

Chr1_QTLs_D1Mit498-D1Mit361_Genes_protein_altering_variants		
Gene	Variant type(s)	Gene ontology terms
2310009B15Rik	missense_variant	molecular_function;biological_process
3110045C21Rik	feature_elongation,intron_variant,non_coding_transcript_variant,splice_region_variant	molecular_function;biological_process
4930500M09Rik	inframe_insertion,missense_variant	molecular_function;biological_process
4930558K02Rik	missense_variant	molecular_function;biological_process
5730559C18Rik	NMD_transcript_variant,missense_variant	molecular_function;biological_process
Abl2	feature_truncation,missense_variant,splice_donor_variant	behavior;protein kinase activity;protein tyrosine kinase activity;non-membrane spanning protein tyrosine kinase activity;protein binding;ATP binding;protein phosphorylation;phagocytosis;substrate-dependent cell migration, cell extension;actin filament organization;cell adhesion;epidermal growth factor receptor signaling pathway;positive regulation of cytosolic calcium ion concentration;learning;adult walking behavior;visual learning;post-embryonic development;regulation of autophagy;positive regulation of phospholipase C activity;positive regulation of neuron projection development;kinase activity;phosphorylation;neuron remodeling;cell migration;transferase activity;peptidyl-tyrosine phosphorylation;cerebellum morphogenesis;negative regulation of cell-cell adhesion;reproductive process;actin cytoskeleton organization;regulation of endocytosis;manganese ion binding;regulation of cell adhesion;neuron differentiation;auditory behavior;positive regulation of protein binding;cellular protein localization;negative regulation of Rho protein signal transduction;multicellular organism growth;exploration behavior;peptidyl-tyrosine autophosphorylation;regulation of cell proliferation;positive regulation of I-kappaB kinase/NF-kappaB signaling;innate immune response;alpha-beta T cell differentiation;metal ion binding;platelet-derived growth factor receptor signaling pathway;dendrite morphogenesis;neuromuscular process controlling balance;actin filament bundle assembly;positive regulation of oxidoreductase activity;Bergmann glial cell differentiation;neuroepithelial cell differentiation;positive regulation of ERK1 and ERK2 cascade;cellular response to retinoic acid;cardiovascular system development;dendritic spine maintenance;positive regulation of interleukin-2 secretion;positive regulation of interferon-gamma secretion;regulation of extracellular matrix organization;positive regulation of Wnt signaling pathway, planar cell polarity pathway;negative regulation of endothelial cell apoptotic process
Acbd3	missense_variant	fatty-acyl-CoA binding;lipid metabolic process;steroid biosynthetic process;transport;protein kinase A regulatory subunit binding
Ackr1	missense_variant	signal transducer activity;transmembrane signaling receptor activity;G-protein coupled receptor activity;inflammatory response;signal transduction;G-protein coupled receptor signaling pathway;chemokine binding;C-C chemokine binding;regulation of chemokine production;chemokine-mediated signaling pathway
Adamts4	feature_elongation,frameshift_variant,missense_variant	protease binding;metalloendopeptidase activity;protein binding;proteolysis;peptidase activity;metallopeptidase activity;zinc ion binding;hydrolase activity;defense response to bacterium;metal ion binding
Ahctf1	NMD_transcript_variant,inframe_deletion,missense_variant	cytokinesis;DNA binding;transcription factor activity, sequence-specific DNA binding;transcription, DNA-templated;regulation of transcription, DNA-templated;transport;cell cycle;mitotic nuclear division;multicellular organism development;protein transport;hemopoiesis;mRNA transport;nuclear pore complex assembly;cell division

Aida	intron_variant,missense_variant,splice_region_variant	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 regulation of JNK cascade;determination of ventral identity;negative regulation of determination of dorsal identity
Aim2	5_prime_UTR_variant,intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant	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 drug;identical protein binding;innate immune response;interleukin-1 beta secretion;positive regulation of interleukin-1 beta secretion;positive regulation of NF-kappaB transcription factor activity;pyroptosis;positive regulation of cysteine-type endopeptidase activity
Aldh9a1	intron_variant,splice_region_variant	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 activity;NAD binding;oxidation-reduction process
Alyref2	missense_variant	nucleotide binding;nucleic acid binding;single-stranded DNA binding;RNA binding;mRNA processing;transport;RNA splicing;mRNA transport
Angptl1	missense_variant	receptor binding;transmembrane receptor protein tyrosine kinase signaling pathway
Apcs	intron_variant,splice_region_variant	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 metabolic process

Apoa2	missense_variant	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 lipoprotein particle receptor binding
ARHGAP30	feature_truncation,intron_variant,missense_variant,splice_region_variant	GTPase activator activity;signal transduction;small GTPase mediated signal transduction
Ascl5	missense_variant	RNA polymerase II regulatory region sequence-specific DNA binding;transcription factor activity, sequence-specific DNA binding;regulation of transcription from RNA polymerase II promoter
Aspm	feature_elongation,feature_truncation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	neuron migration;positive regulation of neuroblast proliferation;calmodulin binding;cell cycle;spindle organization;mitotic nuclear division;spermatogenesis;brain development;male gonad development;forebrain 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 maintenance
Atf6	intron_variant,missense_variant,splice_region_variant,synonymous_variant	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 transcription from RNA polymerase II promoter in response to endoplasmic reticulum stress

