Appendix 2

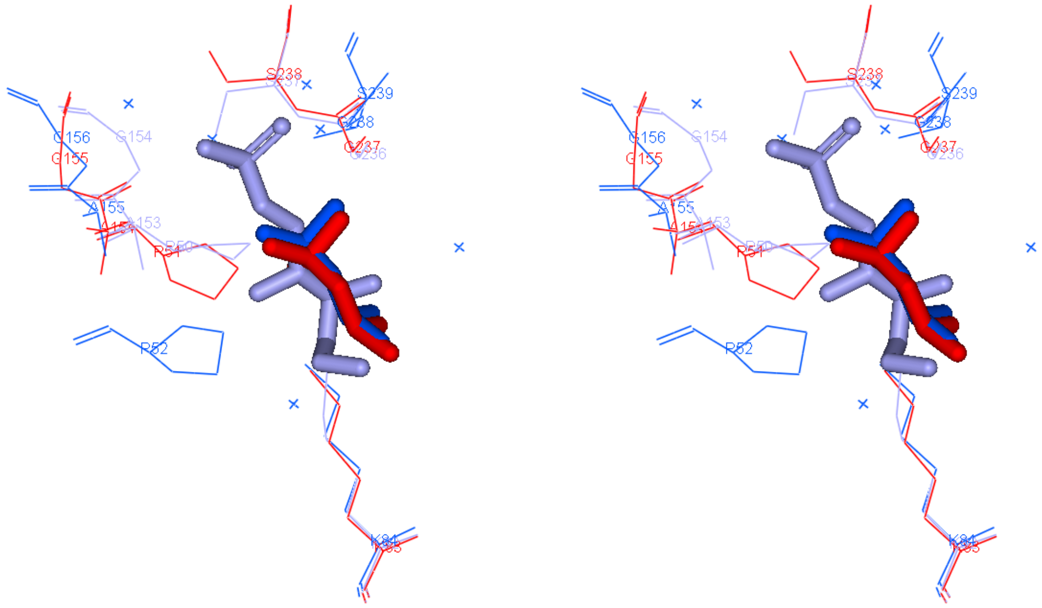

Figure A2.1: Stereoview of *Pf*Pdx1_MPD (red) superimposed with template structures *Tm*Pdx1 (2ISS, dark blue) and *Tt*Pdx1 (2ZBT, light blue). The proline residue (P52 in 2ZBT, P51 in 2ISS and P54 in *Pf*Pdx1) can be seen at the left of the ligand structure indicated as solid stick structure, and adopts a similar conformation to that of *Tm*Pdx1.

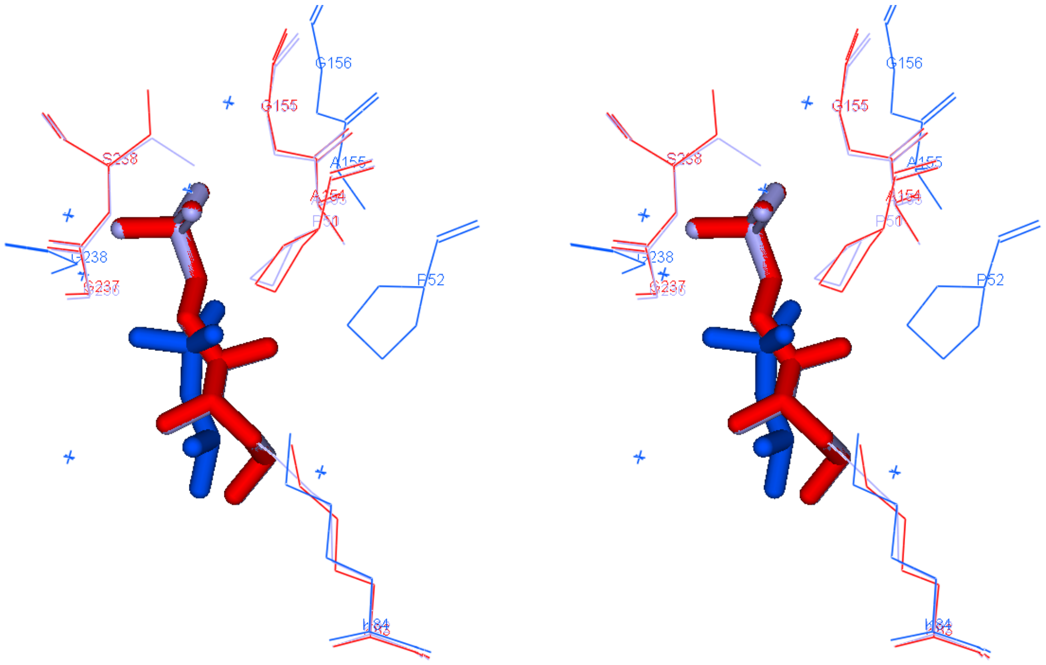

Figure A2.2: Stereoview of *Pf*Pdx1_Ru5P (red) superimposed with template structures *Tm*Pdx1 (2ISS, dark blue) and TtPdx1 (2ZBT, light blue). The proline residue (P52 in 2ZBT, P51 in 2ISS and *Pf*Pdx1) can be seen right of ligand structure indicated in hard solid line, and was comparable to that of *Tm*Pdx1. Similarly S237 was overlaid and more comparable to the *Tm*Pdx1 template.

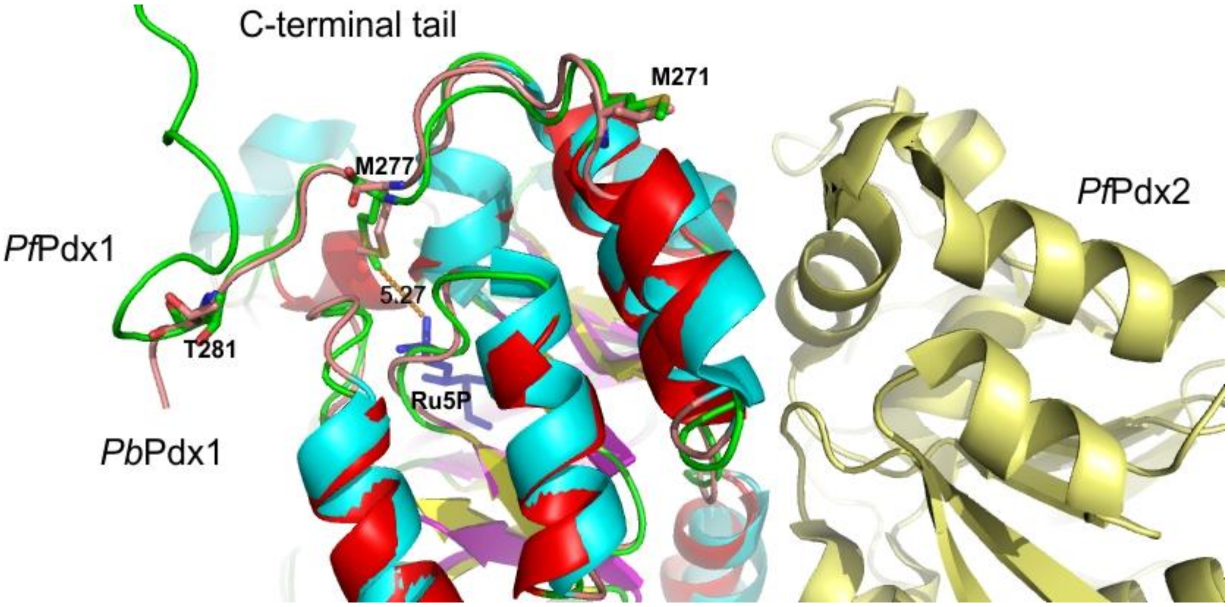

Figure A2.3: Superimposition of minimised *Pf*Pdx1 with *Pb*Pdx1 (PDB ID: 4ADS). The PbPdx1 component of the chimeric *Pb*Pdx1:*Pf*Pdx2 crystal structure was superimposed over the minimised *Pf*Pdx1_Ru5P model. Residues from M271 (*Pf*Pdx1 labelling) to T281 of *Pf*Pdx1 were aligned and spatially similar to those of *Pb*Pdx1. The M277 residue of *Pf*Pdx1 was located 5.27 Å from the phosphate group of the Ru5P substrate in the R5P-active site of *Pf*Pdx1.

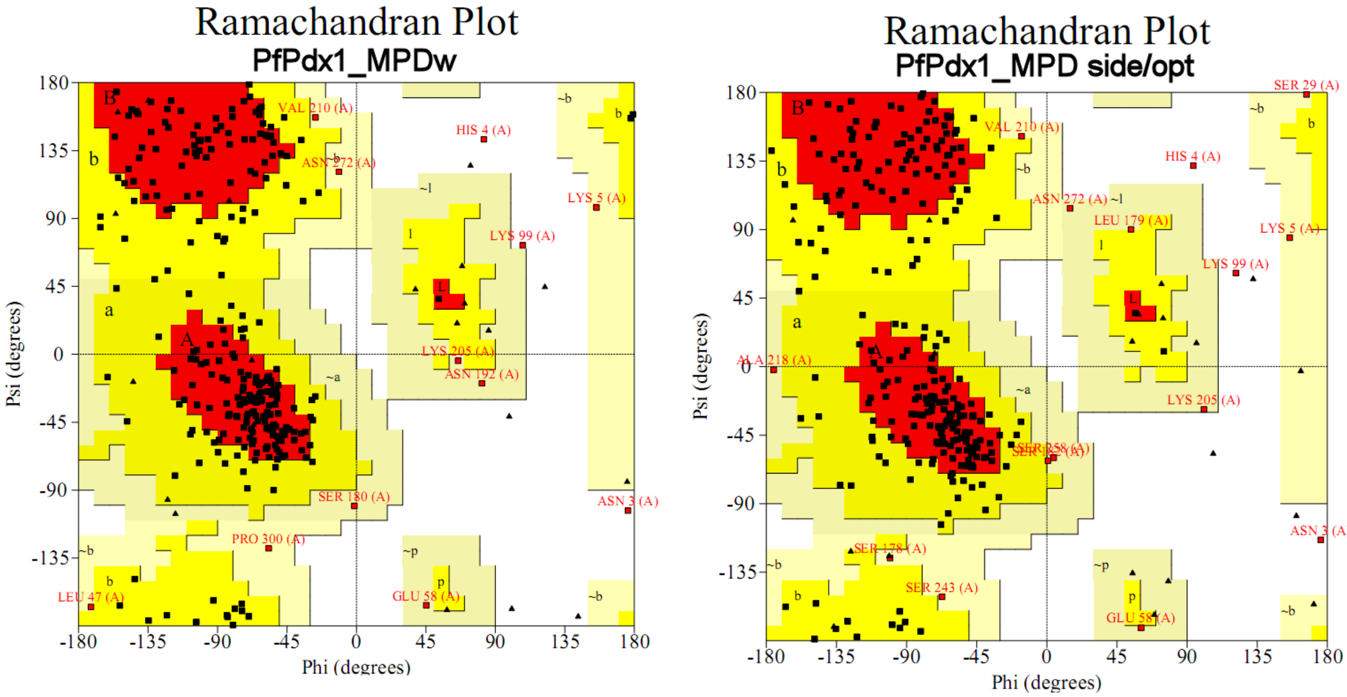

Figure A2.4: Ramachandran plots of *Pf*Pdx1 homology models after protein minimization.

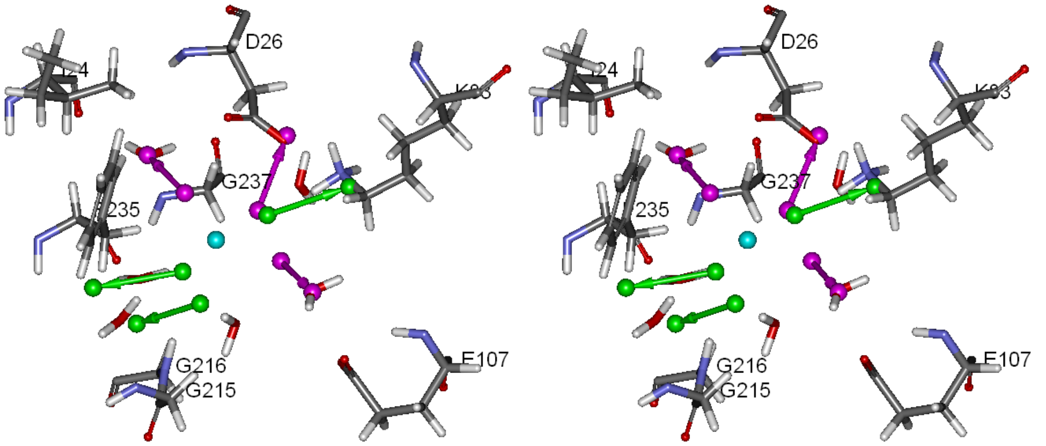

Figure A2.5: A stereo view of the *Pf*Pdx1_MPDw model pharmacophore, in which H-bond donors (green), H-bond acceptors (purple) and hydrophobic features (magenta) additionally involve water molecules, as listed in Table

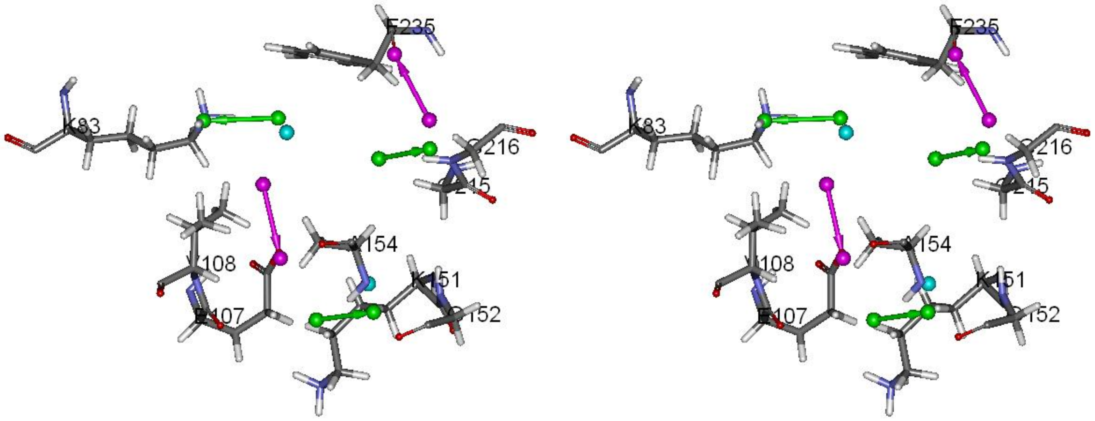

Figure A2.6: Representative stereo view of the *Pf*Pdx1_MPDsco pharmacophore.

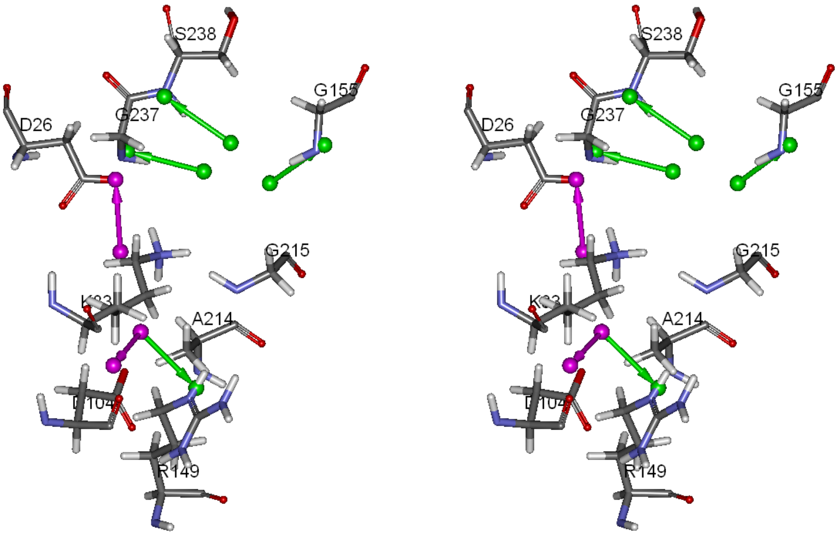

Figure A2.7: Stereo view of the pharmacophore from the *Pf*Pdx1_Ru5P model. Features were manually selected based on interactions between the R5P substrate (not shown in figure). This was termed a custom feature pharmacophore.

Appendix 3

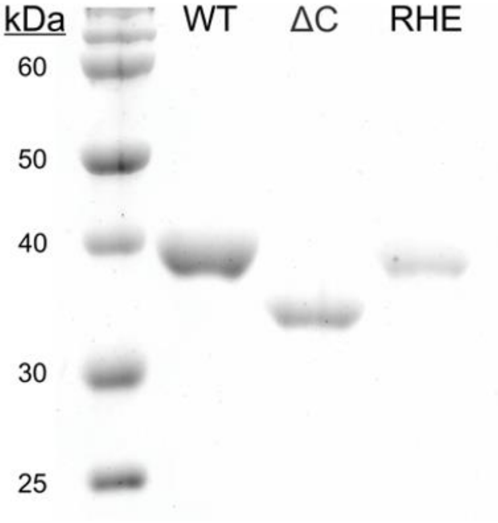

Figure A3.1: Coomassie stained SDS-polyacrylamide gel with 100 µg loaded each of *Pf*Pdx1 wildtype (WT), the C-terminal truncated form of *Pf*Pdx1 (ΔC) and the *Pf*Pdx1 RHE mutant. *Pf*Pdx1-ΔC was shown to be ~ 35 kDa compared to the wild-type (WT) *Pf*PDx1 at 37.5 kDa, confirming the 31 amino acid deletion.

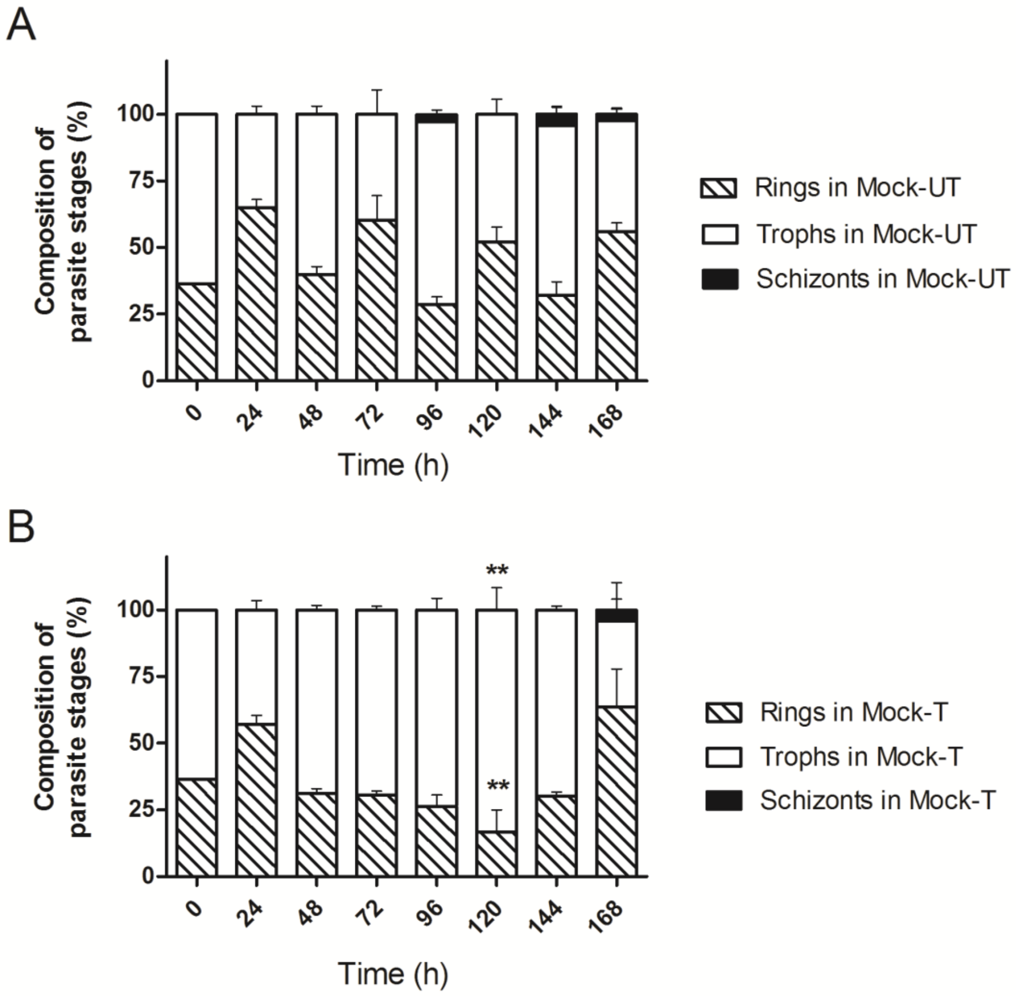

Figure A3.2: Morphological composition of parasite stages in mock control parasites during long-term exposure of 4PEHz. The parasite life-stage composition (percentage of rings, trophozoites or schizonts) of untreated **(A)** and treated **(B)** *P. falciparum* mock cells was determined microscopically during long term growth assays. Results represent average values from two independent experiments performed in triplicate, of which error bars indicate the SEM. Comparisons between treated and untreated mock parasites were made using an unpaired two-tailed Student's t-test in which ** represents statistical significance ($P < 0.05$). The treated mock parasites had significantly different ring and trophozoite life-stage compositions compared to the untreated controls parasites at 120 h.

