

Table 5. GO term enrichment of clusters shown in Fig 4

Cluster key	GO term	log ₁₀ , uncorrected P value	log ₁₀ , corrected P value	GO term genes in cluster	GO term ID	Domain
++-	Cytosol	-47.8318	-3	132	GO:0005829	NA
++-	Cytosolic ribosome (sensu Eukarya)	-41.0607	-3	75	GO:0005830	NA
++-	Biosynthesis	-33.8271	-3	191	GO:0009058	P
++-	Ribosome	-32.6875	-3	92	GO:0005840	NA
++-	Metabolism	-20.092	-3	386	GO:0008152	P
++-	Cytoplasm	-19.8972	-3	423	GO:0005737	NA
++-	Cytosolic small ribosomal subunit (sensu Eukarya)	-19.8562	-3	31	GO:0005843	NA
++-	Oxidoreductase activity	-11.7823	-3	57	GO:0016491	F
++-	Protein metabolism	-11.5394	-3	178	GO:0019538	P
++-	Intracellular	-11.3697	-3	494	GO:0005622	NA
++-	Hexose catabolism	-8.7402	-3	13	GO:0019320	P
++-	Ribosome biogenesis and assembly	-7.9759	-3	50	GO:0042254	P
++-	Nucleotide metabolism	-7.651	-3	21	GO:0009117	P
++-	Ribosome assembly	-7.4322	-3	21	GO:0042255	P
++-	Catabolism	-6.9129	-2.39794	58	GO:0009056	P
++-	Amino acid and derivative metabolism	-6.5057	-2.39794	37	GO:0006519	P
++-	Nucleobase metabolism	-6.4924	-2.39794	13	GO:0009112	P
++-	Organic acid metabolism	-6.4052	-2.39794	47	GO:0006082	P
++-	Endoplasmic reticulum	-5.3214	-1.39794	61	GO:0005783	NA
++-	Energy pathways	-5.0823	-1.22915	36	GO:0006091	P
++*	Biosynthesis	-7.7316	-3	56	GO:0009058	P
++*	Cytoplasm	-6.4233	-2.39794	136	GO:0005737	NA
++*	Cytosol	-5.5464	-1.60206	29	GO:0005829	NA
---+	Cell cycle	-8.193	-3	87	GO:0007049	P
---+	DNA metabolism	-8.0034	-3	78	GO:0006259	P
---+	Regulation of transcription	-7.6716	-3	62	GO:0045449	P
---+	DNA binding	-7.4522	-3	44	GO:0003677	F
---+	Transcription factor activity	-5.0226	-1.16749	16	GO:0003700	F
+*-	Mitochondrial large ribosomal subunit	-6.2114	-2.1549	9	GO:0005762	NA
+++	External	-9.2259	-3	14	GO:0030312	NA

	encapsulating structure					
+++	Glycoprotein biosynthesis	-6.3714	-2.39794	12	GO:0009101	P
*+-	Mitochondrial matrix	-6.1199	-2.09691	15	GO:0005759	NA

