

Supplementary Table S8. Potential DE mRNAs related to fat deposition and lipid metabolism.

RNA ID	Symbol	log2 (DWZ/Yorkshire)	Q value (DWZ/Yorkshire)	KEGG pathway description	GO_C description	GO_F description	GO_P description
NM_213883.2	IGF2	-2.268181338	2.72E-14	04151//PI3K-Akt signaling pathway+++04010//MAPK signaling pathway+++04014//Ras signaling pathway	GO:0016020//membrane+++GO:0005576//extracellular region+++GO:0016021//integral component of membrane+++GO:0005615//extracellular space	GO:0005179//hormone activity+++GO:0005178//integrin binding+++GO:0008083//growth factor activity	GO:0005975//carbohydrate metabolic process+++GO:0008284//positive regulation of cell proliferation+++GO:0001892//embryonic placenta development+++GO:0051781//positive regulation of cell division+++GO:0001503//ossification+++GO:0031056//regulation of histone modification+++GO:0010469//regulation of signaling receptor activity+++GO:0051147//regulation of muscle cell differentiation+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0001701//in utero embryonic development+++GO:0006006//glucose metabolic process+++GO:0060669//embryonic placenta morphogenesis GO:0051781//positive regulation of cell division+++GO:0006006//glucose metabolic process+++GO:0001701//in utero embryonic development+++GO:0005975//carbohydrate metabolic process+++GO:0051147//regulation of muscle cell differentiation+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0060669//embryonic placenta morphogenesis+++GO:0001892//embryonic placenta development+++GO:0001503//ossification+++GO:0010469//regulation of signaling receptor activity+++GO:0031056//regulation of histone modification+++GO:0008284//positive regulation of cell proliferation
XM_021080576.1	IGF2	-2.630210893	7.91E-08	04151//PI3K-Akt signaling pathway+++04014//Ras signaling pathway+++04010//MAPK signaling pathway	GO:0016020//membrane+++GO:0005615//extracellular space+++GO:0005576//extracellular region+++GO:0016021//integral component of membrane	GO:0008083//growth factor activity+++GO:0005179//hormone activity+++GO:0005178//integrin binding	GO:0005975//carbohydrate metabolic process+++GO:0008284//positive regulation of cell proliferation+++GO:0001892//embryonic placenta development+++GO:0001503//ossification+++GO:0010469//regulation of signaling receptor activity+++GO:0031056//regulation of histone modification+++GO:0008284//positive regulation of cell proliferation
XM_021097872.1	SLA-2	2.756366494	1.56E-04	04145//Phagosome+++04514//Cell adhesion molecules (CAMs)+++04144//Endocytosis+++04218//Cellular senescence+++04612//Antigen processing and presentation	GO:0016021//integral component of membrane+++GO:0042612//MHC class I protein complex		GO:0002474//antigen processing and presentation of peptide antigen via MHC class I+++GO:0006955//immune response

NM_214201.1	GPX1	1.180518799	2.35E-06	00480//Glutathione metabolism+++04918//Thyroid hormone synthesis+++00590//Arachidonic acid metabolism	GO:0005737//cytoplasm+++GO:0097413//Lewy body+++GO:0005829//cytosol+++GO:0005739//mitochondrion	GO:0004602//glutathione peroxidase activity+++GO:0017124//SH3 domain binding+++GO:0004601//peroxidase activity+++GO:0016491//oxidoreductase activity	GO:0042311//vasodilation+++GO:0090201//negative regulation of release of cytochrome c from mitochondria+++GO:0060055//angiogenesis involved in wound healing+++GO:1902042//negative regulation of extrinsic apoptotic signaling pathway via death domain receptors+++GO:0043523//regulation of neuron apoptotic process+++GO:0051702//interaction with symbiont+++GO:0043534//blood vessel endothelial cell migration+++GO:0042542//response to hydrogen peroxide+++GO:0002862//negative regulation of inflammatory response to antigenic stimulus+++GO:0000302//response to reactive oxygen species+++GO:0001885//endothelial cell development+++GO:0051897//positive regulation of protein kinase B signaling+++GO:0010332//response to gamma radiation+++GO:0018158//protein oxidation+++GO:0048741//skeletal muscle fiber development+++GO:0033194//response to hydroperoxide+++GO:0040029//regulation of gene expression, epigenetic+++GO:0043403//skeletal muscle tissue regeneration+++GO:0055114//oxidation-reduction process+++GO:0061136//regulation of proteasomal protein catabolic process+++GO:0008631//intrinsic apoptotic signaling pathway in response to oxidative stress+++GO:0009650//UV protection+++GO:0043066//negative regulation of apoptotic process+++GO:0009611//response to wounding+++GO:0045444//fat cell differentiation+++GO:0051450//myoblast proliferation+++GO:0008283//cell proliferation+++GO:1902176//negative regulation of oxidative stress-induced intrinsic apoptotic signaling pathway+++GO:0006979//response to oxidative stress+++GO:0001659//temperature homeostasis+++GO:0009410//response to xenobiotic stimulus+++GO:0014902//myotube differentiation+++GO:0043154//negative regulation of cysteine-type endopeptidase activity involved in anontotic
NM_001115155.1	GPX3	2.154452184	3.74E-05	04918//Thyroid hormone synthesis+++00480//Glutathione metabolism+++00590//Arachidonic acid metabolism	GO:0005615//extracellular space	GO:0004601//peroxidase activity+++GO:0016491//oxidoreductase activity+++GO:0004602//glutathione peroxidase activity+++GO:0008430//selenium binding	GO:0006979//response to oxidative stress+++GO:0098869//cellular oxidant detoxification+++GO:0042744//hydrogen peroxide catabolic process+++GO:0051289//protein homotetramerization+++GO:0055114//oxidation-reduction process

NM_214366.1	PPP2CA	1.609945047	5.59E-04	<p>04152//AMPK signaling pathway+++04013//MAPK signaling pathway - fly+++03015//mRNA surveillance pathway+++04728//Dopaminergic synapse+++04261//Adrenergic signaling in cardiomyocytes+++04350//TGF-beta signaling pathway+++04530//Tight junction+++04151//PI3K-Akt signaling pathway+++04138//Autophagy - yeast+++04140//Autophagy - animal+++04071//Sphingolipid signaling pathway+++04391//Hippo signaling pathway - fly+++04114//Oocyte meiosis+++04390//Hippo signaling pathway+++04730//Long-term depression+++04113//Meiosis - yeast+++04111//Cell cycle - yeast+++04136//Autophagy - other</p>	<p>GO:0000159//protein phosphatase type 2A complex+++GO:0005856//cytoskeleton+++GO:005886//plasma membrane+++GO:0045121//membrane raft+++GO:0045202//synapse+++GO:0005737//cytoplasm+++GO:0005694//chromosome+++GO:000922//spindle pole+++GO:0005634//nucleus+++GO:0005829//cytosol+++GO:0000775//chromosome, centromeric region</p>	<p>GO:0046872//metal ion binding+++GO:0046982//protein heterodimerization activity+++GO:0050811//GABA receptor binding+++GO:0016787//hydrolase activity+++GO:0004721//phosphoprotein phosphatase activity+++GO:0008022//protein C-terminus binding</p>	<p>GO:0007498//mesoderm development+++GO:0010719//negative regulation of epithelial to mesenchymal transition+++GO:0006470//protein dephosphorylation+++GO:0071902//positive regulation of protein serine/threonine kinase activity+++GO:0051321//meiotic cell cycle</p>
XR_002345546.1	SLA-2	1.429697533	0.010705227	<p>04612//Antigen processing and presentation+++04514//Cell adhesion molecules (CAMs)+++04218//Cellular senescence+++04144//Endocytosis+++04145//Phagosome</p>	<p>GO:0000159//Golgi membrane+++GO:0005886//plasma membrane+++GO:0005887//integral component of plasma membrane+++GO:0030670//phagocytic vesicle membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0005783//endoplasmic reticulum+++GO:0055038//recycling endosome membrane+++GO:0071556//integral component of luminal side of endoplasmic reticulum membrane+++GO:0009986//cell surface+++GO:0012507//ER to Golgi transport vesicle membrane+++GO:0016020//membrane+++GO:0042612//MHC class I protein complex+++GO:0031901//early endosome</p>	<p>GO:0046977//TAP binding+++GO:0030881//beta-2-microglobulin binding+++GO:0042605//peptide antigen binding</p>	<p>GO:0016567//protein ubiquitination+++GO:0006955//immune response+++GO:0060337//type I interferon signaling pathway+++GO:0050776//regulation of immune response+++GO:0002474//antigen processing and presentation of peptide antigen via MHC class I+++GO:0002480//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent+++GO:0060333//interferon-gamma-mediated signaling pathway+++GO:0002479//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent</p>
XM_021099123.1	PKM	-2.733557111	0.008946525	<p>00230//Purine metabolism+++01230//Biosynthesis of amino acids+++01100//Metabolic pathways+++01130//Biosynthesis of antibiotics+++01110//Biosynthesis of secondary metabolites+++00010//Glycolysis / Gluconeogenesis+++04922//Glucagon signaling pathway+++01120//Microbial metabolism in diverse environments+++01200//Carbon metabolism+++00620//Pyruvate metabolism</p>	<p>GO:0043209//myelin sheath+++GO:0005634//nucleus+++GO:0005929//cilium+++GO:0005829//cytosol+++GO:0005737//cytoplasm</p>	<p>GO:0016740//transferase activity+++GO:0000287//magnesium ion binding+++GO:0004743//pyruvate kinase activity+++GO:0030955//potassium ion binding+++GO:0016301//kinase activity+++GO:0003824//catalytic activity</p>	<p>GO:0032869//cellular response to insulin stimulus+++GO:1903672//positive regulation of sprouting angiogenesis+++GO:0012501//programmed cell death+++GO:0016310//phosphorylation+++GO:006096//glycolytic process</p>

XM_003123639.4	SQSTM1	1.204257295	0.006062215	04380//Osteoclast differentiation+++04137//Mitophagy - animal+++04218//Cellular senescence+++04217//Necroptosis	GO:0000407//phagophore assembly site+++GO:0016235//aggresome+++GO:0016605//PML body+++GO:0016234//inclusion body+++GO:0005737//cytoplasm+++GO:0005776//autophagosome+++GO:0043231//intracellular membrane-bounded organelle+++GO:0005829//cytosol+++GO:0097225//sperm midpiece+++GO:0000932//P-body+++GO:0044754//autolysosome+++GO:004753//amphisome	GO:0046872//metal ion binding+++GO:0031625//ubiquitin protein ligase binding+++GO:0043130//ubiquitin binding+++GO:0019899//enzyme binding+++GO:0005080//protein kinase C binding+++GO:0019901//protein kinase binding+++GO:0042169//SH2 domain binding+++GO:0008270//zinc ion binding+++GO:0035255//ionotropic glutamate receptor binding+++GO:0070530//K63-linked polyubiquitin modification-dependent protein binding+++GO:0042802//identical protein binding	GO:0061635//regulation of protein complex stability+++GO:0098780//response to mitochondrial depolarisation+++GO:1905719//protein localization to perinuclear region of cytoplasm+++GO:0044130//negative regulation of growth of symbiont in host+++GO:0061912//selective autophagy+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0043122//regulation of I-kappaB kinase/NF-kappaB signaling+++GO:0035973//aggrephagy+++GO:0016236//macroautophagy+++GO:0006914//autophagy+++GO:0007005//mitochondrion organization+++GO:1900273//positive regulation of long-term synaptic potentiation+++GO:0000423//mitophagy+++GO:0007032//endosome organization+++GO:1903078//positive regulation of protein localization to plasma membrane
NM_001099931.1	FABP3	2.919151334	0.024281225	03320//PPAR signaling pathway	GO:0005737//cytoplasm	GO:0008289//lipid binding	
XM_013977556.2	SLA-1	-7.513247337	7.91E-08	04514//Cell adhesion molecules (CAMs)+++04144//Endocytosis+++04612//Antigen processing and presentation+++04145//Phagosome+++04218//Cellular senescence	GO:0042612//MHC class I protein complex+++GO:0016021//integral component of membrane		GO:0006955//immune response+++GO:0002474//antigen processing and presentation of peptide antigen via MHC class I
XM_021080648.1	IGF2	-8.066590296	5.39E-07	04010//MAPK signaling pathway+++04014//Ras signaling pathway+++04151//PI3K-Akt signaling pathway	GO:0016020//membrane+++GO:0016021//integral component of membrane+++GO:0005615//extracellular space+++GO:0005576//extracellular region	GO:0005178//integrin binding+++GO:0008083//growth factor activity+++GO:0005179//hormone activity	GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0008284//positive regulation of cell proliferation+++GO:0051781//positive regulation of cell division+++GO:0051147//regulation of muscle cell differentiation+++GO:0001503//ossification+++GO:0006006//glucose metabolic process+++GO:0001701//in utero embryonic development+++GO:0060669//embryonic placenta morphogenesis+++GO:0031056//regulation of histone modification+++GO:0005975//carbohydrate metabolic process+++GO:0010469//regulation of signaling receptor activity+++GO:0001892//embryonic placenta development

NM_001113702.1	SLA-2	-23.83174519	4.64E-07	04514//Cell adhesion molecules (CAMs)+++04144//Endocytosis+++04145//Phagosome+++04218//Cellular senescence+++04612//Antigen processing and presentation	GO:0009986//cell surface+++GO:0005789//endoplasmic reticulum membrane+++GO:000139//Golgi membrane+++GO:0012507//ER to Golgi transport vesicle membrane+++GO:0031901//early endosome membrane+++GO:0005886//plasma membrane+++GO:0030670//phagocytic vesicle membrane+++GO:0005887//integral component of plasma membrane+++GO:0016020//membrane+++GO:0005783//endoplasmic reticulum+++GO:0071556//integral component of luminal side of endoplasmic reticulum membrane+++GO:0042612//MHC class I protein complex+++GO:0055038//recycling endosome membrane+++GO:0005794//Golgi apparatus	GO:0046977//TAP binding+++GO:0030881//beta-2-microglobulin binding+++GO:0042605//peptide antigen binding	GO:0060333//interferon-gamma-mediated signaling pathway+++GO:0002474//antigen processing and presentation of peptide antigen via MHC class I+++GO:0050776//regulation of immune response+++GO:0002479//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent+++GO:0006955//immune response+++GO:0002480//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent+++GO:0016567//protein ubiquitination+++GO:0060337//type I interferon signaling pathway
NM_001136511.1	HUS1	-4.573817745	0.005775176	04218//Cellular senescence	GO:0035861//site of double-strand break+++GO:0005634//nucleus+++GO:0030896//checkpoint clamp complex+++GO:0005730//nucleolus		GO:0000125//telomere maintenance+++GO:0006289//nucleotide-excision repair+++GO:0007093//mitotic cell cycle checkpoint+++GO:0044778//meiotic DNA integrity checkpoint+++GO:0009792//embryo development ending in birth or egg hatching+++GO:0031573//intra-S DNA damage checkpoint+++GO:0033314//mitotic DNA replication checkpoint+++GO:0000724//double-strand break repair via homologous recombination+++GO:0001932//regulation of protein phosphorylation+++GO:0008156//negative regulation of DNA replication+++GO:0000077//DNA damage checkpoint+++GO:0006974//cellular response to DNA damage stimulus+++GO:0006468//protein phosphorylation+++GO:0000075//cell cycle checkpoint+++GO:0009411//response to UV+++GO:0071479//cellular response to ionizing radiation
XM_021072575.1	PPP3CB	-6.228823559	6.20E-06	04724//Glutamatergic synapse+++04650//Natural killer cell mediated cytotoxicity+++04020//Calcium signaling pathway+++04658//Th1 and Th2 cell differentiation+++04010//MAPK signaling pathway+++04114//Oocyte meiosis+++04662//B cell receptor signaling pathway+++04659//Th17 cell differentiation+++04728//Dopaminergic synapse+++04660//T cell receptor signaling pathway+++04370//VEGF signaling pathway+++04924//Renin secretion+++04921//Oxytocin signaling pathway+++04022//cGMP-PKG signaling pathway+++04218//Cellular senescence+++04360//Axon guidance+++04922//Glucagon signaling pathway+++04380//Osteoclast differentiation+++04625//C-type lectin receptor signaling pathway+++04310//Wnt signaling	GO:0005955//calcineurin complex+++GO:0005886//plasma membrane+++GO:0030018//Z disc+++GO:0098978//glutamatergic synapse+++GO:0030315//T-tubule+++GO:0005737//cytoplasm	GO:0008144//drug binding+++GO:0033192//calmodulin-dependent protein phosphatase activity+++GO:0004722//protein serine/threonine phosphatase activity+++GO:0004721//phosphoprotein phosphatase activity+++GO:0016787//hydrolase activity+++GO:0005516//calmodulin binding+++GO:0019899//enzyme binding+++GO:0005509//calcium ion binding+++GO:0030346//protein phosphatase 2B binding	GO:0003569//cellular response to drug+++GO:1900242//regulation of synaptic vesicle endocytosis+++GO:0006468//protein phosphorylation+++GO:0031987//locomotion involved in locomotory behavior+++GO:0043029//T cell homeostasis+++GO:0030217//T cell differentiation+++GO:0006470//protein dephosphorylation+++GO:0001915//negative regulation of T cell mediated cytotoxicity+++GO:0097720//calcineurin-mediated signaling+++GO:0007507//heart development+++GO:0017156//calcium ion regulated exocytosis+++GO:0035774//positive regulation of insulin secretion involved in cellular response to glucose stimulus+++GO:0001946//lymphangiogenesis+++GO:0034097//response to

XM_013980816.2	MAP2K6	-1.770223162	3.54E-07	04218//Cellular senescence+++04015//Rap1 signaling pathway+++04620//Toll-like receptor signaling pathway+++04212//Longevity regulating pathway - worm+++04664//Fc epsilon RI signaling pathway+++04668//TNF signaling pathway+++04010//MAPK signaling pathway+++04380//Osteoclast differentiation+++04912//GnRH signaling pathway+++04750//Inflammatory mediator regulation of TRP channels	GO:0005829//cytosol+++GO:0005634//nucleus	GO:0004674//protein serine/threonine kinase activity+++GO:0000166//nucleotide binding+++GO:0004708//MAP kinase kinase activity+++GO:0019901//protein kinase binding+++GO:0016301//kinase activity+++GO:0005524//ATP binding+++GO:0004672//protein kinase activity	GO:0120163//negative regulation of cold-induced thermogenesis+++GO:0016310//phosphorylation+++GO:0000165//MAPK cascade+++GO:0000187//activation of MAPK activity+++GO:0006468//protein phosphorylation+++GO:0060048//cardiac muscle contraction
XM_021075038.1	PPP1R3B	-1.762376476	0.032147271	04910//Insulin signaling pathway	GO:0000164//protein phosphatase type 1 complex	GO:0019888//protein phosphatase regulator activity	GO:0005977//glycogen metabolic process+++GO:0005981//regulation of glycogen catabolic process+++GO:0043666//regulation of phosphoprotein phosphatase activity+++GO:0005975//carbohydrate metabolic process
XM_005669518.3	PFKFB4	-1.028598195	0.011980256	00051//Fructose and mannose metabolism+++04152//AMPK signaling pathway	GO:0005829//cytosol	GO:0005524//ATP binding+++GO:0004331//fructose-2,6-bisphosphate 2-phosphatase activity+++GO:0003873//6-phosphofructo-2-kinase activity+++GO:0003824//catalytic activity	GO:0006000//fructose metabolic process+++GO:0046835//carbohydrate phosphorylation+++GO:0016311//dephosphorylation+++GO:0006003//fructose 2,6-bisphosphate metabolic process
XM_021096633.1	GPX7	-1.338056783	0.029188595	00590//Arachidonic acid metabolism+++00480//Glutathione metabolism+++04918//Thyroid hormone synthesis	GO:0005783//endoplasmic reticulum+++GO:0005576//extracellular region	GO:0004601//peroxidase activity+++GO:0016491//oxidoreductase activity+++GO:0004602//glutathione peroxidase activity	GO:0098869//cellular oxidant detoxification+++GO:0055114//oxidation-reduction process+++GO:0006979//response to oxidative stress
XM_021080641.1	IGF2	-10.55693293	1.71E-10	04151//PI3K-Akt signaling pathway+++04010//MAPK signaling pathway+++04014//Ras signaling pathway	GO:0005615//extracellular space+++GO:0016020//membrane+++GO:0016021//integral component of membrane+++GO:0005576//extracellular region	GO:0005179//hormone activity+++GO:0008083//growth factor activity+++GO:0005178//integrin binding	GO:0006006//glucose metabolic process+++GO:0008284//positive regulation of cell proliferation+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0060669//embryonic placenta morphogenesis+++GO:0051781//positive regulation of cell division+++GO:0010469//regulation of signaling receptor activity+++GO:0001503//ossification+++GO:0001892//embryonic placenta development+++GO:0005975//carbohydrate metabolic process+++GO:0001701//in utero embryonic development+++GO:0031056//regulation of histone modification+++GO:0051147//regulation of muscle cell differentiation

