

Table S4. The enrichment of protein-coding genes in KEGG pathway and GO terms.

Term	Database	ID	Input number	P_Value
Other glycan degradation	KEGG PATHWAY	ssc00511	1	0.014797786
Metabolic pathways	KEGG PATHWAY	ssc01100	4	0.021403412
Glyoxylate and dicarboxylate metabolism	KEGG PATHWAY	ssc00630	1	0.024036051
Apoptosis - multiple species	KEGG PATHWAY	ssc04215	1	0.025567719
Tryptophan metabolism	KEGG PATHWAY	ssc00380	1	0.035467895
Type II diabetes mellitus	KEGG PATHWAY	ssc04930	1	0.03698247
Sphingolipid metabolism	KEGG PATHWAY	ssc00600	1	0.03698247
Pyrimidine metabolism	KEGG PATHWAY	ssc00240	1	0.042265666
Lysine degradation	KEGG PATHWAY	ssc00310	1	0.045272229
negative regulation of ruffle assembly	Gene Ontology	GO:1900028	1	0.004695702
'de novo' NAD biosynthetic process from tryptophan	Gene Ontology	GO:0034354	1	0.004695702
positive regulation of exit from mitosis	Gene Ontology	GO:0031536	1	0.004695702
peptidyl-lysine dimethylation	Gene Ontology	GO:0018027	1	0.004695702
chromosome passenger complex protein	Gene Ontology	GO:0032133	1	0.005476275
deglycosylation	Gene Ontology	GO:0006517	1	0.005476275
cyclin/CDK positive transcription elongation factor complex	Gene Ontology	GO:0008024	1	0.005476275
profilin binding	Gene Ontology	GO:0005522	1	0.006256264
outer dynein arm histone	Gene Ontology	GO:0036157	1	0.006256264
methyltransferase activity (H3-K36 specific)	Gene Ontology	GO:0046975	1	0.006256264
response to organic substance	Gene Ontology	GO:0010033	1	0.006256264

peptidyl-lysine trimethylation	Gene			
positive regulation of DNA-templated transcription, elongation	Ontology	GO:0018023	1	0.006256264
condensed chromosome kinetochore	Gene			
negative regulation of membrane protein ectodomain proteolysis	Ontology	GO:0032786	1	0.006256264
peptidyl-lysine monomethylation	Gene			
placenta blood vessel development	Ontology	GO:0000777	1	0.006256264
mitotic spindle midzone	Gene			
negative regulation of platelet aggregation	Ontology	GO:0051045	1	0.006256264
cyclin-dependent protein serine/threonine kinase activator activity	Gene			
branching involved in labyrinthine layer morphogenesis	Ontology	GO:0018026	1	0.007035671
NAD biosynthetic process	Gene			
ATP-dependent microtubule motor activity, minus-end-directed	Ontology	GO:0060674	1	0.007035671
actin nucleation	Gene			
negative regulation of epithelial cell migration	Ontology	GO:1990023	1	0.007035671
negative regulation of tyrosine phosphorylation of STAT protein	Gene			
microtubule binding	Ontology	GO:0090331	1	0.007035671
1-phosphatidylinositol-3-kinase regulator activity	Gene			
	Ontology	GO:0061575	1	0.007035671
	Gene			
	Ontology	GO:0060670	1	0.007035671
	Gene			
	Ontology	GO:0009435	1	0.007814496
	Gene			
	Ontology	GO:0008569	1	0.007814496
	Gene			
	Ontology	GO:0045010	1	0.007814496
	Gene			
	Ontology	GO:0010633	1	0.007814496
	Gene			
	Ontology	GO:0042532	1	0.007814496
	Gene			
	Ontology	GO:0008017	2	0.008036249
	Gene			
	Ontology	GO:0046935	1	0.008592738

trophoblast giant cell differentiation	Gene			
	Ontology	GO:0060707	1	0.008592738
dynein complex	Gene			
protein-lysine N-methyltransferase activity	Ontology	GO:0030286	1	0.0093704
histone methyltransferase activity (H3-K4 specific)	Gene			
	Ontology	GO:0016279	1	0.0093704
regulation of insulin secretion involved in cellular response to glucose stimulus	Gene			
proteoglycan biosynthetic process	Ontology	GO:0061178	1	0.0093704
regulation of glucose metabolic process	Gene			
metalloendopeptidase inhibitor activity	Ontology	GO:0030166	1	0.0093704
RNA polymerase II CTD heptapeptide repeat kinase activity	Gene			
chromosome, centromeric region	Ontology	GO:0010906	1	0.01014748
outer dynein arm assembly	Gene			
dynein light intermediate chain binding	Ontology	GO:0008191	1	0.01014748
neuroblast proliferation	Gene			
negative regulation of apoptotic process	Ontology	GO:0008353	1	0.01014748
	Gene			
	Ontology	GO:0000775	1	0.01014748
amino acid transport	Gene			
phosphatidylinositol 3-kinase complex regulation of phosphatidylinositol 3-kinase activity	Ontology	GO:000775	1	0.01014748
	Gene			
	Ontology	GO:0036158	1	0.01092398
PcG protein complex positive regulation of cell differentiation	Gene			
ARF guanyl-nucleotide exchange factor activity	Ontology	GO:0051959	1	0.01092398
	Gene			
	Ontology	GO:0007405	1	0.01092398
	Gene			
	Ontology	GO:00043066	2	0.011229508
	Gene			
	Ontology	GO:0006865	1	0.0116999
	Gene			
	Ontology	GO:0005942	1	0.01247524
	Gene			
	Ontology	GO:0043551	1	0.01247524
	Gene			
	Ontology	GO:0031519	1	0.01247524
	Gene			
	Ontology	GO:0045597	1	0.01247524
	Gene			
	Ontology	GO:0005086	1	0.013250001

