

Table S1-1. Gene ontology enrichment analysis results (Biological Process)

ID	Description	GeneRatio
GO:0001764	neuron migration	7/104
GO:0038007	netrin-activated signaling pathway	2/104
GO:0070528	protein kinase C signaling	3/104
GO:0046320	regulation of fatty acid oxidation	3/104
GO:0043647	inositol phosphate metabolic process	4/104
GO:0006551	leucine metabolic process	2/104
GO:0044262	cellular carbohydrate metabolic process	7/104
GO:0097553	calcium ion transmembrane import into cytosol	5/104
GO:0034765	regulation of ion transmembrane transport	9/104
GO:0003012	muscle system process	9/104
GO:1904062	regulation of cation transmembrane transport	7/104
GO:0034762	regulation of transmembrane transport	9/104
GO:0060402	calcium ion transport into cytosol	5/104
GO:0000301	retrograde transport, vesicle recycling within Golgi	2/104
GO:0038065	collagen-activated signaling pathway	2/104
GO:0060401	cytosolic calcium ion transport	5/104
GO:0016049	cell growth	9/104
GO:0051056	regulation of small GTPase mediated signal transduction	7/104
GO:0007229	integrin-mediated signaling pathway	4/104
GO:0010566	regulation of ketone biosynthetic process	2/104
GO:0032230	positive regulation of synaptic transmission, GABAergic	2/104
GO:0019395	fatty acid oxidation	4/104
GO:0034440	lipid oxidation	4/104
GO:0046321	positive regulation of fatty acid oxidation	2/104
GO:1900024	regulation of substrate adhesion-dependent cell spreading	3/104
GO:0010565	regulation of cellular ketone metabolic process	5/104
GO:0019722	calcium-mediated signaling	5/104
GO:0032409	regulation of transporter activity	6/104
GO:0019362	pyridine nucleotide metabolic process	5/104
GO:0046496	nicotinamide nucleotide metabolic process	5/104
GO:0090036	regulation of protein kinase C signaling	2/104
GO:0006939	smooth muscle contraction	4/104
GO:0010676	positive regulation of cellular carbohydrate metabolic process	3/104
GO:0072524	pyridine-containing compound metabolic process	5/104
GO:0032460	negative regulation of protein oligomerization	2/104
GO:0046885	regulation of hormone biosynthetic process	2/104
GO:0071871	response to epinephrine	2/104
GO:2000310	regulation of NMDA receptor activity	2/104
GO:0006109	regulation of carbohydrate metabolic process	5/104
GO:0010769	regulation of cell morphogenesis involved in differentiation	6/104
GO:0051209	release of sequestered calcium ion into cytosol	4/104
GO:0051283	negative regulation of sequestering of calcium ion	4/104
GO:0007040	lysosome organization	3/104
GO:0080171	lytic vacuole organization	3/104
GO:0051282	regulation of sequestering of calcium ion	4/104
GO:0098739	import across plasma membrane	3/104
GO:0019751	polyol metabolic process	4/104
GO:0006198	cAMP catabolic process	2/104

GO:0051208	sequestering of calcium ion	4/104
GO:0006733	oxidoreduction coenzyme metabolic process	5/104
GO:0006936	muscle contraction	7/104
GO:0010810	regulation of cell-substrate adhesion	5/104
GO:0019216	regulation of lipid metabolic process	7/104
GO:0010920	negative regulation of inositol phosphate biosynthetic process	1/104
GO:0010924	regulation of inositol-polyphosphate 5-phosphatase activity	1/104
GO:0010925	positive regulation of inositol-polyphosphate 5-phosphatase activity	1/104
GO:0030845	phospholipase C-inhibiting G-protein coupled receptor signaling pathway	1/104
GO:0031549	negative regulation of brain-derived neurotrophic factor receptor signaling	1/104
GO:0036250	peroxisome transport along microtubule	1/104
GO:0044721	protein import into peroxisome matrix, substrate release	1/104
GO:0048033	heme o metabolic process	1/104
GO:0048034	heme O biosynthetic process	1/104
GO:0060305	regulation of cell diameter	1/104
GO:0071250	cellular response to nitrite	1/104
GO:0080033	response to nitrite	1/104
GO:1902076	regulation of lateral motor column neuron migration	1/104
GO:1902078	positive regulation of lateral motor column neuron migration	1/104
GO:1902769	regulation of choline O-acetyltransferase activity	1/104
GO:1902771	positive regulation of choline O-acetyltransferase activity	1/104
GO:1902948	negative regulation of tau-protein kinase activity	1/104
GO:1902955	positive regulation of early endosome to recycling endosome transport	1/104
GO:1902960	negative regulation of aspartic-type endopeptidase activity involved in am	1/104
GO:1902997	negative regulation of neurofibrillary tangle assembly	1/104
GO:1903210	glomerular visceral epithelial cell apoptotic process	1/104
GO:1904633	regulation of glomerular visceral epithelial cell apoptotic process	1/104
GO:1904635	positive regulation of glomerular visceral epithelial cell apoptotic process	1/104
GO:1905483	regulation of motor neuron migration	1/104
GO:1905485	positive regulation of motor neuron migration	1/104
GO:2000184	positive regulation of progesterone biosynthetic process	1/104
GO:2000287	positive regulation of myotome development	1/104
GO:2000290	regulation of myotome development	1/104
GO:2001029	regulation of cellular glucuronidation	1/104
GO:2001031	positive regulation of cellular glucuronidation	1/104
GO:0009135	purine nucleoside diphosphate metabolic process	4/104
GO:0009179	purine ribonucleoside diphosphate metabolic process	4/104
GO:0010634	positive regulation of epithelial cell migration	4/104
GO:0005996	monosaccharide metabolic process	6/104
GO:0009083	branched-chain amino acid catabolic process	2/104
GO:0086003	cardiac muscle cell contraction	3/104
GO:0009185	ribonucleoside diphosphate metabolic process	4/104
GO:0010675	regulation of cellular carbohydrate metabolic process	4/104
GO:0045834	positive regulation of lipid metabolic process	4/104
GO:0006644	phospholipid metabolic process	8/104
GO:0046434	organophosphate catabolic process	4/104
GO:0009214	cyclic nucleotide catabolic process	2/104
GO:0051968	positive regulation of synaptic transmission, glutamatergic	2/104
GO:0046324	regulation of glucose import	3/104
GO:0007204	positive regulation of cytosolic calcium ion concentration	6/104

