

Table S3. Putative gene ontology of 54 genes used in this study.

Gene	Gene ontology	Gene ontology term	Term number
ABCA1	Component	membrane fraction; Golgi apparatus; plasma membrane; integral to plasma membrane; membrane raft; phagocytic vesicle;	GO:0005624; GO:0005794; GO:0005886; GO:0005887; GO:0045121; GO:0045335;
ABCA1	Function	nucleotide binding; protein binding; protein binding; ATP binding; phospholipid binding; phospholipid transporter activity; anion transmembrane transporter activity; cholesterol binding; ATPase activity; cholesterol transporter activity; syntaxin-13 binding; small GTPase binding; apolipoprotein A-I receptor activity;	GO:0001166; GO:0005515; GO:0005515; GO:0005524; GO:0005543; GO:0005548; GO:0008509; GO:0015485; GO:0016887; GO:0017127; GO:0030349; GO:0031267; GO:0034188;
ABCA1	Process	peptide secretion; protein amino acid lipidation; lipid metabolic process; transport; phagocytosis, engulfment; lysosome organization and biogenesis; G-protein coupled receptor protein signaling pathway; steroid metabolic process; cholesterol metabolic process; endosome transport; positive regulation of cAMP biosynthetic process; intracellular cholesterol transport; Cdc42 protein signal transduction; cholesterol efflux; phospholipid efflux; phospholipid efflux; cholesterol homeostasis; reverse cholesterol transport; phospholipid translocation; interleukin-1 beta secretion; phospholipid homeostasis; platelet dense granule organization and biogenesis;	GO:0002790; GO:0006497; GO:0006629; GO:0006810; GO:0006911; GO:0007040; GO:0007186; GO:0008202; GO:0008203; GO:0016197; GO:0030819; GO:0032367; GO:0032488; GO:0033344; GO:0033700; GO:0033700; GO:0042632; GO:0043691; GO:0045332; GO:0050702; GO:0055091; GO:0060155;
ADORA3	Component	plasma membrane; integral to plasma membrane;	GO:0005886; GO:0005887;
ADORA3	Function	rhodopsin-like receptor activity; adenosine receptor activity; G-protein coupled; receptor activity;	GO:0001584; GO:0001609; GO:0004872;
ADORA3	Process	inflammatory response; signal transduction; G-protein coupled receptor protein signaling pathway; activation of adenylate cyclase activity; regulation of heart contraction;	GO:0006954; GO:0007165; GO:0007186; GO:0007190; GO:0008016;
AFF2	Component	nucleus; cytoplasm;	GO:0005634; GO:0005737;
AFF2	Process	brain development; learning and/or memory;	GO:0007420; GO:0007611;
APP	Component	extracellular region; extracellular region; cytoplasm; Golgi apparatus; plasma membrane; integral to plasma membrane; coated pit; cell surface; platelet alpha granule lumen;	GO:0005576; GO:0005576; GO:0005737; GO:0005794; GO:0005886; GO:0005887; GO:0005905; GO:0009986; GO:0031093;
APP	Function	serine-type endopeptidase inhibitor activity; serine-type endopeptidase inhibitor activity; iron ion binding; copper ion binding; heparin binding; zinc ion binding; acetylcholine receptor binding; identical protein binding; metal ion binding;	GO:0004867; GO:0004867; GO:0005506; GO:0005507; GO:0008201; GO:0008270; GO:0031330; GO:0042802; GO:0046872;
APP	Process	cellular copper ion homeostasis; endocytosis; apoptosis; cell adhesion; Notch signaling pathway; neuromuscular process;	GO:0006878; GO:0006897; GO:0006915; GO:0007155; GO:0007219; GO:00050905;
ATXN7	Component	intracellular; nucleus; nucleus; cytoplasm; nuclear matrix;	GO:0005622; GO:0005634; GO:0005634; GO:0005737; GO:0016363;
ATXN7	Function	chromatin binding; protein binding; protein binding; zinc ion binding;	GO:0003682; GO:0005515; GO:0005515; GO:0008270;
