

		protein binding;multicellular organism development;dorsal/ventral pattern
		formation; protein domain specific binding; negative regulation of Wnt
		signaling pathway;phosphatidylinositol binding;regulation of protein
		homodimerization activity;negative regulation of JUN kinase activity;negative
	intron_variant,missense_variant,splice_re	regulation of JNK cascade;determination of ventral identity;negative
Aida	gion_variant	regulation of determination of dorsal identity
		activation of innate immune response; positive regulation of defense
		response to virus by host;immune system process;DNA binding;double-
		stranded DNA binding;protein binding;apoptotic process;inflammatory
		response;negative regulation of NF-kappaB transcription factor
		activity; positive regulation of protein oligomerization; positive regulation of
		interleukin-1 beta production; tumor necrosis factor-mediated signaling
		pathway;cellular response to interferon-beta;cellular response to
	5_prime_UTR_variant,intron_variant,miss	drug;identical protein binding;innate immune response;interleukin-1 beta
	ense_variant,non_coding_transcript_exon	secretion;positive regulation of interleukin-1 beta secretion;positive
	_variant,non_coding_transcript_variant,sp	regulation of NF-kappaB transcription factor activity;pyroptosis;positive
Aim2	lice_region_variant	regulation of cysteine-type endopeptidase activity
		aldehyde dehydrogenase (NAD) activity;cellular aldehyde metabolic
		process;metabolic process;carnitine metabolic process;oxidoreductase
		activity;oxidoreductase activity, acting on the aldehyde or oxo group of
		donors, NAD or NADP as acceptor;aminobutyraldehyde dehydrogenase
		activity; neurotransmitter biosynthetic process; protein homodimerization
		activity;amine binding;4-trimethylammoniobutyraldehyde dehydrogenase
Aldh9a1	intron_variant,splice_region_variant	activity;NAD binding;oxidation-reduction process
		nucleotide binding;nucleic acid binding;single-stranded DNA binding;RNA
Alyref2	missense_variant	binding;mRNA processing;transport;RNA splicing;mRNA transport
		receptor binding;transmembrane receptor protein tyrosine kinase signaling
Angptl1	missense_variant	pathway
		complement component C1q binding;calcium ion binding;protein complex
		assembly;carbohydrate binding;negative regulation by host of viral exo-alpha-
		sialidase activity;negative regulation by host of viral glycoprotein metabolic
		process;innate immune response;negative regulation of monocyte
		differentiation;negative regulation of viral entry into host cell;virion
		binding;metal ion binding;negative regulation of viral process;negative
		regulation of exo-alpha-sialidase activity;negative regulation of glycoprotein
Apcs	intron_variant,splice_region_variant	metabolic process

		negative regulation of cytokine secretion involved in immune response;lipid
		transporter activity;phospholipid binding;fatty acid metabolic
		process;phosphatidylcholine biosynthetic process;transport;lipid
		transport;high-density lipoprotein particle binding;cholesterol metabolic
		process;lipid binding;phospholipid catabolic process;response to
		glucose; positive regulation of cholesterol esterification; negative regulation of
		very-low-density lipoprotein particle remodeling;cholesterol binding;beta-
		glucoside transport;cholesterol transporter activity;protein
		oxidation;peptidyl-methionine modification;regulation of intestinal
		cholesterol absorption; cholesterol transport; animal organ
		regeneration;phosphatidylcholine binding;regulation of protein
		stability;negative regulation of cholesterol transport;cholesterol
		efflux;phospholipid efflux;apolipoprotein receptor binding;triglyceride-rich
		lipoprotein particle remodeling;low-density lipoprotein particle
		remodeling;high-density lipoprotein particle remodeling;high-density
		lipoprotein particle assembly;high-density lipoprotein particle
		clearance; lipoprotein metabolic process; cholesterol homeostasis; protein
		homodimerization activity;reverse cholesterol transport;positive regulation
		of interleukin-8 biosynthetic process; diacylglycerol catabolic process; protein
		heterodimerization activity;negative regulation of lipid catabolic
		process; positive regulation of lipid catabolic process; lipase inhibitor
		activity;negative regulation of lipase activity;phosphatidylcholine-sterol O-
		acyltransferase activator activity;negative regulation of cholesterol
		import; negative regulation of cholesterol transporter activity; high-density
Apoa2	missense_variant	lipoprotein particle receptor binding
	feature_truncation,intron_variant,missens	GTPase activator activity;signal transduction;small GTPase mediated signal
ARHGAP30	e_variant,splice_region_variant	transduction
		RNA polymerase II regulatory region sequence-specific DNA
		binding;transcription factor activity, sequence-specific DNA
Ascl5	missense_variant	binding;regulation of transcription from RNA polymerase II promoter
		neuron migration; positive regulation of neuroblast proliferation; calmodulin
		binding;cell cycle;spindle organization;mitotic nuclear
		division; spermatogenesis; brain development; male gonad
		development; for ebrain neuroblast division; cerebral cortex
		development;negative regulation of neuron differentiation;negative
		regulation of asymmetric cell division;oogenesis;developmental growth;cell
		division; regulation of meiotic cell cycle; spindle localization; maintenance of
		centrosome location;positive regulation of canonical Wnt signaling
		pathway; spindle assembly involved in meiosis; neuronal stem cell population
Aspm	_transcript_variant,splice_region_variant	maintenance
		transcription regulatory region sequence-specific DNA binding;RNA
		polymerase II regulatory region sequence-specific DNA binding;eye
		development;DNA binding;transcription factor activity, sequence-specific
		DNA binding;protein binding;transcription, DNA-templated;regulation of
		transcription, DNA-templated;response to unfolded protein;visual
		perception;endoplasmic reticulum unfolded protein response;ubiquitin
		protein ligase binding;cAMP response element binding;identical protein
		binding; positive regulation of apoptotic process; sequence-specific DNA
		binding; positive regulation of transcription from RNA polymerase II
		promoter; protein heterodimerization activity; positive regulation of
	intron_variant,missense_variant,splice_re	transcription from RNA polymerase II promoter in response to endoplasmic
Atf6	gion_variant,synonymous_variant	reticulum stress

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		nucleotide binding;neurotransmitter uptake;regulation of the force of heart
		contraction; regulation of respiratory gaseous exchange by neurological
		system process;sodium:potassium-exchanging ATPase activity;protein
		binding;ATP binding;transport;ion transport;potassium ion transport;sodium
		ion transport;cellular sodium ion homeostasis;regulation of muscle
		contraction;regulation of smooth muscle contraction;regulation of striated
		muscle contraction;drug binding;regulation of blood pressure;adult
		locomotory behavior;visual learning;potassium ion import;ATP hydrolysis
		coupled proton transport;hydrolase activity;ATPase activity;regulation of
		vasoconstriction; cation-transporting ATPase activity; cellular potassium ion
		homeostasis; potassium ion binding; sodium ion binding; response to
		nicotine;sodium ion export from cell;locomotion;negative regulation of heart
		contraction;negative regulation of striated muscle contraction;ATP metabolic
		process;metal ion binding;chaperone binding;negative regulation of cytosolic
		calcium ion concentration;cellular response to mechanical stimulus;cellular
		response to steroid hormone stimulus; regulation of cardiac muscle cell
	feature_elongation,feature_truncation,int	contraction; negative regulation of calcium ion transmembrane
	ron_variant,missense_variant,non_coding	transport;negative regulation of calcium:sodium antiporter activity;response
Atp1a2	_transcript_variant,splice_region_variant	to glycoside;steroid hormone binding
		nucleotide binding;sodium:potassium-exchanging ATPase activity;ATP
		binding;transport;ion transport;potassium ion transport;sodium ion
		transport;cellular sodium ion
		homeostasis;spermatogenesis;fertilization;potassium ion import;ATP
		hydrolysis coupled proton transport;hydrolase activity;cellular potassium ion
	feature_truncation,intron_variant,missens	homeostasis;flagellated sperm motility;regulation of cellular pH;sodium ion
Atp1a4	e_variant,splice_region_variant	export from cell;regulation of membrane potential;metal ion binding
	feature_truncation,intron_variant,missens	
Axdnd1	e_variant,splice_region_variant	molecular_function;biological_process
	intron_variant,missense_variant,splice_re	
BC026585	gion_variant	zinc ion binding;oxidoreductase activity;oxidation-reduction process
		magnesium ion binding;inositol-1,4-bisphosphate 1-phosphatase
		activity;nucleobase-containing compound metabolic process;3'(2'),5'-
	feature_elongation,intron_variant,missens	bisphosphate nucleotidase activity; hydrolase activity; phosphatidylinositol
Bpnt1	e_variant,splice_region_variant	phosphorylation;metal ion binding
Brox	missense_variant	molecular_function;biological_process
C130074G19Rik	missense_variant	molecular_function;biological_process
		skeletal system development; extraocular skeletal muscle development; ion
		channel activity;voltage-gated ion channel activity;voltage-gated calcium
		channel activity;calcium channel activity;transport;ion transport;calcium ion
		transport;muscle contraction;striated muscle contraction;endoplasmic
		reticulum organization;skeletal muscle tissue development;myoblast
		fusion;neuromuscular junction development;high voltage-gated calcium
		channel activity;regulation of ion transmembrane transport;skeletal muscle
	intron_variant,missense_variant,non_codi	adaptation;metal ion binding;skeletal muscle fiber development;muscle cell
	ng_transcript_variant,splice_region_varian	development;transmembrane transport;calcium ion transmembrane
Cacna1s	t	transport;membrane depolarization during action potential
		receptor activity;receptor binding;protein binding;cell adhesion;homophilic
		cell adhesion via plasma membrane adhesion molecules;heterophilic cell-cell
	feature_truncation,intron_variant,non_co	adhesion via plasma membrane cell adhesion molecules;cell
	ding_transcript_variant,splice_region_vari	recognition; protein localization; protein homodimerization activity; cell
Cadm3	ant	adhesion molecule binding
		microtubule cytoskeleton organization;protein binding;calmodulin
		binding;microtubule binding;spectrin binding;neuron projection
	intron_variant,missense_variant,splice_re	development;regulation of organelle organization;microtubule minus-end
Camsap2	gion_variant	binding
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		blastocyst development;calcium-dependent cysteine-type endopeptidase
		activity;calcium ion binding;proteolysis;myoblast fusion;cytoskeletal protein
		binding;peptidase activity;cysteine-type peptidase activity;protein
		autoprocessing;hydrolase activity;metal ion binding;protein
		heterodimerization activity;regulation of cytoskeleton
	feature_elongation,intron_variant,splice_r	organization; proteolysis involved in cellular protein catabolic process; cellular
Capn2	egion_variant	response to amino acid stimulus
		calcium-dependent cysteine-type endopeptidase activity;calcium ion
	missense_variant,splice_region_variant,sy	binding;proteolysis;digestion;peptidase activity;cysteine-type peptidase
Capn8	nonymous_variant	activity;hydrolase activity;metal ion binding
		calcium ion binding; regulation of muscle contraction; endoplasmic reticulum
		organization; response to heat; regulation of release of sequestered calcium
	inframe_deletion,inframe_insertion,non_c	ion into cytosol by sarcoplasmic reticulum; regulation of skeletal muscle
	oding_transcript_exon_variant,non_codin	contraction by regulation of release of sequestered calcium ion;sarcomere
	g_transcript_variant,splice_region_variant	organization;metal ion binding;protein polymerization;regulation of
Casq1	,synonymous_variant	sequestering of calcium ion
Ccdc121	missense_variant	molecular_function;biological_process
Ccdc185	inframe_insertion,missense_variant	molecular_function;biological_process
		myeloid dendritic cell activation; adaptive immune response; natural killer cell
		activation involved in immune response;immune system process;receptor
		activity;protein binding;immune response;positive regulation of natural killer
		cell proliferation;MHC class I protein binding;innate immune
		response; positive regulation of inositol phosphate biosynthetic
		process; positive regulation of granzyme B production; positive regulation of
	feature_elongation,intron_variant,missens	interferon-gamma secretion; positive regulation of interleukin-8
Cd244	e_variant,splice_region_variant	secretion;positive regulation of CD8-positive, alpha-beta T cell proliferation
		regulation of adaptive immune response;antigen binding;receptor
		activity;protein binding;signal transduction;T cell activation;mast cell
Cd48	missense_variant	activation
		adaptive immune response;immune system process;cell adhesion;regulation
		of lipopolysaccharide-mediated signaling pathway;negative regulation of
		granulocyte macrophage colony-stimulating factor production;negative
		regulation of interleukin-18 production;negative regulation of mast cell
		activation;regulation of macrophage activation;negative regulation of mast
		cell degranulation;positive regulation of MAPK cascade;innate immune
		response;positive regulation of NF-kappaB transcription factor
		activity;positive regulation of monocyte chemotactic protein-1
		production; negative regulation of interleukin-6 secretion; positive regulation
		of tumor necrosis factor secretion; negative regulation of interleukin-10
Cd84	missense_variant	secretion;regulation of store-operated calcium entry
		nucleotide binding;microtubule cytoskeleton organization;magnesium ion
		binding;protein kinase activity;protein serine/threonine kinase activity;ATP
		binding;protein phosphorylation;cytoskeleton organization;nuclear
		migration;kinase activity;phosphorylation;cell migration;transferase
		activity;actomyosin structure organization;actin cytoskeleton
	feature elongation intron variant missens	reorganization;intracellular signal transduction;identical protein
		binding;metal ion binding;regulation of small GTPase mediated signal