GO:0010632	regulation of epithelial cell migration	5/104
GO:0014910	regulation of smooth muscle cell migration	3/104
GO:0042440	pigment metabolic process	3/104
GO:0030325	adrenal gland development	2/104
GO:0050996	positive regulation of lipid catabolic process	2/104
GO:0045913	positive regulation of carbohydrate metabolic process	3/104
GO:0009081	branched-chain amino acid metabolic process	2/104
GO:0046578	regulation of Ras protein signal transduction	5/104
GO:0016358	dendrite development	5/104
GO:2000021	regulation of ion homeostasis	5/104
GO:0009127	purine nucleoside monophosphate biosynthetic process	3/104
GO:0009168	purine ribonucleoside monophosphate biosynthetic process	3/104
GO:0010770	positive regulation of cell morphogenesis involved in differentiation	4/104
GO:1901615	organic hydroxy compound metabolic process	8/104
GO:0051235	maintenance of location	6/104
GO:0003148	outflow tract septum morphogenesis	2/104
GO:0006700	C21-steroid hormone biosynthetic process	2/104
GO:0032350	regulation of hormone metabolic process	2/104
GO:0001508	action potential	4/104
GO:0070588	calcium ion transmembrane transport	6/104
GO:0010827	regulation of glucose transport	3/104
GO:1903169	regulation of calcium ion transmembrane transport	4/104
GO:0042391	regulation of membrane potential	7/104
GO:0008202	steroid metabolic process	6/104
GO:0014909	smooth muscle cell migration	3/104
GO:0009132	nucleoside diphosphate metabolic process	4/104
GO:0032412	regulation of ion transmembrane transporter activity	5/104
GO:0009167	purine ribonucleoside monophosphate metabolic process	6/104
GO:0009126	purine nucleoside monophosphate metabolic process	6/104
GO:0051279	regulation of release of sequestered calcium ion into cytosol	3/104
GO:0046323	glucose import	3/104
GO:0031589	cell-substrate adhesion	6/104
GO:0002121	inter-male aggressive behavior	1/104
GO:0006784	heme a biosynthetic process	1/104
GO:0009082	branched-chain amino acid biosynthetic process	1/104
GO:0009098	leucine biosynthetic process	1/104
GO:0009099	valine biosynthetic process	1/104
GO:0009257	10-formyltetrahydrofolate biosynthetic process	1/104
GO:0016561	protein import into peroxisome matrix, translocation	1/104
GO:0021691	cerebellar Purkinje cell layer maturation	1/104
GO:0021730	trigeminal sensory nucleus development	1/104
GO:0021740	principal sensory nucleus of trigeminal nerve development	1/104
GO:0031548	regulation of brain-derived neurotrophic factor receptor signaling pathway	1/104
GO:0035585	calcium-mediated signaling using extracellular calcium source	1/104
GO:0035668	TRAM-dependent toll-like receptor signaling pathway	1/104
GO:0035669	TRAM-dependent toll-like receptor 4 signaling pathway	1/104
GO:0042351	'de novo' GDP-L-fucose biosynthetic process	1/104
GO:0045053	protein retention in Golgi apparatus	1/104
GO:0046160	heme a metabolic process	1/104
GO:0046168	glycerol-3-phosphate catabolic process	1/104

GO:0070560	protein secretion by platelet	1/104
GO:0090038	negative regulation of protein kinase C signaling	1/104
GO:0098582	innate vocalization behavior	1/104
GO:1901090	regulation of protein tetramerization	1/104
GO:1901091	negative regulation of protein tetramerization	1/104
GO:1901093	regulation of protein homotetramerization	1/104
GO:1901094	negative regulation of protein homotetramerization	1/104
GO:1901558	response to metformin	1/104
GO:1901860	positive regulation of mitochondrial DNA metabolic process	1/104
GO:1901898	negative regulation of relaxation of cardiac muscle	1/104
GO:1902612	regulation of anti-Mullerian hormone signaling pathway	1/104
GO:1902613	negative regulation of anti-Mullerian hormone signaling pathway	1/104
GO:1902954	regulation of early endosome to recycling endosome transport	1/104
GO:1902962	regulation of metalloendopeptidase activity involved in amyloid precursor	1/104
GO:1902963	negative regulation of metalloendopeptidase activity involved in amyloid	1/104
GO:1902996	regulation of neurofibrillary tangle assembly	1/104
GO:1904638	response to resveratrol	1/104
GO:1904639	cellular response to resveratrol	1/104
GO:1905246	negative regulation of aspartic-type peptidase activity	1/104
GO:1990262	anti-Mullerian hormone signaling pathway	1/104
GO:2000324	positive regulation of glucocorticoid receptor signaling pathway	1/104
GO:2000620	positive regulation of histone H4-K16 acetylation	1/104
GO:0022898	regulation of transmembrane transporter activity	5/104
GO:0051480	regulation of cytosolic calcium ion concentration	6/104
GO:0007411	axon guidance	5/104
GO:0006066	alcohol metabolic process	6/104
GO:0042180	cellular ketone metabolic process	5/104
GO:0097485	neuron projection guidance	5/104
GO:0009161	ribonucleoside monophosphate metabolic process	6/104
GO:0035066	positive regulation of histone acetylation	2/104
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	2/104
GO:0043255	regulation of carbohydrate biosynthetic process	3/104
GO:0051186	cofactor metabolic process	7/104
GO:0016311	dephosphorylation	7/104
GO:0009156	ribonucleoside monophosphate biosynthetic process	3/104
GO:0032365	intracellular lipid transport	2/104
GO:0032743	positive regulation of interleukin-2 production	2/104
GO:2000758	positive regulation of peptidyl-lysine acetylation	2/104
GO:0090257	regulation of muscle system process	5/104
GO:0034446	substrate adhesion-dependent cell spreading	3/104
GO:0021537	telencephalon development	5/104
GO:0019217	regulation of fatty acid metabolic process	3/104
GO:0048640	negative regulation of developmental growth	3/104
GO:0022604	regulation of cell morphogenesis	7/104
GO:0007409	axonogenesis	7/104
GO:0014812	muscle cell migration	3/104
GO:0010543	regulation of platelet activation	2/104
GO:0032228	regulation of synaptic transmission, GABAergic	2/104
GO:0045923	positive regulation of fatty acid metabolic process	2/104
GO:0090218	positive regulation of lipid kinase activity	2/104

GO:0009123	nucleoside monophosphate metabolic process	6/104
GO:0060996	dendritic spine development	3/104
GO:0050768	negative regulation of neurogenesis	5/104
GO:0007616	long-term memory	2/104
GO:0009154	purine ribonucleotide catabolic process	2/104
GO:0046621	negative regulation of organ growth	2/104
GO:0006937	regulation of muscle contraction	4/104
GO:0046486	glycerolipid metabolic process	7/104
GO:0031532	actin cytoskeleton reorganization	3/104
GO:0071222	cellular response to lipopolysaccharide	4/104
GO:0009261	ribonucleotide catabolic process	2/104
GO:0010907	positive regulation of glucose metabolic process	2/104
GO:0050775	positive regulation of dendrite morphogenesis	2/104
GO:1900026	positive regulation of substrate adhesion-dependent cell spreading	2/104
GO:1901985	positive regulation of protein acetylation	2/104
GO:2001222	regulation of neuron migration	2/104
GO:0048010	vascular endothelial growth factor receptor signaling pathway	3/104
GO:0002378	immunoglobulin biosynthetic process	1/104
GO:0021590	cerebellum maturation	1/104
GO:0021699	cerebellar cortex maturation	1/104
GO:0042350	GDP-L-fucose biosynthetic process	1/104
GO:0060083	smooth muscle contraction involved in micturition	1/104
GO:0071873	response to norepinephrine	1/104
GO:0090107	regulation of high-density lipoprotein particle assembly	1/104
GO:0090258	negative regulation of mitochondrial fission	1/104
GO:0097477	lateral motor column neuron migration	1/104
GO:0098912	membrane depolarization during atrial cardiac muscle cell action potential	1/104
GO:1902988	neurofibrillary tangle assembly	1/104
GO:1904640	response to methionine	1/104
GO:1904694	negative regulation of vascular smooth muscle contraction	1/104
GO:2000182	regulation of progesterone biosynthetic process	1/104
GO:0009124	nucleoside monophosphate biosynthetic process	3/104
GO:0035265	organ growth	4/104
GO:0006891	intra-Golgi vesicle-mediated transport	2/104
GO:0086005	ventricular cardiac muscle cell action potential	2/104
GO:0002931	response to ischemia	2/104
GO:0008207	C21-steroid hormone metabolic process	2/104
GO:1900449	regulation of glutamate receptor signaling pathway	2/104
GO:0006650	glycerophospholipid metabolic process	6/104
GO:0070838	divalent metal ion transport	7/104
GO:0006732	coenzyme metabolic process	6/104
GO:0010631	epithelial cell migration	5/104
GO:0071219	cellular response to molecule of bacterial origin	4/104
GO:0010522	regulation of calcium ion transport into cytosol	3/104
GO:0072511	divalent inorganic cation transport	7/104
GO:0006734	NADH metabolic process	2/104
GO:0071867	response to monoamine	2/104
GO:0071869	response to catecholamine	2/104
GO:0090132	epithelium migration	5/104
GO:0006096	glycolytic process	3/104