ATXN7	Process	transcription; regulation of transcription, DNA-dependent; nuclear organization and biogenesis; visual perception; cell death;	GO:0006350; GO:0006355; GO:0006997; GO:0007601; GO:0008219;
AXIN1	Component	intracellular; nucleus; cytoplasm; cytosol; cytoplasmic membrane-bounded vesicle; lateral plasma membrane; beta-catenin destruction complex;	GO:0005622; GO:0005634; GO:0005737; GO:0005829; GO:0016023; GO:0016328; GO:0030877;
AXIN1	Function	signal transducer activity; protein binding; protein homodimerization activity;	GO:0004871; GO:0005515; GO:0042803;
AXIN1	Process	apoptosis; multicellular organismal development; oocyte axis determination; sensory perception of sound; protein catabolic process; negative regulation of Wnt receptor signaling pathway; negative regulation of cell cycle; positive regulation of JNK cascade; Wnt receptor signaling pathway through beta-catenin;	GO:0006915; GO:0007275; GO:0007309; GO:0007605; GO:0030163; GO:0030178; GO:0045786; GO:0046330; GO:0060070;
BCHE	Component	extracellular region; nuclear envelope lumen; endoplasmic reticulum; membrane;	GO:0005576; GO:0005641; GO:0005783; GO:0016020;
BCHE	Function	beta-amyloid binding; carboxylesterase activity; cholinesterase activity; hydrolase activity; enzyme binding;	GO:0001540; GO:0004091; GO:0004104; GO:0016787; GO:0019899;
BCHE	Process	cocaine metabolic process;	GO:0050783;
BCOR	Component	nucleus;	GO:0005634;
BCOR	Function	transcription corepressor activity; transcription factor binding; histone deacetylase binding;	GO:0003714; GO:0008134; GO:0042826;
BCOR	Process	transcription; chromatin modification; negative regulation of transcription, DNA-dependent;	GO:0006350; GO:0016568; GO:0045892;
BDNF	Component	extracellular region; cytoplasmic membrane-bounded vesicle;	GO:0005576; GO:0016023;
BDNF	Function	growth factor activity; growth factor activity;	GO:0008083; GO:0008083;
BDNF	Process	ureteric bud development; anti-apoptosis; negative regulation of neuroblast proliferation; axon guidance; axon target recognition; learning and/or memory; feeding behavior; neuron recognition; glutamate secretion; dendrite development; regulation of metabolic process; nerve development; mechanoreceptor differentiation; response to drug; fear response; negative regulation of neuron apoptosis; positive regulation of neuron differentiation; regulation of retinal cell programmed cell death; regulation of synaptic plasticity; inner ear development;	GO:0001657; GO:0006916; GO:0007406; GO:0007411; GO:0007412; GO:0007611; GO:0007631; GO:0008038; GO:0014047; GO:0016358; GO:0019222; GO:0021675; GO:0042490; GO:0042493; GO:0042596; GO:0043524; GO:0045666; GO:0046668; GO:0048167; GO:0048839;
BRCA2	Component	nucleus; nucleoplasm; cytoplasm; centrosome; secretory granule; BRCA2-MAGE-D1 complex;	GO:0005634; GO:0005654; GO:0005737; GO:0005813; GO:0030141; GO:0033593;
BRCA2	Function	single-stranded DNA binding; histone acetyltransferase activity; protein binding; transcription activator activity; gamma-tubulin binding;	GO:0003697; GO:0004402; GO:0005515; GO:0016563; GO:0043015;
