

GO enrichments of biological processes and molecular functions in *E. falciformis* gene clusters in figure 3b. In addition to enriched GO terms (GO id and Term), tables include total numbers of annotated genes for a given GO id, number of genes per cluster belong to the listed GO id (Sign. genes), expected number by random distribution (Expected), p-value, and p-value corrected for mutiple testing (Adj. P-value). Each page contains a list for a given gene cluster (see headings).

Enrichments of biological processes *E. falciformis* cluster 1

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0006352	DNA-templated transcription, initiation	10	4	0.81	0.0059	0.1144

Enrichments of biological processes in E. falciformis cluster 2

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0005975	carbohydrate metabolic process	67	22	7.43	8.90e-07	0.0000
GO:0009144	purine nucleoside triphosphate metabolic...	32	14	3.55	2.00e-06	0.0000
GO:0009199	ribonucleoside triphosphate metabolic pr...	32	14	3.55	2.00e-06	0.0000
GO:0009205	purine ribonucleoside triphosphate metab...	32	14	3.55	2.00e-06	0.0000
GO:0009141	nucleoside triphosphate metabolic proces...	33	14	3.66	3.20e-06	0.0001
GO:0046034	ATP metabolic process	29	13	3.21	3.50e-06	0.0001
GO:0006163	purine nucleotide metabolic process	38	15	4.21	4.20e-06	0.0001
GO:0006928	movement of cell or subcellular componen...	40	15	4.43	8.80e-06	0.0001
GO:0072521	purine-containing compound metabolic pro...	40	15	4.43	8.80e-06	0.0001
GO:0009150	purine ribonucleotide metabolic process	37	14	4.10	1.60e-05	0.0001
GO:0042278	purine nucleoside metabolic process	37	14	4.10	1.60e-05	0.0001
GO:0046128	purine ribonucleoside metabolic process	37	14	4.10	1.60e-05	0.0001
GO:0019693	ribose phosphate metabolic process	42	15	4.66	1.80e-05	0.0001
GO:0009259	ribonucleotide metabolic process	38	14	4.21	2.30e-05	0.0002
GO:0007017	microtubule-based process	48	16	5.32	2.50e-05	0.0002
GO:0009126	purine nucleoside monophosphate metaboli...	34	13	3.77	2.90e-05	0.0002
GO:0009167	purine ribonucleoside monophosphate meta...	34	13	3.77	2.90e-05	0.0002
GO:0009161	ribonucleoside monophosphate metabolic p...	35	13	3.88	4.10e-05	0.0002
GO:0009119	ribonucleoside metabolic process	40	14	4.43	4.50e-05	0.0002
GO:0009117	nucleotide metabolic process	56	17	6.21	5.50e-05	0.0003
GO:0009123	nucleoside monophosphate metabolic proce...	36	13	3.99	5.80e-05	0.0003
GO:0032501	multicellular organismal process	6	5	0.67	8.70e-05	0.0004
GO:0044707	single-multicellular organism process	6	5	0.67	8.70e-05	0.0004
GO:0007018	microtubule-based movement	38	13	4.21	1.10e-04	0.0004
GO:0006753	nucleoside phosphate metabolic process	59	17	6.54	1.10e-04	0.0004
GO:0044723	single-organism carbohydrate metabolic p...	39	13	4.32	1.50e-04	0.0006
GO:1901135	carbohydrate derivative metabolic proces...	78	20	8.65	1.70e-04	0.0006
GO:0009116	nucleoside metabolic process	46	14	5.10	2.50e-04	0.0009
GO:1901657	glycosyl compound metabolic process	46	14	5.10	2.50e-04	0.0009
GO:0006022	aminoglycan metabolic process	5	4	0.55	6.70e-04	0.0018
GO:0006030	chitin metabolic process	5	4	0.55	6.70e-04	0.0018
GO:0007596	blood coagulation	5	4	0.55	6.70e-04	0.0018
GO:0007599	hemostasis	5	4	0.55	6.70e-04	0.0018
GO:0009611	response to wounding	5	4	0.55	6.70e-04	0.0018
GO:0042060	wound healing	5	4	0.55	6.70e-04	0.0018
GO:0050817	coagulation	5	4	0.55	6.70e-04	0.0018
GO:0050878	regulation of body fluid levels	5	4	0.55	6.70e-04	0.0018
GO:0044699	single-organism process	667	94	73.93	9.60e-04	0.0025
GO:0055086	nucleobase-containing small molecule met...	71	17	7.87	1.26e-03	0.0032
GO:0006165	nucleoside diphosphate phosphorylation	17	7	1.88	1.36e-03	0.0034
GO:0006091	generation of precursor metabolites and ...	27	9	2.99	1.65e-03	0.0040
GO:0006040	amino sugar metabolic process	6	4	0.67	1.83e-03	0.0043
GO:1901071	glucosamine-containing compound metaboli...	6	4	0.67	1.83e-03	0.0043
GO:0046939	nucleotide phosphorylation	18	7	2.00	2.01e-03	0.0045
GO:0019637	organophosphate metabolic process	87	19	9.64	2.14e-03	0.0045
GO:0006096	glycolytic process	14	6	1.55	2.40e-03	0.0045
GO:0006757	ATP generation from ADP	14	6	1.55	2.40e-03	0.0045
GO:0009135	purine nucleoside diphosphate metabolic ...	14	6	1.55	2.40e-03	0.0045
GO:0009179	purine ribonucleoside diphosphate metabo...	14	6	1.55	2.40e-03	0.0045
GO:0009185	ribonucleoside diphosphate metabolic pro...	14	6	1.55	2.40e-03	0.0045
GO:0016052	carbohydrate catabolic process	14	6	1.55	2.40e-03	0.0045
GO:0044724	single-organism carbohydrate catabolic p...	14	6	1.55	2.40e-03	0.0045
GO:0046031	ADP metabolic process	14	6	1.55	2.40e-03	0.0045
GO:0009132	nucleoside diphosphate metabolic process	19	7	2.11	2.89e-03	0.0054
GO:0006090	pyruvate metabolic process	15	6	1.66	3.63e-03	0.0066
GO:0019362	pyridine nucleotide metabolic process	20	7	2.22	4.04e-03	0.0070
GO:0046496	nicotinamide nucleotide metabolic proces...	20	7	2.22	4.04e-03	0.0070
GO:0072524	pyridine-containing compound metabolic p...	20	7	2.22	4.04e-03	0.0070
GO:0006733	oxidoreduction coenzyme metabolic proces...	21	7	2.33	5.50e-03	0.0093
GO:0051186	cofactor metabolic process	38	10	4.21	6.43e-03	0.0105
GO:0065008	regulation of biological quality	38	10	4.21	6.43e-03	0.0105
GO:0009142	nucleoside triphosphate biosynthetic pro...	13	5	1.44	9.70e-03	0.0149
GO:0009145	purine nucleoside triphosphate biosynthe...	13	5	1.44	9.70e-03	0.0149
GO:0009201	ribonucleoside triphosphate biosynthetic...	13	5	1.44	9.70e-03	0.0149
GO:0009206	purine ribonucleoside triphosphate biosy...	13	5	1.44	9.70e-03	0.0149