GO:0035335	peptidyl-tyrosine dephosphorylation	3/104
GO:0010677	negative regulation of cellular carbohydrate metabolic process	2/104
GO:0051932	synaptic transmission, GABAergic	2/104
GO:0006757	ATP generation from ADP	3/104
GO:0051961	negative regulation of nervous system development	5/104
GO:0030900	forebrain development	6/104
GO:0051899	membrane depolarization	3/104
GO:0000266	mitochondrial fission	2/104
GO:0045017	glycerolipid biosynthetic process	5/104
GO:0090130	tissue migration	5/104
GO:0061564	axon development	7/104
GO:0003199	endocardial cushion to mesenchymal transition involved in heart valve formation	1/104
GO:0006651	diacylglycerol biosynthetic process	1/104
GO:0014878	response to electrical stimulus involved in regulation of muscle adaptation	1/104
GO:0032345	negative regulation of aldosterone metabolic process	1/104
GO:0032348	negative regulation of aldosterone biosynthetic process	1/104
GO:0034465	response to carbon monoxide	1/104
GO:0035022	positive regulation of Rac protein signal transduction	1/104
GO:0038026	reelin-mediated signaling pathway	1/104
GO:0046368	GDP-L-fucose metabolic process	1/104
GO:0055098	response to low-density lipoprotein particle stimulus	1/104
GO:0061055	myotome development	1/104
GO:0061502	early endosome to recycling endosome transport	1/104
GO:0070294	renal sodium ion absorption	1/104
GO:0070777	D-aspartate transport	1/104
GO:0070779	D-aspartate import	1/104
GO:0097026	dendritic cell dendrite assembly	1/104
GO:0097114	NMDA glutamate receptor clustering	1/104
GO:0097476	spinal cord motor neuron migration	1/104
GO:0097490	sympathetic neuron projection extension	1/104
GO:0097491	sympathetic neuron projection guidance	1/104
GO:1902953	positive regulation of ER to Golgi vesicle-mediated transport	1/104
GO:1904636	response to ionomycin	1/104
GO:1904637	cellular response to ionomycin	1/104
GO:2000065	negative regulation of cortisol biosynthetic process	1/104
GO:2001137	positive regulation of endocytic recycling	1/104
GO:0042181	ketone biosynthetic process	2/104
GO:0086004	regulation of cardiac muscle cell contraction	2/104
GO:0006694	steroid biosynthetic process	4/104
GO:0030258	lipid modification	5/104
GO:0032459	regulation of protein oligomerization	2/104
GO:0045912	negative regulation of carbohydrate metabolic process	2/104
GO:0099601	regulation of neurotransmitter receptor activity	2/104
GO:0046031	ADP metabolic process	3/104
GO:0043551	regulation of phosphatidylinositol 3-kinase activity	2/104
GO:1903727	positive regulation of phospholipid metabolic process	2/104
GO:0010811	positive regulation of cell-substrate adhesion	3/104
GO:0046326	positive regulation of glucose import	2/104
GO:0098659	inorganic cation import across plasma membrane	2/104
GO:0099587	inorganic ion import across plasma membrane	2/104

GO:0006006	glucose metabolic process	4/104
GO:0070252	actin-mediated cell contraction	3/104
GO:0045665	negative regulation of neuron differentiation	4/104
GO:0010721	negative regulation of cell development	5/104
GO:0003096	renal sodium ion transport	1/104
GO:0006552	leucine catabolic process	1/104
GO:0009256	10-formyltetrahydrofolate metabolic process	1/104
GO:0010572	positive regulation of platelet activation	1/104
GO:0010841	positive regulation of circadian sleep/wake cycle, wakefulness	1/104
GO:0021942	radial glia guided migration of Purkinje cell	1/104
GO:0031547	brain-derived neurotrophic factor receptor signaling pathway	1/104
GO:0031944	negative regulation of glucocorticoid metabolic process	1/104
GO:0031947	negative regulation of glucocorticoid biosynthetic process	1/104
GO:0032353	negative regulation of hormone biosynthetic process	1/104
GO:0033564	anterior/posterior axon guidance	1/104
GO:0033625	positive regulation of integrin activation	1/104
GO:0045794	negative regulation of cell volume	1/104
GO:0071332	cellular response to fructose stimulus	1/104
GO:0071362	cellular response to ether	1/104
GO:0090032	negative regulation of steroid hormone biosynthetic process	1/104
GO:0090500	endocardial cushion to mesenchymal transition	1/104
GO:1901078	negative regulation of relaxation of muscle	1/104
GO:1902965	regulation of protein localization to early endosome	1/104
GO:1902966	positive regulation of protein localization to early endosome	1/104
GO:2000618	regulation of histone H4-K16 acetylation	1/104
GO:2000969	positive regulation of AMPA receptor activity	1/104
GO:0071216	cellular response to biotic stimulus	4/104
GO:1903115	regulation of actin filament-based movement	2/104
GO:0001558	regulation of cell growth	6/104
GO:0051090	regulation of DNA binding transcription factor activity	6/104
GO:0032845	negative regulation of homeostatic process	4/104
GO:0006195	purine nucleotide catabolic process	2/104
GO:0010828	positive regulation of glucose transport	2/104
GO:0048588	developmental cell growth	4/104
GO:0006165	nucleoside diphosphate phosphorylation	3/104
GO:0006754	ATP biosynthetic process	2/104
GO:2000273	positive regulation of receptor activity	2/104
GO:2000649	regulation of sodium ion transmembrane transporter activity	2/104
GO:0015758	glucose transport	3/104
GO:0019932	second-messenger-mediated signaling	5/104
GO:0045598	regulation of fat cell differentiation	3/104
GO:0086010	membrane depolarization during action potential	2/104
GO:0030010	establishment of cell polarity	3/104
GO:0001957	intramembranous ossification	1/104
GO:0003406	retinal pigment epithelium development	1/104
GO:0007185	transmembrane receptor protein tyrosine phosphatase signaling pathway	1/104
GO:0010840	regulation of circadian sleep/wake cycle, wakefulness	1/104
GO:0010887	negative regulation of cholesterol storage	1/104
GO:0015917	aminophospholipid transport	1/104
GO:0015942	formate metabolic process	1/104

