Table 2. Functional annotation analysis (also presented in Fig. 3*A* as pie charts)

Biological processes level 5	Differentially expressed genes in category (n)	(%)	P value (Fishers Exact)
RNA metabolism	39	5.36	3.72E-10
Protein biosynthesis	41	5.63	1.59E-06
Cellular macromolecule Catabolism	25	3.43	5.23E-06
Macromolecule biosynthesis	42	5.77	1.19E-05
ER to Golgi vesicle-mediated transport	9	1.24	3.48E-04
Protein transport	44	6.04	9.32E-07
Establishment of cellular localization	44	6.04	3.57E-06
Biopolymer catabolism	21	2.88	1.12E-05
Intracellular protein transport	30	4.12	8.64E-05
Cellular protein metabolism	132	18.13	7.91E-08
Intracellular transport	44	6.04	3.02E-06
Ribosome biogenesis and assembly	15	2.06	9.13E-06
Protein catabolism	20	2.75	1.81E-05
Golgi vesicle transport	10	1.37	6.05E-04
Secretory pathway	14	1.92	0.004632
Cellular component level 4			
Mitochondrion	91	12.50	1.25E-21
Ribosome	32	4.40	2.26E-12
Small nucleolar ribonucleoprotein complex	10	1.37	3.41E-07
Cytosol	33	4.53	6.62E-07
Mitochondrial envelope	29	3.98	2.72E-06
Proteasome core complex	14	1.92	8.34E-15
Mitochondrial matrix	15	2.06	2.27E-08
Organelle inner membrane	29	3.98	4.65E-07
Intracellular membrane-bound organelle	282	38.74	5.09E-15
Organellar ribosome	15	2.06	6.86E-11
Mitochondrial inner membrane	28	3.85	4.61E-07
Nucleolus	18	2.47	1.24E-06
Large ribosomal subunit	9	1.24	1.62E-05
Mitochondrial membrane	28	3.85	2.03E-06
Intracellular non-membr.-bound organelle	73	10.03	6.26E-04
Molecular function level 2			
Structural constituent of ribosome	36	4.95	5.71E-18
Electron transporter activity	20	2.75	1.12E-05
DNA-directed RNA polymerase III activity	6	0.82	1.59E-04
DNA-directed RNA polymerase I activity	6	0.82	1.59E-04
Protein binding	151	20.74	6.49E-04
Carrier activity	28	3.85	9.71E-04
Isomerase activity	11	1.51	0.011384

Selenium binding	5	0.69	0.017377
Proteasome endopeptidase activity	13	1.79	4.38E-15
Hydrolase activity	94	12.91	4.97E-05
DNA-directed RNA polymerase II activity	6	0.82	1.59E-04
Oxidoreductase activity	42	5.77	2.04E-04
Protein transporter activity	12	1.65	7.25E-04
FK506-sensitive peptidyl-prolyl cis-trans isomerase	5	0.69	0.006072
Metal cluster binding	4	0.55	0.045287
Transcription cofactor activity	8	1.10	0.097029
RNA polymerase II transcription factor activity	7	0.96	0.014161
KEGG pathways			
Proteasome	15	2.06	3.91E-12
Pyrimidine metabolism	16	2.20	3.13E-06
Purine metabolism	18	2.47	1.01E-04
Basal transcription factors	6	0.82	0.006238
Nucleotide sugars metabolism	4	0.55	0.036632
Oxidative phosphorylation	20	2.75	2.79E-07
RNA polymerase	9	1.24	4.53E-06
Protein export	5	0.69	7.64E-04
Bisphenol A degradation	4	0.55	0.036632
Snare interactions in vesicular transport	5	0.69	0.038108