Enrichments of molecular functions in E. falciformis cluster 3

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0003676	nucleic acid binding	485	29	15.7	0.00033	0.033

Enrichments of biological processes in E. falciformis cluster 4

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0006506	GPI anchor biosynthetic process	4	3	0.44	0.0049	0.0544
GO:0006661	phosphatidylinositol biosynthetic proces...	4	3	0.44	0.0049	0.0544
GO:0009247	glycolipid biosynthetic process	4	3	0.44	0.0049	0.0544
GO:0032507	maintenance of protein location in cell	4	3	0.44	0.0049	0.0544
GO:0045185	maintenance of protein location	4	3	0.44	0.0049	0.0544
GO:0046467	membrane lipid biosynthetic process	4	3	0.44	0.0049	0.0544
GO:0051220	cytoplasmic sequestering of protein	4	3	0.44	0.0049	0.0544
GO:0051235	maintenance of location	4	3	0.44	0.0049	0.0544
GO:0051651	maintenance of location in cell	4	3	0.44	0.0049	0.0544
GO:0043412	macromolecule modification	229	37	25.38	0.0076	0.0595

Enrichments of molecular functions in *E. falciformis* cluster 4

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0016773	phosphotransferase activity, alcohol gro...	163	29	17.36	0.0030	0.1412
GO:0003824	catalytic activity	1318	162	140.33	0.0033	0.1412
GO:0005543	phospholipid binding	13	5	1.38	0.0083	0.1412

Enrichments of biological processes in E. falciformis cluster 5

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0006281	DNA repair	39	15	5.95	0.00030	0.0100
GO:0006974	cellular response to DNA damage stimulus	39	15	5.95	0.00030	0.0100
GO:0033554	cellular response to stress	39	15	5.95	0.00030	0.0100
GO:0051716	cellular response to stimulus	97	27	14.81	0.00076	0.0190
GO:0006259	DNA metabolic process	90	25	13.74	0.00124	0.0248
GO:0050896	response to stimulus	121	30	18.47	0.00301	0.0448
GO:0030154	cell differentiation	3	3	0.46	0.00352	0.0448
GO:0006950	response to stress	62	18	9.46	0.00358	0.0448
GO:0006468	protein phosphorylation	133	31	20.30	0.00704	0.0782
GO:0006464	cellular protein modification process	202	43	30.83	0.00912	0.0829
GO:0036211	protein modification process	202	43	30.83	0.00912	0.0829



