



# APPENDIX A

## DIFFERENTIAL TRANSCRIPT ABUNDANCE DATASET (LIMMA)

#	FUNCTIONAL CLASSIFICATION	PLASMID ID	OLIGO	ANNOTATION	GO ID	FUNCTIONAL ANNOTATION	FOLD CHANGE TO RELATIVE IS WITH F-VALUES ADJUSTED FOR MDR								
							T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value
1	CYTOKINESIS/CELL CYCLE	PF10_0094	J73_4	tubulin beta chain, putative: PF10_0094 (J73_4)	GO:000226	microtubule cytoskeleton organization and organization (GO:000226)	-0.877117856	0.544454029	1.73E-06	-0.695815503	0.621654329	1.51E-06	-0.386724309	0.764864296	0.000462446
2		PF11_0056	K879_2	putative: PF11_0056 (K879_2)	GO:000707	mitosis	-0.615929357	0.562839424	4.00E-05	-0.820345517	0.57293941	1.79E-06			
3		PF13_0328	M9264_1	antigen: PF13_0328 (M9264_1)	GO:000275	regulation of DNA replication (cyclic signature)	-1.706908296	0.306315803	7.54E-07	-1.241921596	0.422809121	1.19E-05	-0.8904367	0.53736832	3.01E-05
4		PF14_0443	N151_04	centrin, putative: PF14_0443 (N151_04)	GO:0008150	biological_process	-0.848623885	0.595007834	0.000471307	-0.848623885	0.595007834	0.000471307	-0.893345456	0.521492093	0.002198876
5		PF14_0504	N136_76	hypothetical protein: PF14_0504 (N136_76)	DAVID	cyclic-related protein	-0.430976269	0.741760183	0.002057867	-0.430976269	0.741760183	0.002057867	-0.791235864	0.577648934	7.11E-06
6		PFAD190c	AG01_16	actin: PFAD190c (AG01_16)	GO:001628	actin cytoskeleton	-0.999594919	0.501042587	0.012324662	-0.999594919	0.501042587	0.012324662	-0.797480159	0.575383224	0.021713375
7		PFAD520c	A13725_9	domain, putative: PFAD520c (A13725_9)	GO:0006334	nucleosome assembly	-1.048414161	0.483164334	2.83E-06	-0.87768062	0.544239637	1.39E-05	-0.684803092	0.522093728	1.70E-05
8		PFCE060w	C569	kinase, putative: PFCE060w (C569)	GO:0007018	microtubule-based movement	-0.558289134	0.679130564	0.009316004	-0.774708401	0.584050753	0.000121797	-0.38676511	0.764864296	0.000462446
9		PFEB165w	E13013_1	actin, depolymerizing factor, putative: PFEB165w (E13013_1)	GO:0030042	actin filament depolymerization	-0.832326233	0.561612662	2.15E-06	-1.189394342	0.438399966	2.13E-09	-0.987152039	0.50447265	8.31E-09
10		PFEB175c	OPFBL08060	unconventional myosin IIb, putative: PFEB175c (OPFBL08060)	GO:0016459	myosin complex	-0.826336897	0.563959368	4.34E-05	-0.826336897	0.563959368	4.34E-05	-0.810386212	0.570224443	4.30E-05
11		PFEB175c	E1E509_5	unconventional myosin IIb, putative: PFEB175c (E1E509_5)	GO:0016459	myosin complex	-1.188434644	0.438778587	7.94E-05	-1.188434644	0.438778587	7.94E-05	-0.704370306	0.474878286	1.48E-05
12		PFEP1320c	PVAL6P1_156_432	tropomyosin-like protein, putative: PFEP1320c (PVAL6P1_156_432)	GO:0006509	calcium ion binding	-0.924538687	0.526848962	1.48E-06	-0.788517967	0.580103421	4.48E-07	-0.752079108	0.63747275	0.03816505
11		PFEP180w	OPF17633	alpha tubulin, putative: PFEP180w (OPF17633)	GO:0007017	microtubule-based process	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784
13		PFEP180w	I16830_2	alpha tubulin, putative: PFEP180w (I16830_2)	GO:0007017	microtubule-based process	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784
14		PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784
15	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
14	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
15	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
16	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
17	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
18	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
19	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
20	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
21	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
22	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
23	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
24	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
25	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
26	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
27	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
28	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
29	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
30	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
31	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
32	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
33	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
34	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
35	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
36	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
37	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
38	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
39	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
40	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
41	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
42	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
43	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
44	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
45	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
46	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481489	1.04E-05	-0.72099311	0.606717131	0.000167784	
47	PFEP180w	I16830_1	hypothetical protein: PFEP180w (I16830_1)	GO:0007018	microtubule-based movement	-1.142784503	0.452814896	2.19E-05	-0.996079589	0.515481					



#	FUNCTIONAL CLASSIFICATION	FLASMOOB ID	OLIGO	ANNOTATION	GO ID	FUNCTIONAL ANNOTATION	FOLD CHANGE TO RELATIVE 0 WITH P-VALUES ADJUSTED FOR MDR DATA WITH P<0.05 ARE PRESENTED								
							T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value
		PF00830w	OPFD6954	bifunctional dihydroxyacetone reductase/thymidylate synthase:PF00830w:(OPFD6954)	GO:0006231	dTMP biosynthetic process	-0.905177893	0.53396687	0.0004105	-0.77419848	0.584713384	0.00110919	-0.722171625	0.506184293	0.000184442
46		PF00950w	D1263_36	ran binding protein 1:PF00950w:(D1263_36)	GO:0006260	DNA replication	1.001957896	2.002160989	0.011627336	0.881620395	1.842688572	0.00547603			
47		PF00975c	OPFD0352	deoxythymidylate synthase (phosphotransferase domain):PF00975c:(OPFD0352)	GO:0006261	DNA replication	-0.848048988	0.55630617	2.73E-05	-0.72350359	0.605622475	1.38E-05	-0.62607405	0.547607947	4.14E-05
48		PF00975c	F1748L_1	deoxythymidylate synthase (phosphotransferase domain):PF00975c:(F1748L_1)	GO:0006261	DNA replication	-1.507194144	0.351794748	4.81E-06	-0.80941946	0.570913211	0.000397407			
49		PF0236w	OPFI1721	DNA polymerase epsilon, catalytic subunit a, putative:PF0236w:(OPFI1721)	GO:0006260	DNA replication	-0.88862636	0.55147896	2.63E-06	-0.82144625	0.787298179	0.00070861			
50		PF0236w	F18417_1	DNA polymerase epsilon, catalytic subunit a, putative:PF0236w:(F18417_1)	GO:0006260	DNA replication	-1.201008797	0.434870723	1.13E-06	-0.931971996	0.69180052	0.00230647	-0.27186648	0.838261139	0.03229814
51	HOST PARASITE INTERACTION	PF0330c	I11401_2	DNA primase large subunit 1:PF0330c:(I11401_2)	GO:0006568	apna DNA polymerase primase complex	-0.833283283	0.56142384	0.00252301	-0.65296762	0.83969731	2.81E-05	-0.28526569	0.8206952	0.01828990
52		MAL13P1.176	I895L_1	hyaluronate lyase:PF0330c:(I895L_1)	GO:0006260	DNA replication	-1.10795808	0.46308874	0.00146886						
53		MAL13P1.176	I1487L_1	hyaluronate lyase:PF0330c:(I1487L_1)	GO:0006260	DNA replication	1.06461678	2.077022407	0.00358752						
54		MAL13P1.176	F739_1	erythrocyte membrane protein 1 (PEMP1) precursor:MAL13P1.176:(F739_1)	GO:0006405	pathogenesis	0.69864448	1.51451352	0.00180674	-0.19937014	0.566466873	4.97E-07	-0.874807625	0.54843911	1.53E-07
55		MAL13P1.176	F1754L_3	erythrocyte membrane protein 1 (PEMP1) precursor:MAL13P1.176:(F1754L_3)	GO:0006405	pathogenesis	0.64572884	1.564229524	0.00180674	-1.041773487	0.485732005	7.30E-08	-1.195475396	0.439374974	8.31E-05
56		PF07_049	F244L_1	erythrocyte membrane protein 1 (PEMP1):PF07_049:(F244L_1)	GO:0006405	pathogenesis	0.68793372	1.78607878	0.02896674						
57		PF10_019	J33_16	early transcribed membrane protein 11.1:PF10_019:(J33_16)	GO:0006150	biological process	0.439593218	1.407947184	0.02416421						
58		PF10_028	J17C_10	early transcribed membrane protein 11.1:PF10_028:(J17C_10)	GO:0006150	biological process	1.01352395	2.0138364	6.84E-05						
59		PF10_034	J11E_3	early transcribed membrane protein 11.1:PF10_034:(J11E_3)	GO:0006150	biological process	0.852102723	1.80512979	0.00579259	-0.42993589	0.74432931	0.01896242	-0.41978048	0.74908329	0.01988748
60		PF11_010	K84_10	early transcribed membrane protein 11.1:PF11_010:(K84_10)	GO:0006150	biological process	0.787081392	1.72644156	0.00194238						
61		PF11_039	OPPK1284	early transcribed membrane protein 11.1:PF11_039:(OPPK1284)	GO:0006150	biological process	0.79969054	1.74071573	0.00131977	-0.73741634	0.58603209	0.00283034	-1.644003413	0.319967347	3.86E-08
62		PF11_040	K87L_16	early transcribed membrane protein 11.2:PF11_040:(K87L_16)	GO:0006150	biological process	0.544237892	1.488248977	0.01134384	-0.75236605	0.93244576	0.00181917	-1.227893146	0.42894478	3.50E-05
63		PF11_040	K87L_16	early transcribed membrane protein 11.2:PF11_040:(K87L_16)	GO:0006150	biological process	0.93646773	1.99230373	0.00128213						
64		PF13_017	M366L_1	erythrocyte membrane protein 1 (PEMP1):PF13_017:(M366L_1)	GO:0006150	biological process	0.80542678	1.74774912	0.00173815						
65		PF14_012	N150_50	erythrocyte membrane protein 1 (PEMP1):PF14_012:(N150_50)	GO:0006150	biological process	0.834090549	1.660619392	0.00173815						
66		PF0910w	B11	erythrocyte membrane protein 3:PF0910w:(B11)	GO:0006150	biological process	1.580284638	2.98028204	5.73E-05	0.234025237	1.43798963	0.00234682			
67		PF0910w	OPF0917	erythrocyte membrane protein 3:PF0910w:(OPF0917)	GO:0006150	biological process	0.52688038	1.436621867	0.00928674	-0.402170524	0.786718984	0.00178326	-1.016395361	0.494364293	1.16E-06
68		PF0910w	B70	erythrocyte membrane protein 3:PF0910w:(B70)	GO:0006150	biological process	0.756234231	1.71265407	9.38E-05	-0.563300027	0.678752398	0.00198387	-0.569786564	0.60174822	0.000147582
69		PF13_030	B188	erythrocyte membrane protein 1 (PEMP1):PF13_030:(B188)	GO:0006150	biological process	0.973635203	1.963782704	0.00250239						
70		PF0010w	OPF00789	erythrocyte membrane protein 1 (PEMP1):PF0010w:(OPF00789)	GO:0006150	biological process	0.346418272	1.271400246	0.01455412	-0.19021553	0.801607797	0.00629889	-0.764133462	0.588802922	1.47E-06
71		PF00115c	C74	erythrocyte membrane protein 1 (PEMP1):PF00115c:(C74)	GO:0006150	biological process	1.025342496	2.049620164	0.00202739						
72		PF0156c	C639L_1	erythrocyte membrane protein 1 (PEMP1):PF0156c:(C639L_1)	GO:0006150	biological process	0.822203128	1.76816626	0.00184584						
73		PF0156c	OPFF2421	erythrocyte membrane protein 1 (PEMP1):PF0156c:(OPFF2421)	GO:0006150	biological process	0.83741538	1.84615438	0.00184584						
74		PF0156c	OPFL08064	erythrocyte membrane protein 1 (PEMP1):PF0156c:(OPFL08064)	GO:0006150	biological process	0.846461648	1.82089939	0.00292293						
75		PF0265c	I1144L_5	mothy protein, putative:PF0265c:(I1144L_5)	GO:0002008	mothy	-0.87197603	0.546548473	7.13E-05	-0.386897056	0.784793461	0.02935644			
76		PF1475w	Z_4_30	control oligonucleotide to mercuric surface protein 1, precursor:PF1475w:(Z_4_30)	GO:0006405	pathogenesis	0.36872533	1.288628291	0.04962862	-0.67497301	0.625248978	0.00071426	-0.78975819	0.579632601	3.44E-05
77		PF1475w	Z_4_100	control oligonucleotide to mercuric surface protein 1, precursor:PF1475w:(Z_4_100)	GO:0006405	pathogenesis	-0.896898499	0.53706342	2.43E-07	-0.792520771	0.577334464	7.07E-07			
78		PF1475w	I663L_2	control oligonucleotide to mercuric surface protein 1, precursor:PF1475w:(I663L_2)	GO:0006405	pathogenesis	0.70966592	1.63641306	0.0024481	-0.809631463	0.570268163	1.11E-06	-0.610489382	0.649670402	0.000170388
79		PF1475w	F861L_1	control oligonucleotide to mercuric surface protein 1, precursor:PF1475w:(F861L_1)	GO:0006405	pathogenesis	-0.9306287	0.524644893	0.02241773						
80	POLYAMINE & METHIONINE METABOLISM	PF10_040c	OPFL0212	polyamine oxidase (N-methyltransferase domain):PF10_040c:(OPFL0212)	GO:0006405	pathogenesis	0.302034448	1.27639984	0.0021075	-0.39798216	0.71635425	0.01058664	-0.76457462	0.530679497	2.96E-06
81		PF10_040c	I105L_2	polyamine oxidase (N-methyltransferase domain):PF10_040c:(I105L_2)	GO:0006405	pathogenesis	-0.628780023	0.448723077	0.01058664						
82		PF10_040c	I105L_1	polyamine oxidase (N-methyltransferase domain):PF10_040c:(I105L_1)	GO:0006405	pathogenesis	-0.86701889	0.550846478	0.02482807						
83		PF1420w	OPFL0399	homolog, putative:PF1420w:(OPFL0399)	GO:0002012	eviction of host immune response	-0.74526595	0.58962363	5.37E-05	-0.95479995	0.5163836	2.43E-07	-0.389893	0.500349017	8.02E-08

