Appendix A

The List of proteins identified by MS/MS for Colloidal Coomassie Blue, MS compatible silver stain, SYPRO Ruby and Flamingo Pink

Spot nr[a]	Accession number[b]	PlasmoDB ID[c]	Name	Mr	pI	Mascot Score MS/MS[d]	Seq cov[e]	Match[f]
List of proteins identified by MS/MS for Colloidal Coomassie Blue								
C1	Q25883	PF07_0029	Heat shock protein 86	86468	4.94	866	20	18
C2	Q8I2X4	PFI0875w	Heat shock protein	72457	5.18	1344	32	17
C3	Q8I0V4	PFL1070c	Endoplasmin homolog, putative	95301	5.28	453	16	12
C4	Q8IB24	PF08_0054	Heat shock 70 kDa protein	74382	5.51	1296	35	21
C5	Q8II24	PF11_0351	Heat shock protein hsp70 homologue	73651	6.51	1084	33	19
C6	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	417	18	11
C7	Q8IJN9	PF10_0153	Hsp60	62911	6.71	371	20	11
C8	Q8I6S6	MAL8P1.17	Disulfide isomerase, putative	55808	5.56	906	32	14
C9	Q8IJN7	PF10_0155	Enolase	48989	6.21	391	20	7
C10	Q9GN14	PFI1090w	S-adenosylmethionine synthetase	45272	6.28	313	19	6
C11	Q6LFH8	PFF0435w	Ornithine aminotransferase	46938	6.47	258	19	7
C12	Q8II61	PF11_0313	Ribosomal phosphoprotein P0	35002	6.28	343	38	9
C13	Q8T6B1	PF14_0598	Glyceraldehyde-3-phosphate dehydrogenase	37068	7.59	453	32	10
C15	Q8IM15	PF14_0078	HAP protein	51889	8.05	442	20	9
C16	Q8IIR7	PF11_0098	Endoplasmic reticulum-resident calcium binding protein	39464	4.49	539	26	8
C17	Q8I3F3	PFE1590w	Early transcribed membrane protein	19132	5.26	80	7	1
C18	Q8I3F3	PFE1590w	Early transcribed membrane protein	19132	5.26	65	7	1
C19	Q8IKC8	PF14_0678	Exported protein 2	33619	5.1	201	15	6
C20	Q8I6U5	PF11_0161	Falcipain-2, putative	56281	8.14	276	10	5
C21	Q8IIU5	PF11_0069	Hypothetical protein	32112	4.91	148	20	5
C22	Q8IDQ9	MAL13P1.214	Phosphoethanolamine N-methyltransferase, putative	31309	5.43	522	39	9
C23	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	166	14	3
C24	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	137	14	3
C26	O97249	PFC0295c	40S Ribosomal protein S12, putative	15558	4.9	262	35	5
C27	Q8IIF0	PF11_0224	Circumsporozoite-related antigen	17285	5.64	278	22	5
C28	P00441	-	Human Superoxide dismutase	16154	5.7	217	27	4
C29	P32119	-	Human Peroxiredoxin-2	21918	5.67	371	32	8
C30	P32119	-	Human Peroxiredoxin-2	21918	5.67	351	35	9
C34	Q8IB17	MAL8P1.69	14-3-3 protein	30470	4.86	579	49	16
CM1	P00489	-	Rabbit Glycogen phosphorylase	97610	6.76	1348	29	24
CM2	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	762	20	14
CM3	P01012	-	Chicken ovalbumin	43196	5.19	913	40	14
CM4	P00921	-	Bovine carbonic anhydrase II	29096	6.41	517	45	8
CM5	1AVXB	-	Soybean trypsin inhibitor, chain B	19295	4.79	274	26	7
CM6	LABO	-	Bovine alpha lactalbumin	16692	4.93	48	7	1
List of proteins identified by MS/MS for the MS compatible silver stain								
M1	Q25883	PF07_0029	Heat shock protein 86	86468	4.94	848	20	16
M2	Q8I2X4	PFI0875w	Heat shock protein	72457	5.18	1639	39	20
M3	Q8I0V4	PFL1070c	Endoplasmin homolog, putative	95301	5.28	809	29	18
M4	Q8IB24	PF08_0054	Heat shock 70 kDa protein	74382	5.51	1455	39	21
M5	Q8II24	PF11_0351	Heat shock protein hsp70 homologue	73651	6.51	1060	29	18
M6	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	926	29	19
M7	Q8IJN9	PF10_0153	Hsp60	62911	6.71	333	11	5
M8	Q8I6S6	MAL8P1.17	Disulfide isomerase, putative	55808	5.56	939	38	16
M9	Q8IJN7	PF10_0155	Enolase	48989	6.21	1044	50	18
M10	Q9GN14	PFI1090w	S-adenosylmethionine synthetase	45272	6.28	488	28	9
M11	Q6LFH8	PFF0435w	Ornithine aminotransferase	46938	6.47	667	40	14
M12	Q8II61	PF11_0313	Ribosomal phosphoprotein P0	35002	6.28	519	40	10
M13	Q8T6B1	PF14_0598	Glyceraldehyde-3-phosphate dehydrogenase	37068	7.59	720	42	9
M16	Q8IIR7	PF11_0098	Endoplasmic reticulum-resident calcium binding protein	39464	4.49	1050	53	15
M22	Q8IDQ9	MAL13P1.214	Phosphoethanolamine N-methyltransferase, putative	31309	5.43	794	56	12
M23	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	244	25	5
M24	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	245	25	5
M25	Q8I3Z5	PFE0545c	Histamine releasing factor, putative	20024	4.48	189	26	4

M26	O97249	PFC0295c	40S Ribosom	15558	4.9	302	35	5
M27	Q8IIF0	PF11_0224	Circumsporozoite-related antigen	17285	5.64	357	22	6
M29	P32119	-	Human peroxiredoxin-2	21918	5.67	591	36	9
M30	P32119	-	Human peroxiredoxin-2	21918	5.67	381	26	7
M35	Q8IBP0	PF07_0087	Hypothetical protein PF07_0087	29631	8.76	271	31	8
M38	Q71T02	PF13_0141	L-lactate dehydrogenase	34314	7.12	582	35	12
M39	P00915	-	Human carbonic anhydrase 1	28778	6.63	568	48	9
M41	Q8IK90	PF14_0716	Proteosome subunit alpha type 1, putative	29219	5.51	309	23	4
M43	Q7Z0H0		Adenylate kinase 2	27822	8.97	518	45	10
MM1	P00489	-	Rabbit Glycogen phosphorylase	97610	6.76	275	15	11
MM2	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	510	16	10
MM3	P01012	-	Chicken ovalbumin	43196	5.19	922	40	15
MM4	P00921	-	Bovine carbonic anhydrase II	29096	6.41	469	38	6
MM5	1AVXB	-	Soybean trypsin inhibitor, chain B	19295	4.79	323	36	8
MM6	LABO	-	Bovine alpha lactalbumin	16692	4.93	57	7	1
List of proteins identified by MS/MS for SYPRO Ruby								
S1	Q25883	PF07_0029	Heat shock protein 86	86770	4.91	829	20	16
S2	Q8I2X4	PFI0875w	Heat shock protein					
S3	Q8I0V4	PFL1070c	Endoplasmin homolog, putative	95301	5.28	208	7	5
S4	Q8IB24	PF08_0054	Heat shock 70 kDa protein	74382	5.51	1345	38	19
S5	Q8II24	PF11_0351	Heat shock protein hsp70 homologue	73651	6.51	827	23	14
S6	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	745	22	14
S7	Q8IJN9	PF10_0153	Hsp60	62911	6.71	350	13	6
S8	Q8I6S6	MAL8P1.17	Disulfide isomerase, putative	55808	5.56	1075	40	16
S9	Q8IJN7	PF10_0155	Enolase	48989	6.21	727	31	10
S10	Q9GN14	PFI1090w	S-adenosylmethionine synthetase	45272	6.28	317	24	8
S11	Q6LFH8	PFF0435w	Ornithine aminotransferase	46938	6.47	378	19	8
S12	Q8II61	PF11_0313	Ribosomal phosphoprotein P0	35002	6.28	299	18	4
S13	Q8T6B1	PF14_0598	Glyceraldehyde-3-phosphate dehydrogenase	37068	7.59	425	30	7
S15	Q8IM15	PF14_0078	HAP protein	51889	8.05	494	25	10
S16	Q8IIR7	PF11_0098	Endoplasmic reticulum-resident calcium binding protein	39464	4.49	584	35	8
S18	Q8I3F3	PFE1590w	Early transcribed membrane protein	19132	5.26	202	20	2
S19	Q8IKC8	PF14_0678	Exported protein 2	33619	5.1	433	23	7
S20	Q8I6U5	PF11_0161	Falcipain 2, putative	56405	7.12	184	10	5
S21	Q8IIU5	PF11_0069	Hypothetical protein	32112	4.91	305	36	10
S22	Q8IDQ9	MAL13P1.214	Phosphoethanolamine N-methyltransferase, putative	31309	5.43	649	39	9
S23	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	116	15	3
S24	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	104	11	2
S25	Q8I3Z5	PFE0545c	Histamine releasing factor, putative	20024	4.48	129	11	3
S26	O97249	PFC0295c	40S Ribosomal protein S12, putative	15558	4.9	205	35	5
S27	Q8IIF0	PF11_0224	Circumsporozoite-related antigen	17285	5.64	293	21	4
S28	P00441	-	Human superoxide dismutase	16154	5.7	242	27	4
S32	Q8II72	PF11_0302	Hypothetical protein	52147	4.97	148	8	5
S33	Q7KQL5	PF10_0084	tubulin beta chain	50232	4.73	527	31	12
SM1	P00489	-	Rabbit Glycogen phosphorylase	97741	6.77	887	25	19
SM2	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	489	16	10
SM3	P01012	-	Chicken ovalbumin	43116	5.19	824	39	11
SM4	P00921	-	Bovine carbonic anhydrase II	28965	6.4	422	38	6
SM5	1AVXB	-	Soybean trypsin inhibitor, chain B	24346	4.99	265	26	6
List of proteins identified by MS/MS for Flamingo Pink								
F1	Q25883	PF07_0029	Heat shock protein 86	86770	4.91	848	17	16
F2	Q8I2X4	PFI0875w	Heat shock protein	72457	5.18	1518	36	18
F3	Q8I0V4	PFL1070c	Endoplasmin homolog, putative	95301	5.28	623	19	14
F4	Q8IB24	PF08_0054	Heat shock 70 kDa protein	74382	5.51	1401	42	23
F5	Q8II24	PF11_0351	Heat shock protein hsp70 homologue	73651	6.51	515	15	11
F6	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	612	20	11
F7	Q8IJN9	PF10_0153	Hsp60	62911	6.71	271	10	5
F8	Q8I6S6	MAL8P1.17	Disulfide isomerase, putative	55808	5.56	916	38	15
F9	Q8IJN7	PF10_0155	Enolase	48989	6.21	871	39	13
F10	Q9GN14	PFI1090w	S-adenosylmethionine synthetase	45272	6.28	678	40	13
F11	Q6LFH8	PFF0435w	Ornithine aminotransferase	46938	6.47	548	24	10
F12	Q8II61	PF11_0313	Ribosomal phosphoprotein P0	35002	6.28	569	45	13
F13	Q8T6B1	PF14_0598	Glyceraldehyde-3-phosphate dehydrogenase	37068	7.59	774	54	15
F15	Q8IM15	PF14_0078	HAP protein	51889	8.05	444	24	10
F16	Q8IIR7	PF11_0098	Endoplasmic reticulum-resident calcium binding protein	39464	4.49	849	48	13
F19	Q8IKC8	PF14_0678	Exported protein 2	33619	5.1	433	26	9
F20	Q8I6U5	PF11_0161	Falcipain 2, putative	56281	8.14	306	14	6
F21	Q8I2Q0	PFI1270w	Hypothetical protein PFI1270w	24911	5.49	299	31	7

F22	Q8IDQ9	MAL13P1.214	Phosphoetha	31309	5.43	910	59	13
F27	Q8IIF0	PF11_0224	Circumsporozoite-related antigen	17285	5.64	190	22	5
F28	DSHUCZ	-	Human superoxide dismutase	16154	5.7	198	37	4
F29	P32119	-	Human peroxiredoxin-2	21918	5.67	522	35	9
F30	P32119	-	Human peroxiredoxin-2	21918	5.67	523	29	8
F38	Q71T02	PF13_0141	L-lactate dehydrogenase	34314	7.12	622	43	13
F39	P00915	-	Human carbonic anhydrase 1	28778	6.63	624	55	11
F40	Q8IDQ9	MAL13P1.214	Phosphoethanolamine N-methyltransferase, putative	31309	5.43	499	39	9
F41	Q8IK90	PF14_0716	Proteosome subunit alpha type 1, putative	29218	5.51	100	5	1
F42	Q8IDQ9	MAL13P1.214	Phosphoethanolamine N-methyltransferase, putative	31309	5.43	632	44	10
F80	Q8IM15	PF14_0078	HAP protein	51889	8.05	288	21	9
F81	Q8IM15	PF14_0078	HAP protein	51889	8.05	629	35	13
F82	Q8IM15	PF14_0078	HAP protein	51889	8.05	614	30	12
F89	Q8I6U4	PF11_0165	Falcipain 2	56405	7.12	393	16	8
F90	Q8I6U5	PF11_0161	Falcipain 2, putative	56281	8.14	306	14	6
FM1	P00489	-	Rabbit Glycogen phosphorylase	97610	6.76	1375	34	28
FM2	P02769	-	Bovine Serum albumin [Precursor]	71274	5.82	807	19	13
FM3	P01012	-	Chicken ovalbumin	43196	5.19	922	40	15
FM4	P00921	-	Bovine carbonic anhydrase II	29096	6.41	583	47	9
FM5	1AVXB	-	Soybean trypsin inhibitor, chain B	24419	5	323	29	8
FM6	LABO	-	Bovine alpha lactalbumin	16692	4.93	57	7	1

[a]Spot number corresponds to marked spots on the various stain master images in Figure 3.4. [b]Accession number is obtained from the SwissProt UniProt database. [c]PlasmoDB ID is obtained from the PlasmoDB 6.0 database. [d]Mascot scores are based on MS/MS ion searches and is only taken when the score is significant ($p<0.05$). [e]Sequence coverage is given by Mascot for detected peptide sequences. [f]Matched is the number of peptides matched to the particular protein. C followed by number is indicative of spot number that was cut and identified by MS. CM is indicative of the standard molecular weight markers that was cut. M followed by number is indicative of spot number that was cut and identified by MS. MM is indicative of the standard molecular weight markers that was cut. S followed by number is indicative of spot number that was cut and identified by MS. SM is indicative of the standard molecular weight markers that was cut. F followed by number is indicative of spot number that was cut and identified by MS. FM is indicative of the standard molecular weight markers that was cut.

Appendix B

The differentially affected transcripts due to the inhibition of AdoMetDC

Total	Nr	PlasmoDB ID	Product Description	GO ID	Annotated GO Process	LogFC	FC	adj.P.Val
DNA metabolism								
1	1	MAL13P1.328	DNA topoisomerase VI, B subunit, putative	GO:0006259	Catalytic activity, ATP binding	1.48987	2.80864	1.32E-06
2	2	MAL13P1.346	DNA repair endonuclease, putative	GO:0006281	DNA repair	-1.0594	-2.084	0.001996
3	3	MAL13P1.42	recombinase, putative	GO:0015074	DNA recombination, DNA integration	-1.0702	-2.0997	0.001121
4	4	PF07_0023	DNA replication licensing factor mcm7 homologue, putative	GO:0006270	DNA replication initiation	-1.2721	-2.4151	3.61E-06
5	5	PF08_0126	DNA repair protein rad54, putative	GO:0006310	DNA recombination, double-strand break repair via homologous recombination	-0.8399	-1.7899	0.001887
6	6	PF10_0154	ribonucleotide reductase small subunit, putative	GO:0006260	DNA replication	-2.4224	-5.3606	1.14E-07
7	7	PF10_0165	DNA polymerase delta catalytic subunit	GO:0006260	DNA replication	-1.0257	-2.0359	0.000632
8	8	PF11_0061	histone H4	GO:0006334	nucleosome assembly, transcription initiation	-1.7751	-3.4225	4.76E-07
9	9	PF11_0062	histone H2B	GO:0006334	nucleosome assembly	-1.543	-2.914	0.000868
10	10	PF11_0087	Rad51 homolog	GO:0006281	DNA repair, DNA recombination	-0.7996	-1.7406	0.003805
11	11	PF11_0117	replication factor C subunit 5, putative	GO:0006271	DNA replication	-0.8698	-1.8275	0.001285
12	12	PF11_0241	Myb-like DNA-binding domain, putative	GO:0006259	null	0.75277	1.68502	0.034824
13	13	PF11_0282	deoxyuridine 5'-triphosphate nucleotidohydrolase, putative	GO:0006260	DNA replication	-2.6609	-6.3245	5.82E-06
14	14	PF13_0080	conserved Plasmodium protein, unknown function	GO:0006259	RNA-dependent DNA replication	-1.0513	-2.0724	0.002504
15	15	PF13_0095	DNA replication licensing factor MCM4-related	GO:0006268	DNA unwinding during replication	-1.631	-3.0973	3.24E-05
16	16	PF13_0149	chromatin assembly factor 1 subunit, putative	GO:0006333	chromatin assembly or disassembly	-1.5123	-2.8527	0.000207
17	17	PF13_0176	apurinic/apyrimidinic endonuclease Apn1	GO:0006281	DNA repair	-0.8765	-1.8359	0.023412
18	18	PF13_0291	replication licensing factor, putative	GO:0006270	DNA replication initiation	-1.3354	-2.5235	0.000325
19	19	PF13_0328	proliferating cell nuclear antigen	GO:0006275	regulation of DNA replication	-2.5146	-5.7144	1.51E-11
20	20	PF14_0053	ribonucleotide reductase small subunit	GO:0006260	DNA replication	-1.9647	-3.9034	6.96E-06
21	21	PF14_0148	uracil-DNA glycosylase, putative	GO:0006284	base-excision repair	-0.7987	-1.7395	0.015932
22	22	PF14_0177	DNA replication licensing factor MCM2	GO:0006270	DNA replication initiation	-1.0135	-2.0187	0.004041
23	23	PF14_0254	DNA mismatch repair protein Msh2p, putative	GO:0006298	mismatch repair	-0.9089	-1.8776	0.000548
24	24	PF14_0352	ribonucleoside-diphosphate reductase, large subunit	GO:0006260	DNA replication	-1.0587	-2.083	0.00041
25	25	PF14_0366	small subunit DNA primase	GO:0006269	DNA replication	-0.7398	-1.6699	0.044267
26	26	PF14_0374	CCAAT-binding transcription factor, putative	GO:0006259	null	0.78164	1.71908	0.029176
27	27	PF14_0602	DNA polymerase alpha subunit, putative	GO:0006269	DNA replication	-1.2062	-2.3073	0.000868
28	28	PFB0840w	replication factor C, subunit 2	GO:0006260	DNA replication	-1.7554	-3.3762	1.32E-06
29	29	PFB0895c	replication factor C subunit 1, putative	GO:0006260	DNA replication	-0.9455	-1.9259	0.001076
30	30	PFC0250c	AP endonuclease (DNA-[apurinic or apyrimidinic site] lyase), putative	GO:0006281	DNA repair	-0.776	-1.7123	0.00579
31	31	PFC0765c	conserved Plasmodium protein, unknown function	GO:0006260	DNA replication	-1.3613	-2.5691	0.006478
32	32	PFD0590c	DNA polymerase alpha	GO:0006260	DNA replication	-1.0291	-2.0407	0.000163
33	33	PFD0685c	chromosome associated protein, putative	GO:0006259	chromosome organization	-1.0345	-2.0484	0.005887
34	34	PFE0215w	ATP-dependent helicase, putative	GO:0006259	null	-0.7904	-1.7296	0.026565
35	35	PFE0270c	DNA repair protein, putative	GO:0006298	mismatch repair, DNA repair	-1.7925	-3.4641	0.000104
36	36	PFE0450w	chromosome condensation protein, putative	GO:0006259	chromosome organization	-1.381	-2.6045	0.001282