BRCA2	Process	double-strand break repair via homologous recombination; oocyte maturation; inner cell mass cell proliferation; nucleotide-excision repair; DNA recombination; regulation of transcription, DNA-dependent; DNA damage response, signal transduction by p53 class mediator resulting in transcription of p21 class mediator; regulation of S phase of mitotic cell cycle; male meiosis I; spermatogenesis; brain development; cell aging; female gonad development; response to X-ray; response to UV-C; response to gamma radiation; cytokinesis during cell cycle; response to genistein; negative regulation of mammary gland epithelial cell proliferation; DNA damage response, signal transduction by p53 class mediator resulting in induction of apoptosis; chordate embryonic development; response to estrogen stimulus; positive regulation of mitotic cell cycle; replication fork protection; chromosome organization and biogenesis; centrosome duplication;	GO:0000724; GO:0001156; GO:0001833; GO:0006289; GO:0006310; GO:0006355; GO:0006978; GO:0007090; GO:0007141; GO:0007283; GO:0007420; GO:0007569; GO:0008585; GO:0010165; GO:0010225; GO:0010332; GO:0033205; GO:0033595; GO:0033600; GO:0042771; GO:0043009; GO:0043627; GO:0045931; GO:0048478; GO:0051276; GO:0051298;
CFTR	Component	membrane; integral to membrane; basolateral plasma membrane; apical plasma membrane;	GO:0016020; GO:0016021; GO:0016323; GO:0016324;
CFTR	Function	nucleotide binding; ion channel activity; ATP-binding and phosphorylation-dependent chloride channel activity; chloride channel activity; channel-conductance-controlling ATPase activity; protein binding; ATP binding; ATPase activity; PDZ domain binding; chloride ion binding; ATPase activity, coupled to transmembrane movement of substances;	GO:0000166; GO:0005216; GO:0005224; GO:0005254; GO:0005260; GO:0005515; GO:0005524; GO:0005524; GO:0016887; GO:0030165; GO:0031404; GO:0042626;
CFTR	Process	ion transport; respiratory gaseous exchange;	GO:0006811; GO:0007585;
CHRNA1	Component	plasma membrane; nicotinic acetylcholine-gated receptor-channel complex; integral to membrane; cell junction; neuromuscular junction; postsynaptic membrane;	GO:0005886; GO:0005892; GO:0016021; GO:0030054; GO:0031594; GO:0045211;
CHRNA1	Function	nicotinic acetylcholine-activated cation-selective channel activity; ion channel activity; extracellular ligand-gated ion channel activity; acetylcholine receptor activity;	GO:0004889; GO:0005216; GO:0005230; GO:0015464;
CHRNA1	Process	ion transport; muscle contraction; signal transduction; neuromuscular synaptic transmission; neuromuscular junction development; regulation of membrane potential;	GO:0006811; GO:0006936; GO:0007165; GO:0007274; GO:0007528; GO:0042391;
CNR1	Component	plasma membrane; integral to plasma membrane;	GO:0005886; GO:0005887;
CNR1	Function	receptor activity; cannabinoid receptor activity;	GO:0004872; GO:0004949;
CNR1	Process	signal transduction; G-protein signaling, coupled to cyclic nucleotide second messenger; behavior;	GO:0007165; GO:0007187; GO:0007610;
CREM	Component	nucleus; nucleus; transcription factor complex; cytoplasm; Golgi apparatus;	GO:0005634; GO:0005634; GO:0005667; GO:0005737; GO:0005794;
CREM	Function	transcription factor activity; protein binding; cAMP response element binding protein binding; sequence-specific DNA binding; protein dimerization activity;	GO:0003700; GO:0005515; GO:0008140; GO:0043565; GO:0046983;
CREM	Process	transcription; regulation of transcription, DNA-dependent; regulation of transcription, DNA-dependent; regulation of transcription, DNA-dependent; signal transduction; multicellular organismal development; spermatogenesis; cell differentiation;	GO:0006350; GO:0006355; GO:0006355; GO:0006355; GO:0007165; GO:0007275; GO:0007283; GO:0030154;
DACH1	Component	nucleus;	GO:0005634;
DACH1	Function	nucleotide binding; DNA binding; protein binding;	GO:0000166; GO:0003677; GO:0005515;