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							T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value
81		MAL13P1.214	OPFM0499	phosphotransferase (N-methyltransferase domain):MAL13P1.214:(OPFM0499)	GO:0006555	phosphatidylcholine biosynthetic process	-1.432709056	0.37043531	2.86E-07	-1.48425923	0.387419539	7.61E-09	-1.4380441	0.36900732	3.97E-09
82		PF10_028	J15L_11	adenosylmethionine decarboxylase	GO:0006168	biological process	-1.38576843	0.38279808	1.93E-06	-1.28119873	0.40782533	2.43E-07	-1.24466577	0.421917907	2.87E-07
83		PF10_032	J65L_1	adenosylmethionine decarboxylase-ortholog decarboxylase:PF10_032:(J65L_1)	GO:0006555	polyamine biosynthetic process	-0.711910586	0.610611093	0.00049846	-0.90791033	0.53232688	4.02E-06	-0.689565	0.52156007	6.79E-06
84		PF14_030	N13L_32	polyamine oxidase (N-methyltransferase domain):PF14_030:(N13L_32)	GO:0006464	protein modification	-0.83866384	0.5422558	0.00214628						
85		PF14_032	N16L_17	polyamine oxidase (N-methyltransferase domain):PF14_032:(N16L_17)	DAVID	genetic, men/transferase (SAM dep meth domain)	-1.508416047	0.351487164	0.00069983	-1.17943704	0.441524774	9.61E-06	-1.07520493	0.474602639	0.00019323
86		PF0265c	D4917L_36	lysine decarboxylase	GO:0006464	lysine catabolic process	0.87703237	1.83230333	0.0058696	1.14213943	2.48660068	1.79E-06	1.47993865	2.78172423	3.97E-07
87		PF0659c	E296L_11	adenosylmethionine decarboxylase (S-adenosyl-L-homocysteine)	GO:0009116	nucleotide metabolic process	-1.69132568	0.30964336	8.43E-09	-1.54271629	0.34232004	5.77E-10	-1.431794173	0.37066352	3.98E-10
88		PF0156w	I803L_5	homocysteine	GO:0006430	one-carbon compound metabolic process	-0.80241128	0.538776517	6.49E-06	-0.620270011	0.646931375	2.23E-06	-0.619302636	0.5793248	6.70E-06
89		PF0436w	OPFF2412	ornithine	GO:0006691	ornithine metabolic process	0.54471675	1.458492204	0.03058218	0.510326591	1.8747347	0.00219986	0.84152649	1.79195543	0.00377336
90		PF10_050	I1481L_1	S-adenosylmethionine synthase, putative:PF10_050:(I1481L_1)	GO:0006730	one-carbon compound metabolic process	-1.25218962	0.41981163	2.63E-06	-0.80339936	0.584647679	1.38E-05	-0.57289469	0.572263401	0.00057934
91	PRIMARY METABOLISM	Col	F404L_2	putative cytochrome oxidase 1:Col:(F404L_2)		oxidative phosphorylation	-0.491915853	0.711020179	0.03921615	-0.871709374	0.502901549	4.84E-05	-0.862154119	0.552956994	0.000151481
92		Col	E2296L_4	putative cytochrome oxidase 1:Col:(E2296L_4)		oxidative phosphorylation	-0.78408843	0.58071903	0.00203228	-0.629317431	0.646932047	0.001273794			
93		colM12	OPFL08002	mitochondrial encoded cytochrome oxidase subunit 3:colM12:(OPFL08002)		oxidative phosphorylation	-0.479948051	0.71003437	0.00099862	-0.88476639	0.505307462	4.40E-06	-0.697001197	0.516885701	1.71E-06
94		MAL13P1.210	M1918L_9	hydroxymethyltransferase III	GO:0006416	mannosyltransferase_III	-0.801066412	0.570363059	0.0002597	-0.432875993	0.746418298	0.004167585			
95		MAL13P1.76	PMAL13P1.76_101	mitochondria ATP synthase F1, epsilon subunit	GO:0016986	ATP synthase coupled proton transport	-0.866700349	0.48639986	0.001998385	-0.688951461	0.616211943				