37	37	PFE0675c	deoxyribodipyrimidine photolyase (photoreactivating enzyme, DNA photolyase), putative	GO:0006281	DNA repair	-1.4742	-2.7783	0.000104
38	38	PFE1255w	conserved Plasmodium protein, unknown function	GO:0006259	chromosome organization	-0.7247	-1.6525	0.004461
39	39	PFE1345c	minichromosome maintenance protein 3, putative	GO:0006270	DNA replication initiation	-1.2134	-2.3189	0.000104
40	40	PFF0510w	histone H3	GO:0006333	nucleosome assembly	-2.1132	-4.3265	0.000524
41	41	PFF0865w	histone H3	GO:0006334	chromosome organization	-0.8174	-1.7622	0.000934
42	42	PFF1225c	DNA polymerase 1, putative	GO:0006260	DNA replication	-1.021	-2.0294	0.008609
43	43	PFF1470c	DNA polymerase epsilon, catalytic subunit a, putative	GO:0006261	DNA-dependent DNA replication	-0.812	-1.7556	0.000789
44	44	PFI0530c	DNA primase large subunit, putative	GO:0006269	DNA replication, synthesis of RNA primer	-1.9163	-3.7745	2.11E-06
45	45	PFL0150w	origin recognition complex 1 protein	GO:0006270	DNA replication initiation	-1.3542	-2.5565	0.00025
46	46	PFL0580w	DNA replication licensing factor MCM5, putative	GO:0006270	DNA replication initiation, DNA strand elongation	-1.8999	-3.7318	1.33E-05
47	47	PFL1180w	chromatin assembly protein (ASF1), putative	GO:0016458	gene silencing	-1.1375	-2.2	0.000169
48	48	PFL1285c	proliferating cell nuclear antigen 2	GO:0006275	regulation of DNA replication	-1.4194	-2.6748	0.011427
49	49	PFL1655c	DNA polymerase epsilon subunit B, putative	GO:0006260	DNA replication	-1.0389	-2.0546	0.015356
50	50	PFL2005w	replication factor C subunit 4	GO:0006260	DNA replication	-2.009	-4.0249	2.70E-07
Proteolysis								
51	1	MAL13P1.25	conserved Plasmodium protein, unknown function	GO:0006508	null	-1.2518	-2.3813	0.000944
52	2	MAL13P1.270	proteasome subunit, putative	GO:0006511	ubiquitin-dependent protein catabolic process	-0.8733	-1.8318	0.000339
53	3	MAL8P1.113	Peptidase family C50, putative	GO:0006508	proteolysis	-0.734	-1.6632	0.034431
54	4	MAL8P1.140	methionine aminopeptidase, putative	GO:0006508	proteolysis	-1.0168	-2.0234	0.003717
55	5	MAL8P1.75	ubiquitin-activating enzyme, putative	GO:0006464	protein modification process	-0.8558	-1.8098	0.03803
56	6	MAL8P1.99	GTPase, putative	GO:0006508	proteolysis	-1.0411	-2.0577	0.016593
57	7	PF11_0174	cathepsin C, homolog	GO:0006508	proteolysis	0.75926	1.69262	0.029384
58	8	PF13_0084	ubiquitin-like protein, putative	GO:0006464	protein modification process, modification-	0.72972	1.65832	0.010017
59	9	PF14_0348	ATP-dependent Clp protease proteolytic subunit, putative	GO:0006508	proteolysis	-1.0124	-2.0173	0.006525
60	10	PFB0330c	serine repeat antigen 7 (SERA-7)	GO:0006508	proteolysis	-0.7234	-1.6511	0.008836
61	11	PFC0855w	ubiquitin conjugating enzyme, putative	GO:0006464	regulation of protein metabolic process	-0.8927	-1.8567	0.012616
62	12	PFE0870w	transcriptional regulator, putative	GO:0006508	proteolysis, transcription	-0.7907	-1.7299	0.0263
63	13	PFE1355c	ubiquitin carboxyl-terminal hydrolase, putative	GO:0006511	ubiquitin-dependent protein catabolic process	-0.9467	-1.9275	0.006556
64	14	PFF0420c	proteasome subunit alpha type 2, putative	GO:0006511	ubiquitin-dependent protein catabolic process	-0.9812	-1.9741	4.01E-05
65	15	PFI0135c	serine repeat antigen 9 (SERA-9)	GO:0006508	proteolysis	-2.4916	-5.6239	1.21E-08
66	16	PFI0810c	apicoplast Ufd1 precursor	GO:0006511	ubiquitin-dependent protein catabolic process	-1.0179	-2.025	0.000159
67	17	PFL1465c	Heat shock protein hslv	GO:0006511	ubiquitin-dependent protein catabolic process	-1.0168	-2.0234	0.001997
Translation								
68	1	MAL8P1.110	apicoplast ribosomal protein L33 precursor, putative	GO:0006412	translation	-0.9003	-1.8664	0.002779
69	2	PF11_0113	mitochondrial ribosomal protein L11 precursor, putative	GO:0006412	translation	-1.0129	-2.018	0.002101
70	3	PF11_0181	tyrosine-tRNA ligase, putative	GO:0006437	tyrosyl-tRNA aminoacylation	-0.9572	-1.9416	0.005929
71	4	PF11_0182	conserved Plasmodium protein, unknown function	GO:0006415	translational termination	-0.8945	-1.8589	0.004045
72	5	PF11_0386	apicoplast ribosomal protein S14p/S29e precursor, putative	GO:0006412	translation	-1.0163	-2.0227	0.004578
73	6	PF14_0289	mitochondrial ribosomal protein L17-2 precursor, putative	GO:0006412	translation	-1.864	-3.64	3.49E-07
74	7	PF14_0606	mitochondrial ribosomal protein S6-2 precursor, putative	GO:0006412	translation	-1.1322	-2.192	0.000215
75	8	PF14_0709	mitochondrial ribosomal protein L20 precursor, putative	GO:0006412	translation	-1.0767	-2.1092	0.001788
76	9	PFB0390w	apicoplast ribosomal releasing factor precursor, putative	GO:0006412	translation	-0.9242	-1.8977	0.047945
77	10	PFB0645c	mitochondrial large ribosomal subunit, putative	GO:0006412	translation	-1.2275	-2.3417	0.003213
78	11	PFC0675c	mitochondrial ribosomal protein L29/L47 precursor, putative	GO:0006412	translation	-0.9066	-1.8747	0.00679
79	12	PFC0701w	mitochondrial ribosomal protein L27 precursor, putative	GO:0006412	translation	-1.32	-2.4967	2.29E-05
80	13	PFD0675w	apicoplast ribosomal protein L10 precursor, putative	GO:0006412	translation	-1.5395	-2.9069	0.048763
81	14	PFD0780w	glutamyl-tRNA(Gln) amidotransferase subunit A, putative	GO:0006412	translation	-0.9774	-1.969	0.002314
82	15	PFE0960w	mitochondrial ribosomal protein L14 precursor, putative	GO:0006412	translation	-0.9493	-1.9309	0.020063
83	16	PFF0495w	mitochondrial ribosomal protein L19 precursor, putative	GO:0006412	translation	-1.0037	-2.0051	0.003254
84	17	PFF0650w	apicoplast ribosomal protein L18 precursor, putative	GO:0042254	ribosome biogenesis, translation	-0.9535	-1.9366	0.001777
85	18	PFF1395c	glutamyl-tRNA(Gln) amidotransferase subunit B, putative	GO:0006424	glutamyl-tRNA aminoacylation, translation	-0.789	-1.7279	0.004166

86	19	PFI0380c	formylmethionine deformylase, putative	GO:0006412	translation	-0.8662	-1.8229	0.006232
87	20	PFI0890c	organelle ribosomal protein L3 precursor, putative	GO:0006412	translation	-1.1291	-2.1873	0.003978
88	21	PFI1240c	prolyl-t-RNA synthase, putative	GO:0006418	tRNA aminoacylation for protein translation	-1.4703	-2.7708	0.000225
89	22	PFI1575c	peptide release factor, putative	GO:0006415	translational termination	-1.4527	-2.7373	0.000503
90	23	PFI1585c	mitochondrial ribosomal protein S6 precursor, putative	GO:0006412	translation	-0.8202	-1.7657	0.01119
91	24	PFL1150c	mitochondrial ribosomal protein L24-2 precursor, putative	GO:0006412	translation, ribosome biogenesis	-0.7627	-1.6966	0.002721
92	25	PFL1590c	elongation factor G, putative	GO:0006414	translational elongation	-0.7568	-1.6898	0.006525
93	26	PFL1895w	mitochondrial ribosomal protein L23 precursor, putative	GO:0006412	translation	-0.7497	-1.6815	0.038466
Phosphorylation								
94	1	MAL13P1.278	serine/threonine protein kinase, putative	GO:0006468	protein amino acid phosphorylation	1.05398	2.07626	0.035788
95	2	MAL7P1.132	conserved Plasmodium protein, unknown function	GO:0006468	protein amino acid phosphorylation	-0.9639	-1.9505	0.019017
96	3	MAL7P1.144	Serine/Threonine protein kinase, FIKK family	GO:0006468	protein amino acid phosphorylation	0.98588	1.98052	0.016411
97	4	PF11_0377	casein kinase 1, PfCK1	GO:0006468	protein amino acid phosphorylation	-1.0443	-2.0623	0.009823
98	5	PF13_0258	serine/threonine protein kinase	GO:0006468	protein amino acid phosphorylation	-1.3263	-2.5076	0.000776
99	6	PF14_0142	serine/threonine protein phosphatase	GO:0006470	protein amino acid dephosphorylation	-1.328	-2.5106	0.000346
100	7	PFA0130c	Serine/Threonine protein kinase, FIKK family, putative	GO:0006468	protein amino acid phosphorylation	1.21443	2.32049	0.001022
101	8	PFB0815w	Calcium-dependent protein kinase 1	GO:0006468	protein amino acid phosphorylation	1.57348	2.97621	0.04031
102	9	PFC0485w	protein kinase, putative	GO:0006468	protein amino acid phosphorylation	-0.7621	-1.6959	0.005929
103	10	PFC0710w	inorganic pyrophosphatase, putative	GO:0006796	phosphate metabolic process	-1.4027	-2.6439	8.19E-05
104	11	PFC0755c	protein kinase, putative	GO:0006468	protein amino acid phosphorylation	-1.0395	-2.0555	0.009593
105	12	PFD1165w	Serine/Threonine protein kinase, FIKK family	GO:0006468	protein amino acid phosphorylation	0.99581	1.99421	0.016855
106	13	PFD1175w	Serine/Threonine protein kinase, FIKK family	GO:0006468	protein amino acid phosphorylation	1.23584	2.35518	1.84E-05
107	14	PFF0260w	serine/threonine protein kinase, Pfnek-5	GO:0006468	protein amino acid phosphorylation	-0.792	-1.7314	0.011966
108	15	PFF1370w	protein kinase PK4	GO:0006468	protein amino acid phosphorylation	0.74596	1.67709	0.012842
109	16	PFL1110c	CAMP-dependent protein kinase regulatory subunit, putative	GO:0006468	regulation of protein amino acid phosphorylation	-1.0569	-2.0804	0.007751
110	17	PFL1885c	calcium/calmodulin-dependent protein kinase 2	GO:0006468	protein amino acid phosphorylation	1.1697	2.24966	0.003213
Transport								
111	1	MAL13P1.16	SNARE protein, putative	GO:0006810	vesicle-mediated transport	-1.1293	-2.1875	0.020178
112	2	MAL13P1.23	CorA-like Mg2+ transporter protein, putative	GO:0030001	metal ion transport	0.82698	1.77397	0.021423
113	3	MAL7P1.340	ATP synthase subunit C, putative	GO:0015986	ATP synthesis coupled proton transport	-0.9988	-1.9984	0.001997
114	4	MAL8P1.32	nucleoside transporter, putative	GO:0015986	nucleoside transport	-1.4673	-2.765	1.67E-05
115	5	PF07_0065	zinc transporter, putative	GO:0030001	zinc ion transport	-2.2527	-4.7658	1.77E-07
116	6	PF11_0098	endoplasmic reticulum-resident calcium binding protein	GO:0006810	intracellular protein transport	-0.8198	-1.7652	0.011936
117	7	PF13_0041	conserved Plasmodium protein	GO:0006810	intracellular protein transport	-0.7443	-1.6752	0.026774
118	8	PF14_0211	Ctr copper transporter domain containing protein, putative	GO:0030001	copper ion transport	-1.2123	-2.3171	0.001022
119	9	PF14_0321	ABC transporter, putative	GO:0006810	transport	-0.8365	-1.7857	0.009928
120	10	PF14_0662	nucleoside transporter, putative	GO:0006810	transport	0.83567	1.78468	0.024563
121	11	PFA0590w	ABC transporter, (CT family), putative	GO:0006810	transport	-1.2602	-2.3953	2.17E-05
122	12	PFB0500c	Rab5a, GTPase	GO:0015031	protein transport	-0.8045	-1.7466	0.008088
123	13	PFC0125w	ABC transporter, (TAP family), putative	GO:0006810	multidrug transport	-0.915	-1.8856	0.003674
124	14	PFE0410w	triose phosphate transporter	GO:0006810	Transport	-0.7265	-1.6546	0.036221
125	15	PFE1510c	triose phosphate transporter	GO:0006810	transport	-1.327	-2.5088	0.00256
126	16	PFI0240c	Cu2+ -transporting ATPase, Cu2+ transporter	GO:0030001	metal ion transport, metabolic process	-0.9036	-1.8707	0.025984
127	17	PFI0300w	developmental protein, putative	GO:0015031	protein transport	-1.6875	-3.2211	4.07E-07
128	18	PFL1410c	ABC transporter, (CT family)	GO:0006810	transport	0.76578	1.70029	0.00209
129	19	PFL2220w	conserved Plasmodium protein, unknown function	GO:0006810	vesicle-mediated transport	0.75398	1.68644	0.019658
Polyamine methionine								
130	1	MAL13P1.214	phosphoethanolamine N-methyltransferase	GO:0006656	phosphatidylcholine biosynthetic process	-2.35	-5.0984	2.48E-05
131	2	PF10_0121	hypoxanthine phosphoribosyltransferase	GO:0006730	purine ribonucleoside salvage	-0.7731	-1.7089	0.014128
132	3	PF10_0289	adenosine deaminase, putative	GO:0009168	purine ribonucleoside monophosphate biosynthetic	-1.6534	-3.1458	5.35E-05
133	4	PF13_0016	methyl transferase-like protein, putative	GO:0006464	methylation	-0.9245	-1.898	0.001369
134	5	PF14_0309	protein-L-isoaspartate O-methyltransferase beta-aspartate	GO:0006464	protein modification process, protein repair	-1.9495	-3.8625	2.34E-07