DACH1	Process	transcription; regulation of transcription, DNA-dependent; multicellular organismal development;	GO:0006350; GO:0006355; GO:0007275;

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DCTN2	Component	kinetochore; cytoplasm; centrosome; cytoskeleton; dynactin complex; microtubule; membrane; dynein complex; growth cone; nucleus;	GO:0000776; GO:0005737; GO:0005813; GO:0005856; GO:0005869; GO:0005874; GO:0016020; GO:0030286; GO:0030426; GO:0005634;
DCTN2	Function	motor activity; protein binding; DNA binding;	GO:0003774; GO:0005515; GO:0003677;
DCTN2	Process	microtubule-based process; mitosis; cell proliferation;	GO:0007017; GO:0007067; GO:0008283;
DENND5A	Component	Golgi apparatus;	GO:0005794;
DENND5A	Function	Rab GTPase binding; protein binding;	GO:0017137; GO:0005515;
DMRT1	Component	nucleus;	GO:0005634;
DMRT1	Function	transcription factor activity; transcription factor activity; zinc ion binding; metal ion binding;	GO:0003700; GO:0003700; GO:0008270; GO:0046872;
DMRT1	Process	transcription; regulation of transcription, DNA-dependent; multicellular organismal development; sex determination; sex differentiation; male gonad development; cell differentiation;	GO:0006350; GO:0006355; GO:0007275; GO:0007530; GO:0007548; GO:0008584; GO:0030154;
ERC2	Component	cytoplasm; cytoskeleton; synaptosome; cell junction; growth cone; presynaptic membrane; synapse;	GO:0005737; GO:0005856; GO:0019717; GO:0030054; GO:0030426; GO:0042734; GO:0045202;
ERC2	Function	protein binding; protein binding;	GO:0005515; GO:0005515;
FAM123B	Component	nucleus; cytoplasm; plasma membrane;	GO:0005634; GO:0005737; GO:0005886;
FAM123B	Process	Wnt receptor signaling pathway	GO:0016055;
FBN1	Component	microfibril; extracellular region; basement membrane; extracellular space; intracellular; membrane;	GO:0001527; GO:0005576; GO:0005604; GO:0005615; GO:0005622; GO:0016020;
FBN1	Function	transmembrane receptor activity; extracellular matrix structural constituent; extracellular matrix structural constituent; binding; calcium ion binding; calcium ion binding; calcium ion binding; protein binding; zinc ion binding;	GO:0004888; GO:0005201; GO:0005201; GO:0005488; GO:0005509; GO:0005509; GO:0005509; GO:0005515; GO:0008270;
FBN1	Process	skeletal development; heart development; blood coagulation;	GO:0001501; GO:0007507; GO:0007596;
FES	Component	nucleus;	GO:0005634;
FES	Function	nucleotide binding; protein kinase activity; protein tyrosine kinase activity; non-membrane spanning protein tyrosine kinase activity; protein binding; ATP binding; transferase activity;	GO:0000166; GO:0004672; GO:0004713; GO:0004715; GO:0005515; GO:0005524; GO:0016740;
FES	Process	protein amino acid phosphorylation; protein amino acid phosphorylation; multicellular organismal development; cell proliferation;	GO:0006468; GO:0006468; GO:0007275; GO:0008283;
FOXP1	Component	intracellular; nucleus; nucleolus;	GO:0005622; GO:0005634; GO:0005730;
FOXP1	Function	transcription factor activity; RNA polymerase II transcription factor activity; enhancer binding; zinc ion binding; specific transcriptional repressor activity; protein homodimerization activity; sequence-specific DNA binding; metal ion binding; protein heterodimerization activity;	GO:0003700; GO:0003700; GO:0008270; GO:0016566; GO:0042803; GO:0043565; GO:0046872; GO:0046982;