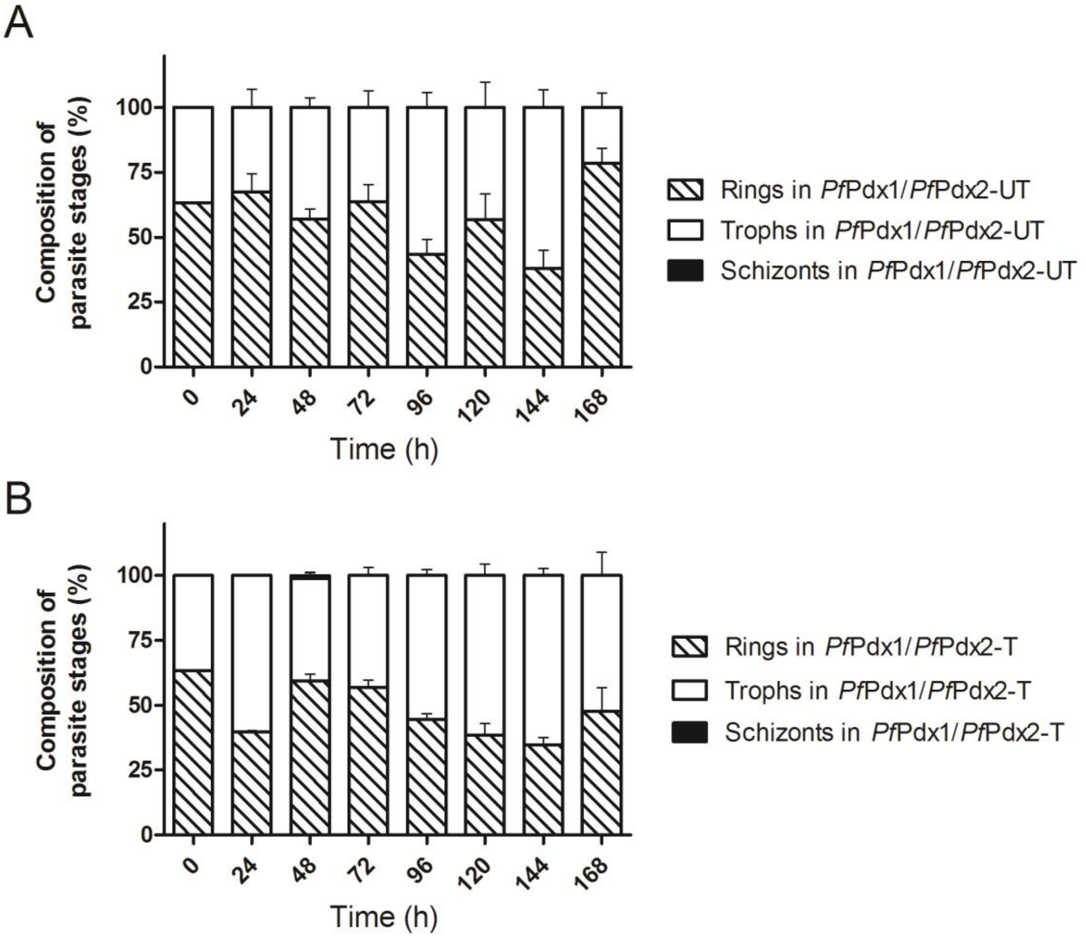

Figure A3.3: Morphological composition of parasite stages in *Pf*Pdx1/*Pf*Pdx2-complemented parasites during long-term exposure of 4PEHz. The parasite life-stage composition (percentage of rings, trophozoites or schizonts) of untreated **(A)** and treated **(B)** *P. falciparum Pf*Pdx1/*Pf*Pdx2-overexpressing parasites was determined microscopically during long term growth assays. Results represent average values from two independent experiments performed in triplicate, of which error bars indicate the SEM. Comparisons between treated and untreated mock parasites were made using an unpaired two-tailed Student’s t-test in which ** represents statistical significance ($P < 0.05$). There were no significant differences in the life-stage compositions between untreated and treated *Pf*Pdx1/*Pf*Pdx2 parasites at any of the time points. This confirmed that complementation of PLP biosynthesis protected the parasites from the effects of 4PEHz, and the parasites grew normally compared to untreated cells.

Appendix 4

Table A4.1: Differentially expressed transcripts from t$_3$ and their associated metabolic processes

No	PlasmoDB ID	PlasmoDB description	$\log_2$FC Tt$_3$:UTt$_3$	aj.P.Val	PlasmoDB annotated processes	Additional process involvement	GO term
Protein amino acid phosphorylation							
1	PF13_0211	calcium dependent protein kinase 5	-2.56	1.29E-07	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
2	PFI1285w	protein kinase, putative	-2.35	1.26E-06	protein amino acid phosphorylation		GO:0009536~plastid
3	MAL13P1.278	serine/threonine protein kinase, putative	-2.23	3.37E-07	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
4	PF11_0464	serine/threonine protein kinase, putative	-2.17	8.33E-08	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
5	PFB0665w	serine/threonine protein kinase, putative	-2.11	2.09E-05	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
6	PF11_0060	calcium/calmodulin-dependent protein kinase, putative	-2.09	7.20E-06	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
7	PFB0815w	calcium dependent protein kinase 1	-2.02	2.47E-07	protein amino acid phosphorylation		
8	PFL1885c	protein kinase 2	-1.91	7.20E-08	protein amino acid phosphorylation		
9	MAL13P1.114	conserved *Plasmodium* protein, unknown function	-1.80	4.53E-07	protein amino acid phosphorylation		GO:0009536~plastid
10	MAL7P1.18	serine/threonine protein kinase, putative	-1.66	6.20E-07	protein amino acid phosphorylation		
11	PFC0945w	protein kinase, putative	-1.58	5.34E-06	protein amino acid phosphorylation		
12	PFC0385c	serine/threonine protein kinase, putative	-1.55	8.77E-07	protein amino acid phosphorylation		
13	PFI0100c	serine/threonine protein kinase, FIKK family	-1.50	1.42E-06	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
14	PFL1110c	cAMP-dependent protein kinase regulatory subunit	-1.49	2.75E-07	regulation of protein amino acid phosphorylation		
15	PFD1165w	serine/threonine protein kinase, FIKK family	-1.28	8.62E-06	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
16	PF14_0346	cGMP-dependent protein kinase	-1.22	2.59E-05	protein amino acid phosphorylation	regulation of protein amino acid phosphorylation	
17	PFB0150c	protein kinase, putative	-1.16	1.51E-04	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
18	PFE0045c	serine/threonine protein kinase, FIKK family	-0.89	2.11E-03	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
19	PFL2280w	serine/threonine protein kinase, putative	-0.89	3.54E-04	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
20	PF14_0734	serine/threonine protein kinase, FIKK family	-0.89	1.42E-03	protein amino acid phosphorylation		
21	PFI0120c	serine/threonine protein kinase, FIKK family	-0.89	8.23E-05	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
22	PF07_0072	calcium dependent protein kinase 4	-0.89	8.53E-05	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
23	PF11_0281	protein phosphatase, putative	-0.86	9.81E-05	dephosphorylation		GO:0006793~phosphorus metabolic process
24	PFD1175w	serine/threonine protein kinase, FIKK family	-0.77	1.08E-04	protein amino acid phosphorylation		GO:0006468~protein amino acid

							phosphorylation
25	PFF0260w	serine/threonine protein kinase, putative	0.91	1.21E-03	protein amino acid phosphorylation		GO:0004674~protein serine/threonine kinase activity
Intracellular signaling pathway							
26	PFI1005w	ADP-ribosylation factor, putative	-2.07	8.59E-09	small GTPase mediated signal transduction		GO:0005525~GTP binding
27	MAL8P1.150	adenylyl cyclase beta, putative	-1.50	1.08E-07	cGMP biosynthetic process	intracellular signaling pathway	
28	PFI1485c	diacylglycerol kinase, putative	-1.39	8.62E-06	activation of protein kinase C activity by G-protein coupled receptor protein signaling pathway	intracellular signaling pathway	GO:0007166~cell surface receptor linked signal transduction
29	MAL13P1.118	3',5'-cyclic nucleotide phosphodiesterase, putative	-1.30	1.35E-05	signal transduction		GO:0004114~3'
30	MAL13P1.297	ADP-ribosylation factor, putative	-1.17	9.97E-05	protein amino acid ADP-ribosylation	small GTPase mediated signal transduction	GO:0006471~protein amino acid ADP-ribosylation
31	PF11_0107	conserved *Plasmodium* protein, unknown function	-1.00	1.91E-05	intracellular signaling pathway		
32	MAL7P1.108	phosphoinositide-binding protein, putative	-0.94	5.51E-05	cell communication		
33	PFL0475w	cGMP-specific phosphodiesterase	-0.85	1.22E-02	cGMP catabolic process	signal transduction	
34	PF11_0147	mitogen-activated protein kinase 2	-0.81	5.62E-05	MAPKKK cascade	protein amino acid phosphorylation	
35	PF10_0071	rhoGAP GTPase, putative	-0.76	5.36E-04	Rho protein signal transduction		GO:0007242~intracellular signaling cascade
36	MAL7P1.92	cysteine repeat modular protein 2	-0.76	9.18E-03	intracellular receptor mediated signaling pathway	intracellular transport	GO:0009536~plastid
37	MAL7P1.73	calcium/calmodulin-dependent protein kinase, putative	0.82	1.67E-02	protein amino acid phosphorylation	signal transduction	GO:0006468~protein amino acid phosphorylation
38	PFL2250c	RAC-beta serine/threonine protein kinase	0.96	6.69E-05	protein amino acid autophosphorylation		
39	PF10_0161	*Plasmodium* exported protein (PHISTc), unknown function	1.16	1.20E-04	small GTPase mediated signal transduction	translational initiation	
Regulation of cell cycle process							
40	PFD0900w	conserved *Plasmodium* protein, unknown function	-1.76	1.09E-04	cell cycle		
41	PFI1685w	cAMP-dependent protein kinase catalytic subunit	-1.67	4.76E-08	cell differentiation	protein amino acid phosphorylation	GO:0006468~protein amino acid phosphorylation
42	PFF0270c	cyclin dependent kinase binding protein, putative	0.79	1.61E-03	regulation of cell cycle	regulation of cell division	GO:0051726~regulation of cell cycle
43	PFI0810c	apicoplast Ufd1 precursor	0.79	1.08E-04	ER-associated protein catabolic process	regulation of cell cycle process	
44	PF14_0178	ubiquitin fusion degradation protein UFD1, putative	0.92	2.16E-04	ER-associated protein catabolic process	regulation of cell cycle process	
45	MAL13P1.279	protein kinase 5	0.92	4.35E-05	cell cycle	protein amino acid phosphorylation	GO:0006468~protein amino acid phosphorylation
46	PF14_0498	DER1-like protein	1.10	5.63E-05	ER-associated protein catabolic process	regulation of cell cycle process	
Apicoplast associated transcripts							
47	PF10_0138	conserved *Plasmodium* protein, unknown function	-3.69	2.92E-10	null		GO:0009536~plastid

48	MAL7P1.119	rhoptry-associated leucine zipper-like protein 1	-3.17	2.93E-09	null		GO:0009536~plastid
49	MAL7P1.141	conserved *Plasmodium* protein, unknown function	-3.16	9.73E-10	null		GO:0009536~plastid
50	MAL8P1.73	rhoptry neck protein 5, putative	-2.78	1.02E-09	null		GO:0009536~plastid
51	PF10_0119	conserved *Plasmodium* protein, unknown function	-2.53	7.16E-09	null		GO:0009536~plastid
52	PF14_0607	conserved *Plasmodium* membrane protein, unknown function	-2.23	4.83E-07	null		GO:0009536~plastid
53	PF10_0166	conserved *Plasmodium* protein, unknown function	-2.09	2.90E-07	null		GO:0009536~plastid
54	PFL2505c	conserved *Plasmodium* protein, unknown function	-2.07	4.83E-07	null		GO:0009536~plastid
55	PF13_0039	conserved *Plasmodium* protein, unknown function	-2.01	1.60E-07	null		GO:0009536~plastid
56	PF11_0304	conserved *Plasmodium* protein, unknown function	-1.93	5.83E-05	null		GO:0009536~plastid
57	PFE0575c	conserved *Plasmodium* protein, unknown function	-1.62	4.91E-07	null		GO:0009536~plastid
58	MAL13P1.49	conserved *Plasmodium* protein, unknown function	-1.57	1.48E-06	null		GO:0009536~plastid
59	PFL1835w	conserved *Plasmodium* protein, unknown function	-1.39	1.69E-06	null		GO:0009536~plastid
60	PF13_0125	conserved *Plasmodium* protein, unknown function	-1.32	8.67E-05	null		GO:0009536~plastid
61	PFL2410w	conserved *Plasmodium* membrane protein, unknown function	-1.24	1.79E-06	null		GO:0009536~plastid
62	PF08_0047	conserved *Plasmodium* protein, unknown function	-1.19	7.63E-07	null		GO:0009536~plastid
63	PFL0840c	conserved *Plasmodium* protein, unknown function	-1.14	9.24E-05	null		GO:0009536~plastid
64	PF11_0135	conserved *Plasmodium* protein, unknown function	-1.13	1.26E-03	null		GO:0009536~plastid
65	PFI1470c	leucine-rich repeat protein	-1.06	6.47E-06	null		GO:0009536~plastid
66	PFC0065c	alpha/beta hydrolase, putative	-1.01	5.04E-05	null		GO:0009536~plastid
67	MAL13P1.61	*Plasmodium* exported protein (hyp8), unknown function	-1.00	1.14E-03	null		GO:0009536~plastid
68	PF11_0231	conserved *Plasmodium* protein, unknown function	-0.99	1.63E-03	null		GO:0009536~plastid
69	PFB0110w	*Plasmodium* exported protein (hyp11), unknown function	-0.95	2.55E-02	null		GO:0009536~plastid
70	PFF0660w	conserved *Plasmodium* protein, unknown function	-0.92	8.97E-06	null		GO:0009536~plastid
71	PFL0875w	conserved *Plasmodium* protein, unknown function	-0.91	4.43E-04	null		GO:0009536~plastid
72	MAL13P1.70	conserved *Plasmodium* membrane protein, unknown function	-0.90	5.85E-05	null		GO:0009536~plastid
73	PF11_0470	conserved *Plasmodium* protein, unknown function	-0.88	5.10E-03	null		GO:0009536~plastid
74	MAL7P1.6	*Plasmodium* exported protein (hyp12), unknown	-0.79	3.77E-04	null		GO:0009536~plastid

		function					
75	PF14_0440	conserved *Plasmodium* membrane protein, unknown function	-0.75	5.40E-04	null		GO:0009536~plastid
76	PFE0215w	ATP-dependent helicase, putative	0.78	2.13E-03	null		GO:0009536~plastid
77	PFB0180w	5'-3' exonuclease, N-terminal resolvase-like domain, putative	0.80	8.80E-04	null		GO:0009536~plastid
78	PFB0395w	conserved *Plasmodium* protein, unknown function	0.83	1.50E-04	null		GO:0009536~plastid
79	PFL2330w	conserved *Plasmodium* protein, unknown function	0.89	1.08E-05	null		GO:0009536~plastid
80	MAL8P1.138	alpha/beta hydrolase, putative	0.89	1.13E-04	null		GO:0009536~plastid
81	PF11_0285	conserved *Plasmodium* protein, unknown function	0.89	2.09E-05	null		GO:0009536~plastid
82	PF14_0696	conserved *Plasmodium* protein, unknown function	0.92	7.11E-04	null		GO:0009536~plastid
83	PF11_0323	conserved *Plasmodium* protein, unknown function	0.94	1.81E-03	null		GO:0009536~plastid
84	MAL13P1.87	sec20 homolog, putative	0.99	2.36E-05	null		GO:0009536~plastid
85	PFL0700w	conserved *Plasmodium* protein, unknown function	1.05	1.34E-05	null		GO:0009536~plastid
86	PFF1090c	conserved *Plasmodium* membrane protein, unknown function	1.07	3.41E-05	null		GO:0009536~plastid
87	PFI0205w	conserved *Plasmodium* protein, unknown function	1.27	2.91E-04	null		GO:0009536~plastid
88	MAL13P1.342	conserved *Plasmodium* protein, unknown function	1.35	2.58E-06	null		GO:0009536~plastid
89	MAL13P1.254	conserved *Plasmodium* protein, unknown function	1.47	2.76E-05	null		GO:0009536~plastid
90	PF14_0155	serine C-palmitoyltransferase, putative	1.48	2.66E-05	biosynthetic process		GO:0009536~plastid
Pathogenesis and invasion							
91	MAL7P1.176	erythrocyte binding antigen-175	-4.93	2.99E-12	entry into host cell	pathogenesis	GO:0009405~pathogenesis
92	PF10_0346	merozoite surface protein 6	-3.33	6.50E-10	entry into host cell		
93	MAL13P1.176	reticulocyte binding protein 2 homologue b	-3.33	5.53E-09	entry into host cell		GO:0030260~entry into host cell
94	PFE0080c	rhoptry-associated protein 2	-3.03	2.99E-10	entry into host cell		
95	PF13_0198	reticulocyte binding protein 2 homologue a	-2.72	2.06E-06	entry into host cell		GO:0007155~cell adhesion
96	PFB0680w	rhoptry neck protein 6	-2.36	6.27E-08	entry into host		
97	PF10_0281	merozoite TRAP-like protein	-1.60	1.07E-06	entry into host cell		
98	PFF1420w	phosphatidylcholine-sterol acyltransferase precursor, putative	-1.60	4.83E-07	entry into host cell	lipid metabolic process	GO:0009536~plastid
99	PF11_0344	apical membrane antigen 1	-1.30	3.74E-06	entry into host cell	pathogenesis	
100	PF10_0345	merozoite surface protein 3	-0.92	2.48E-04	entry into host cell		
101	PF13_0197	merozoite surface protein 7 precursor	-0.87	2.77E-04	entry into host cell		
Transcription							
102	PF10_0357	probable protein, unknown function	-2.19	8.86E-09	transcription		
103	PF11_0442	transcription factor with AP2 domain(s), putative	-2.11	2.13E-08	regulation of transcription	DNA-dependent	
104	PFF0200c	transcription factor with AP2 domain(s), putative,SPE2-interacting protein	-1.89	7.63E-07	regulation of transcription	DNA-dependent	
105	PF11_0091	transcription factor with AP2 domain(s), putative	-1.74	4.76E-08	regulation of transcription	DNA-dependent	GO:0006355~regulation of transcription