135	6	PF14_0526	conserved Plasmodium protein, unknown function	GO:0016787	metabolic process, biological_process	-1.6173	-3.0681	1.05E-05
136	7	PFD0285c	lysine decarboxylase, putative	GO:0006554	lysine catabolic process	1.30051	2.46316	8.63E-06
137	8	PFE0660c	purine nucleotide phosphorylase, putative	GO:0009116	nucleoside metabolic process	-1.6031	-3.0379	1.14E-07
138	9	PFE1050w	adenosylhomocysteinase	GO:0006730	one-carbon compound metabolic process	-1.0572	-2.0808	4.40E-05
139	10	PFI1090w	S-adenosylmethionine synthetase	GO:0006730	one-carbon compound metabolic process	-1.2189	-2.3276	0.000462
140	11	PFL1475w	sun-family protein, putative	GO:0016787	metabolic process	-0.8098	-1.7529	0.011921
141	12	PFL1775c	s-adenosyl-methyltransferase, putative	GO:0006464	biological_process	-0.7291	-1.6576	0.023176
142	13	PFL2465c	thymidylate kinase	GO:0016787	dTDP biosynthetic process, dTTP biosynthetic process	-1.4418	-2.7166	3.17E-06
oxidative stress								
143	1	PF08_0071	Fe-superoxide dismutase	GO:0000679	response to oxidative stress	-1.0267	-2.0374	0.000597
144	2	PF08_0131	1-cys peroxiredoxin	GO:0000679	response to oxidative stress	-1.4511	-2.7341	0.000389
145	3	PF14_0187	glutathione S-transferase	GO:0000679	response to oxidative stress	-0.8293	-1.7768	0.010656
146	4	PF14_0192	glutathione reductase	GO:0000679	response to oxidative stress	-1.108	-2.1555	0.001222
147	5	PF14_0545	thioredoxin, putative	GO:0000679	response to oxidative stress	-1.6222	-3.0784	0.000829
148	6	PFL0595c	glutathione peroxidase	GO:0000679	response to oxidative stress	-1.1247	-2.1805	0.00664
Primary metabolism								
149	1	MAL13P1.218	UDP-N-acetylglucosamine pyrophosphorylase, putative	GO:0006047	UDP-N-acetylglucosamine metabolic process	-0.7698	-1.705	0.048791
150	2	MAL13P1.220	lipoate synthase, putative	GO:0009107	lipoate biosynthetic process	-0.7551	-1.6877	0.008278
151	3	MAL13P1.285	patatin-like phospholipase, putative	GO:0006629	lipid metabolic process	-0.8129	-1.7567	0.010297
152	4	MAL8P1.81	Phosphopantothenoylcysteine decarboxylase, putative	GO:0009152	null	0.96039	1.94584	0.000789
153	5	PF07_0129	acyl-coA synthetase, PfACS5	GO:0006631	fatty acid metabolic process	-0.956	-1.9399	0.000462
154	6	PF10_0016	acyl CoA binding protein, isoform 2, ACBP2	GO:0006631	fatty acid metabolic process	-1.5763	-2.9821	2.48E-05
155	7	PF10_0155	enolase	GO:0006096	glycolysis, gluconeogenesis	-1.4245	-2.6842	4.16E-06
156	8	PF10_0169	phosphomannomutase, putative	GO:0019307	GDP-mannose biosynthetic process	1.04627	2.06519	0.000254
157	9	PF10_0334	flavoprotein subunit of succinate dehydrogenase	GO:0006099	tricarboxylic acid cycle	-0.8543	-1.8079	0.008835
158	10	PF11_0257	ethanolamine kinase, putative	GO:0006629	lipid metabolic process, phosphatidylcholine	-1.3081	-2.4761	8.37E-06
159	11	PF13_0121	dihydrolipamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex	GO:0006103	2-oxoglutarate metabolic process	-1.4046	-2.6475	0.000609
160	12	PF13_0141	L-lactate dehydrogenase	GO:0006100	anaerobic glycolysis	-0.8966	-1.8617	0.001996
161	13	PF13_0242	isocitrate dehydrogenase (NADP), mitochondrial precursor	GO:0006102	isocitrate metabolic process	-1.1511	-2.2209	1.05E-05
162	14	PF13_0349	nucleoside diphosphate kinase b, putative	GO:0009152	GTP biosynthetic process	-1.8054	-3.4954	0.009466
163	15	PF14_0378	triosephosphate isomerase	GO:0006096	glycolysis	-0.7757	-1.7121	0.023504
164	16	PFA0555c	UMP-CMP kinase, putative	GO:0006221	pyrimidine nucleotide biosynthetic process	-1.5145	-2.8571	0.003737
165	17	PFB0385w	apicoplast ACP	GO:0006633	fatty acid biosynthetic process	-1.4011	-2.6411	0.000326
166	18	PFB0505c	3-oxoacyl-(acyl carrier protein) synthase III, putative	GO:0006633	fatty acid biosynthetic process	-1.0612	-2.0866	0.002393
167	19	PFC0275w	FAD-dependent glycerol-3-phosphate dehydrogenase,	GO:0006072	glycerol-3-phosphate metabolic process	-0.8709	-1.8288	0.007514
168	20	PFC0395w	asparagine synthetase, putative	GO:0006529	asparagine biosynthetic process	-0.7346	-1.6639	0.003331
169	21	PFD0311w	cytosolic glyoxalase II	GO:0006089	Lactate metabolic process	0.78996	1.72902	0.03332
170	22	PFD0830w	bifunctional dihydrofolate reductase-thymidylate synthase	GO:0006730	one-carbon compound metabolic process	-2.2973	-4.9153	1.07E-08
171	23	PFE0555w	stearoyl-CoA Delta 9 desaturase, putative	GO:0006629	fatty acid biosynthetic process	-1.85	-3.605	0.000831
172	24	PFF0680c	thiamin-phosphate pyrophosphorylase, putative	GO:0009228	thiamin biosynthetic process	-1.629	-3.0931	1.52E-06
173	25	PFF0895w	malate dehydrogenase	GO:0006100	glycolysis, tricarboxylic acid cycle	-1.1707	-2.2513	0.017555
174	26	PFF1300w	pyruvate kinase	GO:0006096	glycolysis	-0.7933	-1.733	0.004025
175	27	PFI0960w	dolichyl-diphosphooligosaccharide-protein glycosyltransferase, putative	GO:0018279	protein amino acid N-linked glycosylation via asparagine	-0.7505	-1.6824	0.048293
176	28	PFL0415w	mitochondrial ACP precursor	GO:0006633	fatty acid biosynthetic process	-0.738	-1.6679	0.030195
177	29	PFL1720w	serine hydroxymethyltransferase	GO:0006544	one-carbon compound metabolic process	-2.2755	-4.8417	1.55E-06
178	30	PFL2030w	queuine tRNA-ribosyltransferase, putative	GO:0008616	queuosine biosynthetic process	-0.7346	-1.6639	0.031713
Cytoskeleton organization and								
179	1	PF10_0084	tubulin beta chain, putative	GO:0007017	microtubule cytoskeleton organization	-2.3862	-5.228	3.53E-07
180	2	PF10_0224	dynein heavy chain, putative	GO:0007017	microtubule-based movement	-1.3601	-2.5671	0.001384
181	3	PF11_0478	kinesin-like protein, putative	GO:0007018	microtubule-based movement	1.06545	2.09283	0.046894

182	4	PF14_0314	chromatin assembly factor 1 P55 subunit, putative	GO:0006334	nucleosome assembly	1.03554	2.04988	0.013309
183	5	PFA0520c	chromatin assembly factor 1 protein WD40 domain, putative	GO:0006334	nucleosome assembly	-2.2285	-4.6864	1.07E-08
184	6	PFE0165w	actin-depolymerizing factor, putative	GO:0030042	actin filament depolymerization	-1.1342	-2.195	5.88E-05
185	7	PFI0180w	alpha tubulin	GO:0007017	microtubule-based movement, protein	-2.8643	-7.2816	1.13E-11
186	8	PFI1565w	profilin, putative	GO:0007010	cytoskeleton organization	-1.5753	-2.9799	4.40E-05
187	9	PFL0925w	formin 2, putative	GO:0000910	actin cytoskeleton organization, cytokinesis	0.96744	1.95536	0.027169
188	10	PFL2215w	actin I	GO:0007010	cytoskeleton organization	-1.3261	-2.5073	4.14E-06
RNA metabolic process								
189	1	MAL13P1.303	polyadenylate-binding protein, putative	GO:0006396	RNA processing	-2.0479	-4.1351	2.23E-08
190	2	MAL8P1.101	RNA binding protein, putative	GO:0006396	RNA processing	-0.7539	-1.6864	0.01538
191	3	MAL8P1.72	high mobility group protein	GO:0006359	regulation of transcription from RNA polymerase III promoter	-0.7429	-1.6736	0.025947
192	4	PF08_0096	RNA helicase, putative	GO:0006396	RNA processing	-0.777	-1.7136	0.017932
193	5	PF10_0313	mitochondrial preribosomal assembly protein rimM	GO:0006364	rRNA processing	-0.9406	-1.9194	0.001973
194	6	PF13_0043	CCAAT-binding transcription factor, putative	GO:0006355	regulation of transcription, DNA-dependent	-0.8209	-1.7665	0.030195
195	7	PFD0750w	nuclear cap-binding protein, putative	GO:0006397	mRNA processing	-0.8402	-1.7903	0.04735
196	8	PFF1425w	RNA binding protein, putative	GO:0006396	RNA processing	-1.1017	-2.146	0.004767
197	9	PFL0465c	Zinc finger transcription factor (krox1)	GO:0006355	regulation of transcription, DNA-dependent	0.80926	1.75231	0.01026
198	10	PFL2115c	glucose inhibited division protein A homologue, putative	GO:0008033	tRNA processing	-1.5443	-2.9166	1.05E-05
Protein folding								
199	1	MAL13P1.283	TCP-1/cpn60 chaperonin family, putative	GO:0006457	protein folding	-0.7294	-1.6579	0.02857
200	2	PF11_0188	heat shock protein 90, putative	GO:0006457	protein folding, response to unfolded protein	-0.9595	-1.9447	0.016142
201	3	PF11_0352	protein disulfide isomerase	GO:0006467	cell redox homeostasis, protein folding	-0.8667	-1.8235	0.034431
202	4	PF11_0513	DNAJ protein, putative	GO:0006457	protein folding	0.77122	1.70671	0.004744
203	5	PFB0920w	DNAJ protein, putative	GO:0006457	protein folding	1.24227	2.3657	0.008609
204	6	PFL0120c	cyclophilin, putative	GO:0006457	protein folding	-0.8693	-1.8268	0.001361
205	7	PFL2550w	DNAJ domain protein, putative	GO:0006457	protein folding	-1.0136	-2.019	0.000707
Signal transduction								
206	1	MAL13P1.165	GPI transamidase subunit PIG-U, putative	GO:0006506	GPI anchor biosynthetic process	-0.7413	-1.6717	0.017537
207	2	MAL13P1.19	peptidase, putative	GO:0032012	null	-1.2705	-2.4125	0.001134
208	3	MAL13P1.205	Rab11b, GTPase	GO:0007264	small GTPase mediated signal transduction	-0.9526	-1.9353	0.004701
209	4	PF14_0317	Microsomal signal peptidase protein, putative	GO:0006465	signal peptide processing	-0.7569	-1.6899	0.020048
210	5	PFA0335w	Rab5c, GTPase	GO:0007264	small GTPase mediated signal transduction	-1.129	-2.1871	0.001276
211	6	PFE0690c	PfRab1a	GO:0007264	small GTPase mediated signal transduction	-0.8196	-1.7649	0.012142
212	7	PFI0155c	PfRab7, GTPase	GO:0007264	small GTPase mediated signal transduction	-0.777	-1.7136	0.003503
213	8	PFI0215c	signal peptidase, putative	GO:0006465	signal peptide processing	-0.8082	-1.7511	0.015665
214	9	PFI1005w	ADP-ribosylation factor-like protein	GO:0007264	small GTPase mediated signal transduction	-0.9795	-1.9718	0.017957
Coenzyme metabolic process								
215	1	MAL7P1.130	3-demethylubiquinone-9 3-methyltransferase, putative	GO:0006744	ubiquinone biosynthetic process	-0.7675	-1.7023	0.007692
216	2	PF13_0140	dihydrofolate synthase/folylpolyglutamate synthase	GO:0009396	folic acid and derivative biosynthetic process	-0.8106	-1.754	0.0165
217	3	PF14_0200	pantothenate kinase, putative	GO:0015937	coenzyme A biosynthetic process	-0.7489	-1.6805	0.014431
218	4	PF14_0415	dephospho-CoA kinase, putative	GO:0015937	coenzyme A biosynthetic process	-1.3524	-2.5533	0.000208
219	5	PFB0220w	ubiE/COQ5 methyltransferase family, putative	GO:0045426	quinone cofactor biosynthetic process	-1.23	-2.3456	0.000346
220	6	PFL1725w	ATP synthase beta chain, mitochondrial precursor, putative	GO:0006754	hydrogen transport, ATP synthesis coupled proton transport	-1.0458	-2.0646	0.003596
Hydrolase activity								
221	1	MAL13P1.121	adenosine-diphosphatase	GO:0016787	null	-0.8305	-1.7783	0.004701
222	2	PF14_0015	aminopeptidase, putative	GO:0016787	biological_process	1.30733	2.47483	0.032832
223	3	PF14_0017	lysophospholipase, putative	GO:0016787	biological_process	1.24572	2.37137	0.000344
224	4	PF14_0738	lysophospholipase, putative	GO:0016787	biological_process	0.84297	1.79374	0.026576

225	5	PFE1305c	ADP-ribosylation factor GTPase-activating protein, putative	GO:0043087	regulation of ARF GTPase activity, regulation of GTPase activity	-0.792	-1.7315	0.019802
Binding activity								
226	1	MAL13P1.122	SET domain protein, putative	GO:0008270	protein binding, zinc ion binding	0.74727	1.67861	0.030594
227	2	MAL13P1.337	Skp1 family protein, putative	GO:0005488	protein binding	-0.9096	-1.8785	0.010945
228	3	MAL8P1.69	14-3-3 protein, putative	GO:0019904	protein domain specific binding	-0.8588	-1.8136	0.015714
229	4	PF07_0035	cg1 protein	GO:0005488	protein binding	-1.4136	-2.664	0.000713
230	5	PF08_0054	heat shock 70 kDa protein	GO:0005488	response to unfolded protein, heat, ATP binding	-0.9421	-1.9213	0.012616
231	6	PF08_0063	ClpB protein, putative	GO:0005488	protein binding	-0.7873	-1.7259	0.014017
232	7	PF08_0118	conserved Plasmodium protein, unknown function	GO:0008270	zinc ion binding	1.16145	2.23682	0.034051
233	8	PF10_0271	centrin-3	GO:0005509	calcium ion binding	-1.4616	-2.7542	0.001222
234	9	PF11_0044	iron-sulfur assembly protein, sufD, putative	GO:0003674	protein binding	-0.8102	-1.7535	0.001205
235	10	PF11_0074	exonuclease, putative	GO:0005488	nucleic acid binding	-0.8399	-1.7899	0.03318
236	11	PF11_0486	MAEBL, putative	GO:0005488	binding	-0.8387	-1.7884	0.036834
237	12	PF13_0314	conserved Plasmodium protein, unknown function	GO:0008270	zinc ion binding, nucleic acid binding	1.98741	3.96525	0.000462
238	13	PF14_0061	PPR repeat protein	GO:0003674	nucleic acid binding	-0.9161	-1.887	0.011912
239	14	PF14_0257	conserved protein, unknown function	GO:0005515	protein binding	-1.5217	-2.8714	2.05E-06
240	15	PF14_0305	leucine-rich repeat protein 5, LRR5	GO:0005515	protein binding	-1.5022	-2.8327	0.000375
241	16	PF14_0413	CAF1 family ribonuclease, putative	GO:0005488	nucleic acid binding	-0.8857	-1.8477	0.006339
242	17	PF14_0443	centrin-2	GO:0005509	calcium ion binding	-2.2899	-4.8904	8.75E-09
243	18	PF14_0479	conserved Plasmodium protein, unknown function	GO:0008270	zinc ion binding, protein binding	0.83169	1.77977	0.036486
244	19	PFC0190c	EH (Eps15 homology) protein	GO:0005525	protein binding, GTP binding	0.7825	1.72011	0.01579
245	20	PFD0440w	peptidase, M22 family, putative	GO:0005488	zinc ion binding	-1.4319	-2.6981	0.000215
246	21	PFF0155w	Bcs1 protein, putative	GO:0005488	protein complex assembly	-0.8055	-1.7477	0.029559
247	22	PFF1180w	anaphase-promoting complex subunit, putative	GO:0005515	zinc ion binding, protein binding	-1.6559	-3.1512	6.96E-06
248	23	PFF1440w	SET domain protein, putative	GO:0005488	zinc ion binding	0.92613	1.90017	0.015665
249	24	PFI0235w	replication factor A-related protein, putative	GO:0003676	nucleic acid binding	-1.1043	-2.15	0.000713
250	25	PFI0490c	ran-binding protein, putative	GO:0005488	binding	-0.7284	-1.6568	0.007949
251	26	PFI0855w	conserved Plasmodium protein, unknown function	GO:0031072	heat shock protein binding	-0.9763	-1.9674	0.011163
Electron transport								
252	1	PF13_0353	NADH-cytochrome B5 reductase, putative	GO:0006118	electron carrier activity	-1.0751	-2.1068	0.042408
253	2	PF14_0248	ubiquinol-cytochrome c reductase hinge protein, putative	GO:0006122	mitochondrial electron transport, ubiquinol to cytochrome c	-0.839	-1.7888	0.011016
254	3	PF14_0597	cytochrome c1 precursor, putative	GO:0006118	electron carrier activity	-1.6755	-3.1943	0.001094
255	4	PFI1170c	thioredoxin reductase	GO:0006118	cell redox homeostasis	-0.9212	-1.8937	0.008668
256	5	PFI1250w	thioredoxin-like protein 2	GO:0045454	cell redox homeostasis	-0.8073	-1.7499	0.003539
257	6	PFL1550w	lipoamide dehydrogenase	GO:0006118	cell redox homeostasis	-1.2073	-2.309	0.013234
Host parasite								
258	1	MAL13P1.176	reticulocyte binding protein 2, homolog b	GO:0030260	entry into host cell	0.91731	1.88859	0.04735
259	2	PF07_0051	erythrocyte membrane protein 1, PfEMP1	GO:0002033	cell-cell adhesion, pathogenesis	0.96956	1.95824	0.000894
260	3	PF07_0138	rifin	GO:0002033	antigenic variation	-1.0778	-2.1108	0.024047
261	4	PF10_0002	rifin	GO:0002033	antigenic variation	-1.3987	-2.6366	2.65E-05
262	5	PF14_0138	conserved protein, unknown function	GO:0007155	null	-0.8143	-1.7585	0.006096
263	6	PFA0010c	rifin	GO:0002033	antigenic variation	-1.3952	-2.6303	0.029559
264	7	PFA0760w	rifin	GO:0002033	antigenic variation	-1.0321	-2.045	0.000896
265	8	PFD0015c	rifin	GO:0002033	antigenic variation	-0.8845	-1.8461	0.02176
266	9	PFD0995c	erythrocyte membrane protein 1, PfEMP1	GO:0002033	antigenic variation, pathogenesis, rosetting	0.83443	1.78316	0.002942
267	10	PFF0010w	erythrocyte membrane protein 1, PfEMP1	GO:0002033	pathogenesis, antigenic variation	-1.2507	-2.3796	0.000217
268	11	PFF0020c	erythrocyte membrane protein 1 (PfEMP1)-like protein	GO:0009405	pathogenesis	0.77516	1.71137	0.007514
269	12	PFL1420w	macrophage migration inhibitory factor homologue	GO:0020012	evasion or tolerance of host immune response	-1.0704	-2.1	0.000186
270	13	PFL1955w	erythrocyte membrane protein 1, PfEMP1	GO:0002033	cell-cell adhesion, pathogenesis, rosetting,	0.75069	1.68259	0.016669

