

## GO enrichment analysis for clusters of TreeFam families

**Table 1.** GO term enrichment analysis for clusters of co-functioning protein families identified with affinity propagation. Listed are clusters with significant biological process annotations to a given term in at least two species ( $p$ -value  $< 0.001$  after correcting for multiple testing).

ID	GO term	Description
1	GO:0043285	biopolymer catabolic process
1	GO:0030163	protein catabolic process
1	GO:0044267	cellular protein metabolic process
1	GO:0044265	cellular macromolecule catabolic process
1	GO:0044260	cellular macromolecule metabolic process
1	GO:0006511	ubiquitin-dependent protein catabolic process
1	GO:0044248	cellular catabolic process
1	GO:0006508	proteolysis
1	GO:0051603	proteolysis involved in cellular protein catabolic process
1	GO:0019941	modification-dependent protein catabolic process
1	GO:0044257	cellular protein catabolic process
1	GO:0043632	modification-dependent macromolecule catabolic process
1	GO:0009056	catabolic process
1	GO:0009057	macromolecule catabolic process
1	GO:0008152	metabolic process
1	GO:0009987	cellular process
1	GO:0043283	biopolymer metabolic process
1	GO:0019538	protein metabolic process
1	GO:0043170	macromolecule metabolic process
1	GO:0044238	primary metabolic process
1	GO:0044237	cellular metabolic process
3	GO:0019538	protein metabolic process
3	GO:0044267	cellular protein metabolic process
3	GO:0044260	cellular macromolecule metabolic process
3	GO:0006508	proteolysis
3	GO:0043285	biopolymer catabolic process
3	GO:0030163	protein catabolic process
3	GO:0009056	catabolic process
3	GO:0009057	macromolecule catabolic process
7	GO:0042493	response to drug
10	GO:0007165	signal transduction
10	GO:0007154	cell communication
11	GO:0016311	dephosphorylation
12	GO:0006464	protein modification process
12	GO:0043283	biopolymer metabolic process
12	GO:0000398	nuclear mRNA splicing, via spliceosome
12	GO:0043170	macromolecule metabolic process
12	GO:0000375	RNA splicing, via transesterification reactions
12	GO:0008380	RNA splicing
12	GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile
12	GO:0044238	primary metabolic process

Continued on next page

Table 1 – continued from previous page

ID	GO term	Description
12	GO:0044237	cellular metabolic process
12	GO:0006397	mRNA processing
12	GO:0016310	phosphorylation
12	GO:0043687	post-translational protein modification
12	GO:0006468	protein amino acid phosphorylation
12	GO:0006796	phosphate metabolic process
12	GO:0006793	phosphorus metabolic process
13	GO:0007283	spermatogenesis
13	GO:0048232	male gamete generation
14	GO:0007091	mitotic metaphase/anaphase transition
16	GO:0006457	protein folding
17	GO:0000165	MAPKKK cascade
17	GO:0045454	cell redox homeostasis
17	GO:0045859	regulation of protein kinase activity
17	GO:0051347	positive regulation of transferase activity
17	GO:0050790	regulation of catalytic activity
17	GO:0051338	regulation of transferase activity
17	GO:0043406	positive regulation of MAPK activity
17	GO:0043405	regulation of MAPK activity
17	GO:0043549	regulation of kinase activity
17	GO:0065009	regulation of a molecular function
17	GO:0043085	positive regulation of enzyme activity
17	GO:0045860	positive regulation of protein kinase activity
17	GO:0000187	activation of MAPK activity
18	GO:0009161	ribonucleoside monophosphate metabolic process
18	GO:0009156	ribonucleoside monophosphate biosynthetic process
18	GO:0009260	ribonucleotide biosynthetic process
18	GO:0009123	nucleoside monophosphate metabolic process
18	GO:0009259	ribonucleotide metabolic process
18	GO:0009124	nucleoside monophosphate biosynthetic process
18	GO:0009116	nucleoside metabolic process
22	GO:0007059	chromosome segregation
23	GO:0051169	nuclear transport
23	GO:0008104	protein localization
23	GO:0033036	macromolecule localization
23	GO:0006606	protein import into nucleus
23	GO:0006605	protein targeting
23	GO:0045184	establishment of protein localization
23	GO:0006886	intracellular protein transport
23	GO:0046907	intracellular transport
23	GO:0006913	nucleocytoplasmic transport
23	GO:0017038	protein import
23	GO:0051170	nuclear import
23	GO:0051649	establishment of cellular localization
23	GO:0051641	cellular localization
23	GO:0015031	protein transport
23	GO:0016043	cellular component organization and biogenesis