		negative regulation of transcription from RNA polymerase II promoter;RNA
		polymerase II core binding;transcription factor activity, RNA polymerase II
		transcription factor binding;regulation of cell growth;endodermal cell fate
		commitment;protein binding;transcription, DNA-templated;regulation of
		transcription from RNA polymerase II promoter; transcription elongation from
		RNA polymerase II promoter;mRNA polyadenylation;cell cycle;negative
		regulation of cell proliferation; histone monoubiquitination; Wnt signaling
		pathway;histone modification;stem cell population maintenance;positive
		regulation of Wnt signaling pathway;positive regulation of mRNA 3'-end
		processing; protein destabilization; positive regulation of transcription
		elongation from RNA polymerase II promoter;histone H2B
		ubiquitination;recruitment of 3'-end processing factors to RNA polymerase II
		holoenzyme complex;negative regulation of apoptotic process;negative
		regulation of myeloid cell differentiation; positive regulation of transcription
	NMD_transcript_variant,feature_elongatio	from RNA polymerase II promoter; negative regulation of fibroblast
	n,feature_truncation,frameshift_variant,in	proliferation;negative regulation of epithelial cell proliferation;cellular
	tron_variant,missense_variant,splice_regi	response to lipopolysaccharide;negative regulation of G1/S transition of
Cdc73	on_variant	mitotic cell cycle
	intron_variant,missense_variant,splice_re	
Cep170	gion_variant	molecular_function;biological_process
	feature_truncation,intron_variant,missens	
	e_variant,non_coding_transcript_variant,s	
Cep350	plice_region_variant	molecular_function;biological_process
Cfhr1	missense_variant,stop_gained	molecular_function;biological_process
		GDP-dissociation inhibitor activity;GTPase activator activity;intracellular
		protein transport;small GTPase mediated signal transduction;oxidoreductase
Charal		activity;Rab GTPase binding;protein geranylgeranylation;oxidation-reduction
Chml	missense_variant	process
		transport; channel regulator activity; synaptic transmission,
		glutamatergic;regulation of membrane potential;localization within
C-:h2	internal continue and in a continue continue	membrane; regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole
Cnih3	intron_variant,splice_region_variant	propionate selective glutamate receptor activity
Craile 4		transport;ER to Golgi vesicle-mediated transport;protein transport;vesicle-
Cnih4	ce_region_variant	mediated transport;CCR5 chemokine receptor binding
		protein binding;negative regulation of phosphatase activity;phosphatase
Cost	missansa variant	binding; positive regulation of Golgi to plasma membrane protein
Cnst	missense_variant	transport;connexin binding molecular_function;biological_process;transferase activity;transferase
Calaalka	NINAD transport regions relicant relicant	activity, transferring glycosyl groups;procollagen galactosyltransferase
Colgalt2	NMD_transcript_variant,missense_variant	activity
	NMD transcript variant feature elegation	hormone activity;structural molecule activity;transport;intracellular protein
		transport;ER to Golgi vesicle-mediated transport;retrograde vesicle-mediated
	ding_transcript_variant,splice_region_vari	transport, Golgi to ER;intra-Golgi vesicle-mediated transport, Feti ograde vesicle-mediated
Сора	ant	transport; vesicle-mediated transport; pancreatic juice secretion
Сора	unt	calcium ion binding;protein binding;plasma membrane organization;eye
Crb1	missense_variant	photoreceptor cell development;membrane organization
CIDI	masense_variant	priotoreceptor cen development, membrane organization