Enrichments of molecular functions in E. falciformis cluster 5

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0043167	ion binding	912	164	134.10	0.00035	0.0230
GO:0016538	cyclin-dependent protein serine/threonin...	4	4	0.59	0.00046	0.0230
GO:0043168	anion binding	627	117	92.19	0.00099	0.0330
GO:0004672	protein kinase activity	126	31	18.53	0.00181	0.0452
GO:0003684	damaged DNA binding	8	5	1.18	0.00256	0.0489
GO:0032553	ribonucleotide binding	554	100	81.46	0.00810	0.0489
GO:0046914	transition metal ion binding	224	46	32.94	0.00824	0.0489
GO:0005524	ATP binding	468	86	68.81	0.00906	0.0489
GO:0032559	adenyl ribonucleotide binding	468	86	68.81	0.00906	0.0489
GO:0001882	nucleoside binding	550	99	80.87	0.00922	0.0489
GO:0001883	purine nucleoside binding	550	99	80.87	0.00922	0.0489
GO:0032549	ribonucleoside binding	550	99	80.87	0.00922	0.0489
GO:0032550	purine ribonucleoside binding	550	99	80.87	0.00922	0.0489
GO:0032555	purine ribonucleotide binding	550	99	80.87	0.00922	0.0489
GO:0035639	purine ribonucleoside triphosphate bindi...	550	99	80.87	0.00922	0.0489
GO:0030554	adenyl nucleotide binding	469	86	68.96	0.00961	0.0489
GO:0017076	purine nucleotide binding	551	99	81.02	0.00975	0.0489
GO:0003677	DNA binding	157	34	23.08	0.00999	0.0489

# Enrichments of biological processes in E. falciformis cluster 6

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0016070	RNA metabolic process	239	85	49.07	3.10e−09	0.0000
GO:0090304	nucleic acid metabolic process	324	100	66.53	5.30e−07	0.0000
GO:0046483	heterocycle metabolic process	427	124	87.68	5.90e−07	0.0000
GO:1901360	organic cyclic compound metabolic proces...	429	124	88.09	8.00e−07	0.0000
GO:0006725	cellular aromatic compound metabolic pro...	422	121	86.65	2.00e−06	0.0000
GO:0006139	nucleobase-containing compound metabolic...	405	116	83.16	4.00e−06	0.0001
GO:0034641	cellular nitrogen compound metabolic pro...	562	148	115.40	2.30e−05	0.0003
GO:0018130	heterocycle biosynthetic process	164	55	33.67	2.70e−05	0.0003
GO:0010467	gene expression	351	100	72.07	3.50e−05	0.0004
GO:0006396	RNA processing	70	29	14.37	3.80e−05	0.0004
GO:1901362	organic cyclic compound biosynthetic pro...	166	55	34.08	4.10e−05	0.0004
GO:0006807	nitrogen compound metabolic process	590	152	121.14	6.70e−05	0.0006
GO:0019438	aromatic compound biosynthetic process	157	51	32.24	1.50e−04	0.0012
GO:0034654	nucleobase-containing compound biosynthe...	141	46	28.95	2.90e−04	0.0021
GO:0044271	cellular nitrogen compound biosynthetic ...	339	93	69.61	3.70e−04	0.0025
GO:0034660	ncRNA metabolic process	79	29	16.22	4.90e−04	0.0031
GO:0009987	cellular process	1232	276	252.97	6.30e−04	0.0037
GO:0034470	ncRNA processing	36	16	7.39	9.10e−04	0.0051
GO:0032774	RNA biosynthetic process	105	35	21.56	1.05e−03	0.0055
GO:0008033	tRNA processing	21	11	4.31	1.13e−03	0.0056
GO:0006351	transcription, DNA-templated	103	34	21.15	1.51e−03	0.0069
GO:0097659	nucleic acid-templated transcription	103	34	21.15	1.51e−03	0.0069
GO:0006399	tRNA metabolic process	62	23	12.73	1.61e−03	0.0070
GO:1901565	organonitrogen compound catabolic proces...	6	5	1.23	1.78e−03	0.0072
GO:0044237	cellular metabolic process	900	209	184.80	1.80e−03	0.0072
GO:0044260	cellular macromolecule metabolic process	706	169	144.96	1.93e−03	0.0074
GO:0022613	ribonucleoprotein complex biogenesis	29	13	5.95	2.52e−03	0.0090
GO:0042254	ribosome biogenesis	29	13	5.95	2.52e−03	0.0090
GO:0044249	cellular biosynthetic process	426	108	87.47	2.98e−03	0.0103
GO:0009058	biosynthetic process	446	112	91.58	3.48e−03	0.0116
GO:0044085	cellular component biogenesis	56	20	11.50	5.37e−03	0.0173
GO:0043170	macromolecule metabolic process	810	187	166.32	6.94e−03	0.0216
GO:0009063	cellular amino acid catabolic process	5	4	1.03	7.34e−03	0.0216
GO:1901606	alpha-amino acid catabolic process	5	4	1.03	7.34e−03	0.0216
GO:1901576	organic substance biosynthetic process	428	106	87.88	7.75e−03	0.0221