Hypotheticals								
271	1	PF08_0060	asparagine-rich antigen	GO:0008150	biological_process	1.15728	2.23037	0.044795
272	2	PF10_0188	conserved Plasmodium membrane protein, unknown function	GO:0008150	biological_process	-1.3966	-2.6329	0.002101
273	3	PF10_0195	kinesin, putative	GO:0008150	biological_process	-0.8107	-1.7541	0.041116
274	4	PF10_0213	10b antigen, putative	GO:0008150	biological_process	-1.0633	-2.0896	0.000208
275	5	PF10_0246	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.1112	-2.1603	0.010342
276	6	PF11_0046	CPW-WPC family protein	GO:0008150	biological_process	-0.8724	-1.8307	0.010623
277	7	PF11_0049	NOT family protein, putative	GO:0008150	biological_process	-0.8906	-1.854	0.030109
278	8	PF11_0059	metabolite/drug transporter, putative	GO:0008150	biological_process	-1.0445	-2.0627	0.002158
279	9	PF11_0069	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-0.7906	-1.7298	0.002186
280	10	PF11_0146	conserved Plasmodium membrane protein, unknown function	GO:0008150	biological_process	-0.9831	-1.9768	0.008195
281	11	PF11_0215	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.353	-2.5544	0.002721
282	12	PF11_0231	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	0.8138	1.75784	0.02359
283	13	PF11_0271	ThiF family protein, putative	GO:0008150	biological_process	-0.7408	-1.6711	0.03215
284	14	PF11_0307	phosphatidylinositol-4-phosphate-5-kinase,putative	GO:0008150	biological_process	0.81025	1.75352	0.032281
285	15	PF11_0319	mitochondrial rpoD precursor, putative	GO:0008150	biological_process	-0.9923	-1.9893	0.047682
286	16	PF11_0321	serpentine receptor, putative	GO:0008150	biological_process	1.00129	2.00179	0.00028
287	17	PF11_0355	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.7709	-3.4127	9.83E-06
288	18	PF11_0423	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-0.8207	-1.7662	0.002777
289	19	PF13_0011	plasmodium falciparum gamete antigen 27/25	GO:0008150	biological_process	-1.2549	-2.3865	0.008317
290	20	PF14_0014	Plasmodium exported protein, unknown function	GO:0008150	biological_process	-0.87	-1.8277	0.020408
291	21	PF14_0016	early transcribed membrane protein 14.1, etramp14.1	GO:0008150	biological_process	0.91963	1.89162	0.034832
292	22	PF14_0018	Plasmodium exported protein (PHISTb), unknown function	GO:0008150	biological_process	1.18603	2.27526	1.25E-05
293	23	PF14_0045	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	1.04114	2.05786	0.001997
294	24	PF14_0105	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.2169	-2.3245	0.007714
295	25	PF14_0110	rhomboid protease ROM8	GO:0008150	biological_process	0.91907	1.8909	0.000993
296	26	PF14_0297	apyrase, putative	GO:0008150	biological_process	-1.0218	-2.0305	0.011507
297	27	PF14_0329	conserved protein, unknown function	GO:0008150	biological_process	-1	-2	0.024581
298	28	PF14_0463	chloroquine resistance marker protein	GO:0008150	biological_process	-0.7902	-1.7293	0.010523
299	29	PF14_0498	Degradation in the ER (DER1) like protein, putative	GO:0008150	biological_process	-1.0217	-2.0304	0.007714
300	30	PF14_0617	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.2055	-2.3061	5.88E-05
301	31	PF14_0680	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.6512	-3.141	1.54E-05
302	32	PF14_0696	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-0.9997	-1.9995	0.000519
303	33	PF14_0698	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	1.32537	2.50598	0.034291
304	34	PF14_0758	Plasmodium exported protein (hyp17), unknown function	GO:0008150	biological_process	0.73928	1.66935	0.049948
305	35	PFB0075c	Plasmodium exported protein (hyp9), unknown function	GO:0008150	biological_process	0.82587	1.77261	0.015081
306	36	PFB0194w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	0.74353	1.67427	0.030454
307	37	PFB0365w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-0.752	-1.6841	0.017957
308	38	PFB0590w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.1625	-2.2385	0.001022
309	39	PFB0600c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.1414	-2.2059	7.25E-05
310	40	PFB0923c	Plasmodium exported protein, unknown function	GO:0008150	biological_process	1.34746	2.54464	0.01753
311	41	PFB0953w	Plasmodium exported protein (hyp15), unknown function	GO:0008150	biological_process	-0.8516	-1.8045	0.001513
312	42	PFC0730w	HVA22/TB2/DP1 family protein, putative	GO:0008150	biological_process	-0.9235	-1.8967	0.019456
313	43	PFF1535w	Plasmodium exported protein (hyp5), unknown function	GO:0008150	biological_process	0.90252	1.86932	0.002996
314	44	PFL0065w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	0.79007	1.72916	0.012931
315	45	PFL0130c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	0.92295	1.89599	0.018093
316	46	PFL0170w	transporter, putative	GO:0008150	biological_process	-0.9434	-1.9231	0.03411
317	47	PFL0745c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.0419	-2.0589	0.003161
318	48	PFL1065c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-0.7318	-1.6607	0.032882
319	49	PFL1250c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.0844	-2.1204	0.003737
320	50	PFL1330c	cyclin-related protein, Pfcyc-2	GO:0008150	biological_process	-1.4192	-2.6743	0.000309
321	51	PFL1630c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.4052	-2.6485	0.000197

322	52	PFL1670c	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.9615	-3.8948	7.25E-05
323	53	PFL1685w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.2729	-2.4164	2.35E-06
324	54	PFL2205w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-0.8776	-1.8373	0.00567
325	55	PFL2240w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	-1.1238	-2.1791	0.00133
326	56	PFL2455w	conserved Plasmodium protein, unknown function	GO:0008150	biological_process	0.86553	1.82201	0.015428
327	57	PF13_0126	translation initiation factor EIF-2B subunit related	GO:0009987	cellular metabolic process	-0.8703	-1.8281	0.001361
328	58	PF10_0039	membrane skeletal protein IMC1-related	GO:0008150	cytoskeleton organization	1.07352	2.10456	0.003737
329	59	MAL13P1.307	conserved Plasmodium protein, unknown function	GO:0008150	iron-sulfur cluster assembly	-1.3596	-2.5661	0.000421
330	60	PF14_0557	conserved Plasmodium protein, unknown function	GO:0008152	metabolic process	0.96467	1.95162	0.036516
331	61	PFL0685w	Phosphatidylinositol-glycan biosynthesis class O protein,	GO:0008152	metabolic process	-0.9077	-1.8761	0.012798
332	62	MAL13P1.103	conserved Plasmodium protein, unknown function		null	-1.1218	-2.1762	0.019949
333	63	MAL13P1.138	conserved Plasmodium protein, unknown function		null	-1.1296	-2.1879	0.001072
334	64	MAL13P1.180	conserved Plasmodium protein, unknown function		null	-0.8791	-1.8393	0.002039
335	65	MAL13P1.188	conserved Plasmodium protein, unknown function		null	0.83428	1.78297	0.003813
336	66	MAL13P1.189	conserved Plasmodium membrane protein, unknown function		null	-0.8322	-1.7804	0.026901
337	67	MAL13P1.193	conserved Plasmodium protein, unknown function		null	-1.5222	-2.8723	1.54E-05
338	68	MAL13P1.203	conserved Plasmodium protein, unknown function		null	0.8874	1.84984	0.003737
339	69	MAL13P1.222	conserved Plasmodium protein, unknown function		null	0.7822	1.71975	0.00671
340	70	MAL13P1.239	conserved Plasmodium protein, unknown function		null	-0.8439	-1.7949	0.032832
341	71	MAL13P1.251	conserved Plasmodium protein, unknown function		null	-1.7989	-3.4795	1.42E-05
342	72	MAL13P1.260	conserved Plasmodium protein, unknown function		null	0.75977	1.69322	0.010017
343	73	MAL13P1.293	conserved Plasmodium protein, unknown function		null	0.82108	1.76673	0.016179
344	74	MAL13P1.298	conserved Plasmodium membrane protein, unknown function		null	0.72547	1.65344	0.028704
345	75	MAL13P1.332	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	1.05808	2.08216	0.000489
346	76	MAL13P1.470	Plasmodium exported protein (PHISTa), unknown function		null	0.78368	1.72152	0.013371
347	77	MAL13P1.57	conserved Plasmodium protein, unknown function		null	-0.8417	-1.7922	0.003543
348	78	MAL13P1.75	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-0.7546	-1.6871	0.020825
349	79	MAL7P1.102	conserved Plasmodium protein, unknown function		null	-0.8471	-1.7989	0.005775
350	80	MAL7P1.107	conserved Plasmodium protein, unknown function		null	-1.331	-2.5158	0.000596
351	81	MAL7P1.124	conserved Plasmodium protein, unknown function		null	-1.1578	-2.2312	2.42E-05
352	82	MAL7P1.167	conserved Plasmodium protein, unknown function		null	-0.7703	-1.7056	0.017932
353	83	MAL7P1.173	Plasmodium exported protein, unknown function		null	0.87972	1.84002	0.042563
354	84	MAL7P1.174	Plasmodium exported protein (PHISTb), unknown function		null	1.04538	2.06391	0.000154
355	85	MAL7P1.208	rifin-like protein		null	0.78769	1.72631	0.045589
356	86	MAL7P1.23	RAP protein, putative	GO:0020011	apicoplast	-0.7512	-1.6832	0.021764
357	87	MAL7P1.230	hypothetical protein, pseudogene		null	0.75845	1.69167	0.015641
358	88	MAL7P1.3	Plasmodium exported protein (hyp5), unknown function		null	0.7584	1.69162	0.032281
359	89	MAL7P1.33	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-1.3569	-2.5614	0.018747
360	90	MAL7P1.61	null		null	0.72546	1.65343	0.030195
361	91	MAL7P1.77	conserved Plasmodium protein, unknown function		null	-1.3846	-2.611	0.000755
362	92	MAL8P1.2	Plasmodium exported protein (PHISTb), unknown function		null	1.05545	2.07837	0.006518
363	93	MAL8P1.206	Plasmodium exported protein, unknown function		null	-1.5654	-2.9596	0.002017
364	94	MAL8P1.216	rifin		null	-1.2427	-2.3664	0.001369
365	95	MAL8P1.50	conserved Plasmodium protein, unknown function		null	-0.7268	-1.655	0.008317
366	96	MAL8P1.53	conserved Plasmodium protein, unknown function		null	-1.8738	-3.6651	2.70E-07
367	97	MAL8P1.74	conserved Plasmodium protein, unknown function		null	-1.0044	-2.0061	0.000755
368	98	MAL8P1.82	Vacuolar sorting protein VPS9, putative		null	0.8157	1.76015	0.043532
369	99	MAL8P1.86	Sel3 protein	GO:0020011	apicoplast	-1.2598	-2.3947	3.24E-05
370	100	PF07_0022	conserved Plasmodium protein, unknown function		null	-0.9995	-1.9993	0.00154
371	101	PF07_0039	conserved Plasmodium protein, unknown function		null	-0.8494	-1.8018	0.03388
372	102	PF07_0053	conserved Plasmodium protein, unknown function		null	0.86441	1.82059	0.01039
373	103	PF07_0078	transmembrane protein, putative	GO:0016020	membrane	-0.9754	-1.9662	0.000704

374	104	PF07_0082	conserved Plasmodium membrane protein, unknown function		null	0.85888	1.81363	0.024958
375	105	PF07_0084	conserved Plasmodium protein, unknown function		null	0.82274	1.76876	0.011456
376	106	PF07_0087	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-1.3125	-2.4837	0.001103
377	107	PF07_0101	conserved Plasmodium protein, unknown function		null	-0.7944	-1.7344	0.017814
378	108	PF07_0106	conserved Plasmodium protein, unknown function		null	0.93347	1.90987	0.002223
379	109	PF08_0001	Plasmodium exported protein, unknown function	GO:0020011	apicoplast	1.10517	2.15124	7.72E-05
380	110	PF08_0002	surface-associated interspersed gene 8.2 (SURFIN8.2)		null	0.75416	1.68665	0.002869
381	111	PF08_0016	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-1.0013	-2.0018	0.012775
382	112	PF08_0029	conserved Plasmodium protein, unknown function		null	-1.0739	-2.1051	0.019949
383	113	PF08_0030	conserved Plasmodium protein, unknown function		null	-1.3401	-2.5317	0.002264
384	114	PF08_0051	conserved Plasmodium protein, unknown function		null	-1.0001	-2.0001	0.003978
385	115	PF08_0134	conserved Plasmodium protein, unknown function		null	-0.8979	-1.8633	0.035574
386	116	PF10_0020	alpha/beta hydrolase, putative		null	-2.0211	-4.059	4.77E-06
387	117	PF10_0034	conserved Plasmodium protein, unknown function		null	1.21687	2.32442	9.59E-06
388	118	PF10_0052	conserved Plasmodium protein, unknown function		null	-1.4009	-2.6407	0.000515
389	119	PF10_0212	conserved Plasmodium protein, unknown function		null	-0.9745	-1.9649	0.002777
390	120	PF10_0243	conserved Plasmodium protein, unknown function		null	-0.7407	-1.671	0.03332
391	121	PF10_0253	conserved Plasmodium protein, unknown function		null	-0.7996	-1.7406	0.003791
392	122	PF10_0258	conserved Plasmodium protein, unknown function		null	0.91189	1.8815	0.010323
393	123	PF10_0286	conserved Plasmodium protein, unknown function		null	-1.2289	-2.3439	0.006304
394	124	PF10_0291	RAP protein, putative		null	-1.1628	-2.2388	0.015295
395	125	PF10_0307	conserved Plasmodium protein, unknown function		null	1.23334	2.35111	0.000298
396	126	PF10_0319	conserved Plasmodium protein, unknown function		null	0.85248	1.8056	0.011225
397	127	PF10_0336	conserved Plasmodium protein, unknown function		null	-1.4303	-2.6949	0.000934
398	128	PF10_0352	merozoite surface protein		null	0.7875	1.72609	0.017056
399	129	PF11_0035	Plasmodium exported protein, unknown function		null	0.78009	1.71724	0.002088
400	130	PF11_0093	IWS1-like protein, putative		null	0.73478	1.66415	0.023412
401	131	PF11_0206	conserved Plasmodium protein, unknown function		null	1.07565	2.10767	0.005257
402	132	PF11_0278	conserved Plasmodium protein, unknown function		null	0.7906	1.7298	0.0198
403	133	PF11_0290	conserved Plasmodium protein, unknown function		null	0.82433	1.77072	0.016387
404	134	PF11_0296	conserved protein, unknown function		null	0.76255	1.69649	0.019017
405	135	PF11_0371	conserved Plasmodium protein, unknown function		null	-1.0398	-2.0559	0.016977
406	136	PF11_0404	transcription factor with AP2 domain(s), putative		null	0.94238	1.9217	0.033309
407	137	PF11_0413	conserved Plasmodium protein, unknown function		null	0.74028	1.67049	0.048387
408	138	PF11_0425	conserved Plasmodium protein, unknown function		null	-1.213	-2.3182	0.000126
409	139	PF11_0508	Plasmodium exported protein, unknown function		null	-1.1405	-2.2046	0.021309
410	140	PF11_0514	Plasmodium exported protein (PHISTa), unknown function		null	0.96452	1.95141	0.017555
411	141	PF11_0560	conserved protein, unknown function		null	-0.9175	-1.8888	0.006687
412	142	PF13_0024	conserved Plasmodium protein, unknown function		null	-0.8017	-1.7431	0.045163
413	143	PF13_0032	hydrolase, putative	GO:0020011	apicoplast	-2.2264	-4.6797	0.002217
414	144	PF13_0097	transcription factor with AP2 domain(s), putative		null	0.78312	1.72084	0.007879
415	145	PF13_0104	conserved Plasmodium protein, unknown function		null	-0.7584	-1.6916	0.034431
416	146	PF13_0175	conserved protein, unknown function		null	0.89675	1.86186	0.015932
417	147	PF13_0189	conserved Plasmodium protein, unknown function		null	-0.8035	-1.7454	0.030161
418	148	PF13_0192	conserved Plasmodium protein, unknown function	GO:0016020	membrane	-2.0706	-4.2006	5.51E-08
419	149	PF13_0200	conserved Plasmodium protein, unknown function		null	-0.7553	-1.688	0.03309
420	150	PF13_0202	conserved Plasmodium protein, unknown function		null	-1.234	-2.3522	0.001512
421	151	PF13_0241	rhomboid protease ROM6, putative	GO:0016020	null	-0.7978	-1.7385	0.001088
422	152	PF13_0267	conserved Plasmodium protein, unknown function		null	0.7819	1.71939	0.003543
423	153	PF13_0296	splicing factor 3b subunit, putative		null	-0.8722	-1.8305	0.00434
424	154	PF13_0307	conserved Plasmodium protein, unknown function		null	-0.7945	-1.7345	0.001553
425	155	PF13_0338	cysteine-rich surface protein		null	-0.8841	-1.8456	0.039883

426	156	PF13_0348	rhoptry protein		null	-1.0309	-2.0432	0.001644
427	157	PF14_0031	conserved Plasmodium protein, unknown function		null	-1.4697	-2.7696	5.69E-06
428	158	PF14_0101	conserved Plasmodium protein, unknown function		null	-0.8496	-1.802	0.024125
429	159	PF14_0170	NOT family protein, putative		null	0.73112	1.65993	0.01662
430	160	PF14_0186	conserved Plasmodium protein, unknown function		null	-1.0318	-2.0446	0.000432
431	161	PF14_0226	conserved Plasmodium protein, unknown function		null	0.74205	1.67255	0.016411
432	162	PF14_0344	conserved Plasmodium protein, unknown function		null	0.85787	1.81236	0.003387
433	163	PF14_0347	conserved Plasmodium protein, unknown function		null	-0.8823	-1.8434	0.028026
434	164	PF14_0402	conserved Plasmodium protein, unknown function		null	0.83517	1.78407	0.024501
435	165	PF14_0430	mitochondrial ribosomal protein S29 precursor, putative		null	-0.8085	-1.7514	0.00671
436	166	PF14_0488	conserved Plasmodium protein, unknown function		null	-0.7861	-1.7244	0.039144
437	167	PF14_0502	conserved Plasmodium protein, unknown function		null	-0.8699	-1.8275	0.00671
438	168	PF14_0570	pyridoxal 5'-phosphate synthase, putative		null	-1.215	-2.3214	0.002779
439	169	PF14_0583	conserved Plasmodium protein, unknown function		null	-1.0339	-2.0476	0.005929
440	170	PF14_0609	conserved Plasmodium protein, unknown function		null	-0.9309	-1.9064	0.010137
441	171	PF14_0631	conserved Plasmodium protein, unknown function		null	0.7291	1.65761	0.04483
442	172	PF14_0703	conserved Plasmodium protein, unknown function		null	1.13702	2.19926	0.007252
443	173	PF14_0705	conserved Plasmodium protein, unknown function		null	-1.1044	-2.1501	0.017941
444	174	PF14_0706	conserved Plasmodium protein, unknown function		null	0.85094	1.80367	0.019075
445	175	PF14_0760	Plasmodium exported protein, unknown function		null	0.99433	1.99215	0.004045
446	176	PFA0115w	Plasmodium exported protein, unknown function	GO:0020011	apicoplast	-1.6653	-3.1717	0.000435
447	177	PFA0195w	conserved Plasmodium protein, unknown function		null	-1.0273	-2.0382	0.000405
448	178	PFA0245w	transporter, putative		null	-1.9419	-3.8421	6.97E-06
449	179	PFA0350c	conserved Plasmodium protein, unknown function		null	-0.7938	-1.7337	0.04735
450	180	PFA0385w	conserved Plasmodium membrane protein, unknown function	GO:0020011	apicoplast	-1.1384	-2.2013	0.000346
451	181	PFB0115w	conserved Plasmodium protein, unknown function		null	1.68929	3.22498	0.001885
452	182	PFB0161c	conserved Plasmodium protein, unknown function		null	-1.5041	-2.8365	0.003117
453	183	PFB0315w	41 kDa antigen		null	-1.0472	-2.0666	0.013449
454	184	PFB0475c	conserved Plasmodium protein, unknown function		null	1.61727	3.06794	0.00715
455	185	PFB0530c	conserved Plasmodium protein, unknown function		null	-1.1239	-2.1794	0.013309
456	186	PFB0535w	GDP-fructose:GMP antiporter, putative		null	-1.5443	-2.9167	0.001134
457	187	PFB0835c	conserved Plasmodium protein, unknown function		null	-2.094	-4.2693	1.55E-06
458	188	PFB0970c	Plasmodium exported protein, unknown function		null	0.75959	1.69301	0.009621
459	189	PFB0973c	hypothetical protein		null	0.83022	1.77796	0.015439
460	190	PFC0085c	Plasmodium exported protein, unknown function		null	0.85591	1.8099	0.003979
461	191	PFC0262c	conserved Plasmodium protein, unknown function		null	-1.798	-3.4773	6.80E-05
462	192	PFC0315c	conserved Plasmodium protein, unknown function		null	-1.3138	-2.486	0.003569
463	193	PFC0371w	conserved protein, unknown function		null	-1.0759	-2.1081	0.000328
464	194	PFC0390w	N2227-like protein, putative		null	0.72608	1.65413	0.046637
465	195	PFC0435w	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-1.0274	-2.0383	0.000934
466	196	PFC0571c	conserved Plasmodium protein, unknown function		null	-0.9606	-1.9461	0.001222
467	197	PFC0590c	DER1-like protein, putative	GO:0020011	apicoplast	-1.4047	-2.6477	0.002903
468	198	PFC0715c	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-1.4806	-2.7906	0.017237
469	199	PFC0760c	conserved Plasmodium protein, unknown function		null	0.77417	1.7102	0.015278
470	200	PFC0886w	conserved Plasmodium protein, unknown function		null	-1.1253	-2.1814	6.82E-05
471	201	PFC0912w	signal peptidase, putative		null	-1.6703	-3.1828	0.000131
472	202	PFC0965w	conserved Plasmodium protein, unknown function		null	0.73803	1.6679	0.002939
473	203	PFC0990c	conserved Plasmodium protein, unknown function		null	0.76261	1.69656	0.041639
474	204	PFC1110w	null		null	0.89672	1.86183	0.002216
475	205	PFD0080c	Plasmodium exported protein (PHISTb), unknown function		null	-0.9388	-1.9169	0.02204
476	206	PFD0225w	conserved Plasmodium membrane protein, unknown function		null	-0.9649	-1.9519	0.018337
477	207	PFD0495c	conserved Plasmodium protein, unknown function		null	0.85184	1.8048	0.00422