Atp1a2	feature_elongation,feature_truncation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	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 contraction;negative regulation of calcium ion transmembrane transport;negative regulation of calcium:sodium antiporter activity;response to glycoside;steroid hormone binding
Atp1a4	feature_truncation,intron_variant,missense_variant,splice_region_variant	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 homeostasis;flagellated sperm motility;regulation of cellular pH;sodium ion export from cell;regulation of membrane potential;metal ion binding
Axdnd1	feature_truncation,intron_variant,missense_variant,splice_region_variant	molecular_function;biological_process
BC026585	intron_variant,missense_variant,splice_region_variant	zinc ion binding;oxidoreductase activity;oxidation-reduction process
Bpnt1	feature_elongation,intron_variant,missense_variant,splice_region_variant	magnesium ion binding;inositol-1,4-bisphosphate 1-phosphatase activity;nucleobase-containing compound metabolic process;3'(2'),5'-bisphosphate nucleotidase activity;hydrolase activity;phosphatidylinositol phosphorylation;metal ion binding
Brox	missense_variant	molecular_function;biological_process
C130074G19Rik	missense_variant	molecular_function;biological_process
Cacna1s	intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	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 adaptation;metal ion binding;skeletal muscle fiber development;muscle cell development;transmembrane transport;calcium ion transmembrane transport;membrane depolarization during action potential
Cadm3	feature_truncation,intron_variant,non_coding_transcript_variant,splice_region_variant	receptor activity;receptor binding;protein binding;cell adhesion;homophilic cell adhesion via plasma membrane adhesion molecules;heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules;cell recognition;protein localization;protein homodimerization activity;cell adhesion molecule binding
Camsap2	intron_variant,missense_variant,splice_region_variant	microtubule cytoskeleton organization;protein binding;calmodulin binding;microtubule binding;spectrin binding;neuron projection development;regulation of organelle organization;microtubule minus-end binding

Capn2	feature_elongation,intron_variant,splice_region_variant	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 organization;proteolysis involved in cellular protein catabolic process;cellular response to amino acid stimulus
Capn8	missense_variant,splice_region_variant,synonymous_variant	calcium-dependent cysteine-type endopeptidase activity;calcium ion binding;proteolysis;digestion;peptidase activity;cysteine-type peptidase activity;hydrolase activity;metal ion binding
Casq1	inframe_deletion,inframe_insertion,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	calcium ion binding;regulation of muscle contraction;endoplasmic reticulum organization;response to heat;regulation of release of sequestered calcium ion into cytosol by sarcoplasmic reticulum;regulation of skeletal muscle contraction by regulation of release of sequestered calcium ion;sarcomere organization;metal ion binding;protein polymerization;regulation of sequestering of calcium ion
Ccdc121	missense_variant	molecular_function;biological_process
Ccdc185	inframe_insertion,missense_variant	molecular_function;biological_process
Cd244	feature_elongation,intron_variant,missense_variant,splice_region_variant	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 interferon-gamma secretion;positive regulation of interleukin-8 secretion;positive regulation of CD8-positive, alpha-beta T cell proliferation
Cd48	missense_variant	regulation of adaptive immune response;antigen binding;receptor activity;protein binding;signal transduction;T cell activation;mast cell activation
Cd84	missense_variant	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 secretion;regulation of store-operated calcium entry
Cdc42bpa	feature_elongation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	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 reorganization;intracellular signal transduction;identical protein binding;metal ion binding;regulation of small GTPase mediated signal transduction

Cdc73	NMD_transcript_variant,feature_elongation,feature_truncation,frameshift_variant,intron_variant,missense_variant,splice_region_variant	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 from RNA polymerase II promoter;negative regulation of fibroblast proliferation;negative regulation of epithelial cell proliferation;cellular response to lipopolysaccharide;negative regulation of G1/S transition of mitotic cell cycle
Cep170	intron_variant,missense_variant,splice_region_variant	molecular_function;biological_process
Cep350	feature_truncation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	molecular_function;biological_process
Cfhr1	missense_variant,stop_gained	molecular_function;biological_process
Chml	missense_variant	GDP-dissociation inhibitor activity;GTPase activator activity;intracellular protein transport;small GTPase mediated signal transduction;oxidoreductase activity;Rab GTPase binding;protein geranylgeranylation;oxidation-reduction process
Cnih3	intron_variant,splice_region_variant	transport;channel regulator activity;synaptic transmission, glutamatergic;regulation of membrane potential;localization within membrane;regulation of alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionate selective glutamate receptor activity
Cnih4	intron_variant,splice_acceptor_variant,splice_region_variant	transport;ER to Golgi vesicle-mediated transport;protein transport;vesicle-mediated transport;CCR5 chemokine receptor binding
Cnst	missense_variant	protein binding;negative regulation of phosphatase activity;phosphatase binding;positive regulation of Golgi to plasma membrane protein transport;connexin binding
Colgalt2	NMD_transcript_variant,missense_variant	molecular_function;biological_process;transferase activity;transferase activity, transferring glycosyl groups;procollagen galactosyltransferase activity
Copa	NMD_transcript_variant,feature_elongation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	hormone activity;structural molecule activity;transport;intracellular protein transport;ER to Golgi vesicle-mediated transport;retrograde vesicle-mediated transport, Golgi to ER;intra-Golgi vesicle-mediated transport;protein transport;vesicle-mediated transport;pancreatic juice secretion
Crb1	missense_variant	calcium ion binding;protein binding;plasma membrane organization;eye photoreceptor cell development;membrane organization