GO:0018242	protein O-linked glycosylation via serine	1/104
GO:0021578	hindbrain maturation	1/104
GO:0021626	central nervous system maturation	1/104
GO:0032344	regulation of aldosterone metabolic process	1/104
GO:0032347	regulation of aldosterone biosynthetic process	1/104
GO:0032351	negative regulation of hormone metabolic process	1/104
GO:0035634	response to stilbenoid	1/104
GO:0036072	direct ossification	1/104
GO:0042746	circadian sleep/wake cycle, wakefulness	1/104
GO:0042940	D-amino acid transport	1/104
GO:0051552	flavone metabolic process	1/104
GO:0051964	negative regulation of synapse assembly	1/104
GO:0070257	positive regulation of mucus secretion	1/104
GO:0086045	membrane depolarization during AV node cell action potential	1/104
GO:1901857	positive regulation of cellular respiration	1/104
GO:1902285	semaphorin-plexin signaling pathway involved in neuron projection guidance	1/104
GO:1902947	regulation of tau-protein kinase activity	1/104
GO:1902959	regulation of aspartic-type endopeptidase activity involved in amyloid precursor processing	1/104
GO:2000064	regulation of cortisol biosynthetic process	1/104
GO:2000504	positive regulation of blood vessel remodeling	1/104
GO:2000507	positive regulation of energy homeostasis	1/104
GO:0006816	calcium ion transport	6/104
GO:0036092	phosphatidylinositol-3-phosphate biosynthetic process	2/104
GO:0048706	embryonic skeletal system development	3/104
GO:0043550	regulation of lipid kinase activity	2/104
GO:0046148	pigment biosynthetic process	2/104
GO:0050771	negative regulation of axonogenesis	2/104
GO:0050994	regulation of lipid catabolic process	2/104
GO:0045444	fat cell differentiation	4/104
GO:0046939	nucleotide phosphorylation	3/104
GO:0018209	peptidyl-serine modification	5/104
GO:0006874	cellular calcium ion homeostasis	6/104
GO:0008645	hexose transport	3/104
GO:0043467	regulation of generation of precursor metabolites and energy	3/104
GO:0032663	regulation of interleukin-2 production	2/104
GO:0014065	phosphatidylinositol 3-kinase signaling	3/104
GO:0015749	monosaccharide transport	3/104
GO:0048813	dendrite morphogenesis	3/104
GO:0007632	visual behavior	2/104
GO:0035065	regulation of histone acetylation	2/104
GO:0072523	purine-containing compound catabolic process	2/104
GO:0086002	cardiac muscle cell action potential involved in contraction	2/104
GO:0030326	embryonic limb morphogenesis	3/104
GO:0035113	embryonic appendage morphogenesis	3/104
GO:0000042	protein targeting to Golgi	1/104
GO:0006072	glycerol-3-phosphate metabolic process	1/104
GO:0006701	progesterone biosynthetic process	1/104
GO:0007221	positive regulation of transcription of Notch receptor target	1/104
GO:0014832	urinary bladder smooth muscle contraction	1/104
GO:0014848	urinary tract smooth muscle contraction	1/104

GO:0018243	protein O-linked glycosylation via threonine	1/104
GO:0019673	GDP-mannose metabolic process	1/104
GO:0030091	protein repair	1/104
GO:0031946	regulation of glucocorticoid biosynthetic process	1/104
GO:0032489	regulation of Cdc42 protein signal transduction	1/104
GO:0035360	positive regulation of peroxisome proliferator activated receptor signaling	1/104
GO:0038027	apolipoprotein A-I-mediated signaling pathway	1/104
GO:0045906	negative regulation of vasoconstriction	1/104
GO:0046886	positive regulation of hormone biosynthetic process	1/104
GO:0048702	embryonic neurocranium morphogenesis	1/104
GO:0060073	micturition	1/104
GO:0090240	positive regulation of histone H4 acetylation	1/104
GO:0097475	motor neuron migration	1/104
GO:1901858	regulation of mitochondrial DNA metabolic process	1/104
GO:1901897	regulation of relaxation of cardiac muscle	1/104
GO:1902430	negative regulation of amyloid-beta formation	1/104
GO:1902946	protein localization to early endosome	1/104
GO:1905245	regulation of aspartic-type peptidase activity	1/104
GO:0098900	regulation of action potential	2/104
GO:0002576	platelet degranulation	3/104
GO:0010977	negative regulation of neuron projection development	3/104
GO:0001933	negative regulation of protein phosphorylation	6/104
GO:0055074	calcium ion homeostasis	6/104
GO:0046488	phosphatidylinositol metabolic process	4/104
GO:0060048	cardiac muscle contraction	3/104
GO:0010975	regulation of neuron projection development	6/104
GO:0033627	cell adhesion mediated by integrin	2/104
GO:0071398	cellular response to fatty acid	2/104
GO:0090303	positive regulation of wound healing	2/104
GO:0030048	actin filament-based movement	3/104
GO:0051057	positive regulation of small GTPase mediated signal transduction	2/104
GO:0070527	platelet aggregation	2/104
GO:0002433	immune response-regulating cell surface receptor signaling pathway invol	3/104
GO:0038096	Fc-gamma receptor signaling pathway involved in phagocytosis	3/104
GO:0050773	regulation of dendrite development	3/104
GO:0097306	cellular response to alcohol	2/104
GO:2000756	regulation of peptidyl-lysine acetylation	2/104
GO:0050806	positive regulation of synaptic transmission	3/104
GO:0006814	sodium ion transport	4/104
GO:0051924	regulation of calcium ion transport	4/104
GO:0002118	aggressive behavior	1/104
GO:0003056	regulation of vascular smooth muscle contraction	1/104
GO:0007172	signal complex assembly	1/104
GO:0007270	neuron-neuron synaptic transmission	1/104
GO:0009750	response to fructose	1/104
GO:0014732	skeletal muscle atrophy	1/104
GO:0021800	cerebral cortex tangential migration	1/104
GO:0030007	cellular potassium ion homeostasis	1/104
GO:0035331	negative regulation of hippo signaling	1/104
GO:0035865	cellular response to potassium ion	1/104

GO:0046654	tetrahydrofolate biosynthetic process	1/104
GO:0052646	alditol phosphate metabolic process	1/104
GO:0060013	righting reflex	1/104
GO:0060155	platelet dense granule organization	1/104
GO:0060373	regulation of ventricular cardiac muscle cell membrane depolarization	1/104
GO:0071313	cellular response to caffeine	1/104
GO:0072102	glomerulus morphogenesis	1/104
GO:0072578	neurotransmitter-gated ion channel clustering	1/104
GO:0072600	establishment of protein localization to Golgi	1/104
GO:0098712	L-glutamate import across plasma membrane	1/104
GO:1900451	positive regulation of glutamate receptor signaling pathway	1/104
GO:1903802	L-glutamate(1-) import across plasma membrane	1/104
GO:1904684	negative regulation of metalloendopeptidase activity	1/104
GO:1905666	regulation of protein localization to endosome	1/104
GO:1905668	positive regulation of protein localization to endosome	1/104
GO:2000322	regulation of glucocorticoid receptor signaling pathway	1/104
GO:2001135	regulation of endocytic recycling	1/104
GO:2001171	positive regulation of ATP biosynthetic process	1/104
GO:0045600	positive regulation of fat cell differentiation	2/104
GO:1902305	regulation of sodium ion transmembrane transport	2/104
GO:0006090	pyruvate metabolic process	3/104
GO:0072503	cellular divalent inorganic cation homeostasis	6/104
GO:0038094	Fc-gamma receptor signaling pathway	3/104
GO:0032623	interleukin-2 production	2/104
GO:0051966	regulation of synaptic transmission, glutamatergic	2/104
GO:0002431	Fc receptor mediated stimulatory signaling pathway	3/104
GO:0030335	positive regulation of cell migration	6/104
GO:0072006	nephron development	3/104