478	208	PFD0545w	conserved Plasmodium protein, unknown function		null	0.86339	1.81931	0.029731
479	209	PFD0550c	conserved Plasmodium protein, unknown function		null	-1.073	-2.1038	0.003745
480	210	PFD0655w	null		null	-0.7577	-1.6908	0.008418
481	211	PFD0670c	lysine decarboxylase-like protein, putative		null	-0.9665	-1.9541	0.002013
482	212	PFD0850c	Memo-like protein		null	-1.1069	-2.1538	0.017596
483	213	PFD0920w	conserved Plasmodium protein, unknown function		null	-0.9168	-1.888	0.013578
484	214	PFD1140w	Plasmodium exported protein (PHISTc), unknown function		null	1.06876	2.09763	0.001184
485	215	PFE0050w	Plasmodium exported protein, unknown function		null	0.83732	1.78673	0.00451
486	216	PFE0265c	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-0.8716	-1.8297	0.03803
487	217	PFE0310c	conserved Plasmodium protein, unknown function		null	-1.0931	-2.1333	0.003117
488	218	PFE0340c	rhomboid protease ROM4	GO:0016020	membrane	1.12723	2.18438	0.032882
489	219	PFE0345c	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-0.7931	-1.7328	0.022939
490	220	PFE0390w	conserved Plasmodium protein, unknown function		null	0.80204	1.74356	0.013578
491	221	PFE0500c	conserved Plasmodium protein, unknown function		null	-1.3206	-2.4978	9.55E-06
492	222	PFE0620c	conserved Plasmodium protein, unknown function		null	-1.0746	-2.1061	0.004441
493	223	PFE0635c	conserved Plasmodium protein, unknown function		null	-0.9004	-1.8666	0.001384
494	224	PFE1220w	conserved Plasmodium protein, unknown function		null	-0.7528	-1.685	0.020816
495	225	PFE1280w	conserved Plasmodium protein, unknown function		null	-1.1552	-2.2271	0.01052
496	226	PFE1365w	conserved Plasmodium protein, unknown function		null	0.9661	1.95355	0.010247
497	227	PFE1515w	conserved Plasmodium membrane protein, unknown function		null	-1.0758	-2.1079	0.004908
498	228	PFE1610w	Plasmodium exported protein, unknown function	GO:0020011	apicoplast	1.03126	2.04381	0.000462
499	229	PFF0075c	Plasmodium exported protein (PHISTb), unknown function		null	0.80949	1.75259	0.014759
500	230	PFF0205w	mitochondrial ribosomal protein L41 precursor, putative		null	-1.0659	-2.0935	0.001534
501	231	PFF0295c	conserved Plasmodium protein, unknown function		null	0.9298	1.90502	0.001297
502	232	PFF0480w	conserved Plasmodium protein, unknown function		null	0.9663	1.95382	0.000525
503	233	PFF0545c	conserved Plasmodium protein, unknown function		null	-0.9718	-1.9613	5.88E-05
504	234	PFF0550w	transcription factor with AP2 domain(s), putative		null	-0.8717	-1.8299	0.00671
505	235	PFF0630c	conserved Plasmodium protein, unknown function		null	-1.9912	-3.9756	2.70E-07
506	236	PFF0640w	conserved Plasmodium protein, unknown function		null	-1.6463	-3.1304	4.56E-05
507	237	PFF0725w	conserved Plasmodium protein, unknown function		null	0.72405	1.65182	0.003117
508	238	PFF0805c	conserved Plasmodium protein, unknown function		null	-0.902	-1.8687	0.004663
509	239	PFF0935c	conserved Plasmodium protein, unknown function		null	-1.175	-2.2579	0.007034
510	240	PFF1005w	conserved Plasmodium protein, unknown function		null	0.86301	1.81883	0.032073
511	241	PFF1160w	conserved Plasmodium protein, unknown function		null	-0.7971	-1.7376	0.031041
512	242	PFF1290c	conserved Plasmodium protein, unknown function		null	-0.7837	-1.7216	0.010045
513	243	PFF1460c	conserved Plasmodium protein, unknown function		null	0.91097	1.88031	0.003215
514	244	PFI0175w	conserved Plasmodium protein, unknown function		null	0.95386	1.93705	0.048791
515	245	PFI0210c	cysteine repeat modular protein, putative	GO:0020011	apicoplast	-0.9129	-1.8829	0.015639
516	246	PFI0405w	conserved Plasmodium protein, unknown function	GO:0020011	apicoplast	-1.1638	-2.2405	0.018385
517	247	PFI0765w	conserved Plasmodium protein, unknown function		null	0.86861	1.8259	0.007258
518	248	PFI0795w	conserved Plasmodium protein, unknown function		null	-0.8596	-1.8146	0.049904
519	249	PFI0880c	glideosome-associated protein 50		null	-1.5084	-2.8449	0.000146
520	250	PFI0905w	probable protein, unknown function		null	-2.6442	-6.2515	1.58E-09
521	251	PFI0975c	conserved Plasmodium protein, unknown function		null	-0.9179	-1.8894	0.005257
522	252	PFI1040c	conserved Plasmodium membrane protein, unknown function		null	0.992	1.98894	0.014819
523	253	PFI1185c	conserved Plasmodium protein, unknown function		null	0.75797	1.6911	0.030932
524	254	PFI1270w	conserved Plasmodium protein, unknown function		null	-1.5415	-2.911	0.01753
525	255	PFI1500w	conserved Plasmodium membrane protein, unknown function		null	-0.9484	-1.9297	0.041354
526	256	PFI1520w	asparagine-rich antigen, putative		null	0.96767	1.95569	0.027249
527	257	PFI1610c	calcyclin binding protein, putative		null	-0.8053	-1.7475	0.00457
528	258	PFI1630c	conserved Plasmodium protein, unknown function		null	-1.0553	-2.0782	0.048667
529	259	PFI1665w	transcription factor with AP2 domain(s), putative		null	-0.9113	-1.8808	0.004328

530	260	PFI1690c	conserved Plasmodium protein, unknown function		null	1.02675	2.03743	0.023976
531	261	PFI1770w	Plasmodium exported protein (PHISTb), unknown function		null	0.90449	1.87189	0.025947
532	262	PFI1780w	Plasmodium exported protein (PHISTc), unknown function		null	1.29911	2.46078	3.15E-05
533	263	PFL0235w	conserved Plasmodium protein, unknown function		null	-1.8419	-3.5847	9.93E-05
534	264	PFL0280c	histone binding protein, putative		null	-0.7982	-1.739	0.035574
535	265	PFL0975w	conserved Plasmodium protein, unknown function		null	-0.9113	-1.8807	0.032882
536	266	PFL1040w	conserved Plasmodium protein, unknown function		null	-0.7873	-1.7258	0.032281
537	267	PFL1300c	conserved Plasmodium protein, unknown function		null	-0.7312	-1.6601	0.003762
538	268	PFL1335w	cyclin related protein, putative		null	-1.2522	-2.382	0.001752
539	269	PFL1560c	conserved protein, unknown function		null	0.87151	1.82957	0.022843
540	270	PFL1645w	conserved Plasmodium protein, unknown function		null	0.76003	1.69352	0.002158
541	271	PFL1900w	transcription factor with AP2 domain(s), putative		null	-1.4485	-2.7293	0.000386
542	272	PFL2435w	conserved Plasmodium protein, unknown function		null	-0.8135	-1.7575	0.006073
543	273	PFL2535w	Plasmodium exported protein (PHISTb), unknown function		null	-1.4081	-2.6539	0.000375
544	274	MAL8P1.14	mitochondrial inner membrane translocase, putative	GO:0051205	protein insertion into membrane	-1.1011	-2.1452	4.56E-05
545	275	MAL8P1.330	conserved Plasmodium protein, unknown function		null	1.22718	2.3411	0.005232
546	276	PF14_0182	conserved Plasmodium protein, unknown function		null	1.68436	3.21398	0.007421
547	277	PFD1045w	conserved Plasmodium protein, unknown function		null	-1.5894	-3.0093	5.29E-06
548	278	PFE0240c	conserved Plasmodium protein, unknown function		null	-0.9274	-1.9019	0.01841
549	279	PFE0685w	conserved Plasmodium protein, unknown function		null	-1.3974	-2.6342	0.011921

Appendix C

The complete interacting binding partners of AdoMetDC, DHPS/HPPK and AdoMet synthase

Nr	PlasmoDB ID	Name	Score	Present in dataset
		AdoMetDC interactome		
1	PF11_0317	structural maintenance of chromosome protein, putative	9.53	
2	PFE0195w	P-type ATPase, putative	8.31	
3	PFA0390w	DNA repair exonuclease, putative	7.98	
4	MAL8P1.99	hypothetical protein	6.62	Yes
5	PF11_0427	dolichyl-phosphate b-D-mannosyltransferase, putative	6.62	
6	PF07_0129	ATP-dept. acyl-coa synthetase	6.62	Yes
7	PFA0590w	ABC transporter, putative	6.62	Yes
8	PF10_0260	hypothetical protein	5.90	
9	PF13_0348	PfRhop148,Rhoptry protein	5.90	Yes
10	PF14_0053	ribonucleotide reductase small subunit	5.70	Yes
11	PFD0685c	chromosome associated protein, putative	4.71	Yes
12	PFC0125w	ABC transporter, putative	4.71	Yes
13	PF14_0709	ribosomal protein L20, putative	4.71	Yes
14	PF08_0131	1-cys peroxidoxin	4.71	Yes
15	PF11_0117	replication factor C subunit 5, putative	4.71	Yes
16	PF11_0181	tyrosine --tRNA ligase, putative	4.71	Yes
17	PFB0180w	5'-3' exonuclease, N-terminal resolvase-like domain, putative	4.71	
18	PFL2180w	50S ribosomal protein L3, putative	4.71	
19	PF14_0097	cytidine diphosphate-diacylglycerol synthase	4.71	
20	PF14_0081	DNA repair helicase, putative	4.71	
21	PF11_0044	hypothetical protein	4.71	Yes
22	PF11_0197	hypothetical protein	4.71	
23	PF14_0338	hypothetical protein	4.52	
24	PF14_0397	hypothetical protein, conserved	4.52	
25	PF10_0362	DNA polymerase zeta catalytic subunit, putative	4.52	
26	PFB0605w	Ser/Thr protein kinase, putative	4.52	
27	PF08_0034	histone acetyltransferase Gcn5, putative	4.52	
28	PF10_0132	phospholipase C-like, putative	4.52	
29	PFI1310w	NAD synthase, putative	4.52	
30	PF13_0016	methyl transferase-like protein, putative	4.52	Yes
31	PFB0520w	protein kinase, putative	4.52	
32	PF11_0049	hypothetical protein, conserved	4.52	Yes
33	PF11_0074	hypothetical protein	4.52	Yes
34	PF14_0161	hypothetical protein, conserved	4.52	
35	PF14_0441	pyruvate dehydrogenase E1 beta subunit, putative	4.52	
36	PFE0040c	Mature parasite-infected erythrocyte surface antigen (MESA)	4.52	
37	MAL13P1.95	ferredoxin	4.52	
38	PFE0585c	myo-inositol 1-phosphate synthase, putative	4.52	
39	PF13_0021	small heat shock protein, putative	4.52	
40	PFC0915w	ATP-dependent RNA helicase, putative	4.52	
41	PFA0520c	chromatin assembly factor 1 protein WD40 domain, putative	4.52	Yes
42	PF08_0031	oxoglutarate/malate translocator protein, putative	4.52	
43	PFI0910w	DNA helicase, putative	4.52	
44	PF14_0200	hypothetical protein	4.52	Yes
45	PFL1545c	chaperonin cpn60	4.39	
46	PF11_0077	hypothetical protein	3.96	
47	MAL8P1.17	disulfide isomerase precursor, putative	3.96	
48	PF14_0570	hypothetical protein, conserved	3.96	Yes
49	PFE1155c	mitochondrial processing peptidase alpha subunit, putative	3.68	
50	PF14_0309	protein-L-isoaspartate O-methyltransferase beta-aspartate	3.68	Yes
51	PFC0955w	ATP-dependent RNA helicase	3.38	
52	PFI0490c	hypothetical protein	3.38	Yes
53	MAL8P1.157	hypothetical protein	3.38	
54	MAL13P1.138	hypothetical protein	3.38	Yes
55	PF14_0255	hypothetical protein	3.38	

56	PF13_0242	isocitrate dehyc rsor	3.38	Yes
57	PFE1320w	hypothetical protein	3.38	
58	PFL2245w	hypothetical protein	3.38	
59	PFI0670w	hypothetical protein, conserved	3.38	
60	PF14_0354	hypothetical protein	3.38	
61	PFB0215c	3'-5' exonuclease, putative	3.38	
62	PF14_0101	hypothetical protein	3.38	Yes
63	PFL0660w	dynein light chain 1, putative	3.38	
64	PF14_0112	POM1, putative	3.38	
65	PF14_0348	ATP-dependent Clp protease proteolytic subunit, putative	3.38	Yes
66	PF13_0322	falcilysin	3.38	
67	PF14_0192	glutathione reductase	3.38	Yes
68	PF10_0235	hypothetical protein	3.38	
69	PFE0675c	deoxyribodipyrimidine photolyase (photoreactivating enzyme, DNA	3.38	Yes
70	PFL1070c	endoplasmin homolog precursor, putative	3.38	
71	PFC0165w	hypothetical protein, conserved	3.38	
72	PF13_0117	hypothetical protein, conserved	3.38	
73	PF14_0318	hypothetical protein	3.34	
74	PFE0645w	hypothetical protein	3.34	
75	PFI1120c	hypothetical protein	3.34	
76	PF08_0010	hypothetical protein	3.34	
77	PF10_0234	hypothetical protein	3.34	
78	MAL13P1.107	hypothetical protein	3.34	
79	PF13_0077	DEAD box helicase, putative	3.34	
80	MAL13P1.180	hypothetical protein	3.34	Yes
81	PF11_0365	hypothetical protein	3.34	
82	PF14_0394	hypothetical protein	3.34	
83	MAL13P1.295	hypothetical protein	3.34	
84	PF14_0014	hypothetical protein	3.34	Yes
85	PF14_0471	hypothetical protein	3.34	
86	MAL13P1.90	hypothetical protein	3.34	
87	PF11_0219	hypothetical protein	3.34	
88	PFA0615w	hypothetical protein	3.34	
89	PFF0115c	elongation factor G, putative	3.34	
90	PFA0195w	hypothetical protein	3.34	Yes
91	PFA0175w	hypothetical protein	3.34	
92	PFL0485w	hypothetical protein	3.34	
93	PF14_0310	hypothetical protein	3.34	
94	PFI0610w	hypothetical protein	3.34	
95	MAL7P1.111	hypothetical protein	3.34	
96	PF11_0054	hypothetical protein	3.34	
97	PFE0310c	hypothetical protein	3.34	Yes
98	PF10_0226	hypothetical protein, conserved	3.34	
99	PF08_0046	hypothetical protein	3.34	
100	PFL0965c	hypothetical protein	3.34	
101	MAL13P1.332	hypothetical protein	3.34	Yes
102	PFF0655c	adapter-related protein, putative	3.34	
103	PF14_0176	hypothetical protein	3.34	
104	MAL8P1.55	hypothetical protein	3.34	
105	MAL13P1.127	hypothetical protein	3.34	
106	PFF0555w	hypothetical protein	3.34	
107	MAL8P1.11	hypothetical protein	3.34	
108	MAL8P1.86	hypothetical protein	3.34	Yes
109	MAL13P1.266	hypothetical protein	3.34	
110	PFL0605c	hypothetical protein	3.34	
111	PF13_0192	hypothetical protein	3.34	Yes
112	PF11_0248	hypothetical protein	3.34	
113	PFB0185w	hypothetical protein, conserved	3.34	
114	MAL13P1.325	hypothetical protein	3.34	
115	PF08_0067	hypothetical protein	3.34	
116	PFL1675c	hypothetical protein	3.34	
117	PFC0230c	hypothetical protein, conserved	3.34	
118	PFA0460c	tubulin-specific chaperone a, putative	3.34	
119	PF14_0306	hypothetical protein	3.34	
120	PF13_0134	hypothetical protein	3.34	
121	MAL7P1.114	P36-like protein homologue, putative	3.34	
122	PFI0585c	hypothetical protein	3.34	
123	PF14_0253	hypothetical protein	3.34	

124	PF13_0080	hypothetical pr	3.34	Yes
125	PFF0225w	DNA helicase, putative	3.34	
126	PFL1275c	hypothetical protein	3.34	
127	PF14_0498	hypothetical protein	3.34	Yes
128	PFF1175c	hypothetical protein, conserved	3.34	
129	PFF0770c	hypothetical protein with PP2C domain	3.34	
130	PFF1395c	glutamyl-tRNA(Gln) amidotransferase subunit B, putative	3.34	Yes
131	MAL7P1.157	hypothetical protein	3.34	
132	PFF0935c	hypothetical protein	3.34	Yes
133	PFF0400w	hypothetical protein	3.34	
134	PF14_0356	hypothetical protein	3.34	
135	PF14_0300	syntaxin, putative	3.34	
136	MAL7P1.74	hypothetical protein, conserved	3.34	
137	MAL13P1.390	#N/A	3.34	
138	PFF1140c	ATP-dependent DEAD box helicase, putative	3.34	
139	PF10_0032	hypothetical protein	3.34	
140	PF14_0186	hypothetical protein	3.34	Yes
141	PF14_0430	hypothetical protein	3.34	Yes
142	PFL0095c	hypothetical protein	3.34	
143	PF08_0080	hypothetical protein	3.34	
144	PFB0600c	hypothetical protein	3.34	Yes
145	PF13_0241	hypothetical protein	3.34	Yes
146	PF11_0258	co-chaperone GrpE, putative	3.00	
147	PFB0685c	acyl-CoA synthetase, PfACS9	3.00	