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							T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>1</sub> FC	adj. p value						
120		PF0559w	OPFL06105	streny-CoA dehydrase (acyl-CoA dehydrase, fatty acid dehydrase), putative:PF0559w (OPFL06105)	GO:006629	lipid metabolic process															
121		PF0558w	F10423_3	myo-inositol 1-phosphate synthase, putative:PF0558w (F10423_3)	GO:006021	myo-inositol biosynthetic process	-0.52866745	0.52834361	0.00202926	-0.483429739	0.57137082	0.00491446	-0.5530779	0.67664933	0.03494352						
122		PF02970w	E10189_5	long chain polyunsaturated fatty acid elongation enzyme, putative:PF02970w (E10189_5)	GO:006783	heme biosynthetic process															
123		PF0220w	PMALSP1_62_738	pyruvate kinase, putative:PF0220w (PMALSP1_62_738)	GO:011936	fat acid elongation, unsaturated fatty acid synthase kinase															
124		PF01300w	OPFF72425	pyruvate kinase, putative:PF01300w (OPFF72425)	GO:006036	glycolysis	-0.2620528	0.50625992	1.32E-05	-0.77496287	0.55403365	1.11E-05	-0.62946479	0.65540204	0.00012352						
125		PF01300w	A141_1	pyruvate kinase, putative:PF01300w (A141_1)	GO:006036	glycolysis	-0.80466398	0.570897316	0.00620746	-0.15697226	0.603818293	0.01586231									
126		PF01376w	OPFF72461	epsilon-aminocaproate, putative:PF01376w (OPFF72461)	GO:006629	lipid metabolic process															
127		PF01763w	OPPI17653	heme binding, putative:PF01763w (OPPI17653)	GO:002037	heme binding															
126	PROTEIN FOLDING	PF0303c	L1_28	acyl-CoA synthetase-like LIPID METABOLISM	DAVID		1.0	0.44342281		-1.12327614	0.458397915	9.33E-07	-1.98551306	0.25291994	4.01E-10						
128		PF10_2163	J63_43	hsc70:PF10_2163 (J63_43)	GO:006457	protein folding															
129		PF1_1216	K81_18	hypothetical protein:PF1_1216 (K81_18)	GO:006457	Hsp shock factor binding															
130		PF1_1343	K88_17	hypothetical protein:PF1_1343 (K88_17)	DAVID	hsp shock protein (DnaJ)															
131		PF1_2509	K51_17_11	ring-fingered erythrocyte surface antigen, putative:PF1_2509 (K51_17_11)	GO:006457	protein folding															
132		PF1_2013	N145_36	hypothetical protein:PF1_2013 (N145_36)	GO:001072	hsp shock protein binding															
133		PF01100w	A10235_32	ring-fingered erythrocyte surface antigen precursor:PF01100w (A10235_32)	GO:001072	hsp shock protein binding	0.74516087	1.67610949	0.00511689	-1.50002389	0.34105941	1.80E-09	-1.87046361	0.25117079	3.98E-08						
134		PF01100w	A10235_30	ring-fingered erythrocyte surface antigen precursor:PF01100w (A10235_30)	GO:001072	hsp shock protein binding															
134		PF0205c	B90	Maurea parasite-induced erythrocyte surface antigen (MESA), or PBMF2:PF0205c (B90)	GO:006457	protein folding	0.95436994	1.93773233	0.00080603	-0.88980675	0.62029198	0.0012737	-1.41826104	0.37401873	1.48E-06						
136		PF0204c	F2247_17	Maurea parasite-induced erythrocyte surface antigen (MESA), or PBMF2:PF0204c (F2247_17)	GO:001072	hsp shock protein binding	-0.97310061	0.50282511	2.57E-05	-0.83078961	0.59338907	9.18E-06	-0.68887723	0.25869294	8.06E-05						
136	PF0204c	E02062_1	hypothetical protein:PF0204c (E02062_1)	GO:001072	hsp shock protein binding	-0.93486919	0.52304346	2.53E-05	-0.92337662	0.52729768	1.99E-07	-0.74061349	0.59477333	1.84E-06							
136	PF01170w	OPFL06146	hypothetical protein:PF01170w (OPFL06146)	GO:006457	protein folding																
137	PF0355w	E0135_5	hypothetical protein:PF0355w (E0135_5)	GO:006457	protein folding																
137	PF0355w	I190_2_1	hypothetical protein:PF0355w (I190_2_1)	GO:001072	hsp shock protein binding	-0.98720877	0.51149713	0.00238745	-0.5231395	0.63144483	0.02535888										
138	PF0435w	KM469_1	hypothetical protein:PF0435w (KM469_1)	GO:001072	hsp shock protein binding	-0.85818963	0.58113622	0.00260276	-0.25257251	0.68612225	0.02467252	-0.62036668	0.65026019	0.001194731							
139	PF1_1545c	OPR1018	chaperonin (Cpn60):PF1_1545c (OPR1018)	GO:006457	protein folding																
140	PF1_2650w	OPFL0587	hypothetical protein, conserved in P. falciparum:PF1_2650w (OPFL0587)	GO:006457	protein folding	-0.76302625	0.59237076	0.00242675	-1.07383688	0.48704139	1.51E-05	-1.40311715	0.45265259	3.84E-07							
141		MALSP1_113	E4387_1	hypothetical protein:MALSP1_113 (E4387_1)	GO:006036	proteolysis															
141		PRD_2042	F1783_1	hypothetical protein:PRD_2042 (F1783_1)	GO:006036	proteolysis	-0.63693142	0.64307868	0.00154748	-0.74203291	0.58476501	0.00253834	-0.70574689	0.513117343	0.00025746						
142		PF1_1216	K78_31	hypothetical protein:PF1_1216 (K78_31)	GO:006036	proteolysis	-0.59373796	0.580437913	2.24E-05	-0.46207399	0.72941396	8.57E-05	-0.20418804	0.86846124	0.03212386						
143		PF1_1216	K818_5	conserved:PF1_1216 (K818_5)	GO:006456	protein modification															
144		PF1_2382	M5605_3	proteasome subunit, putative:PF1_2382 (M5605_3)	GO:006651	ubiquitin-dependent protein catabolic process	-0.87116486	0.54670314	5.48E-05	-0.35204693	0.73471688	0.00244489									
145		PF1_2015	OPPN267	aminopeptidase, putative:PF1_2015 (OPPN267)	GO:008110	biological process	0.93262048	1.91764079	2.38E-05	0.79313783	1.66490889	2.28E-05	0.38273705	1.1240041	0.00540317						
145		PF1_2015	N145_28	aminopeptidase, putative:PF1_2015 (N145_28)	GO:008110	biological process	0.32665012	1.30292875	0.03514426	0.94281381	1.97464077	2.11E-05	0.89578967	1.64923916	5.37E-06						
146		PF1_2382	N132_119	ATP-dependent O <sub>6</sub> prolylase, putative:PF1_2382 (N132_119)	GO:006036	proteolysis	-0.83177169	0.56118883	0.00250449	-0.74966261	0.59895826	7.38E-06	-0.60770901	0.53416632	0.000218429						
146		PF1_2382	N132_119	ATP-dependent O <sub>6</sub> prolylase, putative:PF1_2382 (N132_119)	DAVID	proteasome M <sub>1</sub> dric metalloprotease															
148		PF1_2439	OPPN263	lysine aminopeptidase, putative:PF1_2439 (OPPN263)	GO:006036	proteolysis	-0.28163978	0.76226717	0.005419329	-0.59851502	0.56490294	1.23E-05	-0.81487485	0.558571037	4.02E-07						
149		PF1_2476	N137_50	ubiquitin-dependent protein catabolic process, putative:PF1_2476 (N137_50)	GO:006651	ubiquitin-dependent protein catabolic process															
150		PF0225w	D6287_70	hypothetical protein:PF0225w (D6287_70)	DAVID	proteasome M <sub>1</sub> dric metalloprotease	-0.58162643	0.66826361	0.01682138	-0.82792456	0.56324274	6.23E-05	-1.13872923	0.45414908	7.01E-07						
150		PF0225w	D4917_1	hypothetical protein:PF0225w (D4917_1)	DAVID	proteasome M <sub>1</sub> dric metalloprotease	-0.79449168	0.57683208	0.00101846	-0.48051234	0.72736331	0.01092351	-0.72728641	0.60404475	0.00082695						
151		PF0225w	D4917_2	hypothetical protein:PF0225w (D4917_2)	GO:006036	proteolysis															
151		PF0244w	OPFL06010	hypothetical protein:PF0244w (OPFL06010)	DAVID	peptidase M22, glyprotease	-1.27921251	0.41181787	9.88E-07	-0.89951228	0.50326265	8.99E-07	-0.85146323	0.55423374	3.52E-06						
151		PF0244w	D1771_57	hypothetical protein:PF0244w (D1771_57)	DAVID	peptidase M22, glyprotease	-1.13292142	0.40282837	0.00101506	-0.78762927	0.57929006	0.00811935	-0.81911609	0.45674912							
152		PF0244w	M22_4	hypothetical protein:PF0244w (M22_4)	DAVID	peptidase M22, glyprotease	-1.22981074	0.42649344	2.63E-05	-0.89269787	0.62150264	0.0014748	-0.60024688	0.56961306	0.000325421						
153		PF0550c	E824_4	hypothetical protein:PF0550c (E824_4)	DAVID	ubiquitin dependent protein catabolic process, zinc finger, RING-type, protein ubiquitination	-0.83209593	0.56397793	1.68E-05	-0.81280599	0.70077193	0.00021744									
154		PF0107c	F3831_2	hypothetical protein:PF0107c (F3831_2)	GO:006515	ubiquitin dependent protein catabolic process															
154		PF01120w	E898_2	hypothetical protein:PF01120w (E898_2)	GO:006036	proteolysis	1.17148532	2.25248189	0.00255867	1.03379183	2.14887378	7.52E-05	0.89721566	1.86248852	0.00044839						
154		PF01120w	E117_12	hypothetical protein:PF01120w (E117_12)	GO:006036	proteolysis	0.99932136	1.99345696	0.00052587												
157		PF0267c	PMALSP1_306_1519	hypothetical protein:PF0267c (PMALSP1_306_1519)	DAVID	ubiquitin dependent protein catabolic process															
157		PF0393c	E802_2	hypothetical protein:PF0393c (E802_2)	GO:006036	proteolysis	-0.75877939	0.60222641	0.0122689	-0.81821462	0.87342416	0.00029472	-0.68459182	0.6218163	0.002087078						
158		PF1166c	F843_1	hypothetical protein:PF1166c (F843_1)	GO:006456	protein modification															
158		PF1166c	E2044_1	hypothetical protein:PF1166c (E2044_1)	GO:006456	protein modification	0.70981827	1.70418598	0.01293524	0.87913332	1.97154916	0.01397384									
158		PF1166c	E2044_2	hypothetical protein:PF1166c (E2044_2)	GO:006456	protein modification															
159		PF0135c	OPPI17588	serpin family cysteine protease, putative:PF0135c (OPPI17588)	GO:006036	proteolysis	-0.31029555	0.524483772	0.01730824	-1.09034655	0.465667665	0.001236771	-0.77594611	0.532555042	0.01278427						
160		PF0135c	OPFL06011	serpin family cysteine protease, putative:PF0135c (OPFL06011)	GO:006036	proteolysis	-0.64300275	0.54637989	0.00363912	-0.588317997	0.511108597	9.71E-07	-0.65588325	0.53031680	4.34E-05						
161		PF1_1216	D6470_1	hypothetical protein:PF1_1216 (D6470_1)	DAVID	ubiquitin dependent protein catabolic process															
161		PF1_2559w	L2_187	PF048 Plasmodium falciparum, conserved:PF1_2559w (L2_187)																	