BgRatio	pvalue	geneID	Count
141/17381	2.20E-05	APBB2/AUTS2/KIRREL3/PTK2/RELN/SPOCK1/ULK4	7
5/17381	0.00035	PTK2/UNC5C	2
27/17381	0.000548	GPD1L/PLEK/ULK4	3
28/17381	0.000611	IRS1/PPARGC1A/PRKAG2	3
67/17381	0.000694	INPP4B/MTMR7/PLCE1/PLEK	4
7/17381	0.00073	AUH/BCAT1	2
250/17381	0.000761	FGGY/IRS1/MTMR7/PLEK/PPARGC1A/PRKAG2/PRKCE	7
128/17381	0.001029	CACNA1C/FAM155A/PRKCE/TPCN2/UBASH3B	5
444/17381	0.001378	CACNA1C/GPD1L/KCNMA1/PDE4B/PPARGC1A/PRKCE/RE	9
448/17381	0.001465	CACNA1C/DOCK5/GPD1L/KCNMA1/PDE4B/PLCE1/PPARG	9
288/17381	0.001723	CACNA1C/GPD1L/PDE4B/PPARGC1A/PRKCE/RELN/UBASH	7
459/17381	0.00173	CACNA1C/GPD1L/KCNMA1/PDE4B/PPARGC1A/PRKCE/RE	9
145/17381	0.001789	CACNA1C/FAM155A/PRKCE/TPCN2/UBASH3B	5
11/17381	0.001883	CUX1/SORL1	2
11/17381	0.001883	ITGA11/UBASH3B	2
157/17381	0.00253	CACNA1C/FAM155A/PRKCE/TPCN2/UBASH3B	5
486/17381	0.002546	APBB2/AUTS2/FSTL4/NRP2/PLCE1/SGK1/SORBS2/SPOCK	9
309/17381	0.002561	ABCA1/AUTS2/CGNL1/PLCE1/PSD3/RELN/TRIO	7
96/17381	0.002636	DOCK1/ITGA11/PLEK/PTK2	4
13/17381	0.002649	DKK3/PPARGC1A	2
13/17381	0.002649	NPS/PRKCE	2
98/17381	0.00284	AUH/IRS1/PPARGC1A/PRKAG2	4
100/17381	0.003055	AUH/IRS1/PPARGC1A/PRKAG2	4
14/17381	0.003079	IRS1/PPARGC1A	2
49/17381	0.00314	DOCK1/DOCK5/PTK2	3
166/17381	0.003217	DKK3/IRS1/PPARGC1A/PRKAG2/PRKCE	5
167/17381	0.0033	CACNA1C/NCALD/PLCE1/PLEK/TPCN2	5
243/17381	0.003407	GPD1L/PDE4B/PPARGC1A/PRKCE/RELN/SGK1	6
169/17381	0.003473	GPD1L/H6PD/PFKP/PPARGC1A/PRKAG2	5
169/17381	0.003473	GPD1L/H6PD/PFKP/PPARGC1A/PRKAG2	5
15/17381	0.003539	GPD1L/ULK4	2
106/17381	0.003767	DOCK5/KCNMA1/PLCE1/TPCN2	4
53/17381	0.003924	IRS1/PPARGC1A/PRKCE	3
174/17381	0.003932	GPD1L/H6PD/PFKP/PPARGC1A/PRKAG2	5
16/17381	0.004029	PEX14/SORL1	2
16/17381	0.004029	DKK3/PPARGC1A	2
16/17381	0.004029	PDE4B/PPARGC1A	2
16/17381	0.004029	PPARGC1A/RELN	2
176/17381	0.004127	IRS1/PLEK/PPARGC1A/PRKAG2/PRKCE	5
258/17381	0.00456	CUX1/DOCK1/DOCK5/FSTL4/PTK2/RELN	6
112/17381	0.004583	CACNA1C/PRKCE/TPCN2/UBASH3B	4
112/17381	0.004583	CACNA1C/PRKCE/TPCN2/UBASH3B	4
56/17381	0.004584	ABCA1/CLVS2/TPCN2	3
56/17381	0.004584	ABCA1/CLVS2/TPCN2	3
113/17381	0.00473	CACNA1C/PRKCE/TPCN2/UBASH3B	4
57/17381	0.004818	FAM155A/SLC1A2/SLC9A9	3
114/17381	0.004879	INPP4B/MTMR7/PLCE1/PLEK	4
18/17381	0.005097	PDE4B/PDE7B	2

116/17381	0.005188	CACNA1C/PRKCE/TPCN2/UBASH3B	4
186/17381	0.005208	GPD1L/H6PD/PFKP/PPARGC1A/PRKAG2	5
352/17381	0.005223	CACNA1C/DOCK5/GPD1L/KCNMA1/PDE4B/PLCE1/TPCN2	7
189/17381	0.005568	DOCK1/DOCK5/PRKCE/PTK2/SPOCK1	5
360/17381	0.005889	ABCA1/DKK3/IRS1/PPARGC1A/PRKAG2/PRKCE/PTK2	7
1/17381	0.005984	PLEK	1
1/17381	0.005984	PLEK	1
1/17381	0.005984	PLEK	1
1/17381	0.005984	PLEK	1
1/17381	0.005984	FSTL4	1
1/17381	0.005984	PEX14	1
1/17381	0.005984	PEX14	1
1/17381	0.005984	COX10	1
1/17381	0.005984	COX10	1
1/17381	0.005984	PLEK	1
1/17381	0.005984	PPARGC1A	1
1/17381	0.005984	PPARGC1A	1
1/17381	0.005984	RELN	1
1/17381	0.005984	RELN	1
1/17381	0.005984	SORL1	1
1/17381	0.005984	SORL1	1
1/17381	0.005984	SORL1	1
1/17381	0.005984	SORL1	1
1/17381	0.005984	SORL1	1
1/17381	0.005984	SORL1	1
1/17381	0.005984	PPARGC1A	1
1/17381	0.005984	PPARGC1A	1
1/17381	0.005984	PPARGC1A	1
1/17381	0.005984	RELN	1
1/17381	0.005984	RELN	1
1/17381	0.005984	PPARGC1A	1
1/17381	0.005984	DMRT2	1
1/17381	0.005984	DMRT2	1
1/17381	0.005984	PRKCE	1
1/17381	0.005984	PRKCE	1
121/17381	0.006018	CARD11/PFKP/PPARGC1A/PRKAG2	4
121/17381	0.006018	CARD11/PFKP/PPARGC1A/PRKAG2	4
121/17381	0.006018	DOCK1/DOCK5/NRP2/PRKCE	4
274/17381	0.006084	FGGY/H6PD/IRS1/PFKP/PPARGC1A/PRKCE	6
20/17381	0.00628	AUH/BCAT1	2
63/17381	0.006372	CACNA1C/GPD1L/PDE4B	3
123/17381	0.006373	CARD11/PFKP/PPARGC1A/PRKAG2	4
123/17381	0.006373	IRS1/PLEK/PPARGC1A/PRKCE	4
123/17381	0.006373	IRS1/PPARGC1A/PRKCE/PTK2	4
461/17381	0.006454	GPD1L/INPP4B/IRS1/MTMR7/OSBPL10/PLCE1/PLEK/PTK2	8
124/17381	0.006556	GPD1L/MTMR7/PDE4B/PDE7B	4
21/17381	0.006914	PDE4B/PDE7B	2
21/17381	0.006914	NPS/RELN	2
65/17381	0.006948	IRS1/PRKAG2/SLC1A2	3
285/17381	0.007328	CACNA1C/FAM155A/PLCE1/PRKCE/TPCN2/UBASH3B	6