106	MAL7P1.125	conserved *Plasmodium* protein, unknown function	-1.56	4.63E-07	regulation of transcription	DNA-dependent	
107	PF11_0477	CCAAT-box DNA binding protein subunit B	-1.36	6.13E-07	regulation of transcription	DNA-dependent	GO:0006355~regulation of transcription
108	PFD0985w	transcription factor with AP2 domain(s), putative	-1.35	9.88E-07	regulation of transcription	DNA-dependent	
109	PF07_0052	conserved *Plasmodium* protein, unknown function	-1.34	5.53E-05	regulation of transcription	DNA-dependent	
110	PFL1510c	conserved *Plasmodium* protein, unknown function	-1.31	1.50E-04	regulation of transcription	DNA-dependent	
111	PFD0380c	conserved *Plasmodium* protein, unknown function	-1.25	8.18E-06	regulation of transcription	DNA-dependent	
112	PF11_0204	conserved *Plasmodium* protein, unknown function	-1.15	2.23E-05	regulation of transcription	DNA-dependent	GO:0006355~regulation of transcription
113	PF07_0126	transcription factor with AP2 domain(s), putative	-1.07	1.72E-06	regulation of transcription	DNA-dependent	GO:0006355~regulation of transcription
114	PFD0485w	conserved *Plasmodium* protein, unknown function	-0.99	1.71E-05	regulation of transcription	DNA-dependent	GO:0043167~ion binding
115	PFD0535w	conserved *Plasmodium* protein, unknown function	-0.91	3.09E-05	regulation of transcription	DNA-dependent	
116	PFF0670w	transcription factor with AP2 domain(s), putative	-0.84	5.14E-05	regulation of transcription	DNA-dependent	
117	PFL0465c	zinc finger transcription factor (krox1)	-0.77	6.67E-03	regulation of transcription	DNA-dependent	GO:0006355~regulation of transcription
118	MAL7P1.78	conserved *Plasmodium* protein, unknown function	0.80	2.35E-04	regulation of transcription	DNA-dependent	GO:0006350~transcription
119	PF14_0665	conserved *Plasmodium* protein, unknown function	0.89	1.32E-04	regulation of transcription	DNA-dependent	
120	PF11_0163	transcription factor with AP2 domain(s), putative	1.05	8.98E-06	regulation of transcription	DNA-dependent	
121	PFI1630c	conserved *Plasmodium* protein, unknown function	1.18	1.14E-05	transcription		
122	PF14_0580	conserved *Plasmodium* protein, unknown function	1.20	1.21E-03	regulation of transcription	DNA-dependent	
Translation							
123	PFI0540w	conserved *Plasmodium* protein, unknown function	-3.34	1.37E-09	translation	translational initiation	
124	PF13_0173	conserved *Plasmodium* protein, unknown function	-2.64	4.85E-09	translational initiation		
125	PFD1100c	conserved *Plasmodium* protein, unknown function	-2.28	6.22E-07	translation	translational initiation	GO:0009536~plastid
126	PFI1675w	conserved *Plasmodium* protein, unknown function	-1.96	1.63E-07	translation		
127	PFL0570c	mitochondrial ribosomal protein S18 precursor, putative	-1.95	9.22E-07	translation		GO:0006412~translation
128	PFF0705c	conserved *Plasmodium* protein, unknown function	-1.66	3.17E-04	translation	translational initiation	
129	PFF1095w	leucyl tRNA synthase	-1.63	9.61E-07	leucyl-tRNA aminoacylation	translation	GO:0006399~tRNA metabolic process
130	MAL7P1.81	eukaryotic translation initiation factor 3 37.28 kDa subunit, putative	-1.12	1.38E-04	regulation of translational initiation		GO:0006417~regulation of translation
131	PFI1725w	*Plasmodium* exported protein, unknown function	-1.06	1.20E-05	translation	valyl-tRNA aminoacylation	
132	PFD0525w	conserved *Plasmodium* protein, unknown function	-0.94	2.00E-05	regulation of translation		
133	PFI0645w	elongation factor 1-beta	-0.89	8.60E-05	translational elongation		GO:0006412~translation
134	MAL7P1.17	conserved *Plasmodium* membrane protein,	-0.82	4.12E-05	translation	translational initiation	

		unknown function					
135	PFL2180w	mitochondrial ribosomal protein L3 precursor, putative	0.76	8.55E-05	translation		GO:0006412~translation
136	PFL2430c	eukaryotic translation initiation factor 2b, subunit 2, putative	0.80	5.59E-04	cellular metabolic process	translational initiation	GO:0006412~translation
137	MAL13P1.164	elongation factor Tu, putative	0.81	6.83E-05	translational elongation		GO:0006412~translation
138	PF13_0069	translation initiation factor IF-2, putative	0.82	1.10E-03	translation	translational initiation	GO:0006412~translation
139	PFA0480w	phenylalanyl-tRNA synthetase, putative	0.85	6.71E-04	phenylalanyl-tRNA aminoacylation	translation	
140	PFB0645c	mitochondrial ribosomal protein L13 precursor, putative	0.85	4.55E-05	translation		GO:0006412~translation
141	PF14_0606	mitochondrial ribosomal protein S6-2 precursor, putative	0.86	1.26E-02	translation		GO:0006412~translation
142	PFL1895w	mitochondrial ribosomal protein L23 precursor, putative	0.86	1.96E-04	translation		GO:0006412~translation
143	PF11_0182	conserved *Plasmodium* protein, unknown function	0.86	7.18E-05	translation	translational termination	
144	PF14_0289	mitochondrial ribosomal protein L17-2 precursor, putative	0.87	1.60E-05	translation		GO:0006412~translation
145	PFC0241w	conserved *Plasmodium* protein, unknown function	0.89	1.26E-04	translation		
146	PF13_0205	tryptophan--tRNA ligase, putative	0.89	8.20E-05	translation	tryptophanyl-tRNA aminoacylation	GO:0006399~tRNA metabolic process
147	PFI1645c	histidyl-tRNA synthetase, putative	0.93	3.74E-05	histidyl-tRNA aminoacylation	translation	GO:0006399~tRNA metabolic process
148	PFI1120c	conserved *Plasmodium* protein, unknown function	0.99	1.00E-04	translation	translational initiation	
149	PFL1910c	conserved *Plasmodium* protein, unknown function	2.05	1.96E-06	translation		
Antigenic variation, defense response and pathogenesis							
150	MAL13P1.60	erythrocyte binding antigen-140	-4.74	2.89E-11	cell-cell adhesion	pathogenesis	GO:0009405~pathogenesis
151	PFD0110w	normocyte binding protein 1,reticulocyte binding protein homologue 1	-3.72	2.53E-09	cell-cell adhesion		
152	PF10_0003	rifin	-3.70	6.50E-10	antigenic variation		GO:0006952~defense response
153	PFA0125c	erythrocyte binding antigen-181	-3.05	1.48E-08	cell-cell adhesion	entry into host cell	
154	PFD1155w	erythrocyte binding antigen-165	-3.00	2.56E-08	pathogenesis		GO:0009405~pathogenesis
155	MAL7P1.208	rhoptry-associated membrane antigen	-2.95	2.31E-08	attachment of GPI anchor to protein	cell-cell adhesion	
156	PFD0955w	apical merozoite protein	-2.79	6.50E-10	attachment of GPI anchor to protein		
157	PFC0120w	cytoadherence linked asexual protein 3.1	-2.70	2.56E-08	cytoadherence to microvasculature	mediated by parasite protein	
158	PFC0110w	cytoadherence linked asexual protein 3.2	-2.56	6.69E-08	cytoadherence to microvasculature	mediated by parasite protein	
159	PF08_0008	GPI-anchored micronemal antigen	-2.47	2.59E-06	attachment of GPI anchor to protein		
160	PFD0295c	apical sushi protein	-2.47	1.00E-07	attachment of GPI anchor to protein		
161	PFD1105w	asparagine-rich protein	-2.19	9.66E-07	cell-cell adhesion		
162	PF11_0373	conserved *Plasmodium* protein, unknown function	-2.17	4.02E-08	attachment of GPI anchor to protein		
163	PFF1545w	rifin	-2.09	4.93E-04	antigenic variation		
164	PF14_0325	conserved *Plasmodium* membrane protein, unknown function	-2.01	1.13E-04	attachment of GPI anchor to protein		
165	PFD1145c	reticulocyte binding protein homologue 5	-1.82	4.76E-08	cell-cell adhesion	entry into host	
166	PF14_0293	conserved *Plasmodium* protein, unknown function	-1.80	3.68E-07	attachment of GPI anchor to protein		

167	PFI1730w	cytoadherence linked asexual protein 9	-1.69	5.10E-08	cell-cell adhesion		
168	PFI1475w	merozoite surface protein 1	-1.65	3.72E-07	attachment of GPI anchor to protein	pathogenesis	GO:0009405~pathogenesis
169	PF10_0348	duffy binding-like merozoite surface protein	-1.46	4.09E-06	cell-cell adhesion	pathogenesis	GO:0009405~pathogenesis
170	PFF0615c	6-cysteine protein	-1.35	5.69E-07	attachment of GPI anchor to protein		
171	PFL1960w	erythrocyte membrane protein 1, PfEMP1	-1.32	1.90E-05	antigenic variation	cell-cell adhesion	
172	PF11_0008	erythrocyte membrane protein 1, PfEMP1	-1.23	2.58E-06	antigenic variation	cell-cell adhesion	GO:0006952~defense response
173	PFL0030c	erythrocyte membrane protein 1, PfEMP1	-1.12	1.42E-04	antigenic variation	cell-cell adhesion	
174	PF07_0132	rifin	-1.12	3.26E-03	antigenic variation		
175	PFB0300c	merozoite surface protein 2	-1.04	4.91E-05	attachment of GPI anchor to protein	cell adhesion	
176	PFB0570w	secreted protein altered thrombospondin repeat protein	-1.01	6.37E-06	cell-cell adhesion		GO:0009536~plastid
177	PFF0380w	conserved *Plasmodium* protein, unknown function	-1.01	3.51E-04	cell adhesion	phosphate transport	
178	PFF0995c	merozoite surface protein 10	-0.98	5.10E-04	attachment of GPI anchor to protein		
179	PFB0010w	erythrocyte membrane protein 1, PfEMP1	-0.92	7.65E-04	antigenic variation	cell-cell adhesion	GO:0006952~defense response
180	PF10_0404	rifin	-0.87	7.48E-05	antigenic variation		GO:0006952~defense response
181	PFL1970w	erythrocyte membrane protein 1, PfEMP1	-0.86	4.48E-03	pathogenesis		
182	PF14_0723	LCCL domain-containing protein	-0.82	3.58E-04	cell adhesion	signal transduction	
183	PF08_0142	erythrocyte membrane protein 1, PfEMP1	-0.81	1.25E-03	antigenic variation	cell-cell adhesion	GO:0009405~pathogenesis
184	PFA0005w	erythrocyte membrane protein 1, PfEMP1	-0.78	5.37E-03	antigenic variation	cell-cell adhesion	
185	PF11_0229	conserved *Plasmodium* protein, unknown function	0.87	1.54E-03	GPI anchor biosynthetic process	attachment of GPI anchor to protein	
186	PFF0975c	conserved *Plasmodium* protein, unknown function	0.88	1.10E-02	attachment of GPI anchor to protein		
187	MAL13P1.348	glycosylphosphatidylinositol anchor attachment 1 protein, putative	0.89	2.21E-04	GPI anchor biosynthetic process	attachment of GPI anchor to protein	
188	PFB0575c	conserved *Plasmodium* protein, unknown function	0.91	1.78E-04	cell adhesion	phosphate transport	
189	PFE1630w	rifin	0.95	2.23E-02	antigenic variation		
190	MAL7P1.50	erythrocyte membrane protein 1, PfEMP1	0.97	2.62E-04	antigenic variation	cell-cell adhesion	GO:0009405~pathogenesis
191	PFI0535w	phosphatidylinositol N-acetylglucosaminyltransferase, putative	0.99	7.77E-05	GPI anchor biosynthetic process		
Cytokinesis							
192	PF10_0039	membrane skeletal protein IMC1-related	-3.75	1.71E-10	cytoskeleton organization		
193	PFL2460w	coronin	-3.52	1.71E-10	cellular component movement	cytokinesis	GO:0000910~cytokinesis
194	PFL1435c	myosin D	-3.46	2.99E-10	actin filament organization	actin filament-based movement	GO:0007010~cytoskeleton organization
195	PF10_0368	dynamin-like protein	-1.88	8.61E-08	microtubule-based process	receptor-mediated endocytosis	GO:0006897~endocytosis
196	PF14_0626	dynein beta chain, putative	-1.35	3.33E-05	microtubule-based movement		GO:0007017~microtubule-based process
197	PFL2215w	actin I	-1.30	7.85E-07	cytoskeleton organization		
198	PFA0260c	cyclase-associated protein, putative	-1.21	5.19E-05	cytoskeleton organization		
199	PFL2165w	kinesin-like protein, putative	0.90	9.96E-05	microtubule-based movement		GO:0007017~microtubule-based process
200	PFE1420w	f-actin capping protein alpha subunit, putative	1.15	3.41E-05	actin cytoskeleton organization		GO:0007010~cytoskeleton organization
201	PFL0115w	dynein heavy chain, putative	1.51	1.42E-03	microtubule-based movement		GO:0007017~microtubule-based process
202	MAL7P1.162	dynein heavy chain, putative	1.81	1.29E-07	microtubule-based movement		GO:0007017~microtubule-based process
203	PFD1050w	alpha tubulin 2	2.71	2.68E-09	microtubule-based movement	protein polymerization	GO:0006461~protein complex assembly
DNA repair and replication							

204	PF14_0527	conserved *Plasmodium* protein, unknown function	-3.16	4.22E-09	DNA recombination	mismatch repair	
205	PF11_0383	conserved *Plasmodium* protein, unknown function	-1.68	6.58E-06	DNA-dependent DNA replication		
206	PFE0420c	guanidine nucleotide exchange factor	-1.49	6.09E-07	DNA packaging		GO:0006323~DNA packaging
207	MAL13P1.112	conserved *Plasmodium* protein, unknown function	-1.01	2.74E-04	DNA integration	DNA recombination	
208	PFI0510c	conserved *Plasmodium* protein, unknown function	-0.76	6.83E-05	DNA repair	DNA-dependent DNA replication	GO:0006259~DNA metabolic process
209	PFF1470c	DNA polymerase epsilon, catalytic subunit a, putative	0.77	2.87E-04	DNA-dependent DNA replication		GO:0006259~DNA metabolic process
210	PFE1345c	minchromosome maintenance (MCM) complex subunit, putative	0.79	1.59E-02	DNA replication	DNA-dependent DNA replication initiation	GO:0006259~DNA metabolic process
211	PF14_0366	small subunit DNA primase	0.87	4.41E-05	DNA replication	synthesis of RNA primer	GO:0006259~DNA metabolic process
212	PF11_0087	Rad51 homolog	0.89	6.81E-05	DNA recombination	DNA repair	
213	PFL2005w	replication factor C subunit 4	0.92	9.38E-05	DNA replication		GO:0006259~DNA metabolic process
214	PFI0530c	DNA primase large subunit, putative	0.93	6.71E-04	DNA replication	synthesis of RNA primer	
215	PFL0150w	origin recognition complex subunit 1	0.99	1.01E-04	DNA-dependent DNA replication initiation		
216	MAL13P1.191	conserved *Plasmodium* protein, unknown function	1.01	8.69E-04	DNA repair		
217	MAL13P1.346	DNA repair endonuclease, putative	1.09	3.22E-05	DNA repair		GO:0006259~DNA metabolic process
Fatty acid, lipid and phospholipid metabolism							
218	PF07_0005	lysophospholipase, putative	-1.57	1.71E-06	phospholipid metabolic process		GO:0006644~phospholipid metabolic process
219	PFI1015w	conserved *Plasmodium* protein, unknown function	-1.39	2.57E-06	lipid transport		
220	PFI1370c	phosphatidylserine decarboxylase	-0.94	1.09E-04	phospholipid biosynthetic process		GO:0006644~phospholipid metabolic process
221	PFB0695c	acyl-CoA synthetase, PfACS8	-0.91	2.00E-04	fatty acid metabolic process	long-chain fatty acid transport	
222	PFF0290w	long chain polyunsaturated fatty acid elongation enzyme, putative	-0.90	3.53E-04	fatty acid elongation	unsaturated fatty acid	GO:0006631~fatty acid metabolic process
223	PF13_0078	conserved *Plasmodium* membrane protein, unknown function	-0.86	1.81E-03	lipid catabolic process		
224	PFE0485w	phosphatidylinositol 4-kinase	-0.85	5.49E-05	phosphoinositide phosphorylation	phosphoinositide-mediated signaling	GO:0006644~phospholipid metabolic process
225	PF14_0020	choline kinase	-0.81	3.11E-05	lipid metabolic process	phosphatidylcholine biosynthetic process	
226	PF10_0015	acyl-CoA binding protein, isoform 1, ACBP1	-0.79	1.26E-02	fatty acid metabolic process		
227	PFL1055c	conserved *Plasmodium* membrane protein, unknown function	-0.78	9.58E-04	lipid catabolic process		
228	PFB0505c	beta-ketoacyl-ACP synthase III	-0.77	5.90E-04	fatty acid biosynthetic process		
229	PFI1180w	patatin-like phospholipase, putative	-0.76	7.06E-05	lipid metabolic process		GO:0016042~lipid catabolic process
230	PF14_0664	biotin carboxylase subunit of acetyl CoA carboxylase, putative	0.80	1.34E-03	fatty acid biosynthetic process		
231	PFD1035w	steroid dehydrogenase, putative	0.82	2.52E-04	fatty acid biosynthetic process		GO:0006631~fatty acid metabolic process
232	PF14_0441	pyruvate dehydrogenase E1 beta subunit	0.91	1.07E-04	acetyl-CoA biosynthetic process from pyruvate	fatty acid biosynthetic process	GO:0009536~plastid