response;complement activation, classical pathway;positive regulation of gene expression,negative regulation of macrophage derived froam cell differentiation;negative regulation of lipid storage; regulation of low-den lipoprotein particle clearance;cholesterol binding;low-density lipoprotein particle binding;negative regulation of superoxide anion generation;positive regulation of superoxide anion generation;positive regulation of superoxide anion generation;positive regulation of intricoxide biosynthetic process;negative regulation of valoritive regulation of the obting;positive regulation of the obting;positive regulation of the obting process;negative regulation of the obting;positive regulation of the obtin			Control of the state of the sta
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regulation of superoide anion generation,wound healing;protein homodimerization activity;positive regulation of intric oxide biosynthetic process,negative regulation of intric oxide biosynthetic process,negative regulation of variety regulation of intric oxide biosynthetic process,negative regulation of variety regulation of process, negative regulation of dendrite development;regulation of interleukin-8 secretion nucleotide process calculor, protein translation;figsae activity;ATP binding;translation;fiRNA aminoacylation for protein translation;figsae activity;protein homodimerization activity;RNA aminoacylation apartate-tRNA[(asn) lig activity;mitochondrial asparaginyl-tRNA aminoacylation) are considered activity;mitochondrial asparaginyl-tRNA aminoacylation aspartate-tRNA[(asn) lig activity;mitochondrial asparaginyl-tRNA aminoacylation) are considered binding;possification;endochondrial bone growth;protein kinas activity;protein prosphorylation;ransmembrane receptor protein tyrosine kinase activity;protein prosphorylation;transmembrane receptor protein tyrosine kinase activity;protein prosphorylation;transferase activity;poption;transmembrane receptor protein tyrosine kinase activity;poption;transferase activity;peptidyl-tryosine phosphorylation;collage fibril organization;regulation of cell proliferation;positive regulation of fibroblast migration;tinase activity;positive protein tyrosine kinase collagen receptor activity;positive regulation of sequence-specific DNA bind transcription factor activity;positive regulation positive regulation of protein kinase activity;protein autophosphorylation;positive regulation for sequence-specific DNA bind transcription factor activity;positive regulation of sequence-specific DNA bind transcription factor activity;positive regulation of sequence-specific DNA bind transcription factor activity;positive regulation of sequence-specific DNA binding-transcription factor binding-transcription factor binding-transcription factor binding-transcription factor binding-transcripti			lipoprotein particle clearance; cholesterol binding; low-density lipoprotein
homodimerization activity;postive regulation of nitric oxide biosymbic regulation of vasodilation;metal ion binding;low-densi lipoprotein particle receptor binding;protein polymerization;cellular rest to calcium ion;positive regulation of dendrite development;regulation of interleukin-8 secretion nucleotide binding;mucleic acid binding;aminoacyl-tRNA ligase activity;aspartate-tRNA ligase activity;ATP binding;translation;tRNA aminoacylation for protein translation;tgsae activity;reprine homodimerization activity;rRNA aminoacylation;gsae activity;reprine homodimerization activity;rRNA aminoacylation;gsae activity;reprine homodimerization activity;rRNA aminoacylation;psapartate-tRNA[Ans] liga activity;mitochondrial sparaginyl-tRNA aminoacylation activity;mitochondrial sparaginyl-tRNA aminoacylation. Deaf8 splice_region_variant,synonymous_variant molecular_function;biological_process nucleotide binding;ossification;endochondrial bone growth;protein kinas activity;protein pyrosine kinase activity;transmembrane receptor protein tyrosine kinase activity;transmembrane receptor signaling pathway;positive regulation of solution; protein tyrosine kinase activity;transmembrane receptor signaling pathway;positive regulation of solution; protein tyrosine kinase activity;transmembrane receptor signaling pathway;positive regulation of solution; protein tyrosine kinase activity;transmembrane receptor signaling pathway;positive regulation of solution;transmembrane receptor signa			particle binding;negative regulation of superoxide anion generation;positive
process;negative regulation of vasodilation;metal ion binding;low-densit lipoprotein particle receptor binding;protein polymerization;cellular responses to calcium ion;positive regulation of dendrite development; edulation of dendrite development; edulation of dendrite development; regulation of underdrite development; edulation of dendrite development; particle receptor binding;mose; dendrite development; particle receptor protein translation; ligase activity; protein inhomodimerization activity; RNA aminoacylation; paspartate-tRNA[Asn] ligase; activity; protein productivity; protein productivit; productivity; protein productivit; productivity; protein productivit; productivity; protein productivit; productivity; protein productivity; pro			regulation of superoxide anion generation; wound healing; protein
Ilipoprotein particle receptor bindingsprotein polymerization; cellular resy to calcium ion; positive regulation of dendrite development; regulation of interleukin-8 secretion nucleotide binding; nucleic acid binding; aminoacyl-tRNA ligase activity; paptratate tRNA ligase activity; protein homodimerization activity; tRNA aminoacylation, aspartate-tRNA(Asn) lig activity; minoacylation saparaginyl-tRNA aminoacylation sativity; more in the sativity; trosine kinase activity; trosine kinase saparaginyl-tRNA aminoacylation sativity; trosine kinase sativity			homodimerization activity; positive regulation of nitric oxide biosynthetic
to calcium ion;positive regulation of dendrite development;regulation of interleukin-8 secretion of dendrite development; and interleukin-8 secretion interleukin-8 secretion decided binding; aminoacyl-tRNA ligase activity; appraisation, activity, appraisation, activity, aminoacyl-tRNA aminoacylation, appartate-RNA ligase activity, appraisation, activity, aminoacylation, appartate-RNA(asn) lig activity, aminoacylation, aminoacylation, appartate-RNA(asn) lig activity, aminoacylation, aminoacylation, appartate-RNA(asn) lig activity, aminoacylation,			process;negative regulation of vasodilation;metal ion binding;low-density
Crp missense_variant interleukin-8 secretion nucleotide binding;mucleic acid binding;aminoacyl-tRNA ligase activity;papartate-tRNA ligase activity;papartate-tRNA ligase activity;papartate-tRNA ligase activity;protein homodimerization activity;tRNA aminoacylation for protein translation;ligase activity;protein homodimerization activity;tRNA aminoacylation Dcaf8 splice_region_variant,synonymous_variant molecular_function;biological_process nucleotide binding;cossification;endochondral bone growth;protein kinas activity;protein tyrosine kinase activity;collagen inding;ATP binding;ATP binding;protein phosphorylation;transmembrane receptor protein tyrosine kinase activity;collagen activity;posphorylation;protein phosphorylation;positive regulation of fibroblast migration;hispapa-travity;phosphorylation;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hispapa-travity;hisp			lipoprotein particle receptor binding; protein polymerization; cellular response
nucleotide binding;nucleic acid binding;aminoacy!tRNA ligase activity,ATP binding;translation;RNA aminoacylation for protein translation;ligase activity;protein homodimerization activity;RNA aminoacylation,aspartate-tRNA[asn] ligase activity;protein homodimerization activity;RNA aminoacylation,aspartate-tRNA[asn] ligase activity;mitochondrial asparaginyl-tRNA aminoacylation Dar52 missense_variant activity;mitochondrial asparaginyl-tRNA aminoacylation splice_region_variant,synonymous_variant molecular_function;biological_process nucleotide binding;ossification;endochondral bone growth;protein kinas activity;protein tyrosine kinase activity;transmembrane receptor protein tyrosine kinase activity;protein phosphorylation;ransmembrane receptor protein tyrosine kinase activity;protein phosphorylation;ransmembrane receptor protein tyrosine kinase activity;peptidyl-tyrosine phosphorylation;rosile kinase activity;peptidyl-tyrosine phosphorylation;rosile kinase activity;peptidyl-tyrosine phosphorylation;rosile kinase activity;peptidyl-tyrosine phosphorylation;rosile kinase collagen pathway;positive regulation of for portein kinase activity;peptidyl-tyrosine phosphorylation;rosile kinase activity;peptidyl-tyrosine phosphorylation;rosile kinase signal pathway;positive regulation of fell prolliferation;positive regulation of fibroblast migration,kinase activity;peptidyl-tyrosine phosphorylation;positive regulation of fibroblast proliferation;positive regulation of portein kinase activity;positive regulation of protein kinase activity;peptidyl-tyrosine phosphorylation;positive regulation of fibroblast migration,kinase activity;positive regulation of fibroblast proliferation;positive regulation of protein kinase activity;positive regulation;positive regulation of protein kinase activity;positi			to calcium ion;positive regulation of dendrite development;regulation of
nucleotide binding;nucleic acid binding;aminoacy14RNA ligase activity;Arp binding;translation;RNA aminoacy14tion for protein translation;ligase activity;protein homodimerization activity;RNA aminoacy14tion,aspartate-tRNA(asyn) lig activity;mitochondrial asparaginy1-tRNA aminoacy14tion of protein translation;ligase activity;protein homodimerization activity;RNA aminoacy14tion,aspartate-tRNA(asyn) lig activity;mitochondrial asparaginy1-tRNA aminoacy14tion Deaf8 splice_region_variant,synonymous_variant molecular_function;biological_process nucleotide binding;ossification;endochondrial bone growth;protein kinas activity;protein tyrosine kinase activity;transmembrane receptor protein kinas activity;protein tyrosine kinase activity;protein tyrosine kinase activity;protein phosphorylation;ransmembrane receptor protein kinas activity;protein tyrosine kinase activity;protein phosphorylation;ransmembrane receptor protein kinas activity;protein tyrosine kinase activity;protein phosphorylation;rose kinase signal pathway;positive regulation of cell proliferation;positive regulation of fibroblast migration,kinase activity;protein phosphorylation;transferase activity;peptidity-frosine phosphorylation;transferase activity;positive regulation of servity;positive regulation of protein kinase activity;positive regulation of fibroblast migration;intransmembrane receptor protein kinas activity;positive regulation of fibroblast migration;intransmembrane receptor protein kinase activity;positive regulation of fibroblast migration;intransperages activity;positive regulation of fibroblast migration;positive regulation of fibroblast proliferation;positive regulation of sequence-specific DNA bind pathway;positive regulation of sequence-specific DNA bind protein kinase activity;positive regulation of sequence-specific protein kinase activity;posi	Crp	missense variant	 interleukin-8 secretion
activity;aspartate-tRNA ligase activity;ATP binding;translation;tRNA aminoacylation for protein translation;figase activity;protein process activity;protein protein translation;figase activity;protein protein translation;figase activity;protein protein protein transport; protein			nucleotide binding;nucleic acid binding;aminoacyl-tRNA ligase
aminoacylation for protein translation; ligase activity; protein homodimerization activity; RNA aminoacylation; aspartate-tRNA(Asn) lig activity; missense_variant activity; mitochondrial asparaginy-tRNA aminoacylation; activity; mitochondrial sparaginy-tRNA aminoacylation; activity; mitochondrial process activity; protein tyrosine kinase collagen receptor activity; protein autophosphorylation; positive regulation of protein kinase activity; protein kinase activity; protein kinase understantion; positive regulation of protein kinase activity; protein kinase understantion; positive regulation of protein kinase activity; protein kinase understantion; positive			
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nucleotide binding:ossification;endochondral bone growth;protein kinase activity;protein tyrosine kinase activity;transmembrane receptor protein tyrosine kinase activity;trolagen binding;ATP binding:protein phosphorylation;transmembrane receptor protein tyrosine kinase signal pathway;positive regulation of cell proliferation;positive regulation of fibroblast migration;kinase activity;phosphorylation;transferase activity;peltidyl-tyrosine phosphorylation;transferase activity;peltidyl-tyrosine phosphorylation;transferase activity;position;positive regulation of bone mineralization;biomineral tissue development;chondrocyte proliferation;positive rigulation of protein tyrosine kinase receptor signaling pathway;positive regulation of seteoblast differentiation;positive regulation of protein kinase activity;protein autophosphorylation;positive regulation of protein kinase activity;positive regulation of sequence-specific DNA bind transcription factor activity;positive regulation of sequence-specific DNA binding;notein transport;positive regulation of protein transport;positive regulation of protein transport;positive regulation of protein transport;positive regulation of protein transport;positive regulation of contractivity;positive regulation of contractivity;positive regulation of contractivity;positive regulation;positive regu	Dcaf8	splice region variant synonymous variant	 molecular_function:biological_process
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differentiation;nucleic acid binding;DNA binding;RNA binding;ATP-deper RNA helicase activity;helicase activity;protein binding;ATP binding;RNA processing;circadian rhythm;ATP-dependent helicase activity;hydrolase activity;cellular response to heat;poly(A) RNA binding;rhythmic process; mediated mRNA stabilization;protein localization to cytoplasmic stress granule smoothened signaling pathway;patched ligand maturation;multicellular organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pat formation;peptide transporter activity;peptide transport;diaphragm development intron_variant,missense_variant,non_codi	Deliliaib	ice_region_variant	
RNA helicase activity;helicase activity;protein binding;ATP binding;RNA processing;circadian rhythm;ATP-dependent helicase activity;hydrolase activity;cellular response to heat;poly(A) RNA binding;rhythmic process; mediated mRNA stabilization;protein localization to cytoplasmic stress granule Dhx9			
processing;circadian rhythm;ATP-dependent helicase activity;hydrolase activity;cellular response to heat;poly(A) RNA binding;rhythmic process; NMD_transcript_variant,feature_elongatio mediated mRNA stabilization;protein localization to cytoplasmic stress granule smoothened signaling pathway;patched ligand maturation;multicellular organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pat formation;peptide transporter activity;peptide transport;diaphragm development lintron_variant,missense_variant,non_codi			
activity;cellular response to heat;poly(A) RNA binding;rhythmic process; NMD_transcript_variant,feature_elongatio Dhx9 n,intron_variant,splice_region_variant smoothened signaling pathway;patched ligand maturation;multicellular organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pat intron_variant,missense_variant,splice_re Disp1 gion_variant intron_variant,missense_variant,non_codi			
NMD_transcript_variant,feature_elongatio			
Dhx9 n,intron_variant,splice_region_variant granule smoothened signaling pathway;patched ligand maturation;multicellular organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pat intron_variant,missense_variant,splice_re Disp1 gion_variant development intron_variant,missense_variant,non_codi			
smoothened signaling pathway;patched ligand maturation;multicellular organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pat intron_variant,missense_variant,splice_re Disp1 gion_variant development intron_variant,missense_variant,non_codi			· · · · · · · · · · · · · · · · · · ·
organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pat intron_variant,missense_variant,splice_re plication;peptide transporter activity;peptide transport;diaphragm development intron_variant,missense_variant,non_codi	Dhx9	n,intron_variant,splice_region_variant	5
specification process;embryonic pattern specification;dorsal/ventral pat intron_variant,missense_variant,splice_re Disp1 gion_variant development intron_variant,missense_variant,non_codi			
intron_variant,missense_variant,splice_re properties transporter activity;peptide transport;diaphragm development properties transporter activity;peptide transporter activity;peptide transport;diaphragm development properties transporter activity;peptide			
Disp1 gion_variant development intron_variant,missense_variant,non_codi			specification process; embryonic pattern specification; dorsal/ventral pattern
intron_variant,missense_variant,non_codi		intron_variant,missense_variant,splice_re	formation; peptide transporter activity; peptide transport; diaphragm
	Disp1	gion_variant	development
ng_transcript_variant,splice_region_varian		intron_variant,missense_variant,non_codi	
Dnah14 t molecular_function;biological_process	Dnah14	t	