FOXP1	Process	negative regulation of transcription from RNA polymerase II promoter; positive regulation of mesenchymal cell proliferation; pre-B cell differentiation; positive regulation of immunoglobulin production; regulation of transcription, DNA-dependent; heart development; skeletal muscle development; embryonic development; negative regulation of transcription; lung development; immunoglobulin V(D)J recombination; smooth muscle development; positive regulation of epithelial cell proliferation; cardiac muscle cell differentiation;	GO:0000122; GO:0002053; GO:0002329; GO:0002639; GO:0006355; GO:0007507; GO:0007519; GO:0009790; GO:0016481; GO:0030324; GO:0033152; GO:0048745; GO:0050679; GO:0055007;
GHR	Component	extracellular region; plasma membrane; integral to plasma membrane;	GO:0005576; GO:0005886; GO:0005887;
GHR	Function	receptor activity; growth hormone receptor activity; protein binding;	GO:0004872; GO:0004903; GO:0005515;
GHR	Process	skeletal development; endocytosis; growth;	GO:0001501; GO:0006897; GO:0040007;
KCNMA1	Component	voltage-gated potassium channel complex; external side of plasma membrane; membrane; integral to membrane; apical plasma membrane; terminal button; postsynaptic membrane;	GO:0008076; GO:0009897; GO:0016020; GO:0016021; GO:0016324; GO:0043195; GO:0045211;
KCNMA1	Function	magnesium ion binding; catalytic activity; voltage-gated ion channel activity; voltage-gated potassium channel activity; calcium ion binding; protein binding; calcium-activated potassium channel activity; potassium ion binding; large conductance calcium-activated potassium channel activity;	GO:0000287; GO:0003824; GO:0005244; GO:0005249; GO:0005509; GO:0005515; GO:0015269; GO:0030955; GO:0060072;
KCNMA1	Process	response to hypoxia; ion transport; potassium ion transport; potassium ion transport; response to osmotic stress; synaptic transmission; sensory perception of sound; sensory perception of sound; circadian rhythm; adult walking behavior; metabolic process; regulation of action potential in neuron; cellular potassium ion homeostasis; regulation of aldosterone metabolic process; response to carbon monoxide; response to carbon monoxide; regulation of membrane potential; auditory receptor cell differentiation; positive regulation of apoptosis; locomotor rhythm; negative regulation of cell volume; saliva secretion; cell maturation; neuromuscular process controlling balance; response to calcium ion; eye blink reflex; smooth muscle contraction involved in micturition; relaxation of vascular smooth muscle;	GO:0001666; GO:0006811; GO:0006813; GO:0006813; GO:0006813; GO:0006970; GO:0007268; GO:0007605; GO:0007605; GO:0007623; GO:0007628; GO:0008152; GO:0019228; GO:0030007; GO:0032344; GO:00034465; GO:0034465; GO:0042391; GO:0042491; GO:0043065; GO:0045475; GO:0045794; GO:0046541; GO:0048469; GO:0050885; GO:0051592; GO:0060082; GO:0060083; GO:0060087;
KDM5C	Component	cellular component; intracellular; nucleus;	GO:0005575; GO:0005622; GO:0005634;
KDM5C	Function	molecular function; DNA binding; iron ion binding; protein binding; zinc ion binding; oxidoreductase activity; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; metal ion binding;	GO:0003674; GO:0003677; GO:0005506; GO:0005515; GO:0008270; GO:0016491; GO:0016702; GO:0046872;
KDM5C	Process	transcription; regulation of transcription, DNA-dependent; biological process; chromatin modification; oxidation reduction;	GO:0006350; GO:0006355; GO:0008150; GO:0016568; GO:0055114;
KDM5D	Component	cellular component; intracellular; nucleus;	GO:0005575; GO:0005622; GO:0005634;
