

Table 1. Biological process GO terms and their p-values for co-expressed proteins.

GO ID	GO term	Protein (SSP) ^{a)}	P adj. ^{b)}	Cluster ^{c)}
16570	Histone modification	Prohibitin (176), ruvB-like 1 (77, 87), ruvB-like 2 (89, 90)	0.0536	2
16569	Covalent chromatin modification	Prohibitin (176), ruvB-like 1 (77, 87), ruvB-like 2 (89, 90)	0.0536	2
6119	Oxidative phosphorylation	ATP synthase β (93), dihydrolipoyl dehydrogenase (66), cytochrome b-c1 (101)	0.0536	2
16568	Chromatin modification	CBX2 (80), prohibitin (176), ruvB-like 1 (77, 87), ruvB-like 2 (89, 90)	0.0306	3
9117	Nucleotide metabolic	Aldolase A (134), dUTPase (215), IDH3A (136), LDH-B (147, 149), malate dehydrogenase 1 (Mdh1) (151), NDK A (217), phosphoglycerate mutase 1 (187), PURH (47), transaldolase (137), triosephosphate isomerase (193, 194)	0.0021	15
19362	Pyridine nucleotide metabolic	IDH3A (136), LDH-B (147, 149), Mdh1 (151), phosphoglycerate mutase 1 (187), transaldolase (137), triosephosphate isomerase (193, 194)	0.0055	15
6007	Glucose catabolic	Aldolase A (134), aldolase C (132), α -enolase (95, 104, 105, 106, 110), LDH-B (147, 149), Mdh1 (151), phosphoglycerate mutase 1 (187), transaldolase (137), triosephosphate isomerase (193, 194)	0.0055	15
46496	Nicotinamide nucleotide metabolic	IDH3A (136), LDH-B (147, 149), Mdh1 (151), phosphoglycerate mutase 1 (187), transaldolase (137), triosephosphate isomerase (193, 194)	0.0055	15
6096	Glycolysis	Aldolase A (134), aldolase C (132), α -enolase (95, 104, 105, 106, 110), LDH-B (147, 149), Mdh1 (151), phosphoglycerate mutase 1 (187), triosephosphate isomerase (193, 194)	0.0093	15
8360	Regulation of cell shape	Aldolase A (134), coronin-1A (59), ezrin (21)	0.0499	15
6098	Pentose-phosphate shunt	phosphoglycerate mutase 1 (187), transaldolase (137), triosephosphate isomerase (193, 194)	0.0138	16
6913	Nucleocytoplasmic transport	DDX39B (82), eIF-5A-1 (224), Prdx-1 (212)	0.0467	18
6406	mRNA export from nucleus	DDX39B (82), eIF-5A-1 (224)	0.0467	18

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6417	Regulation of translation	eIF-5A-1 (224), HspB1 (197)	0.0534	18
6917	Induction of apoptosis	eIF-5A-1 (224), Prdx-1 (212)	0.0534	18
6955	Immune response	Rho GDI 2 (206), Prdx-1 (212)	0.0378	19
35308	Negative regulation of protein amino acid dephosphorylation	14-3-3 β/α (185), 14-3-3 ϵ (172)	0.021	1R
44248	Cellular catabolic	Aldolase A (134), α -enolase (103), citrate synthase (118), mAspAT (129), LDH-B (147, 149), Mdh2 (152), proteasome α 3 (181), Sod1 (220)	0.03	8R
44262	Cellular carbohydrate metabolic	Aldolase A (134), citrate synthase (118), α -enolase (103), LDH-B (147, 149), Mdh2 (152)	0.03	8R
6107	Oxaloacetate metabolic	Citrate synthase (118), mAspAT (129), malate dehydrogenase (152)	0.03	8R
6096	Glycolysis	Aldolase A (134), α -enolase (103), LDH-B (147, 149), Mdh2 (152)	0.03	8R
30097	Hemopoiesis	NDK A (217), Sod1 (220), Ku80 (17)	0.0317	8R
50793	Regulation of developmental process	Aldolase A (134), Ku80 (17), NDK A (217), Sod1 (220)	0.0347	8R
46496	Nicotinamide nucleotide metabolic	Aldolase A (134), LDH-B (147, 149), Mdh2 (152), NDK A (217)	0.0374	8R
48523	Negative regulation of cellular process	α -Enolase (103), HspB1 (199), NDK A (217), SET (125, 139), Sod1 (220), Ku80 (17)	0.045	8R
8152	Metabolic	Aldolase A (134), citrate synthase (118), α -enolase (103), HspB1 (199), Ku80 (17), LDH-B (147, 149), mAspAT (129), Mdh2 (152), NDK A (217), proteasome α 3 (181), SET (125, 139), Sod1 (220)	0.0482	8R
7010	Cytoskeleton organization	Cofilin-1 (222), plastin-2 (42, 43), stathmin (219)	0.0487	11R
51261	Protein depolymerization	Cofilin-1 (222), stathmin (219)	0.0513	11R

^{a)} SSP referring to those numbers in Figure 2 and short protein names referring to those proteins listed in Table S2.

^{b)} P-value adjusted by the Benjamini multiple test adjustment.

Table 1. Biological process GO terms and their p-values for co-expressed proteins.

^{c)} Cluster numbers referring to those in Figures 3 and 4.