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							T <sub>0</sub> log <sub>2</sub> FC	T <sub>0</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>0</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>0</sub> FC	adj. p value	T <sub>0</sub> log <sub>2</sub> FC	T <sub>0</sub> FC	adj. p value
414		PF14_0570	N130_6	hypothetical protein, conserved:PF14_0570_(N130_6)	GO:0008150	biological_process	-1.12359847	0.46615635	0.00181255	-0.75504789	0.93262241	0.001091389						
415		PF14_0582	OPFN2027	hypothetical protein:PF14_0582_(OPFN2027)			-0.82711730	0.64748583	0.00514401	-0.73413650	0.90177739	0.00493361	-0.76299404	0.58927318	0.000317596			
416		PF14_0582	N134_126	hypothetical protein:PF14_0582_(N134_126)			-0.72088009	0.58868899	0.00238323	-0.62921506	0.94629975	0.00226293	-0.46843345	0.72724921	0.00232623			
417		PF14_0582	N134_23	hypothetical protein:PF14_0582_(N134_23)			-0.78102048	0.58841295	0.00211705									
418		PF14_0582	N137_4	hypothetical protein:PF14_0582_(N137_4)	GO:0008150	biological_process	-0.42872308	0.74291909	0.02374527	0.15647692	1.68818946	3.81E-07	0.89582491	1.84762362	3.27E-08			
419		PF14_0586	N137_23	hypothetical protein:PF14_0586_(N137_23)			-0.80202381	0.47863313	5.60E-07	-0.73179777	0.90232779	5.24E-06	-0.72113914	0.902662879	2.38E-06			
420		PF14_0586	N137_21	hypothetical protein:PF14_0586_(N137_21)			-0.80466773	0.47820318	5.34E-05	-0.73951169	0.93922995	7.75E-07	-0.63418161	0.64411978	3.27E-06			
421		PF14_0590	PF14_0590_16	hypothetical protein:PF14_0590_(PF14_0590_16)	GO:0008150	biological_process	-1.00755219	0.45729026	2.36E-06	-0.60951955	0.95899037	3.99E-05	-0.39924214	0.73222399	0.00199932			
422		PF14_0730	PF14_0730_170	hypothetical protein:PF14_0730_(PF14_0730_170)	GO:0008150	biological_process	-0.47498977	1.38942050	0.00309569	-0.69702682	0.91649052	3.20E-04	-0.64437414	0.944789233	2.97E-07			
423		PF14_0732	N125_33	hypothetical protein:PF14_0732_(N125_33)	GO:0008150	biological_process	-1.17370147	0.45240743	1.07E-06	-0.75021042	0.96200583	0.02010731	-0.43243361	0.71269477	0.00037189			
424		PF14_0732	N125_34	hypothetical protein:PF14_0732_(N125_34)	GO:0008150	biological_process	0.875404145	1.828340573	4.73E-06	0.49517823	1.42049473	3.95E-05	-0.41348199	0.526893719	0.00037189			
426		PF14018w	PF14018w_278	hypothetical protein:PF14018w_(PF14018w_278)	GO:0020111	apoptosis	-1.17895362	0.20378987	7.48E-07	-1.61816967	0.34965247	1.06E-08	-1.46318985	0.36473993	2.20E-08			
427		PF14249w	PF14249w	hypothetical protein:PF14249w			-1.18959682	0.20378987	7.48E-07	-1.61816967	0.34965247	1.06E-08	-1.46318985	0.36473993	2.20E-08			
428		PF14255c	A4704_11	hypothetical protein:PF14255c_(A4704_11)			-0.83027483	0.52478399	0.00521281	-0.79310373	0.97898221	1.32E-05	-0.56021436	0.87060261	0.001490036			
430		PF14255c	A8109_21	hypothetical protein:PF14255c_(A8109_21)	GO:0010712	heat shock protein binding	-0.53136814	0.69176935	0.01120697	-0.79310373	0.97898221	1.32E-05	-0.56021436	0.87060261	0.001490036			
430		PF14255c	A1185_2	hypothetical protein:PF14255c_(A1185_2)			-0.82329624	0.58280263	0.00247078	-0.62329624	0.96280263	0.00247078	-0.63320442	0.83740591	0.00247078			
431		PF14255c	A3114_2	hypothetical protein:PF14255c_(A3114_2)			-0.81902812	0.56802439	0.00219024	-0.71972641	0.92526291	0.00190212	-1.14451335	0.45146924	1.18E-06			
433		PF14255c	A1480_24	hypothetical protein:PF14255c_(A1480_24)			-0.45132936	0.73168905	0.04894230	-0.68204158	0.94221237	0.00146520						
434		PF14255c	PF14255c_135	hypothetical protein:PF14255c_(PF14255c_135)			-0.34449464	0.73962959	0.01307194	-0.62449464	0.97962959	0.01307194	-0.29124229	0.46929732	6.81E-06			
436		PF14255c	880	hypothetical protein:PF14255c_(880)	GO:0008150	biological_process	-0.82049462	0.67846414	0.02277058	-0.68204158	0.94221237	0.00146520	-0.51167874	0.64972738	0.00107442			
437		PF14255c	884	hypothetical protein:PF14255c_(884)	GO:0008150	biological_process	-0.73012972	0.80280389	0.00107013	-1.37183111	0.34637118	6.48E-06						
437		PF14255c	889	hypothetical protein:PF14255c_(889)			1.34247957	0.32646474	7.23E-05	1.72928297	0.31613989	4.83E-06						
438		PF14255c	8161	hypothetical protein:PF14255c_(8161)			1.00141301	2.0019519	0.00032047	0.64511076	1.56933958	0.04830731						
439		PF14255c	8310	hypothetical protein:PF14255c_(8310)	GO:0008150	biological_process	0.80808029	1.75175475	0.00194236	0.46859406	1.38192036	0.01907497						
440		PF14255c	8310	hypothetical protein:PF14255c_(8310)			-0.54610478	0.58481843	0.00116629	-0.71452876	0.94409599	0.00296333	-0.68642674	0.90272686	0.00072629			
441		PF14255c	8370	hypothetical protein:PF14255c_(8370)	GO:0008150	biological_process	-0.78446729	0.83048936	0.00170273	-0.84428252	0.91864261	4.42E-06	-1.01944479	0.430308179	3.43E-06			
441		PF14255c	8389	hypothetical protein:PF14255c_(8389)			-0.79732846	0.57533047	0.00507626	-0.67021929	0.92341118	0.02436181	-0.95415959	0.51412036	0.000711061			
442		PF14255c	8392	hypothetical protein:PF14255c_(8392)	GO:0008150	biological_process	-1.5493798	0.34166907	0.01192077	-1.09775266	0.46724793	0.00540599	-1.08081003	0.47038663	0.02116748			
443		PF14255c	8392	hypothetical protein:PF14255c_(8392)			-0.46810478	0.58481843	0.00116629	-0.71452876	0.94409599	0.00296333	-0.68642674	0.90272686	0.00072629			
443		PF14255c	8536	hypothetical protein:PF14255c_(8536)	GO:0008150	biological_process	-0.489991161	0.70701415	0.02476588	-0.78452876	0.94409599	0.00296333	-0.68642674	0.90272686	0.00072629			
444		PF14255c	8665	hypothetical protein:PF14255c_(8665)	GO:0008150	biological_process	-0.72949439	1.72059637	0.00179983	-0.67021929	0.92341118	0.02436181	-0.95415959	0.51412036	0.000711061			
447		PF14255c	8572	liver stage antigen 3-PF0915c_(8572)	GO:0008150	biological_process	-0.7744997	0.98924315	7.22E-04	-0.7744997	0.98924315	7.22E-04	-0.7744997	0.98924315	7.22E-04			
447		PF14255c	8577	hypothetical protein:PF14255c_(8577)	GO:0008150	biological_process	0.50159197	1.41577495	0.006584194	0.32487405	0.98919094	2.93E-06	1.03929294	2.05612896	6.51E-07			
449		PF14255c	OPF0859	hypothetical protein:PF14255c_(OPF0859)	GO:0008150	biological_process	-0.93104874	0.52447835	0.00147202	-0.62961251	0.94343662	0.00306033	-0.41914749	0.74623119	0.01274929			
449		PF14255c	8603	hypothetical protein:PF14255c_(8603)	GO:0008150	biological_process	-1.30022294	0.47859748	1.74E-07	-0.62961251	0.94343662	0.00306033	-0.41914749	0.74623119	0.01274929			
450		PF14255c	C49	hypothetical protein:PF14255c_(C49)			0.39302629	1.91708285	0.04848691	0.79364578	0.48926979	0.00012036						
451		PF14255c	C54	hypothetical protein:PF14255c_(C54)	GO:0020111	apoptosis	0.78194694	1.60251184	0.00311416	0.93241622	0.52397901	0.00101128	-0.16776718	0.47073442	0.0012036			
453		PF14255c	C33	hypothetical protein:PF14255c_(C33)	GO:005622	intracellular	1.17489507	2.28789302	0.004134871									
453		PF14255c	C239	hypothetical protein:PF14255c_(C239)	GO:0020111	apoptosis	0.89190489	1.85630352	0.00042142	0.70930089	1.63572924	0.00489696						
456		PF14255c	OPF0768	hypothetical protein:PF14255c_(OPF0768)			-0.81216493	0.56939305	0.00427082	-0.76277611	0.98930632	0.00170722	-0.61178474	0.55411776	5.00E-05			
456		PF14255c	C385	hypothetical protein:PF14255c_(C385)			-0.54555451	0.63439547	0.02354817	-0.54555451	0.63439547	0.02354817	-0.54555451	0.63439547	0.02354817			
457		PF14255c	OPF0773	hypothetical protein:PF14255c_(OPF0773)	GO:0020111	apoptosis	-0.51449599	0.70037911	0.00114114	-0.51449599	0.70037911	0.00114114	-0.51449599	0.70037911	0.00114114			
457		PF14255c	C419	hypothetical protein:PF14255c_(C419)	GO:0020111	apoptosis	-0.68985952	0.62339984	0.01192858	-0.68985952	0.62339984	0.01192858	-0.68985952	0.62339984	0.01192858			
458		PF14255c	OPF0730w	hypothetical protein:PF14255c_(OPF0730w)	GO:0008150	biological_process	-0.60214468	0.69876472	3.78E-05	-0.60214468	0.69876472	3.78E-05	-0.60214468	0.69876472	3.78E-05			
458		PF14255c	OPF0730w	hypothetical protein:PF14255c_(OPF0730w)	GO:0008150	biological_process	-0.66223901	0.61367029	2.45E-05	-0.66223901	0.61367029	2.45E-05	-0.66223901	0.61367029	2.45E-05			
459		PF14255c	C541	hepatocyte stage antigen:PF14255c_(C541)			-0.73964324	0.59931827	0.00114264	-1.20074229	0.420178349	0.00078349						
459		PF14255c	C622	hypothetical protein:PF14255c_(C622)			-0.786761297	0.579643874	0.04995994									
461		PF14255c	OPF0775	hypothetical protein:PF14255c_(OPF0775)			-1.08709938	0.47279617	9.52E-05	-1.15532829	0.90977987	0.00242234	-0.64662389	0.58405271	0.00219934			
462		PF14255c	C604	hypothetical protein:PF14255c_(C604)			-0.82701166	0.52939348	0.00179158	-0.48193719	0.71123461	0.00397629	-0.40724613	0.75414646	0.02851519			
462		PF14255c	C129	hypothetical protein:PF14255c_(C129)			-0.74441702	0.59503912	0.02045163	-0.74441702	0.59503912	0.02045163	-0.74441702	0.59503912	0.02045163			
463		PF14255c	C243_42	hypothetical protein:PF14255c_(C243_42)			-0.74423238	0.59628499	0.02042841	-0.71734417	0.64811654	1.5						