		 inactivation of MAPK activity;regulation of adaptive immune
		response; phosphoprotein phosphatase activity; protein tyrosine phosphatase
		activity;protein dephosphorylation;protein tyrosine/serine/threonine
		phosphatase activity;dephosphorylation;hydrolase activity;phosphatase
		activity;MAP kinase tyrosine/serine/threonine phosphatase activity;response
		to lipopolysaccharide;negative regulation of stress-activated MAPK
		cascade; MAP kinase phosphatase activity; negative regulation of JUN kinase
		activity;negative regulation of protein kinase activity by regulation of protein
		phosphorylation;regulation of innate immune response;negative regulation
		of JNK cascade; oligodendrocyte differentiation; negative regulation of
		oligodendrocyte differentiation;negative regulation of respiratory burst
Dusp10	intron_variant,splice_region_variant	involved in inflammatory response; regulation of brown fat cell differentiation
		phosphoprotein phosphatase activity; protein dephosphorylation; protein
		tyrosine/serine/threonine phosphatase activity;zinc ion
	riant,intron_variant,missense_variant,splic	binding;dephosphorylation;phosphatase activity;kinase binding;positive
Dusp12	e_region_variant	regulation of glucokinase activity
		neural tube closure; actin binding; protein binding; profilin binding; movement
		of cell or subcellular component;actin filament organization;multicellular
		organism development;nervous system development;axon guidance;actin
	inframe_deletion,intron_variant,missense	polymerization or depolymerization;SH3 domain binding;actin cytoskeleton
Enah	_variant,splice_region_variant	organization;cell differentiation;WW domain binding
		catalytic activity;epoxide hydrolase activity;cellular aromatic compound
		metabolic process;response to toxic substance;response to organic cyclic
	5_prime_UTR_variant,intron_variant,miss	compound; hydrolase activity; aromatic compound catabolic process; enzyme
Ephx1	ense_variant,splice_region_variant	binding;cis-stilbene-oxide hydrolase activity;diol biosynthetic process
		nucleotide binding;RNA binding;catalytic activity;aminoacyl-tRNA ligase
		activity;glutamate-tRNA ligase activity;proline-tRNA ligase activity;ATP
		binding;translation;regulation of translation;tRNA aminoacylation for protein
		translation;glutamyl-tRNA aminoacylation;prolyl-tRNA
		aminoacylation; metabolic process; ligase activity; ligase activity, forming
		aminoacyl-tRNA and related compounds; negative regulation of
	intron_variant,missense_variant,splice_re	translation;RNA stem-loop binding;tRNA aminoacylation;GTPase
Eprs	gion_variant	binding;cellular response to interferon-gamma
	8001_1011011	immune system process;humoral immune response mediated by circulating
		immunoglobulin;DNA binding;chromatin binding;catalytic activity;nuclease
		activity;endonuclease activity;exonuclease activity;nucleobase-containing
		compound metabolic process; DNA metabolic process; DNA repair; mismatch
		repair;DNA recombination;cellular response to DNA damage stimulus;5'-3'
		exonuclease activity;somatic hypermutation of immunoglobulin
		genes;hydrolase activity;hydrolase activity, acting on ester bonds;5'-3'
		exodeoxyribonuclease activity; single-stranded DNA 5'-3'
		exodeoxyribonuclease activity;single-stranded bNA 5 -5 exodeoxyribonuclease activity;isotype switching;metal ion binding;flap
	facture truncation intron variant as lies a	
Fvo1	feature_truncation,intron_variant,splice_r	endonuclease activity;meiotic cell cycle;double-stranded DNA 5'-3'
Exo1	egion_variant	exodeoxyribonuclease activity;nucleic acid phosphodiester bond hydrolysis
		regulation of cytokine production; protein binding; cell adhesion; PDZ domain
		binding;epithelial cell differentiation;actomyosin structure
		organization;negative regulation of GTPase activity;positive regulation of
		GTPase activity;positive regulation of blood pressure;intestinal
		absorption;establishment of protein localization to plasma
	feature_elongation,feature_truncation,int	membrane;establishment of endothelial intestinal barrier;regulation of
	ron_variant,non_coding_transcript_varian	membrane permeability;cadherin binding involved in cell-cell
F11r	t,splice_region_variant	adhesion;regulation of actin cytoskeleton reorganization
F13b	missense_variant	blood coagulation;hemostasis

		negative regulation of protein phosphorylation; positive regulation of protein
	NMD transcript variant,inframe insertion	phosphorylation;molecular function;regulation of translation;response to
Fam129a	,missense_variant	endoplasmic reticulum stress; positive regulation of translation
Fam163a	missense_variant	molecular_function;biological_process
		negative regulation of transcription from RNA polymerase II promoter;death
		receptor binding;cytokine activity;tumor necrosis factor receptor
		binding;transcription, DNA-templated;regulation of transcription, DNA-
		templated;apoptotic process;activation of cysteine-type endopeptidase
		activity involved in apoptotic process; inflammatory cell apoptotic
		process;immune response;positive regulation of cell proliferation;extrinsic
		apoptotic signaling pathway via death domain receptors;negative regulation
		of angiogenesis;cellular chloride ion homeostasis;positive regulation of
		apoptotic process; positive regulation of neuron apoptotic process; positive
		regulation of epidermal growth factor receptor signaling pathway;retinal cell
		programmed cell death;endosomal lumen acidification;T cell apoptotic
		process;necroptotic process;apoptotic signaling pathway;extrinsic apoptotic
		signaling pathway;necroptotic signaling pathway;positive regulation of
Fasl	missense_variant	endothelial cell apoptotic process
	feature_truncation,intron_variant,splice_r	Chaotherial cell apoptotic process
Fbxo28	egion_variant	 molecular_function;biological_process
		activation of MAPK activity;positive regulation of type I
		hypersensitivity;serotonin secretion;protein binding;signal transduction;cell
		surface receptor signaling pathway; activation of JUN kinase
		activity;leukotriene biosynthetic process;lgE receptor activity;lgE
		binding; positive regulation of mast cell degranulation; positive regulation of
		interleukin-3 biosynthetic process; positive regulation of granulocyte
		macrophage colony-stimulating factor biosynthetic process; positive
		regulation of peptidyl-tyrosine phosphorylation;positive regulation of calcium
Fcer1a	missense_variant	mediated signaling
	-	negative regulation of type I hypersensitivity;immune complex
		clearance;negative regulation of immunoglobulin production;negative
		regulation of inflammatory response to antigenic stimulus;negative
		regulation of acute inflammatory response to antigenic stimulus;negative
		regulation of humoral immune response mediated by circulating
		immunoglobulin;signal transducer activity, downstream of receptor;protein
		binding;receptor-mediated endocytosis;phagocytosis, engulfment;defense
		response;immune response;cell surface receptor signaling pathway;response
		to bacterium;immunoglobulin mediated immune response;IgG
		binding;immunoglobulin binding;antigen processing and presentation of
		exogenous peptide antigen via MHC class II; negative regulation of B cell
		proliferation;endocytic recycling;negative regulation of interleukin-10
		production;negative regulation of neutrophil apoptotic process;mast cell
		activation;negative regulation of phagocytosis;positive regulation of
		phagocytosis;negative regulation of immune response;cellular response to
Fcgr2b	missense_variant	molecule of bacterial origin
		antibody-dependent cellular cytotoxicity;positive regulation of type IIa
		hypersensitivity;positive regulation of type III hypersensitivity;positive
		regulation of type I hypersensitivity;serotonin secretion;phagocytosis,
		recognition;phagocytosis, engulfment;cell surface receptor signaling
	intron_variant,missense_variant,non_codi	pathway; IgG receptor activity; IgG binding; neutrophil chemotaxis; positive
	ng_transcript_exon_variant,non_coding_t	regulation of tumor necrosis factor biosynthetic process;antigen processing
		and presentation of exogenous peptide antigen via MHC class I;mast cell
Fcgr3	nonymous_variant	activation; positive regulation of phagocytosis; regulation of immune response

		lgE receptor activity;lgG receptor activity;neutrophil activation;positive
	intron_variant,missense_variant,splice_re	regulation of bone resorption;regulation of sensory perception of
Fcgr4	gion_variant	pain;cellular response to lipopolysaccharide
Fcrl6	missense_variant	biological_process;protein phosphatase binding
	NMD_transcript_variant,feature_truncatio	
	n,inframe_deletion,intron_variant,missens	
	e_variant,non_coding_transcript_variant,s	
Fcrla	plice_region_variant	protein binding;cell differentiation
F	intron_variant,missense_variant,splice_re	
Fcrlb	gion_variant	molecular_function;negative regulation of immune response
		catalistic activity of magrata budgetaca activity utricarbavulic acid avelogium arata
	NMD transcript variant intron variant mi	catalytic activity;fumarate hydratase activity;tricarboxylic acid cycle;fumarate
FL 1		
Fh1	ssense_variant,splice_region_variant	number of cells within a tissue;protein tetramerization
		actin binding;transport;cellular response to DNA damage
		stimulus;multicellular organism development;microtubule binding;protein
		transport; vesicle-mediated transport; meiotic chromosome movement
		towards spindle pole;polar body extrusion after meiotic divisions;negative
		regulation of protein catabolic process;negative regulation of apoptotic
		process;actin nucleation;intracellular transport;oogenesis;actin filament
		bundle assembly;establishment of meiotic spindle localization;homologous
		chromosome movement towards spindle pole involved in homologous
_	intron_variant,missense_variant,splice_re	chromosome segregation;formin-nucleated actin cable assembly;cellular
Fmn2	gion_variant,synonymous_variant	response to hypoxia
	feature_truncation,intron_variant,non_co	
	ding_transcript_variant,splice_region_vari	
Gas5	ant	molecular_function;biological_process
		transport;electron carrier activity;response to organic substance;protein
	,non_coding_transcript_exon_variant,non	disulfide oxidoreductase activity;response to hydrogen peroxide;cell redox
Cl. 2	_coding_transcript_variant,splice_region_	homeostasis;metal ion binding;iron-sulfur cluster binding;2 iron, 2 sulfur
Glrx2	variant	cluster binding;oxidation-reduction process
Gm10176	missense_variant	molecular_function;biological_process
Gm10517	missense_variant	molecular_function;biological_process
Gm10521	feature_elongation,frameshift_variant	molecular_function;biological_process
	intron_variant,missense_variant,splice_re	microtubule motor activity;microtubule-based movement;ATPase
Gm1305	gion_variant	activity;cytoskeleton-dependent intracellular transport
	feature_truncation,intron_variant,non_co	
	ding_transcript_variant,splice_region_vari	
Gm2061	ant	molecular_function;biological_process
	intron_variant,missense_variant,splice_re	
Gm4788	gion_variant	molecular_function;biological_process
		molecular_function;signal transducer activity;G-protein coupled receptor
C - 25		activity;signal transduction;G-protein coupled receptor signaling
Gpr25	missense_variant	pathway;biological_process
		RNA polymerase II core promoter sequence-specific DNA binding;RNA
		polymerase II distal enhancer sequence-specific DNA binding;osteoblast
		differentiation;nucleosome assembly;spermatogenesis;single fertilization;cell
		proliferation;nucleosomal DNA binding;pericentric heterochromatin
		assembly;telomeric heterochromatin assembly;multicellular organism
110.50		growth;histone binding;muscle cell differentiation;oogenesis;negative
H3f3a	intron_variant,splice_region_variant	regulation of chromosome condensation
		molecular_function;catalytic activity;carbohydrate metabolic
	intron_variant,missense_variant,splice_ac	process;biological_process;oxidoreductase activity, acting on the CH-OH
Hhipl2	ceptor_variant,splice_region_variant	group of donors, quinone or similar compound as acceptor; quinone binding