Crp	missense_variant	complement component C1q binding;calcium ion binding;acute-phase response;complement activation, classical pathway;positive regulation of gene expression;negative regulation of macrophage derived foam cell differentiation;negative regulation of lipid storage;regulation of low-density lipoprotein particle clearance;cholesterol binding;low-density lipoprotein particle binding;negative regulation of superoxide anion generation;positive regulation of superoxide anion generation;wound healing;protein homodimerization activity;positive regulation of nitric oxide biosynthetic process;negative regulation of vasodilation;metal ion binding;low-density lipoprotein particle receptor binding;protein polymerization;cellular response to calcium ion;positive regulation of dendrite development;regulation of interleukin-8 secretion
Dars2	missense_variant	nucleotide binding;nucleic acid binding;aminoacyl-tRNA ligase activity;aspartate-tRNA ligase activity;ATP binding;translation;tRNA aminoacylation for protein translation;ligase activity;protein homodimerization activity;tRNA aminoacylation;aspartate-tRNA(Asn) ligase activity;mitochondrial asparaginyl-tRNA aminoacylation
Dcaf8	splice_region_variant,synonymous_variant	molecular_function;biological_process
Ddr2	intron_variant,missense_variant,splice_region_variant	nucleotide binding;ossification;endochondral bone growth;protein kinase activity;protein tyrosine kinase activity;transmembrane receptor protein tyrosine kinase activity;collagen binding;ATP binding;protein phosphorylation;transmembrane receptor protein tyrosine kinase signaling pathway;positive regulation of cell proliferation;positive regulation of fibroblast migration;kinase activity;phosphorylation;transferase activity;peptidyl-tyrosine phosphorylation;collagen fibril organization;regulation of bone mineralization;biomineral tissue development;chondrocyte proliferation;protein tyrosine kinase collagen receptor activity;collagen-activated tyrosine kinase receptor signaling pathway;positive regulation of osteoblast differentiation;positive regulation of protein kinase activity;protein autophosphorylation;positive regulation of fibroblast proliferation;positive regulation of sequence-specific DNA binding transcription factor activity;positive regulation of extracellular matrix disassembly
Ddx59	missense_variant	nucleotide binding;nucleic acid binding;RNA binding;ATP-dependent RNA helicase activity;helicase activity;ATP binding;RNA secondary structure unwinding;hydrolase activity;metal ion binding
Dennd1b	NMD_transcript_variant,intron_variant,splice_region_variant	guanyl-nucleotide exchange factor activity;transport;protein transport;Rab guanyl-nucleotide exchange factor activity;Rab GTPase binding;endocytic recycling;T-helper 2 cell cytokine production;positive regulation of GTPase activity;regulation of immune response;T cell receptor signaling pathway
Dhx9	NMD_transcript_variant,feature_elongation,intron_variant,splice_region_variant	nucleotide binding;RNA polymerase II transcription factor binding;osteoblast differentiation;nucleic acid binding;DNA binding;RNA binding;ATP-dependent 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;CRD-mediated mRNA stabilization;protein localization to cytoplasmic stress granule
Disp1	intron_variant,missense_variant,splice_region_variant	smoothed signaling pathway;patched ligand maturation;multicellular organism development;determination of left/right symmetry;pattern specification process;embryonic pattern specification;dorsal/ventral pattern formation;peptide transporter activity;peptide transport;diaphragm development
Dnah14	intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	molecular_function;biological_process

Dusp10	intron_variant,splice_region_variant	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 involved in inflammatory response;regulation of brown fat cell differentiation
Dusp12	3_prime_UTR_variant,NMD_transcript_variant,intron_variant,missense_variant,splice_region_variant	phosphoprotein phosphatase activity;protein dephosphorylation;protein tyrosine/serine/threonine phosphatase activity;zinc ion binding;dephosphorylation;phosphatase activity;kinase binding;positive regulation of glucokinase activity
Enah	inframe_deletion,intron_variant,missense_variant,splice_region_variant	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 polymerization or depolymerization;SH3 domain binding;actin cytoskeleton organization;cell differentiation;WW domain binding
Ephx1	5_prime_UTR_variant,intron_variant,missense_variant,splice_region_variant	catalytic activity;epoxide hydrolase activity;cellular aromatic compound metabolic process;response to toxic substance;response to organic cyclic compound;hydrolase activity;aromatic compound catabolic process;enzyme binding;cis-stilbene-oxide hydrolase activity;diol biosynthetic process
Eprs	intron_variant,missense_variant,splice_region_variant	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 translation;RNA stem-loop binding;tRNA aminoacylation;GTPase binding;cellular response to interferon-gamma
Exo1	feature_truncation,intron_variant,splice_region_variant	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;isotype switching;metal ion binding;flap endonuclease activity;meiotic cell cycle;double-stranded DNA 5'-3' exodeoxyribonuclease activity;nucleic acid phosphodiester bond hydrolysis
F11r	feature_elongation,feature_truncation,intron_variant,non_coding_transcript_variant,splice_region_variant	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 membrane;establishment of endothelial intestinal barrier;regulation of membrane permeability;cadherin binding involved in cell-cell adhesion;regulation of actin cytoskeleton reorganization
F13b	missense_variant	blood coagulation;hemostasis



Fam129a	NMD_transcript_variant,inframe_insertion,missense_variant	negative regulation of protein phosphorylation;positive regulation of protein phosphorylation;molecular_function;regulation of translation;response to endoplasmic reticulum stress;positive regulation of translation
Fam163a	missense_variant	molecular_function;biological_process
FasI	missense_variant	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 endothelial cell apoptotic process
Fbxo28	feature_truncation,intron_variant,splice_region_variant	molecular_function;biological_process
Fcgr1a	missense_variant	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;IgE receptor activity;IgE 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-mediated signaling
Fcgr2b	missense_variant	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 molecule of bacterial origin
Fcgr3	intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	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 pathway;IgG receptor activity;IgG binding;neutrophil chemotaxis;positive regulation of tumor necrosis factor biosynthetic process;antigen processing and presentation of exogenous peptide antigen via MHC class I;mast cell activation;positive regulation of phagocytosis;regulation of immune response