# APPENDIX B

## DIFFERENTIAL TRANSCRIPT ABUNDANCE DATASET (EDGE)

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PlasmoDB IDs	NAME
chr13-tRNA-Thr-1	chr13-tRNA-Thr-1::chr13-tRNA-Thr-1::(PCHR13-TRNA-THR-1_2)
chr14.gen_473_MND1	chr14.gen_473_MND1::chr14.gen_473_MND1::(PCHR14.GEN_473_MND1_168)
chr7.rRNA-1-ITS1	chr7.rRNA-1-ITS1, putative::chr7.rRNA-1-ITS1::(PCHR7.RRNA-1-ITS1_17)
chr8.rRNA-1-5.8s-pseudo	chr8.rRNA-1-5.8s, pseudo::chr8.rRNA-1-5.8s-pseudo::(PCHR8.RRNA-1-5.8S-PSEUDO_90)
MAL13P1.103	hypothetical protein::MAL13P1.103::(M10202_2)
MAL13P1.109	conserved hypothetical protein, conserved in <i>P. falciparum</i> ::MAL13P1.109::(OPFM60490)
MAL13P1.118	cAMP-specific 3',5'-cyclic phosphodiesterase 4D, putative::MAL13P1.118::(M16622_2)
MAL13P1.131	hypothetical protein::MAL13P1.131::(M33739_10)
MAL13P1.141	hypothetical protein::MAL13P1.141::(M24561_22)
MAL13P1.142	hypothetical protein::MAL13P1.142::(M24561_19)
MAL13P1.15	hypothetical protein::MAL13P1.15::(PMAL13P1.15_12)
MAL13P1.150	hypothetical protein::MAL13P1.150::(PMAL13P1.150_1377)
MAL13P1.158	hypothetical protein::MAL13P1.158::(J4848_2)
MAL13P1.162	DNAJ-like protein, putative::MAL13P1.162::(PMAL13P1.162_176)
MAL13P1.164	elongation factor tu, putative::MAL13P1.164::(M8032_4)
MAL13P1.167	signal peptidase, putative::MAL13P1.167::(M18924_16)
MAL13P1.168	hypothetical protein::MAL13P1.168::(PMAL13P1.168_448)
MAL13P1.182	hypothetical protein, conserved::MAL13P1.182::(PMAL13P1.182_635)
MAL13P1.183	hypothetical protein::MAL13P1.183::(PMAL13P1.183_168)
MAL13P1.184	endopeptidase, putative::MAL13P1.184::(M32813_2)
MAL13P1.19	hypothetical protein::MAL13P1.19::(I4256_1)
MAL13P1.190	proteasome regulatory component, putative::MAL13P1.190::(M54626_1)
MAL13P1.194	hypothetical protein::MAL13P1.194::(M37794_2)
MAL13P1.217	hypothetical protein::MAL13P1.217::(J8570_1)
MAL13P1.218	UDP-N-acetylglucosamine pyrophosphorylase, putative::MAL13P1.218::(M55888_8)
MAL13P1.227	ubiquitin-conjugating enzyme, putative::MAL13P1.227::(M35930_10)
MAL13P1.232	hypothetical protein::MAL13P1.232::(KN1115_2)
MAL13P1.234	hypothetical protein::MAL13P1.234::(I4738_1)
MAL13P1.238	hypothetical protein::MAL13P1.238::(M15752_2)
MAL13P1.24	hypothetical protein::MAL13P1.24::(M29079_4)
MAL13P1.243	elongation factor Tu, putative::MAL13P1.243::(M45339_1)
MAL13P1.248	nucleoside diphosphate hydrolase::MAL13P1.248::(M24933_5)
MAL13P1.250	hypothetical protein::MAL13P1.250::(PMAL13P1.250_736)
MAL13P1.254	hypothetical protein::MAL13P1.254::(PMAL13P1.254_185)
MAL13P1.255	hypothetical protein::MAL13P1.255::(OPFM60555)
MAL13P1.256	phosphatidylinositol transfer protein, putative::MAL13P1.256::(PMAL13P1.256_3773)
MAL13P1.261	hypothetical protein::MAL13P1.261::(M24315_1)
MAL13P1.277	DnaJ-like protein, putative::MAL13P1.277::(PMAL13P1.277_207)
MAL13P1.28	hypothetical protein::MAL13P1.28::(M16281_2)
MAL13P1.281	glutamate--tRNA ligase, putative::MAL13P1.281::(M21508_6)
MAL13P1.292	riboflavin kinase / FAD synthase family protein, putative::MAL13P1.292::(PMAL13P1.292_332)
MAL13P1.299	hypothetical protein, conserved::MAL13P1.299::(M26245_8)
MAL13P1.300	hypothetical protein::MAL13P1.300::(M26245_9)
MAL13P1.303	polyadenylate binding protein, putative::MAL13P1.303::(M2931_3)
MAL13P1.308	hypothetical protein, conserved::MAL13P1.308::(M36754_2)
MAL13P1.318	hypothetical protein::MAL13P1.318::(OPFM60527)
MAL13P1.323	hypothetical protein::MAL13P1.323::(M1222_1)
MAL13P1.332	hypothetical protein::MAL13P1.332::(M3696_3)
MAL13P1.341	hypothetical protein, conserved::MAL13P1.341::(M38913_6)
MAL13P1.343	proteasome regulatory subunit, putative::MAL13P1.343::(M33419_1)
MAL13P1.354	erythrocyte membrane protein 1 (PEMP1), pseudogene::MAL13P1.354::(L1_21)
MAL13P1.40	hypothetical protein::MAL13P1.40::(OPFM60513)
MAL13P1.45	hypothetical protein, conserved::MAL13P1.45::(M25032_3)
MAL13P1.48	hypothetical protein::MAL13P1.48::(M3590_1)
MAL13P1.480	Histidine Rich protein III (HRPIII)::MAL13P1.480::(PHRPIII_502)
MAL13P1.54	hypothetical protein, conserved::MAL13P1.54::(M2511_2)
MAL13P1.61	hypothetical protein::MAL13P1.61::(M26214_1)
MAL13P1.65	hypothetical protein::MAL13P1.65::(PMAL13P1.65_103)
MAL13P1.74	hypothetical protein::MAL13P1.74::(M364_1)
MAL13P1.82	phosphatidylinositol synthase, putative::MAL13P1.82::(PMAL13P1.82_71)
MAL13P1.89	hypothetical protein::MAL13P1.89::(M5172_2)
MAL7P1.110	hypothetical protein, conserved::MAL7P1.110::(PMAL7P1.110_303)
MAL7P1.119	hypothetical protein::MAL7P1.119::(F53897_2)
MAL7P1.138	hypothetical protein::MAL7P1.138::(F35197_1)
MAL7P1.141	hypothetical protein::MAL7P1.141::(PMAL7P1.141_100)
MAL7P1.145	DNA mismatch repair protein pms1 homologue, putative::MAL7P1.145::(D52830_1)
MAL7P1.149	hypothetical protein::MAL7P1.149::(PMAL7P1.149_1727)
MAL7P1.170	ring stage expressed protein::MAL7P1.170::(OPFBLOB0026)
MAL7P1.25	hypothetical protein::MAL7P1.25::(F42062_1)
MAL7P1.27	chloroquine resistance transporter, putative::MAL7P1.27::(F35774_1)
MAL7P1.29	hypothetical protein::MAL7P1.29::(E12238_1)
MAL7P1.6	hypothetical protein::MAL7P1.6::(PMAL7P1.6_11)
MAL7P1.61	erythrocyte membrane protein 1 (PEMP1) pseudogene::MAL7P1.61::(F17545_3)
MAL7P1.76	hypothetical protein::MAL7P1.76::(F403_1)
MAL7P1.77	hypothetical protein::MAL7P1.77::(F25543_1)



MAL7P1.83 hypothetical protein::MAL7P1.83::(F66828\_2)  
MAL7P1.88 thioredoxin-like protein::MAL7P1.88::(F71224\_1)  
MAL7P1.93 mitochondrial ribosomal protein S8, putative::MAL7P1.93::(F68670\_1)  
MAL8P1.101 hypothetical protein::MAL8P1.101::(E22273\_1)  
MAL8P1.108 protein phosphatase, putative::MAL8P1.108::(PMAL8P1.108\_541)  
MAL8P1.109 hypothetical protein, conserved::MAL8P1.109::(F26666\_3)  
MAL8P1.113 hypothetical protein::MAL8P1.113::(E4387\_1)  
MAL8P1.114 hypothetical protein::MAL8P1.114::(F55001\_5)  
MAL8P1.145 hypothetical protein, conserved::MAL8P1.145::(PMAL8P1.145\_328)  
MAL8P1.146 hypothetical protein::MAL8P1.146::(F4732\_2)  
MAL8P1.157 hypothetical protein::MAL8P1.157::(F27536\_1)  
MAL8P1.17 disulfide isomerase precursor, putative::MAL8P1.17::(F53081\_1)  
MAL8P1.21 hypothetical protein::MAL8P1.21::(F19190\_1)  
MAL8P1.3 integral membrane protein, conserved in *P. falciparum*::MAL8P1.3::(OPFBLOB0144)  
MAL8P1.30 hypothetical protein::MAL8P1.30::(PMAL8P1.30\_1158)  
MAL8P1.32 nucleoside transporter, putative::MAL8P1.32::(F4541\_1)  
MAL8P1.34 hypothetical protein::MAL8P1.34::(F31053\_2)  
MAL8P1.51 protein-transport protein sec61 beta 1 subunit, putative::MAL8P1.51::(PMAL8P1.51\_168)  
MAL8P1.53 hypothetical protein::MAL8P1.53::(PMAL8P1.53\_1127)  
MAL8P1.55 hypothetical protein::MAL8P1.55::(F20870\_2)  
MAL8P1.62 hypothetical protein, conserved in other *Plasmodium* species::MAL8P1.62::(F70676\_1)  
MAL8P1.79 hypothetical protein::MAL8P1.79::(KN2562\_1)  
MAL8P1.99 hypothetical protein::MAL8P1.99::(F4481\_1)  
PF00\_0001 hypothetical protein::PF00\_0001::(F5510\_1)  
PF00\_0003 hypothetical protein::PF00\_0003::(F39902\_1)  
PF07\_0006 starp antigen::PF07\_0006::(OPFG0007)  
PF07\_0010 hypothetical protein::PF07\_0010::(F20792\_1)  
PF07\_0011 hypothetical protein, conserved::PF07\_0011::(OPFG0025)  
PF07\_0023 DNA replication licensing factor mcm7 homologue, putative::PF07\_0023::(OPFG0035)  
PF07\_0032 Cg8 protein::PF07\_0032::(D35303\_1)  
PF07\_0034 Cg3 protein::PF07\_0034::(OPFG0001)  
PF07\_0039 hypothetical protein::PF07\_0039::(F47864\_1)  
PF07\_0042 hypothetical protein::PF07\_0042::(F17836\_1)  
PF07\_0052 hypothetical protein::PF07\_0052::(PPF07\_0052\_366)  
PF07\_0059 4-nitrophenylphosphatase, putative::PF07\_0059::(F7288\_1)  
PF07\_0062 GTP-binding translation elongation factor tu family protein, putative::PF07\_0062::(F11707\_1)  
PF07\_0064 hypothetical protein::PF07\_0064::(F69212\_1)  
PF07\_0075 hypothetical protein, expressed::PF07\_0075::(F56229\_4)  
PF07\_0112 proteasome subunit alpha type 5, putative::PF07\_0112::(F960\_4)  
PF07\_0113 hypothetical protein::PF07\_0113::(F71022\_1)  
PF07\_0118 hypothetical protein::PF07\_0118::(E18957\_1)  
PF07\_0121 hypothetical protein, conserved::PF07\_0121::(E14340\_1)  
PF08\_0003 tryptophan/threonine-rich antigen::PF08\_0003::(OPFBLOB0065)  
PF08\_0006 prohibitin, putative::PF08\_0006::(OPFH0005)  
PF08\_0010 hypothetical protein::PF08\_0010::(F5206\_2)  
PF08\_0021 hypothetical protein::PF08\_0021::(F36803\_1)  
PF08\_0029 hypothetical protein::PF08\_0029::(OPFH0035)  
PF08\_0032 hypothetical protein::PF08\_0032::(F1761\_1)  
PF08\_0041 ribosome biogenesis protein nep1 homologue, putative::PF08\_0041::(OPFBLOB0134)  
PF08\_0045 2-oxoglutarate dehydrogenase e1 component::PF08\_0045::(F10318\_1)  
PF08\_0053 hypothetical protein::PF08\_0053::(PPF08\_0053\_743)  
PF08\_0056 zinc finger protein, putative::PF08\_0056::(F65493\_3)  
PF08\_0063 hypothetical protein::PF08\_0063::(F39343\_3)  
PF08\_0075 60S ribosomal protein L13, putative::PF08\_0075::(F21981\_2)  
PF08\_0080 hypothetical protein::PF08\_0080::(F17989\_1)  
PF08\_0083 hypothetical protein::PF08\_0083::(OPFH0037)  
PF08\_0091 hypothetical protein::PF08\_0091::(F28313\_1)  
PF08\_0097 hypothetical protein::PF08\_0097::(PPF08\_0097\_1500)  
PF08\_0098 abc transporter, putative::PF08\_0098::(F61881\_1)  
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PF08\_0116 hypothetical protein::PF08\_0116::(F53446\_1)  
PF08\_0119 hypothetical protein::PF08\_0119::(PPF08\_0119\_76)  
PF08\_0125 tubulin gamma chain::PF08\_0125::(F20448\_4)  
PF08\_0131 1-cys peroxidoxin::PF08\_0131::(F46816\_2)  
PF10\_0014 hypothetical protein::PF10\_0014::(PPF10\_0014\_381)  
PF10\_0015 acyl CoA binding protein, putative::PF10\_0015::(OPFJ12802)  
PF10\_0016 acyl CoA binding protein, putative::PF10\_0016::(J33\_21)  
PF10\_0017 hypothetical protein::PF10\_0017::(J33\_20)  
PF10\_0019 early transcribed membrane protein::PF10\_0019::(J33\_16)  
PF10\_0021 hypothetical protein::PF10\_0021::(J33\_12)  
PF10\_0022 hypothetical protein::PF10\_0022::(J33\_11)  
PF10\_0025 PF70 protein::PF10\_0025::(F67629\_1)  
PF10\_0033 hypothetical protein::PF10\_0033::(J120\_2)  
PF10\_0034 hypothetical protein::PF10\_0034::(J120\_6)  
PF10\_0036 N-acetyltransferase, putative::PF10\_0036::(J120\_11)  
PF10\_0047 hypothetical protein::PF10\_0047::(KS2508\_1)  
PF10\_0051 ADP/ATP carrier protein, putative::PF10\_0051::(J43\_12)  
PF10\_0052 hypothetical protein::PF10\_0052::(J43\_15)  
PF10\_0053 tRNA ligase, putative::PF10\_0053::(J43\_16)  
PF10\_0065 hypothetical protein::PF10\_0065::(J163\_7)  
PF10\_0066 hypothetical protein::PF10\_0066::(J163\_6)  
PF10\_0068 hypothetical protein::PF10\_0068::(J634\_1)  
PF10\_0079 hypothetical protein::PF10\_0079::(J73\_15)  
PF10\_0084 tubulin beta chain, putative::PF10\_0084::(J73\_4)  
PF10\_0092 hypothetical protein::PF10\_0092::(PPF10\_0092\_84)  
PF10\_0093 hypothetical protein::PF10\_0093::(J267\_2)  
PF10\_0097 hypothetical protein::PF10\_0097::(J647\_6)  
PF10\_0100 hypothetical protein::PF10\_0100::(J1417\_2)  
PF10\_0101 hypothetical protein::PF10\_0101::(J920\_3)  
PF10\_0108 hypothetical protein::PF10\_0108::(J252\_1)  
PF10\_0116 hypothetical protein::PF10\_0116::(J293\_1)  
PF10\_0120 hypothetical protein::PF10\_0120::(KM827\_4)