XM_021093026.1	APAF1	-4.477990917	2.73E-04	04210//Apoptosis+++04215//Apoptosis - multiple species+++04214//Apoptosis - fly+++04115//p53 signaling pathway	GO:0032991//protein-containing complex+++GO:0005634//nucleus+++GO:0005737//cytoplasm+++GO:0043293//apoptosome+++GO:0005829//cytosol	GO:0043531//ADP binding+++GO:0000166//nucleotide binding+++GO:0042802//identical protein binding+++GO:0008233//peptidase activity+++GO:0005524//ATP binding+++GO:0008656//cysteine-type endopeptidase activator activity involved in apoptotic process	GO:0008635//activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c+++GO:0007275//multicellular organism development+++GO:0007420//brain development+++GO:1902510//regulation of apoptotic DNA fragmentation+++GO:0006508//proteolysis+++GO:0042981//regulation of apoptotic process+++GO:0001843//neural tube closure+++GO:0030900//forebrain development+++GO:2001235//positive regulation of apoptotic signaling pathway+++GO:0006919//activation of cysteine-type endopeptidase activity involved in apoptotic process+++GO:0051402//neuron apoptotic process+++GO:0097190//apoptotic signaling pathway+++GO:0006915//apoptotic signaling pathway+++GO:0009411//response to UV+++GO:0035518//histone H2A monoubiquitination+++GO:0006281//DNA repair+++GO:0010224//response to UV-B+++GO:0070914//UV-damage excision repair+++GO:0000209//protein polyubiquitination+++GO:0006290//pyrimidine dimer repair
XM_013994354.2	DDB2	-1.855766191	1.36E-06	04120//Ubiquitin mediated proteolysis+++03420//Nucleotide excision repair+++04115//p53 signaling pathway	GO:0030054//cell junction+++GO:0080008//Cul4-RING E3 ubiquitin ligase complex+++GO:0032991//protein-containing complex+++GO:0005634//nucleus+++GO:0005654//nucleoplasm+++GO:0031465//Cul4B-RING E3 ubiquitin ligase complex	GO:0004842//ubiquitin-protein transferase activity+++GO:0003684//damaged DNA binding+++GO:0044877//protein-containing complex binding	

NM_001044525.1	KIT	-2.195084256	0.007324293	04014//Ras signaling pathway+++04151//PI3K-Akt signaling pathway+++04072//Phospholipase D signaling pathway+++04640//Hematopoietic cell lineage+++04015//Rap1 signaling pathway+++04916//Melanogenesis+++04010//MAP K signaling pathway	GO:0043235//receptor complex+++GO:0005887//integral component of plasma membrane+++GO:0005886//plasma membrane+++GO:0016021//integral component of membrane+++GO:0005615//extracellular space+++GO:0005737//cytoplasm+++GO:0009897//external side of plasma membrane+++GO:0009986//cell surface+++GO:0016020//membrane+++GO:0005911//cell-cell junction+++GO:0042629//mast cell granule	GO:0002020//protease binding+++GO:0046872//metal ion binding+++GO:0004888//transmembrane signaling receptor activity+++GO:0016301//kinase activity+++GO:0042803//protein homodimerization activity+++GO:0005524//ATP binding+++GO:0004713//protein tyrosine kinase activity+++GO:0004672//protein kinase activity+++GO:0000166//nucleotide binding+++GO:0004714//transmembrane receptor protein tyrosine kinase activity+++GO:0005020//stem cell factor receptor activity+++GO:0019955//cytokine binding+++GO:0016740//transferase activity	GO:0050910//detection of mechanical stimulus involved in sensory perception of sound+++GO:0046777//protein autophosphorylation+++GO:0043410//positive regulation of MAPK cascade+++GO:0030217//T cell differentiation+++GO:0097067//cellular response to thyroid hormone stimulus+++GO:0043473//pigmentation+++GO:0035556//intracellular signal transduction+++GO:0060374//mast cell differentiation+++GO:0035855//megakaryocyte development+++GO:0018108//peptidyl-tyrosine phosphorylation+++GO:0043069//negative regulation of programmed cell death+++GO:0008360//regulation of cell shape+++GO:0007283//spermatogenesis+++GO:0008284//positive regulation of cell proliferation+++GO:0030318//melanocyte differentiation+++GO:0060326//cell chemotaxis+++GO:0043406//positive regulation of MAP kinase activity+++GO:0007286//spermatid development+++GO:0002320//lymphoid progenitor cell differentiation+++GO:0048863//stem cell differentiation+++GO:0042531//positive regulation of tyrosine phosphorylation of STAT protein+++GO:0006954//inflammatory response+++GO:0002327//immature B cell differentiation+++GO:0051091//positive regulation of DNA-binding transcription factor activity+++GO:0002371//dendritic cell cytokine production+++GO:0030032//lamellipodium assembly+++GO:0038109//Kit signaling pathway+++GO:0009314//response to radiation+++GO:0035162//embryonic hemopoiesis+++GO:0030097//hemopoiesis+++GO:0070374//positive regulation of ERK1 and ERK2 cascade+++GO:0006687//glycosphingolipid metabolic process+++GO:0035701//hematopoietic stem cell migration+++GO:0097324//melanocyte migration+++GO:0000187//activation of MAPK activity+++GO:0031532//actin cytoskeleton reorganization+++GO:0032762//mast cell
XM_013997432.2	PKN2	-1.06853347	0.009550899	04151//PI3K-Akt signaling pathway	GO:0005737//cytoplasm+++GO:0030027//lamellipodium+++GO:0030496//midbody+++GO:0016604//nuclear body+++GO:0032991//protein-containing complex+++GO:0045111//intermediate filament cytoskeleton+++GO:0005654//nucleoplasm+++GO:0005634//nucleus+++GO:0005886//plasma membrane+++GO:0005829//cytosol+++GO:0032154//cleavage furrow+++GO:0043296//apical junction complex+++GO:0048471//perinuclear region of cytoplasm+++GO:0005813//centrosome	GO:0004674//protein serine/threonine kinase activity+++GO:0017049//GTP-Rho binding+++GO:0070063//RNA polymerase binding+++GO:0004672//protein kinase activity+++GO:0016740//transferase activity+++GO:0042826//histone deacetylase binding+++GO:0000166//nucleotide binding+++GO:0016301//kinase activity+++GO:0005524//ATP binding	GO:0007165//signal transduction+++GO:2000145//regulation of cell motility+++GO:0016310//phosphorylation+++GO:0006468//protein phosphorylation+++GO:0045931//positive regulation of mitotic cell cycle+++GO:0043297//apical junction assembly+++GO:00101631//epithelial cell migration+++GO:0032467//positive regulation of cytokinesis+++GO:0018105//peptidyl-serine phosphorylation+++GO:0035556//intracellular signal transduction+++GO:0045070//positive regulation of viral genome replication

XM_021071473.1	RXRA	-1.270846026	0.02998124	04919//Thyroid hormone signaling pathway+++04659//Th17 cell differentiation+++04928//Parathyroid hormone synthesis, secretion and action+++03320//PPAR signaling pathway+++04976//Bile secretion+++04151//PI3K-Akt signaling pathway+++04920//Adipocytokine signaling pathway	GO:0090575//RNA polymerase II transcription factor complex+++GO:0000790//nuclear chromatin+++GO:0005634//nucleus+++GO:0043235//receptor complex+++GO:0032991//protein-containing complex	GO:0004886//9-cis retinoic acid receptor activity+++GO:0046982//protein heterodimerization activity+++GO:0043565//sequence-specific DNA binding+++GO:0019899//enzyme binding+++GO:0008270//zinc ion binding+++GO:0008134//transcription factor binding+++GO:0016922//nuclear receptor binding+++GO:0050692//DBD domain binding+++GO:0044323//retinoic acid-responsive element binding+++GO:0000977//RNA polymerase II regulatory region sequence-specific DNA binding+++GO:0003677//DNA binding+++GO:0050693//LBD domain binding+++GO:0046872//metal ion binding+++GO:0042277//peptide binding+++GO:0001972//retinoic acid binding+++GO:0003690//double-stranded DNA binding+++GO:0031490//chromatin DNA binding+++GO:0003700//DNA-binding transcription factor activity+++GO:0044212//transcription regulatory region DNA binding+++GO:0004879//nuclear receptor activity+++GO:0070644//vitamin D response element binding+++GO:0042809//vitamin D receptor binding+++GO:0003707//steroid hormone receptor activity	GO:0055010//ventricular cardiac muscle tissue morphogenesis+++GO:0006357//regulation of transcription by RNA polymerase II+++GO:0007566//embryo implantation+++GO:0060528//secretory columnar luminal epithelial cell differentiation involved in prostate glandular acinus development+++GO:0001890//placenta development+++GO:0001701//in utero embryonic development+++GO:0045893//positive regulation of transcription, DNA-templated+++GO:0007507//heart development+++GO:0032526//response to retinoic acid+++GO:0019048//modulation by virus of host morphology or physiology+++GO:0048384//retinoic acid receptor signaling pathway+++GO:0060038//cardiac muscle cell proliferation+++GO:0045994//positive regulation of translational initiation by iron+++GO:0043401//steroid hormone mediated signaling pathway+++GO:0045944//positive regulation of transcription by RNA polymerase II+++GO:0043010//camera-type eye development+++GO:0001893//maternal placenta development+++GO:0055012//ventricular cardiac muscle cell differentiation+++GO:0051289//protein homotetramerization+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0035357//peroxisome proliferator activated receptor signaling pathway+++GO:0006355//regulation of transcription, DNA-templated+++GO:0060687//regulation of branching involved in prostate gland
XM_013988572.2	HIPK4	-1.373123645	0.001941764	04218//Cellular senescence	GO:0005737//cytoplasm+++GO:0005634//nucleus	GO:0004672//protein kinase activity+++GO:0005524//ATP binding	GO:0016572//histone phosphorylation+++GO:1901796//regulation of signal transduction by p53 class mediator+++GO:0018105//peptidyl-serine phosphorylation+++GO:0006468//protein phosphorylation+++GO:0046777//protein autophosphorylation

XM_021095197.1	TMEM52	-1.748299409	5.42E-04	<p>04912//GnRH signaling pathway+++04728//Dopaminergic synapse+++04745//Phototransduction - fly+++04070//Phosphatidylinositol signaling system+++04916//Melanogenesis+++04713//Circadi an entrainment+++04014//Ras signaling pathway+++04218//Cellular senescence+++04024//cAMP signaling pathway+++04915//Estrogen signaling pathway+++04910//Insulin signaling pathway+++04625//C-type lectin receptor signaling pathway+++04750//Inflammatory mediator regulation of TRP channels+++04261//Adrenergic signaling in cardiomyocytes+++04744//Phototransduction+++04 925//Aldosterone synthesis and secretion+++04722//Neurotrophin signaling pathway+++04971//Gastric acid secretion+++04921//Oxytocin signaling pathway+++04922//Glucagon signaling pathway+++04016//MAPK signaling pathway - plant+++04740//Olfactory transduction+++04924//Renin secretion+++04020//Calcium signaling pathway+++04015//Rap1 signaling pathway+++04114//Oocyte meiosis+++04022//cGMP-PKG signaling pathway+++04270//Vascular smooth muscle contraction+++04626//Plant-pathogen interaction+++04720//Long-term potentiation+++04970//Salivary</p>	<p>GO:0016020//membrane+++GO:0016021//integra l component of membrane</p>
XR_002340201.1	HUS1	-1.567164014	0.019212631	<p>04218//Cellular senescence</p>	<p>GO:0030896//checkpoint clamp complex+++GO:0005730//nucleolus+++GO:0005 634//nucleus+++GO:0035861//site of double- strand break</p>
					<p>GO:0001932//regulation of protein phosphorylation+++GO:0031573//intra-S DNA damage checkpoint+++GO:0033314//mitotic DNA replication checkpoint+++GO:0071479//cellular response to ionizing radiation+++GO:0000723//telomere maintenance+++GO:0044778//meiotic DNA integrity checkpoint+++GO:0006289//nucleotide- excision repair+++GO:0000075//cell cycle checkpoint+++GO:0008156//negative regulation of DNA replication+++GO:0006468//protein phosphorylation+++GO:0000724//double-strand break repair via homologous recombination+++GO:0009411//response to UV+++GO:0009792//embryo development ending in birth or egg hatching+++GO:0000077//DNA damage checkpoint+++GO:0007093//mitotic cell cycle checkpoint+++GO:0006974//cellular response to DNA damage stimulus</p>

XM_021098438.1	LOC100515902	-2.403201879	0.00163902	04145//Phagosome+++04612//Antigen processing and presentation+++04218//Cellular senescence+++04514//Cell adhesion molecules (CAMs)+++04144//Endocytosis	GO:0009986//cell surface+++GO:0005887//integral component of plasma membrane+++GO:0016020//membrane+++GO:0055038//recycling endosome membrane+++GO:0012507//ER to Golgi transport vesicle membrane+++GO:0030670//phagocytic vesicle membrane+++GO:0005783//endoplasmic reticulum+++GO:0031901//early endosome membrane+++GO:0042612//MHC class I protein complex+++GO:0005789//endoplasmic reticulum membrane+++GO:0005794//Golgi apparatus+++GO:0005886//plasma membrane+++GO:0071556//integral component of luminal side of endoplasmic reticulum membrane+++GO:0000139//Golgi membrane	GO:0042605//peptide antigen binding+++GO:0046977//TAP binding+++GO:0030881//beta-2-microglobulin binding	GO:0002474//antigen processing and presentation of peptide antigen via MHC class I+++GO:0060337//type I interferon signaling pathway+++GO:0002479//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent+++GO:0002480//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent+++GO:0050776//regulation of immune response+++GO:0060333//interferon-gamma-mediated signaling pathway+++GO:0006955//immune response+++GO:0016567//protein ubiquitination
XM_005660928.3	DDB2	-1.871301977	0.026124862	03420//Nucleotide excision repair+++04115//p53 signaling pathway+++04120//Ubiquitin mediated proteolysis	GO:0005654//nucleoplasm+++GO:0080008//Cu14-RING E3 ubiquitin ligase complex+++GO:0032991//protein-containing complex+++GO:0030054//cell junction+++GO:0031465//Cu14B-RING E3 ubiquitin ligase complex+++GO:0005634//nucleus	GO:0044877//protein-containing complex binding+++GO:0004842//ubiquitin-protein transferase activity+++GO:0003684//damaged DNA binding	GO:0006290//pyrimidine dimer repair+++GO:0070914//UV-damage excision repair+++GO:0035518//histone H2A monoubiquitination+++GO:0051865//protein autoubiquitination+++GO:0006281//DNA repair+++GO:0009411//response to UV+++GO:0000209//protein polyubiquitination+++GO:0010224//response to UV-B
XM_021081655.1	LDHA	-1.592368404	0.004577741	01120//Microbial metabolism in diverse environments+++01110//Biosynthesis of secondary metabolites+++01100//Metabolic pathways+++00620//Pyruvate metabolism+++00270//Cysteine and methionine metabolism+++04922//Glucagon signaling pathway+++00010//Glycolysis / Gluconeogenesis+++00640//Propanoate metabolism+++01130//Biosynthesis of antibiotics	GO:0005737//cytoplasm	GO:0016616//oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor+++GO:0003824//catalytic activity+++GO:0016491//oxidoreductase activity+++GO:0004459//L-lactate dehydrogenase activity	GO:0019752//carboxylic acid metabolic process+++GO:0055114//oxidation-reduction process+++GO:0005975//carbohydrate metabolic process
XM_005656555.3	EIF4E	8.120614695	1.46E-04	04151//PI3K-Akt signaling pathway+++03013//RNA transport+++04910//Insulin signaling pathway+++04211//Longevity regulating pathway+++04066//HIF-1 signaling pathway+++04150//mTOR signaling pathway	GO:0036464//cytoplasmic ribonucleoprotein granule+++GO:0010494//cytoplasmic stress granule+++GO:0005829//cytosol+++GO:0098978//glutamatergic synapse+++GO:0048471//perinuclear region of cytoplasm+++GO:0000932//P-body+++GO:0005845//mRNA cap binding complex+++GO:0016442//RISC complex+++GO:0005737//cytoplasm+++GO:0098794//postsynapse+++GO:0033391//chromatoid body+++GO:0016281//eukaryotic translation initiation factor 4F complex	GO:0031370//eukaryotic initiation factor 4G binding+++GO:0019899//enzyme binding+++GO:0000340//RNA 7-methylguanosine cap binding+++GO:0003723//RNA binding+++GO:0003743//translation initiation factor activity+++GO:0045182//translation regulator activity+++GO:0070491//repressing transcription factor binding	GO:0099578//regulation of translation at postsynapse, modulating synaptic transmission+++GO:0017148//negative regulation of translation+++GO:0001662//behavioral fear response+++GO:0071549//cellular response to dexamethasone stimulus+++GO:0006413//translational initiation+++GO:0019827//stem cell population maintenance+++GO:0045931//positive regulation of mitotic cell cycle+++GO:0006417//regulation of translation+++GO:0000082//G1/S transition of mitotic cell cycle+++GO:0006412//translation+++GO:0045665//negative regulation of neuron differentiation

XM_021072576.1	PPP3CB	22.47669815	2.61E-06	<p>04010//MAPK signaling pathway+++04218//Cellular senescence+++04625//C-type lectin receptor signaling pathway+++04724//Glutamatergic synapse+++04310//Wnt signaling pathway+++04360//Axon guidance+++04114//Oocyte meiosis+++04662//B cell receptor signaling pathway+++04720//Long-term potentiation+++04658//Th1 and Th2 cell differentiation+++04924//Renin secretion+++04921//Oxytocin signaling pathway+++04728//Dopaminergic synapse+++04659//Th17 cell differentiation+++04022//cGMP-PKG signaling pathway+++04660//T cell receptor signaling pathway+++04380//Osteoclast differentiation+++04922//Glucagon signaling pathway+++04370//VEGF signaling pathway+++04020//Calcium signaling pathway+++04650//Natural killer cell mediated cytotoxicity</p> <p>04371//Apelin signaling pathway+++04723//Retrograde endocannabinoid signaling+++04744//Phototransduction+++04062//C hemokine signaling pathway+++04727//GABAergic synapse+++04926//Relaxin signaling pathway+++04740//Olfactory transduction+++04724//Glutamatergic synapse+++04151//PI3K-Akt signaling pathway+++04011//MAPK signaling pathway - yeast+++04726//Serotonergic synapse+++04725//Cholinergic synapse+++04728//Dopaminergic synapse+++04014//Ras signaling pathway+++04713//Circadian entrainment</p>	<p>GO:0098978//glutamatergic synapse+++GO:0005737//cytoplasm+++GO:0005955//calcineurin complex+++GO:0030315//T-tubule+++GO:0005886//plasma membrane+++GO:0030018//Z disc</p>	<p>GO:0016787//hydrolase activity+++GO:0019899//enzyme binding+++GO:0005516//calmodulin binding+++GO:0004721//phosphoprotein phosphatase activity+++GO:0005509//calcium ion binding+++GO:0033192//calmodulin-dependent protein phosphatase activity+++GO:0008144//drug binding+++GO:0004722//protein serine/threonine phosphatase activity+++GO:0030346//protein phosphatase 2B binding</p>	<p>GO:0006470//protein dephosphorylation+++GO:0001946//lymphangiogenesis+++GO:1900242//regulation of synaptic vesicle endocytosis+++GO:0030217//T cell differentiation+++GO:0035690//cellular response to drug+++GO:0097720//calcineurin-mediated signaling+++GO:0006468//protein phosphorylation+++GO:0035774//positive regulation of insulin secretion involved in cellular response to glucose stimulus+++GO:0010468//regulation of gene expression+++GO:0043029//T cell homeostasis+++GO:0001915//negative regulation of T cell mediated cytotoxicity+++GO:0031987//locomotion involved in locomotory behavior+++GO:0007507//heart development+++GO:0034097//response to cytokine+++GO:0017156//calcium ion regulated exocytosis</p>
XM_021097492.1	GNB1	21.16167518	1.02E-05	<p>00590//Arachidonic acid metabolism+++01100//Metabolic pathways+++04270//Vascular smooth muscle contraction+++00830//Retinol metabolism+++04750//Inflammatory mediator regulation of TRP channels+++00071//Fatty acid degradation+++03320//PPAR signaling pathway</p>	<p>GO:0005834//heterotrimeric G-protein complex+++GO:0043209//myelin sheath+++GO:0001750//photoreceptor outer segment</p>	<p>GO:0003924//GTPase activity+++GO:0044877//protein-containing complex binding+++GO:0051020//GTPase binding</p>	<p>GO:0007186//G protein-coupled receptor signaling pathway+++GO:0007200//phospholipase C-activating G protein-coupled receptor signaling pathway+++GO:0050909//sensory perception of taste+++GO:0060041//retina development in camera-type eye+++GO:0007165//signal transduction+++GO:0008283//cell proliferation</p>
XM_021096707.1	LOC100737897	7.634489128	0.011585609	<p>00590//Arachidonic acid metabolism+++01100//Metabolic pathways+++04270//Vascular smooth muscle contraction+++00830//Retinol metabolism+++04750//Inflammatory mediator regulation of TRP channels+++00071//Fatty acid degradation+++03320//PPAR signaling pathway</p>	<p>GO:0005783//endoplasmic reticulum+++GO:0016020//membrane+++GO:0016021//integral component of membrane+++GO:0005789//endoplasmic reticulum membrane</p>	<p>GO:0004497//monooxygenase activity+++GO:0046872//metal ion binding+++GO:0005506//iron ion binding+++GO:0020037//heme binding+++GO:0016491//oxidoreductase activity+++GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen</p>	<p>GO:0055114//oxidation-reduction process</p>