Enrichments of molecular functions in E. falciformis cluster  
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GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0003676	nucleic acid binding	485	155	110.85	1.7e-07	0.0000
GO:0004386	helicase activity	90	40	20.57	3.2e-06	0.0002
GO:0008026	ATP-dependent helicase activity	60	28	13.71	3.4e-05	0.0008
GO:0070035	purine NTP-dependent helicase activity	60	28	13.71	3.4e-05	0.0008
GO:0005488	binding	1845	451	421.67	1.1e-03	0.0220
GO:1901363	heterocyclic compound binding	1040	267	237.69	3.0e-03	0.0457
GO:0097159	organic cyclic compound binding	1041	267	237.92	3.2e-03	0.0457
GO:0042623	ATPase activity, coupled	108	37	24.68	3.9e-03	0.0487
GO:0016887	ATPase activity	129	42	29.48	6.1e-03	0.0678

## Enrichments of biological processes in *E. falciformis* cluster 7

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0006518	peptide metabolic process	181	73	29.49	8.60e−17	0.0000
GO:0006412	translation	175	71	28.51	1.80e−16	0.0000
GO:0043043	peptide biosynthetic process	177	71	28.84	3.70e−16	0.0000
GO:0043603	cellular amide metabolic process	189	73	30.79	1.50e−15	0.0000
GO:0043604	amide biosynthetic process	185	71	30.14	6.40e−15	0.0000
GO:1901564	organonitrogen compound metabolic proces...	294	93	47.90	1.90e−13	0.0000
GO:1901566	organonitrogen compound biosynthetic pro...	240	81	39.10	2.50e−13	0.0000
GO:0009059	macromolecule biosynthetic process	325	88	52.95	1.80e−08	0.0000
GO:0044271	cellular nitrogen compound biosynthetic ...	339	90	55.23	3.40e−08	0.0000
GO:0034645	cellular macromolecule biosynthetic proc...	324	87	52.79	3.50e−08	0.0000
GO:0044249	cellular biosynthetic process	426	105	69.41	1.20e−07	0.0000
GO:1901576	organic substance biosynthetic process	428	105	69.73	1.60e−07	0.0000
GO:0009058	biosynthetic process	446	106	72.67	8.50e−07	0.0000
GO:0044267	cellular protein metabolic process	423	101	68.92	1.50e−06	0.0000
GO:0010467	gene expression	351	86	57.19	4.40e−06	0.0000
GO:0019538	protein metabolic process	520	110	84.72	2.30e−04	0.0014
GO:0034641	cellular nitrogen compound metabolic pro...	562	117	91.57	2.70e−04	0.0016
GO:0006807	nitrogen compound metabolic process	590	120	96.13	6.50e−04	0.0036
GO:0006414	translational elongation	15	7	2.44	5.58e−03	0.0294
GO:0008152	metabolic process	1224	216	199.43	6.32e−03	0.0316

Enrichments of molecular functions in E. falciformis cluster 7

GO id	Term	Annot. genes	Sign. genes	Expected	P-value	Adj. P-value
GO:0005198	structural molecule activity	124	58	16.59	1.10e-20	0.0000
GO:0003735	structural constituent of ribosome	103	52	13.78	1.70e-20	0.0000
GO:0031177	phosphopantetheine binding	4	4	0.54	3.20e-04	0.0080
GO:0072341	modified amino acid binding	4	4	0.54	3.20e-04	0.0080
GO:0016491	oxidoreductase activity	143	33	19.13	7.80e-04	0.0156
GO:0033218	amide binding	8	5	1.07	1.65e-03	0.0227
GO:0016746	transferase activity, transferring acyl ...	46	14	6.15	1.89e-03	0.0227
GO:0016875	ligase activity, forming carbon-oxygen b...	42	13	5.62	2.30e-03	0.0227
GO:0016876	ligase activity, forming aminoacyl-tRNA ...	42	13	5.62	2.30e-03	0.0227
GO:0004298	threonine-type endopeptidase activity	12	6	1.61	2.50e-03	0.0227
GO:0070003	threonine-type peptidase activity	12	6	1.61	2.50e-03	0.0227
GO:0004812	aminoacyl-tRNA ligase activity	41	12	5.48	5.61e-03	0.0468
GO:0000049	tRNA binding	4	3	0.54	8.56e-03	0.0658