KDM5D	Function	molecular function; DNA binding; protein binding; zinc ion binding; oxidoreductase activity; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; metal ion binding;	GO:0003674; GO:0003677; GO:0005515; GO:0008270; GO:0016491; GO:0016702; GO:0046872;
KDM5D	Process	chromatin modification; oxidation reduction; spermatogenesis	GO:0016568; GO:0055114; GO:0007283;
LRPPRC	Component	condensed nuclear chromosome; nucleus; nuclear inner membrane; nuclear outer membrane; mitochondrion; cytoskeleton; membrane; perinuclear region of cytoplasm;	GO:0000794; GO:0005634; GO:0005637; GO:0005640; GO:0005739; GO:0005856; GO:0016020; GO:0048471;
LRPPRC	Function	DNA binding; RNA binding; protein binding; microtubule binding; beta-tubulin binding; actin filament binding;	GO:0003677; GO:0003723; GO:0005515; GO:0008017; GO:0048487; GO:0051015;
LRPPRC	Process	transcription; regulation of transcription, DNA-dependent; transport; mitochondrion transport along microtubule; mRNA transport;	GO:0006350; GO:0006355; GO:0006810; GO:0047497; GO:0051028;
LUC7L	Component	nucleus;	GO:0005634;
LUC7L	Function	protein binding; zinc ion binding; metal ion binding;	GO:0005515; GO:0008270; GO:0046872;
LUC7L	Process	negative regulation of striated muscle development;	GO:0045843;
MAPKAP1	Component	cellular component; nucleus; cytosol; plasma membrane; cytoplasmic vesicle;	GO:0005575; GO:0005634; GO:0005829; GO:0005886; GO:0031410;
MAPKAP1	Function	kinase activity; Ras GTPase binding;	GO:0016301; GO:0017016;
MAPKAP1	Process	biological process;	GO:0008150;
MBD5	Component	nucleus;	GO:0005634;
MBD5	Function	DNA binding;	GO:0003677;
NEGR1	Component	plasma membrane; anchored to membrane;	GO:0005886; GO:0031225;
NEGR1	Function	protein binding;	GO:0005515;
NEGR1	Process	cell adhesion;	GO:0007155;
NPAS3	Component	nucleus; cytoplasm;	GO:0005634; GO:0005737;
NPAS3	Function	DNA binding; signal transducer activity; transcription regulator activity;	GO:0003677; GO:0004871; GO:0030528;
NPAS3	Process	regulation of transcription, DNA-dependent; signal transduction; locomotory behavior; social behavior; maternal behavior;	GO:0006355; GO:0007165; GO:0007626; GO:0035176; GO:0042711;
PLCB4	Component	nucleus; smooth endoplasmic reticulum; microsome; postsynaptic density; dendrite;	GO:0005634; GO:0005790; GO:0005792; GO:0014069; GO:0030425;
PLCB4	Function	phosphoinositide phospholipase C activity; signal transducer activity; calcium ion binding; protein binding; protein binding; hydrolase activity;	GO:0004435; GO:0004871; GO:0005509; GO:0005515; GO:0005515; GO:0016787;
PLCB4	Process	lipid metabolic process; intracellular signaling cascade; lipid catabolic process;	GO:0006629; GO:0007242; GO:0016042;
PNO	Component	extracellular region;	GO:0005576;
PNO	Function	opioid peptide activity; neuropeptide hormone activity;	GO:0001515; GO:0005184;

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PNO	Process	signal transduction; neuropeptide signaling pathway; synaptic transmission; sensory perception;	GO:0007165; GO:0007218; GO:0007268; GO:0007600;
POLA1	Component	chromatin; nucleus; nuclear envelope; nucleoplasm; nucleoplasm; alpha DNA polymerase:primase complex; alpha DNA polymerase:primase complex; nucleolus; cytoplasm; nuclear matrix;	GO:0000785; GO:0005634; GO:0005635; GO:0005654; GO:0005654; GO:0005658; GO:0005658; GO:0005730; GO:0005737; GO:0016363;
POLA1	Function	nucleotide binding; DNA binding; DNA binding; chromatin binding; DNA-directed DNA polymerase activity; DNA-directed DNA polymerase activity; DNA primase activity; protein binding; zinc ion binding; transferase activity; nucleotidyltransferase activity; metal ion binding; protein heterodimerization activity;	GO:0000166; GO:0003677; GO:0003677; GO:0003677; GO:0003682; GO:0003887; GO:0003887; GO:0003896; GO:0005515; GO:0008270; GO:0016740; GO:0016779; GO:0046872; GO:0046982;