233	PFB0685c	acyl-CoA synthetase, PfACS9	1.07	3.47E-04	fatty acid metabolic process	long-chain fatty acid transport	
234	PF14_0123	conserved *Plasmodium* protein, unknown function	1.12	1.46E-06	phosphatidylinositol metabolic process		GO:0006644~phospholipid metabolic process
235	PF13_0066	malonyl CoA-acyl carrier protein transacylase precursor	1.19	1.76E-02	fatty acid biosynthetic process		GO:0004314~[acyl-carrier-protein] S-malonyltransferase activity
236	PF11_0256	pyruvate dehydrogenase E1 alpha subunit	1.65	4.28E-08	acetyl-CoA biosynthetic process from pyruvate	fatty acid biosynthetic process	GO:0006084~acetyl-CoA metabolic process
Stress response							
237	PF13_0019	sodium/hydrogen exchanger, Na , H antiporter	-0.93	2.10E-05	response to drug	sodium ion transport	GO:0006811~ion transport
238	PFB0320c	iron-sulfur assembly protein, putative	-0.79	1.57E-04	iron-sulfur cluster assembly		GO:0016226~iron-sulfur cluster assembly
239	PF11_0169	pyridoxine biosynthesis protein Pdx2	0.77	5.98E-05	response to singlet oxygen	vitamin B6 biosynthetic process	
240	PF11_0044	iron-sulfur assembly protein, sufD, putative	0.92	6.29E-05	iron-sulfur cluster assembly		GO:0016226~iron-sulfur cluster assembly
241	PF14_0368	thioredoxin peroxidase 1	0.95	1.14E-04	DNA protection	cell redox homeostasis	
242	PF14_0186	conserved *Plasmodium* protein, unknown function	0.97	4.74E-03	cell redox homeostasis		
243	PF13_0021	small heat shock protein, putative	1.09	4.19E-05	response to heat	response to unfolded protein	GO:0006986~response to unfolded protein
244	MAL13P1.100	conserved *Plasmodium* protein, unknown function	1.11	1.01E-05	cell redox homeostasis		
245	PF08_0066	lipoamide dehydrogenase	1.28	8.55E-05	acetyl-CoA biosynthetic process from pyruvate	cell redox homeostasis	GO:0006084~acetyl-CoA metabolic process
Transport							
246	PF10_0262	conserved *Plasmodium* protein, unknown function	-3.35	6.38E-10	phosphate transport		
247	PF10_0059	conserved *Plasmodium* membrane protein, unknown function	-2.39	1.39E-08	transport		
248	PFL0245w	probable protein, unknown function	-1.59	4.29E-06	transport		GO:0009536~plastid
249	PFD1110w	glideosome associated protein with multiple membrane spans 2	-1.47	9.02E-07	transport		
250	PFL1700c	V-type K -independent H -translocating inorganic pyrophosphatase	-1.47	1.38E-07	proton transport		
251	PF13_0271	ABC transporter, (heavy metal transporter family), putative	-1.23	1.91E-06	transport		GO:0009536~plastid
252	PF14_0260	metabolite/drug transporter, putative	-1.19	1.14E-04	transport		
253	PFI0270w	conserved *Plasmodium* protein, unknown function	-1.15	1.78E-06	transport		
254	PFI1560c	conserved *Plasmodium* membrane protein, unknown function	-1.04	1.70E-04	transport		
255	PF10_0129	conserved *Plasmodium* protein, unknown function	-1.03	1.14E-05	phosphate transport		
256	PF11_0287	CRAL/TRIO domain-containing protein, putative	-0.95	4.31E-05	transport		
257	PF13_0238	kelch protein, putative	-0.81	4.59E-05	potassium ion transport		GO:0006811~ion transport
258	PF11_0340	conserved *Plasmodium* protein, unknown function	-0.77	2.10E-03	potassium ion transport		

259	PFD0725c	arsenical pump-driving ATPase, putative	0.80	1.14E-04	cellular metal ion homeostasis	ion transport	GO:0006873~cellular ion homeostasis
260	PF08_0097	conserved *Plasmodium* membrane protein, unknown function	0.82	3.93E-05	transport		
261	PF14_0133	SufC ATPase, putative	0.88	3.50E-05	transport		GO:0009536~plastid
262	PFF0170w	cation/H antiporter	0.90	3.83E-05	calcium ion transport		GO:0006811~ion transport
263	PF10_0216	zinc transporter, putative	1.03	1.70E-04	ion transport	transport	
264	PFI0400c	conserved *Plasmodium* membrane protein, unknown function	1.20	1.99E-06	ion transport		
Metabolic processes							
265	PFL0035c	acyl-CoA synthetase, PfACS7	-1.89	2.32E-07	metabolic process		
266	PF11_0190	haloacid dehalogenase-like hydrolase, putative	-1.13	8.38E-05	metabolic process		GO:0016791~phosphatase activity
267	PFC0260w	P-loop containing nucleoside triphospahte hydrolase, putative	-0.88	7.55E-04	metabolic process		
268	PF10_0147	FAD synthetase, putative	-0.79	7.18E-04	metabolic process		GO:0016779~nucleotidyltransferase activity
269	PF10_0036	N-acetyltransferase, putative	-0.77	8.59E-04	metabolic process		GO:0016407~acetyltransferase activity
270	PF11_0145	glyoxalase I	0.76	2.74E-04	methylglyoxal metabolic process		
271	MAL13P1.186	1-deoxy-D-xylulose 5-phosphate synthase	0.77	6.06E-05	metabolic process		GO:0016744~transferase activity
272	PFE1510c	triose phosphate transporter	0.80	2.67E-03	glucose import		GO:0009536~plastid
273	PF14_0060	glycerophodiester phosphodiesterase, putative	0.82	3.78E-04	glycerol metabolic process	intracellular signaling pathway	GO:0006071~glycerol metabolic process
274	PF13_0131	acetyltransferase, GNAT family, putative	0.86	2.38E-04	metabolic process		GO:0016407~acetyltransferase activity
275	PF10_0210	deoxyribose-phosphate aldolase, putative	0.86	1.01E-05	deoxyribonucleotide catabolic process	pentose-phosphate shunt	GO:0005996~monosaccharide metabolic process
276	PF11_0311	N-acetyl glucosamine phosphate mutase, putative	0.88	6.49E-05	carbohydrate metabolic process	glucosamine metabolic process	GO:0005996~monosaccharide metabolic process
277	PF14_0286	glutamate dehydrogenase, putative	0.90	2.92E-04	cellular amino acid metabolic process	oxidation reduction	GO:0055114~oxidation reduction
278	PF14_0357	succinyl CoA ligase, putative	0.91	3.26E-03	glycolysis	tricarboxylic acid cycle	GO:0005996~monosaccharide metabolic process
279	PFF1265w	oxidoreductase, short-chain dehydrogenase family, putative	0.91	1.12E-05	metabolic process		GO:0055114~oxidation reduction
280	PF14_0295	ATP-specific succinyl-CoA synthetase beta subunit, putative	0.92	6.79E-05	succinyl-CoA metabolic process	tricarboxylic acid cycle	GO:0006084~acetyl-CoA metabolic process
281	MAL13P1.319	indole-3-glycerol-phosphate synthase, putative	0.92	1.03E-03	metabolic process		GO:0016831~carboxy-lyase activity
282	PF10_0122	phosphoglucomutase, putative	0.94	3.07E-04	carbohydrate metabolic process		GO:0016866~intramolecular transferase activity
283	PFL0285w	targeted glyoxalase II	1.07	9.33E-06	methylglyoxal metabolic process		GO:0006081~cellular aldehyde metabolic process
Cofactor related processes							
284	PFD0830w	bifunctional dihydrofolate reductase-thymidylate synthase	0.76	4.08E-04	dTMP biosynthetic process	glycine biosynthetic process	
285	PFL1920c	hydroxyethylthiazole kinase, putative	0.76	2.19E-03	thiamin biosynthetic process		GO:0006766~vitamin metabolic process
Vesicle-mediated transport							
286	PF13_0090	ADP-ribosylation factor, putative	-1.92	1.09E-06	intracellular protein transport	small GTPase mediated signal transduction	GO:0006886~intracellular protein transport
287	PFI0515w	SNARE protein, putative	-1.08	3.55E-06	intracellular protein transport	regulation of vesicle fusion	GO:0016192~vesicle-mediated transport
288	PFL0885w	adaptor protein subunit, putative	-0.92	2.07E-05	intracellular protein transport	vesicle-mediated transport	GO:0006886~intracellular protein transport

289	PFB0480w	syntaxin, Qa-SNARE family	-0.90	6.25E-04	intracellular protein transport	regulation of vesicle fusion	
290	MAL13P1.135	SNARE protein, putative	-0.85	1.78E-04	intracellular protein transport	regulation of vesicle fusion	GO:0006886~intracellular protein transport
291	PFF0830w	alpha adaptin-like protein, putative	-0.84	6.76E-04	intracellular protein transport	protein complex assembly	GO:0006461~protein complex assembly
292	PF14_0034	translocation associated membrane protein, putative	1.07	1.84E-04	intracellular protein transmembrane transport		GO:0016021~integral to membrane
Post-translational protein modification							
293	PFE0340c	rhomboid protease ROM4	-1.34	2.28E-06	signal peptide processing		GO:0016021~integral to membrane
294	PF13_0301	ubiquitin conjugating enzyme, putative	-1.01	8.42E-05	post-translational protein modification	regulation of protein metabolic process	GO:0006508~proteolysis
295	PFE0835w	ubiquitin carboxyl-terminal hydrolase 2, putative	-0.96	1.67E-05	protein deubiquitination	ubiquitin-dependent protein catabolic process	GO:0006508~proteolysis
296	PFL2545c	*Plasmodium* exported protein, unknown function	-0.95	3.76E-04	post-translational protein modification	regulation of protein metabolic process	
297	PFL2100w	ubiquitin conjugating enzyme E2, putative	-0.88	2.84E-04	post-translational protein modification	regulation of protein metabolic process	forming carbon-nitrogen bonds
298	PFC0855w	ubiquitin conjugating enzyme, putative	0.77	1.25E-03	post-translational protein modification	regulation of protein metabolic process	
299	PFL1790w	ubiquitin-activating enzyme, putative	0.78	1.10E-04	ER-associated protein catabolic process	protein modification process	GO:0001882~nucleoside binding
300	PF08_0085	ubiquitin conjugating enzyme, putative	0.85	1.69E-05	post-translational protein modification	regulation of protein metabolic process	GO:0006508~proteolysis
301	PF10_0330	ubiquitin conjugating enzyme, putative	0.98	3.76E-05	post-translational protein modification	protein ubiquitination	GO:0006508~proteolysis
Proteolysis							
302	PF08_0108	plasmepsin X	-3.01	6.47E-10	proteolysis		GO:0006508~proteolysis
303	PFE0370c	subtilisin-like protease 1	-3.00	2.36E-08	proteolysis		GO:0006508~proteolysis
304	PFF1365c	HECT-domain (ubiquitin-transferase), putative	-2.69	9.72E-10	protein modification process		
305	PFD0230c	dipeptidyl peptidase 3	-2.17	6.31E-08	protein catabolic process	proteolysis	GO:0006508~proteolysis
306	PF10_0094	tubulin-tyrosine ligase, putative	-2.06	4.17E-08	protein modification process		GO:0016879~ligase activity
307	MAL8P1.126	serine protease, putative	-1.53	6.46E-06	proteolysis		GO:0006508~proteolysis
308	MAL13P1.38	conserved *Plasmodium* membrane protein, unknown function	-1.44	7.09E-07	proteolysis		
309	PF11_0381	subtilisin-like protease 2	-1.36	5.42E-06	protein maturation	proteolysis	
310	PFE0355c	subtilisin-like protease 3, putative	-1.08	1.54E-04	proteolysis		GO:0006508~proteolysis
311	PFE1235c	ubiquitin fusion degradation protein UFD1, putative	-1.04	2.55E-02	ubiquitin-dependent protein catabolic process		GO:0006508~proteolysis
312	PFB0585w	Leu/Phe-tRNA protein transferase, putative	-0.90	2.98E-05	protein catabolic process		GO:0009057~macromolecule catabolic process
313	MAL13P1.56	M1-family alanyl aminopeptidase	0.80	1.03E-02	proteolysis		GO:0006508~proteolysis
314	PFC0495w	plasmepsin VI	0.86	2.36E-02	proteolysis		
315	PFB0355c	serine repeat antigen 2	2.40	9.86E-07	immunoglobulin production	proteolysis	
Protein folding							
316	PF11_0509	ring-infected erythrocyte surface antigen	-3.03	2.93E-09	protein folding		GO:0006457~protein folding
317	PFD0095c	*Plasmodium* exported protein (PHISTb), unknown function	-2.38	7.17E-09	protein folding		
318	PF11_0513	DnaJ protein, putative	-1.52	3.86E-06	protein folding		GO:0006457~protein folding
319	PFD1170c	*Plasmodium* exported protein (PHISTb), unknown function	-1.17	3.58E-06	protein folding		

320	PF11_0175	heat shock protein 101	-0.96	3.08E-05	protein folding	protein hexamerization	GO:0006986~response to unfolded protein
321	PF08_0115	DnaJ protein, putative	-0.80	7.91E-04	protein folding		GO:0006457~protein folding
322	PFI0985c	chaperone, putative	0.78	9.21E-04	protein folding		
323	PFA0460c	tubulin-specific chaperone a, putative	1.11	8.42E-06	protein complex assembly	protein folding	
Protein transport						
324	PFD0720w	conserved ARM repeats protein, unknown function	-3.02	2.93E-09	protein import into nucleus		
325	PFA0155c	conserved *Plasmodium* protein, unknown function	-1.30	3.52E-06	exocytosis	protein transport	
326	PFL2220w	conserved *Plasmodium* protein, unknown function	-1.11	1.30E-05	endocytosis	intracellular protein transport	GO:0006886~intracellular protein transport
327	PF13_0024	conserved *Plasmodium* protein, unknown function	-0.87	2.24E-04	autophagy	protein transport	
328	MAL13P1.51	secretory complex protein 61 alpha,Rab GTPase 5b	-0.83	8.72E-05	protein transport	protein transport by the Sec complex	GO:0006355~regulation of transcription
329	PF14_0171	conserved *Plasmodium* protein, unknown function	-0.80	3.61E-02	autophagy	protein transport	
330	PFE1120w	conserved *Plasmodium* protein, unknown function	-0.79	1.49E-03	protein localization	protein transport	
331	PFF1125c	RNA-binding protein mei2 homologue, putative	0.75	3.98E-03	positive regulation of meiosis		GO:0010564~regulation of cell cycle process
332	PF14_0283	conserved *Plasmodium* protein, unknown function	0.81	6.23E-03	autophagy	cytolysis	GO:0006914~autophagy
333	PFF0155w	mitochondrial chaperone BCS1, putative	0.88	1.10E-02	protein complex assembly		GO:0006461~protein complex assembly
334	MAL8P1.14	mitochondrial inner membrane protein, putative	0.89	1.61E-03	protein insertion into membrane		GO:0008104~protein localization
Protein amino acid dephosphorylation						
335	PF14_0224	serine/threonine protein phosphatase	-2.65	7.57E-10	protein amino acid dephosphorylation		
336	PF08_0129	serine/threonine protein phosphatase, putative	-1.20	2.43E-04	protein amino acid dephosphorylation		GO:0006470~protein amino acid dephosphorylation
337	MAL8P1.108	protein phosphatase, putative	0.85	6.29E-05	protein amino acid dephosphorylation		GO:0006470~protein amino acid dephosphorylation
338	PF14_0280	phosphotyrosyl phosphatase activator, putative	1.01	5.96E-05	protein amino acid dephosphorylation		GO:0006470~protein amino acid dephosphorylation
Chromatin modification						
339	PF13_0152	transcriptional regulatory protein sir2a	-1.24	3.11E-04	chromatin silencing	protein amino acid deacetylation	GO:0006342~chromatin silencing
340	PF10_0211	conserved *Plasmodium* membrane protein, unknown function	-1.05	1.43E-06	ATP synthesis coupled electron transport	transport	
341	MAL13P1.328	DNA topoisomerase VI, b subunit, putative	-0.96	2.61E-04	null		GO:0001882~nucleoside binding
342	PFA0555c	UMP-CMP kinase, putative	-0.95	2.00E-05	nucleobase	nucleoside	
343	PFF0350w	MYND finger protein, putative	-0.93	6.94E-03	negative regulation of transcription from RNA polymerase II promoter		GO:0000122~negative regulation of transcription from RNA polymerase II promoter
344	PF14_0314	chromatin assembly factor 1 P55 subunit, putative	-0.89	6.05E-04	nucleosome assembly		GO:0006323~DNA packaging
345	PF13_0185	histone H3 variant, putative	-0.88	6.41E-05	chromatin assembly or disassembly	nucleosome assembly	GO:0006323~DNA packaging
346	PF11_0429	conserved *Plasmodium* protein, unknown	-0.81	1.65E-04	chromatin modification	regulation of transcription	GO:0043167~ion binding

		function					
347	PF14_0234	DNA-directed DNA polymerase, putative	-0.77	1.94E-04	null		GO:0001882~nucleoside binding
348	PFE1390w	RNA helicase 1	0.77	1.77E-04	null		GO:0001882~nucleoside binding
349	MAL13P1.146	AMP deaminase, putative	0.79	5.44E-04	AMP catabolic process	purine ribonucleoside monophosphate biosynthetic process	GO:0006163~purine nucleotide metabolic process
350	PFD0685c	chromosome associated protein, putative	0.84	1.57E-04	chromosome organization		GO:0000070~mitotic sister chromatid segregation
351	PF13_0349	nucleoside diphosphate kinase	0.89	1.55E-04	CTP biosynthetic process	GTP biosynthetic process	GO:0006163~purine nucleotide metabolic process
352	PFL1725w	ATP synthase beta chain, mitochondrial precursor, putative	0.93	1.10E-05	ATP synthesis coupled proton transport	hydrogen transport	GO:0006091~generation of precursor metabolites and energy
353	PF08_0042	ATP-dependent RNA helicase prh1, putative	1.04	1.06E-02	null		GO:0001882~nucleoside binding
354	PF14_0672	phosphodiesterase delta, putative	1.72	4.82E-06	cyclic nucleotide metabolic process	signal transduction	GO:0009123~nucleoside monophosphate metabolic process
RNA-related processes							
355	PFD0495c	conserved *Plasmodium* protein, unknown function	-2.44	4.87E-09	RNA splicing	mRNA processing	
356	PF11_0255	ribonucleoprotein, putative	-0.82	3.51E-04	RNA splicing	mRNA processing	
357	PFC0145c	conserved *Plasmodium* protein, unknown function	-0.81	2.10E-04	rRNA processing		
358	PF14_0028	pre-mRNA splicing factor, putative	0.80	2.06E-05	RNA processing		GO:0006396~RNA processing
359	PFL1525c	pre-mRNA splicing factor RNA helicase, putative	0.82	3.80E-05	RNA splicing	regulation of cell cycle	GO:0006396~RNA processing
360	PFE1245w	conserved *Plasmodium* protein, unknown function	0.92	2.68E-04	mRNA processing		GO:0043167~ion binding
361	PFD0700c	RNA binding protein, putative	1.48	8.85E-07	RNA metabolic process		
Other processes							
362	PFA0110w	ring-infected erythrocyte surface antigen	-3.77	1.15E-10	regulation of immune response		
363	PF14_0344	translocon component PTEX150	-1.26	2.85E-06	translocation of peptides or proteins into host cell cytoplasm		
364	PFL2285c	conserved *Plasmodium* protein, unknown function	-1.04	1.66E-04	tetrapyrrole biosynthetic process		GO:0018130~heterocycle biosynthetic process
365	PFD0930w	CGI-141 protein homolog, putative	-1.00	1.87E-06	vesicle-mediated transport		GO:0016192~vesicle-mediated transport
366	PF14_0054	conserved protein, unknown function	-1.00	2.34E-06	histone ubiquitination		GO:0043167~ion binding
367	PF13_0159	nicotinic acid mononucleotide adenyltransferase	-0.95	1.55E-04	NAD biosynthetic process		GO:0006732~coenzyme metabolic process
368	PFI0345w	GTPase activator, putative	-0.81	6.34E-04	regulation of Rab GTPase activity		GO:0032313~regulation of Rab GTPase activity
369	PF10_0158	conserved *Plasmodium* protein, unknown function	-0.78	1.06E-03	regulation of GTPase activity		
370	PF13_0221	conserved *Plasmodium* protein, unknown function	0.80	4.92E-03	multicellular organismal development		
371	PF10_0227	HORMA domain protein, putative	0.81	1.79E-03	mitosis		GO:0000087~M phase of mitotic cell cycle
372	PF14_0699	GTPase activator, putative	0.83	5.40E-04	regulation of Rab GTPase activity		GO:0032313~regulation of Rab GTPase activity
373	PFE0970w	cytochrome c oxidase assembly protein (heme A:	0.86	1.26E-05	heme O biosynthetic process		GO:0006778~porphyrin metabolic