Nr	PlasmoDB ID	Name	Score	Present in dataset
		DHPS/HPPK interactome		
1	PF13_0140	dihydrofolate synthase/folylpolyglutamate synthase	10.32	Yes
2	PFL0740c	10 kd chaperonin, putative	8.31	
3	PF11_0258	co-chaperone GrpE, putative	8.31	
4	PF13_0180	chaperonin, putative	8.31	
5	PF08_0006	prohibitin, putative	7.98	
6	PFL1475w	sun-family protein, putative	7.98	Yes
7	PF13_0234	phosphoenolpyruvate carboxykinase	5.96	
8	PF11_0188	heat shock protein 90, putative	5.96	Yes
9	PF14_0656	U2 snRNP auxiliary factor, putative	5.96	
10	PF14_0242	arginine n-methyltransferase, putative	5.96	
11	PFB0953w	hypothetical protein	5.90	Yes
12	MAL7P1.209	#N/A	5.90	
13	PFF0945c	bi-functional enzyme: long-chain fatty- acid Co-A ligase and oxalyl Co-A	5.90	
14	PFE0060w	hypothetical protein	5.90	
15	PF11_0076	hypothetical protein	5.90	
16	PFF0775w	pyridoxal kinase-like protein, putative	5.90	
17	PF10_0013	hypothetical protein	5.90	
18	MAL8P1.124	hypothetical protein	5.90	
19	PF14_0705	hypothetical protein	5.90	Yes
20	PFE1230c	hypothetical protein, conserved	5.90	
21	PF13_0300	mitochondrial inner membrane translocase, putative	5.90	
22	MAL8P1.15	hypothetical protein	5.90	
23	PFE1245w	zinc finger protein, putative	5.90	
24	PF11_0511	hypothetical protein	5.90	
25	PFC0790w	hypothetical protein	5.90	
26	PF13_0015	hypothetical protein	5.90	
27	PFA0160c	hypothetical protein	5.90	
28	MAL13P1.73	hypothetical protein	5.90	
29	PF14_0674	hypothetical protein	5.90	
30	MAL13P1.318	hypothetical protein	5.90	
31	PFB0525w	asparagine -- tRNA ligase, putative	4.71	
32	PFL1210w	hypothetical protein	4.71	
33	PF07_0079	60S ribosomal protein L11a, putative	4.71	
34	PFL1425w	t-complex protein 1, gamma subunit, putative	4.71	
35	MAL13P1.284	pyrroline carboxylate reductase	4.71	
36	PFI1100w	Para-aminobenzoic acid synthetase	4.71	
37	PFE0475w	asparagine -- t RNA ligase, putative	4.71	
38	PF14_0370	RNA helicase, putative	4.71	
39	PFC0285c	T-complex protein beta subunit, putative	4.71	
40	PFL0705c	adrenodoxin-type ferredoxin, putative	4.52	

41	PFB0545c	ribosomal protei	4.52	
42	PF14_0023	hypothetical protein, conserved	4.52	
43	PF11_0339	hypothetical protein	4.52	
44	PFA0145c	aspartyl-tRNA synthetase	4.52	
45	PF14_0517	peptidase, putative	4.52	
46	PF14_0230	Ribosomal protein family L5, putative	4.52	
47	PF13_0345	aminomethyltransferase, mitochondrial precursor	4.52	
48	PFB0595w	heat shock 40 kDa protein, putative	4.52	
49	PFD0755c	adenylate kinase 1	4.52	
50	PF11_0077	hypothetical protein	4.52	
51	PF08_0018	translation initiation factor-like protein	4.52	
52	PFL2395c	dimethyladenosine transferase, putative	4.52	
53	PFL1150c	ribosomal protein L24, putative	4.52	Yes
54	PF10_0121	hypoxanthine phosphoribosyltransferase	4.52	Yes
55	PF10_0325	hypothetical protein, conserved	4.52	
56	PF14_0668	hypothetical protein	4.39	
57	PF14_0036	acid phosphatase, putative	4.39	
58	PFB0115w	hypothetical protein	4.39	Yes
59	PF14_0297	ecto-nucleoside triphosphate diphosphohydrolase 1, putative	4.39	Yes
60	PFE0605c	glutathione synthetase	4.39	
61	PFL0255c	uga suppressor tRNA-associated antigenic protein, putative	4.39	
62	PFL1310c	ATP-dependent RNA helicase, putative	4.39	
63	PF11_0264	DNA-dependent RNA polymerase	4.39	
64	PF11_0351	heat shock protein hsp70 homologue	4.39	
65	PF13_0243	hypothetical protein	4.39	
66	PFI1570c	aminopeptidase, putative	4.39	
67	PF14_0022	exopolyphosphatase, putative	4.39	
68	PFE0630c	orotate phosphoribosyltransferase, putative	3.38	
69	MAL13P1.54	hypothetical protein, conserved	3.38	
70	PF14_0378	triose-phosphate isomerase	3.38	Yes
71	PF10_0153	hsp60	3.38	
72	PFC0271c	glutaredoxin, putative	3.38	
73	PF11_0165	falcipain 2 precursor	3.38	
74	PFD0980w	holo-(acyl-carrier protein) synthase, putative	3.38	
75	PFB0200c	aspartate aminotransferase, putative	3.38	
76	PFE1080w	ribosomal large subunit pseudouridylate synthase, putative	3.38	
77	PF14_0381	delta-aminolevulinic acid dehydratase	3.38	
78	PF11_0507	antigen 332, putative	3.38	
79	PF14_0147	ATP-dependent protease, putative	3.38	
80	PFC0550w	hypothetical protein	3.38	
81	PF14_0166	lysine -- tRNA ligase, putative	3.38	
82	PF13_0141	L-lactate dehydrogenase	3.38	Yes
83	PFD0555c	hypothetical protein	3.38	
84	PF11_0301	spermidine synthase	3.38	
85	PFC0205c	PfGLP-1, 1-cys-glutaredoxin-like protein-1	3.38	
86	PFL1710c	tetQ family GTPase, putative	3.38	
87	PF10_0152	hypothetical protein	3.38	
88	PFL0690c	hypothetical protein conserved	3.38	
89	PF07_0100	hypothetical protein	3.38	
90	PF14_0341	glucose-6-phosphate isomerase	3.38	
91	PF14_0096	hypothetical protein	3.38	
92	PF14_0209	hypothetical protein	3.34	
93	PF10_0064	hypothetical protein	3.34	
94	MAL13P1.221	aspartate carbamoyltransferase	3.34	
95	PFI1750c	hypothetical protein	3.34	
96	PFF0105w	MYND finger domain protein	3.34	
97	PF13_0029	hypothetical protein	3.34	
98	PFF1330c	mitochondrial import inner membrane translocase subunit, putative	3.34	
99	PF08_0029	hypothetical protein	3.34	Yes
100	PFD0365c	hypothetical protein	3.34	
101	PF14_0410	hypothetical protein	3.34	
102	PFE0295w	hypothetical protein	3.34	
103	PF11_0319	hypothetical protein	3.34	Yes
104	PF13_0183	hypothetical protein	3.34	
105	PFB0470w	hypothetical protein	3.34	
106	PF14_0037	hypothetical protein	3.34	
107	PFA0630c	hypothetical protein	3.34	
108	PFF0820w	hypothetical protein	3.34	

109	PFL2355w	hypothetical pro	3.34	
110	PFB0620w	hypothetical protein	3.34	
111	PFB0560w	hypothetical protein	3.34	
112	PFF0120w	geranylgeranyltransferase, putative	3.34	
113	PF11_0404	malaria antigen	3.34	Yes
114	PFE1605w	DNAJ protein	3.34	
115	PF13_0098	hypothetical protein	3.34	
116	PF14_0312	hypothetical protein	3.34	
117	PF08_0051	hypothetical protein	3.34	Yes
118	PFE0670w	hypothetical protein	3.34	
119	MAL8P1.32	nucleoside transporter, putative	3.34	Yes
120	PFI1415w	Serine/Threonine protein kinase, putative	3.34	
121	PF13_0191	hypothetical protein	3.34	
122	MAL13P1.46	hypothetical protein	3.34	
123	PFI1615c	#N/A	3.34	
124	PF14_0180	hypothetical protein	3.34	
125	PFB0921c	hypothetical protein	3.34	
126	PF14_0687	hypothetical protein	3.34	
127	PFF1335c	4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosynthesis enzyme	3.34	
128	PFI0430c	hypothetical protein	3.34	
129	PFA0100c	hypothetical protein	3.34	
130	MAL13P1.333	hypothetical protein	3.34	
131	PFE0800w	hypothetical protein	3.34	
132	PFB0110w	hypothetical protein	3.34	
133	PF13_0281	hypothetical protein	3.34	
134	PFC0166w	#N/A	3.34	
135	PF13_0101	hypothetical protein	3.34	
136	PFF0590c	homologue of human HSPC025	3.34	
137	PF13_0252	nucleoside transporter 1	3.34	
138	PF11_0247	hypothetical protein	3.34	
139	PFC0085c	hypothetical protein, conserved	3.34	Yes
140	PF11_0254	hypothetical protein	3.34	
141	PF10_0324	hypothetical protein	3.34	
142	MAL7P1.225	#N/A	3.34	
143	PFF0435w	ornithine aminotransferase	3.34	
144	PFL0640w	hypothetical protein	3.34	
145	PF13_0097	hypothetical protein	3.34	Yes
146	PFB0930w	hypothetical protein	3.34	
147	MAL13P1.352	hypothetical protein	3.34	
148	PFF1400w	hypothetical protein	3.34	
149	PF07_0075	hypothetical protein, expressed	3.34	
150	PF11_0508	hypothetical protein	3.34	Yes
151	PF11_0506	hypothetical protein	3.34	
152	MAL7P1.31	hypothetical protein	3.34	
153	PF13_0071	hypothetical protein	3.34	
154	PF13_0099	hypothetical protein	3.34	
155	MAL7P1.201	#N/A	3.34	
156	PF10_0265	hypothetical protein	3.34	
157	PF10_0029	hypothetical protein	3.34	
158	PF13_0112	hypothetical protein	3.34	
159	PFE0595w	hypothetical protein	3.34	
160	PFA0255c	hypothetical protein	3.34	
161	MAL13P1.274	serine/threonine protein phosphatase pfPp5	3.34	
162	PFI1385c	hypothetical protein	3.34	
163	PF14_0308	hypothetical protein	3.34	
164	PFE1615c	hypothetical protein	3.34	

Nr	PlasmoDB ID	Name	Score	Present in dataset
		AdoMet synthase interactome		
1	PFE1345c	minichromosome maintenance protein 3, putative	11.69	Yes
2	PFB0895c	replication factor C subunit 1, putative	11.69	Yes
3	PFL0835w	GTP-binding protein, putative	8.31	
4	PFI1575c	peptide release factor, putative	8.31	Yes
5	PF13_0095	DNA replication licensing factor mcm4-related	8.31	Yes
6	PF14_0177	DNA replication licensing factor MCM2	8.31	Yes
7	PFB0795w	ATP synthase F1, alpha subunit, putative	8.31	

8	PFE0450w	chromosome cc	7.98	Yes
9	PFD0420c	flap exonuclease, putative	7.98	
10	MAL13P1.96	chromosome segregation protein, putative	7.98	
11	PFD0590c	DNA polymerase alpha	7.98	Yes
12	PFC0745c	proteasome component C8, putative	6.62	
13	PF13_0061	ATP synthase gamma chain, mitochondrial precursor, putative	6.62	
14	PF07_0023	DNA replication licensing factor mcm7 homologue, putative	6.62	Yes
15	MAL8P1.128	proteasome subunit alpha, putative	6.62	
16	PF13_0353	NADH-cytochrome b5 reductase, putative	5.96	Yes
17	MAL8P1.101	hypothetical protein	5.96	Yes
18	PF14_0063	ATP-dependent Clp protease, putative	5.96	
19	PFI0240c	E1-E2_ATPase/hydrolase, putative	5.96	Yes
20	PF11_0249	hypothetical protein	5.96	
21	MAL13P1.244	TBC domain protein, putative	5.96	
22	PFI0530c	DNA primase, large subunit, putative	5.96	Yes
23	PF14_0309	protein-L-isoaspartate O-methyltransferase beta-aspartate	5.96	Yes
24	PFB0750w	vacuolar protein-sorting protein VPS45, putative	5.96	
25	PFB0500c	rab5 protein, putative	5.96	Yes
26	PFI1240c	prolyl-t-RNA synthase, putative	5.96	Yes
27	PF14_0132	ribosomal protein S9, putative	5.96	
28	PFA0345w	centrin, putative	5.96	
29	MAL13P1.196	protein kinase, putative	5.96	
30	MAL8P1.138	hypothetical protein, conserved	5.96	
31	PF11_0352	protein disulfide isomerase related protein	5.96	Yes
32	PFF1190c	N-acetylglucosaminyl- phosphatidylinositol de-n-acetylase, putative	5.90	
33	MAL7P1.203	#N/A	5.90	
34	PFE0240c	hypothetical protein	5.90	Yes
35	PF11_0420	hypothetical protein	5.90	
36	MAL13P1.147	hypothetical protein	5.90	
37	MAL13P1.194	hypothetical protein	5.90	
38	PF11_0425	hypothetical protein	5.90	Yes
39	PFI0665w	hypothetical protein	5.90	
40	MAL13P1.103	hypothetical protein	5.90	Yes
41	MAL13P1.229	hypothetical protein	5.90	
42	PF13_0131	hypothetical protein	5.90	
43	PFD0465c	hypothetical protein, conserved	5.90	
44	PFB0835c	hypothetical protein	5.90	Yes
45	PF14_0351	hypothetical protein	5.90	
46	PF10_0133	hypothetical protein	5.90	
47	PF14_0105	hypothetical protein	5.90	Yes
48	PFL1430c	hypothetical protein	5.90	
49	MAL13P1.217	hypothetical protein	5.90	
50	PFD0175c	hypothetical protein	5.90	
51	PF11_0459	hypothetical protein	5.90	
52	PFB0530c	hypothetical protein	5.90	Yes
53	PF14_0138	hypothetical protein	5.90	Yes
54	PF10_0228	hypothetical protein, conserved	5.90	
55	PFB0170w	hypothetical protein, conserved	5.90	
56	MAL13P1.123	hypothetical protein	5.90	
57	PF10_0246	hypothetical protein	5.90	Yes
58	PFF1470c	DNA polymerase epsilon, catalytic subunit a, putative	5.90	Yes
59	PFF1225c	DNA polymerase 1, putative	5.90	Yes
60	PFC0320w	hypothetical protein	5.90	
61	PFB0590w	hypothetical protein	5.90	Yes
62	PF10_0249	hypothetical protein	5.90	
63	MAL7P1.77	hypothetical protein	5.90	Yes
64	PFE0760w	hypothetical protein	5.90	
65	PFL0265w	hypothetical protein	5.90	
66	PFB0535w	hypothetical protein	5.90	Yes
67	MAL13P1.161	unknown	5.90	
68	PFC0275w	FAD-dependent glycerol-3-phosphate dehydrogenase, putative	4.71	Yes
69	PFI0380c	formylmethionine deformylase, putative	4.71	Yes
70	MAL8P1.140	methionine aminopeptidase, putative	4.71	Yes
71	PF13_0291	replication licensing factor, putative	4.71	Yes
72	PF11_0317	structural maintenance of chromosome protein, putative	4.71	
73	PF13_0328	proliferating cell nuclear antigen	4.71	Yes
74	PF13_0251	DNA topoisomerase III, putative	4.71	
75	PFL0150w	origin recognition complex 1 protein	4.71	Yes

76	PF11_0087	Rad51 homolog	4.71	Yes
77	PFB0840w	replication factor C, subunit 2	4.71	Yes
78	PF14_0053	ribonucleotide reductase small subunit	4.52	Yes
79	PF11_0427	dolichyl-phosphate b-D-mannosyltransferase, putative	4.52	
80	PF11_0348	hypothetical protein	4.52	
81	MAL8P1.17	disulfide isomerase precursor, putative	4.52	
82	PF10_0362	DNA polymerase zeta catalytic subunit, putative	4.52	
83	PF11_0099	heat shock protein DnaJ homologue Pfj2	4.52	
84	MAL13P1.47	mitochondrial ATP synthase delta subunit, putative	4.52	
85	PF07_0105	exonuclease i, putative	4.52	
86	PFI1170c	Thioredoxin reductase	4.52	Yes
87	PF14_0064	vacuolar protein sorting 29, putative	4.52	
88	PFB0385w	acyl carrier protein, putative	4.52	Yes
89	PFL0595c	glutathione peroxidase	4.52	Yes
90	PFD0685c	chromosome associated protein, putative	4.52	Yes
91	PFD0790c	DNA replication licensing factor, putative	4.52	
92	PF13_0272	thioredoxin-related protein, putative	4.52	
93	MAL8P1.142	proteasome beta-subunit	4.52	
94	PF14_0695	DNA-directed RNA polymerase, alpha subunit, truncated, putative	4.52	
95	PFC0170c	dihydrolipoamide acyltransferase, putative	4.52	
96	PF14_0060	hypothetical protein	4.39	
97	PFL0090c	hypothetical protein	4.39	
98	PF14_0641	1-deoxy-D-xylulose 5-phosphate reductoisomerase	4.39	
99	PFB0365w	hypothetical protein, conserved	4.39	Yes
100	PFD0595w	hypothetical protein	4.39	
101	PFD0585c	hypothetical protein	4.39	
102	PF11_0112	vacuolar sorting protein 35, putative	4.39	
103	PF10_0140	hypothetical protein	4.39	
104	PF10_0360	hypothetical protein	4.39	
105	PFI0135c	papain family cysteine protease, putative	4.39	Yes
106	PF14_0252	hypothetical protein	4.39	
107	MAL13P1.105	hypothetical protein	4.39	
108	PFC0525c	glycogen synthase kinase, putative	4.39	
109	PF11_0098	endoplasmic reticulum-resident calcium binding protein	4.39	Yes
110	MAL13P1.42	hypothetical protein	4.39	Yes
111	MAL7P1.132	hypothetical protein	4.39	Yes
112	PF13_0189	hypothetical protein	4.39	Yes
113	PFE0090w	hypothetical protein	4.39	
114	PF14_0148	uracil-DNA glycosylase, putative	4.39	Yes
115	PFE1225w	50S ribosomal subunit protein L12, putative	4.39	
116	PF08_0014	plastid 50S ribosomal protein, putative	4.39	
117	PFC0510w	zinc finger protein, putative	4.39	
118	PF11_0131	hypothetical protein	3.96	
119	PF11_0282	deoxyuridine 5'-triphosphate nucleotidohydrolase, putative	3.38	Yes
120	PFE0270c	DNA repair protein, putative	3.38	Yes
121	PFI1360c	serine/threonine protein phosphatase, putative	3.38	
122	PF08_0126	DNA repair protein rad54, putative	3.38	Yes
123	PFL1180w	Chromatin assembly protein (ASF1), putative	3.38	Yes
124	PF13_0149	chromatin assembly factor 1 subunit, putative	3.38	Yes
125	PF14_0088	hypothetical protein	3.38	
126	PF11_0386	30S ribosomal protein S14, putative	3.38	Yes
127	PF14_0323	calmodulin	3.38	
128	MAL13P1.202	hypothetical protein	3.38	
129	PFI0155c	ras family GTP-ase, putative	3.38	Yes
130	PFC0310c	ATP-dependent CLP protease, putative	3.38	
131	PFC0710w	inorganic pyrophosphatase, putative	3.38	Yes
132	PFL1370w	NIMA-related protein kinase (Pfnek-1)	3.38	
133	PFL0630w	iron-sulfur subunit of succinate dehydrogenase	3.38	
134	PFA0225w	LytB protein	3.38	
135	PF11_0227	hypothetical protein	3.38	
136	PF14_0254	DNA mismatch repair protein Msh2p, putative	3.38	Yes
137	PFD0810w	small GTP-binding protein sar1	3.38	
138	PF07_0078	hypothetical protein, conserved	3.38	Yes
139	PF11_0061	histone H4, putative	3.38	Yes
140	PFC0250c	AP endonuclease (DNA-(apurinic or apyrimidinic site) lyase), putative	3.38	Yes
141	PF11_0145	glyoxalase I, putative	3.38	
142	PFC0955w	ATP-dependent RNA helicase	3.38	
143	PFA0545c	replication factor c protein, putative	3.38	