XR_309303.3	IKBK	20.05226809	3.65E-05	<p>04010//MAPK signaling pathway+++04622//RIG-I-like receptor signaling pathway+++04668//TNF signaling pathway+++04151//PI3K-Akt signaling pathway+++04380//Osteoclast differentiation+++04625//C-type lectin receptor signaling pathway+++04062//Chemokine signaling pathway+++04620//Toll-like receptor signaling pathway+++04659//Th17 cell differentiation+++04662//B cell receptor signaling pathway+++04210//Apoptosis+++04014//Ras signaling pathway+++04623//Cytosolic DNA-sensing pathway+++04660//T cell receptor signaling pathway+++04064//NF-kappa B signaling pathway+++04621//NOD-like receptor signaling pathway+++04920//Adipocytokine signaling pathway+++04657//IL-17 signaling pathway+++04658//Th1 and Th2 cell differentiation</p>	<p>GO:0000151//ubiquitin ligase complex+++GO:0072686//mitotic spindle+++GO:0005737//cytoplasm+++GO:0000922//spindle pole+++GO:0008385//IkkappaB kinase complex+++GO:0005634//nucleus+++GO:0005829//cytosol</p>	<p>GO:0042803//protein homodimerization activity+++GO:0046872//metal ion binding+++GO:1990450//linear polyubiquitin binding+++GO:0046982//protein heterodimerization activity+++GO:0016740//transferase activity+++GO:0031625//ubiquitin protein ligase binding+++GO:0019904//protein domain specific binding+++GO:0016301//kinase activity+++GO:0042802//identical protein binding+++GO:0070530//K63-linked polyubiquitin modification-dependent protein binding</p>	<p>GO:0006974//cellular response to DNA damage stimulus+++GO:0043123//positive regulation of I-kappaB kinase/NF-kappaB signaling+++GO:0051650//establishment of vesicle localization+++GO:0016310//phosphorylation+++GO:0045944//positive regulation of transcription by RNA polymerase II+++GO:0051092//positive regulation of NF-kappaB transcription factor activity</p>
XM_021079417.1	PFKFB1	21.93516869	4.74E-06	<p>04152//AMPK signaling pathway+++04922//Glucagon signaling pathway+++00051//Fructose and mannose metabolism</p>	<p>GO:0043540//6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase complex+++GO:0005829//cytosol</p>	<p>GO:0042802//identical protein binding+++GO:0003873//6-phosphofructo-2-kinase activity+++GO:0004331//fructose-2,6-bisphosphate 2-phosphatase activity+++GO:0016301//kinase activity+++GO:0005524//ATP binding+++GO:0003824//catalytic activity</p>	<p>GO:0016310//phosphorylation+++GO:0016311//dephosphorylation+++GO:0006003//fructose 2,6-bisphosphate metabolic process+++GO:0006000//fructose metabolic process+++GO:0046835//carbohydrate phosphorylation</p>
NM_214425.1	CYP4A21	8.227945773	0.005538316	<p>04750//Inflammatory mediator regulation of TRP channels+++00590//Arachidonic acid metabolism+++03320//PPAR signaling pathway+++04270//Vascular smooth muscle contraction+++01100//Metabolic pathways+++00071//Fatty acid degradation+++00830//Retinol metabolism</p>	<p>GO:0016020//membrane+++GO:0016021//integral component of membrane+++GO:0005783//endoplasmic reticulum+++GO:0005789//endoplasmic reticulum membrane</p>	<p>GO:0046872//metal ion binding+++GO:0005506//iron ion binding+++GO:0004497//monooxygenase activity+++GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen+++GO:0020037//heme binding+++GO:0016491//oxidoreductase activity</p>	<p>GO:0055114//oxidation-reduction process</p>
XM_021074019.1	CYP2C34	7.783404598	0.03971261	<p>04726//Serotonergic synapse+++01100//Metabolic pathways+++00830//Retinol metabolism</p>	<p>GO:0031090//organelle membrane+++GO:0005789//endoplasmic reticulum membrane</p>	<p>GO:0016491//oxidoreductase activity+++GO:0046872//metal ion binding+++GO:0004497//monooxygenase activity+++GO:0005506//iron ion binding+++GO:0020037//heme binding+++GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen</p>	<p>GO:0055114//oxidation-reduction process</p>
XM_013998328.2	LIN37	6.382196727	0.021016084	<p>04218//Cellular senescence</p>	<p>GO:0017053//transcriptional repressor complex</p>		<p>GO:0007049//cell cycle</p>

XM_021090010.1	HIPK1	23.49485944	7.31E-07	04218//Cellular senescence	GO:0016605//PML body+++GO:0016607//nuclear speck+++GO:0005737//cytoplasm+++GO:0005654//nucleoplasm+++GO:0005813//centrosome+++GO:0005829//cytosol+++GO:0005634//nucleus	GO:0005524//ATP binding+++GO:0004672//protein kinase activity	GO:0060235//lens induction in camera-type eye+++GO:0042771//intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator+++GO:0007224//smoothed signaling pathway+++GO:0008284//positive regulation of cell proliferation+++GO:0060059//embryonic retina morphogenesis in camera-type eye+++GO:0010803//regulation of tumor necrosis factor-mediated signaling pathway+++GO:0097191//extrinsic apoptotic signaling pathway+++GO:0072577//endothelial cell apoptotic process+++GO:0009952//anterior/posterior pattern specification+++GO:0010842//retina layer formation+++GO:0061072//iris morphogenesis+++GO:0030182//neuron differentiation+++GO:0048596//embryonic camera-type eye morphogenesis+++GO:0006468//protein phosphorylation+++GO:0034333//adherens junction assembly
NM_214424.1	CYP4A24	8.62469727	0.004407793	00590//Arachidonic acid metabolism+++04750//Inflammatory mediator regulation of TRP channels+++00830//Retinol metabolism+++04270//Vascular smooth muscle contraction+++03320//PPAR signaling pathway+++00071//Fatty acid degradation+++01100//Metabolic pathways	GO:0005789//endoplasmic reticulum membrane+++GO:0016021//integral component of membrane	GO:0004497//monooxygenase activity+++GO:0020037//heme binding+++GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen+++GO:0005506//iron ion binding	
NM_214420.1	CYP2C49	8.397166552	0.025282449	01100//Metabolic pathways+++00830//Retinol metabolism+++04726//Serotonergic synapse	GO:0005789//endoplasmic reticulum membrane+++GO:0031090//organelle membrane	GO:0070330//aromatase activity+++GO:0005506//iron ion binding+++GO:0004497//monooxygenase activity+++GO:0020037//heme binding+++GO:0008392//arachidonic acid epoxygenase activity+++GO:0008395//steroid hydroxylase activity+++GO:0019825//oxygen binding	GO:0006805//xenobiotic metabolic process+++GO:0019373//epoxygenase P450 pathway
XM_021093492.1	LEPR	2.228967987	0.04327926	04060//Cytokine-cytokine receptor interaction+++04152//AMPK signaling pathway+++04630//Jak-STAT signaling pathway+++04080//Neuroactive ligand-receptor interaction+++04920//Adipocytokine signaling pathway	GO:0016323//basolateral plasma membrane+++GO:0016021//integral component of membrane	GO:0038021//leptin receptor activity	GO:0030217//T cell differentiation+++GO:0060259//regulation of feeding behavior+++GO:0001525//angiogenesis+++GO:0098868//bone growth+++GO:0010507//negative regulation of autophagy+++GO:0046850//regulation of bone remodeling+++GO:0019953//sexual reproduction+++GO:0033210//leptin-mediated signaling pathway+++GO:0042593//glucose homeostasis+++GO:0097009//energy homeostasis+++GO:0044321//response to leptin+++GO:0006909//phagocytosis

XM_021098329.1	TNXB	2.32106685	0.005204574	04151//PI3K-Akt signaling pathway+++04512//ECM-receptor interaction+++04510//Focal adhesion	GO:0031012//extracellular matrix+++GO:0062023//collagen-containing extracellular matrix+++GO:0005576//extracellular region+++GO:0043005//neuron projection+++GO:0005615//extracellular space	GO:0005201//extracellular matrix structural constituent+++GO:0046982//protein heterodimerization activity+++GO:0042803//protein homodimerization activity+++GO:0050839//cell adhesion molecule binding+++GO:0005518//collagen binding+++GO:0008201//heparin binding	GO:0048666//neuron development+++GO:0006631//fatty acid metabolic process+++GO:0098609//cell-cell adhesion+++GO:0043506//regulation of JUN kinase activity+++GO:0030199//collagen fibril organization+++GO:0030198//extracellular matrix organization+++GO:0007160//cell-matrix adhesion+++GO:0007157//heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules+++GO:0006641//triglyceride metabolic process+++GO:0006629//lipid metabolic process
XM_021088844.1	PTK2	1.457558501	0.009348031	04012//ErbB signaling pathway+++04151//PI3K-Akt signaling pathway+++04810//Regulation of actin cytoskeleton+++04670//Leukocyte transendothelial migration+++04360//Axon guidance+++04370//VEGF signaling pathway+++04062//Chemokine signaling pathway+++04510//Focal adhesion	GO:0005856//cytoskeleton+++GO:0005737//cytoplasm+++GO:0005925//focal adhesion+++GO:0005886//plasma membrane+++GO:0005634//nucleus+++GO:0016324//apical plasma membrane+++GO:0005829//cytosol+++GO:0030027//lamellipodium+++GO:0001725//stress fiber	GO:0005524//ATP binding+++GO:0016301//kinase activity+++GO:0004715//non-membrane spanning protein tyrosine kinase activity+++GO:0019901//protein kinase binding+++GO:0003779//actin binding+++GO:0042169//SH2 domain binding+++GO:0004672//protein kinase activity+++GO:0019903//protein phosphatase binding+++GO:0008432//JUN kinase binding+++GO:0004713//protein tyrosine kinase activity	GO:0051964//negative regulation of synapse assembly+++GO:0001568//blood vessel development+++GO:0050771//negative regulation of axonogenesis+++GO:0007229//integrin-mediated signaling pathway+++GO:0007179//transforming growth factor beta receptor signaling pathway+++GO:0051893//regulation of focal adhesion assembly+++GO:0001570//vasculogenesis+++GO:0008284//positive regulation of cell proliferation+++GO:0001932//regulation of protein phosphorylation+++GO:0014068//positive regulation of phosphatidylinositol 3-kinase signaling+++GO:0043542//endothelial cell migration+++GO:2000060//positive regulation of ubiquitin-dependent protein catabolic process+++GO:0060396//growth hormone receptor signaling pathway+++GO:0010632//regulation of epithelial cell migration+++GO:0071560//cellular response to transforming growth factor beta stimulus+++GO:0021955//central nervous system neuron axonogenesis+++GO:0010507//negative regulation of autophagy+++GO:0045860//positive regulation of protein kinase activity+++GO:0018108//peptidyl-tyrosine phosphorylation+++GO:0048013//ephrin receptor signaling pathway+++GO:0043066//negative regulation of apoptotic process+++GO:0046777//protein autophosphorylation+++GO:0045667//regulation of osteoblast differentiation+++GO:0030335//positive regulation of cell migration+++GO:0008360//regulation of cell shape+++GO:0006468//protein phosphorylation+++GO:0046621//negative regulation of organ growth+++GO:0001934//positive regulation of protein phosphorylation+++GO:0051897//positive regulation of protein kinase B signaling+++GO:0001764//neuron migration+++GO:0001525//angiogenesis+++GO:0022408//negative regulation of cell-cell

XM_021101866.1	LIN54	1.556411155	1.16E-04	04218//Cellular senescence	GO:0005634//nucleus	GO:0003677//DNA binding+++GO:0046872//metal ion binding	GO:0007049//cell cycle+++GO:0006355//regulation of transcription, DNA-templated+++GO:0006351//transcription, DNA-templated
				04722//Neurotrophin signaling pathway+++04630//Jak-STAT signaling pathway+++04072//Phospholipase D signaling pathway+++04670//Leukocyte transendothelial migration+++04360//Axon guidance+++04013//MAPK signaling pathway - fly+++04920//Adipocytokine signaling pathway+++04650//Natural killer cell mediated cytotoxicity+++04014//Ras signaling pathway+++04625//C-type lectin receptor signaling pathway			GO:0046676//negative regulation of insulin secretion+++GO:0046825//regulation of protein export from nucleus+++GO:0046326//positive regulation of glucose import+++GO:0061582//intestinal epithelial cell migration+++GO:0048873//homeostasis of number of cells within a tissue+++GO:0030220//platelet formation+++GO:0048013//ephrin receptor signaling pathway+++GO:0048008//platelet-derived growth factor receptor signaling pathway+++GO:0007173//epidermal growth factor receptor signaling pathway+++GO:0051463//negative regulation of cortisol secretion+++GO:0040014//regulation of multicellular organism growth+++GO:0048609//multicellular organismal reproductive process+++GO:0060125//negative regulation of growth hormone secretion+++GO:0006629//lipid metabolic process+++GO:0033277//abortive mitotic cell cycle+++GO:0009755//hormone-mediated signaling pathway+++GO:0032760//positive regulation of tumor necrosis factor production+++GO:0021697//cerebellar cortex formation+++GO:0048806//genitalia development+++GO:0007507//heart development+++GO:0045931//positive regulation of mitotic cell cycle+++GO:0071364//cellular response to epidermal growth factor stimulus+++GO:0060325//face morphogenesis+++GO:0000187//activation of MAPK activity+++GO:0038127//ERBB signaling pathway+++GO:0042593//glucose homeostasis+++GO:0006470//protein dephosphorylation+++GO:0006641//triglyceride metabolic process+++GO:0007229//integrin-mediated signaling pathway+++GO:0048011//neurotrophin TRK receptor signaling pathway+++GO:0007420//brain development+++GO:0048839//inner ear development+++GO:0046887//positive regulation of hormone secretion+++GO:0032755//positive regulation of interleukin-6 production+++GO:0035264//multicellular
XM_021073562.1	PTPN11	1.282613951	0.003171929		GO:0005737//cytoplasm+++GO:0005634//nucleus+++GO:0032991//protein-containing complex	GO:0001784//phosphotyrosine residue binding+++GO:0016791//phosphatase activity+++GO:0051428//peptide hormone receptor binding+++GO:0019901//protein kinase binding+++GO:0050839//cell adhesion molecule binding+++GO:0030971//receptor tyrosine kinase binding+++GO:0004726//non-membrane spanning protein tyrosine phosphatase activity+++GO:0016787//hydrolase activity+++GO:0005070//SH3/SH2 adaptor activity+++GO:0005158//insulin receptor binding+++GO:0004725//protein tyrosine phosphatase activity+++GO:0004721//phosphoprotein phosphatase activity	

XM_021097491.1	GNB1	-22.08924085	4.01E-06	<p>04728//Dopaminergic synapse+++04727//GABAergic synapse+++04151//PI3K-Akt signaling pathway+++04726//Serotonergic synapse+++04740//Olfactory transduction+++04371//Apelin signaling pathway+++04723//Retrograde endocannabinoid signaling+++04725//Cholinergic synapse+++04014//Ras signaling pathway+++04744//Phototransduction+++04926//R elaxin signaling pathway+++04062//Chemokine signaling pathway+++04713//Circadian entrainment+++04724//Glutamatergic</p>	<p>GO:0043209//myelin sheath+++GO:0001750//photoreceptor outer segment+++GO:0005834//heterotrimeric G- protein complex</p>	<p>GO:0003924//GTPase activity+++GO:0051020//GTPase binding+++GO:0044877//protein-containing complex binding</p>	<p>GO:0007165//signal transduction+++GO:0008283//cell proliferation+++GO:0050909//sensory perception of taste+++GO:0060041//retina development in camera-type eye+++GO:0007200//phospholipase C-activating G protein-coupled receptor signaling pathway+++GO:0007186//G protein-coupled receptor signaling pathway</p>
XM_021088840.1	PTK2	-8.314774955	6.06E-07	<p>04151//PI3K-Akt signaling pathway+++04670//Leukocyte transendothelial migration+++04510//Focal adhesion+++04810//Regulation of actin cytoskeleton+++04062//Chemokine signaling pathway+++04012//ErbB signaling pathway+++04360//Axon guidance+++04370//VEGF signaling pathway</p>	<p>GO:0016324//apical plasma membrane+++GO:0030027//lamellipodium+++GO :0001725//stress fiber+++GO:0005829//cytosol+++GO:0005856//c ytoskeleton+++GO:0005886//plasma membrane+++GO:0005737//cytoplasm+++GO:00 05925//focal adhesion+++GO:0005634//nucleus</p>	<p>GO:0003779//actin binding+++GO:0019903//protein phosphatase binding+++GO:0008432//JUN kinase binding+++GO:0004715//non-membrane spanning protein tyrosine kinase activity+++GO:0004713//protein tyrosine kinase activity+++GO:0004672//protein kinase activity+++GO:0016301//kinase activity+++GO:0019901//protein kinase binding+++GO:0042169//SH2 domain binding+++GO:0005524//ATP binding</p>	<p>GO:0051897//positive regulation of protein kinase B signaling+++GO:0010613//positive regulation of cardiac muscle hypertrophy+++GO:0051893//regulation of focal adhesion assembly+++GO:0001764//neuron migration+++GO:0051964//negative regulation of synapse assembly+++GO:0030335//positive regulation of cell migration+++GO:0001932//regulation of protein phosphorylation+++GO:0000226//microtubule cytoskeleton organization+++GO:0001934//positive regulation of protein phosphorylation+++GO:0007172//signal complex assembly+++GO:0042127//regulation of cell proliferation+++GO:0001568//blood vessel development+++GO:0010632//regulation of epithelial cell migration+++GO:0038083//peptidyl-tyrosine autophosphorylation+++GO:0048013//ephrin receptor signaling pathway+++GO:0050771//negative regulation of axonogenesis+++GO:0071560//cellular response to transforming growth factor beta stimulus+++GO:0045860//positive regulation of protein kinase activity+++GO:0018108//peptidyl- tyrosine phosphorylation+++GO:0014068//positive regulation of phosphatidylinositol 3-kinase signaling+++GO:0046621//negative regulation of organ growth+++GO:0006468//protein phosphorylation+++GO:0007179//transforming growth factor beta receptor signaling pathway+++GO:0022408//negative regulation of cell-cell adhesion+++GO:0001525//angiogenesis+++GO:0 007229//integrin-mediated signaling pathway+++GO:0043066//negative regulation of apoptotic process+++GO:0046777//protein autophosphorylation+++GO:2000060//positive regulation of ubiquitin-dependent protein catabolic process+++GO:1900024//regulation of substrate adhesion-dependent cell spreading+++GO:0033628//regulation of cell adhesion mediated by</p>

XM_021084221.1	FOXO3	-9.00078075	0.044059527	<p>04722//Neurotrophin signaling pathway+++04213//Longevity regulating pathway - multiple species+++04917//Prolactin signaling pathway+++04068//FoxO signaling pathway+++04211//Longevity regulating pathway+++04151//PI3K-Akt signaling pathway+++04218//Cellular senescence+++04137//Mitophagy - animal+++04152//AMPK signaling pathway+++04062//Chemokine signaling pathway+++04212//Longevity regulating pathway - worm</p>	<p>GO:0005737//cytoplasm+++GO:0005634//nucleus+++GO:0005759//mitochondrial matrix+++GO:0005739//mitochondrion+++GO:0032991//protein-containing complex+++GO:0005654//nucleoplasm+++GO:0005829//cytosol+++GO:0005741//mitochondrial outer membrane+++GO:0016020//membrane</p>	<p>GO:0019901//protein kinase binding+++GO:0000978//RNA polymerase II proximal promoter sequence-specific DNA binding+++GO:0000981//DNA-binding transcription factor activity, RNA polymerase II-specific+++GO:0003700//DNA-binding transcription factor activity+++GO:0001227//DNA-binding transcription repressor activity, RNA polymerase II-specific+++GO:0001228//DNA-binding transcription activator activity, RNA polymerase II-specific+++GO:0043565//sequence-specific DNA binding+++GO:0003677//DNA binding+++GO:0008013//beta-catenin binding+++GO:0034246//mitochondrial sequence-specific DNA-binding transcription factor activity+++GO:0031490//chromatin DNA binding+++GO:0008134//transcription factor binding</p>	<p>GO:0042593//glucose homeostasis+++GO:0043525//positive regulation of neuron apoptotic process+++GO:0048854//brain morphogenesis+++GO:0045944//positive regulation of transcription by RNA polymerase II+++GO:0001544//initiation of primordial ovarian follicle growth+++GO:0045893//positive regulation of transcription, DNA-templated+++GO:0043065//positive regulation of apoptotic process+++GO:0006357//regulation of transcription by RNA polymerase II+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0030330//DNA damage response, signal transduction by p53 class mediator+++GO:0045648//positive regulation of erythrocyte differentiation+++GO:0033209//tumor necrosis factor-mediated signaling pathway+++GO:0006390//mitochondrial transcription+++GO:0034599//cellular response to oxidative stress+++GO:0001556//oocyte maturation+++GO:0097192//extrinsic apoptotic signaling pathway in absence of ligand+++GO:0030336//negative regulation of cell migration+++GO:0006355//regulation of transcription, DNA-templated+++GO:0008286//insulin receptor signaling pathway+++GO:0001547//antral ovarian follicle growth+++GO:0097150//neuronal stem cell population maintenance+++GO:0090090//negative regulation of canonical Wnt signaling pathway+++GO:0006417//regulation of translation+++GO:2000177//regulation of neural precursor cell</p>
XM_021097493.1	GNB1	-22.00961843	4.38E-06	<p>04926//Relaxin signaling pathway+++04725//Cholinergic synapse+++04014//Ras signaling pathway+++04371//Apelin signaling pathway+++04740//Olfactory transduction+++04726//Serotonergic synapse+++04011//MAPK signaling pathway - yeast+++04744//Phototransduction+++04723//Retinoid signaling+++04724//Glutamatergic synapse+++04151//PI3K-Akt signaling pathway+++04062//Chemokine signaling pathway+++04713//Circadian entrainment+++04728//Dopaminergic</p>	<p>GO:0005834//heterotrimeric G-protein complex+++GO:0001750//photoreceptor outer segment+++GO:0043209//myelin sheath</p>	<p>GO:0003924//GTPase activity+++GO:0044877//protein-containing complex binding+++GO:0051020//GTPase binding</p>	<p>GO:0007186//G protein-coupled receptor signaling pathway+++GO:0008283//cell proliferation+++GO:0007165//signal transduction+++GO:0007200//phospholipase C-activating G protein-coupled receptor signaling pathway+++GO:0060041//retina development in camera-type eye+++GO:0050909//sensory perception of taste</p>