		farnesyltransferase), putative					process
374	PF11_0295	farnesyl pyrophosphate synthase, putative	0.86	9.96E-05	isoprenoid biosynthetic process		GO:0006720~isoprenoid metabolic process
375	MAL13P1.183	conserved *Plasmodium* protein, unknown function	0.89	1.17E-02	respiratory electron transport chain		
376	PFB0220w	ubiE/COQ5 methyltransferase, putative	0.89	1.40E-04	quinone cofactor biosynthetic process		GO:0006732~coenzyme metabolic process
377	PF13_0353	NADH-cytochrome b5 reductase, putative	0.89	4.51E-05	null		GO:0055114~oxidation reduction
378	PFF1075w	conserved *Plasmodium* protein, unknown function	0.94	2.17E-04	vacuolar transport	vacuole fusion	
379	PF10_0374	Pf11-1 protein	1.07	5.96E-05	SRP-dependent cotranslational protein targeting to membrane	gamete generation	GO:0007276~gamete generation
380	MAL13P1.251	conserved *Plasmodium* protein, unknown function	1.26	1.40E-05	arginyl-tRNA aminoacylation		GO:0009536~plastid
Transcripts with hypothetical or unknown function							
381	PFL2520w	reticulocyte binding protein homologue 3, pseudogene	-4.63	8.53E-10	null		
382	PF08_0035	conserved *Plasmodium* protein, unknown function	-3.96	6.99E-10	null		
383	PF13_0058	conserved *Plasmodium* protein, unknown function	-3.93	6.47E-10	null		
384	PF07_0061	conserved *Plasmodium* protein, unknown function	-3.56	3.94E-09	null		
385	MAL8P1.70	conserved *Plasmodium* protein, unknown function	-3.49	2.93E-09	null		GO:0043167~ion binding
386	PF11_0268	kelch protein, putative	-3.44	6.50E-10	null		
387	PFE1285w	membrane skeletal protein IMC1-related	-3.22	2.73E-09	null		
388	PFA0440w	photosensitized INA-labeled protein 1, PhIL1, putative	-3.17	3.80E-10	null		
389	PF10_0170	conserved *Plasmodium* protein, unknown function	-3.16	3.04E-10	null		
390	PFC0185w	membrane skeletal protein IMC1-related	-3.09	2.57E-07	null		
391	PFC0830w	trophozoite stage antigen	-2.83	8.33E-08	null		
392	PFB0935w	cytoadherence linked asexual protein 2	-2.79	2.42E-08	null		GO:0020035~cytoadherence to microvasculature
393	PFI0675w	conserved *Plasmodium* protein, unknown function	-2.78	6.38E-10	null		
394	PFF0645c	integral membrane protein, putative	-2.78	3.21E-07	null		GO:0016021~integral to membrane
395	PFC1045c	conserved *Plasmodium* protein, unknown function	-2.74	3.22E-08	null		
396	MAL8P1.141	conserved *Plasmodium* protein, unknown function	-2.71	4.73E-09	null		
397	PFD0195c	conserved *Plasmodium* protein, unknown function	-2.70	3.31E-06	null		
398	PFB0120w	early transcribed membrane protein 2	-2.67	8.58E-09	null		
399	PF11_0039	early transcribed membrane protein 11.1	-2.60	3.58E-08	null		
400	PF13_0233	myosin A	-2.59	4.02E-08	null		GO:0005856~cytoskeleton
401	PF14_0572	conserved *Plasmodium* membrane protein, unknown function	-2.58	6.98E-08	null		

402	PF14_0343	conserved *Plasmodium* protein, unknown function	-2.58	1.65E-07	null		
403	PF13_0079	conserved *Plasmodium* protein, unknown function	-2.56	4.76E-08	null		
404	MAL13P1.268	conserved *Plasmodium* protein, unknown function	-2.54	1.99E-06	null		
405	PF14_0495	rhoptry neck protein 2	-2.51	2.05E-07	null		
406	PFI0410c	conserved *Plasmodium* protein, unknown function	-2.49	1.86E-08	null		
407	PFB0926c	*Plasmodium* exported protein (hyp2), unknown function	-2.45	5.30E-09	null		
408	PFB0670c	conserved *Plasmodium* protein, unknown function	-2.45	3.31E-06	null		
409	PFE0075c	rhoptry-associated protein 3	-2.42	8.59E-09	null		
410	PFI0690c	conserved *Plasmodium* protein, unknown function	-2.38	3.86E-05	null		
411	PF11_0277	conserved *Plasmodium* protein, unknown function	-2.35	9.09E-10	null		
412	PF10_0351	probable protein, unknown function	-2.35	1.17E-08	null		
413	PFF0870w	conserved *Plasmodium* membrane protein, unknown function	-2.34	2.71E-07	null		
414	PFI1800w	lysophospholipase, putative	-2.31	1.25E-06	null		
415	PF11_0213	conserved *Plasmodium* protein, unknown function	-2.28	2.56E-08	null		GO:0016021~integral to membrane
416	MAL7P1.229	cytoadherence linked asexual protein	-2.27	4.31E-09	null		
417	PF14_0337	conserved *Plasmodium* protein, unknown function	-2.25	5.01E-07	null		
418	PFL0300c	protein phosphatase, putative	-2.25	5.90E-08	null		
419	PF08_0058	conserved *Plasmodium* protein, unknown function	-2.24	5.53E-09	null		
420	PFF0710w	conserved *Plasmodium* protein, unknown function	-2.23	4.89E-08	null		
421	PF11_0168	rhoptry neck protein 4	-2.23	8.33E-08	null		
422	PFE0770w	conserved *Plasmodium* protein, unknown function	-2.20	1.63E-07	null		
423	PFD1150c	reticulocyte binding protein homologue 4	-2.18	1.89E-07	null		
424	PF10_0306	MORN repeat protein, putative	-2.15	4.22E-09	null		
425	PF14_0222	ankyrin, putative	-2.14	2.95E-06	null		
426	MAL7P1.66	mitochondrial ribosomal protein S5 precursor, putative	-2.12	8.30E-08	null		GO:0005840~ribosome
427	PF14_0102	rhoptry-associated protein 1	-2.10	1.20E-06	null		GO:0020007~apical complex
428	MAL13P1.260	alveolin, putative	-2.09	2.76E-07	null		
429	PFF0675c	myosin E, putative	-2.09	2.32E-07	null		GO:0008092~cytoskeletal protein binding
430	PFL2225w	myosin A tail domain interacting protein	-2.08	3.20E-09	null		
431	PFI0785c	sugar transporter, putative	-2.08	6.16E-07	null		GO:0008643~carbohydrate transport
432	PF10_0352	merozoite surface protein	-2.05	8.33E-08	null		
433	PF11_0528	conserved *Plasmodium* protein, unknown function	-2.03	1.04E-06	null		

434	PFC0355c	conserved *Plasmodium* protein, unknown function	-2.03	1.74E-07	null		
435	PF14_0018	*Plasmodium* exported protein (PHISTb), unknown function	-2.02	3.40E-09	null		
436	PFL1090w	glideosome-associated protein 45	-2.00	2.76E-06	null		
437	PF10_0135	conserved *Plasmodium* protein, unknown function	-1.99	9.40E-08	null		
438	PF10_0193	microtubule-associated protein 1 light chain 3, putative	-1.97	1.27E-08	null		
439	PFI1445w	high molecular weight rhoptry protein 2	-1.97	4.02E-08	null		
440	PFB0475c	conserved *Plasmodium* protein, unknown function	-1.96	3.58E-08	null		
441	PF11_0094	conserved *Plasmodium* protein, unknown function	-1.96	9.40E-08	null		
442	PF08_0130	rRNA processing WD-repeat protein, putative	-1.92	1.36E-06	null		
443	PFD0100c	surface-associated interspersed gene 4.1, (SURFIN4.1)	-1.90	9.64E-07	null		
444	MAL13P1.405	conserved protein, unknown function	-1.90	1.63E-07	null		
445	PF10_0146	conserved *Plasmodium* protein, unknown function	-1.89	9.40E-08	null		
446	PFE1260c	conserved *Plasmodium* protein, unknown function	-1.89	8.48E-08	null		
447	PF10_0184	conserved *Plasmodium* protein, unknown function	-1.89	2.56E-07	null		
448	PF10_0072	conserved *Plasmodium* protein, unknown function	-1.88	8.77E-07	null		GO:0043167~ion binding
449	PFL1785c	conserved *Plasmodium* protein, unknown function	-1.88	5.76E-09	null		
450	PFD0395c	conserved *Plasmodium* protein, unknown function	-1.87	9.90E-09	null		
451	PF07_0127	conserved *Plasmodium* protein, unknown function	-1.87	4.76E-08	null		
452	MAL13P1.94	conserved *Plasmodium* membrane protein, unknown function	-1.84	7.09E-08	null		
453	PF14_0652	conserved *Plasmodium* protein, unknown function	-1.82	3.95E-08	null		GO:0043167~ion binding
454	PF10_0220	phospholipid scramblase 1, putative	-1.80	1.84E-07	null		
455	PF14_0119	p1/s1 nuclease, putative	-1.80	8.11E-06	null		
456	PF11_0180	conserved *Plasmodium* protein, unknown function	-1.76	7.46E-07	null		
457	PFF1020c	conserved *Plasmodium* protein, unknown function	-1.76	5.57E-07	null		
458	PFL0060w	*Plasmodium* exported protein, unknown function	-1.74	8.68E-07	null		
459	PFE0175c	myosin B	-1.73	1.17E-06	null		GO:0005856~cytoskeleton
460	PF14_0732	*Plasmodium* exported protein (PHISTb), unknown function	-1.72	4.65E-07	null		
461	PF13_0255	conserved *Plasmodium* protein, unknown function	-1.70	3.13E-06	null		
462	PF14_0578	conserved *Plasmodium* protein, unknown	-1.68	1.42E-07	null		

		function					
463	PFI0265c	high molecular weight rhoptry protein 3	-1.67	7.22E-07	null		
464	PF10_0308	OTU-like cysteine protease, putative	-1.67	7.91E-08	null		
465	PFC0820w	conserved *Plasmodium* protein, unknown function	-1.67	8.59E-06	null		
466	PFE0365c	conserved *Plasmodium* protein, unknown function	-1.66	4.16E-05	null		
467	PFB0275w	metabolite/drug transporter, putative	-1.66	4.18E-07	null		
468	PF14_0586	conserved *Plasmodium* protein, unknown function	-1.64	2.26E-06	null		
469	PF11_0415	conserved *Plasmodium* protein, unknown function	-1.64	1.61E-07	null		
470	PF11_0267	kelch protein, putative	-1.63	7.74E-06	null		
471	PF13_0036	DnaJ protein, putative	-1.63	1.66E-06	null		
472	PFF0480w	conserved *Plasmodium* protein, unknown function	-1.62	1.54E-07	null		
473	PF10_0347	merozoite surface protein	-1.60	9.22E-07	null		
474	PFD0385w	conserved *Plasmodium* protein, unknown function	-1.60	6.44E-07	null		
475	PF10_0295	conserved *Plasmodium* protein, unknown function	-1.59	9.48E-05	null		
476	MAL8P1.144	AAA family ATPase, putative	-1.57	1.89E-07	null		GO:0006355~regulation of transcription
477	PFI1720w	gametocytogenesis-implicated protein	-1.57	2.03E-05	null		
478	PFE0440w	conserved *Plasmodium* protein, unknown function	-1.52	1.05E-05	null		
479	PFD0765w	RING zinc finger protein, putative	-1.52	6.05E-07	null		GO:0043167~ion binding
480	PFD0185c	conserved *Plasmodium* protein, unknown function	-1.52	5.19E-07	null		
481	PFF0990c	conserved *Plasmodium* protein, unknown function	-1.51	4.17E-07	null		
482	PFE1415w	cell cycle regulator with zn-finger domain, putative	-1.51	1.40E-05	null		GO:0043167~ion binding
483	PFC0370w	conserved *Plasmodium* protein, unknown function	-1.50	9.61E-07	null		
484	MAL13P1.102	conserved *Plasmodium* protein, unknown function	-1.50	4.84E-04	null		
485	PFI0360c	conserved *Plasmodium* protein, unknown function	-1.49	4.43E-07	null		
486	MAL7P1.29	conserved *Plasmodium* membrane protein, unknown function	-1.49	6.72E-06	null		
487	PF14_0660	protein phosphatase, putative	-1.48	1.91E-06	null		
488	MAL8P1.13	folate/biopterin transporter, putative	-1.47	1.27E-06	null		GO:0016021~integral to membrane
489	PF08_0119	conserved *Plasmodium* protein, unknown function	-1.47	1.66E-06	null		
490	PF10_0151	conserved *Plasmodium* protein, unknown function	-1.45	1.07E-05	null		
491	PF14_0044	conserved *Plasmodium* protein, unknown function	-1.44	3.22E-05	null		
492	PF13_0169	conserved *Plasmodium* protein, unknown	-1.42	1.68E-05	null		

		function					
493	PF14_0092	conserved *Plasmodium* membrane protein, unknown function	-1.41	2.05E-07	null		
494	PFF0485c	zinc finger protein, putative	-1.41	2.02E-07	null		GO:0016021~integral to membrane
495	PF10_0037	conserved *Plasmodium* protein, unknown function	-1.41	4.88E-06	null		
496	PF10_0223	conserved *Plasmodium* membrane protein, unknown function	-1.41	1.90E-06	null		
497	MAL13P1.331	conserved *Plasmodium* protein, unknown function	-1.41	3.74E-06	null		
498	MAL13P1.130	glideosome associated protein with multiple membrane spans 1	-1.40	1.57E-06	null		
499	PF14_0213	conserved *Plasmodium* protein, unknown function	-1.40	1.53E-05	null		
500	PFI0940c	PPPDE peptidase, putative	-1.40	4.01E-06	null		
501	PF14_0013	DnaJ protein, putative	-1.39	4.82E-06	null		GO:0016021~integral to membrane
502	MAL8P1.146	filament assembling protein, putative	-1.39	3.47E-04	null		GO:0005200~structural constituent of cytoskeleton
503	PF10_0292	conserved *Plasmodium* protein, unknown function	-1.38	9.18E-06	null		
504	PFA0265c	conserved *Plasmodium* protein, unknown function	-1.38	6.53E-06	null		
505	MAL13P1.245	conserved *Plasmodium* protein, unknown function	-1.37	1.15E-05	null		
506	PFB0106c	*Plasmodium* exported protein, unknown function	-1.37	1.99E-04	null		
507	PFL1025c	conserved *Plasmodium* protein, unknown function	-1.37	3.65E-07	null		
508	PFD0255w	ag-1 blood stage membrane protein homologue	-1.37	1.28E-06	null		
509	PFI0845w	conserved *Plasmodium* membrane protein, unknown function	-1.36	6.88E-06	null		
510	PF11_0193	conserved *Plasmodium* protein, unknown function	-1.36	1.33E-04	null		
511	PFI0705w	conserved *Plasmodium* protein, unknown function	-1.36	2.89E-06	null		
512	PF11_0300	conserved *Plasmodium* protein, unknown function	-1.36	6.53E-07	null		
513	PF08_0003	tryptophan/threonine-rich antigen	-1.36	1.17E-06	null		
514	PF14_0363	metacaspase-like protein	-1.35	2.41E-05	null		
515	PF11_0362	protein phosphatase, putative	-1.33	7.73E-07	null		
516	PFL1505c	conserved *Plasmodium* protein, unknown function	-1.32	6.62E-04	null		
517	PFL0315c	conserved *Plasmodium* protein, unknown function	-1.32	8.41E-07	null		
518	PF14_0135	conserved *Plasmodium* protein, unknown function	-1.31	4.71E-05	null		
519	PF11_0040	early transcribed membrane protein 11.2	-1.31	8.62E-06	null		
520	PF10_0248	conserved *Plasmodium* membrane protein, unknown function	-1.29	8.77E-06	null		
521	PF11_0167	conserved *Plasmodium* membrane protein,	-1.29	8.49E-07	null		GO:0043167~ion binding

		unknown function					
522	MAL7P1.170	*Plasmodium* exported protein, unknown function	-1.29	3.82E-07	null		
523	PF13_0162	conserved *Plasmodium* protein, unknown function	-1.29	2.61E-06	null		
524	PF08_0081	conserved *Plasmodium* protein, unknown function	-1.29	2.77E-06	null		
525	PF14_0110	rhomboid protease ROM8	-1.28	6.59E-07	null		
526	PF07_0019	conserved *Plasmodium* protein, unknown function	-1.27	7.73E-07	null		
527	PF10_0073	conserved *Plasmodium* protein, unknown function	-1.27	9.02E-06	null		
528	PF14_0374	CCAAT-binding transcription factor, putative	-1.27	5.78E-06	null		
529	PF10_0019	early transcribed membrane protein 10.1	-1.26	8.67E-05	null		
530	PFB0625w	conserved *Plasmodium* protein, unknown function	-1.23	6.86E-06	null		
531	PF14_0106	ankyrin-repeat protein, putative	-1.23	2.03E-04	null		
532	PF10_0254	conserved *Plasmodium* protein, unknown function	-1.23	1.80E-05	null		
533	PFI1555w	conserved *Plasmodium* protein, unknown function	-1.23	1.59E-06	null		
534	PF13_0161	conserved *Plasmodium* protein, unknown function	-1.23	8.65E-06	null		
535	PF11_0505	probable protein, unknown function	-1.23	7.09E-06	null		
536	PF08_0118	conserved *Plasmodium* protein, unknown function	-1.22	4.36E-06	null		GO:0043167~ion binding
537	PFE0650c	conserved *Plasmodium* protein, unknown function	-1.21	7.07E-06	null		
538	PFD1130w	conserved *Plasmodium* protein, unknown function	-1.21	5.85E-05	null		
539	MAL13P1.228	conserved *Plasmodium* protein, unknown function	-1.20	1.45E-06	null		
540	PFC0700c	conserved *Plasmodium* protein, unknown function	-1.19	7.99E-06	null		
541	PF11_0379	conserved *Plasmodium* protein, unknown function	-1.19	2.66E-03	null		
542	PF14_0045	conserved *Plasmodium* protein, unknown function	-1.19	2.74E-05	null		GO:0016021~integral to membrane
543	PFC0090w	*Plasmodium* exported protein, unknown function	-1.19	4.56E-04	null		
544	PFL1795c	conserved *Plasmodium* protein, unknown function	-1.18	7.24E-05	null		
545	PFC0345w	conserved *Plasmodium* protein, unknown function	-1.18	1.01E-05	null		
546	PFB0105c	*Plasmodium* exported protein (PHISTc), unknown function	-1.17	1.17E-04	null		
547	PFL1870c	sphingomyelin phosphodiesterase, putative	-1.17	5.92E-05	null		
548	MAL13P1.480	histidine-rich protein III	-1.17	2.19E-04	null		
549	PFC0235w	conserved *Plasmodium* protein, unknown function	-1.17	7.60E-06	null		
550	MAL13P1.215	conserved *Plasmodium* protein, unknown	-1.16	4.50E-05	null		

		function					
551	PFB0615c	conserved *Plasmodium* protein, unknown function	-1.16	2.41E-05	null		
552	PFI1040c	conserved *Plasmodium* membrane protein, unknown function	-1.16	4.44E-03	null		
553	PF10_0163	*Plasmodium* exported protein (PHISTc), unknown function	-1.16	4.91E-05	null		
554	PF10_0301	calmodulin, putative	-1.15	1.99E-04	null		GO:0043167~ion binding
555	PF07_0107	*Plasmodium* exported protein, unknown function	-1.15	8.38E-05	null		
556	PF14_0065	glideosome associated protein with multiple membrane spans 3, putative	-1.11	3.85E-06	null		
557	PF14_0016	early transcribed membrane protein 14.1	-1.11	3.35E-05	null		
558	PF10_0315	conserved *Plasmodium* protein, unknown function	-1.10	1.18E-04	null		
559	PFA0210c	conserved *Plasmodium* protein, unknown function	-1.10	9.25E-06	null		
560	PF14_0353	conserved *Plasmodium* protein, unknown function	-1.10	1.41E-05	null		
561	MAL13P1.413	membrane associated histidine-rich protein	-1.10	5.15E-04	null		
562	MAL13P1.380	conserved *Plasmodium* protein, unknown function	-1.09	1.40E-04	null		
563	MAL8P1.62	conserved *Plasmodium* protein, unknown function	-1.08	3.86E-06	null		
564	PFF1475c	conserved *Plasmodium* protein, unknown function	-1.08	7.54E-06	null		
565	MAL13P1.308	conserved *Plasmodium* protein, unknown function	-1.08	1.65E-06	null		
566	PF14_0388	conserved *Plasmodium* protein, unknown function	-1.08	1.67E-05	null		
567	PFE0785c	metabolite/drug transporter, putative	-1.08	5.61E-06	null		
568	PF14_0472	conserved *Plasmodium* protein, unknown function	-1.07	1.33E-04	null		
569	PF11_0417	conserved *Plasmodium* protein, unknown function	-1.06	6.25E-05	null		
570	PFI1380c	conserved *Plasmodium* protein, unknown function	-1.06	1.90E-03	null		
571	PFA0295c	conserved *Plasmodium* protein, unknown function	-1.05	1.22E-03	null		
572	PFE0200c	AN1-like zinc finger family protein	-1.05	8.48E-05	null		GO:0043167~ion binding
573	PFE0590w	conserved *Plasmodium* protein, unknown function	-1.05	1.33E-04	null		
574	MAL13P1.37	conserved *Plasmodium* protein, unknown function	-1.04	7.66E-05	null		GO:0043167~ion binding
575	PF13_0086	conserved *Plasmodium* protein, unknown function	-1.04	1.33E-04	null		
576	PFC0905c	oocyst capsule protein	-1.04	5.51E-05	null		
577	PF11_0172	folate/biopterin transporter, putative	-1.04	8.97E-05	null		
578	PFE0425w	conserved *Plasmodium* protein, unknown function	-1.03	2.13E-03	null		GO:0043167~ion binding