		liver development;DNA binding;transcription, DNA-templated;regulation of
		transcription, DNA-templated;skeletal muscle tissue development;positive
		regulation of cell proliferation;cell differentiation;sequence-specific DNA
		binding;positive regulation of T-helper 1 cell differentiation;negative
		regulation of T-helper 2 cell differentiation; positive regulation of organ
Hlx	sense_variant	development;embryonic digestive tract morphogenesis
		molecular_function;calcium ion binding;cell cycle;biological_process;cell
Hmcn1	e_variant,splice_region_variant	division
		3-keto sterol reductase activity;estradiol 17-beta-dehydrogenase
		activity;prolactin receptor binding;lipid metabolic process;steroid
		biosynthetic process;cholesterol biosynthetic process;oxidoreductase
Hsd17b7	missense_variant	activity;oxidation-reduction process
lfi202b	missense_variant	cellular response to interferon-beta
		RNA polymerase II core promoter proximal region sequence-specific DNA
		binding;core promoter binding;transcriptional repressor activity, RNA
		polymerase II core promoter proximal region sequence-specific
		binding;double-stranded DNA binding;transcription factor binding;cellular
Ifi203	initiator_codon_variant,missense_variant	response to interferon-beta;identical protein binding;poly(A) RNA binding
		RNA polymerase II core promoter proximal region sequence-specific DNA
		binding;core promoter binding;transcriptional repressor activity, RNA
		polymerase II core promoter proximal region sequence-specific
		binding;double-stranded DNA binding;transcription cofactor activity;protein
		binding;transcription, DNA-templated;regulation of transcription, DNA-
		templated;regulation of transcription from RNA polymerase II
		promoter;multicellular organism development;transcription factor
		binding;cellular response to interferon-beta;intrinsic apoptotic signaling
		pathway in response to DNA damage by p53 class mediator; identical protein
	intron_variant,missense_variant,splice_re	binding;poly(A) RNA binding;positive regulation of osteoblast
Ifi204	gion_variant	differentiation;inner ear development
		RNA polymerase II core promoter proximal region sequence-specific DNA
		binding;core promoter binding;transcriptional repressor activity, RNA
		polymerase II core promoter proximal region sequence-specific
		binding;double-stranded DNA binding;transcription, DNA-
		templated;regulation of transcription, DNA-templated;transcription factor
	intron_variant,missense_variant,splice_re	 binding;cellular response to interferon-beta;identical protein binding;poly(A)
Ifi205	gion_variant	RNA binding
	NMD transcript variant,inframe deletion,	
	intron_variant,missense_variant,splice_re	
	gion_variant,stop_gained,synonymous_va	
lgfn1	riant	 molecular_function;biological_process
	feature_elongation,feature_truncation,int	
	ron_variant,missense_variant,splice_regio	
lgsf8	n_variant	protein binding;regulation of cell motility
U		homophilic cell adhesion via plasma membrane adhesion
		molecules;multicellular organism development;nervous system
		development;dendrite development;cell differentiation;regulation of
		synapse organization; cell-cell adhesion; protein binding involved in cell-cell

		I
		MAPK cascade; regulation of protein phosphorylation; myeloid cell
		homeostasis;cell surface receptor signaling pathway;inositol-1,4,5-
		trisphosphate 3-kinase activity; T cell differentiation; inositol trisphosphate
		metabolic process;negative regulation of neutrophil apoptotic
		process;common myeloid progenitor cell proliferation;positive thymic T cell
		selection;thymic T cell selection;negative regulation of myeloid cell
	intron_variant,missense_variant,splice_re	differentiation; positive regulation of Ras protein signal transduction; positive
Itpkb	gion_variant	regulation of alpha-beta T cell differentiation;cellular response to calcium ion
Ivns1abp	missense variant	protein binding;negative regulation of intrinsic apoptotic signaling pathway
TVIISTUDP	imissense_variane	nucleotide binding;receptor binding;inward rectifier potassium channel
		activity;voltage-gated ion channel activity;potassium channel activity;protein
		binding;ATP binding;transport;ion transport;potassium ion transport;visual
		perception;adult walking behavior;potassium ion import;oligodendrocyte
		development;ATP-activated inward rectifier potassium channel
		activity; central nervous system myelination; regulation of ion transmembrane
		transport;regulation of membrane potential;identical protein
		binding;regulation of long-term neuronal synaptic plasticity;protein
		homotetramerization; regulation of sensory perception of pain; glutamate
		reuptake;L-glutamate import;potassium ion homeostasis;regulation of
		resting membrane potential;membrane hyperpolarization;potassium ion
Kcnj10	missense_variant	transmembrane transport
Kenjio	imissense_variane	inward rectifier potassium channel activity;voltage-gated ion channel
		activity;transport;ion transport;potassium ion transport;potassium ion
		import;G-protein activated inward rectifier potassium channel activity;PDZ
Kcnj9	intron_variant,splice_region_variant	domain binding;regulation of ion transmembrane transport
ikenjo	introl_variant,spiice_region_variant	demand sharing, egalation of fort transmembrane transport
		voltage-gated potassium channel activity; potassium channel
Kcnt2	missense_variant	activity; potassium ion transport; calcium-activated potassium channel activity
		nucleotide binding;regulation of cell growth;microtubule motor activity;ATP
		binding;microtubule-based movement;microtubule depolymerization;mitotic
		metaphase plate congression;microtubule binding;positive regulation of cell
		proliferation;ATP-dependent microtubule motor activity, plus-end-
		directed;regulation of G2/M transition of mitotic cell cycle;tubulin
		binding;ATPase activity;protein kinase binding;cerebellar granular layer
		structural organization; cerebellar Purkinje cell layer structural
		organization;cerebellar cortex development;hippocampus
		development; olfactory bulb development; cell proliferation in
		forebrain;cerebral cortex development;regulation of cell adhesion;PDZ
		domain binding;regulation of cell migration;cytoskeleton-dependent
		intracellular transport;SCF-dependent proteasomal ubiquitin-dependent
		protein catabolic process;regulation of myelination;activation of protein
		kinase activity; positive regulation of cytokinesis; regulation of Rap protein
		signal transduction;negative regulation of integrin activation;substrate
		adhesion-dependent cell spreading; negative regulation of apoptotic
		process;proteasome-mediated ubiquitin-dependent protein catabolic
	feature_elongation,intron_variant,missens	process; regulation of neuron apoptotic process; negative regulation of
		neuron apoptotic process;establishment of protein localization;cell
		division;mitotic cell cycle process;regulation of cell maturation;regulation of
Kif14	nt	G1/S transition of mitotic cell cycle
	NMD_transcript_variant,feature_truncatio	
	n,intron_variant,missense_variant,non_co	
		nucleotide binding;microtubule motor activity;ATP binding;microtubule-
Kif21b	ant	based movement;microtubule binding;ATPase activity
Klhdc9	missense_variant	molecular_function;biological_process
	1	

		monooxygenase activity;kynurenine 3-monooxygenase activity;tryptophan
		catabolic process;response to salt stress;NAD(P)H oxidase
		activity;oxidoreductase activity;pyridine nucleotide biosynthetic
		process;tryptophan catabolic process to kynurenine;NAD metabolic
	ding_transcript_exon_variant,non_coding	process; quinolinate biosynthetic process; secondary metabolite biosynthetic
	_transcript_variant,splice_region_variant,s	process;flavin adenine dinucleotide binding;oxidation-reduction
Kmo	ynonymous_variant	process;kynurenine metabolic process;FAD binding
	intron_variant,missense_variant,non_codi	
	ng_transcript_variant,splice_donor_varian	structural molecule activity;cell-cell adhesion;cadherin binding involved in
Lad1	t,splice_region_variant	cell-cell adhesion
		extracellular matrix structural constituent;protein binding;protein complex
		assembly;cell adhesion;cell migration;extracellular matrix
	intron_variant,missense_variant,non_codi	disassembly; neuron projection development; hemides mosome
	ng_transcript_exon_variant,non_coding_t	assembly;substrate adhesion-dependent cell spreading;glycosphingolipid
Lamc1	ranscript_variant,splice_region_variant	binding
		DNA binding;nuclear localization sequence binding;sterol biosynthetic
		process;oxidoreductase activity, acting on the CH-CH group of
		donors; oxidoreductase activity, acting on the CH-CH group of donors, NAD or
	feature truncation intron variant missens	NADP as acceptor;poly(A) RNA binding;chaperone binding;oxidation-
Lbr	e_variant,splice_region_variant	reduction process;chromo shadow domain binding
	e_ranant/spince_region_ranant	negative regulation of transcription from RNA polymerase II promoter;heart
		morphogenesis;cytokine activity;transforming growth factor beta receptor
		binding;multicellular organism development;determination of left/right
		symmetry;growth factor activity;negative regulation of cell
		proliferation;anterior/posterior axis specification;positive regulation of
	takan and takan arang	pathway-restricted SMAD protein phosphorylation;cell growth;response to
		retinoic acid;nodal binding;growth;cell migration involved in
	ng_transcript_exon_variant,non_coding_t	gastrulation;regulation of apoptotic process;regulation of MAPK cascade;cell
	ranscript_variant,splice_region_variant,sy	development;SMAD protein signal transduction;negative regulation of nodal
Lefty1	nonymous_variant	signaling pathway;negative regulation of nodal receptor complex assembly
		cytokine activity;transforming growth factor beta receptor
		binding;multicellular organism development;growth factor activity;positive
		regulation of pathway-restricted SMAD protein phosphorylation;cell
		growth;growth;regulation of apoptotic process;regulation of MAPK
Lefty2	missense_variant	cascade;cell development;SMAD protein signal transduction
	missense_variant,splice_region_variant,sy	
Lin9	nonymous_variant	transcription, DNA-templated;cell cycle;DNA biosynthetic process
	NMD_transcript_variant,feature_truncatio	
	n,intron_variant,missense_variant,non_co	adaptive immune response;immune system process;cell adhesion;positive
	ding_transcript_variant,splice_region_vari	regulation of interleukin-17 production; innate immune response; T-helper 17
Ly9	ant	cell lineage commitment
		protein depalmitoylation;palmitoyl-(protein) hydrolase activity;hydrolase
		activity;negative regulation of Golgi to plasma membrane protein
Lyplal1	missense_variant	transport;carboxylic ester hydrolase activity
		catalytic activity;nitrate reductase activity;oxidoreductase
		activity;molybdenum ion binding;pyridoxal phosphate binding;nitrate
	intron_variant,missense_variant,splice_re	metabolic process;molybdopterin cofactor binding;oxidation-reduction
Marc1	gion_variant	process
	<u>0</u>	catalytic activity;nitrate reductase activity;oxidoreductase
	NMD transcript variant feature truncation	activity;molybdenum ion binding;pyridoxal phosphate binding;nitrate
		metabolic process;molybdopterin cofactor binding;oxidation-reduction
Marc2	ariant,splice_region_variant	process
IVIGICZ	unant,spince_region_variant	lhi occas