XM_021093571.1	PGM1	-7.764412041	0.032759186	01100//Metabolic pathways+++01130//Biosynthesis of antibiotics+++01110//Biosynthesis of secondary metabolites+++00230//Purine metabolism+++00520//Amino sugar and nucleotide sugar metabolism+++00030//Pentose phosphate pathway+++00052//Galactose metabolism+++00521//Streptomycin biosynthesis+++00010//Glycolysis / Gluconeogenesis+++01120//Microbial metabolism in diverse environments+++00500//Starch and sucrose metabolism	GO:0015629//actin cytoskeleton+++GO:0005829//cytosol	GO:0004614//phosphoglucomutase activity+++GO:0046872//metal ion binding+++GO:0016868//intramolecular transferase activity, phosphotransferases+++GO:0000287//magnesium ion binding	GO:0019388//galactose catabolic process+++GO:0071704//organic substance metabolic process+++GO:0006006//glucose metabolic process+++GO:0005975//carbohydrate metabolic process+++GO:0005978//glycogen biosynthetic process
XM_013998997.2	CASP9	-7.494066932	3.41E-04	04210//Apoptosis+++04215//Apoptosis - multiple species+++04919//Thyroid hormone signaling pathway+++04370//VEGF signaling pathway+++04115//p53 signaling pathway+++04151//PI3K-Akt signaling pathway	GO:0005829//cytosol+++GO:0032991//protein-containing complex+++GO:0043293//apoptosome+++GO:005737//cytoplasm+++GO:0005634//nucleus	GO:0008233//peptidase activity+++GO:0017124//SH3 domain binding+++GO:0019901//protein kinase binding+++GO:0097153//cysteine-type endopeptidase activity involved in apoptotic process+++GO:0008234//cysteine-type peptidase activity+++GO:0097199//cysteine-type endopeptidase activity involved in apoptotic signaling pathway+++GO:0004197//cysteine-type endopeptidase activity+++GO:0016787//hydrolase activity	GO:0071549//cellular response to dexamethasone stimulus+++GO:0042770//signal transduction in response to DNA damage+++GO:0006915//apoptotic process+++GO:0043525//positive regulation of neuron apoptotic process+++GO:0009411//response to UV+++GO:0006919//activation of cysteine-type endopeptidase activity involved in apoptotic process+++GO:2001020//regulation of response to DNA damage stimulus+++GO:0043065//positive regulation of apoptotic process+++GO:0008630//intrinsic apoptotic signaling pathway in response to DNA damage+++GO:0006508//proteolysis+++GO:0034644//cellular response to UV+++GO:0006974//cellular response to DNA damage stimulus+++GO:0042981//regulation of apoptotic process GO:0030900//forebrain development+++GO:0042981//regulation of apoptotic process+++GO:0097190//apoptotic signaling pathway+++GO:0051402//neuron apoptotic process+++GO:0070059//intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress+++GO:0007275//multicellular organism development+++GO:0006508//proteolysis+++GO:0006915//apoptotic process+++GO:0007420//brain development+++GO:0008635//activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c+++GO:0006919//activation of cysteine-type endopeptidase activity involved in apoptotic process+++GO:2001235//positive regulation of apoptotic signaling
XM_021093024.1	APAF1	-1.925932415	0.024281225	04215//Apoptosis - multiple species+++04214//Apoptosis - fly+++04115//p53 signaling pathway+++04210//Apoptosis	GO:0005829//cytosol+++GO:0005737//cytoplasm+++GO:0043293//apoptosome+++GO:0005634//nucleus+++GO:0032991//protein-containing complex	GO:0043531//ADP binding+++GO:0042802//identical protein binding+++GO:0008233//peptidase activity+++GO:0000166//nucleotide binding+++GO:0005524//ATP binding+++GO:0008656//cysteine-type endopeptidase activator activity involved in apoptotic process	GO:0018107//peptidyl-threonine phosphorylation+++GO:0043508//negative regulation of JUN kinase activity+++GO:0009299//mRNA transcription+++GO:0043066//negative regulation of apoptotic process+++GO:0006468//protein phosphorylation+++GO:0018105//peptidyl-serine phosphorylation
XM_021083201.1	HIPK3	-23.95018874	3.93E-07	04218//Cellular senescence	GO:0005829//cytosol+++GO:0016605//PML body+++GO:0016604//nuclear body+++GO:0005737//cytoplasm	GO:0005524//ATP binding+++GO:0004672//protein kinase activity+++GO:0004674//protein serine/threonine kinase activity	

XM_021083203.1	HIPK3	-23.99488457	3.71E-07	04218//Cellular senescence	GO:0016604//nuclear body+++GO:0016605//PML body+++GO:0005737//cytoplasm+++GO:0005829//cytosol	GO:0004674//protein serine/threonine kinase activity+++GO:0004672//protein kinase activity+++GO:0005524//ATP binding	GO:0043508//negative regulation of JUN kinase activity+++GO:0006468//protein phosphorylation+++GO:0043066//negative regulation of apoptotic process+++GO:0018107//peptidyl-threonine phosphorylation+++GO:0018105//peptidyl-serine phosphorylation+++GO:0009299//mRNA transcription
XM_021072578.1	PPP3CB	-10.15951945	0.007719386	04380//Osteoclast differentiation+++04310//Wnt signaling pathway+++04658//Th1 and Th2 cell differentiation+++04218//Cellular senescence+++04922//Glucagon signaling pathway+++04625//C-type lectin receptor signaling pathway+++04921//Oxytocin signaling pathway+++04659//Th17 cell differentiation+++04114//Oocyte meiosis+++04650//Natural killer cell mediated cytotoxicity+++04724//Glutamatergic synapse+++04370//VEGF signaling pathway+++04728//Dopaminergic synapse+++04924//Renin secretion+++04360//Axon guidance+++04022//cGMP-PKG signaling pathway+++04010//MAPK signaling pathway+++04020//Calcium signaling pathway+++04660//T cell receptor signaling pathway+++04720//Long-term	GO:0030315//T-tubule+++GO:0098978//glutamatergic synapse+++GO:0005955//calcineurin complex+++GO:0005886//plasma membrane+++GO:0005737//cytoplasm+++GO:0030018//Z disc	GO:0008144//drug binding+++GO:0005509//calcium ion binding+++GO:0004722//protein serine/threonine phosphatase activity+++GO:0016787//hydrolase activity+++GO:0005516//calmodulin binding+++GO:0019899//enzyme binding+++GO:0033192//calmodulin-dependent protein phosphatase activity+++GO:0004721//phosphoprotein phosphatase activity+++GO:0030346//protein phosphatase 2B binding	GO:0031987//locomotion involved in locomotory behavior+++GO:0097720//calcineurin-mediated signaling+++GO:0035690//cellular response to drug+++GO:0006468//protein phosphorylation+++GO:0035774//positive regulation of insulin secretion involved in cellular response to glucose stimulus+++GO:0034097//response to cytokine+++GO:0043029//T cell homeostasis+++GO:1900242//regulation of synaptic vesicle endocytosis+++GO:0007507//heart development+++GO:0006470//protein dephosphorylation+++GO:0001915//negative regulation of T cell mediated cytotoxicity+++GO:0017156//calcium ion regulated exocytosis+++GO:0010468//regulation of gene expression+++GO:0030217//T cell
XR_002343984.1	LOC100626199	-7.440815787	0.01795358	00830//Retinol metabolism+++01100//Metabolic pathways	GO:0016021//integral component of membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0031090//organelle membrane+++GO:0043231//intracellular membrane-bounded organelle	GO:0009055//electron transfer activity+++GO:0004745//retinol dehydrogenase activity	GO:0006629//lipid metabolic process
XM_021081605.1	PPP2R5C	6.30476285	0.027589485	04151//PI3K-Akt signaling pathway+++04114//Oocyte meiosis+++04152//AMPK signaling pathway+++04113//Meiosis - yeast+++04728//Dopaminergic synapse+++03015//mRNA surveillance pathway+++04261//Adrenergic signaling in cardiomyocytes+++04071//Sphingolipid signaling pathway	GO:0005794//Golgi apparatus+++GO:0000159//protein phosphatase type 2A complex+++GO:0005654//nucleoplasm+++GO:0005634//nucleus+++GO:0005829//cytosol+++GO:0000775//chromosome, centromeric region	GO:0072542//protein phosphatase activator activity+++GO:0019888//protein phosphatase regulator activity	GO:0007165//signal transduction+++GO:0008285//negative regulation of cell proliferation+++GO:0031952//regulation of protein autophosphorylation+++GO:0043666//regulation of phosphoprotein phosphatase activity+++GO:0043161//proteasome-mediated ubiquitin-dependent protein catabolic process

XM_013987480.2	JAK3	7.052183413	0.002188111	<p>04630//Jak-STAT signaling pathway+++04217//Necroptosis+++04151//PI3K-Akt signaling pathway+++04062//Chemokine signaling pathway+++04550//Signaling pathways regulating pluripotency of stem cells+++04658//Th1 and Th2 cell differentiation+++04659//Th17 cell differentiation</p>	<p>GO:0016020//membrane+++GO:0005856//cytoskeleton</p>	<p>GO:0016301//kinase activity+++GO:0000166//nucleotide binding+++GO:0019903//protein phosphatase binding+++GO:0004715//non-membrane spanning protein tyrosine kinase activity+++GO:0004713//protein tyrosine kinase activity+++GO:0005524//ATP binding+++GO:0016740//transferase activity+++GO:0004672//protein kinase activity</p>	<p>GO:0070670//response to interleukin-4+++GO:0030218//erythrocyte differentiation+++GO:0016310//phosphorylation+++GO:0035771//interleukin-4-mediated signaling pathway+++GO:0043029//T cell homeostasis+++GO:0006468//protein phosphorylation+++GO:0007260//tyrosine phosphorylation of STAT protein+++GO:0030183//B cell differentiation+++GO:0019221//cytokine-mediated signaling pathway+++GO:0018108//peptidyl-tyrosine phosphorylation+++GO:0042102//positive regulation of T cell proliferation+++GO:1903660//negative regulation of complement-dependent cytotoxicity+++GO:0035556//intracellular signal transduction</p>
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XM_021088688.1	ANGPT1	4.992650994	0.030651025	04010//MAPK signaling pathway+++04015//Rap1 signaling pathway+++04151//PI3K-Akt signaling pathway+++04066//HIF-1 signaling pathway+++04014//Ras signaling pathway	GO:0005902//microvillus+++GO:0005615//extracellular space+++GO:0045121//membrane raft+++GO:0005886//plasma membrane+++GO:0005576//extracellular region	GO:0005102//signaling receptor binding+++GO:0030971//receptor tyrosine kinase binding	GO:0045785//positive regulation of cell adhesion+++GO:0031589//cell-substrate adhesion+++GO:0007171//activation of transmembrane receptor protein tyrosine kinase activity+++GO:0001701//in utero embryonic development+++GO:0050731//positive regulation of peptidyl-tyrosine phosphorylation+++GO:0002040//sprouting angiogenesis+++GO:0034394//protein localization to cell surface+++GO:0050918//positive chemotaxis+++GO:0010595//positive regulation of endothelial cell migration+++GO:0030154//cell differentiation+++GO:0043066//negative regulation of apoptotic process+++GO:0030097//hemopoiesis+++GO:0032680//regulation of tumor necrosis factor production+++GO:0031398//positive regulation of protein ubiquitination+++GO:0007275//multicellular organism development+++GO:0001525//angiogenesis+++GO:0030210//heparin biosynthetic process+++GO:0033138//positive regulation of peptidyl-serine phosphorylation+++GO:0014068//positive regulation of phosphatidylinositol 3-kinase signaling+++GO:0043536//positive regulation of blood vessel endothelial cell migration+++GO:0070374//positive regulation of ERK1 and ERK2 cascade+++GO:0043122//regulation of I-kappaB kinase/NF-kappaB signaling+++GO:2000446//regulation of macrophage migration inhibitory factor signaling pathway+++GO:0072012//glomerulus vasculature development+++GO:0007162//negative regulation of cell adhesion+++GO:0007169//transmembrane receptor protein tyrosine kinase signaling pathway+++GO:0014842//regulation of skeletal muscle satellite cell proliferation+++GO:0002740//negative regulation of cytokine secretion involved in immune response+++GO:0043116//negative regulation of vascular permeability+++GO:0048014//Tie signaling pathway+++GO:0043393//regulation of
XM_021079731.1	CYP4F55	6.307434669	0.031848562	00590//Arachidonic acid metabolism+++01100//Metabolic pathways	GO:0005789//endoplasmic reticulum membrane+++GO:0016021//integral component of membrane+++GO:0031090//organelle membrane	GO:000449//monooxygenase activity+++GO:0005506//iron ion binding+++GO:0097259//20-aldehyde-leukotriene B4 20-monoxygenase activity+++GO:0050051//leukotriene-B4 20-monoxygenase activity+++GO:0097258//20-hydroxy-leukotriene B4 omega oxidase activity+++GO:0000037//heme binding	GO:0006690//icosanoid metabolic process+++GO:0006691//leukotriene metabolic process

XM_005662959.3	CCNE2	6.643013568	0.026498754	04151//PI3K-Akt signaling pathway+++04218//Cellular senescence+++04114//Oocyte meiosis+++04115//p53 signaling pathway+++04391//Hippo signaling pathway - fly+++04110//Cell cycle	GO:0000307//cyclin-dependent protein kinase holoenzyme complex+++GO:0097135//cyclin E2-CDK2 complex+++GO:0005634//nucleus+++GO:0005737//cytoplasm+++GO:0005813//centrosome	GO:0004672//protein kinase activity+++GO:0016538//cyclin-dependent protein serine/threonine kinase regulator activity+++GO:0019901//protein kinase binding	GO:0001129//synapsis+++GO:0000278//mitotic cell cycle+++GO:0000082//G1/S transition of mitotic cell cycle+++GO:0045787//positive regulation of cell cycle+++GO:0051726//regulation of cell cycle+++GO:0006270//DNA replication initiation+++GO:0000723//telomere maintenance+++GO:0007088//regulation of mitotic nuclear division+++GO:1903827//regulation of cellular protein localization+++GO:0000079//regulation of cyclin-dependent protein serine/threonine kinase activity+++GO:0070192//chromosome organization involved in meiotic cell cycle+++GO:0008284//positive regulation of cell proliferation+++GO:0006468//protein
XM_021063797.1	LAMC2	1.127612033	0.034671933	04510//Focal adhesion+++04512//ECM-receptor interaction+++04151//PI3K-Akt signaling pathway	GO:0005604//basement membrane	GO:0008201//heparin binding	GO:0048731//system development+++GO:0070831//basement membrane assembly+++GO:0030333//positive regulation of cell migration+++GO:0008284//positive regulation of cell proliferation
XM_021085872.1	IL4R	7.552520643	0.001706112	04630//Jak-STAT signaling pathway+++04658//Th1 and Th2 cell differentiation+++04640//Hematopoietic cell lineage+++04060//Cytokine-cytokine receptor interaction+++04659//Th17 cell differentiation+++04151//PI3K-Akt signaling pathway	GO:0005615//extracellular space+++GO:0043235//receptor complex+++GO:0005576//extracellular region+++GO:0016021//integral component of membrane+++GO:0016020//membrane	GO:0008083//growth factor activity+++GO:0005125//cytokine activity+++GO:0004896//cytokine receptor activity+++GO:0005136//interleukin-4 receptor binding+++GO:0005126//cytokine receptor binding	GO:0019221//cytokine-mediated signaling pathway+++GO:0001934//positive regulation of protein phosphorylation+++GO:0046825//regulation of protein export from nucleus+++GO:0042531//positive regulation of tyrosine phosphorylation of STAT protein+++GO:0042113//B cell activation+++GO:1903142//positive regulation of establishment of endothelial barrier+++GO:0006955//immune response+++GO:0010633//negative regulation of epithelial cell migration+++GO:0042976//activation of Janus kinase activity+++GO:0010469//regulation of signaling receptor activity+++GO:0016239//positive regulation of macroautophagy+++GO:0097028//dendritic cell differentiation+++GO:0046427//positive regulation of JAK-STAT cascade+++GO:0010628//positive regulation of gene expression+++GO:0042110//T cell activation+++GO:0035745//T-helper 2 cell cytokine production+++GO:0045892//negative regulation of transcription, DNA-templated+++GO:0032736//positive regulation of interleukin-13 production+++GO:0045582//positive regulation of T cell differentiation+++GO:0002532//production of molecular mediator involved in inflammatory response+++GO:1903660//negative regulation of complement-dependent cytotoxicity+++GO:2000357//negative regulation

XR_002338387.1 ULK1

8.253415417

2.00E-05

04152//AMPK signaling
pathway+++04140//Autophagy -
animal+++04137//Mitophagy -
animal+++04211//Longevity regulating
pathway+++04150//mTOR signaling pathway

GO:1990316//Atg1/ULK1 kinase
complex+++GO:0034045//phagophore assembly
site membrane+++GO:0097632//extrinsic
component of phagophore assembly site
membrane+++GO:0097629//extrinsic component
of omegasome
membrane+++GO:0000407//phagophore assembly
site+++GO:0032045//guanyl-nucleotide exchange
factor
complex+++GO:0016020//membrane+++GO:0097
635//extrinsic component of autophagosome
membrane+++GO:0005776//autophagosome+++G
O:0005829//cytosol
GO:0042802//identical protein
binding+++GO:0004674//protein serine/threonine
kinase activity+++GO:0016740//transferase
activity+++GO:0017137//Rab GTPase
binding+++GO:0016301//kinase
activity+++GO:0000166//nucleotide
binding+++GO:0005524//ATP
binding+++GO:0004672//protein kinase
activity+++GO:0051020//GTPase
binding+++GO:0044877//protein-containing
complex binding

GO:0006914//autophagy+++GO:0006104//protei
n localization+++GO:0031175//neuron projection
development+++GO:0006468//protein
phosphorylation+++GO:0018105//peptidyl-serine
phosphorylation+++GO:0016310//phosphorylato
n+++GO:0010506//regulation of
autophagy+++GO:0000045//autophagosome
assembly+++GO:0046777//protein
autophosphorylation+++GO:0031333//negative
regulation of protein complex
assembly+++GO:0018107//peptidyl-threonine
phosphorylation+++GO:0048675//axon
extension+++GO:0016236//macroautophagy+++
GO:0042594//response to
starvation+++GO:0075044//autophagy of host
cells involved in interaction with
symbiont+++GO:0007165//signal