579	PFL2120w	conserved *Plasmodium* protein, unknown function	-1.03	2.77E-06	null		
580	MAL8P1.109	protein phosphatase, putative	-1.01	5.39E-05	null		
581	PFL0325w	Tat binding protein 1(TBP-1)-interacting protein, putative	-1.01	5.17E-03	null		
582	PFD0080c	*Plasmodium* exported protein (PHISTb), unknown function	-0.99	3.20E-05	null		
583	PFC0875w	ABC transporter, putative	-0.99	2.97E-05	null		
584	PF14_0149	conserved *Plasmodium* protein, unknown function	-0.99	1.22E-03	null		
585	PFI0885w	cytochrome b5-like heme/steroid binding protein, putative	-0.98	2.69E-05	null		
586	PFD0715c	conserved *Plasmodium* protein, unknown function	-0.98	3.86E-04	null		
587	PFD0940w	conserved *Plasmodium* protein, unknown function	-0.98	6.48E-05	null		
588	PFE1410c	conserved *Plasmodium* protein, unknown function	-0.97	1.93E-03	null		
589	PFL1565c	CG2-related protein, putative	-0.96	8.78E-06	null		
590	PF10_0156	conserved *Plasmodium* protein, unknown function	-0.96	1.92E-03	null		
591	PFL2110c	conserved protein, unknown function	-0.96	5.96E-03	null		
592	PF14_0143	atypical protein kinase, ABC-1 family, putative	-0.96	2.14E-05	null		
593	PF14_0530	ferlin, putative	-0.95	2.37E-04	null		
594	PFF0610c	PP-loop family protein, putative	-0.94	4.36E-05	null		
595	PF14_0173	cyclic nucleotide-binding protein, putative	-0.94	3.40E-05	null		
596	PFE1130w	conserved protein, unknown function	-0.93	4.12E-05	null		
597	PF14_0303	conserved *Plasmodium* protein, unknown function	-0.93	3.52E-04	null		
598	MAL7P1.7	*Plasmodium* exported protein (PHISTb), unknown function	-0.93	3.39E-04	null		
599	MAL13P1.264	conserved *Plasmodium* protein, unknown function	-0.93	1.90E-05	null		
600	PF14_0604	conserved *Plasmodium* protein, unknown function	-0.93	5.31E-04	null		
601	PFL1385c	merozoite surface protein 9	-0.93	1.24E-03	null		
602	PF10_0020	alpha/beta hydrolase, putative	-0.92	3.90E-04	null		
603	PFB0955w	stevor	-0.91	1.88E-04	null		GO:0005576~extracellular region
604	PF10_0283	conserved *Plasmodium* protein, unknown function	-0.91	4.60E-04	null		
605	PFB0190c	conserved *Plasmodium* protein, unknown function	-0.90	1.69E-04	null		
606	MAL13P1.188	conserved *Plasmodium* protein, unknown function	-0.90	1.47E-05	null		
607	MAL7P1.13	conserved *Plasmodium* protein, unknown function	-0.90	5.86E-04	null		
608	PF10_0342	probable protein, unknown function	-0.89	2.30E-03	null		
609	PFI0975c	conserved *Plasmodium* protein, unknown function	-0.89	1.45E-04	null		

610	PFF0295c	conserved *Plasmodium* protein, unknown function	-0.88	9.52E-05	null		
611	MAL7P1.222	rifin	-0.88	8.25E-03	null		
612	PF07_0028	conserved *Plasmodium* protein, unknown function	-0.88	2.00E-02	null		
613	PFL2205w	conserved *Plasmodium* protein, unknown function	-0.88	3.08E-04	null		
614	PF10_0244	formin 2, putative	-0.87	6.76E-05	null		GO:0043167~ion binding
615	PFD0300w	conserved *Plasmodium* protein, unknown function	-0.87	1.67E-03	null		
616	PF08_0082	conserved *Plasmodium* protein, unknown function	-0.87	6.97E-04	null		
617	PFL1945c	early transcribed membrane protein 12	-0.86	1.14E-03	null		
618	MAL8P1.12	conserved *Plasmodium* protein, unknown function	-0.86	3.45E-03	null		
619	PF10_0304	conserved *Plasmodium* protein, unknown function	-0.86	1.30E-03	null		
620	PFF0605c	conserved *Plasmodium* protein, unknown function	-0.86	2.03E-02	null		
621	PFL1650w	conserved *Plasmodium* protein, unknown function	-0.86	1.09E-04	null		
622	PF10_0023	*Plasmodium* exported protein (hyp16), unknown function	-0.85	3.86E-02	null		
623	PFD0910w	conserved *Plasmodium* protein, unknown function	-0.85	4.31E-03	null		
624	PF13_0055	conserved *Plasmodium* protein, unknown function	-0.85	2.14E-04	null		GO:0043167~ion binding
625	PFI0850w	conserved *Plasmodium* protein, unknown function	-0.84	4.89E-04	null		
626	PFB0145c	conserved *Plasmodium* protein, unknown function	-0.84	2.22E-05	null		
627	PFB0310c	merozoite surface protein 4	-0.84	4.16E-05	null		
628	PFF1460c	conserved *Plasmodium* protein, unknown function	-0.83	2.25E-04	null		
629	PF14_0703	conserved *Plasmodium* protein, unknown function	-0.83	1.25E-03	null		
630	PF10_0025	PF70 protein	-0.83	2.14E-04	null		
631	PFE1095w	conserved *Plasmodium* protein, unknown function	-0.83	4.31E-04	null		
632	PF10_0118	conserved *Plasmodium* protein, unknown function	-0.83	1.43E-02	null		
633	PF14_0196	tetratricopeptide repeat family protein, putative	-0.83	2.39E-04	null		
634	PF13_0303	regulator of chromosome condensation, putative	-0.82	3.30E-05	null		
635	MAL13P1.287	conserved *Plasmodium* protein, unknown function	-0.82	7.23E-04	null		
636	PF11_0390	conserved *Plasmodium* protein, unknown function	-0.82	5.30E-03	null		
637	PF10_0034	conserved *Plasmodium* protein, unknown function	-0.82	4.20E-04	null		

638	MAL13P1.137	conserved *Plasmodium* protein, unknown function	-0.81	1.47E-04	null		
639	PFI1735c	ring-exported protein 1	-0.81	1.57E-04	null		
640	MAL13P1.296	conserved *Plasmodium* protein, unknown function	-0.81	2.49E-04	null		
641	PF14_0151	RNA-binding protein Nova-1, putative	-0.81	8.68E-04	null		
642	PF11_0290	conserved *Plasmodium* protein, unknown function	-0.81	4.91E-05	null		
643	PFE0400w	SET domain protein, putative	-0.81	4.02E-04	null		
644	PFF1505w	TRAP-like protein, putative	-0.80	2.64E-04	null		
645	PF10_0185	conserved *Plasmodium* protein, unknown function	-0.80	4.02E-02	null		
646	PF14_0233	conserved *Plasmodium* protein, unknown function	-0.80	1.42E-04	null		
647	PFC0760c	conserved *Plasmodium* protein, unknown function	-0.80	1.88E-03	null		
648	PF10_0157	conserved *Plasmodium* protein, unknown function	-0.80	9.25E-03	null		
649	MAL13P1.175	MSP7-like protein, fragment	-0.79	7.11E-04	null		
650	PFI0355c	ATP-dependent heat shock protein, putative	-0.79	2.42E-03	null		GO:0009376~HslUV protease complex
651	MAL8P1.160	*Plasmodium* exported protein (hyp7), unknown function	-0.79	6.62E-03	null		
652	PF10_0024	*Plasmodium* exported protein (hyp2), unknown function	-0.78	1.29E-03	null		
653	PF14_0136	diphthamide synthesis protein, putative	-0.78	7.75E-05	null		
654	PF13_0285	inositol-polyphosphate 5-phosphatase, putative	-0.78	4.26E-04	null		GO:0004445~inositol-polyphosphate 5-phosphatase activity
655	PFI1755c	ring-exported protein 3	-0.78	8.67E-05	null		
656	MAL13P1.329	conserved *Plasmodium* membrane protein, unknown function	-0.77	1.71E-02	null		
657	PFD0580c	conserved *Plasmodium* protein, unknown function	-0.77	3.39E-02	null		
658	PFB0915w	liver stage antigen 3	-0.77	5.35E-03	null		
659	PFB0910w	*Plasmodium* exported protein, unknown function	-0.77	1.56E-04	null		
660	MAL8P1.209	var-like protein	-0.77	1.07E-02	null		
661	PFI0385c	P1 nuclease, putative	-0.77	6.62E-04	null		
662	PF08_0001	*Plasmodium* exported protein, unknown function	-0.76	5.99E-04	null		
663	PFC0130c	conserved *Plasmodium* protein, unknown function	-0.76	8.12E-04	null		
664	PF11_0179	conserved *Plasmodium* protein, unknown function	-0.76	8.87E-05	null		
665	PF14_0621	conserved *Plasmodium* protein, unknown function	-0.76	1.74E-04	null		
666	PFI1225w	conserved *Plasmodium* protein, unknown function	-0.76	6.58E-03	null		
667	PF11_0392	conserved *Plasmodium* protein, unknown function	-0.76	3.18E-02	null		
668	PF14_0140	conserved *Plasmodium* protein, unknown function	-0.76	1.51E-04	null		

669	PF10_0145	conserved *Plasmodium* protein, unknown function	-0.76	2.42E-03	null		GO:0043167~ion binding
670	MAL13P1.152	conserved *Plasmodium* protein, unknown function	-0.76	1.88E-02	null		
671	PF13_0064	conserved *Plasmodium* protein, unknown function	-0.75	2.72E-04	null		
672	PF14_0197	zinc finger protein, putative	-0.75	1.33E-04	null		
673	PFF0570c	conserved *Plasmodium* protein, unknown function	-0.75	2.61E-03	null		
674	PF11_0421	conserved *Plasmodium* protein, unknown function	-0.75	2.87E-04	null		
675	MAL13P1.127	conserved *Plasmodium* protein, unknown function	0.75	2.80E-04	null		
676	PFB0365w	conserved *Plasmodium* protein, unknown function	0.75	3.32E-05	null		
677	PFI0580c	falstatin	0.75	2.13E-04	null		
678	PF14_0032	conserved *Plasmodium* protein, unknown function	0.76	2.18E-03	null		
679	PFL2315c	conserved *Plasmodium* membrane protein, unknown function	0.76	4.06E-03	null		
680	MAL13P1.195	CPW-WPC family protein	0.76	3.78E-04	null		
681	PF10_0253	conserved *Plasmodium* protein, unknown function	0.77	6.24E-03	null		
682	PFI1430w	conserved *Plasmodium* protein, unknown function	0.77	1.03E-03	null		
683	PF07_0039	conserved *Plasmodium* protein, unknown function	0.77	2.78E-03	null		
684	PFF1070c	radical SAM protein, putative	0.77	2.08E-04	null		
685	MAL13P1.236	conserved *Plasmodium* protein, unknown function	0.78	2.31E-04	null		
686	PF08_0040	clp1-related protein, putative	0.78	9.61E-05	null		
687	PF11_0403	conserved *Plasmodium* protein, unknown function	0.78	2.42E-03	null		
688	PFD0415c	conserved *Plasmodium* protein, unknown function	0.79	4.32E-04	null		
689	PF14_0220	conserved *Plasmodium* protein, unknown function	0.79	1.14E-02	null		
690	PFE0760w	conserved *Plasmodium* protein, unknown function	0.79	3.66E-02	null		
691	PFC0915w	ATP-dependent RNA helicase, putative	0.79	3.40E-05	null		
692	PFI1610c	calcyclin binding protein, putative	0.79	5.14E-05	null		
693	PFC0570c	conserved *Plasmodium* protein, unknown function	0.80	5.35E-04	null		
694	PF14_0310	conserved *Plasmodium* protein, unknown function	0.80	1.15E-04	null		
695	PFL1140w	integral membrane protein, putative	0.80	5.28E-05	null		
696	PF11_0322	conserved *Plasmodium* protein, unknown function	0.80	9.39E-04	null		
697	PF08_0021	SPRY domain, putative	0.81	3.43E-03	null		

698	PFL1845c	calcyclin binding protein, putative	0.81	6.55E-04	null		
699	PF14_0103	conserved *Plasmodium* protein, unknown function	0.81	9.21E-05	null		
700	PF13_0114	conserved *Plasmodium* protein, unknown function	0.82	1.26E-02	null		
701	PF13_0194	probable protein, unknown function	0.82	2.87E-05	null		
702	PF10_0238	conserved *Plasmodium* protein, unknown function	0.82	5.75E-04	null		
703	MAL13P1.351	conserved *Plasmodium* protein, unknown function	0.82	1.35E-03	null		
704	PF13_0028	membrane integral peptidase, M50 family, putative	0.82	4.34E-04	null		
705	PF11_0357	zinc finger protein, putative	0.82	4.46E-03	null		GO:0043167~ion binding
706	PFF0640w	conserved *Plasmodium* protein, unknown function	0.82	2.80E-04	null		
707	PFA0235w	conserved *Plasmodium* protein, unknown function	0.83	1.27E-03	null		
708	PFI0605c	conserved *Plasmodium* protein, unknown function	0.83	8.28E-04	null		
709	PF11_0186	conserved *Plasmodium* protein, unknown function	0.83	1.98E-05	null		
710	PFL0610w	conserved *Plasmodium* protein, unknown function	0.84	2.72E-02	null		
711	PF14_0542	conserved protein, unknown function	0.84	2.83E-04	null		
712	MAL13P1.149	conserved *Plasmodium* protein, unknown function	0.85	7.75E-04	null		
713	PFI1330c	conserved *Plasmodium* protein, unknown function	0.85	2.16E-04	null		
714	MAL7P1.124	conserved *Plasmodium* protein, unknown function	0.86	3.98E-04	null		
715	PF13_0223	conserved protein, unknown function	0.86	4.55E-04	null		
716	PF13_0035	U3 small nucleolar RNA-associated protein 6, putative	0.86	4.35E-03	null		
717	PF07_0114	conserved *Plasmodium* protein, unknown function	0.86	2.33E-03	null		
718	PFL0800c	cell traversal protein for ookinetes and sporozoites	0.87	2.27E-02	null		
719	PF11_0308	conserved *Plasmodium* protein, unknown function	0.87	2.23E-04	null		
720	MAL8P1.56	conserved *Plasmodium* membrane protein, unknown function	0.87	7.73E-05	null		
721	MAL13P1.347	conserved *Plasmodium* protein, unknown function	0.88	3.64E-04	null		
722	PF10_0092	metallopeptidase, putative	0.88	2.05E-05	null		
723	PFL1065c	conserved *Plasmodium* protein, unknown function	0.88	3.70E-04	null		
724	MAL7P1.115	conserved *Plasmodium* membrane protein, unknown function	0.88	1.18E-02	null		
725	PF14_0176	conserved *Plasmodium* protein, unknown	0.91	2.62E-04	null		

		function					
726	PF07_0110	protein phosphatase, putative	0.91	2.69E-05	null		
727	PFI0440w	conserved *Plasmodium* membrane protein, unknown function	0.92	2.11E-03	null		
728	PFI1080w	dynein intermediate chain 2, ciliary	0.94	3.54E-04	null		
729	PFI1705w	phosphatidylinositol N-acetylglucosaminyltransferase subunit P, putative	0.94	4.56E-05	null		
730	MAL8P1.84	conserved *Plasmodium* protein, unknown function	0.96	5.92E-05	null		
731	PF07_0014	conserved *Plasmodium* protein, unknown function	0.97	1.88E-02	null		GO:0016021~integral to membrane
732	PFD0915w	conserved *Plasmodium* protein, unknown function	0.98	5.40E-04	null		
733	MAL8P1.111	JmjC domain containing protein	0.98	2.24E-05	null		
734	PFL0340w	conserved *Plasmodium* protein, unknown function	0.99	7.80E-05	null		
735	MAL8P1.97	hypothetical protein	1.00	6.32E-05	null		
736	PF07_0118	conserved *Plasmodium* membrane protein, unknown function	1.00	4.73E-05	null		
737	PF13_0202	conserved *Plasmodium* protein, unknown function	1.00	4.76E-05	null		
738	PFA0190c	actin-related protein	1.01	3.47E-04	null		
739	PFL0710w	conserved *Plasmodium* protein, unknown function	1.01	8.83E-06	null		
740	PF13_0266	conserved *Plasmodium* protein, unknown function	1.01	5.51E-04	null		
741	PF14_0358	41-2 protein antigen precursor,transport protein particle (TRAPP) component, Bet3	1.02	1.67E-04	null		GO:0016192~vesicle-mediated transport
742	PF14_0648	conserved *Plasmodium* protein, unknown function	1.02	3.65E-05	null		
743	PF13_0164	conserved *Plasmodium* protein, unknown function	1.03	3.99E-04	null		
744	PFI0950w	protein disulfide isomerase	1.03	2.79E-06	null		GO:0016860~intramolecular oxidoreductase activity
745	MAL13P1.182	conserved *Plasmodium* protein, unknown function	1.04	1.94E-05	null		
746	PF08_0099	acyl-CoA binding protein, putative	1.07	5.91E-05	null		GO:0005504~fatty acid binding
747	PFC0505c	conserved *Plasmodium* protein, unknown function	1.09	3.36E-04	null		
748	PFL1260w	hydrolase/phosphatase, putative	1.10	5.38E-05	null		
749	MAL13P1.106	probable protein, unknown function	1.13	2.67E-04	null		
750	PF10_0273	DHHC-type zinc finger protein, putative	1.16	1.17E-06	null		GO:0043167~ion binding
751	PFL1695c	conserved *Plasmodium* protein, unknown function	1.18	1.47E-04	null		
752	PF11_0486	merozoite adhesive erythrocytic binding protein	1.18	1.83E-04	null		GO:0020007~apical complex
753	PFI0615w	conserved *Plasmodium* protein, unknown function	1.20	9.89E-04	null		
754	PFL0995c	conserved *Plasmodium* protein, unknown function	1.20	2.03E-04	null		