		Landa at the binding of the state of the sta
		nucleotide binding;microtubule cytoskeleton organization;magnesium ion
		binding; neuron migration; phosphatidylserine binding; protein kinase
		activity;protein serine/threonine kinase activity;ATP
		binding;phosphatidylinositol-4,5-bisphosphate binding;protein
		phosphorylation;cytoskeleton organization;lipid binding;Wnt signaling
		pathway;kinase activity;phosphorylation;transferase activity;establishment
		of cell polarity;intracellular signal transduction;metal ion binding;tau-protein
Mark1	e_variant,splice_region_variant	kinase activity;phosphatidic acid binding
		chondrocyte development;positive regulation of leukocyte
		migration;transport;exocytosis;ER to Golgi vesicle-mediated
		transport;negative regulation of cell adhesion;protein transport;vesicle-
		mediated transport;collagen fibril organization;negative regulation of cell
		migration;positive regulation of bone mineralization;wound
		healing;lipoprotein transport;lipoprotein transporter activity;cargo loading
Mia3	_variant	into COPII-coated vesicle
		RNA polymerase II core promoter proximal region sequence-specific DNA
		binding;RNA polymerase II distal enhancer sequence-specific DNA
		binding;core promoter proximal region sequence-specific DNA
		binding;transcriptional activator activity, RNA polymerase II core promoter
		proximal region sequence-specific binding;RNA polymerase II transcription
		factor binding;RNA polymerase II repressing transcription factor
		binding;transcriptional activator activity, RNA polymerase II transcription
		factor binding;transcriptional activator activity, RNA polymerase II distal
		enhancer sequence-specific binding;endoderm formation;hematopoietic
		progenitor cell differentiation; DNA binding; transcription, DNA-
		templated;regulation of transcription, DNA-templated;multicellular organism
		development;gastrulation;endoderm development;heart
		development;hemopoiesis;cell differentiation;endodermal cell
		differentiation;cell migration involved in gastrulation;protein
		homodimerization activity;sequence-specific DNA binding;positive regulation
		of transcription from RNA polymerase II promoter; digestive tract
		development;negative regulation of hematopoietic progenitor cell
Mixl1	missense_variant	differentiation;positive regulation of mesoderm development
		RNA polymerase II core promoter proximal region sequence-specific DNA
		binding;core promoter binding;transcriptional repressor activity, RNA
		polymerase II core promoter proximal region sequence-specific
		binding;double-stranded DNA binding;transcription factor binding;negative
		regulation of cell growth;regulation of growth;identical protein
Mndal	NMD_transcript_variant,missense_variant	
Mptx1	missense_variant	molecular_function;biological_process;metal ion binding
	feature elongation, feature truncation, int	
	ron_variant,missense_variant,splice_regio	protein binding;negative regulation of apoptotic process;cell-cell junction
Mpz	n_variant,synonymous_variant	maintenance
	intron_variant,missense_variant,splice_re	
Mroh3	gion variant, synonymous variant	 molecular_function;biological_process
Mroh9	intron variant,splice region variant	molecular function;biological process
		protein binding;NADP catabolic process;superoxide metabolic
		process; protein C-terminus binding; response to glucose; response to organic
		cyclic compound;superoxide-generating NADPH oxidase activity;response to
		lipopolysaccharide; cellular response to hormone stimulus; superoxide anion
		generation; positive regulation of neuron apoptotic process; positive
Ncf2	intron_variant,splice_region_variant	regulation of blood pressure;Rac GTPase binding
14012		myeloid cell homeostasis;endopeptidase activity;protein binding;membrane
		1
		protein ectodomain proteolysis; Notch signaling pathway; peptidase
Nostro	NIMED transcript variant minor and a visit	activity;protein processing;T cell proliferation;positive regulation of catalytic
Ncstn	ַרואואון_transcript_variant,missense_variant	activity;beta-amyloid metabolic process;epithelial cell proliferation

		NADH dehydrogenase activity;transport;response to oxidative stress;NADH
	intron_variant,missense_variant,non_codi	dehydrogenase (ubiquinone) activity;oxidoreductase activity;oxidoreductase
	ng_transcript_exon_variant,non_coding_t	activity, acting on NAD(P)H;ubiquitin protein ligase binding;metal ion
	ranscript_variant,splice_region_variant,sy	binding;quinone binding;NAD binding;iron-sulfur cluster binding;4 iron, 4
Ndufs2	nonymous_variant	sulfur cluster binding;oxidation-reduction process
		RNA polymerase II regulatory region sequence-specific DNA binding;RNA
		polymerase II transcription factor activity, sequence-specific DNA
		binding;transcriptional activator activity, RNA polymerase II transcription
		regulatory region sequence-specific binding; DNA binding; transcription, DNA
		templated;regulation of transcription, DNA-templated;multicellular organism
	1	
Nhlh1	splice_region_variant	RNA polymerase II promoter;protein dimerization activity
	missense_variant,non_coding_transcript_	
	exon_variant,non_coding_transcript_varia	nitrogen compound metabolic process;hydrolase activity;hydrolase activity,
Nit1	nt,splice_region_variant	acting on carbon-nitrogen (but not peptide) bonds
		protease binding;biological_process;PDZ domain binding;nitric-oxide
	intron_variant,missense_variant,non_codi	synthase binding;negative regulation of neuron death;regulation of high
	ng_transcript_variant,splice_donor_varian	voltage-gated calcium channel activity; positive regulation of peptidyl-
Nos1ap	t,splice_region_variant	cysteine S-nitrosylation
	feature_truncation,intron_variant,missens	
Nphs2	e_variant,splice_region_variant	protein binding;excretion;actin cytoskeleton reorganization
		catalytic activity;carbohydrate metabolic process;metabolic process;N-
		acetylneuraminate lyase activity;lyase activity;N-acetylneuraminate catabolic
Npl	intron_variant,splice_region_variant	process;identical protein binding
		RNA polymerase II regulatory region sequence-specific DNA
		binding;transcriptional activator activity, RNA polymerase II transcription
		regulatory region sequence-specific binding;DNA binding;transcription factor
		activity, sequence-specific DNA binding; steroid hormone receptor
		activity;thyroid hormone receptor activity;protein binding;transcription, DNA
		templated;regulation of transcription, DNA-templated;zinc ion
		 binding;steroid hormone mediated signaling pathway;sequence-specific DNA
		binding;negative regulation of transcription, DNA-templated;positive
		regulation of transcription from RNA polymerase II promoter; metal ion
Nr1i3	NMD_transcript_variant,missense_variant	
		molecular_function;cell cycle;mitotic nuclear division;attachment of spindle
Nuf2	intron_variant,splice_region_variant	microtubules to kinetochore;cell division
	feature_truncation,intron_variant,missens	
	e variant,splice acceptor variant,splice r	nucleotide binding;ATP binding;ribosome biogenesis;poly(A) RNA
NvI	egion_variant	binding;positive regulation of telomerase activity;preribosome binding
	·····	extracellular matrix organization; protein homodimerization
Olfml2b	gion variant	activity;extracellular matrix binding
	Bron_runant	transmembrane signaling receptor activity;olfactory receptor activity;G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr1406	missense variant	smell; detection of chemical stimulus involved in sensory perception
0111400	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr218	missense_variant	smell;detection of chemical stimulus involved in sensory perception
	illisselise_variant	olfactory receptor activity; odorant binding; G-protein coupled receptor
Olfr220	missansa variant	signaling pathway;sensory perception of smell
UIII Z Z U	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-
Olf-224	missansa variert	protein coupled receptor signaling pathway; sensory perception of
Olfr231	missense_variant	smell;detection of chemical stimulus involved in sensory perception
		G-protein coupled receptor activity;olfactory receptor activity;cell surface
016 0 : 0		receptor signaling pathway;G-protein coupled receptor signaling
Olfr248	missense_variant	pathway;sensory perception of smell
		olfactory receptor activity; G-protein coupled receptor signaling
Olfr414	missense_variant	pathway;sensory perception of smell

		G-protein coupled receptor activity;olfactory receptor activity;cell surface
		receptor signaling pathway;G-protein coupled receptor signaling
Olfr417	missense_variant	pathway;sensory perception of smell
0111117	missense_variane	transmembrane signaling receptor activity; olfactory receptor activity; G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr420	missense variant	smell;detection of chemical stimulus involved in sensory perception
		transmembrane signaling receptor activity; Olfactory receptor activity; G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr424	missense_variant	smell;detection of chemical stimulus involved in sensory perception
		transmembrane signaling receptor activity;olfactory receptor activity;G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr427	missense variant	smell;detection of chemical stimulus involved in sensory perception
		olfactory receptor activity;G-protein coupled receptor signaling
Olfr429	missense_variant	pathway;sensory perception of smell
		transmembrane signaling receptor activity;olfactory receptor activity;G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr430	missense variant	smell;detection of chemical stimulus involved in sensory perception
<u> </u>		transmembrane signaling receptor activity;olfactory receptor activity;G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr432	missense_variant	smell;detection of chemical stimulus involved in sensory perception
052		transmembrane signaling receptor activity;olfactory receptor activity;G-
		protein coupled receptor signaling pathway;sensory perception of
Olfr433	missense_variant	smell;detection of chemical stimulus involved in sensory perception
		signal transducer activity;G-protein coupled receptor activity;signal
		transduction;G-protein coupled receptor signaling
		pathway;phototransduction;G-protein coupled photoreceptor
		activity;photoreceptor activity;protein-chromophore linkage;response to
Opn3	missense_variant	stimulus;cellular response to light stimulus
- F		activity;NAD+ ADP-ribosyltransferase activity;protein binding;DNA metabolic
		process; lagging strand elongation; DNA repair; base-excision repair; double-
		strand break repair; transcription, DNA-templated; regulation of transcription,
		DNA-templated; protein ADP-ribosylation; cellular response to DNA damage
		stimulus;mitochondrion organization;transforming growth factor beta
		receptor signaling pathway;transcription factor binding;zinc ion
		binding; positive regulation of cardiac muscle hypertrophy; regulation of
		SMAD protein complex assembly; protein autoprocessing; transferase
		activity;transferase activity, transferring glycosyl groups;enzyme
		binding; protein kinase binding; signal transduction involved in regulation of
		gene expression;estrogen receptor binding;mitochondrial DNA metabolic
		process; cellular response to insulin stimulus; positive regulation of
		intracellular estrogen receptor signaling pathway;cellular response to
		oxidative stress; protein modification process; regulation of growth rate; DNA
		damage response, detection of DNA damage; identical protein
		binding;histone deacetylase binding;mitochondrial DNA repair;regulation of
		DNA methylation;poly(A) RNA binding;positive regulation of transcription
		from RNA polymerase II promoter;SMAD binding;metal ion binding;protein N-
		terminus binding;behavioral response to cocaine;DNA ligation involved in
		DNA repair;NAD binding;positive regulation of mitochondrial
		depolarization; positive regulation of SMAD protein import into
		nucleus; protein poly-ADP-ribosylation; R-SMAD binding; cellular response to
		superoxide; cellular response to transforming growth factor beta
		stimulus; positive regulation of protein localization to nucleus; positive
		regulation of neuron death; regulation of oxidative stress-induced neuron
		intrinsic apoptotic signaling pathway;regulation of single strand break
		repair;regulation of cellular protein localization;negative regulation of
Da 1	to the second se	telomere maintenance via telomere lengthening;cellular response to beta-
Parp1	intron_variant,splice_region_variant	amyloid; positive regulation of myofibroblast differentiation; negative

		protein binding;protein targeting to peroxisome;peroxisome
		organization;peroxisome membrane biogenesis;peroxisome
		fission;peroxisome membrane class-1 targeting sequence binding;protein
		import into peroxisome membrane;protein N-terminus binding;protein
	feature_truncation,intron_variant,non_co	stabilization;ATPase binding;chaperone-mediated protein folding;chaperone-
	ding_transcript_variant,splice_region_vari	mediated protein transport; establishment of protein localization to
Pex19	ant	peroxisome;negative regulation of lipid binding
		protein folding;protein binding involved in protein folding;unfolded protein
Pfdn2	inframe_insertion	binding; positive regulation of cytoskeleton organization
		mannosyltransferase activity; GPI anchor biosynthetic process; transferase
		activity;transferase activity, transferring glycosyl groups;transferase activity,
Pigm	missense_variant	transferring hexosyl groups
	NMD_transcript_variant,intron_variant,spl	protein binding;lamin binding;cell adhesion;single organismal cell-cell
Pkp1	ice_region_variant	adhesion;intermediate filament bundle assembly
		ovulation from ovarian follicle;phospholipase activity;lysophospholipase
		activity;phospholipase A2 activity;calcium ion binding;calcium-dependent
		phospholipid binding;lipid metabolic process;metabolic process;positive
		regulation of cell proliferation; phospholipid catabolic process; response to
		organic substance;lipid catabolic process;hydrolase activity;arachidonic acid
		metabolic process; positive regulation of vesicle fusion; positive regulation of
		prostaglandin biosynthetic process; histone acetyltransferase
		binding; regulation of cell proliferation; positive regulation of apoptotic
		process;surfactant homeostasis;icosanoid biosynthetic
	non_coding_transcript_exon_variant,non_	process;decidualization;metal ion binding;calcium-dependent phospholipase
	coding_transcript_variant,splice_region_v	A2 activity; arachidonic acid secretion; positive regulation of inflammatory
Pla2g4a	ariant,synonymous_variant	response;response to calcium ion;cellular response to antibiotic
		oxygen-dependent protoporphyrinogen oxidase activity;porphyrin-containing
		compound biosynthetic process;heme biosynthetic process;oxidoreductase
	intron_variant,non_coding_transcript_vari	activity;protoporphyrinogen IX metabolic process;oxidation-reduction
Ррох	ant,splice_region_variant	process