POLA1	Process	S phase of mitotic cell cycle; DNA synthesis during DNA repair; DNA synthesis during DNA repair; nucleobase, nucleoside, nucleotide and nucleic acid metabolic process; DNA replication initiation; leading strand elongation; lagging strand elongation; double-strand break repair via nonhomologous end joining; cell proliferation;	GO:0000084; GO:0000731; GO:0000731; GO:0006139; GO:0006270; GO:0006272; GO:0006273; GO:0006303; GO:0008283;
RAG1	Component	intracellular; nucleus;	GO:0005622; GO:0005634;
RAG1	Function	DNA binding; endonuclease activity; protein binding; zinc ion binding; hydrolase activity; metal ion binding;	GO:0003677; GO:0004519; GO:0005515; GO:0008270; GO:0016787; GO:0046872;
RAG1	Process	DNA recombination; immune response; B cell differentiation; V(D)J recombination;	GO:0006310; GO:0006955; GO:0030183; GO:0033151;
RAG2	Component	nucleus;	GO:0005634;
RAG2	Function	DNA binding; endonuclease activity; peroxidase activity; hydrolase activity; heme binding;	GO:0003677; GO:0004519; GO:0004601; GO:0016787; GO:0020037;
RAG2	Process	DNA recombination; response to oxidative stress; somatic diversification of immunoglobulins; B cell differentiation; T cell differentiation in the thymus; V(D)J recombination;	GO:0006310; GO:0006979; GO:0016445; GO:0030183; GO:0033077; GO:0033151;
RPGRI1	Component	axoneme; cilium;	GO:0005930; GO:0005929;
RPGRI1	Function	protein binding;	GO:0005515;
RPGRI1	Process	eye photoreceptor cell development; response to stimulus; visual perception;	GO:0042462; GO:0050896; GO:0007601;
S1PR1	Component	plasma membrane; integral to membrane;	GO:0005886; GO:0016021;
S1PR1	Function	lysophospholipid and lysophosphatidic acid receptor activity; receptor activity;	GO:0001619; GO:0004872;
S1PR1	Process	angiogenesis; signal transduction; G-protein coupled receptor protein signaling pathway; G-protein signaling, adenylate cyclase inhibiting pathway; brain development; positive regulation of cell proliferation; regulation of cell adhesion;	GO:0001525; GO:0007165; GO:0007186; GO:0007193; GO:0007420; GO:0008284; GO:0030155;
SGMS1	Component	Golgi trans cisterna; Golgi membrane; nucleus; endoplasmic reticulum; Golgi apparatus; plasma membrane; integral to membrane; integral to Golgi membrane;	GO:0000138; GO:0000139; GO:0005634; GO:0005783; GO:0005794; GO:0005886; GO:0016021; GO:0030173;
SGMS1	Function	kinase activity; transferase activity; sphingomyelin synthase activity; ceramide cholinephosphotransferase activity;	GO:0016301; GO:0016740; GO:0033188; GO:0047493;
SGMS1	Process	lipid metabolic process; sphingolipid metabolic process; sphingomyelin biosynthetic process; apoptosis; cell growth;	GO:0006629; GO:0006665; GO:0006686; GO:0006915; GO:0016049;
SIM1	Component	nucleus; Golgi apparatus;	GO:0005634; GO:0005794;
SIM1	Function	transcription factor activity; signal transducer activity; protein binding; protein heterodimerization activity;	GO:0003700; GO:0004871; GO:0005515; GO:0046982;
SIM1	Process	regulation of transcription, DNA-dependent; signal transduction; multicellular organismal development; nervous system development; cell differentiation;	GO:0006355; GO:0007165; GO:0007275; GO:0007399; GO:0030154;
SRY	Component	nucleus; nucleus; cytoplasm; nuclear speck;	GO:0005634; GO:0005634; GO:0005737; GO:0016607;