144	PF14_0142	serine/threonin	3.38	Yes
145	PFE0690c	Rab1 protein	3.38	Yes
146	PF11_0488	hypothetical protein	3.38	
147	PF07_0064	hypothetical protein	3.38	
148	MAL13P1.167	signal peptidase, putative	3.38	
149	PF10_0154	ribonucleotide reductase small subunit, putative	3.38	Yes
150	PF13_0349	nucleoside diphosphate kinase b; putative	3.38	Yes
151	PFB0220w	UbiE-like methlytransferase, putative	3.38	Yes
152	MAL13P1.141	hypothetical protein	3.34	
153	PFF0670w	hypothetical protein	3.34	
154	PFA0250w	hypothetical protein	3.34	
155	MAL13P1.124	hypothetical protein	3.34	
156	PF13_0249	hypothetical protein	3.34	
157	PF14_0488	hypothetical protein	3.34	Yes
158	PF10_0291	hypothetical protein	3.34	Yes
159	PFE0710w	hypothetical protein	3.34	
160	PFI0990c	hypothetical protein	3.34	
161	PF14_0435	hypothetical protein	3.34	
162	PFL0085c	hypothetical protein	3.34	
163	PFC1035w	hypothetical protein	3.34	
164	PF13_0336	hypothetical protein	3.34	
165	PFD0330w	hypothetical protein	3.34	
166	PFF1485w	hypothetical protein	3.34	
167	PFL2300w	hypothetical protein	3.34	
168	MAL13P1.336	hypothetical protein	3.34	
169	PF14_0153	hypothetical protein	3.34	
170	PF11_0448	hypothetical protein	3.34	
171	PF10_0236	hypothetical protein	3.34	
172	PFL0680c	hypothetical protein	3.34	
173	MAL13P1.307	hypothetical protein	3.34	Yes
174	PF11_0195	hypothetical protein	3.34	
175	MAL7P1.111	hypothetical protein	3.34	
176	PF13_0312	hypothetical protein	3.34	
177	PF11_0146	hypothetical protein	3.34	Yes
178	PFE0265c	hypothetical protein	3.34	Yes
179	PF14_0310	hypothetical protein	3.34	
180	PFI1665w	uncharacterised trophozoite protein	3.34	Yes
181	PFD0335c	hypothetical protein	3.34	
182	PF10_0164	hypothetical protein	3.34	
183	PF14_0445	hypothetical protein	3.34	
184	PF14_0666	hypothetical protein	3.34	
185	PFC0315c	hypothetical protein	3.34	Yes
186	PF11_0484	hypothetical protein	3.34	
187	PF10_0207	hypothetical protein	3.34	
188	PFF0940c	cell division cycle protein 48 homologue, putative	3.34	
189	PF14_0380	hypothetical protein	3.34	
190	PF11_0333	hypothetical protein	3.34	
191	PF13_0246	hypothetical protein	3.34	
192	PF11_0054	hypothetical protein	3.34	
193	PFE0490w	hypothetical protein	3.34	
194	PF13_0338	hypothetical protein	3.34	Yes
195	MAL13P1.57	hypothetical protein	3.34	Yes
196	MAL7P1.128	hypothetical protein	3.34	
197	PFD0655c	ubiquitin carboxyl-terminal hydrolase a, putative	3.34	
198	PFL2360w	hypothetical protein	3.34	
199	MAL13P1.311	hypothetical protein	3.34	
200	PF10_0050	hypothetical protein	3.34	
201	PF14_0444	hypothetical protein	3.34	
202	PFF0765c	hypothetical protein	3.34	
203	PFD0760c	hypothetical protein	3.34	
204	MAL13P1.160	unknown	3.34	
205	PF11_0075	hypothetical protein	3.34	
206	PFF0740c	hypothetical protein	3.34	
207	PF14_0270	ribosomal protein L15, putative	3.34	
208	PF14_0665	hypothetical protein	3.34	
209	PF08_0010	hypothetical protein	3.34	
210	PF14_0613	hypothetical protein	3.34	
211	PFI0565w	hypothetical protein	3.34	

212	PFF0650w	ribosomal prote	3.34	Yes
213	PFF0680c	thiamin-phosphate pyrophosphorylase, putative	3.34	Yes
214	PF14_0268	hypothetical protein	3.34	
215	PF10_0191	hypothetical protein	3.34	
216	PFE1025c	hypothetical protein	3.34	
217	PFL0615w	hypothetical protein	3.34	
218	PF14_0315	hypothetical protein	3.34	
219	PF11_0451	hypothetical protein	3.34	
220	PF14_0300	syntaxin, putative	3.34	
221	MAL13P1.131	hypothetical protein	3.34	
222	PFL0375w	hypothetical protein	3.34	
223	PFD0805w	prohibitin-like protein, putative	3.34	
224	MAL8P1.84	hypothetical protein	3.34	
225	PF14_0617	hypothetical protein	3.34	Yes
226	PFA0370w	hypothetical protein	3.34	
227	PFI0405w	hypothetical protein	3.34	Yes
228	PF14_0306	hypothetical protein	3.34	
229	PF13_0154	hypothetical protein	3.34	
230	MAL7P1.102	hypothetical protein	3.34	Yes
231	PFF0330w	coatomer alpha subunit, putative	3.34	
232	PFI0830c	hypothetical protein	3.34	
233	PFE1330c	hypothetical protein	3.34	
234	PF13_0333	hypothetical protein	3.34	
235	PFD0915w	hypothetical protein	3.34	
236	PFF0665c	syntaxin binding protein, putative	3.34	
237	PFE1165c	hypothetical protein	3.34	
238	PF14_0245	hypothetical protein	3.34	
239	PFI1525w	hypothetical protein	3.34	
240	PFL2045w	hypothetical protein	3.34	
241	PFI0160w	hypothetical protein	3.34	
242	PFE1280w	hypothetical protein	3.34	Yes
243	PFA0405w	hypothetical protein	3.34	
244	PFD0170c	hypothetical protein	3.34	
245	PF13_0155	hypothetical protein	3.34	
246	MAL7P1.74	hypothetical protein, conserved	3.34	
247	PF11_0440	hypothetical protein	3.34	
248	PF13_0200	hypothetical protein	3.34	Yes
249	PFC0500w	hypothetical protein	3.34	
250	PF10_0188	hypothetical protein	3.34	Yes
251	PF13_0188	hypothetical protein	3.34	
252	PF14_0169	hypothetical protein	3.34	
253	PFL0720w	hypothetical protein	3.34	
254	PF11_0324	hypothetical protein	3.34	
255	PF11_0482	hypothetical protein	3.34	
256	PFL1330c	hypothetical protein	3.34	Yes
257	PF11_0435	hypothetical protein	3.34	

Appendix D

Transcripts shared between the AdoMetDC inhibited transcriptome dataset, SpdS inhibition and the co-inhibition of AdoMetDC/ODC

Totall	Nr	PlasmoDB ID	Product Description	Fold change		
				AdoMetDC	A/O	SpdS
			DNA metabolism			
1	1	PF10_0154	ribonucleotide reductase small subunit, putative	-5.4	-1.5	-4.2
2	2	PF11_0087	Rad51 homolog	-1.7	-1.6	-3.5
3	3	PF11_0117	replication factor C subunit 5, putative	-1.8	-1.8	-4.5
4	4	PF11_0241	Myb-like DNA-binding domain, putative	1.7	1.8	2.1
5	5	PF11_0282	deoxyuridine 5'-triphosphate nucleotidohydrolase,	-6.3	-2.9	-2.8
6	6	PF13_0095	DNA replication licensing factor MCM4-related	-3.1	-1.4	
7	7	PF13_0291	replication licensing factor, putative	-2.5	-1.2	-3.5
8	8	PF13_0328	proliferating cell nuclear antigen	-5.7	-1.9	-4.2
9	9	PF14_0053	ribonucleotide reductase small subunit	-3.9	-1.4	-5.0
10	10	PF14_0254	DNA mismatch repair protein Msh2p, putative	-1.9	-1.4	-2.0
11	11	PF14_0366	small subunit DNA primase	-1.7		-2.1
12	12	PF14_0374	CCAAT-binding transcription factor, putative	1.7	2.1	
13	13	PFB0840w	replication factor C, subunit 2	-3.4		-2.8
14	14	PFB0895c	replication factor C subunit 1, putative	-1.9	-1.2	-2.7
15	15	PFD0685c	chromosome associated protein, putative	-2.0	-2.0	-2.0
16	16	PFE0215w	ATP-dependent helicase, putative	-1.7		-2.6
17	17	PFE0450w	chromosome condensation protein, putative	-2.6		-2.5
18	18	PFE0675c	deoxyribodipyrimidine photolyase (photoreactivating	-2.8	-1.5	-4.3
19	19	PFE1345c	minichromosome maintenance protein 3, putative	-2.3		-2.0
20	20	PFF1470c	DNA polymerase epsilon, catalytic subunit a, putative	-1.8	-1.5	
21	21	PFI0530c	DNA primase large subunit, putative	-3.8	-1.2	
22	22	PFL0580w	DNA replication licensing factor MCM5, putative	-3.7		-3.5
23	23	PFL1180w	chromatin assembly protein (ASF1), putative	-2.2		-2.4
24	24	PFL1285c	proliferating cell nuclear antigen 2	-2.7		-2.1
25	25	PFL1655c	DNA polymerase epsilon subunit B, putative	-2.1	-2.2	-2.2
26	26	PFL2005w	replication factor C subunit 4	-4.0		-3.8
			Proteolysis			
27	1	MAL8P1.113	Peptidase family C50, putative	-1.7	-1.6	
28	2	MAL8P1.99	GTPase, putative	-2.1	-2.2	-3.6
29	3	PF14_0348	ATP-dependent Clp protease proteolytic subunit,	-2.0	-1.6	
30	4	PFI0135c	serine repeat antigen 9 (SERA-9)	-5.6	-1.7	-4.0
31	5	PFL1465c	Heat shock protein hslv	-2.0		-2.5
			Translation			
32	1	MAL8P1.110	apicoplast ribosomal protein L33 precursor, putative	-1.9		-2.9
33	2	PF11_0113	mitochondrial ribosomal protein L11 precursor, putative	-2.0		-2.1
34	3	PF11_0181	tyrosine-tRNA ligase, putative	-1.9	-1.4	
35	4	PF11_0182	conserved Plasmodium protein, unknown function	-1.9	-1.9	
36	5	PF11_0386	apicoplast ribosomal protein S14p/S29e precursor,	-2.0		-2.6
37	6	PF14_0606	mitochondrial ribosomal protein S6-2 precursor,	-2.2	-1.7	
38	7	PF14_0709	mitochondrial ribosomal protein L20 precursor, putative	-2.1	-1.9	-2.4
39	8	PFC0675c	mitochondrial ribosomal protein L29/L47 precursor,	-1.9		-2.4
40	9	PFD0780w	glutamyl-tRNA(Gln) amidotransferase subunit A,	-2.0		-3.9
41	10	PFF0495w	mitochondrial ribosomal protein L19 precursor, putative	-2.0		-2.0
42	11	PFF0650w	apicoplast ribosomal protein L18 precursor, putative	-1.9		-2.6
43	12	PFI0380c	formylmethionine deformylase, putative	-1.8		-2.2
44	13	PFI0890c	organelle ribosomal protein L3 precursor, putative	-2.2	-1.6	-2.7
45	14	PFI1240c	prolyl-t-RNA synthase, putative	-2.8	-1.8	
46	15	PFI1585c	mitochondrial ribosomal protein S6 precursor, putative	-1.8	1.8	
47	16	PFL1895w	mitochondrial ribosomal protein L23 precursor, putative	-1.7		-3.0
			Phosphorylation			
48	1	PF13_0258	serine/threonine protein kinase	-2.5		2.2
49	2	PFA0130c	Serine/Threonine protein kinase, FIKK family, putative	2.3	1.8	
50	3	PFC0710w	inorganic pyrophosphatase, putative	-2.6		-2.2
51	4	PFC0755c	protein kinase, putative	-2.1		-2.1
52	5	PFD1165w	Serine/Threonine protein kinase, FIKK family	2.0	-2.0	

53	6	PFD1175w	Serine/Threonine protein kinase, FIKK family	2.4	1.7	2.5
54	7	PFF1370w	protein kinase PK4	1.7		2.0
55	8	PFL1110c	CAMP-dependent protein kinase regulatory subunit,	-2.1		-3.8
56	9	PFL1885c	calcium/calmodulin-dependent protein kinase 2	2.2	2.3	2.4
			Transport			
57	1	MAL13P1.23	CorA-like Mg2+ transporter protein, putative	1.8		2.0
58	2	MAL8P1.32	nucleoside transporter, putative	-2.8	-1.5	-3.0
59	3	PF07_0065	zinc transporter, putative	-4.8	-2.2	-3.4
60	4	PF14_0211	Ctr copper transporter domain containing protein,	-2.3		-3.4
61	5	PF14_0662	nucleoside transporter, putative	1.8	1.8	
62	6	PFA0590w	ABC transporter, (CT family), putative	-2.4	-1.7	
63	7	PFB0500c	Rab5a, GTPase	-1.7		-2.1
64	8	PFC0125w	ABC transporter, (TAP family), putative	-1.9	-1.9	-2.1
65	9	PFE0410w	triose phosphate transporter	-1.7	-1.9	-2.5
66	10	PFE1510c	triose phosphate transporter	-2.5		-3.2
67	11	PFI0240c	Cu2+ -transporting ATPase, Cu2+ transporter	-1.9		-4.4
68	12	PFI0300w	developmental protein, putative	-3.2		-2.7
69	13	PFL2220w	conserved Plasmodium protein, unknown function	1.7		3.3
			Polyamine methionine metabolism			
70	1	MAL13P1.214	phosphoethanolamine N-methyltransferase	-5.1	-2.7	-3.4
71	2	PF10_0289	adenosine deaminase, putative	-3.1	-2.4	-2.3
72	3	PF14_0309	protein-L-isoaspartate O-methyltransferase beta-	-3.9	-1.8	
73	4	PF14_0526	conserved Plasmodium protein, unknown function	-3.1	-2.1	-2.0
74	5	PFD0285c	lysine decarboxylase, putative	2.5	2.8	2.4
75	6	PFE0660c	purine nucleotide phosphorylase, putative	-3.0	-2.7	-3.6
76	7	PFE1050w	adenosylhomocysteinase(S-adenosyl-L-homocystein e	-2.1	-1.5	-1.0
77	8	PFI1090w	S-adenosylmethionine synthetase	-2.3	-1.5	-1.0
			Oxidative stress			
78	1	PF08_0131	1-cys peroxiredoxin	-2.7	-2.8	-4.5
79	2	PF14_0187	glutathione S-transferase	-1.8	-1.5	-2.1
80	3	PF14_0192	glutathione reductase	-2.2	-1.7	-2.6
81	4	PF13_0353	NADH-cytochrome B5 reductase, putative	-2.1		-2.4
82	5	PFI1170c	thioredoxin reductase	-1.9		-3.1
			Primary metabolism			
83	1	MAL8P1.81	Phosphopantothenoylcysteine decarboxylase, putative	1.9		3.1
84	2	PF07_0129	acyl-coA synthetase, PfACS5	-1.9	-1.6	-3.9
85	3	PF10_0016	acyl CoA binding protein, isoform 2, ACBP2	-3.0	-1.5	-6.3
86	4	PF10_0155	enolase	-2.7	-2.0	
87	5	PF10_0334	flavoprotein subunit of succinate dehydrogenase	-1.8		-3.1
88	6	PF11_0257	ethanolamine kinase, putative	-2.5	-1.4	-4.6
89	7	PF13_0121	dihydrolipamide succinyltransferase component of 2-	-2.6	-1.7	-2.5
90	8	PF13_0141	L-lactate dehydrogenase	-1.9	-1.5	-2.4
91	9	PF13_0242	isocitrate dehydrogenase (NADP), mitochondrial	-2.2		-2.1
92	10	PF13_0349	nucleoside diphosphate kinase b, putative	-3.5	-1.9	-4.4
93	11	PF14_0378	triosephosphate isomerase	-1.7	-1.1	
94	12	PFB0385w	apicoplast ACP	-2.6		-2.7
95	13	PFD0830w	bifunctional dihydrofolate reductase-thymidylate	-4.9	-1.6	-2.2
96	14	PFE0555w	stearoyl-CoA Delta 9 desaturase, putative	-3.6	-1.5	-2.9
97	15	PFF1300w	pyruvate kinase	-1.7	-1.5	-2.2
98	16	PF10_0084	tubulin beta chain, putative	-5.2	-1.3	-4.6
99	17	PF14_0314	chromatin assembly factor 1 P55 subunit, putative	2.0	2.4	
100	18	PFA0520c	chromatin assembly factor 1 protein WD40 domain,	-4.7	-1.6	
101	19	PFE0165w	actin-depolymerizing factor, putative	-2.2	-2.0	-2.5
102	20	PFI0180w	alpha tubulin	-7.3	-1.5	-4.5
103	21	PFI1565w	profilin, putative	-3.0	-2.0	-2.2
104	22	PFL0925w	formin 2, putative	2.0	1.9	
105	23	PFL2215w	actin I	-2.5		-2.3
			RNA metabolic process			
106	1	MAL13P1.303	polyadenylate-binding protein, putative	-4.1	-1.3	-3.1
107	2	MAL8P1.101	RNA binding protein, putative	-1.7		-2.8
108	3	PF08_0096	RNA helicase, putative	-1.7	-1.8	
109	4	PFF1425w	RNA binding protein, putative	-2.1		-2.8
110	5	PFL0465c	Zinc finger transcription factor (krox1)	1.8	2.0	
111	6	PFL2115c	glucose inhibited division protein A homologue, putative	-2.9	-1.3	
			Protein folding			
112	1	PFB0920w	DNAJ protein, putative	2.4		2.2
113	2	PFL2550w	DNAJ domain protein, putative	-2.0	-2.2	-2.2
			Signal transduction			