Continued on next page

Table 1 – continued from previous page

ID	GO term	Description
23	GO:0006810	transport
23	GO:0051234	establishment of localization
23	GO:0051179	localization
26	GO:0006413	translational initiation
26	GO:0022618	protein-RNA complex assembly
26	GO:0022613	ribonucleoprotein complex biogenesis and assembly
26	GO:0022607	cellular component assembly
26	GO:0065003	macromolecular complex assembly
26	GO:0009058	biosynthetic process
26	GO:0006412	translation
26	GO:0009059	macromolecule biosynthetic process
27	GO:0006413	translational initiation
29	GO:0006457	protein folding
30	GO:0006468	protein amino acid phosphorylation
30	GO:0044267	cellular protein metabolic process
30	GO:0016310	phosphorylation
30	GO:0007165	signal transduction
30	GO:0007154	cell communication
30	GO:0019538	protein metabolic process
30	GO:0043412	biopolymer modification
30	GO:0043687	post-translational protein modification
30	GO:0006464	protein modification process
30	GO:0006796	phosphate metabolic process
30	GO:0006793	phosphorus metabolic process
30	GO:0044260	cellular macromolecule metabolic process
30	GO:0043170	macromolecule metabolic process
30	GO:0007242	intracellular signaling cascade
31	GO:0019320	hexose catabolic process
31	GO:0006007	glucose catabolic process
31	GO:0046365	monosaccharide catabolic process
31	GO:0006096	glycolysis
32	GO:0016310	phosphorylation
33	GO:0007001	chromosome organization and biogenesis (sensu Eukaryota)
33	GO:0016569	covalent chromatin modification
33	GO:0016570	histone modification
33	GO:0051276	chromosome organization and biogenesis
33	GO:0016575	histone deacetylation
33	GO:0006355	regulation of transcription, DNA-dependent
33	GO:0032774	RNA biosynthetic process
33	GO:0006351	transcription, DNA-dependent
33	GO:0006350	transcription
33	GO:0045449	regulation of transcription
33	GO:0006476	protein amino acid deacetylation
33	GO:0006323	DNA packaging
33	GO:0006325	establishment and/or maintenance of chromatin architecture
33	GO:0016568	chromatin modification
34	GO:0006259	DNA metabolic process

Continued on next page

Table 1 – continued from previous page

ID	GO term	Description
34	GO:0007001	chromosome organization and biogenesis (sensu Eukaryota)
34	GO:0016568	chromatin modification
34	GO:0051276	chromosome organization and biogenesis
34	GO:0006325	establishment and/or maintenance of chromatin architecture
34	GO:0006323	DNA packaging
35	GO:0016575	histone deacetylation
35	GO:0016570	histone modification
35	GO:0016569	covalent chromatin modification
35	GO:0006476	protein amino acid deacetylation
35	GO:0016568	chromatin modification
37	GO:0051301	cell division
37	GO:0000087	M phase of mitotic cell cycle
37	GO:0043283	biopolymer metabolic process
37	GO:0007067	mitosis
37	GO:0000279	M phase
37	GO:0044238	primary metabolic process
37	GO:0000278	mitotic cell cycle
37	GO:0007049	cell cycle
37	GO:0022403	cell cycle phase
37	GO:0022402	cell cycle process
42	GO:0000074	regulation of progression through cell cycle
42	GO:0051726	regulation of cell cycle
42	GO:0022403	cell cycle phase
42	GO:0000279	M phase
42	GO:0022402	cell cycle process
42	GO:0051301	cell division
42	GO:0007049	cell cycle
45	GO:0051301	cell division
46	GO:0006512	ubiquitin cycle
47	GO:0043412	biopolymer modification
47	GO:0006464	protein modification process
47	GO:0043687	post-translational protein modification
47	GO:0006793	phosphorus metabolic process
47	GO:0006796	phosphate metabolic process
47	GO:0016310	phosphorylation
47	GO:0006468	protein amino acid phosphorylation
48	GO:0006950	response to stress
48	GO:0050896	response to stimulus
49	GO:0006886	intracellular protein transport
49	GO:0045039	protein import into mitochondrial inner membrane
49	GO:0007007	inner mitochondrial membrane organization and biogenesis
49	GO:0006626	protein targeting to mitochondrion
49	GO:0043681	protein import into mitochondrion
49	GO:0065002	intracellular protein transport across a membrane
49	GO:0007006	mitochondrial membrane organization and biogenesis
49	GO:0007005	mitochondrion organization and biogenesis
55	GO:0006457	protein folding

Continued on next page

Table 1 – continued from previous page

ID	GO term	Description
57	GO:0022618	protein-RNA complex assembly
57	GO:0022613	ribonucleoprotein complex biogenesis and assembly
57	GO:0006413	translational initiation
61	GO:0016071	mRNA metabolic process
61	GO:0006397	mRNA processing
61	GO:0006396	RNA processing
61	GO:0008380	RNA splicing
62	GO:0006261	DNA-dependent DNA replication
65	GO:0006289	nucleotide-excision repair
65	GO:0000737	DNA catabolic process, endonucleolytic
68	GO:0007031	peroxisome organization and biogenesis
71	GO:0007001	chromosome organization and biogenesis (sensu Eukaryota)
71	GO:0051276	chromosome organization and biogenesis
75	GO:0007264	small GTPase mediated signal transduction
75	GO:0007242	intracellular signaling cascade
75	GO:0007165	signal transduction
75	GO:0000902	cell morphogenesis
75	GO:0030030	cell projection organization and biogenesis
75	GO:0030036	actin cytoskeleton organization and biogenesis
75	GO:0048858	cell projection morphogenesis
75	GO:0048856	anatomical structure development
75	GO:0030029	actin filament-based process
75	GO:0032989	cellular structure morphogenesis
75	GO:0009653	anatomical structure morphogenesis
75	GO:0007010	cytoskeleton organization and biogenesis
75	GO:0032990	cell part morphogenesis
75	GO:0030031	cell projection biogenesis
77	GO:0051301	cell division
77	GO:0007049	cell cycle
83	GO:0006561	proline biosynthetic process
83	GO:0006560	proline metabolic process
83	GO:0009084	glutamine family amino acid biosynthetic process
83	GO:0009064	glutamine family amino acid metabolic process
83	GO:0006520	amino acid metabolic process
83	GO:0008652	amino acid biosynthetic process
83	GO:0009309	amine biosynthetic process
83	GO:0044271	nitrogen compound biosynthetic process