9ac, Cfos, H3K27ac, PolII, H2AZ, DNase1, Gabp, ELF1, Rad21, H3K4me3
		lung (IMR90)	H3K4me3, CTCF, H3K4me2, DNase1
		nervous (NH-A)	DNase1
		skin (NHEK)	DNase1, H3K9ac, H3K4me3, CTCF
		NHLF	DNase1, H3K4me3, CTCF, H3K9ac, H3K27ac
		Osteobl	CTCF, H3K4me2, H3K4me3
		blood (DND-41)	CTCF, H3K27ac, H3K9ac
		breast (HMEC)	H3K27ac, H3K4me3, H3K4me2, CTCF
		cervix (HeLa-S3)	DNase1, CTCF, H3K9ac, H3K4me2, H3K27ac, TAF1, H3K4me3, Gabp, PolII
		monocytes (Monocytes-CD14+)	CTCF, H3K9ac, H3K4me3
		endothelium (HUVEC)	H3K4me3, PolII, CTCF, DNase1
		A549	H3K27ac, DNase1, CTCF, H3K4me2, H3K4me3

Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
ABT1	upstream gene variant, downstream gene variant	2952	ENST00000274849	NM_013375.3	ENSP00000274849	3
BTN1A1	upstream gene variant, downstream gene variant	1094	ENST00000244513	NM_001732.2	ENSP00000244513	3
BTN1A1	upstream gene variant, downstream gene variant	1581	ENST00000613186	?	ENSP00000484707	3
BTN2A1	upstream gene variant	2079	ENST00000312541	NM_007049.4	ENSP00000312158	4
BTN2A1	upstream gene variant	2115	ENST00000429381	NM_078476.3	ENSP00000416945	4
BTN2A1	upstream gene variant	2058	ENST00000541522	NM_001197233.2	ENSP00000443909	4
BTN2A1	upstream gene variant	2076	ENST00000377600	?	ENSP00000366825	4
BTN2A1	upstream gene variant, downstream gene variant	1405	ENST00000480218	?	ENSP00000418936	6
BTN2A1	upstream gene variant, downstream gene variant	93	ENST00000493173	?	ENSP00000420447	8
BTN2A1	upstream gene variant, downstream gene variant	1403	ENST00000469185	NM_001197234.2	ENSP00000419043	5
BTN3A3	downstream gene variant	1320	ENST00000361232	NM_197974.2	ENSP00000355238	4
BTN3A3	downstream gene variant	720	ENST00000244519	NM_006994.4	ENSP00000244519	4
BTN3A3	downstream gene variant	721	ENST00000480110	?	?	4
BTN3A3	downstream gene variant	2218	ENST00000490254	NM_001242803.1	ENSP00000419736	4
BTN3A3	downstream gene variant	2220	ENST00000497681	?	?	4
BTN3A3	downstream gene variant	1974	ENST00000483179	?	?	4
BTN3A3	downstream gene variant	3921	ENST00000477388	?	?	2
CTA-14H9.5	downstream gene variant	2258	ENST00000567732	?	?	2
GUSBP2	upstream gene variant	24	ENST00000479900	?	?	2
GUSBP2	downstream gene variant	2834	ENST00000492832	?	?	1
GUSBP2	downstream gene variant, upstream gene	2183	ENST00000463434	?	?	2

	variant					
HCG11	downstream gene variant	3083	ENST00000411553	?	?	2
HMGN4	downstream gene variant	2730	ENST00000377575	NM_006353.2	ENSP00000366798	2
LINC00240	upstream gene variant	415	ENST00000606878	?	?	2
LINC00240	upstream gene variant, downstream gene variant	414	ENST00000607607	?	?	3
POM121L6P	downstream gene variant	4071	ENST00000441186	?	?	1
RP11-457M11.6	downstream gene variant	2142	ENST00000602994	?	?	1
RP11-457M11.7	upstream gene variant, downstream gene variant	3100	ENST00000616994	?	?	2
RP11-457M11.7	upstream gene variant, downstream gene variant	3100	ENST00000611708	?	?	2
ZNF322	downstream gene variant	910	ENST00000622479	NM_001242797.1	ENSP00000482607	2
ZNF322	downstream gene variant	900	ENST00000415922	NM_024639.4	ENSP00000418897	2
ZNF322	downstream gene variant	2808	ENST00000471278	?	ENSP00000419728	2
ZNF322	downstream gene variant	4993	ENST00000480036	?	ENSP00000420301	1
ZNF322	downstream gene variant	910	ENST00000607204	NM_001242798.1	ENSP00000483223	2
ZNF322	downstream gene variant	910	ENST00000456172	NM_001242799.1	ENSP00000478899	2

Putative effect on transcript

Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
BTN2A1	ENST00000377600	?	ENSP00000366825	4
BTN2A1	ENST00000312541	NM_007049.4	ENSP00000312158	2
BTN2A1	ENST00000429381	NM_078476.3	ENSP00000416945	4
BTN2A1	ENST00000469185	NM_001197234.2	ENSP00000419043	4
BTN2A1	ENST00000541522	NM_001197233.2	ENSP00000443909	2
BTN2A1	ENST00000480218	?	ENSP00000418936	2
BTN2A1	ENST00000493173	?	ENSP00000420447	2
GUSBP2	ENST00000479900	?	?	9
GUSBP2	ENST00000463434	?	?	3
GUSBP2	ENST00000492832	?	?	1
LINC00240	ENST00000607607	?	?	3
LINC00240	ENST00000606878	?	?	5
RP11-457M11.7	ENST00000611708	?	?	1
ZNF322	ENST00000415922	NM_024639.4	ENSP00000418897	1
ZNF322	ENST00000622479	NM_001242797.1	ENSP00000482607	1
ZNF322	ENST00000465674	?	?	1
ZNF322	ENST00000471278	?	ENSP00000419728	1
ZNF322	ENST00000461899	?	?	1
ZNF322	ENST00000607204	NM_001242798.1	ENSP00000483223	1
ZNF322	ENST00000480036	?	ENSP00000420301	1
ZNF322	ENST00000456172	NM_001242799.1	ENSP00000478899	1

3'-UTR variant

5'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
ABT1	ENST00000274849	NM_013375.3	ENSP00000274849	1
BTN2A1	ENST00000377600	?	ENSP00000366825	5
BTN2A1	ENST00000429381	NM_078476.3	ENSP00000416945	2

Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
LINC00240	ENST00000607607	?	1
RP11-457M11.7	ENST00000616994	?	1