PF10\_0132 phospholipase C-like, putative::PF10\_0132::(J53\_7)  
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PF10\_0152 hypothetical protein::PF10\_0152::(J53\_42)  
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PF10\_0163 hypothetical protein::PF10\_0163::(J425\_2)  
PF10\_0168 hypothetical protein::PF10\_0168::(J248\_4)  
PF10\_0174 26s proteasome subunit p55, putative::PF10\_0174::(J110\_4)  
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PF10\_0200 hypothetical protein, conserved::PF10\_0200::(J26\_1)  
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PF10\_0227 hypothetical protein, conserved::PF10\_0227::(PPF10\_0227\_403)  
PF10\_0235 hypothetical protein::PF10\_0235::(J245\_5)  
PF10\_0238 hypothetical protein::PF10\_0238::(J245\_10)  
PF10\_0246 hypothetical protein::PF10\_0246::(J212\_1)  
PF10\_0259 hypothetical protein::PF10\_0259::(J232\_6)  
PF10\_0262 hypothetical protein::PF10\_0262::(J121\_1)  
PF10\_0275 protoporphyrinogen oxidase, putative::PF10\_0275::(J504\_4)  
PF10\_0286 hypothetical protein::PF10\_0286::(J151\_5)  
PF10\_0295 hypothetical protein::PF10\_0295::(J564\_3)  
PF10\_0301 calmodulin, putative::PF10\_0301::(J461\_5)  
PF10\_0311 hypothetical protein, conserved::PF10\_0311::(J352\_5)  
PF10\_0313 hypothetical protein::PF10\_0313::(D38761\_3)  
PF10\_0317 hypothetical protein::PF10\_0317::(J153\_2)  
PF10\_0330 ubiquitin-conjugating enzyme, putative::PF10\_0330::(J1011\_2)  
PF10\_0331 hypothetical protein, conserved::PF10\_0331::(J141\_1)  
PF10\_0334 flavoprotein subunit of succinate dehydrogenase::PF10\_0334::(J167\_8)  
PF10\_0345 merozoite Surface Protein 3, MSP3::PF10\_0345::(J116\_9)  
PF10\_0346 merozoite Surface protein 6, MSP6::PF10\_0346::(J116\_7)  
PF10\_0359 hypothetical protein::PF10\_0359::(J21\_27)  
PF10\_0360 hypothetical protein::PF10\_0360::(J21\_24)  
PF10\_0363 pyruvate kinase, putative::PF10\_0363::(J21\_14)  
PF11\_0036 hypothetical protein, conserved::PF11\_0036::(KS54\_4)  
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PF11\_0040 early transcribed membrane protein 11.2::PF11\_0040::(KS75\_15)  
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PF11\_0048 casein kinase II beta chain, putative::PF11\_0048::(KS375\_3)  
PF11\_0084 hypothetical protein::PF11\_0084::(PPF11\_0084\_251)  
PF11\_0087 Rad51 homolog, putative::PF11\_0087::(KS42\_6)  
PF11\_0105 hypothetical protein::PF11\_0105::(KS2345\_1)  
PF11\_0123 hypothetical protein::PF11\_0123::(KS26\_1)  
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PF11\_0159 hypothetical protein::PF11\_0159::(PPF11\_0159\_288)  
PF11\_0164 peptidyl-prolyl cis-trans isomerase::PF11\_0164::(KS2\_14)  
PF11\_0165 falcipain 2 precursor::PF11\_0165::(KS826\_1)  
PF11\_0166 hypothetical protein::PF11\_0166::(KS826\_2)  
PF11\_0177 ubiquitin C-terminal hydrolase, family 1, putative::PF11\_0177::(KS113\_1)  
PF11\_0179 hypothetical protein::PF11\_0179::(KS509\_7)  
PF11\_0198 hypothetical protein, conserved::PF11\_0198::(KS97\_20)  
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PF11\_0276 hypothetical protein::PF11\_0276::(KS266\_16)  
PF11\_0301 spermidine synthase::PF11\_0301::(KS488\_1)  
PF11\_0306 A/G-specific adenine glycosylase, putative::PF11\_0306::(KS101\_1)  
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PF11\_0347 hypothetical protein::PF11\_0347::(KS44\_10)  
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PF11\_0366 hypothetical protein::PF11\_0366::(KS85\_6)  
PF11\_0393 hypothetical protein, conserved::PF11\_0393::(KS125\_6)  
PF11\_0396 Protein phosphatase 2C::PF11\_0396::(KS81\_2)  
PF11\_0409 hypothetical protein, conserved::PF11\_0409::(KS316\_19)  
PF11\_0412 Vacuolar ATP synthase subunit F, putative::PF11\_0412::(KS667\_1)  
PF11\_0414 hypothetical protein::PF11\_0414::(KS1030\_4)  
PF11\_0419 hypothetical protein::PF11\_0419::(KS694\_2)  
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PF11\_0460 hypothetical protein::PF11\_0460::(KS127\_17)  
PF11\_0469 hypothetical protein::PF11\_0469::(KS225\_10)  
PF11\_0485 hypothetical protein::PF11\_0485::(KS56\_24)  
PF11\_0488 hypothetical protein::PF11\_0488::(KS56\_33)  
PF11\_0489 hypothetical protein::PF11\_0489::(KS222\_1)  
PF11\_0504 hypothetical protein::PF11\_0504::(KS157\_19)  
PF11\_0505 hypothetical protein::PF11\_0505::(KS157\_18)  
PF11\_0507 antigen 332, putative::PF11\_0507::(F40797\_1)  
PF11\_0509 ring-infected erythrocyte surface antigen, putative::PF11\_0509::(KS157\_11)  
PF11\_0512 ring-infected erythrocyte surface antigen 2, RESA-2 - malaria parasite (Plasmodium falciparum)-related::PF11\_0512::(KS157\_1)  
PF11\_0513 hypothetical protein::PF11\_0513::(KS48\_18)  
PF11\_0521 erythrocyte membrane protein 1 (PfEMP1)::PF11\_0521::(E686\_1)  
PF11\_0524 U6 snRNA associated Sm-like protein Ls; U6 snRNA associated Sm-like protein LsM4, putative::PF11\_0524::(KS25\_17)  
PF13\_0011 plasmodium falciparum gamete antigen 27/25::PF13\_0011::(M32775\_1)  
PF13\_0029 hypothetical protein::PF13\_0029::(M27404\_1)  
PF13\_0036 DNAJ protein, putative::PF13\_0036::(M45727\_11)  
PF13\_0043 CCAAT-binding transcription factor, putative::PF13\_0043::(M58024\_1)  
PF13\_0045 40S ribosomal protein S27, putative::PF13\_0045::(M3816\_2)  
PF13\_0051 snornc protein gar1 homologue, putative::PF13\_0051::(M12190\_2)  
PF13\_0058 hypothetical protein::PF13\_0058::(M2610\_1)