XM_013989935.2	BRCA1	4.149392283	0.017574574	<p>03460//Fanconi anemia pathway+++03440//Homologous recombination+++04120//Ubiquitin mediated proteolysis+++04151//PI3K-Akt signaling pathway</p>	<p>GO:0070531//BRCA1-A complex+++GO:0005737//cytoplasm+++GO:1990904//ribonucleoprotein complex+++GO:0032991//protein-containing complex+++GO:0031436//BRCA1-BARD1 complex+++GO:0000794//condensed nuclear chromosome+++GO:0005886//plasma membrane+++GO:0000800//lateral element+++GO:0005634//nucleus+++GO:0000793//condensed chromosome+++GO:0005694//chromosome</p>	<p>GO:0019899//enzyme binding+++GO:0042802//identical protein binding+++GO:0003723//RNA binding+++GO:0003684//damaged DNA binding+++GO:0070063//RNA polymerase binding+++GO:0003677//DNA binding+++GO:0008270//zinc ion binding+++GO:0003713//transcription coactivator activity+++GO:0046872//metal ion binding+++GO:0044212//transcription regulatory region DNA binding+++GO:0031625//ubiquitin protein ligase binding+++GO:0004842//ubiquitin-protein transferase activity</p>	<p>GO:0045893//positive regulation of transcription, DNA-templated+++GO:0043627//response to estrogen+++GO:2000617//positive regulation of histone H3-K9 acetylation+++GO:0007098//centrosome cycle+++GO:0051574//positive regulation of histone H3-K9 methylation+++GO:0006301//postreplication repair+++GO:0051571//positive regulation of histone H3-K4 methylation+++GO:0007049//cell cycle+++GO:0035067//negative regulation of histone acetylation+++GO:0035066//positive regulation of histone acetylation+++GO:2000620//positive regulation of histone H4-K16 acetylation+++GO:1902042//negative regulation of extrinsic apoptotic signaling pathway via death domain receptors+++GO:0043009//chordate embryonic development+++GO:0072425//signal transduction involved in G2 DNA damage checkpoint+++GO:0044818//mitotic G2/M transition checkpoint+++GO:0006281//DNA repair+++GO:0007059//chromosome segregation+++GO:0044030//regulation of DNA methylation+++GO:2000378//negative regulation of reactive oxygen species metabolic process+++GO:0045766//positive regulation of angiogenesis+++GO:0006310//DNA recombination+++GO:0006357//regulation of transcription by RNA polymerase II+++GO:0045892//negative regulation of transcription, DNA-templated+++GO:0010212//response to ionizing radiation+++GO:0051572//negative regulation of histone H3-K4 methylation+++GO:0033147//negative regulation of intracellular estrogen receptor signaling pathway+++GO:0009048//dosage compensation by inactivation of X chromosome+++GO:0031398//positive regulation of protein ubiquitination+++GO:0006349//regulation of gene expression by genetic imprinting+++GO:0045717//negative regulation of fatty acid biosynthetic</p>
XM_021078074.1	ACSS1	3.240991487	0.028933101	<p>00640//Propanoate metabolism+++01200//Carbon metabolism+++00680//Methane metabolism+++01120//Microbial metabolism in diverse environments+++01130//Biosynthesis of antibiotics+++00630//Glyoxylate and dicarboxylate metabolism+++00620//Pyruvate metabolism+++01100//Metabolic pathways+++00010//Glycolysis / Gluconeogenesis+++01110//Biosynthesis of secondary metabolites+++00720//Carbon fixation pathways in prokaryotes</p>	<p>GO:0005759//mitochondrial matrix</p>	<p>GO:0016208//AMP binding+++GO:0003987//acetate-CoA ligase activity+++GO:0003824//catalytic activity+++GO:0005524//ATP binding+++GO:0000166//nucleotide binding+++GO:0016874//ligase activity</p>	<p>GO:0006085//acetyl-CoA biosynthetic process+++GO:0019427//acetyl-CoA biosynthetic process from acetate</p>

XM_013982220.2	ZMAT3	-21.66291004	6.09E-06	04115//p53 signaling pathway	GO:0005886//plasma membrane+++GO:0005654//nucleoplasm	GO:0008270//zinc ion binding+++GO:0003676//nucleic acid binding+++GO:0046872//metal ion binding	GO:0006974//cellular response to DNA damage stimulus+++GO:0072332//intrinsic apoptotic signaling pathway by p53 class mediator+++GO:0015031//protein transport+++GO:0040008//regulation of growth
XM_021063227.1	MDM4	-6.281651299	0.029172568	04115//p53 signaling pathway	GO:0005634//nucleus	GO:0046872//metal ion binding+++GO:0019899//enzyme binding	GO:0030330//DNA damage response, signal transduction by p53 class mediator+++GO:0008283//cell proliferation+++GO:0042177//negative regulation of protein catabolic process+++GO:0065003//protein-containing complex assembly+++GO:0071157//negative regulation of cell cycle arrest+++GO:0071456//cellular response to hypoxia+++GO:0050821//protein stabilization+++GO:0043066//negative regulation of apoptotic process+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0045023//G0 to G1 transition
XM_021069855.1	ZMAT3	-7.113502883	6.35E-04	04115//p53 signaling pathway	GO:0005654//nucleoplasm+++GO:0005886//plasma membrane	GO:0046872//metal ion binding+++GO:0008270//zinc ion binding+++GO:0003676//nucleic acid binding	GO:0006974//cellular response to DNA damage stimulus+++GO:0015031//protein transport+++GO:0072332//intrinsic apoptotic signaling pathway by p53 class mediator+++GO:0040008//regulation of growth
XM_021070801.1	MAG1	-7.021449972	0.024914946	04015//Rap1 signaling pathway+++04151//PI3K-Akt signaling pathway+++04530//Tight junction	GO:0030054//cell junction+++GO:0005737//cytoplasm+++GO:0016020//membrane+++GO:0005654//nucleoplasm+++GO:0005912//adherens junction+++GO:0042995//cell projection+++GO:0005923//bicellular tight junction+++GO:0005634//nucleus	GO:0005515//protein binding+++GO:0051393//alpha-actinin binding+++GO:0032947//protein-containing complex scaffold activity	GO:0065003//protein-containing complex assembly+++GO:0007166//cell surface receptor signaling pathway+++GO:0070997//neuron death+++GO:0007155//cell adhesion
XM_021078612.1	PRKAG2	-7.72515599	4.78E-04	04710//Circadian rhythm+++04920//Adipocytokine signaling pathway+++04922//Glucagon signaling pathway+++04213//Longevity regulating pathway - multiple species+++04371//Apelin signaling pathway+++04921//Oxytocin signaling pathway+++04910//Insulin signaling pathway+++04714//Thermogenesis+++04211//Longevity regulating pathway+++04068//FoxO signaling pathway+++04530//Tight junction+++04152//AMPK signaling pathway	GO:0031588//nucleotide-activated protein kinase complex	GO:0005524//ATP binding+++GO:0032559//adenyl ribonucleotide binding+++GO:0004862//cAMP-dependent protein kinase inhibitor activity+++GO:0019901//protein kinase binding+++GO:0030295//protein kinase activator activity+++GO:0043531//ADP binding+++GO:0008603//cAMP-dependent protein kinase regulator activity+++GO:0008607//phosphorylase kinase regulator activity	GO:0001900//regulation of protein serine/threonine kinase activity+++GO:0071901//negative regulation of protein serine/threonine kinase activity+++GO:0032147//activation of protein kinase activity+++GO:0019217//regulation of fatty acid metabolic process+++GO:0045860//positive regulation of protein kinase activity+++GO:0005977//glycogen metabolic process+++GO:0006110//regulation of glycolytic process+++GO:0035556//intracellular signal transduction+++GO:0006469//negative regulation of protein kinase activity+++GO:0010800//positive regulation of peptide threonine phosphorylation

XM_021097326.1	PLA2G4E	-8.567195919	9.84E-06	<p>01100//Metabolic pathways+++04010//MAPK signaling pathway+++00590//Arachidonic acid metabolism+++00591//Linoleic acid metabolism+++04730//Long-term depression+++00565//Ether lipid metabolism+++04726//Serotonergic synapse+++04270//Vascular smooth muscle contraction+++04014//Ras signaling pathway+++04611//Platelet activation+++04664//Fc epsilon RI signaling pathway+++04370//VEGF signaling pathway+++01110//Biosynthesis of secondary metabolites+++00592//alpha-Linolenic acid metabolism+++04072//Phospholipase D signaling pathway+++04750//Inflammatory mediator regulation of TRP channels+++04217//Necroptosis+++04724//Glutamate synapse+++04912//GnRH signaling pathway+++00564//Glycerophospholipid metabolism+++04913//Ovarian steroidogenesis+++04921//Oxytocin signaling pathway</p>	GO:0005737//cytoplasm	<p>GO:0046872//metal ion binding+++GO:0102568//phospholipase A2 activity consuming 1,2-diacylglycerol+++GO:0004620//phospholipase activity+++GO:0004623//phospholipase A2 activity+++GO:0016787//hydrolase activity+++GO:0102567//phospholipase A2 activity (consuming 1,2-dipalmitoylphosphatidylcholine)</p>	<p>GO:0006629//lipid metabolic process+++GO:0016042//lipid catabolic process+++GO:0009395//phospholipid catabolic process</p>
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XM_021101934.1 ATM

-9.332342337

1.82E-09

04115//p53 signaling pathway+++04068//FoxO signaling pathway+++04210//Apoptosis+++03440//Homologous recombination+++04214//Apoptosis - fly+++04218//Cellular senescence+++04110//Cell cycle+++04064//NF-kappa B signaling pathway

GO:1990391//DNA repair complex+++GO:0005634//nucleus+++GO:0000781//chromosome, telomeric region+++GO:0031410//cytoplasmic vesicle+++GO:0005840//ribosome+++GO:0005730//nucleolus

GO:0016301//kinase activity+++GO:0004674//protein serine/threonine kinase activity+++GO:0016740//transferase activity+++GO:0005524//ATP binding+++GO:0047485//protein N-terminus binding+++GO:0004677//DNA-dependent protein kinase activity+++GO:0003677//DNA binding+++GO:0044877//protein-containing complex binding+++GO:0003735//structural constituent of ribosome+++GO:0046983//protein dimerization activity+++GO:0016303//1-phosphatidylinositol-3-kinase activity+++GO:0000166//nucleotide binding

GO:0071480//cellular response to gamma radiation+++GO:0010506//regulation of autophagy+++GO:0036092//phosphatidylinositol-3-phosphate biosynthetic process+++GO:0046777//protein autophosphorylation+++GO:0000723//telomere maintenance+++GO:0006468//protein phosphorylation+++GO:0000077//DNA damage checkpoint+++GO:0071044//histone mRNA catabolic process+++GO:0097694//establishment of RNA localization to telomere+++GO:1904884//positive regulation of telomerase catalytic core complex assembly+++GO:1904354//negative regulation of telomere capping+++GO:0007050//cell cycle arrest+++GO:0090399//replicative senescence+++GO:0030335//positive regulation of cell migration+++GO:0016310//phosphorylation+++GO:0032210//regulation of telomere maintenance via telomerase+++GO:0018105//peptidyl-serine phosphorylation+++GO:0071481//cellular response to X-ray+++GO:0007049//cell cycle+++GO:0043065//positive regulation of apoptotic process+++GO:0008630//intrinsic apoptotic signaling pathway in response to DNA damage+++GO:0072434//signal transduction involved in mitotic G2 DNA damage checkpoint+++GO:0043517//positive regulation of DNA damage response, signal transduction by p53 class mediator+++GO:0002331//pre-B cell allelic exclusion+++GO:0030889//negative regulation of B cell proliferation+++GO:1904358//positive regulation of telomere maintenance via telomere lengthening+++GO:0016572//histone phosphorylation+++GO:0036289//peptidyl-serine autophosphorylation+++GO:0010628//positive regulation of gene expression+++GO:0006281//DNA repair+++GO:0006975//DNA damage induced protein phosphorylation+++GO:0006412//translation+++GO:1904262//negative regulation of TORC1

XM_021080582.1	IGF2	-7.629361637	5.97E-05	04014//Ras signaling pathway+++04151//PI3K-Akt signaling pathway+++04010//MAPK signaling pathway	GO:0016021//integral component of membrane+++GO:0005576//extracellular region+++GO:0016020//membrane+++GO:0005615//extracellular space	GO:0008083//growth factor activity+++GO:0005179//hormone activity+++GO:0005178//integrin binding	GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0010469//regulation of signaling receptor activity+++GO:0001892//embryonic placenta development+++GO:0031056//regulation of histone modification+++GO:0060669//embryonic placenta morphogenesis+++GO:0005975//carbohydrate metabolic process+++GO:0006006//glucose metabolic process+++GO:0001503//ossification+++GO:0008284//positive regulation of cell proliferation+++GO:0051147//regulation of muscle cell differentiation+++GO:0001701//in utero embryonic development+++GO:0051781//positive regulation of cell division
XM_021093025.1	APAF1	-22.36191102	2.94E-06	04210//Apoptosis+++04214//Apoptosis - fly+++04115//p53 signaling pathway+++04215//Apoptosis - multiple species	GO:0005829//cytosol+++GO:0005737//cytoplasm+++GO:0043293//apoptosome+++GO:0005634//nucleus+++GO:0032991//protein-containing complex	GO:0042802//identical protein binding+++GO:0008656//cysteine-type endopeptidase activator activity involved in apoptotic process+++GO:0000166//nucleotide binding+++GO:0008233//peptidase activity+++GO:0043531//ADP binding+++GO:0005524//ATP binding	GO:2001235//positive regulation of apoptotic signaling pathway+++GO:0030900//forebrain development+++GO:0007275//multicellular organism development+++GO:0051402//neuron apoptotic process+++GO:0042981//regulation of apoptotic process+++GO:0097190//apoptotic signaling pathway+++GO:0001843//neural tube closure+++GO:1902510//regulation of apoptotic DNA fragmentation+++GO:0070059//intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress+++GO:0006919//activation of cysteine-type endopeptidase activity involved in apoptotic process+++GO:0006508//proteolysis+++GO:0006915//apoptotic process+++GO:0007420//brain development+++GO:0008635//activation of cysteine-type endopeptidase activity involved in apoptotic process by cytochrome c
XM_021079541.1	ACSL4	-21.69130157	5.94E-06	00014//Fatty acid degradation+++04920//Adipocytokine signaling pathway+++01100//Metabolic pathways+++01212//Fatty acid metabolism+++00061//Fatty acid biosynthesis+++04216//Ferroptosis+++02024//Quorum sensing+++03320//PPAR signaling pathway+++04714//Thermogenesis+++04146//Peroxisome	GO:0005739//mitochondrion+++GO:0016021//integral component of membrane+++GO:0005737//cytoplasm+++GO:005811//lipid droplet+++GO:0016020//membrane+++GO:0044233//Mitochondria-associated ER Membrane	GO:0016874//ligase activity+++GO:0003824//catalytic activity+++GO:0031957//very long-chain fatty acid-CoA ligase activity+++GO:0004467//long-chain fatty acid-CoA ligase activity+++GO:0102391//decanoate-CoA ligase activity+++GO:0047676//arachidonate-CoA ligase activity	GO:0001676//long-chain fatty acid metabolic process+++GO:0006629//lipid metabolic process+++GO:0060136//embryonic process involved in female pregnancy

XR_002335884.1	LOC106504983	-6.331560217	0.020387217	04920//Adipocytokine signaling pathway+++04979//Cholesterol metabolism+++04152//AMPK signaling pathway+++04975//Fat digestion and absorption+++04512//ECM-receptor interaction+++03320//PPAR signaling pathway+++04640//Hematopoietic cell lineage+++04145//Phagosome	GO:0045121//membrane raft+++GO:0016020//membrane+++GO:0016324//apical plasma membrane+++GO:0005794//Golgi apparatus+++GO:0031526//brush border membrane+++GO:0016021//integral component of membrane	GO:0050909//sensory perception of taste+++GO:0031623//receptor internalization+++GO:0071404//cellular response to low-density lipoprotein particle stimulus+++GO:0007166//cell surface receptor signaling pathway+++GO:0030299//intestinal cholesterol absorption+++GO:0007155//cell adhesion+++GO:0006955//immune response+++GO:0070508//cholesterol import+++GO:1990000//amyloid fibril formation+++GO:0033993//response to lipid+++GO:0044539//long-chain fatty acid import+++GO:0070542//response to fatty acid+++GO:0097009//energy homeostasis+++GO:1900227//positive regulation of NLRP3 inflammasome complex assembly+++GO:0071726//cellular response to diacyl bacterial lipopeptide+++GO:0050702//interleukin-1 beta secretion+++GO:0050892//intestinal absorption+++GO:0007204//positive regulation of cytosolic calcium ion concentration+++GO:0034197//triglyceride transport+++GO:0070374//positive regulation of ERK1 and ERK2 cascade+++GO:0070543//response to linoleic acid	
XM_021079792.1	CYP4F55	-6.599864824	0.028008712	00590//Arachidonic acid metabolism+++01100//Metabolic pathways	GO:0005789//endoplasmic reticulum membrane+++GO:0016021//integral component of membrane+++GO:0031090//organelle membrane	GO:0097258//20-hydroxy-leukotriene B4 omega oxidase activity+++GO:0097259//20-aldehyde-leukotriene B4 20-monoxygenase activity+++GO:0050051//leukotriene-B4 20-monoxygenase activity+++GO:0020037//heme binding+++GO:0005506//iron ion binding+++GO:0004497//monoxygenase activity	GO:0006691//leukotriene metabolic process+++GO:0006690//icosanoid metabolic process
XM_021098332.1	TNXB	1.713106044	8.21E-11	04151//PI3K-Akt signaling pathway+++04510//Focal adhesion+++04512//ECM-receptor interaction	GO:0043005//neuron projection+++GO:0005615//extracellular space+++GO:0031012//extracellular matrix+++GO:0005576//extracellular region+++GO:0062023//collagen-containing extracellular matrix	GO:0046982//protein heterodimerization activity+++GO:0042803//protein homodimerization activity+++GO:0050839//cell adhesion molecule binding+++GO:0005201//extracellular matrix structural constituent+++GO:0005518//collagen binding+++GO:0008201//heparin binding	GO:0006631//fatty acid metabolic process+++GO:0007157//heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules+++GO:0030198//extracellular matrix organization+++GO:0006641//triglyceride metabolic process+++GO:0098609//cell-cell adhesion+++GO:0006629//lipid metabolic process+++GO:0048666//neuron development+++GO:0043506//regulation of JUN kinase activity+++GO:0030199//collagen fibril
XM_021101862.1	LIN54	1.668227562	0.008107107	04218//Cellular senescence	GO:0005654//nucleoplasm	GO:0003677//DNA binding+++GO:0046872//metal ion binding	GO:0006355//regulation of transcription, DNA-templated+++GO:0006351//transcription, DNA-templated+++GO:0007049//cell cycle+++GO:0051726//regulation of cell cycle

XM_021078616.1	PRKAG2	1.259927756	0.038686793	04714//Thermogenesis+++04910//Insulin signaling pathway+++04211//Longevity regulating pathway+++04710//Circadian rhythm+++04921//Oxytocin signaling pathway+++04213//Longevity regulating pathway - multiple species+++04068//FoxO signaling pathway+++04920//Adipocytokine signaling pathway+++04152//AMPK signaling pathway+++04371//Apelin signaling pathway+++04530//Tight junction+++04922//Glucagon signaling pathway	GO:0031588//nucleotide-activated protein kinase complex	GO:0019901//protein kinase binding+++GO:0004862//cAMP-dependent protein kinase inhibitor activity+++GO:0008603//cAMP-dependent protein kinase regulator activity+++GO:0032559//adenyl ribonucleotide binding+++GO:0005524//ATP binding+++GO:0030295//protein kinase activator activity+++GO:0043531//ADP binding+++GO:0008607//phosphorylase kinase regulator activity	GO:0035556//intracellular signal transduction+++GO:0071901//negative regulation of protein serine/threonine kinase activity+++GO:0010800//positive regulation of peptidyl-threonine phosphorylation+++GO:0045860//positive regulation of protein kinase activity+++GO:0019217//regulation of fatty acid metabolic process+++GO:0005977//glycogen metabolic process+++GO:0006110//regulation of glycolytic process+++GO:0006469//negative regulation of protein kinase activity+++GO:0032147//activation of protein kinase activity+++GO:0071900//regulation of protein serine/threonine kinase activity
XM_021099599.1	BCL2	1.273179187	7.51E-07	04215//Apoptosis - multiple species+++04725//Cholinergic synapse+++04915//Estrogen signaling pathway+++04151//PI3K-Akt signaling pathway+++04928//Parathyroid hormone synthesis, secretion and action+++04210//Apoptosis+++04510//Focal adhesion+++04261//Adrenergic signaling in cardiomyocytes+++04115//p53 signaling pathway+++04340//Hedgehog signaling pathway+++04722//Neurotrophin signaling pathway+++04140//Autophagy - animal+++04064//NF-kappa B signaling pathway+++04071//Sphingolipid signaling pathway+++04630//Jak-STAT signaling pathway+++04066//HIF-1 signaling pathway+++04141//Protein processing in endoplasmic reticulum+++04621//NOD-like receptor signaling pathway+++04217//Necroptosis	GO:0016020//membrane+++GO:0016021//integral component of membrane	GO:0042803//protein homodimerization activity+++GO:0046982//protein heterodimerization activity	GO:0006915//apoptotic process+++GO:0043066//negative regulation of apoptotic process+++GO:0042981//regulation of apoptotic process
XM_021101100.1	TBC1D1	2.074576015	0.038896377	04152//AMPK signaling pathway	GO:0005623//cell	GO:0005096//GTPase activator activity+++GO:0017137//Rab GTPase binding	GO:0090630//activation of GTPase activity+++GO:0006886//intracellular protein transport
XM_021083604.1	LOC110255237	2.224526312	0.010767769	01100//Metabolic pathways+++00590//Arachidonic acid metabolism	GO:0005789//endoplasmic reticulum membrane+++GO:0031090//organelle membrane	GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen+++GO:0046872//metal ion binding+++GO:0005506//iron ion binding+++GO:0016491//oxidoreductase activity+++GO:0004497//monooxygenase activity+++GO:0020037//heme binding	GO:0055114//oxidation-reduction process
XM_021074130.1	SORBS1	1.948759414	6.66E-04	04910//Insulin signaling pathway+++03320//PPAR signaling pathway+++04520//Adherens junction	GO:0005813//centrosome+++GO:0005924//cell-substrate adherens junction+++GO:0005899//insulin receptor complex+++GO:0005913//cell-cell adherens junction+++GO:0045121//membrane raft+++GO:0016363//nuclear matrix+++GO:0016020//membrane+++GO:0001725//stress fiber+++GO:0005829//cytosol+++GO:0005634//nucleus+++GO:0005856//cytoskeleton+++GO:0005925//focal adhesion+++GO:0005886//plasma membrane	GO:0019901//protein kinase binding+++GO:0031625//ubiquitin protein ligase binding+++GO:0008134//transcription factor binding+++GO:0005070//SH3/SH2 adaptor activity+++GO:0005158//insulin receptor binding	GO:0007015//actin filament organization