203/17381	0.007484	DOCK1/DOCK5/NRP2/PRKCE/PTK2	5
67/17381	0.007555	DOCK5/PPARGC1A/SORL1	3
67/17381	0.007555	COX10/MTHFD1L/PPARGC1A	3
22/17381	0.007576	DKK3/PBX1	2
22/17381	0.007576	IRS1/PRKCE	2
69/17381	0.008193	IRS1/PPARGC1A/PRKCE	3
23/17381	0.008266	AUH/BCAT1	2
209/17381	0.008431	ABCA1/AUTS2/PLCE1/PSD3/TRIO	5
210/17381	0.008596	ARID1B/CUX1/FSTL4/RELN/RERE	5
210/17381	0.008596	CACNA1C/GPD1L/PRKCE/TPCN2/UBASH3B	5
71/17381	0.008861	LHPP/PPARGC1A/PRKAG2	3
71/17381	0.008861	LHPP/PPARGC1A/PRKAG2	3
137/17381	0.009254	CUX1/DOCK1/DOCK5/RELN	4
492/17381	0.00938	ABCA1/DKK3/INPP4B/MTMR7/PLCE1/PLEK/PRKAG2/SORL1	8
302/17381	0.009598	ABCA1/CACNA1C/PRKCE/SORL1/TPCN2/UBASH3B	6
25/17381	0.009725	NRP2/RARB	2
25/17381	0.009725	DKK3/PPARGC1A	2
25/17381	0.009725	DKK3/PPARGC1A	2
140/17381	0.009965	CACNA1C/GPD1L/NPS/TPCN2	4
305/17381	0.010045	CACNA1C/FAM155A/PDE4B/PRKCE/TPCN2/UBASH3B	6
75/17381	0.01029	IRS1/PRKAG2/SLC1A2	3
142/17381	0.010459	CACNA1C/PDE4B/PRKCE/UBASH3B	4
403/17381	0.010614	CACNA1C/GPD1L/KCNK9/KCNMA1/NPS/RELN/TPCN2	7
309/17381	0.010665	ABCA1/DKK3/PBX1/PPARGC1A/PRKAG2/SORL1	6
76/17381	0.010667	DOCK5/PPARGC1A/SORL1	3
143/17381	0.010711	CARD11/PFKP/PPARGC1A/PRKAG2	4
222/17381	0.010761	GPD1L/PDE4B/PPARGC1A/PRKCE/RELN	5
310/17381	0.010824	CARD11/COX10/LHPP/PFKP/PPARGC1A/PRKAG2	6
311/17381	0.010984	CARD11/COX10/LHPP/PFKP/PPARGC1A/PRKAG2	6
77/17381	0.011052	CACNA1C/PRKCE/UBASH3B	3
78/17381	0.011445	IRS1/PRKAG2/SLC1A2	3
316/17381	0.011813	DOCK1/DOCK5/ITGA11/PRKCE/PTK2/SPOCK1	6
2/17381	0.011932	KIRREL3	1
2/17381	0.011932	COX10	1
2/17381	0.011932	BCAT1	1
2/17381	0.011932	BCAT1	1
2/17381	0.011932	BCAT1	1
2/17381	0.011932	MTHFD1L	1
2/17381	0.011932	PEX14	1
2/17381	0.011932	RERE	1
2/17381	0.011932	KIRREL3	1
2/17381	0.011932	KIRREL3	1
2/17381	0.011932	FSTL4	1
2/17381	0.011932	CACNA1C	1
2/17381	0.011932	PRKCE	1
2/17381	0.011932	PRKCE	1
2/17381	0.011932	GMDS	1
2/17381	0.011932	SORL1	1
2/17381	0.011932	COX10	1
2/17381	0.011932	GPD1L	1

2/17381	0.011932	PLEK	1
2/17381	0.011932	GPD1L	1
2/17381	0.011932	AUTS2	1
2/17381	0.011932	PEX14	1
2/17381	0.011932	PEX14	1
2/17381	0.011932	PEX14	1
2/17381	0.011932	PEX14	1
2/17381	0.011932	PPARGC1A	1
2/17381	0.011932	PPARGC1A	1
2/17381	0.011932	PDE4B	1
2/17381	0.011932	DKK3	1
2/17381	0.011932	DKK3	1
2/17381	0.011932	SORL1	1
2/17381	0.011932	SORL1	1
2/17381	0.011932	SORL1	1
2/17381	0.011932	SORL1	1
2/17381	0.011932	PPARGC1A	1
2/17381	0.011932	PPARGC1A	1
2/17381	0.011932	SORL1	1
2/17381	0.011932	DKK3	1
2/17381	0.011932	LMO3	1
2/17381	0.011932	AUTS2	1
228/17381	0.011972	GPD1L/PDE4B/PPARGC1A/PRKCE/RELN	5
318/17381	0.012157	CACNA1C/FAM155A/PLCE1/PRKCE/TPCN2/UBASH3B	6
229/17381	0.012183	APBB2/NRP2/PTK2/RELN/UNC5C	5
320/17381	0.012508	ABCA1/INPP4B/MTMR7/PLCE1/PLEK/SORL1	6
231/17381	0.012611	DKK3/IRS1/PPARGC1A/PRKAG2/PRKCE	5
231/17381	0.012611	APBB2/NRP2/PTK2/RELN/UNC5C	5
322/17381	0.012865	CARD11/COX10/LHPP/PFKP/PPARGC1A/PRKAG2	6
29/17381	0.012959	AUTS2/PPARGC1A	2
29/17381	0.012959	IRS1/PTK2	2
82/17381	0.013097	IRS1/PLEK/PPARGC1A	3
421/17381	0.013247	COX10/GPD1L/H6PD/MTHFD1L/PFKP/PPARGC1A/PRKAG2	7
422/17381	0.013406	INPP4B/LHPP/MTMR7/PLEK/PTPRT/TMEM132D/UBASH3B	7
83/17381	0.01353	LHPP/PPARGC1A/PRKAG2	3
30/17381	0.013831	ABCA1/PRKAG2	2
30/17381	0.013831	CARD11/PDE4B	2
30/17381	0.013831	AUTS2/PPARGC1A	2
237/17381	0.013958	CACNA1C/DOCK5/PDE4B/PLCE1/PPARGC1A	5
84/17381	0.013971	DOCK1/DOCK5/PTK2	3
238/17381	0.014191	KIRREL3/RARB/RELN/SLC1A2/TRAPPC9	5
85/17381	0.014421	IRS1/PPARGC1A/PRKAG2	3
85/17381	0.014421	FSTL4/PTK2/WWC1	3
432/17381	0.015072	CUX1/DOCK1/DOCK5/FSTL4/PALM2/PTK2/RELN	7
433/17381	0.015246	APBB2/AUTS2/FSTL4/NRP2/PTK2/RELN/UNC5C	7
87/17381	0.015344	DOCK5/PPARGC1A/SORL1	3
32/17381	0.015649	PLEK/UBASH3B	2
32/17381	0.015649	NPS/PRKCE	2
32/17381	0.015649	IRS1/PPARGC1A	2
32/17381	0.015649	IRS1/PTK2	2