regulation of ARF protein signal transduction	Gene Ontology	GO:0032012	1	0.013250001
dynein intermediate chain binding	Gene Ontology	GO:0045505	1	0.013250001
receptor signaling pathway via JAK- STAT	Gene Ontology	GO:0007259	1	0.013250001
mitotic spindle pole	Gene Ontology	GO:0097431	1	0.013250001
nuclear chromatin negative regulation of	Gene Ontology	GO:0000790	2	0.013395221
insulin receptor signaling pathway	Gene Ontology	GO:0046627	1	0.014024183
response to hormone	Gene Ontology	GO:0009725	1	0.014024183
actin polymerization or depolymerization	Gene Ontology	GO:0008154	1	0.014024183
positive regulation of cyclin-dependent protein				
serine/threonine kinase activity	Gene Ontology	GO:0045737	1	0.014024183
mitotic spindle assembly checkpoint	Gene Ontology	GO:0007094	1	0.014024183
cysteine-type endopeptidase inhibitor activity				
involved in apoptotic process	Gene Ontology	GO:0043027	1	0.014797786
cilium movement	Gene Ontology	GO:0003341	1	0.014797786
response to cytokine	Gene Ontology	GO:0034097	1	0.015570811
cyclin-dependent protein				
serine/threonine kinase activity	Gene Ontology	GO:0004693	1	0.017115129
ceramide biosynthetic process	Gene Ontology	GO:0046513	1	0.018657139
mitotic spindle assembly	Gene Ontology	GO:0090307	1	0.020196845
positive regulation of mitotic cell cycle	Gene Ontology	GO:0045931	1	0.020965835
protein	Gene			
phosphorylation	Ontology	GO:0006468	2	0.021286943
phosphotyrosine residue binding	Gene Ontology	GO:0001784	1	0.021734251
spindle microtubule	Gene Ontology	GO:0005876	1	0.021734251

cyclin-dependent protein serine/threonine kinase regulator activity	Gene Ontology	GO:0016538	1	0.022502091
sperm flagellum	Gene Ontology	GO:0036126	1	0.023269358
tubulin binding	Gene Ontology	GO:0015631	1	0.025567719
positive regulation of stress fiber assembly	Gene Ontology	GO:0051496	1	0.025567719
G2/M transition of mitotic cell cycle	Gene Ontology	GO:0000086	1	0.025567719
positive regulation of actin filament polymerization	Gene Ontology	GO:0030838	1	0.026332694
chromosome segregation	Gene Ontology	GO:0007059	1	0.027097096
mitotic spindle organization	Gene Ontology	GO:0007052	1	0.027097096
mitotic cytokinesis	Gene Ontology	GO:0000281	1	0.027860928
collagen trimer	Gene Ontology	GO:0005581	1	0.027860928
cytoplasmic microtubule	Gene Ontology	GO:0005881	1	0.028624188
extracellular space scavenger receptor activity	Gene Ontology	GO:0005615	3	0.029203476
collagen binding	Gene Ontology	GO:0005044	1	0.030910546
negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	Gene Ontology	GO:0005518	1	0.031671525
phosphatidylinositol phosphorylation	Gene Ontology	GO:0043154	1	0.032431936
phagocytic vesicle cysteine-type endopeptidase activity	Gene Ontology	GO:0046854	1	0.033951051
axoneme	Gene Ontology	GO:0045335	1	0.037738908
SH3 domain binding protein homodimerization activity	Gene Ontology	GO:0004197	1	0.03849478
	Gene Ontology	GO:0005930	1	0.039250086
	Gene Ontology	GO:0017124	1	0.040004828
	Gene Ontology	GO:0042803	2	0.041607835

	Gene			
mitotic spindle	Ontology	GO:0072686	1	0.042265666
cellular response to	Gene			
interferon-gamma	Ontology	GO:0071346	1	0.042265666
positive regulation of	Gene			
MAPK cascade	Ontology	GO:0043410	1	0.042265666
	Gene			
protease binding	Ontology	GO:0002020	1	0.043770073
	Gene			
motile cilium	Ontology	GO:0031514	1	0.043770073
	Gene			
cell division	Ontology	GO:0051301	1	0.043770073
positive regulation of				
cytosolic calcium ion	Gene			
concentration	Ontology	GO:0007204	1	0.043770073
hematopoietic				
progenitor cell	Gene			
differentiation	Ontology	GO:0002244	1	0.045272229
microtubule-based	Gene			
movement	Ontology	GO:0007018	1	0.046772138
negative regulation of				
inflammatory	Gene			
response	Ontology	GO:0050728	1	0.046772138
positive regulation of				
protein kinase B	Gene			
signaling	Ontology	GO:0051897	1	0.046772138
protein	Gene			
deubiquitination	Ontology	GO:0016579	1	0.048269802