

Table S3. GO Terms either over- or under-represented in the shotgun proteome of the different treatments, as identified by Fisher's exact test (a)

Category	GO-ID	Term	Control			Cadmium			Zinc		
			FDR	P-Value	Over/Under	FDR	P-Value	Over/Under	FDR	P-Value	Over/Under
Cellular Component	GO:0000786	nucleosome	---	---	---	---	---	---	0.00605	0.000944	under
	GO:0005856	cytoskeleton	---	---	---	---	---	---	0.00605	0.000944	under
	GO:0000015	phosphopyruvate hydratase complex	---	---	---	---	---	---	0.000164	7.98E-06	over
	GO:0000324	fungal-type vacuole	---	---	---	---	---	---	0.00605	0.000931	over
	GO:0009898	internal side of plasma membrane	---	---	---	---	---	---	0.000585	6.31E-05	over
Molecular Function	GO:0003677	DNA binding	---	---	---	---	---	---	0.00119	0.000155	under
	GO:0005524	ATP binding	---	---	---	0.002171	0.000157	over	1.2E-07	2.22E-09	under
	GO:0008135	translation factor activity, nucleic acid binding	---	---	---	---	---	---	0.00749	0.00119	under
	GO:0046982	protein heterodimerization activity	---	---	---	---	---	---	0.00605	0.000944	under
	GO:0003924	GTPase activity	0.000713	1.56E-05	under	4.84E-05	9.39E-07	over	0.00178	0.000248	under
	GO:0005525	GTP binding	0.000256	4.32E-06	under	1.78E-05	2.7E-07	over	0.00111	0.000137	under
	GO:0000287	magnesium ion binding	---	---	---	---	---	---	0.000164	7.98E-06	over
	GO:0004634	phosphopyruvate hydratase activity	---	---	---	---	---	---	0.000164	7.98E-06	over
	GO:0008863	formate dehydrogenase (NAD+) activity	---	---	---	---	---	---	0.000161	6.43E-06	over
	GO:0051287	NAD binding	---	---	---	---	---	---	6.26E-06	1.9E-07	over
	GO:0030060	L-malate dehydrogenase activity	0.004285	0.000148	over	---	---	---	0.00122	0.000163	over
	GO:0003746	translation elongation factor activity	---	---	---	0.002799	0.000205	over	---	---	---
	GO:0004365	glyceraldehyde-3-phosphate dehydrogenase activity	---	---	---	1.78E-05	1.7E-07	under	---	---	---
	GO:0050661	NADP binding	---	---	---	5.08E-05	1.03E-06	under	---	---	---
	GO:0051082	unfolded protein binding	0.00883	0.00032	under	---	---	---	---	---	---
Biological Process	GO:0006334	nucleosome assembly	---	---	---	---	---	---	0.00119	0.000155	under
	GO:0006412	translation	---	---	---	---	---	---	0.00788	0.00127	under
	GO:0006457	protein folding	---	---	---	---	---	---	0.00194	0.000275	under
	GO:0006950	response to stress	---	---	---	---	---	---	0.000164	0.000008	under
	GO:0006184	GTP catabolic process	0.000713	1.56E-05	under	4.84E-05	9.39E-07	over	0.00178	0.000248	under
	GO:0006094	gluconeogenesis	---	---	---	---	---	---	0.000521	4.17E-05	over
	GO:0006096	glycolysis	---	---	---	1.78E-05	2.62E-07	under	0.000161	6.52E-06	over
	GO:0032889	regulation of vacuole fusion, non-autophagic	---	---	---	---	---	---	0.000585	6.31E-05	over
	GO:0006099	tricarboxylic acid cycle	0.002775	8.66E-05	over	---	---	---	0.000759	8.57E-05	over
	GO:0006108	malate metabolic process	0.004285	0.000148	over	---	---	---	0.00122	0.000163	over
	GO:0044262	cellular carbohydrate metabolic process	0.001769	4.1E-05	over	---	---	---	0.00202	0.000292	over
	GO:0006414	translational elongation	---	---	---	0.009527	0.000747	over	---	---	---
	GO:0044267	cellular protein metabolic process	0.000652	1.26E-05	under	---	---	---	---	---	---

(a) GO Terms terms under-represented in the specific treatment are shaded in red, those over-represented are shaded in green