SRY	Function	transcription factor activity; protein binding; protein binding; DNA bending activity; transcription activator activity;	GO:0003700; GO:0005515; GO:0005515; GO:0008301; GO:0016563;
SRY	Process	transcription; regulation of transcription, DNA-dependent; cell differentiation; male sex determination; male sex determination;	GO:0006350; GO:0006355; GO:0030154; GO:0030238; GO:0030238;
TEX2	Component	membrane; integral to membrane;	GO:0016020; GO:0016021;
TEX2	Function	molecular function;	GO:0003674;
TEX2	Process	sphingolipid metabolic process; signal transduction;	GO:0006665; GO:0007165;
TTR	Component	extracellular region;	GO:0005576;
TTR	Function	hormone activity; steroid binding; retinal binding; retinol binding;	GO:0005179; GO:0005496; GO:0016918; GO:0019841;
TTR	Process	thyroid hormone generation; transport;	GO:0006590; GO:0006810;
TYR	Component	cytoplasm; lysosome; Golgi-associated vesicle; membrane; integral to membrane; melanosome membrane; perinuclear region of cytoplasm;	GO:0005737; GO:0005764; GO:0005798; GO:0016020; GO:0016021; GO:0033162; GO:0048471;
TYR	Function	monooxygenase activity; monophenol monooxygenase activity; copper ion binding; protein binding; protein homodimerization activity; metal ion binding; protein heterodimerization activity;	GO:0004497; GO:0004503; GO:0005507; GO:0005515; GO:0042803; GO:0046872; GO:0046982;
TYR	Process	melanin biosynthetic process from tyrosine; eye pigment biosynthetic process; visual perception; sensory perception of sound; cell proliferation; pigmentation; oxidation reduction;	GO:0006583; GO:0006726; GO:0007601; GO:0007605; GO:0008283; GO:0043473; GO:0055114;
USH2A	Component	extracellular region; basement membrane; cytoplasm; plasma membrane; integral to membrane; cell projection;	GO:0005576; GO:0005604; GO:0005737; GO:0005886; GO:0016021; GO:0042995;
USH2A	Function	collagen binding; PDZ domain binding;	GO:0005518; GO:0030165;
USH2A	Process	sensory perception of sound; photoreceptor cell maintenance; maintenance of organ identity; response to stimulus;	GO:0007605; GO:0045494; GO:0048496; GO:0050896;
UTY	Component	cellular component; nucleus;	GO:0005575; GO:0005634;
UTY	Function	molecular function; binding; iron ion binding; oxidoreductase activity; oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen; metal ion binding;	GO:0003674; GO:0005488; GO:0005506; GO:0016491; GO:0016702; GO:0046872;
UTY	Process	biological process; chromatin modification; oxidation reduction;	GO:0008150; GO:0016568; GO:0055114;
ZFX	Component	intracellular; nucleus; nucleolus;	GO:0005622; GO:0005634; GO:0005730;
ZFX	Function	DNA binding; DNA binding; transcription coactivator activity; zinc ion binding; transcription regulator activity; metal ion binding;	GO:0003677; GO:0003677; GO:0003713; GO:0008270; GO:0030528; GO:0046872;
ZFX	Process	regulation of transcription, DNA-dependent; regulation of transcription;	GO:0006355; GO:0045449;
ZFY	Component	intracellular; nucleus;	GO:0005622; GO:0005634;
ZFY	Function	DNA binding; zinc ion binding; transcription regulator activity; metal ion binding;	GO:0003677; GO:0008270; GO:0030528; GO:0046872;
ZFY	Process	regulation of transcription, DNA-dependent;	GO:0006355;
ZIC3	Component	intracellular; nucleus;	GO:0005622; GO:0005634;
ZIC3	Function	DNA binding; zinc ion binding; metal ion binding;	GO:0003677; GO:0008270; GO:0046872;
ZIC3	Process	transcription; regulation of transcription, DNA-dependent; determination of left/right symmetry;	GO:0006350; GO:0006355; GO:0007368;