PF13\_0059 ribosomal protein S15, mitochondrial precursor, putative::PF13\_0059::(M38127\_1)  
 PF13\_0061 ATP synthase gamma chain, mitochondrial precursor, putative::PF13\_0061::(M2511\_7)  
 PF13\_0076 hypothetical protein::PF13\_0076::(M1595\_2)  
 PF13\_0095 DNA replication licensing factor mcm4-related::PF13\_0095::(M4927\_3)  
 PF13\_0096 Ubiquitin Carboxyl-terminal Hydrolase-like zinc finger protein::PF13\_0096::(M4927\_1)  
 PF13\_0101 hypothetical protein::PF13\_0101::(I4500\_1)  
 PF13\_0128 beta-hydroxyacyl-*acp* dehydratase precursor::PF13\_0128::(M44397\_17)  
 PF13\_0129 ribosomal protein L6 homologue, putative::PF13\_0129::(M44397\_14)  
 PF13\_0132 60S ribosomal protein L23a, putative::PF13\_0132::(M44397\_10)  
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 PF13\_0260 hypothetical protein, conserved::PF13\_0260::(M5968\_1)  
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 PF13\_0271 ABC transporter, putative::PF13\_0271::(M26914\_8)  
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 PF13\_0296 hypothetical protein, conserved::PF13\_0296::(PPF13\_0296\_50)  
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 PF13\_0328 proliferating cell nuclear antigen::PF13\_0328::(M36754\_1)  
 PF13\_0330 ATP-dependent DNA helicase, putative::PF13\_0330::(M22193\_8)  
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 PF13\_0344 UBA/THIF-type NAD/FAD binding protein, putative::PF13\_0344::(M34743\_8)  
 PF13\_0349 nucleoside diphosphate kinase b, putative::PF13\_0349::(M38941\_10)  
 PF14\_0015 aminopeptidase, putative::PF14\_0015::(N145\_28)  
 PF14\_0016 hypothetical protein::PF14\_0016::(N145\_23)  
 PF14\_0038 cytochrome c, putative::PF14\_0038::(N165\_2)  
 PF14\_0047 hypothetical protein::PF14\_0047::(N159\_4)  
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 PF14\_0053 ribonucleotide reductase small subunit::PF14\_0053::(N159\_20)  
 PF14\_0054 hypothetical protein, conserved::PF14\_0054::(N159\_23)  
 PF14\_0064 vacuolar protein sorting 29, putative::PF14\_0064::(N159\_39)  
 PF14\_0068 fibrillarin, putative::PF14\_0068::(N159\_46)  
 PF14\_0072 hypothetical protein, conserved::PF14\_0072::(N171\_4)  
 PF14\_0077 plasmepsin 2 precursor::PF14\_0077::(N150\_91)  
 PF14\_0096 hypothetical protein::PF14\_0096::(N150\_60)  
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 PF14\_0107 hypothetical protein, conserved::PF14\_0107::(PPF14\_0107\_497)  
 PF14\_0108 hypothetical protein::PF14\_0108::(N150\_33)  
 PF14\_0109 hypothetical protein::PF14\_0109::(PPF14\_0109\_47)  
 PF14\_0122 nuclear transport factor 2, putative::PF14\_0122::(N150\_3)  
 PF14\_0146 ribonucleoprotein, putative::PF14\_0146::(N175\_12)  
 PF14\_0150 RNA polymerase small subunit, putative::PF14\_0150::(N127\_54)  
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 PF14\_0176 hypothetical protein::PF14\_0176::(N143\_71)  
 PF14\_0192 glutathione reductase::PF14\_0192::(N143\_29)  
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 PF14\_0253 hypothetical protein::PF14\_0253::(N157\_1)  
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 PF14\_0288 cytochrome c oxidase subunit II precursor, putative::PF14\_0288::(N138\_34)  
 PF14\_0300 syntaxin, putative::PF14\_0300::(N138\_61)  
 PF14\_0310 hypothetical protein::PF14\_0310::(N138\_94)  
 PF14\_0314 chromatin assembly factor 1 p55 subunit, putative::PF14\_0314::(N138\_102)  
 PF14\_0316 DNA topoisomerase II, putative::PF14\_0316::(N172\_3)  
 PF14\_0321 ABC transporter, putative::PF14\_0321::(N132\_184)  
 PF14\_0327 methionine aminopeptidase, type II, putative::PF14\_0327::(N132\_172)  
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 PF14\_0380 hypothetical protein::PF14\_0380::(N132\_37)  
 PF14\_0381 delta-aminolevulinic acid dehydratase::PF14\_0381::(N132\_27)  
 PF14\_0382 metalloendopeptidase, putative::PF14\_0382::(N132\_24)  
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 PF14\_0392 Ser/Thr protein kinase, putative::PF14\_0392::(I9716\_1)  
 PF14\_0395 hypothetical protein, conserved::PF14\_0395::(N128\_94)  
 PF14\_0401 methionine -- tRNA ligase, putative::PF14\_0401::(N128\_85)



PF14\_0403 protein prenyltransferase alpha subunit, putative::PF14\_0403::(N128\_76)  
PF14\_0411 small nuclear ribonuclear protein, putative::PF14\_0411::(PPF14\_0411\_230)  
PF14\_0413 hypothetical protein::PF14\_0413::(N128\_62)  
PF14\_0417 heat shock protein, putative::PF14\_0417::(N128\_56)  
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PF14\_0518 nifU protein, putative::PF14\_0518::(N168\_34)  
PF14\_0519 ribosomal protein S11, putative::PF14\_0519::(N168\_32)  
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PF14\_0607 hypothetical protein::PF14\_0607::(N134\_73)  
PF14\_0615 ATP synthase (C/AC39) subunit, putative::PF14\_0615::(N134\_44)  
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PF14\_0630 protein serine/threonine phosphatase::PF14\_0630::(N134\_2)  
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PF14\_0673 hypothetical protein::PF14\_0673::(N137\_43)  
PF14\_0677 RNA 3'-Terminal Phosphate Cyclase-like protein, putative::PF14\_0677::(N187\_5)  
PF14\_0680 hypothetical protein::PF14\_0680::(PPF14\_0680\_16)  
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PF14\_0691 hypothetical protein::PF14\_0691::(N133\_36)  
PF14\_0694 protein disulfide isomerase, putative::PF14\_0694::(N133\_19)  
PF14\_0697 dihydroorotase, putative::PF14\_0697::(N133\_9)  
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PF14\_0716 Proteasome subunit alpha type 1, putative::PF14\_0716::(N147\_25)  
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PF14\_0730 hypothetical protein::PF14\_0730::(PPF14\_0730\_170)  
PF14\_0731 hypothetical protein::PF14\_0731::(N129\_36)  
PF14\_0738 lysophospholipase, putative::PF14\_0738::(N129\_14)  
PFA0110w ring-infected erythrocyte surface antigen precursor::PFA0110w::(A10325\_29)  
PFA0140c hypothetical protein::PFA0140c::(A23157\_1)  
PFA0180w hypothetical protein::PFA0180w::(A8010\_10)  
PFA0210c hypothetical protein::PFA0210c::(A8010\_31)  
PFA0300c vacuolar ATP synthase, putative::PFA0300c::(A8109\_6)  
PFA0335w P. falciparum GTP binding protein RAB5::PFA0335w::(PPFA0335W\_427)  
PFA0345w centrin, putative::PFA0345w::(A12797\_1)  
PFA0395c hypothetical protein::PFA0395c::(PPFA0395C\_496)  
PFA0400c beta3 proteasome subunit, putative::PFA0400c::(A14680\_4)  
PFA0405w hypothetical protein::PFA0405w::(A9766\_1)  
PFA0415c hypothetical protein::PFA0415c::(A21885\_5)  
PFA0420w hypothetical protein::PFA0420w::(A12706\_1)  
PFA0450c mRNA cleavage factor-like protein, putative::PFA0450c::(A31914\_8)  
PFA0485w hypothetical protein::PFA0485w::(A3310\_11)  
PFA0510w hypothetical protein::PFA0510w::(A3310\_1)  
PFA0525w transcription initiation factor TFIIIB, putative::PFA0525w::(A13725\_6)  
PFA0545c replication factor c protein, putative::PFA0545c::(A1718\_1)  
PFA0565c hypothetical protein::PFA0565c::(PPFA0565C\_278)  
PFA0570w hypothetical protein::PFA0570w::(A13231\_2)  
PFA0670c hypothetical protein::PFA0670c::(PPFA0670C\_135)  
PFB0010w erythrocyte membrane protein 1 (PfEMP1)::PFB0010w::(B11)  
PFB0085c hypothetical protein::PFB0085c::(B50)  
PFB0100c knob associated histidine-rich protein::PFB0100c::(A11546\_1)  
PFB0110w hypothetical protein::PFB0110w::(B68)  
PFB0120w early transcribed membrane protein, putative::PFB0120w::(B70)  
PFB0160w ERCC1 nucleotide excision repair protein, putative::PFB0160w::(B95)  
PFB0190c hypothetical protein::PFB0190c::(B114)  
PFB0250w hypothetical protein::PFB0250w::(B149)  
PFB0315w 41 kDa antigen::PFB0315w::(B197)  
PFB0365w hypothetical protein, conserved::PFB0365w::(B251)  
PFB0385w acyl carrier protein, putative::PFB0385w::(B270)  
PFB0390w ribosome releasing factor, putative::PFB0390w::(B272)  
PFB0475c hypothetical protein, conserved::PFB0475c::(B326)  
PFB0575c hypothetical protein::PFB0575c::(B388)  
PFB0580w hypothetical protein::PFB0580w::(B389)  
PFB0595w heat shock 40 kDa protein, putative::PFB0595w::(B396)  
PFB0600c hypothetical protein::PFB0600c::(B397)  
PFB0605w Ser/Thr protein kinase, putative::PFB0605w::(B403)  
PFB0620w hypothetical protein::PFB0620w::(B424)  
PFB0635w T-complex protein 1, putative::PFB0635w::(B432)  
PFB0705w hypothetical protein::PFB0705w::(B467)  
PFB0810w hypothetical protein::PFB0810w::(B513)  
PFB0865w small nuclear ribonucleoprotein, putative::PFB0865w::(B549)  
PFB0900c hypothetical protein::PFB0900c::(B565)