XM_021074132.1	SORBS1	5.79154755	0.024281225	04910//Insulin signaling pathway+++03320//PPAR signaling pathway+++04520//Adherens junction	GO:0005813//centrosome+++GO:0005899//insulin receptor complex+++GO:0005829//cytosol+++GO:0045121//membrane raft+++GO:0005634//nucleus+++GO:0016020//membrane+++GO:0001725//stress fiber+++GO:0005856//cytoskeleton+++GO:0005924//cell-substrate adherens junction+++GO:0005925//focal adhesion+++GO:0005913//cell-cell adherens junction+++GO:0016363//nuclear matrix+++GO:0005886//plasma membrane	GO:0019901//protein kinase binding+++GO:0005070//SH3/SH2 adaptor activity+++GO:0005158//insulin receptor binding+++GO:0031625//ubiquitin protein ligase binding+++GO:0008134//transcription factor binding	GO:0007015//actin filament organization
XM_013980184.2	AQP7	22.60503555	2.23E-06	04923//Regulation of lipolysis in adipocytes+++03320//PPAR signaling pathway	GO:0016021//integral component of membrane+++GO:0016020//membrane	GO:0015267//channel activity	GO:0070295//renal water absorption+++GO:0055085//transmembrane transport+++GO:0015793//glycerol transport
XM_021072176.1	CYP2C33	6.524844759	0.049396438	00590//Arachidonic acid metabolism+++00140//Steroid hormone biosynthesis+++04726//Serotonergic synapse+++04750//Inflammatory mediator regulation of TRP channels+++00830//Retinol metabolism+++01100//Metabolic pathways+++00591//Linoleic acid metabolism	GO:0031090//organelle membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0043231//intracellular membrane-bounded organelle	GO:0020037//heme binding+++GO:0070330//aromatase activity+++GO:0008392//arachidonic acid epoxygenase activity+++GO:0005506//iron ion binding+++GO:0008395//steroid hydroxylase activity	GO:0019369//arachidonic acid metabolic process+++GO:0033574//response to testosterone+++GO:0019373//epoxygenase P450 pathway
NM_214414.1	CYP2C33	8.165599687	0.044853172	04726//Serotonergic synapse+++00140//Steroid hormone biosynthesis+++01100//Metabolic pathways+++04750//Inflammatory mediator regulation of TRP channels+++00591//Linoleic acid metabolism+++00830//Retinol metabolism+++00590//Arachidonic acid metabolism	GO:0005789//endoplasmic reticulum membrane+++GO:0043231//intracellular membrane-bounded organelle+++GO:0031090//organelle membrane	GO:0005506//iron ion binding+++GO:0020037//heme binding+++GO:0008392//arachidonic acid epoxygenase activity+++GO:0070330//aromatase activity+++GO:0008395//steroid hydroxylase activity	GO:0033574//response to testosterone+++GO:0019373//epoxygenase P450 pathway+++GO:0019369//arachidonic acid metabolic process
XM_005654266.3	PRKAG2	21.87227211	4.98E-06	04371//Apelin signaling pathway+++04710//Circadian rhythm+++04530//Tight junction+++04910//Insulin signaling pathway+++04922//Glucagon signaling pathway+++04068//FoxO signaling pathway+++04921//Oxytocin signaling pathway+++04211//Longevity regulating pathway+++04714//Thermogenesis+++04152//AMP K signaling pathway+++04213//Longevity regulating pathway - multiple species+++04920//Adipocytokine signaling pathway	GO:0031588//nucleotide-activated protein kinase complex	GO:0005524//ATP binding+++GO:0019901//protein kinase binding+++GO:0043531//ADP binding+++GO:0008607//phosphorylase kinase regulator activity+++GO:0030295//protein kinase activator activity+++GO:0008603//cAMP-dependent protein kinase regulator activity+++GO:0004862//cAMP-dependent protein kinase inhibitor activity+++GO:0032559//adenyl ribonucleotide binding	GO:0035556//intracellular signal transduction+++GO:0071900//regulation of protein serine/threonine kinase activity+++GO:0005977//glycogen metabolic process+++GO:0071901//negative regulation of protein serine/threonine kinase activity+++GO:0032147//activation of protein kinase activity+++GO:0019217//regulation of fatty acid metabolic process+++GO:0045860//positive regulation of protein kinase activity+++GO:0010800//positive regulation of peptidyl-threonine phosphorylation+++GO:0006469//negative regulation of protein kinase activity+++GO:0006110//regulation of glycolytic process

XM_021098327.1	TNXB	4.353045528	0.023579059	04512//ECM-receptor interaction+++04510//Focal adhesion+++04151//PI3K-Akt signaling pathway	GO:0062023//collagen-containing extracellular matrix+++GO:0043005//neuron projection+++GO:0031012//extracellular matrix+++GO:0005615//extracellular space+++GO:0005576//extracellular region	GO:0005518//collagen binding+++GO:0050839//cell adhesion molecule binding+++GO:0008201//heparin binding+++GO:0005201//extracellular matrix structural constituent+++GO:0046982//protein heterodimerization activity+++GO:0042803//protein homodimerization activity	GO:0048666//neuron development+++GO:0098609//cell-cell adhesion+++GO:0006629//lipid metabolic process+++GO:0006631//fatty acid metabolic process+++GO:0030198//extracellular matrix organization+++GO:0007160//cell-matrix adhesion+++GO:0043506//regulation of JUN kinase activity+++GO:0007157//heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules+++GO:0030199//collagen fibril organization+++GO:0006641//triglyceride metabolic process
NM_001113445.1	G6PC	7.333154638	0.003198036	04151//PI3K-Akt signaling pathway+++04152//AMPK signaling pathway+++04068//FoxO signaling pathway+++04910//Insulin signaling pathway+++00010//Glycolysis / Gluconeogenesis+++01100//Metabolic pathways+++04922//Glucagon signaling pathway+++04973//Carbohydrate digestion and absorption+++00052//Galactose metabolism+++04920//Adipocytokine signaling pathway+++00500//Starch and sucrose metabolism	GO:0005783//endoplasmic reticulum+++GO:0016021//integral component of membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0016020//membrane	GO:0016773//phosphotransferase activity, alcohol group as acceptor+++GO:0016787//hydrolase activity+++GO:0042301//phosphate ion binding+++GO:0004346//glucose-6-phosphatase activity	GO:0010468//regulation of gene expression+++GO:0006094//gluconeogenesis+++GO:0008202//steroid metabolic process+++GO:0006641//triglyceride metabolic process+++GO:0005980//glycogen catabolic process+++GO:0051156//glucose 6-phosphate metabolic process+++GO:0015760//glucose-6-phosphate transport+++GO:0005977//glycogen metabolic process+++GO:0042593//glucose homeostasis+++GO:0046415//urate metabolic process+++GO:0035264//multicellular organism growth+++GO:0016311//dephosphorylation+++G
NM_001315734.1	LOC100739741	9.650004263	1.34E-04	01100//Metabolic pathways+++00140//Steroid hormone biosynthesis+++00590//Arachidonic acid metabolism+++04726//Serotonergic synapse+++04750//Inflammatory mediator regulation of TRP channels+++00830//Retinol metabolism+++00591//Linoleic acid metabolism	GO:0043231//intracellular membrane-bounded organelle+++GO:0005737//cytoplasm+++GO:0016020//membrane+++GO:0016021//integral component of membrane	GO:0046872//metal ion binding+++GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen+++GO:0005506//iron ion binding+++GO:0019825//oxygen binding+++GO:0020037//heme binding+++GO:0004497//monooxygenase activity+++GO:0016712//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen+++GO:0016491//oxidoreductase activity+++GO:0008395//steroid hydroxylase activity+++GO:0008392//arachidonic acid epoxygenase activity	GO:0042738//exogenous drug catabolic process+++GO:0019373//epoxygenase P450 pathway+++GO:0006082//organic acid metabolic process+++GO:0055114//oxidation-reduction process+++GO:0006805//xenobiotic metabolic process
XM_021083612.1	LOC102167481	4.307329713	1.33E-09	01100//Metabolic pathways+++00590//Arachidonic acid metabolism	GO:0031090//organelle membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0016021//integral component of membrane	GO:0097258//20-hydroxy-leukotriene B4 omega oxidase activity+++GO:0004497//monooxygenase activity+++GO:0097259//20-aldehyde-leukotriene B4 20-monooxygenase activity+++GO:0050051//leukotriene-B4 20-monooxygenase activity+++GO:0020037//heme binding+++GO:0005506//iron ion binding	GO:0006691//leukotriene metabolic process+++GO:0006690//icosanoid metabolic process

NM_001243939.1	ADHIC	6.315951874	2.19E-06	01100//Metabolic pathways+++00980//Metabolism of xenobiotics by cytochrome P450+++00982//Drug metabolism - cytochrome P450+++00830//Retinol metabolism+++00010//Glycolysis / Gluconeogenesis+++01110//Biosynthesis of secondary metabolites+++00071//Fatty acid degradation+++00350//Tyrosine metabolism	GO:0005737//cytoplasm	GO:0008270//zinc ion binding+++GO:0004022//alcohol dehydrogenase (NAD) activity	
XM_001926129.6	PTGS1	1.306321694	0.010210229	00590//Arachidonic acid metabolism+++01100//Metabolic pathways+++04923//Regulation of lipolysis in adipocytes+++04611//Platelet activation+++04726//Serotonergic synapse	GO:0043231//intracellular membrane-bounded organelle+++GO:0001750//photoreceptor outer segment+++GO:0005737//cytoplasm+++GO:0005794//Golgi apparatus	GO:0020037//heme binding+++GO:0004666//prostaglandin-endoperoxide synthase activity+++GO:0004601//peroxidase activity	GO:0006693//prostaglandin metabolic process+++GO:0055114//oxidation-reduction process+++GO:0006954//inflammatory response+++GO:0042127//regulation of cell proliferation+++GO:0098869//cellular oxidant detoxification+++GO:0060085//smooth muscle relaxation of the bladder outlet+++GO:0001516//prostaglandin biosynthetic process+++GO:0006979//response to oxidative stress+++GO:0008217//regulation of blood pressure+++GO:0019371//cyclooxygenase pathway
XM_013982357.2	STRADB	1.264412473	0.013957128	04152//AMPK signaling pathway+++04150//mTOR signaling pathway	GO:0005737//cytoplasm+++GO:0016235//aggregome+++GO:0005634//nucleus+++GO:0005829//cytosol	GO:0004672//protein kinase activity+++GO:0005524//ATP binding	GO:2001240//negative regulation of extrinsic apoptotic signaling pathway in absence of ligand+++GO:0006468//protein phosphorylation+++GO:0000902//cell morphogenesis+++GO:0032147//activation of protein kinase activity+++GO:0007254//JNK cascade+++GO:0006611//protein export from nucleus
XM_021074163.1	SORBS1	1.391927743	0.012265876	04910//Insulin signaling pathway+++04520//Adherens junction+++03320//PPAR signaling pathway	GO:0005924//cell-substrate adherens junction+++GO:0005913//cell-cell adherens junction+++GO:0005899//insulin receptor complex+++GO:0016020//membrane+++GO:0005856//cytoskeleton+++GO:0005813//centrosome+++GO:0005925//focal adhesion+++GO:0005829//cytosol+++GO:0016363//nuclear matrix+++GO:0005886//plasma membrane+++GO:0005634//nucleus+++GO:0045121//membrane raft+++GO:0001725//stress fiber	GO:0005158//insulin receptor binding+++GO:0019901//protein kinase binding+++GO:0008134//transcription factor binding+++GO:0031625//ubiquitin protein ligase binding+++GO:0005070//SH3/SH2 adaptor activity	GO:0007015//actin filament organization
XM_021091201.1	PRKAG1	1.229141864	0.022333785	04530//Tight junction+++04922//Glucagon signaling pathway+++04211//Longevity regulating pathway+++04910//Insulin signaling pathway+++04920//Adipocytokine signaling pathway+++04714//Thermogenesis+++04921//Oxytocin signaling pathway+++04152//AMPK signaling pathway+++04068//FoxO signaling pathway+++04213//Longevity regulating pathway - multiple species+++04371//Apelin signaling pathway+++04710//Circadian rhythm	GO:0031588//nucleotide-activated protein kinase complex	GO:0004679//AMP-activated protein kinase activity+++GO:0005524//ATP binding+++GO:0016208//AMP binding+++GO:0000166//nucleotide binding+++GO:0016301//kinase activity+++GO:0004672//protein kinase activity+++GO:0019901//protein kinase binding+++GO:0032559//adenyl ribonucleotide binding+++GO:0043531//ADP binding	GO:0071900//regulation of protein serine/threonine kinase activity+++GO:0006631//fatty acid metabolic process+++GO:0006633//fatty acid biosynthetic process+++GO:0006629//lipid metabolic process+++GO:0006468//protein phosphorylation+++GO:0016310//phosphorylation+++GO:0010628//positive regulation of gene expression

XM_021074134.1	SORBS1	2.141428728	5.32E-04	03320//PPAR signaling pathway+++04910//Insulin signaling pathway+++04520//Adherens junction	GO:0005899//insulin receptor complex+++GO:0001725//stress fiber+++GO:0016020//membrane+++GO:0005913//cell-cell adherens junction+++GO:0005924//cell-substrate adherens junction+++GO:0005634//nucleus+++GO:0005925//focal adhesion+++GO:0005829//cytosol+++GO:0005813//centrosome+++GO:0005886//plasma membrane+++GO:0005856//cytoskeleton+++GO:0045121//membrane raft+++GO:0016363//nuclear matrix	GO:0008134//transcription factor binding+++GO:0031625//ubiquitin protein ligase binding+++GO:0019901//protein kinase binding+++GO:0005070//SH3/SH2 adaptor activity+++GO:0005158//insulin receptor binding	GO:0007015//actin filament organization
XM_021068059.1	MAP2K3	1.893675012	0.007165652	04620//Toll-like receptor signaling pathway+++04750//Inflammatory mediator regulation of TRP channels+++04013//MAPK signaling pathway - fly+++04668//TNF signaling pathway+++04912//GnRH signaling pathway+++04218//Cellular senescence+++04714//Thermogenesis+++04015//Ras p1 signaling pathway+++04664//Fc epsilon RI signaling pathway+++04010//MAPK signaling pathway+++04624//Toll and Imd signaling pathway	GO:0005737//cytoplasm	GO:0004674//protein serine/threonine kinase activity+++GO:0004708//MAP kinase kinase activity+++GO:0005524//ATP binding+++GO:0004672//protein kinase activity+++GO:0019901//protein kinase binding+++GO:0000166//nucleotide binding+++GO:0016301//kinase activity	GO:0038066//p38MAPK cascade+++GO:0045893//positive regulation of transcription, DNA-templated+++GO:0000165//MAPK cascade+++GO:0045860//positive regulation of protein kinase activity+++GO:0006468//protein phosphorylation+++GO:0016310//phosphorylation+++GO:0000187//activation of MAPK activity+++GO:0042035//regulation of cytokine biosynthetic process+++GO:0032147//activation of protein kinase activity+++GO:0035924//cellular response to vascular endothelial growth factor stimulus+++GO:0023014//signal transduction by protein phosphorylation+++GO:0006954//inflammatory response+++GO:0060048//cardiac muscle contraction+++GO:0043536//positive regulation of blood vessel endothelial cell migration+++GO:0031098//stress-activated protein kinase signaling cascade
XM_021074020.1	CYP2C36	10.04821267	1.25E-04	00830//Retinol metabolism+++04726//Serotonergic synapse+++01100//Metabolic pathways	GO:0043231//intracellular membrane-bounded organelle+++GO:0005737//cytoplasm	GO:0008392//arachidonic acid epoxygenase activity+++GO:0016705//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen+++GO:0016712//oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen, reduced flavin or flavoprotein as one donor, and incorporation of one atom of oxygen+++GO:0046872//metal ion binding+++GO:0005506//iron ion binding+++GO:0020037//heme binding+++GO:0016491//oxidoreductase activity+++GO:0008395//steroid hydroxylase activity+++GO:0004497//monooxygenase activity	GO:0006805//xenobiotic metabolic process+++GO:0055114//oxidation-reduction process+++GO:0042738//exogenous drug catabolic process+++GO:0006082//organic acid metabolic process+++GO:0019373//epoxygenase P450 pathway

XM_021097877.1	SLA-2	5.099477482	0.04055044	04145//Phagosome+++04144//Endocytosis+++04218//Cellular senescence+++04612//Antigen processing and presentation+++04514//Cell adhesion molecules (CAMs)	GO:0016020//membrane+++GO:0000139//Golgi membrane+++GO:0071556//integral component of luminal side of endoplasmic reticulum membrane+++GO:0005794//Golgi apparatus+++GO:0055038//recycling endosome membrane+++GO:0012507//ER to Golgi transport vesicle membrane+++GO:0031901//early endosome membrane+++GO:0042612//MHC class I protein complex+++GO:0005789//endoplasmic reticulum membrane+++GO:0005887//integral component of plasma membrane+++GO:0005886//plasma membrane+++GO:0009986//cell surface+++GO:0030670//phagocytic vesicle membrane+++GO:0005783//endoplasmic reticulum	GO:0046977//TAP binding+++GO:0030881//beta-2-microglobulin binding+++GO:0042605//peptide antigen binding	GO:0002474//antigen processing and presentation of peptide antigen via MHC class I+++GO:0002479//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent+++GO:0016567//protein ubiquitination+++GO:0002480//antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-independent+++GO:0006955//immune response+++GO:0060337//type I interferon signaling pathway+++GO:0060333//interferon-gamma-mediated signaling pathway+++GO:0050776//regulation of immune response
NM_213979.1	FBP1	4.892230367	0.002157843	04152//AMPK signaling pathway+++01130//Biosynthesis of antibiotics+++01100//Metabolic pathways+++01200//Carbon metabolism+++00030//Pentose phosphate pathway+++00010//Glycolysis / Gluconeogenesis+++01110//Biosynthesis of secondary metabolites+++00051//Fructose and mannose metabolism+++01120//Microbial metabolism in diverse environments+++04910//Insulin signaling pathway+++00710//Carbon fixation in photosynthetic organisms+++00680//Methane metabolism	GO:0005634//nucleus+++GO:0005829//cytosol+++GO:0005737//cytoplasm	GO:0048029//monosaccharide binding+++GO:0042802//identical protein binding+++GO:0016208//AMP binding+++GO:0042578//phosphoric ester hydrolase activity+++GO:0016787//hydrolase activity+++GO:0016791//phosphatase activity+++GO:0003824//catalytic activity+++GO:0046872//metal ion binding+++GO:0042132//fructose 1,6-bisphosphate 1-phosphatase activity	GO:0045820//negative regulation of glycolytic process+++GO:0005975//carbohydrate metabolic process+++GO:0006000//fructose metabolic process+++GO:0006094//gluconeogenesis+++GO:0016311//dephosphorylation+++GO:0005986//sucrose biosynthetic process+++GO:0030308//negative regulation of cell growth+++GO:0006111//regulation of gluconeogenesis+++GO:0051289//protein homotetramerization+++GO:0008152//metabolic process+++GO:0030388//fructose 1,6-bisphosphate metabolic process+++GO:0046580//negative regulation of Ras protein signal transduction+++GO:0006002//fructose 6-phosphate metabolic process+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0071286//cellular response to magnesium ion+++GO:0035690//cellular response to drug
XM_005673043.3	PCK1	7.516253235	0.001275788	00620//Pyruvate metabolism+++00010//Glycolysis / Gluconeogenesis+++01100//Metabolic pathways+++04964//Proximal tubule bicarbonate reclamation+++04068//FoxO signaling pathway+++04910//Insulin signaling pathway+++01120//Microbial metabolism in diverse environments+++03320//PPAR signaling pathway+++04920//Adipocytokine signaling pathway+++01130//Biosynthesis of antibiotics+++04151//PI3K-Akt signaling pathway+++00020//Citrate cycle (TCA cycle)+++04922//Glucagon signaling pathway+++04152//AMPK signaling pathway+++01110//Biosynthesis of secondary metabolites	GO:0005739//mitochondrion+++GO:0005829//cytosol	GO:0031406//carboxylic acid binding+++GO:0004613//phosphoenolpyruvate carboxykinase (GTP) activity+++GO:0004611//phosphoenolpyruvate carboxykinase activity+++GO:0000287//magnesium ion binding+++GO:0030145//manganese ion binding+++GO:0016301//kinase activity+++GO:0005525//GTP binding+++GO:0017076//purine nucleotide binding	GO:0006475//internal protein amino acid acetylation+++GO:0016310//phosphorylation+++GO:0033993//response to lipid+++GO:0032869//cellular response to insulin stimulus+++GO:0006006//glucose metabolic process+++GO:0006629//lipid metabolic process+++GO:0071549//cellular response to dexamethasone stimulus+++GO:0051365//cellular response to potassium ion starvation+++GO:0071333//cellular response to glucose stimulus+++GO:0009617//response to bacterium+++GO:0061402//positive regulation of transcription from RNA polymerase II promoter in response to acidic pH+++GO:0042594//response to starvation+++GO:0070365//hepatocyte differentiation+++GO:0046327//glycerol biosynthetic process from pyruvate+++GO:0019543//propionate catabolic process+++GO:0006094//gluconeogenesis+++GO:0032868//response to insulin+++GO:0006090//pyruvate metabolic process