755	PFE1540w	CPW-WPC family protein	1.27	2.09E-06	null		
756	PF14_0588	conserved *Plasmodium* protein, unknown function	1.28	7.01E-04	null		
757	PF13_0081	conserved *Plasmodium* protein, unknown function	1.29	3.48E-07	null		
758	PFL0070c	*Plasmodium* exported protein, unknown function	1.31	9.96E-04	null		
759	PF14_0631	conserved *Plasmodium* protein, unknown function	1.32	7.13E-06	null		
760	MAL13P1.197	probable protein, unknown function	1.33	7.27E-04	null		
761	PFE1450c	conserved *Plasmodium* protein, unknown function	1.34	4.79E-06	null		
762	PFF1065c	conserved *Plasmodium* protein, unknown function	1.34	1.40E-04	null		
763	PFF1520w	RESA-like protein	1.35	8.31E-03	null		
764	MAL8P1.6	early transcribed membrane protein 8	1.37	2.21E-06	null		
765	PFI1220w	conserved protein, unknown function	1.43	2.77E-06	null		
766	PF14_0305	leucine-rich repeat protein	1.46	3.85E-06	null		
767	PF14_0452	conserved *Plasmodium* protein, unknown function	1.49	8.00E-03	null		
768	PFL1750c	conserved *Plasmodium* protein, unknown function	1.50	2.79E-06	null		
769	PF11_0451	conserved *Plasmodium* protein, unknown function	1.58	1.95E-07	null		
770	PFC0680w	conserved *Plasmodium* protein, unknown function	1.59	6.00E-05	null		
771	PFI0980w	long chain fatty acid elongation enzyme, putative	1.60	1.23E-05	null		
772	PF14_0131	conserved *Plasmodium* protein, unknown function	1.60	2.79E-06	null		
773	MAL7P1.156	conserved *Plasmodium* protein, unknown function	1.61	2.56E-07	null		
774	PFL0795c	male development gene 1	1.65	4.18E-05	null		
775	MAL13P1.129	conserved *Plasmodium* protein, unknown function	1.66	1.59E-06	null		
776	PF10_0164	early transcribed membrane protein 10.3	1.67	4.17E-08	null		
777	PFI0315c	dynein light intermediate chain 2, cytosolic	1.69	2.83E-03	null		
778	PF14_0040	secreted ookinete adhesive protein	1.81	4.73E-05	null		
779	PF11_0092	mechanosensitive ion channel protein	1.84	3.09E-05	null		
780	PF14_0272	CPW-WPC family protein	1.84	2.31E-08	null		
781	PF11_0479	conserved *Plasmodium* protein, unknown function	1.89	7.35E-05	null		
782	PFL2385c	conserved *Plasmodium* protein, unknown function	2.09	1.44E-07	null		
783	PF14_0467	conserved *Plasmodium* protein, unknown function	2.16	3.50E-06	null		
784	PFE1205c	conserved *Plasmodium* membrane protein, unknown function	2.69	5.40E-09	null		
785	PF14_0708	probable protein, unknown function	3.00	2.31E-08	null		
786	PFI1520w	asparagine-rich antigen, putative	3.10	6.47E-10	null		
787	PFI1230c	conserved *Plasmodium* protein, unknown	3.43	4.15E-08	null		

		function					

Table A4.2: **Transcripts associated with cofactor metabolic processes and folate metabolism at Tt_3 parasites compared to UTt_3.** GSEA identified transcripts involved in cofactor metabolic process as well as folate metabolism were enriched in Tt_3 parasites compared to UTt_3. Listed below are the log_2FC of expressed transcripts belonging to these two different clusters.

PlasmoDB ID	**PlasmoDB description**	**log_2FC $Tt_3:UTt_3$**	**aj.P.Val**	**PlasmoDB annotated processes**	**GO term**
GO.0051186.COFACTOR.METABOLIC.PROCESS					
PF13_0159	nicotinic acid mononucleotide adenyltransferase	-0.95	1.55E-04	NAD biosynthetic process	GO:0006732~coenzyme metabolic process
PFB0320c	iron-sulfur assembly protein, putative	-0.79	1.57E-04	iron-sulfur cluster assembly	GO:0016226~iron-sulfur cluster assembly
PFL1920c	hydroxyethylthiazole kinase, putative	0.76	2.19E-03	thiamin biosynthetic process	GO:0006766~vitamin metabolic process
PFD0830w	bifunctional dihydrofolate reductase-thymidylate synthase	0.76	4.08E-04	dTMP biosynthetic process	
PF11_0169	SNO glutamine amidotransferase family protein	0.77	5.98E-05	response to singlet oxygen and vitamin B6 biosynthetic process	
PFE0970w	cytochrome c oxidase assembly protein (heme A: farnesyltransferase), putative	0.86	1.26E-05	heme O biosynthetic process	GO:0006778~porphyrin metabolic process
PF10_0210	deoxyribose-phosphate aldolase, putative	0.86	1.01E-05	deoxyribonucleotide catabolic process	GO:0005996~monosaccharide metabolic process
PFB0220w	ubiE/COQ5 methyltransferase, putative	0.89	1.40E-04	quinone cofactor biosynthetic process	GO:0006732~coenzyme metabolic process
PF11_0044	iron-sulfur assembly protein, sufD, putative	0.92	6.29E-05	iron-sulfur cluster assembly	GO:0016226~iron-sulfur cluster assembly

PF08_0066	lipoamide dehydrogenase	1.28	8.55E-05	acetyl-CoA biosynthetic process from pyruvate	GO:0006084~acetyl-CoA metabolic process
PF11_0256	pyruvate dehydrogenase E1 alpha subunit	1.65	4.28E-08	acetyl-CoA biosynthetic process from pyruvate	GO:0006084~acetyl-CoA metabolic process
PF14_0441	pyruvate dehydrogenase E1 beta subunit	0.91	1.07E-04	acetyl-CoA biosynthetic process from pyruvate	GO:0009536~plastid
PFB0220w	ubiE/COQ5 methyltransferase, putative	0.89	1.40E-04	quinone cofactor biosynthetic process	GO:0006732~coenzyme metabolic process
PF11_0044	iron-sulfur assembly protein, sufD, putative	0.92	6.29E-05	iron-sulfur cluster assembly	GO:0016226~iron-sulfur cluster assembly
MPM.FOLATE BIOSYNTHESIS					
PF08_0066	lipoamide dehydrogenase (aLipDH)	1.28	8.55E-05	cell redox homeostasis, oxidation-reduction process	GO:0051186~cofactor metabolic process
* PFD0830w	bifunctional dihydrofolate reductase-thymidylate synthase (DHFR-TS)	0.76	4.08E-04	dTMP biosynthetic process	glycine biosynthetic process
PF13_0345	glycine cleavage T protein, putative (GCVT)	0.32	2.95E-02	glycine catabolic process	
PF13_0140	dihydrofolate synthase/folylpolyglutamate synthase (DHFS-FPGS)	0.49	4.92E-03	biosynthetic process, folic acid-containing compound biosynthetic process	GO:0051186~cofactor metabolic process
PF08_0095	dihydropteroate synthetase (DHPS)	0.43	3.23E-02	folic acid-containing compound biosynthetic process	GO:0051188~cofactor biosynthetic process
MAL13P1.67	methionyl-tRNA formyltransferase, putative	0.30	1.54E-01	biosynthetic process,translational initiation	

Footnote: The adjusted P-value (adj. P-value) indicates a normalised standard error from spot or probe results, and is interpreted as a normal t-statistic result. * DHFR-TS (PFD0830w) was not part of the annotated cluster MPM.folate biosynthesis, however is part of folate recycling. This transcript was included for interpretation purposes.

Table A4.3: Uniquely expressed transcripts from 4PEHz-treated parasites at t_3. Comparison of differentially regulated transcripts from t_3 to microarray data of; CQ- ,artesunate- ,WR99210-treated *P. falciparum*, as well as heat-treated *P. falciparum*, including a study involving 20 different compounds which focuses on schizontal expression patterns. Comparisons Transcripts were uniquely expressed during 4PEHz treatment, and not found in other transcriptomes.

No.	**PlasmoDB ID**	**PlasmoDB description**	**$\log_2$FC Tt_3:UTt_3**	**aj.P.Val**	**PlasmoDB annotated processes**	**Additional process involvement**	**GO term**
Protein amino acid dephosphorylation and signal transduction							
1	PFL0475w	cGMP-specific phosphodiesterase	-0.85	1.22E-02	cGMP catabolic process	signal transduction	
2	PF14_0723	LCCL domain-containing protein	-0.82	3.58E-04	cell adhesion	signal transduction	
3	PF14_0672	phosphodiesterase delta, putative	1.72	4.82E-06	cyclic nucleotide metabolic process	signal transduction	GO:0009123~nucleoside monophosphate metabolic process
4	MAL7P1.73	calcium/calmodulin-dependent protein kinase, putative	0.82	1.67E-02	protein amino acid phosphorylation	signal transduction	GO:0006468~protein amino acid phosphorylation
5	PF14_0498	DER1-like protein	1.10	5.63E-05	ER-associated protein catabolic process	regulation of cell cycle process	
6	PFF0270c	cyclin dependent kinase binding protein, putative	0.79	1.61E-03	regulation of cell cycle	regulation of cell division	GO:0051726~regulation of cell cycle
7	PFE0045c	serine/threonine protein kinase, FIKK family	-0.89	2.11E-03	protein amino acid phosphorylation		GO:0006468~protein amino acid phosphorylation
8	PFF0260w	serine/threonine protein kinase, putative	0.91	1.21E-03	protein amino acid phosphorylation		GO:0004674~protein serine/threonine kinase activity
9	MAL13P1.114	conserved *Plasmodium* protein, unknown function	-1.80	4.53E-07	protein amino acid phosphorylation		GO:0009536~plastid
10	PF08_0129	serine/threonine protein phosphatase, putative	-1.15	4.52E-05	protein amino acid dephosphorylation		GO:0006470~protein amino acid dephosphorylation
11	PF14_0224	serine/threonine protein phosphatase	-2.65	7.57E-10	protein amino acid dephosphorylation		
12	MAL13P1.297	ADP-ribosylation factor, putative	-1.17	9.97E-05	protein amino acid ADP-ribosylation	small GTPase mediated signal transduction	GO:0006471~protein amino acid ADP-ribosylation
13	PF11_0147	mitogen-activated protein kinase 2	-0.81	5.62E-05	MAPKKK cascade	protein amino acid phosphorylation	

Apicoplast associated transcripts							
14	MAL13P1.254	conserved *Plasmodium* protein, unknown function	1.47	2.76E-05	null		GO:0009536~plastid
15	MAL13P1.342	conserved *Plasmodium* protein, unknown function	1.35	2.58E-06	null		GO:0009536~plastid
16	MAL13P1.49	conserved *Plasmodium* protein, unknown function	-1.57	1.48E-06	null		GO:0009536~plastid
17	MAL13P1.87	sec20 homolog, putative	0.99	2.36E-05	null		GO:0009536~plastid
18	MAL7P1.6	*Plasmodium* exported protein (hyp12), unknown function	-0.79	3.77E-04	null		GO:0009536~plastid
19	MAL8P1.138	alpha/beta hydrolase, putative	1.39	2.04E-07	null		GO:0009536~plastid
20	MAL8P1.73	rhoptry neck protein 5, putative	-2.78	1.02E-09	null		GO:0009536~plastid
21	PF10_0119	conserved *Plasmodium* protein, unknown function	-2.53	7.16E-09	null		GO:0009536~plastid
22	PF11_0135	conserved *Plasmodium* protein, unknown function	-1.13	1.26E-03	null		GO:0009536~plastid
23	PF11_0285	conserved *Plasmodium* protein, unknown function	0.89	2.09E-05	null		GO:0009536~plastid
24	PF11_0304	conserved *Plasmodium* protein, unknown function	-1.93	5.83E-05	null		GO:0009536~plastid
25	PF11_0323	conserved *Plasmodium* protein, unknown function	0.94	1.81E-03	null		GO:0009536~plastid
26	PF13_0125	conserved *Plasmodium* protein, unknown function	-1.32	8.67E-05	null		GO:0009536~plastid
27	PFB0110w	*Plasmodium* exported protein (hyp11), unknown function	-0.95	2.55E-02	null		GO:0009536~plastid
28	PFE0575c	conserved *Plasmodium* protein, unknown function	-1.62	4.91E-07	null		GO:0009536~plastid
29	PFI0205w	conserved *Plasmodium* protein, unknown function	1.27	2.91E-04	null		GO:0009536~plastid
30	PFL0875w	conserved *Plasmodium* protein, unknown function	-0.91	4.43E-04	null		GO:0009536~plastid
Cytoskeleton organization and antigenic variation							
31	PFE1420w	f-actin capping protein alpha subunit, putative	1.15	3.41E-05	actin cytoskeleton organization		GO:0007010~cytoskeleton organization

32	PFF1545w	rifin	-2.09	4.93E-04	antigenic variation		
33	PFL0030c	erythrocyte membrane protein 1, PfEMP1	-1.12	1.42E-04	antigenic variation	cell-cell adhesion	
34	PF10_0003	rifin	-3.70	6.50E-10	antigenic variation		GO:0006952~defense response
35	MAL7P1.50	erythrocyte membrane protein 1, PfEMP1	0.97	2.62E-04	antigenic variation	cell-cell adhesion	GO:0009405~pathogenesis
36	PFB0010w	erythrocyte membrane protein 1, PfEMP1	-0.92	7.65E-04	antigenic variation	cell-cell adhesion	GO:0006952~defense response
37	PFF1420w	phosphatidylcholine-sterol acyltransferase precursor, putative	-1.60	4.83E-07	entry into host cell	lipid metabolic process	GO:0009536~plastid
38	PFD0955w	apical merozoite protein	-2.79	6.50E-10	attachment of GPI anchor to protein		
39	PFI0535w	phosphatidylinositol N-acetylglucosaminyltransferase, putative	0.99	7.77E-05	GPI anchor biosynthetic process		
40	PFD1105w	asparagine-rich protein	-2.19	9.66E-07	cell-cell adhesion		
41	PFI1730w	cytoadherence linked asexual protein 9	-1.69	5.10E-08	cell-cell adhesion		
42	PFE0175c	myosin B	-1.73	1.17E-06	null		GO:0005856~cytoskeleton
43	PFA0260c	cyclase-associated protein, putative	-1.21	5.19E-05	cytoskeleton organization		
44	PFB0680w	rhoptry neck protein 6	-2.36	6.27E-08	entry into host		
Metabolic process							
45	PFC0260w	P-loop containing nucleoside triphospahte hydrolase, putative	-0.88	7.55E-04	metabolic process		
46	PF11_0190	haloacid dehalogenase-like hydrolase, putative	-1.13	8.38E-05	metabolic process		GO:0016791~phosphatase activity
47	PFL0035c	acyl-CoA synthetase, PfACS7	-1.89	2.32E-07	metabolic process		
48	PF13_0066	malonyl CoA-acyl carrier protein transacylase precursor	1.19	1.76E-02	fatty acid biosynthetic process		GO:0004314~[acyl-carrier-protein] S-malonyltransferase activity
49	PFD1035w	steroid dehydrogenase, putative	0.82	2.52E-04	fatty acid biosynthetic process		GO:0006631~fatty acid metabolic process
50	PFB0505c	beta-ketoacyl-ACP synthase III	-0.77	5.90E-04	fatty acid biosynthetic process		

Transcription, translation and post translational modification							
51	PFD0700c	RNA binding protein, putative	1.48	8.85E-07	RNA metabolic process		
52	PF11_0383	conserved *Plasmodium* protein, unknown function	-1.68	6.58E-06	DNA-dependent DNA replication		
53	PF11_0429	conserved *Plasmodium* protein, unknown function	-0.81	1.65E-04	chromatin modification	regulation of transcription	GO:0043167~ion binding
54	PFI1630c	conserved *Plasmodium* protein, unknown function	1.18	1.14E-05	transcription		
55	PFC0241w	conserved *Plasmodium* protein, unknown function	0.89	1.26E-04	translation		
56	MAL13P1.251	conserved *Plasmodium* protein, unknown function	1.26	1.40E-05	arginyl-tRNA aminoacylation		GO:0009536~plastid
57	PFD1100c	conserved *Plasmodium* protein, unknown function	-2.28	6.22E-07	translation	translational initiation	GO:0009536~plastid
58	PFF0705c	conserved *Plasmodium* protein, unknown function	-1.66	3.17E-04	translation	translational initiation	
59	PFI1675w	conserved *Plasmodium* protein, unknown function	-1.96	1.63E-07	translation		
60	PFI1725w	*Plasmodium* exported protein, unknown function	-1.06	1.20E-05	translation	valyl-tRNA aminoacylation	
61	PFL1910c	conserved *Plasmodium* protein, unknown function	2.05	1.96E-06	translation		
62	PFL1895w	mitochondrial ribosomal protein L23 precursor, putative	0.86	1.96E-04	translation		GO:0006412~translation
63	PFL2545c	*Plasmodium* exported protein, unknown function	-0.95	3.76E-04	post-translational protein modification	regulation of protein metabolic process	
64	PFC0495w	plasmepsin VI	0.86	2.36E-02	proteolysis		
65	PF10_0094	tubulin-tyrosine ligase, putative	-2.06	4.17E-08	protein modification process		GO:0016879~ligase activity
Transport							
66	PF10_0059	conserved *Plasmodium* membrane protein, unknown function	-2.39	1.39E-08	transport		
67	PF11_0287	CRAL/TRIO domain-containing protein, putative	-0.95	4.31E-05	transport		
68	PF10_0216	zinc transporter, putative	1.03	1.70E-04	ion transport	transport	

69	PF11_0340	conserved *Plasmodium* protein, unknown function	-0.77	2.10E-03	potassium ion transport		
70	PFI0400c	conserved *Plasmodium* membrane protein, unknown function	1.20	1.99E-06	ion transport		
71	PFI1560c	conserved *Plasmodium* membrane protein, unknown function	-1.04	1.70E-04	transport		
72	PFF1075w	conserved *Plasmodium* protein, unknown function	0.94	2.17E-04	vacuolar transport	vacuole fusion	
Other processes							
73	MAL13P1.328	DNA topoisomerase VI, b subunit, putative	-0.96	2.61E-04	null		GO:0001882~nucleoside binding
74	PFI1005w	ADP-ribosylation factor, putative	-2.07	8.59E-09	small GTPase mediated signal transduction		GO:0005525~GTP binding
75	PFB0480w	syntaxin, Qa-SNARE family	-0.90	6.25E-04	intracellular protein transport	regulation of vesicle fusion	
76	PF14_0358	41-2 protein antigen precursor,transport protein particle (TRAPP) component, Bet3	1.02	1.67E-04	null		GO:0016192~vesicle-mediated transport
77	PFB0955w	stevor	-0.91	1.88E-04	null		GO:0005576~extracellular region
78	PFE1235c	ubiquitin fusion degradation protein UFD1, putative	-1.04	2.55E-02	ubiquitin-dependent protein catabolic process		GO:0006508~proteolysis
79	PF13_0159	nicotinic acid mononucleotide adenyltransferase	-0.95	1.55E-04	NAD biosynthetic process		GO:0006732~coenzyme metabolic process
80	PFL1920c	hydroxyethylthiazole kinase, putative	0.76	2.19E-03	thiamin biosynthetic process		GO:0006766~vitamin metabolic process
81	PF13_0021	small heat shock protein, putative	1.09	4.19E-05	response to heat	response to unfolded protein	GO:0006986~response to unfolded protein
82	MAL8P1.14	mitochondrial inner membrane protein, putative	0.89	1.61E-03	protein insertion into membrane		GO:0008104~protein localization
83	PF14_0034	translocation associated membrane protein, putative	1.07	1.84E-04	intracellular protein transmembrane transport		GO:0016021~integral to membrane
84	PF07_0014	conserved *Plasmodium* protein, unknown function	0.97	1.88E-02	null		GO:0016021~integral to membrane
85	PFF0485c	zinc finger protein, putative	-1.41	2.02E-07	null		GO:0016021~integral to membrane