337/17381	0.015781	CARD11/COX10/LHPP/PFKP/PPARGC1A/PRKAG2	6
89/17381	0.0163	ARID1B/FSTL4/RELN	3
247/17381	0.016412	FSTL4/PBX1/PTK2/SORL1/SPOCK1	5
33/17381	0.016594	RELN/SGK1	2
33/17381	0.016594	PDE4B/PDE7B	2
33/17381	0.016594	PTK2/WWC1	2
163/17381	0.016612	CACNA1C/DOCK5/PDE4B/PLCE1	4
441/17381	0.016693	GPD1L/INPP4B/IRS1/MTMR7/OSBPL10/PLCE1/PLEK	7
90/17381	0.01679	AUTS2/PHACTR1/PLEK	3
165/17381	0.017294	ABCA1/PDE4B/PPARGC1A/PRKCE	4
34/17381	0.017563	PDE4B/PDE7B	2
34/17381	0.017563	IRS1/PPARGC1A	2
34/17381	0.017563	CUX1/RELN	2
34/17381	0.017563	DOCK1/DOCK5	2
34/17381	0.017563	AUTS2/PPARGC1A	2
34/17381	0.017563	RELN/ULK4	2
92/17381	0.017795	DOCK1/NRP2/PTK2	3
3/17381	0.017844	GALNT2	1
3/17381	0.017844	RERE	1
3/17381	0.017844	RERE	1
3/17381	0.017844	GMDS	1
3/17381	0.017844	KCNMA1	1
3/17381	0.017844	PPARGC1A	1
3/17381	0.017844	ABCA1	1
3/17381	0.017844	PPARGC1A	1
3/17381	0.017844	RELN	1
3/17381	0.017844	CACNA1C	1
3/17381	0.017844	SORL1	1
3/17381	0.017844	PPARGC1A	1
3/17381	0.017844	DOCK5	1
3/17381	0.017844	PPARGC1A	1
93/17381	0.01831	LHPP/PPARGC1A/PRKAG2	3
168/17381	0.01835	PTK2/RARB/SORBS2/WWC1	4
35/17381	0.018556	CUX1/SORL1	2
35/17381	0.018556	CACNA1C/GPD1L	2
36/17381	0.019572	ARID1B/PPARGC1A	2
36/17381	0.019572	DKK3/PPARGC1A	2
36/17381	0.019572	PPARGC1A/RELN	2
354/17381	0.019607	GPD1L/INPP4B/IRS1/MTMR7/OSBPL10/PLEK	6
456/17381	0.019664	CACNA1C/FAM155A/PDE4B/PRKCE/SLC39A11/TPCN2/UB	7
355/17381	0.019851	GPD1L/H6PD/MTHFD1L/PFKP/PPARGC1A/PRKAG2	6
260/17381	0.020012	DOCK1/DOCK5/NRP2/PRKCE/PTK2	5
173/17381	0.020197	ABCA1/PDE4B/PPARGC1A/PRKCE	4
97/17381	0.020452	CACNA1C/PRKCE/UBASH3B	3
460/17381	0.020516	CACNA1C/FAM155A/PDE4B/PRKCE/SLC39A11/TPCN2/UB	7
37/17381	0.02061	GPD1L/PFKP	2
37/17381	0.02061	PDE4B/PPARGC1A	2
37/17381	0.02061	PDE4B/PPARGC1A	2
263/17381	0.020911	DOCK1/DOCK5/NRP2/PRKCE/PTK2	5
99/17381	0.021572	PFKP/PPARGC1A/PRKAG2	3

99/17381	0.021572	MTMR7/PTPRT/UBASH3B	3
38/17381	0.021672	PLEK/PPARGC1A	2
38/17381	0.021672	NPS/PRKCE	2
100/17381	0.022145	PFKP/PPARGC1A/PRKAG2	3
267/17381	0.02215	FSTL4/PBX1/PTK2/SORL1/SPOCK1	5
366/17381	0.022662	KIRREL3/PPARGC1A/RARB/RELN/SLC1A2/TRAPPC9	6
101/17381	0.022726	CACNA1C/GPD1L/TPCN2	3
39/17381	0.022755	COX10/PPARGC1A	2
269/17381	0.022787	GPD1L/INPP4B/IRS1/MTMR7/PLCE1	5
269/17381	0.022787	DOCK1/DOCK5/NRP2/PRKCE/PTK2	5
473/17381	0.02346	APBB2/AUTS2/FSTL4/NRP2/PTK2/RELN/UNC5C	7
4/17381	0.023722	ERG	1
4/17381	0.023722	PLCE1	1
4/17381	0.023722	PPARGC1A	1
4/17381	0.023722	DKK3	1
4/17381	0.023722	DKK3	1
4/17381	0.023722	KCNMA1	1
4/17381	0.023722	AUTS2	1
4/17381	0.023722	RELN	1
4/17381	0.023722	GMDS	1
4/17381	0.023722	ABCA1	1
4/17381	0.023722	DMRT2	1
4/17381	0.023722	SORL1	1
4/17381	0.023722	SGK1	1
4/17381	0.023722	SLC1A2	1
4/17381	0.023722	SLC1A2	1
4/17381	0.023722	ARID1B	1
4/17381	0.023722	RELN	1
4/17381	0.023722	RELN	1
4/17381	0.023722	NRP2	1
4/17381	0.023722	NRP2	1
4/17381	0.023722	SORL1	1
4/17381	0.023722	PPARGC1A	1
4/17381	0.023722	PPARGC1A	1
4/17381	0.023722	DKK3	1
4/17381	0.023722	SORL1	1
40/17381	0.023861	DKK3/PPARGC1A	2
40/17381	0.023861	CACNA1C/PDE4B	2
184/17381	0.024654	DKK3/PBX1/PPARGC1A/PRKAG2	4
275/17381	0.024769	AUH/IRS1/MTMR7/PPARGC1A/PRKAG2	5
41/17381	0.024988	PEX14/SORL1	2
41/17381	0.024988	PLEK/PPARGC1A	2
41/17381	0.024988	PPARGC1A/RELN	2
105/17381	0.025133	PFKP/PPARGC1A/PRKAG2	3
42/17381	0.026137	IRS1/PTK2	2
42/17381	0.026137	IRS1/PTK2	2
107/17381	0.026385	DOCK1/DOCK5/PRKCE	3
43/17381	0.027306	IRS1/SLC1A2	2
43/17381	0.027306	FAM155A/SLC9A9	2
43/17381	0.027306	FAM155A/SLC9A9	2

192/17381	0.02824	H6PD/IRS1/PFKP/PPARGC1A	4
110/17381	0.028327	CACNA1C/GPD1L/PDE4B	3
193/17381	0.028709	FSTL4/PBX1/PTK2/SPOCK1	4
288/17381	0.029436	FSTL4/PBX1/PTK2/SORL1/SPOCK1	5
5/17381	0.029565	SGK1	1
5/17381	0.029565	AUH	1
5/17381	0.029565	MTHFD1L	1
5/17381	0.029565	PLEK	1
5/17381	0.029565	NPS	1
5/17381	0.029565	RERE	1
5/17381	0.029565	FSTL4	1
5/17381	0.029565	DKK3	1
5/17381	0.029565	DKK3	1
5/17381	0.029565	DKK3	1
5/17381	0.029565	UNC5C	1
5/17381	0.029565	PLEK	1
5/17381	0.029565	KCNMA1	1
5/17381	0.029565	PPARGC1A	1
5/17381	0.029565	PPARGC1A	1
5/17381	0.029565	DKK3	1
5/17381	0.029565	ERG	1
5/17381	0.029565	PDE4B	1
5/17381	0.029565	SORL1	1
5/17381	0.029565	SORL1	1
5/17381	0.029565	AUTS2	1
5/17381	0.029565	RELN	1
195/17381	0.029662	ABCA1/PDE4B/PPARGC1A/PRKCE	4
45/17381	0.029708	CACNA1C/PDE4B	2
391/17381	0.030025	APBB2/FSTL4/PLCE1/SGK1/SPOCK1/WISP1	6
391/17381	0.030025	CARD11/PEX14/PPARGC1A/RELN/SGK1/TRAPPC9	6
197/17381	0.030632	CACNA1C/PRKCE/TPCN2/UBASH3B	4
46/17381	0.030939	PDE4B/PDE7B	2
47/17381	0.03219	IRS1/SLC1A2	2
202/17381	0.033141	AUTS2/FSTL4/NRP2/SORBS2	4
117/17381	0.033144	PFKP/PPARGC1A/PRKAG2	3
48/17381	0.033461	PPARGC1A/PRKAG2	2
48/17381	0.033461	PRKCE/RELN	2
48/17381	0.033461	GPD1L/PRKCE	2
118/17381	0.033865	IRS1/PRKAG2/SLC1A2	3
300/17381	0.034209	CACNA1C/NCALD/PLCE1/PLEK/TPCN2	5
119/17381	0.034594	LMO3/TRIO/WDFY2	3
49/17381	0.034751	CACNA1C/TPCN2	2
120/17381	0.035331	FRMD4A/PTK2/WWC1	3
6/17381	0.035374	MN1	1
6/17381	0.035374	RARB	1
6/17381	0.035374	TRIO	1
6/17381	0.035374	NPS	1
6/17381	0.035374	ABCA1	1
6/17381	0.035374	ABCA1	1
6/17381	0.035374	MTHFD1L	1