NM_001123158.1	PCK1	6.369135947	4.82E-05	<p>01120//Microbial metabolism in diverse environments+++04964//Proximal tubule bicarbonate reclamation+++00010//Glycolysis / Gluconeogenesis+++00020//Citrate cycle (TCA cycle)+++04151//PI3K-Akt signaling pathway+++04152//AMPK signaling pathway+++03320//PPAR signaling pathway+++04910//Insulin signaling pathway+++04920//Adipocytokine signaling pathway+++01130//Biosynthesis of antibiotics+++01110//Biosynthesis of secondary metabolites+++04922//Glucagon signaling pathway+++04068//FoxO signaling pathway+++00620//Pyruvate metabolism+++01100//Metabolic pathways</p>	<p>GO:0005829//cytosol+++GO:0005739//mitochondrion</p>	<p>GO:0004611//phosphoenolpyruvate carboxykinase activity+++GO:0000287//magnesium ion binding+++GO:0030145//manganese ion binding+++GO:0031406//carboxylic acid binding+++GO:0004613//phosphoenolpyruvate carboxykinase (GTP) activity+++GO:0005525//GTP binding+++GO:0016301//kinase activity+++GO:0017076//purine nucleotide binding</p>	<p>GO:0006475//internal protein amino acid acetylation+++GO:0046327//glycerol biosynthetic process from pyruvate+++GO:0070365//hepatocyte differentiation+++GO:0071549//cellular response to dexamethasone stimulus+++GO:0019543//propionate catabolic process+++GO:0032869//cellular response to insulin stimulus+++GO:0032868//response to insulin+++GO:0033993//response to lipid+++GO:0006094//gluconeogenesis+++GO:0016310//phosphorylation+++GO:0009617//response to bacterium+++GO:0061402//positive regulation of transcription from RNA polymerase II promoter in response to acidic pH+++GO:0006090//pyruvate metabolic process+++GO:0006629//lipid metabolic process+++GO:0051365//cellular response to potassium ion starvation+++GO:0042594//response to starvation+++GO:0071333//cellular response to glucose stimulus+++GO:0006006//glucose metabolic process</p>
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XM_021093564.1	PRKAA2	-2.088050702	2.80E-07	<p>04920//Adipocytokine signaling pathway+++04714//Thermogenesis+++04213//Longevity regulating pathway - multiple species+++04710//Circadian rhythm+++04140//Autophagy - animal+++04910//Insulin signaling pathway+++04921//Oxytocin signaling pathway+++04211//Longevity regulating pathway+++04151//PI3K-Akt signaling pathway+++04922//Glucagon signaling pathway+++04068//FoxO signaling pathway+++04150//mTOR signaling pathway+++04152//AMPK signaling pathway+++04371//Apelin signaling pathway+++04530//Tight junction</p>	<p>GO:0043025//neuronal cell body+++GO:0016607//nuclear speck+++GO:0005737//cytoplasm+++GO:0005634//nucleus+++GO:0030425//dendrite+++GO:0031588//nucleotide-activated protein kinase complex+++GO:0005794//Golgi apparatus+++GO:0030424//axon+++GO:0010494//cytoplasmic stress granule</p>	<p>GO:0047322//[hydroxymethylglutaryl-CoA reductase (NADPH)] kinase activity+++GO:0046872//metal ion binding+++GO:0050405//[acetyl-CoA carboxylase] kinase activity+++GO:0004674//protein serine/threonine kinase activity+++GO:0004672//protein kinase activity+++GO:0005524//ATP binding+++GO:0000166//nucleotide binding+++GO:0016740//transferase activity+++GO:0004712//protein serine/threonine/tyrosine kinase activity+++GO:0035174//histone serine kinase activity+++GO:0016301//kinase activity+++GO:0003682//chromatin binding+++GO:0004679//AMP-activated protein kinase activity</p>	<p>GO:0042595//glucose homeostasis+++GO:0035404//histone-serine phosphorylation+++GO:0016055//Wnt signaling pathway+++GO:0010468//regulation of gene expression+++GO:0071380//cellular response to prostaglandin E stimulus+++GO:0071333//cellular response to glucose stimulus+++GO:0014850//response to muscle activity+++GO:0016241//regulation of macroautophagy+++GO:0008610//lipid biosynthetic process+++GO:0006629//lipid metabolic process+++GO:0006914//autophagy+++GO:0016126//sterol biosynthetic process+++GO:0006695//cholesterol biosynthetic process+++GO:0070507//regulation of microtubule cytoskeleton organization+++GO:0062028//regulation of stress granule assembly+++GO:0035556//intracellular signal transduction+++GO:0035690//cellular response to drug+++GO:0042752//regulation of circadian rhythm+++GO:0010629//negative regulation of gene expression+++GO:0032007//negative regulation of TOR signaling+++GO:0031669//cellular response to nutrient levels+++GO:0006631//fatty acid metabolic process+++GO:0048511//rhythmic process+++GO:0071277//cellular response to calcium ion+++GO:0008202//steroid metabolic process+++GO:0043066//negative regulation of apoptotic process+++GO:0016310//phosphorylation+++GO:0034599//cellular response to oxidative stress+++GO:2000758//positive regulation of peptidyl-lysine acetylation+++GO:0006468//protein phosphorylation+++GO:0006694//steroid biosynthetic process+++GO:0010508//positive regulation of autophagy+++GO:1903829//positive regulation of cellular protein localization+++GO:0008203//cholesterol metabolic process+++GO:0042149//cellular response to glucose GO:0001503//ossification+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0008284//positive regulation of cell proliferation+++GO:0001701//in utero embryonic development+++GO:0006006//glucose metabolic process+++GO:0051781//positive regulation of cell division+++GO:0051147//regulation of muscle cell differentiation+++GO:0005975//carbohydrate metabolic process+++GO:0060669//embryonic placenta morphogenesis+++GO:0031056//regulation of histone modification+++GO:0010469//regulation of signaling receptor activity+++GO:0001892//embryonic placenta development</p>
XM_021080575.1	IGF2	-2.066171754	1.36E-08	<p>04010//MAPK signaling pathway+++04014//Ras signaling pathway+++04151//PI3K-Akt signaling pathway</p>	<p>GO:0005576//extracellular region+++GO:0016021//integral component of membrane+++GO:0016020//membrane+++GO:0005615//extracellular space</p>	<p>GO:0005178//integrin binding+++GO:0005179//hormone activity+++GO:0008083//growth factor activity</p>	

NM_001038644.1	ANGPTL4	-1.704947066	1.77E-04	03320//PPAR signaling pathway+++04979//Cholesterol metabolism	GO:0005615//extracellular space+++GO:0005576//extracellular region	GO:0004857//enzyme inhibitor activity+++GO:0042802//identical protein binding	GO:0001525//angiogenesis+++GO:0030154//cell differentiation+++GO:0007275//multicellular organism development+++GO:2000352//negative regulation of endothelial cell apoptotic process+++GO:0051005//negative regulation of lipoprotein lipase activity+++GO:0043066//negative regulation of apoptotic process+++GO:0070328//triglyceride homeostasis
XM_021069486.1	PPP2R3A	-1.158642419	0.007753811	04151//PI3K-Akt signaling pathway+++03015//mRNA surveillance pathway+++04261//Adrenergic signaling in cardiomyocytes+++04152//AMPK signaling pathway+++04728//Dopaminergic synapse+++04071//Sphingolipid signaling pathway	GO:0000159//protein phosphatase type 2A complex	GO:0005509//calcium ion binding	GO:0090263//positive regulation of canonical Wnt signaling pathway+++GO:0090090//negative regulation of canonical Wnt signaling pathway+++GO:0061053//somite development+++GO:0045732//positive regulation of protein catabolic process+++GO:0006470//protein dephosphorylation+++GO:0090244//Wnt signaling pathway involved in somitogenesis+++GO:0090249//regulation of cell motility involved in somitogenic axis elongation+++GO:0007525//somatic muscle development+++GO:0001754//eye photoreceptor cell differentiation
XM_021080585.1	IGF2	-4.961226962	5.52E-16	04151//PI3K-Akt signaling pathway+++04014//Ras signaling pathway+++04010//MAPK signaling pathway	GO:0016021//integral component of membrane+++GO:0005615//extracellular space+++GO:0005576//extracellular region+++GO:0016020//membrane	GO:0005179//hormone activity+++GO:0005178//integrin binding+++GO:0008083//growth factor activity	GO:0060669//embryonic placenta morphogenesis+++GO:0001892//embryonic placenta development+++GO:0001503//ossification+++GO:0051781//positive regulation of cell division+++GO:0001701//in utero embryonic development+++GO:0010469//regulation of signaling receptor activity+++GO:0008284//positive regulation of cell proliferation+++GO:0031056//regulation of histone modification+++GO:0051147//regulation of muscle cell differentiation+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0005975//carbohydrate metabolic process+++GO:0006006//glucose metabolic process
XM_013992761.2	LAMA4	-1.149905214	0.010569534	04510//Focal adhesion+++04512//ECM-receptor interaction+++04151//PI3K-Akt signaling pathway	GO:0031594//neuromuscular junction+++GO:0005604//basement membrane+++GO:0043083//synaptic cleft+++GO:0062023//collagen-containing extracellular matrix	GO:0005102//signaling receptor binding+++GO:0005201//extracellular matrix structural constituent	GO:0005102//regulation of cell adhesion+++GO:0120163//negative regulation of cold-induced thermogenesis+++GO:0001568//blood vessel development+++GO:0030334//regulation of cell migration+++GO:0050873//brown fat cell differentiation+++GO:0045995//regulation of embryonic development+++GO:0007155//cell adhesion

XR_002343817.1	GAPDH	-1.31680227	0.008174347	01110//Biosynthesis of secondary metabolites+++01130//Biosynthesis of antibiotics+++01200//Metabolic pathways+++02000//Carbon metabolism+++04066//HIF-1 signaling pathway+++00710//Carbon fixation in photosynthetic organisms+++01230//Biosynthesis of amino acids+++00010//Glycolysis / Gluconeogenesis+++01120//Microbial metabolism in diverse environments	GO:0005634//nucleus+++GO:0097452//GAIT complex+++GO:0098850//extrinsic component of synaptic vesicle membrane+++GO:0005829//cytosol+++GO:0005737//cytoplasm+++GO:0015630//microtubule cytoskeleton	GO:0097718//disordered domain specific binding+++GO:0035605//peptidyl-cysteine S-nitrosylase activity+++GO:0051287//NAD binding+++GO:0050661//NADP binding+++GO:0008017//microtubule binding+++GO:0004365//glyceraldehyde-3-phosphate dehydrogenase (NAD+) (phosphorylating) activity	GO:0099162//regulation of neurotransmitter loading into synaptic vesicle+++GO:0051402//neuron apoptotic process+++GO:0050821//protein stabilization+++GO:0006417//regulation of translation+++GO:0000226//microtubule cytoskeleton organization+++GO:0006006//glucose metabolic process+++GO:0035606//peptidyl-cysteine S-trans-nitrosylation+++GO:0006096//glycolytic process
XM_021066016.1	ACOX1	-1.233611583	2.81E-05	00592//alpha-Linolenic acid metabolism+++00071//Fatty acid degradation+++01110//Biosynthesis of secondary metabolites+++04024//cAMP signaling pathway+++04146//Peroxisome+++01040//Biosynthesis of unsaturated fatty acids+++01100//Metabolic pathways+++01212//Fatty acid metabolism+++03320//PPAR signaling pathway	GO:0043231//intracellular membrane-bounded organelle+++GO:0005886//plasma membrane+++GO:0005730//nucleolus+++GO:0005654//nucleoplasm+++GO:0005777//peroxisome+++GO:0005737//cytoplasm+++GO:0005778//peroxisomal membrane+++GO:0005634//nucleus	GO:0030165//PDZ domain binding+++GO:0003997//acyl-CoA oxidase activity+++GO:0016401//palmitoyl-CoA oxidase activity+++GO:0050660//flavin adenine dinucleotide binding+++GO:0005102//signaling receptor binding+++GO:0071949//FAD binding+++GO:0005504//fatty acid binding+++GO:0047485//protein N-terminus binding+++GO:0016627//oxidoreductase activity, acting on the CH-CH group of donors	GO:0006635//fatty acid beta-oxidation+++GO:0033540//fatty acid beta-oxidation using acyl-CoA oxidase+++GO:0055088//lipid homeostasis+++GO:0055114//oxidation-reduction process+++GO:0000038//very long-chain fatty acid metabolic process+++GO:0006091//generation of precursor metabolites and energy+++GO:0006629//lipid metabolic process+++GO:0007283//spermatogenesis+++GO:0019395//fatty acid oxidation+++GO:0006631//fatty acid metabolic process+++GO:0006693//prostaglandin metabolic process
XM_005671823.3	PPP1R3B	-1.737570686	0.004752355	04910//Insulin signaling pathway	GO:0000164//protein phosphatase type 1 complex	GO:0019888//protein phosphatase regulator activity	GO:0005975//carbohydrate metabolic process+++GO:0005981//regulation of glycogen catabolic process+++GO:0043666//regulation of phosphoprotein phosphatase activity+++GO:0005977//glycogen metabolic process
XM_021068116.1	MAP2K6	-1.751027008	4.28E-19	04380//Osteoclast differentiation+++04750//Inflammatory mediator regulation of TRP channels+++04912//GnRH signaling pathway+++04010//MAPK signaling pathway+++04218//Cellular senescence+++04212//Longevity regulating pathway - worm+++04015//Rap1 signaling pathway+++04620//Toll-like receptor signaling pathway+++04668//TNF signaling pathway+++04664//Fc epsilon RI signaling pathway	GO:0005829//cytosol+++GO:0005634//nucleus	GO:0000166//nucleotide binding+++GO:0005524//ATP binding+++GO:0019901//protein kinase binding+++GO:0004674//protein serine/threonine kinase activity+++GO:0004708//MAP kinase kinase activity+++GO:0004672//protein kinase activity+++GO:0016301//kinase activity	GO:0060048//cardiac muscle contraction+++GO:0016310//phosphorylation+++GO:0000187//activation of MAPK activity+++GO:0006468//protein phosphorylation+++GO:0120163//negative regulation of cold-induced thermogenesis+++GO:0000165//MAPK cascade

XM_021087999.1	ALDOA	-1.93426523	3.50E-09	00680//Methane metabolism+++00710//Carbon fixation in photosynthetic organisms+++00010//Glycolysis / Gluconeogenesis+++00051//Fructose and mannose metabolism+++01200//Carbon metabolism+++01120//Microbial metabolism in diverse environments+++00030//Pentose phosphate pathway+++01110//Biosynthesis of secondary metabolites+++01230//Biosynthesis of amino acids+++01100//Metabolic pathways+++01130//Biosynthesis of antibiotics	GO:0005737//cytoplasm+++GO:0005720//nuclear heterochromatin	GO:0003824//catalytic activity+++GO:0016829//lyase activity+++GO:0004332//fructose-bisphosphate aldolase activity	GO:0006096//glycolytic process
XM_021080692.1	PKA1	2.506151938	4.06E-05	04910//Insulin signaling pathway+++04020//Calcium signaling pathway+++04922//Glucagon signaling pathway	GO:0005886//plasma membrane+++GO:0016020//membrane+++GO:0005964//phosphorylase kinase complex	GO:0005516//calmodulin binding+++GO:0004689//phosphorylase kinase activity+++GO:0003824//catalytic activity	GO:0005977//glycogen metabolic process+++GO:0006468//protein phosphorylation+++GO:0005975//carbohydrate metabolic process

NM_001044526.1	PPARA	1.754195949	0.011302082	<p>04922//Glucagon signaling pathway+++04024//cAMP signaling pathway+++04920//Adipocytokine signaling pathway+++03320//PPAR signaling pathway</p>	<p>GO:0005654//nucleoplasm+++GO:0005634//nucleus+++GO:0090575//RNA polymerase II transcription factor complex</p>	<p>GO:0000981//DNA-binding transcription factor activity, RNA polymerase II-specific+++GO:0030374//nuclear receptor transcription coactivator activity+++GO:0043565//sequence-specific DNA binding+++GO:0000978//RNA polymerase II proximal promoter sequence-specific DNA binding+++GO:0008144//drug binding+++GO:0038023//signaling receptor activity+++GO:0003700//DNA-binding transcription factor activity+++GO:0005504//fatty acid binding+++GO:0000977//RNA polymerase II regulatory region sequence-specific DNA binding+++GO:0001228//DNA-binding transcription activator activity, RNA polymerase II-specific+++GO:0004879//nuclear receptor activity+++GO:0003677//DNA binding+++GO:0001227//DNA-binding transcription repressor activity, RNA polymerase II-specific+++GO:0008134//transcription factor binding+++GO:0008270//zinc ion binding+++GO:0000976//transcription regulatory region sequence-specific DNA binding+++GO:0031624//ubiquitin conjugating enzyme binding+++GO:0008289//lipid binding+++GO:0046872//metal ion binding+++GO:0003707//steroid hormone receptor activity+++GO:0001103//RNA polymerase II repressing transcription factor binding</p>	<p>GO:0019216//regulation of lipid metabolic process+++GO:1902894//negative regulation of pri-miRNA transcription by RNA polymerase II+++GO:0010745//negative regulation of macrophage derived foam cell differentiation+++GO:0050728//negative regulation of inflammatory response+++GO:0030522//intracellular receptor signaling pathway+++GO:0006631//fatty acid metabolic process+++GO:0007275//multicellular organism development+++GO:0008544//epidermis development+++GO:0070166//enamel mineralization+++GO:0045893//positive regulation of transcription, DNA-templated+++GO:0030154//cell differentiation+++GO:0019217//regulation of fatty acid metabolic process+++GO:0045722//positive regulation of gluconeogenesis+++GO:0042752//regulation of circadian rhythm+++GO:0072366//regulation of cellular ketone metabolic process by positive regulation of transcription from RNA polymerase II promoter+++GO:0042060//wound healing+++GO:0046321//positive regulation of fatty acid oxidation+++GO:0010468//regulation of gene expression+++GO:0032922//circadian regulation of gene expression+++GO:0032099//negative regulation of appetite+++GO:0045944//positive regulation of transcription by RNA polymerase II+++GO:0010891//negative regulation of sequestering of triglyceride+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:1903038//negative regulation of leukocyte cell-cell adhesion+++GO:0010887//negative regulation of cholesterol storage+++GO:0072363//regulation of glycolytic process by positive regulation of transcription from RNA polymerase II promoter+++GO:0045892//negative regulation of transcription, DNA-templated+++GO:0006355//regulation of transcription, DNA-</p>
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NM_001122987.1	HK2	1.613495229	0.001906339	04910//Insulin signaling pathway+++01110//Biosynthesis of secondary metabolites+++01120//Microbial metabolism in diverse environments+++01200//Carbon metabolism+++04973//Carbohydrate digestion and absorption+++01130//Biosynthesis of antibiotics+++00500//Starch and sucrose metabolism+++04066//HIF-1 signaling pathway+++01100//Metabolic pathways+++00052//Galactose metabolism+++00010//Glycolysis / Gluconeogenesis+++00051//Fructose and mannose metabolism+++00521//Streptomycin biosynthesis+++00520//Amino sugar and nucleotide sugar metabolism+++00524//Neomycin, kanamycin and gentamicin biosynthesis	GO:0005623//cell+++GO:0005829//cytosol	GO:0016740//transferase activity+++GO:0019158//mannokinase activity+++GO:0004396//hexokinase activity+++GO:0016301//kinase activity+++GO:0004340//glucokinase activity+++GO:0008865//fructokinase activity+++GO:0003824//catalytic activity+++GO:0005524//ATP binding+++GO:0000166//nucleotide binding+++GO:0016773//phosphotransferase activity, alcohol group as acceptor+++GO:0005536//glucose binding	GO:0001678//cellular glucose homeostasis+++GO:0008152//metabolic process+++GO:00046835//carbohydrate phosphorylation+++GO:0016310//phosphorylation+++GO:0051156//glucose 6-phosphate metabolic process+++GO:0019318//hexose metabolic process+++GO:0005975//carbohydrate metabolic process+++GO:0006096//glycolytic process
XM_003124944.4	RETSAT	1.298125017	5.33E-04	00830//Retinol metabolism	GO:0031965//nuclear membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0005640//nuclear outer membrane	GO:0051786//all-trans-retinol 13,14-reductase activity+++GO:0016491//oxidoreductase activity	GO:0042572//retinol metabolic process+++GO:0055114//oxidation-reduction process
XM_021066854.1	ALDOB	9.908947528	7.51E-07	01110//Biosynthesis of secondary metabolites+++01100//Metabolic pathways+++01230//Biosynthesis of amino acids+++00030//Pentose phosphate pathway+++00710//Carbon fixation in photosynthetic organisms+++00051//Fructose and mannose metabolism+++01200//Carbon metabolism+++00010//Glycolysis / Gluconeogenesis+++01120//Microbial metabolism in diverse environments+++00680//Methane metabolism+++01130//Biosynthesis of antibiotics	GO:0034451//centriolar satellite+++GO:0005815//microtubule organizing center	GO:0016829//lyase activity+++GO:0070061//fructose binding+++GO:0008092//cytoskeletal protein binding+++GO:0051117//ATPase binding+++GO:0061609//fructose-1-phosphate aldolase activity+++GO:0042802//identical protein binding+++GO:0003824//catalytic activity+++GO:0004332//fructose-bisphosphate aldolase activity	GO:0030388//fructose 1,6-bisphosphate metabolic process+++GO:0032781//positive regulation of ATPase activity+++GO:0006000//fructose metabolic process+++GO:0006116//NADH oxidation+++GO:0070072//vacuolar proton-transporting V-type ATPase complex assembly+++GO:0006096//glycolytic process
XM_021083611.1	LOC100739101	10.1881759	5.64E-10	01100//Metabolic pathways+++00590//Arachidonic acid metabolism	GO:0016021//integral component of membrane+++GO:0005789//endoplasmic reticulum membrane+++GO:0031090//organelle membrane	GO:0004497//monooxygenase activity+++GO:0005506//iron ion binding+++GO:0097258//20-hydroxy-leukotriene B4 omega oxidase activity+++GO:0050051//leukotriene-B4 20-monooxygenase activity+++GO:0097259//20-aldehyde-leukotriene B4 20-monooxygenase activity+++GO:0020037//heme binding	GO:0006690//icosanoid metabolic process+++GO:0006691//leukotriene metabolic process
XM_001927113.6	ACSS1	2.27019517	0.001047686	01200//Carbon metabolism+++01110//Biosynthesis of secondary metabolites+++01130//Biosynthesis of antibiotics+++01100//Metabolic pathways+++00630//Glyoxylate and dicarboxylate metabolism+++00010//Glycolysis / Gluconeogenesis+++00640//Propanoate metabolism+++00620//Pyruvate metabolism+++00680//Methane metabolism+++01120//Microbial metabolism in diverse environments+++00720//Carbon fixation pathways in prokaryotes	GO:0005759//mitochondrial matrix	GO:0000166//nucleotide binding+++GO:0003987//acetate-CoA ligase activity+++GO:0016874//ligase activity+++GO:0005524//ATP binding+++GO:0016208//AMP binding+++GO:0003824//catalytic activity	GO:0006085//acetyl-CoA biosynthetic process+++GO:0019427//acetyl-CoA biosynthetic process from acetate