Fcgr4	intron_variant,missense_variant,splice_region_variant	IgE receptor activity;IgG receptor activity;neutrophil activation;positive regulation of bone resorption;regulation of sensory perception of pain;cellular response to lipopolysaccharide
Fcrl6	missense_variant	biological_process;protein phosphatase binding
Fcrla	NMD_transcript_variant,feature_truncation,inframe_deletion,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	protein binding;cell differentiation
Fcrlb	intron_variant,missense_variant,splice_region_variant	molecular_function;negative regulation of immune response
Fh1	NMD_transcript_variant,intron_variant,missense_variant,splice_region_variant	catalytic activity;fumarate hydratase activity;tricarboxylic acid cycle;fumarate metabolic process;malate metabolic process;lyase activity;homeostasis of number of cells within a tissue;protein tetramerization
Fmn2	intron_variant,missense_variant,splice_region_variant,synonymous_variant	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 chromosome segregation;formin-nucleated actin cable assembly;cellular response to hypoxia
Gas5	feature_truncation,intron_variant,non_coding_transcript_variant,splice_region_variant	molecular_function;biological_process
Glx2	NMD_transcript_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant	transport;electron carrier activity;response to organic substance;protein disulfide oxidoreductase activity;response to hydrogen peroxide;cell redox homeostasis;metal ion binding;iron-sulfur cluster binding;2 iron, 2 sulfur 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
Gm1305	intron_variant,missense_variant,splice_region_variant	microtubule motor activity;microtubule-based movement;ATPase activity;cytoskeleton-dependent intracellular transport
Gm2061	feature_truncation,intron_variant,non_coding_transcript_variant,splice_region_variant	molecular_function;biological_process
Gm4788	intron_variant,missense_variant,splice_region_variant	molecular_function;biological_process
Gpr25	missense_variant	molecular_function;signal transducer activity;G-protein coupled receptor activity;signal transduction;G-protein coupled receptor signaling pathway;biological_process
H3f3a	intron_variant,splice_region_variant	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 growth;histone binding;muscle cell differentiation;oogenesis;negative regulation of chromosome condensation
Hhip12	intron_variant,missense_variant,splice_acceptor_variant,splice_region_variant	molecular_function;catalytic activity;carbohydrate metabolic process;biological_process;oxidoreductase activity, acting on the CH-OH group of donors, quinone or similar compound as acceptor;quinone binding

Hlx	feature_elongation,frameshift_variant,missense_variant	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 growth;enteric nervous system development;animal organ development;embryonic digestive tract morphogenesis
Hmcn1	feature_elongation,intron_variant,missense_variant,splice_region_variant	molecular_function;calcium ion binding;cell cycle;biological_process;cell division
Hsd17b7	missense_variant	3-keto sterol reductase activity;estradiol 17-beta-dehydrogenase activity;prolactin receptor binding;lipid metabolic process;steroid biosynthetic process;cholesterol biosynthetic process;oxidoreductase activity;oxidation-reduction process
Ifi202b	missense_variant	cellular response to interferon-beta
Ifi203	initiator_codon_variant,missense_variant	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 response to interferon-beta;identical protein binding;poly(A) RNA binding
Ifi204	intron_variant,missense_variant,splice_region_variant	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 binding;poly(A) RNA binding;positive regulation of osteoblast differentiation;inner ear development
Ifi205	intron_variant,missense_variant,splice_region_variant	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 binding;cellular response to interferon-beta;identical protein binding;poly(A) RNA binding
Igfn1	NMD_transcript_variant,inframe_deletion,intron_variant,missense_variant,splice_region_variant,stop_gained,synonymous_variant	molecular_function;biological_process
Igsf8	feature_elongation,feature_truncation,intron_variant,missense_variant,splice_region_variant	protein binding;regulation of cell motility
Igsf9	NMD_transcript_variant,missense_variant	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 adhesion

		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 differentiation;positive regulation of Ras protein signal transduction;positive regulation of alpha-beta T cell differentiation;cellular response to calcium ion
Itpkb	intron_variant,missense_variant,splice_region_variant	
Ivns1abp	missense_variant	protein binding;negative regulation of intrinsic apoptotic signaling pathway
Kcnj10	missense_variant	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 transmembrane transport
Kcnj9	intron_variant,splice_region_variant	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 domain binding;regulation of ion transmembrane transport
Kcnt2	missense_variant	voltage-gated potassium channel activity;potassium channel activity;potassium ion transport;calcium-activated potassium channel activity
Kif14	feature_elongation,intron_variant,missense_variant,non_coding_transcript_variant,splice_acceptor_variant,splice_region_variant	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 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 G1/S transition of mitotic cell cycle
Kif21b	NMD_transcript_variant,feature_truncation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	nucleotide binding;microtubule motor activity;ATP binding;microtubule-based movement;microtubule binding;ATPase activity
Klhdhc9	missense_variant	molecular_function;biological_process