	feature_truncation,intron_variant,missens	pathway;negative regulation of signal transduction;positive regulation of
	1	ion and activator activity, o protein coupled receptor signaling
		GTPase activator activity; G-protein coupled receptor signaling
Rfwd2	missense_variant	ligase activity
		dependent protein catabolic process; metal ion binding; ubiquitin protein
		ubiquitination; ligase activity; positive regulation of proteasomal ubiquitin-
		protein binding;zinc ion binding;response to ionizing radiation;protein
Rasal2	egion_variant	transduction
	feature_elongation,intron_variant,splice_r	GTPase activator activity;negative regulation of Ras protein signal
Ralgps2	gion_variant	signal transduction
	intron_variant,missense_variant,splice_re	mediated signal transduction;biological_process;regulation of Ral protein
		molecular_function;guanyl-nucleotide exchange factor activity;small GTPase
Rab3gap2	gion_variant,synonymous_variant	network organization; positive regulation of autophagosome assembly
	intron_variant,missense_variant,splice_re	protein lipidation; positive regulation of endoplasmic reticulum tubular
		localization to endoplasmic reticulum membrane; positive regulation of
		activity;protein heterodimerization activity;establishment of protein
		GTPase binding;enzyme regulator activity;regulation of GTPase
		GTPase activator activity;Rab guanyl-nucleotide exchange factor activity;Rab
Qsox1	t	process
	ng_transcript_variant,splice_region_varian	activity;thiol oxidase activity;cell redox homeostasis;oxidation-reduction
	intron_variant,missense_variant,non_codi	macroautophagy;oxidoreductase activity;flavin-linked sulfhydryl oxidase
		protein disulfide isomerase activity; protein folding; negative regulation of
Pycr2	nymous_variant	activity;cellular response to oxidative stress;oxidation-reduction process
	intron_variant,splice_region_variant,syno	process;cellular amino acid biosynthetic process;oxidoreductase
		pyrroline-5-carboxylate reductase activity;proline biosynthetic
Psen2	lice_region_variant	regulation of apoptotic signaling pathway
	5_prime_UTR_variant,missense_variant,sp	involved in ubiquitin-dependent protein catabolic process;negative
		death domain receptors;negative regulation of protein ubiquitination
		receptors; positive regulation of extrinsic apoptotic signaling pathway via
		regulation of extrinsic apoptotic signaling pathway via death domain
		maturation; cardiac muscle contraction; neuron cellular homeostasis; negative
		pathway;negative regulation of ubiquitin-protein transferase activity;protein
		metabolic process; positive regulation of coagulation; T cell receptor signaling
		development;thymus development;brain morphogenesis;beta-amyloid
		protein metabolic process;regulation of synaptic plasticity;lung alveolus
		catalytic activity;regulation of protein binding;skin morphogenesis;cellular
		process; positive regulation of apoptotic process; positive regulation of
		transduction;locomotion;anagen;amyloid precursor protein catabolic
		reticulum calcium ion homeostasis;intracellular signal
		of proteasomal ubiquitin-dependent protein catabolic process;endoplasmic
		complex assembly;negative regulation of protein binding;positive regulation
		morphogenesis;forebrain development;negative regulation of protein
		activity;dorsal/ventral neural tube patterning;embryonic limb
		development;protein transport;protein processing;hydrolase
		processing; learning or memory; memory; peptidase activity; embryo
		activated receptor activity; regulation of epidermal growth factor-
		factor-activated receptor activity; regulation of epidermal growth factor-
		proteolysis;calcium ion transport;negative regulation of epidermal growth
		activity;protein binding;proteolysis;membrane protein ectodomain
		differentiation; endopeptidase activity; aspartic-type endopeptidase
		involved in immune response;myeloid leukocyte
		development;hematopoietic progenitor cell differentiation;T cell activation
		fate specification;somitogenesis;positive regulation of receptor recycling;negative regulation of protein phosphorylation;hair follicle
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		G-protein alpha-subunit binding;GTPase activator activity;G-protein coupled
		receptor signaling pathway;negative regulation of signal
		transduction; positive regulation of GTPase activity; negative regulation of G-
Rgs4	missense_variant	protein coupled receptor protein signaling pathway
		GTPase activator activity;signal transduction;G-protein coupled receptor
		signaling pathway;negative regulation of signal transduction;negative
Rgs5	intron_variant,splice_region_variant	regulation of G-protein coupled receptor protein signaling pathway
		signal transducer activity;GTPase activator activity;protein binding;G-protein
		coupled receptor signaling pathway; regulation of G-protein coupled receptor
		protein signaling pathway;negative regulation of signal transduction;G-
	intron_variant,splice_region_variant,syno	protein beta-subunit binding;intracellular signal transduction;positive
Rgs7	nymous_variant	regulation of GTPase activity
		G-protein alpha-subunit binding;GTPase activator activity;G-protein coupled
		receptor signaling pathway; G-protein coupled acetylcholine receptor
		signaling pathway;negative regulation of signal transduction;positive
		regulation of GTPase activity; regulation of dopamine receptor signaling
Rgs8	intron_variant,splice_region_variant	pathway
	NMD_transcript_variant,intron_variant,mi	
	ssense_variant,non_coding_transcript_var	
Rgsl1	iant,splice_region_variant	GTPase activator activity
		nucleotide binding;RNA binding;nuclease activity;endonuclease
		activity;ribonuclease activity;protein kinase activity;ATP binding;rRNA
		processing;mRNA processing;protein phosphorylation;hydrolase
		activity;rRNA binding;ribonucleoprotein complex binding;regulation of mRNA
		stability;negative regulation of viral genome replication;fat cell
	intron_variant,missense_variant,non_codi	differentiation; positive regulation of transcription from RNA polymerase II
	ng_transcript_variant,splice_region_varian	promoter;metal ion binding;defense response to virus;positive regulation of
Rnasel	t	glucose import in response to insulin stimulus
		negative regulation of transcription from RNA polymerase II
		promoter;mitotic cell cycle;gastrulation with mouth forming
		second;chromatin binding;ubiquitin-protein transferase activity;protein
		binding;transcription, DNA-templated;regulation of transcription, DNA-
		templated;germ cell development;zinc ion binding;anterior/posterior axis
		specification;histone ubiquitination;ligase activity;histone H2A
		monoubiquitination;histone H2A-K119 monoubiquitination;negative
		regulation of sequence-specific DNA binding transcription factor
		activity;metal ion binding;ubiquitin protein ligase activity;RING-like zinc
Rnf2	intron_variant,splice_region_variant	finger domain binding
		RNA polymerase II regulatory region sequence-specific DNA binding;DNA
		binding;transcription factor activity, sequence-specific DNA binding;steroid
		hormone receptor activity;9-cis retinoic acid receptor activity;transcription,
		DNA-templated;regulation of transcription, DNA-templated;zinc ion
		binding;regulation of myelination;steroid hormone mediated signaling
		pathway;sequence-specific DNA binding;positive regulation of transcription
		from RNA polymerase II promoter; metal ion binding; retinoic acid receptor
		signaling pathway;protein homotetramerization;positive regulation of
		transcription from RNA polymerase II promoter involved in cellular response
Rxrg	missense_variant	to chemical stimulus
		neuron migration;protein binding;establishment of cell polarity;microtubule
Sdccag8	NMD_transcript_variant,missense_variant	organizing center organization; tube formation; centrosome organization
Sde2	missense_variant	molecular_function;biological_process
		succinate dehydrogenase activity;tricarboxylic acid cycle;mitochondrial
		electron transport, succinate to ubiquinone;transport;electron carrier
	intron_variant,missense_variant,splice_re	activity;oxidoreductase activity, acting on the CH-CH group of donors;metal
Sdhc	gion_variant	ion binding;oxidation-reduction process
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		molecular_function;transport;endoplasmic reticulum
		organization;peroxisome organization;positive regulation of gene
		expression; protein transport; vesicle-mediated transport; peroxisome
	intron_variant,missense_variant,splice_re	fission;COPII vesicle coating;positive regulation of protein exit from
Sec16b	gion_variant	endoplasmic reticulum; protein localization to endoplasmic reticulum
		adaptive immune response;immune system process;protein binding;peptidyl-
		tyrosine phosphorylation;regulation of natural killer cell activation;innate
		immune response;negative regulation of natural killer cell mediated
	intron_variant,missense_variant,splice_re	cytotoxicity;positive regulation of natural killer cell mediated
Sh2d1b2	gion_variant	cytotoxicity;positive regulation of peptidyl-tyrosine phosphorylation
	NMD_transcript_variant,feature_elongatio	
	n,feature_truncation,intron_variant,splice	protein binding;spermatogenesis;cell differentiation;positive regulation of
Shcbp1l	_region_variant	chromosome organization
		natural killer cell differentiation;natural killer cell proliferation;leukocyte
		chemotaxis involved in inflammatory response; adaptive immune
		response;myeloid dendritic cell activation involved in immune
		response;immune system process;negative regulation of T cell cytokine
		production;receptor activity;protein binding;phagocytosis;cell
		adhesion; positive regulation of macrophage chemotaxis; regulation of vesicle
		fusion;negative regulation of interleukin-12 production;negative regulation
		of interleukin-6 production; negative regulation of tumor necrosis factor
		production;T-helper 1 cell cytokine production;positive regulation of
		activated T cell proliferation; identical protein binding; innate immune
		response; positive regulation of JNK cascade; lymphocyte activation; regulation
		of catalytic activity; positive regulation of ERK1 and ERK2 cascade; negative
		regulation of interferon-gamma secretion; positive regulation of interferon-
	intron_variant,non_coding_transcript_vari	
Slamf1	ant,splice_region_variant	regulation of dendritic cell chemotaxis
Sidiffic	and spines_region_variant	natural killer cell differentiation;natural killer cell proliferation;adaptive
		immune response;immune system process;positive regulation of interferon-
		gamma production;positive regulation of interleukin-17 production;innate
	feature_truncation,intron_variant,splice_r	immune response; positive regulation of natural killer cell mediated
Slamf6	egion_variant,synonymous_variant	cytotoxicity;T-helper 17 cell lineage commitment
Sidiffio	egion_variant,3ynonymous_variant	adaptive immune response;immune system process;protein
Slamf7	missense variant	binding;regulation of natural killer cell activation;innate immune response
Sidiliii	inissense_variant	leukocyte chemotaxis involved in inflammatory response;receptor
		activity;negative regulation of macrophage chemotaxis;regulation of
		NAD(P)H oxidase activity;cellular response to drug;defense response to
		bacterium;identical protein binding;regulation of kinase activity;negative
		regulation of respiratory burst involved in inflammatory response; negative
	intron variant missansa variant salica sa	regulation of monocyte chemotaxis;phagosome acidification;negative
Clamfo	intron_variant,missense_variant,splice_re	regulation of neutrophil migration;negative regulation of dendritic cell
Slamf8	gion_variant	chemotaxis
Slamf9	missense_variant	molecular_function;biological_process
		nuclear-transcribed mRNA catabolic process, nonsense-mediated
		decay;ribonuclease activity;mRNA export from nucleus;telomere
		maintenance via telomerase; telomeric DNA binding; ribonucleoprotein
	feature_truncation,intron_variant,missens	complex binding;regulation of RNA stability;protein phosphatase 2A
Smg7	e_variant,splice_region_variant	binding;telomerase RNA binding