86	PFL2285c	conserved *Plasmodium* protein, unknown function	-1.04	1.66E-04	tetrapyrrole biosynthetic process		GO:0018130~heterocycle biosynthetic process
87	PF10_0072	conserved *Plasmodium* protein, unknown function	-1.88	8.77E-07	null		GO:0043167~ion binding
88	PF10_0301	calmodulin, putative	-1.15	1.99E-04	null		GO:0043167~ion binding
89	PFD0765w	RING zinc finger protein, putative	-1.52	6.05E-07	null		GO:0043167~ion binding
Transcripts with hypothetical or unknown function							
90	MAL13P1.102	conserved *Plasmodium* protein, unknown function	-1.50	4.84E-04	null		
91	MAL13P1.106	probable protein, unknown function	1.13	2.67E-04	null		
92	MAL13P1.149	conserved *Plasmodium* protein, unknown function	0.85	7.75E-04	null		
93	MAL13P1.152	conserved *Plasmodium* protein, unknown function	-0.76	1.88E-02	null		
94	MAL13P1.175	MSP7-like protein, fragment	-0.79	7.11E-04	null		
95	MAL13P1.182	conserved *Plasmodium* protein, unknown function	1.04	1.94E-05	null		
96	MAL13P1.188	conserved *Plasmodium* protein, unknown function	-0.90	1.47E-05	null		
97	MAL13P1.215	conserved *Plasmodium* protein, unknown function	-1.16	4.50E-05	null		
98	MAL13P1.245	conserved *Plasmodium* protein, unknown function	-1.37	1.15E-05	null		
99	MAL13P1.287	conserved *Plasmodium* protein, unknown function	-0.82	7.23E-04	null		
100	MAL7P1.124	conserved *Plasmodium* protein, unknown function	0.86	3.98E-04	null		
101	MAL7P1.156	conserved *Plasmodium* protein, unknown function	1.61	2.56E-07	null		
102	MAL7P1.222	rifin	-0.88	8.25E-03	null		
103	MAL8P1.12	conserved *Plasmodium* protein, unknown function	-0.86	3.45E-03	null		
104	MAL8P1.160	*Plasmodium* exported protein (hyp7), unknown function	-0.79	6.62E-03	null		

105	MAL8P1.56	conserved *Plasmodium* membrane protein, unknown function	0.87	7.73E-05	null		
106	PF07_0028	conserved *Plasmodium* protein, unknown function	-0.88	2.00E-02	null		
107	PF07_0127	conserved *Plasmodium* protein, unknown function	-1.87	4.76E-08	null		
108	PF08_0082	conserved *Plasmodium* protein, unknown function	-0.87	6.97E-04	null		
109	PF10_0034	conserved *Plasmodium* protein, unknown function	-0.82	4.20E-04	null		
110	PF10_0092	metallopeptidase, putative	0.88	2.05E-05	null		
111	PF10_0135	conserved *Plasmodium* protein, unknown function	-1.99	9.40E-08	null		
112	PF10_0157	conserved *Plasmodium* protein, unknown function	-0.80	9.25E-03	null		
113	PF10_0184	conserved *Plasmodium* protein, unknown function	-1.89	2.56E-07	null		
114	PF10_0185	conserved *Plasmodium* protein, unknown function	-0.80	4.02E-02	null		
115	PF10_0238	conserved *Plasmodium* protein, unknown function	1.07	3.56E-06	null		
116	PF10_0248	conserved *Plasmodium* membrane protein, unknown function	-1.29	8.77E-06	null		
117	PF10_0254	conserved *Plasmodium* protein, unknown function	-1.23	1.80E-05	null		
118	PF10_0283	conserved *Plasmodium* protein, unknown function	-0.91	4.60E-04	null		
119	PF10_0342	probable protein, unknown function	-0.89	2.30E-03	null		
120	PF11_0180	conserved *Plasmodium* protein, unknown function	-1.76	7.46E-07	null		
121	PF11_0193	conserved *Plasmodium* protein, unknown function	-1.36	1.33E-04	null		
122	PF11_0300	conserved *Plasmodium* protein, unknown function	-1.36	6.53E-07	null		
123	PF11_0379	conserved *Plasmodium* protein, unknown function	-1.19	2.66E-03	null		
124	PF11_0390	conserved *Plasmodium* protein, unknown function	-0.82	5.30E-03	null		

125	PF11_0421	conserved *Plasmodium* protein, unknown function	-0.75	2.87E-04	null		
126	PF11_0451	conserved *Plasmodium* protein, unknown function	1.58	1.95E-07	null		
127	PF13_0114	conserved *Plasmodium* protein, unknown function	0.82	1.26E-02	null		
128	PF13_0194	probable protein, unknown function	0.82	2.87E-05	null		
129	PF13_0266	conserved *Plasmodium* protein, unknown function	1.01	5.51E-04	null		
130	PF14_0040	secreted ookinete adhesive protein	1.81	4.73E-05	null		
131	PF14_0044	conserved *Plasmodium* protein, unknown function	-1.44	3.22E-05	null		
132	PF14_0092	conserved *Plasmodium* membrane protein, unknown function	-1.41	2.05E-07	null		
133	PF14_0119	p1/s1 nuclease, putative	-1.80	8.11E-06	null		
134	PF14_0220	conserved *Plasmodium* protein, unknown function	0.79	1.14E-02	null		
135	PF14_0222	ankyrin, putative	-2.14	2.95E-06	null		
136	PF14_0303	conserved *Plasmodium* protein, unknown function	-0.93	3.52E-04	null		
137	PF14_0337	conserved *Plasmodium* protein, unknown function	-2.25	5.01E-07	null		
138	PF14_0353	conserved *Plasmodium* protein, unknown function	-1.10	1.41E-05	null		
139	PF14_0452	conserved *Plasmodium* protein, unknown function	1.49	8.00E-03	null		
140	PF14_0472	conserved *Plasmodium* protein, unknown function	-1.07	1.33E-04	null		
141	PF14_0530	ferlin, putative	-0.95	2.37E-04	null		
142	PF14_0572	conserved *Plasmodium* membrane protein, unknown function	-2.58	6.98E-08	null		
143	PF14_0578	conserved *Plasmodium* protein, unknown function	-1.68	1.42E-07	null		
144	PF14_0586	conserved *Plasmodium* protein, unknown function	-1.64	2.26E-06	null		

145	PF14_0604	conserved *Plasmodium* protein, unknown function	-0.93	5.31E-04	null		
146	PF14_0660	protein phosphatase, putative	-1.48	1.91E-06	null		
147	PFA0235w	conserved *Plasmodium* protein, unknown function	0.83	1.27E-03	null		
148	PFB0105c	*Plasmodium* exported protein (PHISTc), unknown function	-1.17	1.17E-04	null		
149	PFB0310c	merozoite surface protein 4	-0.84	4.16E-05	null		
150	PFB0625w	conserved *Plasmodium* protein, unknown function	-1.23	6.86E-06	null		
151	PFB0670c	conserved *Plasmodium* protein, unknown function	-2.45	3.31E-06	null		
152	PFC0370w	conserved *Plasmodium* protein, unknown function	-1.50	9.61E-07	null		
153	PFC0830w	trophozoite stage antigen	-2.83	8.33E-08	null		
154	PFC0905c	oocyst capsule protein	-1.04	5.51E-05	null		
155	PFC1045c	conserved *Plasmodium* protein, unknown function	-2.74	3.22E-08	null		
156	PFD0100c	surface-associated interspersed gene 4.1, (SURFIN4.1)	-1.90	9.64E-07	null		
157	PFD0195c	conserved *Plasmodium* protein, unknown function	-2.70	3.31E-06	null		
158	PFD0395c	conserved *Plasmodium* protein, unknown function	-1.87	9.90E-09	null		
159	PFD0580c	conserved *Plasmodium* protein, unknown function	-0.77	3.39E-02	null		
160	PFD0715c	conserved *Plasmodium* protein, unknown function	-0.98	3.86E-04	null		
161	PFD0910w	conserved *Plasmodium* protein, unknown function	-0.85	4.31E-03	null		
162	PFD0915w	conserved *Plasmodium* protein, unknown function	0.98	5.40E-04	null		
163	PFE0590w	conserved *Plasmodium* protein, unknown function	-1.05	1.33E-04	null		
164	PFE0760w	conserved *Plasmodium* protein, unknown function	0.79	3.66E-02	null		

165	PFE1095w	conserved *Plasmodium* protein, unknown function	-0.83	4.31E-04	null		
166	PFE1205c	conserved *Plasmodium* membrane protein, unknown function	2.69	5.40E-09	null		
167	PFE1410c	conserved *Plasmodium* protein, unknown function	-0.97	1.93E-03	null		
168	PFE1540w	CPW-WPC family protein	1.27	2.09E-06	null		
169	PFF0570c	conserved *Plasmodium* protein, unknown function	-0.75	2.61E-03	null		
170	PFF0605c	conserved *Plasmodium* protein, unknown function	-0.86	2.03E-02	null		
171	PFF0640w	conserved *Plasmodium* protein, unknown function	0.82	2.80E-04	null		
172	PFF0990c	conserved *Plasmodium* protein, unknown function	-1.51	4.17E-07	null		
173	PFF1065c	conserved *Plasmodium* protein, unknown function	1.34	1.40E-04	null		
174	PFF1475c	conserved *Plasmodium* protein, unknown function	-1.08	7.54E-06	null		
175	PFI0315c	dynein light intermediate chain 2, cytosolic	1.69	2.83E-03	null		
176	PFI0385c	P1 nuclease, putative	-0.77	6.62E-04	null		
177	PFI0440w	conserved *Plasmodium* membrane protein, unknown function	0.92	2.11E-03	null		
178	PFI0845w	conserved *Plasmodium* membrane protein, unknown function	-1.36	6.88E-06	null		
179	PFI0980w	long chain fatty acid elongation enzyme, putative	1.60	1.23E-05	null		
180	PFI1080w	dynein intermediate chain 2, ciliary	0.94	3.54E-04	null		
181	PFI1220w	conserved protein, unknown function	1.43	2.77E-06	null		
182	PFI1225w	conserved *Plasmodium* protein, unknown function	-0.76	6.58E-03	null		
183	PFI1230c	conserved *Plasmodium* protein, unknown function	3.43	4.15E-08	null		
184	PFI1330c	conserved *Plasmodium* protein, unknown function	0.85	2.16E-04	null		

185	PFI1380c	conserved *Plasmodium* protein, unknown function	-1.06	1.90E-03	null		
186	PFI1705w	phosphatidylinositol N-acetylglucosaminyltransferase subunit P, putative	0.94	4.56E-05	null		
187	PFI1735c	ring-exported protein 1	-0.81	1.57E-04	null		
188	PFI1800w	lysophospholipase, putative	-2.31	1.25E-06	null		
189	PFL0325w	Tat binding protein 1(TBP-1)-interacting protein, putative	-1.01	5.17E-03	null		
190	PFL0795c	male development gene 1	1.65	4.18E-05	null		
191	PFL0995c	conserved *Plasmodium* protein, unknown function	1.20	2.03E-04	null		
192	PFL1785c	conserved *Plasmodium* protein, unknown function	-1.88	5.76E-09	null		
193	PFL1870c	sphingomyelin phosphodiesterase, putative	-1.17	5.92E-05	null		
194	PFL1945c	early transcribed membrane protein 12	-0.86	1.14E-03	null		
195	PFL2110c	conserved protein, unknown function	-0.96	5.96E-03	null		
196	PFL2385c	conserved *Plasmodium* protein, unknown function	2.09	1.44E-07	null		

Table A4.4: Proteins present in protein extracts from 4PEHz-treated parasites.

Accession	Description	Sequest score	% Sequence coverage	Nr of peptides	MW (kDa)	Calc. pI	Predicted GO process
PFL0020w	erythrocyte membrane protein 1, PfEMP1	15.0	7.3	18	333.0	6.8	antigenic variation, cell-cell adhesion
MAL7P1.89	dynein heavy chain, putative	12.8	8.3	37	698.4	8.5	microtubule-based movement
PFB0870w	conserved *Plasmodium* protein, unknown function	12.3	13.6	23	283.4	9.2	metabolic process
MAL7P1.55	erythrocyte membrane protein 1, PfEMP1	12.3	9.9	18	256.4	5.8	pathogenesis
MAL13P1.133	conserved *Plasmodium* membrane protein, unknown function	10.5	11.7	43	658.6	9.3	null
MAL13P1.278	serine/threonine protein kinase, putative	10.2	11.6	35	475.4	8.9	protein phosphorylation
PF14_0722	cysteine repeat modular protein 4	9.5	8.6	36	700.5	8.2	null
PFD0020c	erythrocyte membrane protein 1, PfEMP1	8.8	8.5	21	398.0	5.9	pathogenesis
PFD0995c	erythrocyte membrane protein 1, PfEMP1	8.3	11.8	21	247.5	5.5	pathogenesis
PF14_0594	conserved *Plasmodium* protein, unknown function	7.3	9.1	20	395.4	6.6	null
PF13_0148	conserved *Plasmodium* protein, unknown function	6.7	10.6	33	575.1	8.9	null
PF13_0044	carbamoyl phosphate synthetase	6.7	7.4	10	273.3	6.6	nitrogen compound metabolic process
PFF0445w	conserved *Plasmodium* protein, unknown function	6.6	8.1	33	720.1	7.0	null
PF14_0668	conserved *Plasmodium* protein, unknown function	6.6	10.1	17	294.9	8.0	null
MAL8P1.127	conserved *Plasmodium* protein, unknown function	6.5	7.4	7	158.9	5.1	null
PFL0950c	aminophospholipid-transporting P-ATPase	6.4	8.4	8	179.0	7.1	ATP biosynthesis, phospholipid transport
PF13_0079	conserved *Plasmodium* protein, unknown function	6.2	13.8	17	240.4	8.7	null
PF13_0155	conserved *Plasmodium* protein, unknown function	5.7	6.6	15	319.9	7.5	double-strand break repair
PFC0930c	conserved *Plasmodium* protein, unknown function	5.4	13.3	15	221.4	9.5	null
PFF0285c	DNA repair-like protein, putative	4.6	12.3	19	267.8	8.6	null
PF11_0417	conserved *Plasmodium* protein, unknown function	4.6	7.3	9	219.7	9.6	null
PFE0440w	conserved *Plasmodium* protein, unknown function	4.1	8.4	14	370.0	5.4	null
PF13_0080	telomerase reverse transcriptase, putative	3.8	12.0	26	303.9	9.9	RNA-dependent DNA replication
PF07_0082	conserved *Plasmodium* membrane protein, unknown function	3.8	6.3	15	402.4	8.3	null
PF14_0318	conserved *Plasmodium* protein, unknown function	3.8	10.7	20	252.4	9.5	null
PF14_0278	ATP-dependent DNA helicase, putative	3.8	8.2	7	169.4	8.0	DNA recombination, DNA repair
PFL1130c	conserved *Plasmodium* protein, unknown function	3.7	5.0	14	544.0	8.8	null
PF13_0089	inositol polyphosphate kinase, putative	3.7	10.0	10	192.1	9.2	null
PF14_0160	conserved protein, unknown function	3.7	9.4	17	264.8	9.3	proteolysis
PFL2505c	conserved *Plasmodium* protein, unknown function	3.6	10.0	17	263.0	9.2	null
MAL8P1.150	adenylyl cyclase beta, putative	3.4	7.6	12	269.4	7.5	cyclic nucleotide biosynthetic process, intracellular signal transduction
MAL13P1.246	conserved *Plasmodium* membrane protein, unknown function	3.4	6.8	9	218.4	8.1	null
PF14_0165	conserved *Plasmodium* protein, unknown function	3.3	7.3	18	357.4	8.9	null

Table A4.5: Proteins present in untreated parasite extracts from the 4PEHz study.

Accession	Description	Sequest score	% Sequence coverage	Nr of peptides	MW (kDa)	Calc. pI	Predicted GO process
MAL8P1.208	rifin	54.3	12.4	3	41.1	8.8	NA
PF14_0101	conserved *Plasmodium* protein, unknown function	13.6	8.5	24	526.4	8.9	null
PF14_0627	40S ribosomal protein S3, putative	9.1	22.2	5	24.7	10.2	translation
PF07_0118	conserved *Plasmodium* membrane protein, unknown function	8.4	5.3	18	670.7	9.2	null
PFL0360c	conserved *Plasmodium* protein, unknown function	8.3	12.9	25	326.3	8.7	null
PFB0615c	conserved *Plasmodium* protein, unknown function	8.1	12.6	24	293.1	9.1	null
PFE0245c	conserved *Plasmodium* membrane protein, unknown function	8.1	6.5	17	355.0	5.4	null
PFL0405w	conserved *Plasmodium* protein, unknown function	8.0	7.0	18	533.3	9.0	null
MAL13P1.116	conserved *Plasmodium* membrane protein, unknown function	7.7	7.4	14	404.7	8.5	null
PF14_0419	conserved *Plasmodium* protein, unknown function	7.4	9.5	45	864.5	8.6	null
PFF1440w	SET domain protein, putative	7.2	10.7	51	795.5	8.6	null
PF08_0140	erythrocyte membrane protein 1, PfEMP1	7.1	8.9	18	340.4	5.8	pathogenesis
PF07_0037	Cg2 protein	6.2	8.0	15	325.3	7.8	null
MAL13P1.66	conserved *Plasmodium* protein, unknown function	6.2	12.9	24	345.5	9.3	null
PF14_0547	conserved *Plasmodium* protein, unknown function	6.1	6.6	15	370.8	8.9	null
PF14_0145	ubiquitin carboxyl-terminal hydrolase, putative	5.5	17.4	18	164.3	9.5	ubiquitin-dependent protein catabolic process
PF14_0337	conserved *Plasmodium* protein, unknown function	4.8	10.6	13	210.6	8.6	null
PFI0165c	DEAD/DEAH box helicase, putative	4.5	10.8	17	300.7	6.9	null
PFD1015c	erythrocyte membrane protein 1, PfEMP1	4.4	7.0	10	248.8	5.4	pathogenesis
PFD0965w	phosphatidylinositol 4-kinase, putative	4.3	8.5	28	611.1	9.5	NA
PFC0925w	conserved *Plasmodium* protein, unknown function	4.3	22.6	6	59.8	9.9	null
PF14_0073	conserved *Plasmodium* protein, unknown function	4.2	13.5	22	241.0	9.5	null
PF11_0481	tubulin-tyrosine ligase, putative	4.1	14.4	26	325.1	9.2	protein modification process
PF13_0298	conserved *Plasmodium* protein, unknown function	4.0	21.2	20	166.2	9.4	null
PFF0645c	integral membrane protein, putative	4.0	8.2	8	171.9	8.9	null
MAL7P1.15	conserved *Plasmodium* membrane protein, unknown function	3.9	10.0	30	513.5	8.4	null
PFL1280w	RAP protein, putative	3.8	9.6	10	179.7	9.2	null
PFB0560w	conserved *Plasmodium* protein, unknown function	3.7	7.7	22	477.6	8.3	null
PF10_0045	conserved *Plasmodium* membrane protein, unknown function	3.7	7.9	16	357.8	8.9	null
MAL13P1.26	conserved *Plasmodium* protein, unknown function	3.6	12.5	25	418.3	7.1	null
PFF0935c	conserved *Plasmodium* protein, unknown function	3.5	12.6	33	433.4	9.5	null