

PlasmoDB ID	Annotation	Fold change ^a	IDC time of peak expression (hpi)
Polyamine and methionine metabolism			
PF10_0322	PfAdoMetDC/ODC	-1.9	24
PFD0285c	LDC	2.8	25
PFF0435w	OAT	1.9	18
PF11090w	AdoMet synthetase	-2.4	27
PFE1050w	Adenosylhomocysteinase	-1.9	33
PF10_0289	Adenosine deaminase, putative	-2.6	27
PFE0660c	Uridine phosphorylase, putative	-3.2	27
PF10_0340	Methionine-tRNA ligase	-1.7	33
<i>Methyltransferases</i>			
MAL13P1.214	Phosphoethanolamine N-methyltransferase, putative	-2.8	40
PF14_0309	Protein-L-isoaspartate O-methyl transferase, putative	-1.9	41
PF14_0526	Generic methyltransferase	-2.9	37
Potential polyamine associated effects			
PF14_0316	DNA topoisomerase II	-1.7	50
PFL1885c	Calcium/calmodulin-dependent protein kinase 2, putative	2.4	50
PF07_0065	Zinc transporter, putative	-2.4	40
Oxidative stress defense			
PF08_0131	1-Cys-peroxidoxin	-3.2	34
PF14_0192	Glutathione reductase	-1.7	34
PF14_0187	Glutathione S-transferase	-1.8	-
Energy metabolism			
<i>Oxidative phosphorylation</i>			
Col	Cytochrome oxidase I, putative	-2	-
CoxI	Cytochrome oxidase I, putative	-1.7	53
CoxIII_2	Mitochondrial encoded cytochrome oxidase subunit 3	-2	-
PF11_0412	Vacuolar ATP synthase subunit F, putative	-1.8	34
MAL7P1.75	Mitochondrial ATP synthase F1, epsilon subunit, putative	-1.8	-

PFE0970w	Cytochrome c oxidase assembly, putative	-1.7	24
PF13_0121	Dihydrolipoamide succinyltransferase	-1.7	27
<i>Glycolysis</i>			
PF10_0155	Enolase	-2	18
PF13_0141	L-lactate dehydrogenase	-1.8	18
PF14_0378	Triose-phosphate isomerase	-1.8	18
PF14_0598	Glyceraldehyde-3-phosphate dehydrogenase	-2.1	27
PFF1300w	Pyruvate kinase	-1.9	28
DNA replication			
PF11_0117	Replication factor C subunit 5, putative	-2.1	34
PF11_0087	Rad51 homolog, putative	-2	35
PF13_0095	DNA replication licensing factor mcm4-related	-2.2	42
PF13_0291	Replication licensing factor, putative	-1.8	34
PF14_0081	DNA repair helicase, putative	-1.7	-
PF14_0112	POM1, putative	-2	37
PF14_0254	DNA mismatch repair protein Msh2p, putative	-1.8	32
PF14_0314	Chromatin assembly factor 1 p55 subunit, putative	2.4	-
PF14_0601	Replication factor C3	-2	34
PFB0180w	5'-3' Exonuclease, putative	-1.9	26
PFB0895c	Replication factor C subunit 1, putative	-2	33
PFD0470c	Replication factor A protein, putative	-2.5	34
PFD0685c	Chromosome associated protein, putative	-2	40
PFD0830w	Dihydrofolate reductase-thymidylate synthase	-2	33
PFD0950w	Ran binding protein 1	2	-
PFE0675c	DNA photolyase	-2.2	36
PFF1470c	DNA polymerase epsilon, catalytic subunit A, putative	-1.7	36
PFI0235w	Replication factor A-related protein, putative	-1.8	33
PFI0530c	DNA primase, large subunit, putative	-1.8	35
Transcription factors			
PF11_0241	Hypothetical protein with Myb-like domains	1.8	-

PFL0465c	C2H2-type zinc-finger transcription factor, krox1	2	-
PFE1245w	CCCH-type zinc-finger protein	1.7	26
PFD0560w	Hypothetical protein with a TATA-box -like domain	1.7	32
PFE0415w	Transcription factor IIB, putative	-1.8	-
Translation			
MAL13P1.327	Ribosomal protein S17 homologue, putative	1.7	22
PF07_0080	40S ribosomal protein S10, putative	1.9	16
PF10_0038	Ribosomal protein S20e, putative	2.3	15
PF11_0454	Ribosomal protein, 40S subunit, putative	2	-
PF13_0014	40S ribosomal protein S7 homologue, putative	1.8	15
PF13_0171	60S ribosomal protein L23, putative	2	13
PF13_0228	40S ribosomal subunit protein S6	1.8	13
PF14_0205	Ribosomal protein S25	2.4	23
PF14_0231	Ribosomal protein L7a, putative	1.8	21
PF14_0579	Ribosomal protein L27, putative	2.1	21
PF14_0709	Ribosomal protein L20, putative	-2.6	32
PFB0455w	Ribosomal L37ae protein, putative	1.7	16
PFC0535w	60S ribosomal protein L26, putative	2	-
PFC1020c	40S ribosomal protein S3A, putative	1.7	15
PFE0185c	60S ribosomal subunit protein L31, putative	1.8	14
PFI1585c	30S ribosomal protein S6-like protein, putative	1.8	-
Cell cycle mediators			
PF13_0328	Proliferating cell nuclear antigen	-3.3	40
PF14_0604	Hypothetical protein with cyclin homology	-1.7	2
PFL1330c	Hypothetical protein with cyclin homology	1.8	37

a. Average fold-change calculated at the time point of maximum change