Kmo	NMD_transcript_variant,feature_truncation,intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	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 process;quinolinate biosynthetic process;secondary metabolite biosynthetic process;flavin adenine dinucleotide binding;oxidation-reduction process;kynurenine metabolic process;FAD binding
Lad1	intron_variant,missense_variant,non_coding_transcript_variant,splice_donor_variant,splice_region_variant	structural molecule activity;cell-cell adhesion;cadherin binding involved in cell-cell adhesion
Lamc1	intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant	extracellular matrix structural constituent;protein binding;protein complex assembly;cell adhesion;cell migration;extracellular matrix disassembly;neuron projection development;hemidesmosome assembly;substrate adhesion-dependent cell spreading;glycosphingolipid binding
Lbr	feature_truncation,intron_variant,missense_variant,splice_region_variant	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 NADP as acceptor;poly(A) RNA binding;chaperone binding;oxidation-reduction process;chromo shadow domain binding
Lefty1	intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	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 pathway-restricted SMAD protein phosphorylation;cell growth;response to retinoic acid;nodal binding;growth;cell migration involved in gastrulation;regulation of apoptotic process;regulation of MAPK cascade;cell development;SMAD protein signal transduction;negative regulation of nodal signaling pathway;negative regulation of nodal receptor complex assembly
Lefty2	missense_variant	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 cascade;cell development;SMAD protein signal transduction
Lin9	missense_variant,splice_region_variant,synonymous_variant	transcription, DNA-templated;cell cycle;DNA biosynthetic process
Ly9	NMD_transcript_variant,feature_truncation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	adaptive immune response;immune system process;cell adhesion;positive regulation of interleukin-17 production;innate immune response;T-helper 17 cell lineage commitment
Lyplal1	missense_variant	protein depalmitoylation;palmitoyl-(protein) hydrolase activity;hydrolase activity;negative regulation of Golgi to plasma membrane protein transport;carboxylic ester hydrolase activity
Marc1	intron_variant,missense_variant,splice_region_variant	catalytic activity;nitrate reductase activity;oxidoreductase activity;molybdenum ion binding;pyridoxal phosphate binding;nitrate metabolic process;molybdopterin cofactor binding;oxidation-reduction process
Marc2	NMD_transcript_variant,feature_truncation,intron_variant,non_coding_transcript_variant,splice_region_variant	catalytic activity;nitrate reductase activity;oxidoreductase activity;molybdenum ion binding;pyridoxal phosphate binding;nitrate metabolic process;molybdopterin cofactor binding;oxidation-reduction process

Mark1	feature_truncation,intron_variant,missense_variant,splice_region_variant	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 kinase activity;phosphatidic acid binding
Mia3	feature_elongation,inframe_insertion,intron_variant,missense_variant,splice_region_variant	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 into COPII-coated vesicle
Mixl1	missense_variant	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 differentiation;positive regulation of mesoderm development
Mndal	NMD_transcript_variant,missense_variant	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 binding;poly(A) RNA binding
Mptx1	missense_variant	molecular_function;biological_process;metal ion binding
Mpz	feature_elongation,feature_truncation,intron_variant,missense_variant,splice_region_variant,synonymous_variant	protein binding;negative regulation of apoptotic process;cell-cell junction maintenance
Mroh3	intron_variant,missense_variant,splice_region_variant,synonymous_variant	molecular_function;biological_process
Mroh9	intron_variant,splice_region_variant	molecular_function;biological_process
Ncf2	intron_variant,splice_region_variant	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 regulation of blood pressure;Rac GTPase binding
Ncstn	NMD_transcript_variant,missense_variant	myeloid cell homeostasis;endopeptidase activity;protein binding;membrane protein ectodomain proteolysis;Notch signaling pathway;peptidase activity;protein processing;T cell proliferation;positive regulation of catalytic activity;beta-amyloid metabolic process;epithelial cell proliferation

Ndufs2	intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	NADH dehydrogenase activity;transport;response to oxidative stress;NADH dehydrogenase (ubiquinone) activity;oxidoreductase activity;oxidoreductase activity, acting on NAD(P)H;ubiquitin protein ligase binding;metal ion binding;quinone binding;NAD binding;iron-sulfur cluster binding;4 iron, 4 sulfur cluster binding;oxidation-reduction process
Nhlh1	5_prime_UTR_variant,feature_truncation,splice_region_variant	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 development;cell differentiation;positive regulation of transcription from RNA polymerase II promoter;protein dimerization activity
Nit1	missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant	nitrogen compound metabolic process;hydrolase activity;hydrolase activity, acting on carbon-nitrogen (but not peptide) bonds
Nos1ap	intron_variant,missense_variant,non_coding_transcript_variant,splice_donor_variant,splice_region_variant	protease binding;biological_process;PDZ domain binding;nitric-oxide synthase binding;negative regulation of neuron death;regulation of high voltage-gated calcium channel activity;positive regulation of peptidyl-cysteine S-nitrosylation
Nphs2	feature_truncation,intron_variant,missense_variant,splice_region_variant	protein binding;excretion;actin cytoskeleton reorganization
Npl	intron_variant,splice_region_variant	catalytic activity;carbohydrate metabolic process;metabolic process;N-acetylneuraminase lyase activity;lyase activity;N-acetylneuraminase catabolic process;identical protein binding
Nr1i3	NMD_transcript_variant,missense_variant	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 binding
Nuf2	intron_variant,splice_region_variant	molecular_function;cell cycle;mitotic nuclear division;attachment of spindle microtubules to kinetochore;cell division
Nvl	feature_truncation,intron_variant,missense_variant,splice_acceptor_variant,splice_region_variant	nucleotide binding;ATP binding;ribosome biogenesis;poly(A) RNA binding;positive regulation of telomerase activity;preribosome binding
Olfr12b	intron_variant,missense_variant,splice_region_variant	extracellular matrix organization;protein homodimerization activity;extracellular matrix binding
Olfr1406	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr218	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr220	missense_variant	olfactory receptor activity;odorant binding;G-protein coupled receptor signaling pathway;sensory perception of smell
Olfr231	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr248	missense_variant	G-protein coupled receptor activity;olfactory receptor activity;cell surface receptor signaling pathway;G-protein coupled receptor signaling pathway;sensory perception of smell
Olfr414	missense_variant	olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell

Olfr417	missense_variant	G-protein coupled receptor activity;olfactory receptor activity;cell surface receptor signaling pathway;G-protein coupled receptor signaling pathway;sensory perception of smell
Olfr420	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr424	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr427	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr429	missense_variant	olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell
Olfr430	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr432	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Olfr433	missense_variant	transmembrane signaling receptor activity;olfactory receptor activity;G-protein coupled receptor signaling pathway;sensory perception of smell;detection of chemical stimulus involved in sensory perception
Opn3	missense_variant	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 stimulus;cellular response to light stimulus
Parp1	intron_variant,splice_region_variant	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 telomere maintenance via telomere lengthening;cellular response to beta-amyloid;positive regulation of myofibroblast differentiation;negative



Pex19	feature_truncation,intron_variant,non_coding_transcript_variant,splice_region_variant	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 stabilization;ATPase binding;chaperone-mediated protein folding;chaperone-mediated protein transport;establishment of protein localization to peroxisome;negative regulation of lipid binding
Pfdn2	inframe_insertion	protein folding;protein binding involved in protein folding;unfolded protein binding;positive regulation of cytoskeleton organization
Pigm	missense_variant	mannosyltransferase activity;GPI anchor biosynthetic process;transferase activity;transferase activity, transferring glycosyl groups;transferase activity, transferring hexosyl groups
Pkp1	NMD_transcript_variant,intron_variant,splice_region_variant	protein binding;lamin binding;cell adhesion;single organismal cell-cell adhesion;intermediate filament bundle assembly
Pla2g4a	non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	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 process;decidualization;metal ion binding;calcium-dependent phospholipase A2 activity;arachidonic acid secretion;positive regulation of inflammatory response;response to calcium ion;cellular response to antibiotic
Ppox	intron_variant,non_coding_transcript_variant,splice_region_variant	oxygen-dependent protoporphyrinogen oxidase activity;porphyrin-containing compound biosynthetic process;heme biosynthetic process;oxidoreductase activity;protoporphyrinogen IX metabolic process;oxidation-reduction process

		fate specification;somitogenesis;positive regulation of receptor recycling;negative regulation of protein phosphorylation;hair follicle development;hematopoietic progenitor cell differentiation;T cell activation involved in immune response;myeloid leukocyte differentiation;endopeptidase activity;aspartic-type endopeptidase activity;protein binding;proteolysis;membrane protein ectodomain proteolysis;calcium ion transport;negative regulation of epidermal growth factor-activated receptor activity;regulation of epidermal growth factor-activated receptor activity;Notch signaling pathway;Notch receptor processing;learning or memory;memory;peptidase activity;embryo development;protein transport;protein processing;hydrolase activity;dorsal/ventral neural tube patterning;embryonic limb morphogenesis;forebrain development;negative regulation of protein complex assembly;negative regulation of protein binding;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;endoplasmic reticulum calcium ion homeostasis;intracellular signal transduction;locomotion;anagen;amyloid precursor protein catabolic process;positive regulation of apoptotic process;positive regulation of catalytic activity;regulation of protein binding;skin morphogenesis;cellular protein metabolic process;regulation of synaptic plasticity;lung alveolus development;thymus development;brain morphogenesis;beta-amyloid metabolic process;positive regulation of coagulation;T cell receptor signaling pathway;negative regulation of ubiquitin-protein transferase activity;protein maturation;cardiac muscle contraction;neuron cellular homeostasis;negative regulation of extrinsic apoptotic signaling pathway via death domain receptors;positive regulation of extrinsic apoptotic signaling pathway via death domain receptors;negative regulation of protein ubiquitination
Psen2	5_prime_UTR_variant,missense_variant,splice_region_variant	involved in ubiquitin-dependent protein catabolic process;negative regulation of apoptotic signaling pathway
Pycr2	intron_variant,splice_region_variant,synonymous_variant	pyrroline-5-carboxylate reductase activity;proline biosynthetic process;cellular amino acid biosynthetic process;oxidoreductase activity;cellular response to oxidative stress;oxidation-reduction process
Qsox1	intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	protein disulfide isomerase activity;protein folding;negative regulation of macroautophagy;oxidoreductase activity;flavin-linked sulfhydryl oxidase activity;thiol oxidase activity;cell redox homeostasis;oxidation-reduction process
Rab3gap2	intron_variant,missense_variant,splice_region_variant,synonymous_variant	GTPase activator activity;Rab guanyl-nucleotide exchange factor activity;Rab GTPase binding;enzyme regulator activity;regulation of GTPase activity;protein heterodimerization activity;establishment of protein localization to endoplasmic reticulum membrane;positive regulation of protein lipidation;positive regulation of endoplasmic reticulum tubular network organization;positive regulation of autophagosome assembly
Ralgps2	intron_variant,missense_variant,splice_region_variant	molecular_function;guanyl-nucleotide exchange factor activity;small GTPase mediated signal transduction;biological_process;regulation of Ral protein signal transduction
Rasal2	feature_elongation,intron_variant,splice_region_variant	GTPase activator activity;negative regulation of Ras protein signal transduction
Rfwd2	missense_variant	protein binding;zinc ion binding;response to ionizing radiation;protein ubiquitination;ligase activity;positive regulation of proteasomal ubiquitin-dependent protein catabolic process;metal ion binding;ubiquitin protein ligase activity
Rgs16	feature_truncation,intron_variant,missense_variant,splice_acceptor_variant	GTPase activator activity;G-protein coupled receptor signaling pathway;negative regulation of signal transduction;positive regulation of GTPase activity