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		RNA polymerase II core promoter sequence-specific DNA binding;RNA
		polymerase II core binding;RNA polymerase II intronic transcription
		regulatory region sequence-specific DNA binding;protein binding;nucleosome
		assembly;negative regulation of protein kinase activity;methyltransferase
		activity;myotube cell development;covalent chromatin
		modification;transferase activity;histone-lysine N-methyltransferase
		activity;methylation;positive regulation of peptidyl-serine
	intron_variant,missense_variant,non_codi	phosphorylation;histone lysine methylation;establishment of protein
	ng_transcript_variant,splice_region_varian	localization;positive regulation of transcription from RNA polymerase II
Smyd3	t	promoter;metal ion binding;cellular response to dexamethasone stimulus
		fatty-acyl-CoA binding;sterol O-acyltransferase activity;lipid metabolic
		process;steroid metabolic process;cholesterol metabolic process;O-
		acyltransferase activity;macrophage derived foam cell
		differentiation;cholesterol storage;cholesterol binding;transferase
		activity;transferase activity, transferring acyl groups;cholesterol efflux;very-
		low-density lipoprotein particle assembly;cholesterol
	intron variant missense variant non codi	esterification;cholesterol O-acyltransferase activity;cholesterol
		homeostasis; positive regulation of amyloid precursor protein biosynthetic
Soat1	t	process
Joaci		lymphocyte homeostasis;actin binding;calcium ion binding;porphyrin-
		containing compound biosynthetic process; plasma membrane
	feature elegation feature truncation int	
		organization; regulation of cell shape; actin cytoskeleton
		organization;hemopoiesis;positive regulation of protein binding;positive
		regulation of T cell proliferation;metal ion binding;protein
Spta1	ynonymous_variant	heterodimerization activity;actin filament capping
		ossification;molecular_function;multicellular organism development;positive
	intron_variant,missense_variant,splice_re	regulation of collagen biosynthetic process; positive regulation of osteoblast
Suco	gion_variant	differentiation;regulation of bone remodeling
		molecular_function;regulation of complement activation;negative regulation
	intron_variant,missense_variant,splice_re	of complement activation, alternative pathway;negative regulation of
Susd4	gion_variant	complement activation, classical pathway
	NMD_transcript_variant,intron_variant,mi	
Swt1	ssense_variant,splice_region_variant	molecular_function;transcription, DNA-templated
_		DNA binding;protein binding;transcription, DNA-templated;regulation of
Taf1a	e_variant,splice_region_variant	transcription, DNA-templated;transcription from RNA polymerase I promoter
		molecular_function;multicellular organism
		development;spermatogenesis;spermatid development;cell differentiation;P
Tdrd5	e_variant,splice_region_variant	granule organization;DNA methylation involved in gamete generation
Tex35	missense_variant	molecular_function;biological_process
		positive regulation of cytokine production; toll-like receptor signaling
		pathway; immune system process; MyD88-dependent toll-like receptor
		signaling pathway;receptor activity;transmembrane signaling receptor
		activity;interleukin-1 receptor binding;protein binding;inflammatory
		response;signal transduction;positive regulation of interleukin-8
		production; positive regulation of toll-like receptor signaling pathway; toll-like
	feature_truncation,frameshift_variant,intr	receptor 5 signaling pathway; defense response to bacterium; innate immune
	l e e e e e e e e e e e e e e e e e e e	response; positive regulation of nitric oxide biosynthetic process; regulation of
Tlr5	variant	cytokine secretion; defense response to Gram-negative bacterium
	NMD_transcript_variant,feature_elongatio	
		nucleotide binding;molecular_function;transport;ion
Tmem63a	egion_variant,synonymous_variant	transport;biological_process
	intron_variant,missense_variant,splice_re	
Tmem9	gion_variant	 molecular_function;transport;biological_process
memb	Ipion_variant	inioicealar_ranetion,transport,biological_process

	intron_variant,missense_variant,splice_re	integrin binding;cell-matrix adhesion;axonogenesis;cell growth;cell
Tnn	gion_variant	migration;identical protein binding
		skeletal muscle contraction; actin binding; regulation of muscle
		contraction;transition between fast and slow fiber;metal ion
	intron variant,non coding transcript vari	binding;ventricular cardiac muscle tissue morphogenesis;cardiac muscle
Tnni1	ant,splice_region_variant	contraction
		actin binding;structural constituent of cytoskeleton;tropomyosin
		binding;muscle contraction;regulation of muscle contraction;heart
		development;regulation of heart contraction;ATPase activity;muscle filament
		 sliding;troponin C binding;protein binding, bridging;troponin I
		binding; negative regulation of ATPase activity; positive regulation of ATPase
		activity;regulation of muscle filament sliding speed;sarcomere
	feature_elongation,intron_variant,missens	organization; protein heterooligomerization; response to calcium ion; actin
	e_variant,splice_donor_variant,splice_regi	crosslink formation; atrial cardiac muscle tissue morphogenesis; ventricular
Tnnt2	on_variant	cardiac muscle tissue morphogenesis; cardiac muscle contraction
		integrin binding;cell adhesion;neuron cell-cell adhesion;negative regulation
		of cell adhesion; associative learning; negative regulation of neuron projection
		development; telencephalon cell migration; negative regulation of cell-cell
		adhesion;extracellular matrix organization;negative regulation of axon
		extension;locomotory exploration behavior;sphingolipid binding;negative
		regulation of axon extension involved in regeneration;regulation of
		neurogenesis; modulation of synaptic transmission; negative regulation of
		synaptic transmission;synapse organization;neuromuscular process
		controlling balance; positive regulation of synaptic transmission,
		glutamatergic;positive regulation of transmission of nerve impulse;long-term
Tnr	missense_variant	synaptic potentiation
	NMD_transcript_variant,feature_elongatio	
	n,frameshift_variant,intron_variant,misse	
	nse_variant,non_coding_transcript_exon_	ATPase activator activity; protein binding; lamin binding; cytoskeletal protein
	variant,non_coding_transcript_variant,spli	binding;positive regulation of ATPase activity;protein localization to
Tor1aip1	ce_region_variant,synonymous_variant	nucleus;ATPase binding;nuclear membrane organization
		ATPase activator activity;protein binding;endoplasmic reticulum
		organization;positive regulation of ATPase activity;ATPase binding;protein
Tor1aip2	missense_variant	localization to nuclear envelope
- 0		nucleotide binding;3-dehydroquinate dehydratase activity;protein
Tor3a	NMD_transcript_variant,missense_variant	binding;ATP binding;ATPase activity
		tRNA binding;RNA binding;tRNA (guanine-N2-)-methyltransferase
	NAC A CONTRACTOR OF THE CONTRA	activity;behavior;tRNA processing;methyltransferase activity;adult
T141		locomotory behavior;transferase activity;adult behavior;methylation;poly(A)
Trmt1l	ssense_variant,splice_region_variant	RNA binding;metal ion binding
		immune system development;RNA binding;smoothened signaling
Troug	missansa yariant	pathway;response to UV;cell projection organization;U2 snRNA binding;misfolded RNA binding;metal ion binding;cilium assembly
Trove2	missense_variant	p53 binding;apoptotic process;cell cycle;central nervous system
		development;heart development;embryo development ending in birth or egg
		hatching; response to ionizing radiation; SH3 domain binding; identical protein
	facture truncation introductions	binding;NF-kappaB binding;intrinsic apoptotic signaling pathway by p53 class
TrnE2hn2		mediator; intrinsic apoptotic signaling pathway; positive regulation of
Trp53bp2	e_variant,splice_region_variant	execution phase of apoptosis; positive regulation of neuron death
	missonso variant salica ragion variant av	tRNA-intron endonuclease activity;molecular_function;tRNA splicing, via
Toon1E		endonucleolytic cleavage and ligation;mRNA processing;tRNA
Tsen15	nonymous_variant	processing;biological_process

		UDP-N-acetylglucosamine diphosphorylase activity;UDP-N-acetylglucosamine
		metabolic process;UDP-N-acetylglucosamine biosynthetic process;metabolic
	ranscript_variant,splice_region_variant,sy	process;transferase activity;nucleotidyltransferase activity;carbohydrate
Uap1	nonymous_variant	binding;identical protein binding;uridylyltransferase activity
	NMD_transcript_variant,intron_variant,no	
	n_coding_transcript_variant,splice_region	protein binding;response to endoplasmic reticulum stress;UFM1 transferase
Ufc1	_variant	activity;protein ufmylation;protein K69-linked ufmylation
		positive regulation of transcription from RNA polymerase II promoter by
		glucose;response to hypoxia;DNA binding;double-stranded DNA
		binding;transcription factor activity, sequence-specific DNA
		binding;transcription factor activity, RNA polymerase II distal enhancer
		sequence-specific binding;protein binding;glucose metabolic
		process;transcription, DNA-templated;regulation of transcription, DNA-
		templated;transcription from RNA polymerase II promoter;response to
		UV;late viral transcription;enzyme binding;protein kinase binding;cellular
		response to insulin stimulus; protein homodimerization activity; histone
		deacetylase binding;bHLH transcription factor binding;sequence-specific DNA
		binding;positive regulation of transcription, DNA-templated;positive
		regulation of transcription from RNA polymerase II promoter;protein
Usf1	inframe_deletion	heterodimerization activity;protein dimerization activity;lipid homeostasis
		transcription coactivator activity; thiol-dependent ubiquitin-specific protease
		activity;transcription, DNA-templated;regulation of transcription, DNA-
		templated;proteolysis;ubiquitin-dependent protein catabolic
		process;peptidase activity;cysteine-type peptidase activity;covalent
		chromatin modification;histone deubiquitination;protein
		deubiquitination;hydrolase activity;NEDD8-specific protease activity;neuron
	NMD_transcript_variant,missense_variant	projection development;thiol-dependent ubiquitinyl hydrolase
Usp21	,splice_acceptor_variant	activity; positive regulation of transcription, DNA-templated; metal ion binding

polarity pathway involved in heart morphogenesis; cochlea development; cochlea morphogenesis; establishment of epithelial cell polarity; regulation of establishment of planar polarity; establishment of planar polarity; regulation of establishment of planar polarity; pathway involved in neural tube closure; planar cell polarity pathway involved in axon guidance; non-motile cilium assembly Vmn1r1 missense_variant molecular_function; sensory perception of chemical stimulus NMD_transcript_variant, feature_elongatio			
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Wdr64 intron_variant,splice_region_variant molecular_function;biological_process	Wdr64	intron_variant,splice_region_variant	molecular_function;biological_process
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