6/17381	0.035374	GALNT2	1
6/17381	0.035374	RERE	1
6/17381	0.035374	RERE	1
6/17381	0.035374	DKK3	1
6/17381	0.035374	DKK3	1
6/17381	0.035374	DKK3	1
6/17381	0.035374	PPARGC1A	1
6/17381	0.035374	MN1	1
6/17381	0.035374	NPS	1
6/17381	0.035374	SLC1A2	1
6/17381	0.035374	PPARGC1A	1
6/17381	0.035374	PTK2	1
6/17381	0.035374	PRKCE	1
6/17381	0.035374	CACNA1C	1
6/17381	0.035374	PPARGC1A	1
6/17381	0.035374	NRP2	1
6/17381	0.035374	SORL1	1
6/17381	0.035374	SORL1	1
6/17381	0.035374	DKK3	1
6/17381	0.035374	ERG	1
6/17381	0.035374	PPARGC1A	1
408/17381	0.035841	CACNA1C/FAM155A/PDE4B/PRKCE/TPCN2/UBASH3B	6
50/17381	0.036061	INPP4B/IRS1	2
122/17381	0.036829	DMRT2/MTHFD1L/PBX1	3
51/17381	0.037389	IRS1/PTK2	2
51/17381	0.037389	COX10/MTHFD1L	2
51/17381	0.037389	FSTL4/PTK2	2
51/17381	0.037389	IRS1/PRKCE	2
210/17381	0.037398	LMO3/PPARGC1A/TRIO/WDFY2	4
123/17381	0.037591	PFKP/PPARGC1A/PRKAG2	3
308/17381	0.037644	GALNT2/GPD1L/PRKCE/SGK1/STK32C	5
413/17381	0.037681	CACNA1C/FAM155A/PLCE1/PRKCE/TPCN2/UBASH3B	6
124/17381	0.03836	IRS1/PRKAG2/SLC1A2	3
124/17381	0.03836	IRS1/PPARGC1A/PRKAG2	3
52/17381	0.038736	CARD11/PDE4B	2
126/17381	0.039923	IRS1/PTK2/RELN	3
126/17381	0.039923	IRS1/PRKAG2/SLC1A2	3
126/17381	0.039923	CUX1/RELN/RERE	3
53/17381	0.040101	NPS/SLC1A2	2
53/17381	0.040101	AUTS2/PPARGC1A	2
53/17381	0.040101	PDE4B/PDE7B	2
53/17381	0.040101	CACNA1C/GPD1L	2
127/17381	0.040717	CACNA1C/PBX1/RARB	3
127/17381	0.040717	CACNA1C/PBX1/RARB	3
7/17381	0.041147	SORL1	1
7/17381	0.041147	GPD1L	1
7/17381	0.041147	PPARGC1A	1
7/17381	0.041147	MAML3	1
7/17381	0.041147	KCNMA1	1
7/17381	0.041147	KCNMA1	1

7/17381	0.041147	GALNT2	1
7/17381	0.041147	GMDS	1
7/17381	0.041147	MSRA	1
7/17381	0.041147	DKK3	1
7/17381	0.041147	ABCA1	1
7/17381	0.041147	LMO3	1
7/17381	0.041147	ABCA1	1
7/17381	0.041147	DOCK5	1
7/17381	0.041147	PPARGC1A	1
7/17381	0.041147	MTHFD1L	1
7/17381	0.041147	KCNMA1	1
7/17381	0.041147	AUTS2	1
7/17381	0.041147	RELN	1
7/17381	0.041147	PPARGC1A	1
7/17381	0.041147	PDE4B	1
7/17381	0.041147	SORL1	1
7/17381	0.041147	SORL1	1
7/17381	0.041147	SORL1	1
54/17381	0.041484	CACNA1C/NPS	2
128/17381	0.041518	LHFPL2/PHACTR2/PLEK	3
128/17381	0.041518	FSTL4/PTK2/SPOCK1	3
424/17381	0.041939	GPD1L/LMO3/PPARGC1A/PRKAG2/SORL1/UBASH3B	6
424/17381	0.041939	CACNA1C/FAM155A/PLCE1/PRKCE/TPCN2/UBASH3B	6
218/17381	0.041956	INPP4B/IRS1/MTMR7/PLEK	4
129/17381	0.042328	CACNA1C/GPD1L/PDE4B	3
425/17381	0.042341	CUX1/FSTL4/PTK2/RELN/SPOCK1/ULK4	6
55/17381	0.042885	ITGA11/PTK2	2
55/17381	0.042885	PPARGC1A/PRKCE	2
55/17381	0.042885	PLEK/PRKCE	2
130/17381	0.043145	CACNA1C/GPD1L/PDE4B	3
56/17381	0.044304	AUTS2/RELN	2
56/17381	0.044304	PLEK/UBASH3B	2
132/17381	0.044803	DOCK1/PRKCE/PTK2	3
132/17381	0.044803	DOCK1/PRKCE/PTK2	3
133/17381	0.045644	CUX1/FSTL4/RELN	3
57/17381	0.045739	ABCA1/PRKCE	2
57/17381	0.045739	AUTS2/PPARGC1A	2
134/17381	0.046493	NPS/PRKCE/RELN	3
226/17381	0.046817	GPD1L/PRKCE/SGK1/SLC9A9	4
226/17381	0.046817	CACNA1C/PDE4B/PRKCE/UBASH3B	4
8/17381	0.046887	KIRREL3	1
8/17381	0.046887	DOCK5	1
8/17381	0.046887	PTK2	1
8/17381	0.046887	ARID1B	1
8/17381	0.046887	PPARGC1A	1
8/17381	0.046887	PPARGC1A	1
8/17381	0.046887	RELN	1
8/17381	0.046887	KCNMA1	1
8/17381	0.046887	WWC1	1
8/17381	0.046887	PPARGC1A	1

8/17381	0.046887	MTHFD1L	1
8/17381	0.046887	GPD1L	1
8/17381	0.046887	AUTS2	1
8/17381	0.046887	ABCA1	1
8/17381	0.046887	GPD1L	1
8/17381	0.046887	PPARGC1A	1
8/17381	0.046887	KIRREL3	1
8/17381	0.046887	RELN	1
8/17381	0.046887	SORL1	1
8/17381	0.046887	SLC1A2	1
8/17381	0.046887	RELN	1
8/17381	0.046887	SLC1A2	1
8/17381	0.046887	SORL1	1
8/17381	0.046887	SORL1	1
8/17381	0.046887	SORL1	1
8/17381	0.046887	LMO3	1
8/17381	0.046887	SORL1	1
8/17381	0.046887	PPARGC1A	1
58/17381	0.047192	LMO3/WDFY2	2
58/17381	0.047192	GPD1L/PRKCE	2
135/17381	0.04735	PFKP/PPARGC1A/PRKAG2	3
438/17381	0.047784	CACNA1C/FAM155A/PLCE1/PRKCE/TPCN2/UBASH3B	6
136/17381	0.048214	DOCK1/PRKCE/PTK2	3
59/17381	0.048662	CARD11/PDE4B	2
59/17381	0.048662	NPS/RELN	2
137/17381	0.049087	DOCK1/PRKCE/PTK2	3
442/17381	0.049543	DOCK1/DOCK5/NRP2/PRKCE/PTK2/RELN	6
138/17381	0.049967	KIRREL3/PBX1/PLCE1	3