XM_021099593.1	BCL2	1.291763403	2.37E-04	<p>04722//Neurotrophin signaling pathway+++04510//Focal adhesion+++04340//Hedgehog signaling pathway+++04217//Necroptosis+++04071//Sphingo lipid signaling pathway+++04630//Jak-STAT signaling pathway+++04064//NF-kappa B signaling pathway+++04210//Apoptosis+++04066//HIF-1 signaling pathway+++04725//Cholinergic synapse+++04928//Parathyroid hormone synthesis, secretion and action+++04621//NOD-like receptor signaling pathway+++04115//p53 signaling pathway+++04915//Estrogen signaling pathway+++04261//Adrenergic signaling in cardiomyocytes+++04141//Protein processing in endoplasmic reticulum+++04151//PI3K-Akt signaling pathway+++04140//Autophagy - animal+++04215//Apoptosis - multiple species</p>	<p>GO:0016021//integral component of membrane+++GO:0016020//membrane</p>	<p>GO:0042803//protein homodimerization activity+++GO:0046982//protein heterodimerization activity</p>	<p>GO:0042981//regulation of apoptotic process+++GO:0006915//apoptotic process+++GO:0043066//negative regulation of apoptotic process</p>
NM_001005154.1	MYC	1.564948468	1.80E-04	<p>04012//ErbB signaling pathway+++04350//TGF-beta signaling pathway+++04310//Wnt signaling pathway+++04390//Hippo signaling pathway+++04630//Jak-STAT signaling pathway+++04218//Cellular senescence+++04919//Thyroid hormone signaling pathway+++04151//PI3K-Akt signaling pathway+++04550//Signaling pathways regulating pluripotency of stem cells+++04391//Hippo signaling pathway - fly+++04110//Cell cycle+++04010//MAPK signaling pathway</p>	<p>GO:0005730//nucleolus+++GO:0005819//spindle +++GO:0005634//nucleus+++GO:0016604//nuclear body+++GO:0005654//nucleoplasm</p>	<p>GO:0070888//E-box binding+++GO:0046983//protein dimerization activity+++GO:0003700//DNA-binding transcription factor activity+++GO:0044877//protein-containing complex binding+++GO:0003677//DNA binding+++GO:0000981//DNA-binding transcription factor activity, RNA polymerase II-specific</p>	<p>GO:0006819//cellular iron ion homeostasis+++GO:0006338//chromatin remodeling+++GO:2000573//positive regulation of DNA biosynthetic process+++GO:0032204//regulation of telomere maintenance+++GO:0000165//MAPK cascade+++GO:0097193//intrinsic apoptotic signaling pathway+++GO:0043280//positive regulation of cysteine-type endopeptidase activity involved in apoptotic process+++GO:0043066//negative regulation of apoptotic process+++GO:2001022//positive regulation of response to DNA damage stimulus+++GO:0006355//regulation of transcription, DNA-templated+++GO:0045656//negative regulation of monocyte differentiation+++GO:0048146//positive regulation of fibroblast proliferation+++GO:0051276//chromosome organization+++GO:0051782//negative regulation of cell division+++GO:0045944//positive regulation of transcription by RNA polymerase II+++GO:0042981//regulation of apoptotic process+++GO:0006974//cellular response to DNA damage stimulus+++GO:0042493//response to drug+++GO:0045893//positive regulation of transcription, DNA-templated+++GO:0010332//response to gamma radiation+++GO:0009314//response to radiation+++GO:0008284//positive regulation of cell proliferation+++GO:0032873//negative regulation of stress-activated MAPK</p>

NM_214403.1	IL6R	1.44216946	0.011338353	<p>04066//HIF-1 signaling pathway+++04630//Jak-STAT signaling pathway+++04659//Th17 cell differentiation+++04640//Hematopoietic cell lineage+++04151//PI3K-Akt signaling pathway+++04060//Cytokine-cytokine receptor interaction</p>	<p>GO:0009897//external side of plasma membrane+++GO:0016020//membrane+++GO:0043235//receptor complex+++GO:0005576//extracellular region+++GO:0070110//ciliary neurotrophic factor receptor complex+++GO:0016021//integral component of membrane+++GO:0016324//apical plasma membrane+++GO:0043514//interleukin-12 complex+++GO:0005896//interleukin-6 receptor complex+++GO:0070743//interleukin-23 complex</p>	<p>GO:0042164//interleukin-12 alpha subunit binding+++GO:0004896//cytokine receptor activity+++GO:0019899//enzyme binding+++GO:0008083//growth factor activity+++GO:0004915//interleukin-6 receptor activity+++GO:0045519//interleukin-23 receptor binding+++GO:0005138//interleukin-6 receptor binding+++GO:0042803//protein homodimerization activity+++GO:0019981//interleukin-6 binding+++GO:0004897//ciliary neurotrophic factor receptor activity+++GO:0070119//ciliary neurotrophic factor binding+++GO:0005143//interleukin-12 receptor binding+++GO:0019955//cytokine binding</p>	<p>GO:0032816//positive regulation of natural killer cell activation+++GO:0042104//positive regulation of activated T cell proliferation+++GO:002827//positive regulation of T-helper 1 type immune response+++GO:0032755//positive regulation of interleukin-6 production+++GO:0048661//positive regulation of smooth muscle cell proliferation+++GO:0070120//ciliary neurotrophic factor-mediated signaling pathway+++GO:0010536//positive regulation of activation of Janus kinase activity+++GO:0042531//positive regulation of tyrosine phosphorylation of STAT protein+++GO:0050671//positive regulation of lymphocyte proliferation+++GO:0031018//endocrine pancreas development+++GO:0019221//cytokine-mediated signaling pathway+++GO:0070102//interleukin-6-mediated signaling pathway+++GO:0051135//positive regulation of NK T cell activation+++GO:0034097//response to cytokine+++GO:0010469//regulation of signaling receptor activity+++GO:0050731//positive regulation of peptidyl-tyrosine phosphorylation+++GO:0032729//positive regulation of interferon-gamma production+++GO:0032722//positive regulation of chemokine production+++GO:0008284//positive regulation of cell proliferation</p>
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XM_021088726.1	IL6R	1.327448268	0.009641659	04640//Hematopoietic cell lineage+++04659//Th17 cell differentiation+++04060//Cytokine-cytokine receptor interaction+++04066//HIF-1 signaling pathway+++04151//PI3K-Akt signaling pathway+++04630//Jak-STAT signaling pathway	GO:0005576//extracellular region+++GO:0005896//interleukin-6 receptor complex+++GO:0070743//interleukin-23 complex+++GO:0009897//external side of plasma membrane+++GO:0070110//ciliary neurotrophic factor receptor complex+++GO:0016324//apical plasma membrane+++GO:0043514//interleukin-12 complex+++GO:0016020//membrane+++GO:0016021//integral component of membrane+++GO:0043235//receptor complex	GO:0005576//interleukin-12 receptor binding+++GO:0004896//cytokine receptor activity+++GO:0019981//interleukin-6 binding+++GO:0004897//ciliary neurotrophic factor receptor activity+++GO:0070119//ciliary neurotrophic factor binding+++GO:0045519//interleukin-23 receptor binding+++GO:0042164//interleukin-12 alpha subunit binding+++GO:0005138//interleukin-6 receptor binding+++GO:0004915//interleukin-6 receptor activity+++GO:0019955//cytokine binding+++GO:0019899//enzyme binding+++GO:0008083//growth factor activity+++GO:0042803//protein homodimerization activity	GO:0050671//positive regulation of lymphocyte proliferation+++GO:0042531//positive regulation of tyrosine phosphorylation of STAT protein+++GO:0002827//positive regulation of T-helper 1 type immune response+++GO:0032816//positive regulation of natural killer cell activation+++GO:0051135//positive regulation of NK T cell activation+++GO:0070102//interleukin-6-mediated signaling pathway+++GO:0048661//positive regulation of smooth muscle cell proliferation+++GO:0032729//positive regulation of interferon-gamma production+++GO:0032755//positive regulation of interleukin-6 production+++GO:0019221//cytokine-mediated signaling pathway+++GO:0010469//regulation of signaling receptor activity+++GO:0034097//response to cytokine+++GO:0070120//ciliary neurotrophic factor-mediated signaling pathway+++GO:0010536//positive regulation of activation of Janus kinase activity+++GO:0008284//positive regulation of cell proliferation+++GO:0031018//endocrine pancreas development+++GO:0050731//positive regulation of peptidyl-tyrosine phosphorylation+++GO:0042104//positive regulation of activated T cell proliferation+++GO:0032722//positive regulation of chemokine production GO:0090630//activation of GTPase activity+++GO:0006886//intracellular protein transport	
XM_021101103.1	TBC1D1	1.524432137	5.42E-04	04152//AMPK signaling pathway	GO:0005623//cell	GO:0017137//Rab GTPase binding+++GO:0005096//GTPase activator activity	GO:0005070//SH3/SH2 adaptor activity+++GO:0019901//protein kinase binding+++GO:0008134//transcription factor binding+++GO:0005158//insulin receptor binding+++GO:0031625//ubiquitin protein ligase binding	GO:0007015//actin filament organization
XM_021074155.1	SORBS1	1.402747244	0.008602096	04910//Insulin signaling pathway+++04520//Adherens junction+++03320//PPAR signaling pathway	GO:0016020//membrane+++GO:0005856//cytoskeleton+++GO:0005813//centrosome+++GO:0005886//plasma membrane+++GO:0001725//stress fiber+++GO:0045121//membrane raft+++GO:0005924//cell-substrate adherens junction+++GO:0005634//nucleus+++GO:0005913//cell-cell adherens junction+++GO:0005899//insulin receptor complex+++GO:0005829//cytosol+++GO:000592	GO:0005070//SH3/SH2 adaptor activity+++GO:0019901//protein kinase binding+++GO:0008134//transcription factor binding+++GO:0005158//insulin receptor binding+++GO:0031625//ubiquitin protein ligase binding	GO:0007015//actin filament organization	
XM_021084204.1	MKNK2	1.208324646	0.012681781	04066//HIF-1 signaling pathway+++04010//MAPK signaling pathway+++04910//Insulin signaling pathway	GO:0016604//nuclear body+++GO:0005654//nucleoplasm+++GO:0005737//cytoplasm+++GO:0005634//nucleus	GO:0004683//calmodulin-dependent protein kinase activity+++GO:0004674//protein serine/threonine kinase activity+++GO:0004672//protein kinase activity+++GO:0000166//nucleotide binding+++GO:0009931//calcium-dependent protein serine/threonine kinase activity+++GO:0005524//ATP binding	GO:0071243//cellular response to arsenic-containing substance+++GO:0018105//peptidyl-serine phosphorylation+++GO:0035556//intracellular signal transduction+++GO:0006468//protein phosphorylation+++GO:0030097//hemopoiesis+++GO:0097192//extrinsic apoptotic signaling pathway in absence of ligand	

NM_214152.2	PPARD	2.825732156	7.31E-06	03320//PPAR signaling pathway+++04310//Wnt signaling pathway	GO:0005634//nucleus+++GO:0000790//nuclear chromatin+++GO:0005654//nucleoplasm	GO:0003713//transcription coactivator activity+++GO:0004879//nuclear receptor activity+++GO:0001227//DNA-binding transcription repressor activity, RNA polymerase II-specific+++GO:0051059//NF-kappaB binding+++GO:0070539//linoleic acid binding+++GO:0008270//zinc ion binding+++GO:0003677//DNA binding+++GO:0003700//DNA-binding transcription factor activity+++GO:0008134//transcription factor binding+++GO:0000981//DNA-binding transcription factor activity, RNA polymerase II-specific+++GO:0003707//steroid hormone receptor activity+++GO:0046982//protein heterodimerization activity+++GO:0043565//sequence-specific DNA binding+++GO:0008289//lipid binding+++GO:0008144//drug binding	GO:0008654//phospholipid biosynthetic process+++GO:0043415//positive regulation of skeletal muscle tissue regeneration+++GO:0033189//response to vitamin A+++GO:0046697//decidualization+++GO:0008203//cholesterol metabolic process+++GO:0045684//positive regulation of epidermis development+++GO:0043066//negative regulation of apoptotic process+++GO:0045600//positive regulation of fat cell differentiation+++GO:1902894//negative regulation of pri-miRNA transcription by RNA polymerase II+++GO:0032966//negative regulation of collagen biosynthetic process+++GO:0051546//keratinocyte migration+++GO:0014068//positive regulation of phosphatidylinositol 3-kinase signaling+++GO:2000288//positive regulation of myoblast proliferation+++GO:0009749//response to glucose+++GO:0015908//fatty acid transport+++GO:0045892//negative regulation of transcription, DNA-templated+++GO:0045662//negative regulation of myoblast differentiation+++GO:0006091//generation of precursor metabolites and energy+++GO:0009062//fatty acid catabolic process+++GO:0043616//keratinocyte proliferation+++GO:0000122//negative regulation of transcription by RNA polymerase II+++GO:0014823//response to activity+++GO:0032024//positive regulation of insulin secretion+++GO:0042060//wound healing+++GO:0060612//adipose tissue development+++GO:0006357//regulation of transcription by RNA polymerase II+++GO:0031589//cell-substrate adhesion+++GO:0030308//negative regulation of cell growth+++GO:1904659//glucose transmembrane transport+++GO:0009299//mRNA transcription+++GO:0071456//cellular response to hypoxia+++GO:0006029//proteoglycan metabolic process+++GO:0050728//negative regulation of inflammatory response+++GO:0007566//embryo implantation+++GO:0045893//positive regulation of intracellular signal transduction+++GO:0045860//positive regulation of protein kinase activity+++GO:0032147//activation of protein kinase activity+++GO:0071901//negative regulation of protein serine/threonine kinase activity+++GO:0006469//negative regulation of protein kinase activity+++GO:0005977//glycogen metabolic process+++GO:0071900//regulation of protein serine/threonine kinase activity+++GO:0006110//regulation of glycolytic process+++GO:0010800//positive regulation of peptidyl-threonine phosphorylation+++GO:0019217//regulation of fatty acid metabolic process
XM_021078618.1	PRKAG2	2.830586155	2.91E-06	04530//Tight junction+++04152//AMPK signaling pathway+++04910//Insulin signaling pathway+++04710//Circadian rhythm+++04211//Longevity regulating pathway+++04213//Longevity regulating pathway - multiple species+++04922//Glucagon signaling pathway+++04920//Adipocytokine signaling pathway+++04714//Thermogenesis+++04921//Oxytocin signaling pathway+++04068//FoxO signaling pathway+++04371//Apelin signaling pathway	GO:0031588//nucleotide-activated protein kinase complex	GO:0019901//protein kinase binding+++GO:0032559//adenyl ribonucleotide binding+++GO:0030295//protein kinase activator activity+++GO:0005524//ATP binding+++GO:0004862//cAMP-dependent protein kinase inhibitor activity+++GO:0008607//phosphorylase kinase regulator activity+++GO:0043531//ADP binding+++GO:0008603//cAMP-dependent protein kinase regulator activity	

XM_021079753.1	CYP4F55	3.085266986	0.019442856	01100//Metabolic pathways+++00590//Arachidonic acid metabolism	GO:0016021//integral component of membrane+++GO:0031090//organelle membrane+++GO:0005789//endoplasmic reticulum membrane	GO:0020037//heme binding+++GO:0004497//monooxygenase activity+++GO:0050051//leukotriene-B4 20-monooxygenase activity+++GO:0005506//iron ion binding+++GO:0097258//20-hydroxy-leukotriene B4 omega oxidase activity+++GO:0097259//20-aldehyde-leukotriene B4 20-monooxygenase activity	GO:0006691//leukotriene metabolic process+++GO:0006690//icosanoid metabolic process
NM_213910.1	SERPINE1	2.28842103	0.003987346	04218//Cellular senescence+++04371//Apelin signaling pathway+++04390//Hippo signaling pathway+++04115//p53 signaling pathway+++04610//Complement and coagulation cascades+++04066//HIF-1 signaling pathway	GO:0062023//collagen-containing extracellular matrix+++GO:0005615//extracellular space+++GO:0070062//extracellular exosome+++GO:0005576//extracellular region	GO:0005102//signaling receptor binding+++GO:0004867//serine-type endopeptidase inhibitor activity+++GO:0030414//peptidase inhibitor activity+++GO:0002020//protease binding	GO:1901331//positive regulation of odontoblast differentiation+++GO:0001300//chronological cell aging+++GO:0051918//negative regulation of fibrinolysis+++GO:0030194//positive regulation of blood coagulation+++GO:0048260//positive regulation of receptor-mediated endocytosis+++GO:1902042//negative regulation of extrinsic apoptotic signaling pathway via death domain receptors+++GO:0010466//negative regulation of peptidase activity+++GO:2000098//negative regulation of smooth muscle cell-matrix adhesion+++GO:0071222//cellular response to lipopolysaccharide+++GO:0030336//negative regulation of cell migration+++GO:0014912//negative regulation of smooth muscle cell migration+++GO:2000352//negative regulation of endothelial cell apoptotic process+++GO:0001525//angiogenesis+++GO:0090026//positive regulation of monocyte chemotaxis+++GO:0050729//positive regulation of inflammatory response+++GO:0045766//positive regulation of angiogenesis+++GO:0010757//negative regulation of plasminogen activation+++GO:0050829//defense response to Gram-negative bacterium+++GO:0010469//regulation of signaling receptor activity+++GO:0010951//negative regulation of endopeptidase activity+++GO:0090399//replicative senescence+++GO:0032757//positive regulation of interleukin-8 production+++GO:0097187//dentinogenesis+++GO:0061044//negative regulation of vascular wound healing+++GO:0035491//positive