Rgs4	missense_variant	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-protein coupled receptor protein signaling pathway
Rgs5	intron_variant,splice_region_variant	GTPase activator activity;signal transduction;G-protein coupled receptor signaling pathway;negative regulation of signal transduction;negative regulation of G-protein coupled receptor protein signaling pathway
Rgs7	intron_variant,splice_region_variant,synonymous_variant	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-protein beta-subunit binding;intracellular signal transduction;positive regulation of GTPase activity
Rgs8	intron_variant,splice_region_variant	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 pathway
Rgs11	NMD_transcript_variant,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	GTPase activator activity
Rnasel	intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	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 differentiation;positive regulation of transcription from RNA polymerase II promoter;metal ion binding;defense response to virus;positive regulation of glucose import in response to insulin stimulus
Rnf2	intron_variant,splice_region_variant	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 finger domain binding
Rxrg	missense_variant	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 to chemical stimulus
Sdccag8	NMD_transcript_variant,missense_variant	neuron migration;protein binding;establishment of cell polarity;microtubule organizing center organization;tube formation;centrosome organization
Sde2	missense_variant	molecular_function;biological_process
Sdhc	intron_variant,missense_variant,splice_region_variant	succinate dehydrogenase activity;tricarboxylic acid cycle;mitochondrial electron transport, succinate to ubiquinone;transport;electron carrier activity;oxidoreductase activity, acting on the CH-CH group of donors;metal ion binding;oxidation-reduction process

Sec16b	intron_variant,missense_variant,splice_region_variant	molecular_function;transport;endoplasmic reticulum organization;peroxisome organization;positive regulation of gene expression;protein transport;vesicle-mediated transport;peroxisome fission;COPII vesicle coating;positive regulation of protein exit from endoplasmic reticulum;protein localization to endoplasmic reticulum
Sh2d1b2	intron_variant,missense_variant,splice_region_variant	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 cytotoxicity;positive regulation of natural killer cell mediated cytotoxicity;positive regulation of peptidyl-tyrosine phosphorylation
Shcbp1l	NMD_transcript_variant,feature_elongation,feature_truncation,intron_variant,splice_region_variant	protein binding;spermatogenesis;cell differentiation;positive regulation of chromosome organization
Slamf1	intron_variant,non_coding_transcript_variant,splice_region_variant	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-gamma secretion;negative regulation of CD40 signaling pathway;positive regulation of dendritic cell chemotaxis
Slamf6	feature_truncation,intron_variant,splice_region_variant,synonymous_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 immune response;positive regulation of natural killer cell mediated cytotoxicity;T-helper 17 cell lineage commitment
Slamf7	missense_variant	adaptive immune response;immune system process;protein binding;regulation of natural killer cell activation;innate immune response
Slamf8	intron_variant,missense_variant,splice_region_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 regulation of monocyte chemotaxis;phagosome acidification;negative regulation of neutrophil migration;negative regulation of dendritic cell chemotaxis
Slamf9	missense_variant	molecular_function;biological_process
Smg7	feature_truncation,intron_variant,missense_variant,splice_region_variant	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay;ribonuclease activity;mRNA export from nucleus;telomere maintenance via telomerase;telomeric DNA binding;ribonucleoprotein complex binding;regulation of RNA stability;protein phosphatase 2A binding;telomerase RNA binding

Smyd3	intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	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 phosphorylation;histone lysine methylation;establishment of protein localization;positive regulation of transcription from RNA polymerase II promoter;metal ion binding;cellular response to dexamethasone stimulus
Soat1	intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant	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 esterification;cholesterol O-acyltransferase activity;cholesterol homeostasis;positive regulation of amyloid precursor protein biosynthetic process
Spta1	feature_elongation,feature_truncation,intron_variant,missense_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	lymphocyte homeostasis;actin binding;calcium ion binding;porphyrin-containing compound biosynthetic process;plasma membrane organization;regulation of cell shape;actin cytoskeleton organization;hemopoiesis;positive regulation of protein binding;positive regulation of T cell proliferation;metal ion binding;protein heterodimerization activity;actin filament capping
Suco	intron_variant,missense_variant,splice_region_variant	ossification;molecular_function;multicellular organism development;positive regulation of collagen biosynthetic process;positive regulation of osteoblast differentiation;regulation of bone remodeling
Susd4	intron_variant,missense_variant,splice_region_variant	molecular_function;regulation of complement activation;negative regulation of complement activation, alternative pathway;negative regulation of complement activation, classical pathway
Swt1	NMD_transcript_variant,intron_variant,missense_variant,splice_region_variant	molecular_function;transcription, DNA-templated
Taf1a	feature_elongation,intron_variant,missense_variant,splice_region_variant	DNA binding;protein binding;transcription, DNA-templated;regulation of transcription, DNA-templated;transcription from RNA polymerase I promoter
Tdrd5	feature_truncation,intron_variant,missense_variant,splice_region_variant	molecular_function;multicellular organism development;spermatogenesis;spermatid development;cell differentiation;P granule organization;DNA methylation involved in gamete generation
Tex35	missense_variant	molecular_function;biological_process
Tlr5	feature_truncation,frameshift_variant,intron_variant,missense_variant,splice_region_variant	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 receptor 5 signaling pathway;defense response to bacterium;innate immune response;positive regulation of nitric oxide biosynthetic process;regulation of cytokine secretion;defense response to Gram-negative bacterium
Tmem63a	NMD_transcript_variant,feature_elongation,intron_variant,missense_variant,splice_region_variant,synonymous_variant	nucleotide binding;molecular_function;transport;ion transport;biological_process
Tmem9	intron_variant,missense_variant,splice_region_variant	molecular_function;transport;biological_process