114	1	MAL13P1.165	GPI tran	-1.7		-2.0
115	2	MAL13P1.19	peptidase, putative	-2.4	-2.1	-1.0
116	3	PFE0690c	PfRab1a	-1.8	-3.2	-5.2
117	4	PFI0155c	PfRab7, GTPase	-1.7		-2.5
			Coenzyme metabolic process			
118	1	PF14_0200	pantothenate kinase, putative	-1.7		-2.2
119	2	PF14_0415	dephospho-CoA kinase, putative	-2.6	-1.4	-2.5
120	3	PF14_0570	pyridoxal 5'-phosphate synthase, putative	-2.3	-2.2	-2.5
121	4	PFL1725w	ATP synthase beta chain, mitochondrial precursor,	-2.1		-3.2
			Hydrolase activity			
122	1	MAL13P1.121	adenosine-diphosphatase	-1.8		-2.2
123	2	PF14_0015	aminopeptidase, putative	2.5	1.3	2.3
124	3	PF14_0017	lysophospholipase, putative	2.4		2.9
			Binding activity			
125	1	MAL13P1.122	SET domain protein, putative	1.7		3.1
126	2	PF07_0035	cg1 protein	-2.7		-2.3
127	3	PF14_0061	PPR repeat protein	-1.9	-1.6	-3.2
128	4	PF14_0257	conserved protein, unknown function	-2.9	-1.8	-2.4
129	5	PF14_0443	centrin-2	-4.9	-1.6	-2.0
130	6	PFD0440w	peptidase, M22 family, putative	-2.7	-1.8	-2.4
131	7	PFF1440w	SET domain protein, putative	1.9		2.1
132	8	PFI0235w	replication factor A-related protein, putative	-2.1	-1.8	-4.0
133	9	PFI0490c	ran-binding protein, putative	-1.7	-1.8	2.5
134	10	PFI0855w	conserved Plasmodium protein, unknown function	-2.0	-2.0	
			Host parasite			
135	1	MAL13P1.176	reticulocyte binding protein 2, homolog b	1.9	2.1	
136	2	PFF0020c	erythrocyte membrane protein 1 (PfEMP1)-like protein	1.7		3.4
137	3	PFL1420w	macrophage migration inhibitory factor homologue	-2.1	-2.0	-2.3
138	4	PFL1955w	erythrocyte membrane protein 1, PfEMP1	1.7		2.3
			Hypotheticals			
139	1	PF08_0060	asparagine-rich antigen	2.2	2.4	2.4
140	2	PF10_0188	conserved Plasmodium membrane protein, unknown	-2.6		-2.6
141	3	PF10_0195	kinesin, putative	-1.8		-3.2
142	4	PF10_0246	conserved Plasmodium protein, unknown function	-2.2		-2.4
143	5	PF11_0215	conserved Plasmodium protein, unknown function	-2.6	-1.3	-5.0
144	6	PF11_0231	conserved Plasmodium protein, unknown function	1.8		2.5
145	7	PF11_0321	serpentine receptor, putative	2.0		2.1
146	8	PF13_0011	plasmodium falciparum gamete antigen 27/25	-2.4	-3.9	-2.8
147	9	PF14_0014	Plasmodium exported protein, unknown function	-1.8		-2.5
148	10	PF14_0018	Plasmodium exported protein (PHISTb), unknown	2.3		2.2
149	11	PF14_0045	conserved Plasmodium protein, unknown function	2.1		3.4
150	12	PF14_0105	conserved Plasmodium protein, unknown function	-2.3		-3.2
151	13	PF14_0297	apyrase, putative	-2.0	-1.5	-2.1
152	14	PF14_0329	conserved protein, unknown function	-2.0	-2.1	-3.0
153	15	PF14_0680	conserved Plasmodium protein, unknown function	-3.1	-1.3	
154	16	PF14_0758	Plasmodium exported protein (hyp17), unknown	1.7	1.2	
155	17	PFB0075c	Plasmodium exported protein (hyp9), unknown function	1.8		3.9
156	18	PFB0365w	conserved Plasmodium protein, unknown function	-1.7		-2.9
157	19	PFB0590w	conserved Plasmodium protein, unknown function	-2.2	-2.1	
158	20	PFB0923c	Plasmodium exported protein, unknown function	2.5	2.1	2.2
159	21	PFB0953w	Plasmodium exported protein (hyp15), unknown	-1.8	-1.3	-3.9
160	22	PFC0730w	HVA22/TB2/DP1 family protein, putative	-1.9	-1.7	-2.7
161	23	PFL0130c	conserved Plasmodium protein, unknown function	1.9		2.1
162	24	PFL1330c	cyclin-related protein, Pfcyc-2	-2.7		
163	25	PFL2240w	conserved Plasmodium protein, unknown function	-2.2	-1.5	-2.3
164	26	PF10_0039	membrane skeletal protein IMC1-related	2.1	1.7	
165	27	PFL0685w	Phosphatidylinositol-glycan biosynthesis class O protein,	-1.9	-1.5	-2.3
166	28	MAL13P1.180	conserved Plasmodium protein, unknown function	-1.8		-2.2
167	29	MAL13P1.193	conserved Plasmodium protein, unknown function	-2.9	-1.4	-3.0
168	30	MAL13P1.293	conserved Plasmodium protein, unknown function	1.8		2.6
169	31	MAL13P1.298	conserved Plasmodium membrane protein, unknown	1.7		2.1
170	32	MAL13P1.332	conserved Plasmodium protein, unknown function	-0.5		-2.2
171	33	MAL13P1.57	conserved Plasmodium protein, unknown function	-1.8		-2.9
172	34	MAL7P1.173	Plasmodium exported protein, unknown function	1.8	-3.0	
173	35	MAL7P1.33	conserved Plasmodium protein, unknown function	-2.6	-1.6	-2.2
174	36	MAL7P1.61	null	1.7	-1.8	2.4
175	37	MAL7P1.77	conserved Plasmodium protein, unknown function	-2.6	-2.2	
176	38	MAL8P1.2	Plasmodium exported protein (PHISTb), unknown	2.1		2.1

177	39	MAL8P1.53	conserv ion	-3.7	-1.4	
178	40	MAL8P1.82	Vacuolar sorting protein VPS9, putative	1.8	1.8	
179	41	MAL8P1.86	Sel3 protein	-2.4	-1.7	
180	42	PF07_0039	conserved Plasmodium protein, unknown function	-1.8		-2.8
181	43	PF07_0087	conserved Plasmodium protein, unknown function	-2.5	-1.3	-3.4
182	44	PF07_0106	conserved Plasmodium protein, unknown function	1.9		2.6
183	45	PF08_0001	Plasmodium exported protein, unknown function	2.2	1.7	
184	46	PF08_0029	conserved Plasmodium protein, unknown function	-2.1		-3.7
185	47	PF08_0051	conserved Plasmodium protein, unknown function	-2.0	-1.7	
186	48	PF10_0020	alpha/beta hydrolase, putative	-4.1	-2.5	-6.3
187	49	PF10_0034	conserved Plasmodium protein, unknown function	2.3		-2.0
188	50	PF10_0243	conserved Plasmodium protein, unknown function	-1.7	-1.7	
189	51	PF10_0253	conserved Plasmodium protein, unknown function	-1.7	-2.0	-5.6
190	52	PF10_0286	conserved Plasmodium protein, unknown function	-2.3	-1.7	
191	53	PF10_0307	conserved Plasmodium protein, unknown function	2.4	2.1	
192	54	PF11_0035	Plasmodium exported protein, unknown function	1.7	2.4	-2.1
193	55	PF11_0371	conserved Plasmodium protein, unknown function	-2.1		2.1
194	56	PF11_0404	transcription factor with AP2 domain(s), putative	1.9		2.0
195	57	PF11_0425	conserved Plasmodium protein, unknown function	-2.3	-1.5	-2.2
196	58	PF11_0508	Plasmodium exported protein, unknown function	-2.2	-2.5	-2.5
197	59	PF13_0097	transcription factor with AP2 domain(s), putative	1.7		2.3
198	60	PF13_0192	conserved Plasmodium protein, unknown function	-4.2	-1.7	-8.1
199	61	PF13_0267	conserved Plasmodium protein, unknown function	1.7	1.8	4.8
200	62	PF13_0296	splicing factor 3b subunit, putative	-1.8	-1.8	
201	63	PF13_0338	cysteine-rich surface protein	-1.8		-2.1
202	64	PF14_0031	conserved Plasmodium protein, unknown function	-2.8		3.5
203	65	PF14_0101	conserved Plasmodium protein, unknown function	-1.8		2.0
204	66	PF14_0186	conserved Plasmodium protein, unknown function	-2.0	-1.2	-3.7
205	67	PF14_0402	conserved Plasmodium protein, unknown function	1.8	2.1	2.8
206	68	PF14_0430	mitochondrial ribosomal protein S29 precursor, putative	-1.8	-1.7	-1.0
207	69	PF14_0488	conserved Plasmodium protein, unknown function	-1.7		-2.7
208	70	PF14_0631	conserved Plasmodium protein, unknown function	1.7		2.0
209	71	PF14_0703	conserved Plasmodium protein, unknown function	2.2		3.3
210	72	PF14_0705	conserved Plasmodium protein, unknown function	-2.2		-2.2
211	73	PF14_0706	conserved Plasmodium protein, unknown function	1.8		2.2
212	74	PFA0115w	Plasmodium exported protein, unknown function	-3.2	-2.7	
213	75	PFA0245w	transporter, putative	-3.8	-1.3	
214	76	PFB0115w	conserved Plasmodium protein, unknown function	3.2	3.3	4.0
215	77	PFB0530c	conserved Plasmodium protein, unknown function	-2.2		-3.2
216	78	PFB0535w	GDP-fructose:GMP antiporter, putative	-2.9	-2.1	-3.0
217	79	PFB0835c	conserved Plasmodium protein, unknown function	-4.3	-1.6	-2.8
218	80	PFC0085c	Plasmodium exported protein, unknown function	1.8	1.7	2.1
219	81	PFC0262c	conserved Plasmodium protein, unknown function	-3.5		-2.4
220	82	PFC0571c	conserved Plasmodium protein, unknown function	-1.9		-3.1
221	83	PFC0590c	DER1-like protein, putative	-2.6	-1.5	
222	84	PFC0912w	signal peptidase, putative	-3.2	-1.5	-3.7
223	85	PFD0080c	Plasmodium exported protein (PHISTb), unknown	-1.9	-1.7	
224	86	PFD0225w	conserved Plasmodium membrane protein, unknown	-2.0	-2.2	
225	87	PFD0495c	conserved Plasmodium protein, unknown function	1.8		2.2
226	88	PFD0545w	conserved Plasmodium protein, unknown function	1.8		3.1
227	89	PFD0670c	lysine decarboxylase-like protein, putative	-2.0	-1.6	-3.1
228	90	PFD0850c	Memo-like protein	-2.2		-2.0
229	91	PFD0920w	conserved Plasmodium protein, unknown function	-1.9		2.3
230	92	PFD1140w	Plasmodium exported protein (PHISTc), unknown	2.1	1.3	
231	93	PFE0345c	conserved Plasmodium protein, unknown function	-1.7	-2.1	-2.5
232	94	PFE0500c	conserved Plasmodium protein, unknown function	-2.5	-1.8	-2.3
233	95	PFE1280w	conserved Plasmodium protein, unknown function	-2.2		-2.2
234	96	PFE1610w	Plasmodium exported protein, unknown function	2.0	1.8	
235	97	PFF0480w	conserved Plasmodium protein, unknown function	2.0		2.2
236	98	PFF0630c	conserved Plasmodium protein, unknown function	-4.0	-2.1	
237	99	PFF0935c	conserved Plasmodium protein, unknown function	-2.3	-1.7	
238	100	PFI0210c	cysteine repeat modular protein, putative	-1.9	-1.9	
239	101	PFI0405w	conserved Plasmodium protein, unknown function	-2.2		-4.1
240	102	PFI0880c	glideosome-associated protein 50	-2.8	-1.3	-2.2
241	103	PFI0975c	conserved Plasmodium protein, unknown function	-1.9	1.7	
242	104	PFI1520w	asparagine-rich antigen, putative	2.0		3.4
243	105	PFI1665w	transcription factor with AP2 domain(s), putative	-1.9		-2.2
244	106	PFI1770w	Plasmodium exported protein (PHISTb), unknown	1.9	-1.8	

245	107	PFI1780w	Plasmoc vn	2.5		2.2
246	108	PFL0280c	histone binding protein, putative	-1.7	-1.4	-2.2
247	109	PFL1040w	conserved Plasmodium protein, unknown function	-1.7		-3.5
248	110	PFL1300c	conserved Plasmodium protein, unknown function	-1.7	-0.6	
249	111	PFL1645w	conserved Plasmodium protein, unknown function	1.7	1.6	2.1
250	112	PFL1900w	transcription factor with AP2 domain(s), putative	-2.7	-1.4	-4.9
251	113	PFL2535w	Plasmodium exported protein (PHISTb), unknown	-2.7	-1.5	
252	114	PFE0685w	#N/A	-2.6	-1.9	-3.5

Appendix E

Unique transcripts found only with the inhibition of AdoMetDC

Nr	PlasmoDB ID	Product Description	FC
		DNA metabolism	
1	MAL13P1.328	DNA topoisomerase VI, B subunit, putative	2.8
2	PF14_0053	ribonucleotide reductase small subunit	-3.9
3	PFL1180w	chromatin assembly protein (ASF1), putative	-2.2
		Proteolysis	
4	PF13_0084	ubiquitin-like protein, putative	1.7
5	PF14_0348	ATP-dependent Clp protease proteolytic subunit, putative	-2.0
		Translation	
6	PF11_0113	mitochondrial ribosomal protein L11 precursor, putative	-2.0
7	PFC0675c	mitochondrial ribosomal protein L29/L47 precursor, putative	-1.9
8	PFC0701w	mitochondrial ribosomal protein L27 precursor, putative	-2.5
9	PFD0675w	apicoplast ribosomal protein L10 precursor, putative	-2.9
10	PFF0495w	mitochondrial ribosomal protein L19 precursor, putative	-2.0
11	PFL1150c	mitochondrial ribosomal protein L24-2 precursor, putative	-1.7
12	PFL1895w	mitochondrial ribosomal protein L23 precursor, putative	-1.7
		Phosphorylation	
13	PFC0485w	protein kinase, putative	-1.7
14	PFF0260w	serine/threonine protein kinase, Pfnek-5	-1.7
		Transport	
15	MAL13P1.16	SNARE protein, putative	-2.2
		polyamine methionine metabolism	
16	MAL13P1.214	phosphoethanolamine N-methyltransferase	-5.1
17	PF13_0016	methyl transferase-like protein, putative	-1.9
18	PF14_0526	conserved Plasmodium protein, unknown function	-3.1
		Primary metabolism	
19	MAL13P1.220	lipoate synthase, putative	-1.7
20	PFB0505c	3-oxoacyl-(acyl carrier protein) synthase III, putative	-2.1
21	PFI0960w	dolichyl-diphosphooligosaccharide-protein glycosyltransferase, putative	-1.7
		Cytoskeleton organization and biogenesis	
22	PF11_0478	kinesin-like protein, putative	2.1
		RNA metabolic process	
23	MAL8P1.72	high mobility group protein	-1.7
24	PF10_0313	mitochondrial preribosomal assembly protein rimM precursor, putative	-1.9
25	PF13_0043	CCAAT-binding transcription factor, putative	-1.8
26	PFD0750w	nuclear cap-binding protein, putative	-1.8
		Signal transduction	
27	PF14_0317	Microsomal signal peptidase protein, putative	-1.7
		Coenzyme metabolic process	
28	MAL7P1.130	3-demethylubiquinone-9 3-methyltransferase, putative	-1.7
29	PF14_0570	pyridoxal 5'-phosphate synthase, putative	-2.3
		Host parasite	
30	PF07_0138	rifin	-2.1
31	PFF0010w	erythrocyte membrane protein 1, PfEMP1	-2.4
32	PFF0020c	erythrocyte membrane protein 1 (PfEMP1)-like protein	1.7
		Hypotheticals	
33	PF11_0046	CPW-WPC family protein	-1.8
34	PF11_0355	conserved Plasmodium protein, unknown function	-3.4
35	PF14_0297	apyrase, putative	-2.0
36	PF14_0498	Degradation in the ER (DER1) like protein, putative	-2.0
37	PF14_0698	conserved Plasmodium protein, unknown function	2.5
38	PFB0953w	Plasmodium exported protein (hyp15), unknown function	-1.8

39	PFF1535w	Plasmod...own function	1.9
40	PFL0065w	conserved Plasmodium protein, unknown function	1.7
41	PFL1685w	conserved Plasmodium protein, unknown function	-2.4
42	PFL2455w	conserved Plasmodium protein, unknown function	1.8
43	MAL13P1.307	conserved Plasmodium protein, unknown function	-2.6
44	MAL13P1.188	conserved Plasmodium protein, unknown function	1.8
45	MAL13P1.251	conserved Plasmodium protein, unknown function	-3.5
46	MAL7P1.124	conserved Plasmodium protein, unknown function	-2.2
47	MAL7P1.173	Plasmodium exported protein, unknown function	1.8
48	MAL7P1.23	RAP protein, putative	-1.7
49	MAL7P1.230	hypothetical protein, pseudogene	1.7
50	MAL7P1.33	conserved Plasmodium protein, unknown function	-2.6
51	MAL7P1.61	conserved Plasmodium protein, unknown function	1.7
52	MAL8P1.206	Plasmodium exported protein, unknown function	-3.0
53	MAL8P1.216	rifin	-2.4
54	PF08_0030	conserved Plasmodium protein, unknown function	-2.5
55	PF08_0134	conserved Plasmodium protein, unknown function	-1.9
56	PF10_0034	conserved Plasmodium protein, unknown function	2.3
57	PF10_0258	conserved Plasmodium protein, unknown function	1.9
58	PF11_0514	Plasmodium exported protein (PHISTa), unknown function	2.0
59	PF11_0560	conserved protein, unknown function	-1.9
60	PF14_0226	conserved Plasmodium protein, unknown function	1.7
61	PF14_0488	conserved Plasmodium protein, unknown function	-1.7
62	PF14_0502	conserved Plasmodium protein, unknown function	-1.8
63	PF14_0705	conserved Plasmodium protein, unknown function	-2.2
64	PF14_0760	Plasmodium exported protein, unknown function	2.0
65	PFB0970c	Plasmodium exported protein, unknown function	1.7
66	PFB0973c	hypothetical protein	1.8
67	PFC0990c	conserved Plasmodium protein, unknown function	1.7
68	PFD0550c	conserved Plasmodium protein, unknown function	-2.1
69	PFD0655w	conserved Plasmodium protein, unknown function	-1.7
70	PFD0920w	conserved Plasmodium protein, unknown function	-1.9
71	PFD1140w	Plasmodium exported protein (PHISTc), unknown function	2.1
72	PFE1610w	Plasmodium exported protein, unknown function	2.0
73	PFF0075c	Plasmodium exported protein (PHISTb), unknown function	1.8
74	PFF0545c	conserved Plasmodium protein, unknown function	-2.0
75	PFF0630c	conserved Plasmodium protein, unknown function	-4.0
76	PFF0640w	conserved Plasmodium protein, unknown function	-3.1
77	PFF0725w	conserved Plasmodium protein, unknown function	1.7
78	PFF1005w	conserved Plasmodium protein, unknown function	1.8
79	PFF1160w	conserved Plasmodium protein, unknown function	-1.7
80	PFF1290c	conserved Plasmodium protein, unknown function	-1.7
81	PFI1630c	conserved Plasmodium protein, unknown function	-2.1
82	PFI1690c	conserved Plasmodium protein, unknown function	2.0
83	PFE0685w	conserved Plasmodium protein, unknown function	-2.6