Tnn	intron_variant,missense_variant,splice_region_variant	integrin binding;cell-matrix adhesion;axonogenesis;cell growth;cell migration;identical protein binding
Tnni1	intron_variant,non_coding_transcript_variant,splice_region_variant	skeletal muscle contraction;actin binding;regulation of muscle contraction;transition between fast and slow fiber;metal ion binding;ventricular cardiac muscle tissue morphogenesis;cardiac muscle contraction
Tnnt2	feature_elongation,intron_variant,missense_variant,splice_donor_variant,splice_region_variant	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 organization;protein heterooligomerization;response to calcium ion;actin crosslink formation;atrial cardiac muscle tissue morphogenesis;ventricular cardiac muscle tissue morphogenesis;cardiac muscle contraction
Tnr	missense_variant	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 synaptic potentiation
Tor1aip1	NMD_transcript_variant,feature_elongation,frameshift_variant,intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	ATPase activator activity;protein binding;lamin binding;cytoskeletal protein binding;positive regulation of ATPase activity;protein localization to nucleus;ATPase binding;nuclear membrane organization
Tor1aip2	missense_variant	ATPase activator activity;protein binding;endoplasmic reticulum organization;positive regulation of ATPase activity;ATPase binding;protein localization to nuclear envelope
Tor3a	NMD_transcript_variant,missense_variant	nucleotide binding;3-dehydroquinate dehydratase activity;protein binding;ATP binding;ATPase activity
Trmt1l	NMD_transcript_variant,intron_variant,missense_variant,splice_region_variant	tRNA binding;RNA binding;tRNA (guanine-N2-)-methyltransferase activity;behavior;tRNA processing;methyltransferase activity;adult locomotory behavior;transferase activity;adult behavior;methylation;poly(A) RNA binding;metal ion binding
Trove2	missense_variant	immune system development;RNA binding;smoothed signaling pathway;response to UV;cell projection organization;U2 snRNA binding;misfolded RNA binding;metal ion binding;cilium assembly
Trp53bp2	feature_truncation,intron_variant,missense_variant,splice_region_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 binding;NF-kappaB binding;intrinsic apoptotic signaling pathway by p53 class mediator;intrinsic apoptotic signaling pathway;positive regulation of execution phase of apoptosis;positive regulation of neuron death
Tsen15	missense_variant,splice_region_variant,synonymous_variant	tRNA-intron endonuclease activity;molecular_function;tRNA splicing, via endonucleolytic cleavage and ligation;mRNA processing;tRNA processing;biological_process

Uap1	intron_variant,missense_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant,synonymous_variant	UDP-N-acetylglucosamine diphosphorylase activity;UDP-N-acetylglucosamine metabolic process;UDP-N-acetylglucosamine biosynthetic process;metabolic process;transferase activity;nucleotidyltransferase activity;carbohydrate binding;identical protein binding;uridylyltransferase activity
Ufc1	NMD_transcript_variant,intron_variant,non_coding_transcript_variant,splice_region_variant	protein binding;response to endoplasmic reticulum stress;UFM1 transferase activity;protein ufmylation;protein K69-linked ufmylation
Usf1	inframe_deletion	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 heterodimerization activity;protein dimerization activity;lipid homeostasis
Usp21	NMD_transcript_variant,missense_variant,splice_acceptor_variant	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 projection development;thiol-dependent ubiquitinyl hydrolase activity;positive regulation of transcription, DNA-templated;metal ion binding

		polarity;neural tube closure;hair follicle development;heart looping;outflow tract septum morphogenesis;membranous septum morphogenesis;muscular septum morphogenesis;epicardial cell to mesenchymal cell transition;planar cell polarity pathway involved in axis elongation;protein binding;Rho protein signal transduction;multicellular organism development;anterior/posterior pattern specification;heparan sulfate proteoglycan biosynthetic process;convergent extension involved in neural plate elongation;regulation of Wnt signaling pathway;glomerulus development;regulation of actin cytoskeleton organization;somatic stem cell population maintenance;non-canonical Wnt signaling pathway;cell migration involved in kidney development;post-anal tail morphogenesis;dopaminergic neuron axon guidance;serotonergic neuron axon guidance;wound healing;positive regulation of JUN kinase activity;apical protein localization;establishment or maintenance of epithelial cell apical/basal polarity;somatic stem cell division;establishment of body hair planar orientation;digestive tract morphogenesis;convergent extension involved in axis elongation;convergent extension involved in organogenesis;Wnt signaling pathway, planar cell polarity pathway;inner ear receptor cell development;inner ear receptor stereocilium organization;orthogonal dichotomous subdivision of terminal units involved in lung branching morphogenesis;planar dichotomous subdivision of terminal units involved in lung branching morphogenesis;lateral sprouting involved in lung morphogenesis;cardiac vascular smooth muscle cell differentiation;kidney morphogenesis;planar cell 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 involved in neural tube closure;planar cell polarity pathway involved in neural tube closure;planar cell polarity pathway involved in axon guidance;non-motile cilium assembly
Vangl2	intron_variant,non_coding_transcript_variant,splice_region_variant	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
Wdr26	NMD_transcript_variant,feature_elongation,intron_variant,non_coding_transcript_exon_variant,non_coding_transcript_variant,splice_region_variant	molecular_function;biological_process
Wdr64	intron_variant,splice_region_variant	molecular_function;biological_process
Zfp648	missense_variant	molecular_function;biological_process