PFB0915w liver stage antigen 3::PFB0915w::(B572)  
PFB0953w hypothetical protein::PFB0953w::(B603)  
PFC0090w hypothetical protein, conserved::PFC0090w::(C54)  
PFC0115c erythrocyte membrane protein 1 (PfEMP1) pseudogene::PFC0115c::(C67)  
PFC0145c hypothetical protein, conserved::PFC0145c::(C97)  
PFC0165w hypothetical protein, conserved::PFC0165w::(C114)  
PFC0170c dihydrolipoamide acyltransferase, putative::PFC0170c::(C116)  
PFC0220w hypothetical protein::PFC0220w::(C141)  
PFC0255c ubiquitin-conjugating enzyme E2, putative::PFC0255c::(C161)  
PFC0325c hypothetical protein::PFC0325c::(C223)  
PFC0350c T-complex protein eta subunit, putative::PFC0350c::(C234)  
PFC0405c hypothetical protein::PFC0405c::(C258)  
PFC0440c helicase, putative::PFC0440c::(C281)  
PFC0445w hypothetical protein::PFC0445w::(PPFC0445W\_93)  
PFC0540w hypothetical protein::PFC0540w::(C365)  
PFC0571c hypothetical protein::PFC0571c::(C386)  
PFC0581w hypothetical protein::PFC0581w::(C416)  
PFC0670c hypothetical protein::PFC0670c::(C441)  
PFC0705c hypothetical protein::PFC0705c::(C458)  
PFC0715c hypothetical protein::PFC0715c::(C470)  
PFC0745c proteasome component C8, putative::PFC0745c::(C497)  
PFC0765c hypothetical protein::PFC0765c::(C507)  
PFC0800w band 7-related protein::PFC0800w::(C526)  
PFC0830w trophozoite stage antigen::PFC0830w::(C541)  
PFC0845c ubiquitin-protein ligase, putative::PFC0845c::(C559)  
PFC0890w vesicle transport protein, putative::PFC0890w::(C591)  
PFC0910w hypothetical protein::PFC0910w::(C600)  
PFC0911c hypothetical protein::PFC0911c::(C602)  
PFC0912w hypothetical protein::PFC0912w::(C604)  
PFC0935c N-acetylglucosamine-1-phosphate transferase, putative::PFC0935c::(PPFC0935C\_329)  
PFC1025w F49C12.11-like protein::PFC1025w::(C681)  
PFD0010w unknown::PFD0010w::(OPFD66971)  
PFD0165w ubiquitin-specific protease, putative::PFD0165w::(D6287\_29)  
PFD0175c hypothetical protein::PFD0175c::(D6287\_31)  
PFD0225w hypothetical protein::PFD0225w::(D49176\_1)  
PFD0230c protease, putative::PFD0230c::(D49176\_6)  
PFD0235c hypothetical protein::PFD0235c::(D49176\_8)  
PFD0285c lysine decarboxylase, putative::PFD0285c::(D49176\_36)  
PFD0320c hypothetical protein::PFD0320c::(D49176\_61)  
PFD0330w hypothetical protein::PFD0330w::(D17715\_136)  
PFD0360w hypothetical protein::PFD0360w::(D17715\_110)  
PFD0365c hypothetical protein::PFD0365c::(D17715\_109)  
PFD0440w hypothetical protein::PFD0440w::(D17715\_64)  
PFD0465c hypothetical protein, conserved::PFD0465c::(D17715\_51)  
PFD0595w hypothetical protein::PFD0595w::(D17715\_12)  
PFD0670c hypothetical protein, conserved::PFD0670c::(D23156\_20)  
PFD0685c chromosome associated protein, putative::PFD0685c::(D23156\_27)  
PFD0690c hypothetical protein::PFD0690c::(D23156\_45)  
PFD0755c adenylate kinase 1::PFD0755c::(D33539\_32)  
PFD0760c hypothetical protein::PFD0760c::(D33539\_33)  
PFD0795w hypothetical protein::PFD0795w::(D33539\_55)  
PFD0830w bifunctional dihydrofolate reductase-thymidylate synthase::PFD0830w::(D33539\_76)  
PFD0845w hypothetical protein::PFD0845w::(D33539\_85)  
PFD0850c hypothetical protein, conserved::PFD0850c::(OPFH0015)  
PFD0930w CGI-141 protein homolog, putative::PFD0930w::(D12635\_22)  
PFD0945c hypothetical protein::PFD0945c::(D12635\_33)  
PFD1015c erythrocyte membrane protein 1 (PfEMP1)::PFD1015c::(D53677\_1)  
PFD1090c clathrin assembly protein, putative::PFD1090c::(D16785\_10)  
PFD1135c hypothetical protein::PFD1135c::(D15909\_4)  
PFD1140w hypothetical protein::PFD1140w::(D15909\_8)  
PFD1165w protein kinase, conserved in P. falciparum::PFD1165w::(D34948\_3)  
PFE0045c kinase, putative::PFE0045c::(E20800\_1)  
PFE0065w skeleton binding protein::PFE0065w::(E598\_1)  
PFE0070w interspersed repeat antigen, putative::PFE0070w::(E12394\_2)  
PFE0090w hypothetical protein::PFE0090w::(E17057\_1)  
PFE0110w hypothetical protein::PFE0110w::(F15289\_3)  
PFE0140c hypothetical protein::PFE0140c::(E13140\_2)  
PFE0150c 4-diphosphocytidyl-2c-methyl-D-erythritol kinase (CMK), putative::PFE0150c::(E14176\_1)  
PFE0165w actin depolymerizing factor, putative::PFE0165w::(E13013\_1)  
PFE0175c unconventional myosin pfm-b::PFE0175c::(E15509\_11)  
PFE0215w ATP-dependent helicase, putative::PFE0215w::(E714\_9)  
PFE0265c hypothetical protein::PFE0265c::(E20827\_1)  
PFE0420c guanidine nucleotide exchange factor, putative::PFE0420c::(E21208\_5)  
PFE0435c single-strand binding protein, putative::PFE0435c::(E30064\_1)  
PFE0445c SNAP protein (soluble N-ethylmaleimide-sensitive factor Attachment Protein), putative::PFE0445c::(D13568\_1)  
PFE0730c ribose 5-phosphate epimerase, putative::PFE0730c::(E27247\_7)  
PFE0795c nif-like protein, putative::PFE0795c::(E3215\_6)  
PFE0800w hypothetical protein::PFE0800w::(E3215\_4)  
PFE0810c 40S ribosomal subunit protein S14, putative::PFE0810c::(E3215\_1)  
PFE0855c hypothetical protein::PFE0855c::(E26351\_1)  
PFE0955w hypothetical protein::PFE0955w::(E13038\_9)  
PFE1025c hypothetical protein::PFE1025c::(E26771\_4)  
PFE1040c hypothetical protein::PFE1040c::(E17542\_1)  
PFE1045c hypothetical protein::PFE1045c::(E18031\_10)  
PFE1170w hypothetical protein::PFE1170w::(E6125\_5)  
PFE1175w hypothetical protein::PFE1175w::(E27173\_1)  
PFE1190c hypothetical protein::PFE1190c::(PPFE1190C\_105)  
PFE1230c hypothetical protein, conserved::PFE1230c::(F52907\_2)  
PFE1250w long-chain fatty acid CoA ligase, putative::PFE1250w::(E13599\_1)  
PFE1255w hypothetical protein::PFE1255w::(E24637\_1)  
PFE1280w hypothetical protein::PFE1280w::(E5415\_6)  
PFE1325w hypothetical protein::PFE1325w::(PPFE1325W\_13374)

PFE1340w transmembrane protein, putative::PFE1340w::(F35756\_2)  
PFE1405c eukaryotic translation initiation factor 3, subunit 6, putative::PFE1405c::(E248\_3)  
PFE1425c hypothetical protein::PFE1425c::(D65681\_1)  
PFE1430c cyclophilin, putative::PFE1430c::(E20260\_8)  
PFE1450c hypothetical protein, conserved::PFE1450c::(F53383\_11)  
PFE1595c hypothetical protein::PFE1595c::(E19695\_2)  
PFE1615c hypothetical protein::PFE1615c::(D57574\_1)  
PFF0115c elongation factor G, putative::PFF0115c::(E6534\_1)  
PFF0205w hypothetical protein, conserved::PFF0205w::(PMAL6P1.45\_104)  
PFF0210w hypothetical protein::PFF0210w::(PMAL6P1.46\_2093)  
PFF0230c glyoxalase I, putative::PFF0230c::(PMAL6P1.50\_552)  
PFF0235c hypothetical protein::PFF0235c::(PMAL6P1.51\_1594)  
PFF0290w long chain polyunsaturated fatty acid elongation enzyme, putative::PFF0290w::(PMAL6P1.62\_738)  
PFF0365c conserved hypothetical protein, EXS family::PFF0365c::(OPFF72474)  
PFF0435w ornithine aminotransferase::PFF0435w::(OPFF72412)  
PFF0490w hypothetical protein::PFF0490w::(PMAL6P1.102\_2416)  
PFF0500c step II splicing factor, putative::PFF0500c::(F38861\_1)  
PFF0570c hypothetical protein::PFF0570c::(PMAL6P1.308\_619)  
PFF0580w hypothetical protein::PFF0580w::(OPFF72489)  
PFF0595c hypothetical protein::PFF0595c::(PMAL6P1.303\_4968)  
PFF0620c hypothetical protein::PFF0620c::(OPFF72480)  
PFF0670w hypothetical protein::PFF0670w::(E9475\_1)  
PFF0695w hypothetical protein, conserved::PFF0695w::(OPFF72512)  
PFF0775w pyridoxal kinase-like protein, putative::PFF0775w::(OPFF72459)  
PFF0785w hypothetical protein, conserved::PFF0785w::(PMAL6P1.264\_388)  
PFF0825c mitochondrial import receptor subunit tom40::PFF0825c::(PMAL6P1.256\_494)  
PFF0885w 60S ribosomal protein L27a, putative::PFF0885w::(OPFF72427)  
PFF0905w hypothetical protein::PFF0905w::(PMAL6P1.240\_748)  
PFF0925w hypothetical protein::PFF0925w::(PMAL6P1.236\_640)  
PFF0940c cell division cycle protein 48 homologue, putative::PFF0940c::(F4425\_1)  
PFF0955c hypothetical protein::PFF0955c::(OPFF72446)  
PFF1030w hypothetical protein, conserved::PFF1030w::(F30774\_1)  
PFF1065c hypothetical protein::PFF1065c::(PMAL6P1.207\_638)  
PFF1080w hypothetical protein, conserved::PFF1080w::(PMAL6P1.204\_137)  
PFF1260c hypothetical protein::PFF1260c::(D5782\_1)  
PFF1270c hypothetical protein::PFF1270c::(OPFF72513)  
PFF1280w hypothetical protein::PFF1280w::(E18868\_1)  
PFF1355w hypothetical protein::PFF1355w::(OPFF72509)  
PFF1365c hypothetical protein::PFF1365c::(D27403\_1)  
PFF1375c ethanalaminephosphotransferase, putative::PFF1375c::(OPFF72461)  
PFF1425w RNA binding protein, putative::PFF1425w::(E18025\_1)  
PFI0085c hypothetical protein::PFI0085c::(I3470\_1)  
PFI0130c hypothetical protein::PFI0130c::(I15913\_1)  
PFI0135c papain family cysteine protease, putative::PFI0135c::(I587\_1)  
PFI0145w hypothetical protein::PFI0145w::(PFI0145W\_292)  
PFI0155c ras family GTP-ase, putative::PFI0155c::(I17263\_1)  
PFI0160w hypothetical protein::PFI0160w::(E25749\_1)  
PFI0180w alpha tubulin::PFI0180w::(I16837\_2)  
PFI0215c signal peptidase, putative::PFI0215c::(OPFI17697)  
PFI0235w replication factor A-related protein, putative::PFI0235w::(F18417\_1)  
PFI0280c hypothetical protein, conserved::PFI0280c::(I4355\_3)  
PFI0335w hypothetical protein::PFI0335w::(I15927\_5)  
PFI0380c formylmethionine deformylase, putative::PFI0380c::(I9302\_2)  
PFI0475w small nuclear ribonucleoprotein (snRNP), putative::PFI0475w::(I5180\_1)  
PFI0505c selenophosphate synthetase, putative::PFI0505c::(I3489\_1)  
PFI0540w hypothetical protein::PFI0540w::(E25593\_1)  
PFI0570w GTP-binding protein, putative::PFI0570w::(F5048\_1)  
PFI0575c hypothetical protein::PFI0575c::(KN1713\_1)  
PFI0590c hypothetical protein::PFI0590c::(OPFI17707)  
PFI0610w hypothetical protein::PFI0610w::(OPFI17724)  
PFI0645w EF-1B::PFI0645w::(F19787\_1)  
PFI0670w hypothetical protein, conserved::PFI0670w::(I6724\_2)  
PFI0675w hypothetical protein::PFI0675w::(F67796\_1)  
PFI0725c hypothetical protein::PFI0725c::(I4179\_1)  
PFI0730w hypothetical protein::PFI0730w::(F48839\_1)  
PFI0750c hypothetical protein::PFI0750c::(I884\_1)  
PFI0760w hypothetical protein::PFI0760w::(I17631\_1)  
PFI0820c RNA-binding protein, putative::PFI0820c::(I16748\_1)  
PFI0860c ATP-dependant RNA helicase, putative::PFI0860c::(F51170\_1)  
PFI0870w hypothetical protein::PFI0870w::(E11286\_1)  
PFI0890c large ribosomal subunit protein L3, prokaryotic (50S)-like, putative::PFI0890c::(I6033\_4)  
PFI0895c hypothetical protein, conserved::PFI0895c::(I15861\_1)  
PFI0910w DNA helicase, putative::PFI0910w::(I3002\_1)  
PFI0925w gamma-glutamylcysteine synthetase::PFI0925w::(F46067\_3)  
PFI0975c hypothetical protein::PFI0975c::(F37098\_2)  
PFI1000w hypothetical protein::PFI1000w::(I4780\_1)  
PFI1005w ADP-ribosylation factor-like protein, putative::PFI1005w::(I3555\_1)  
PFI1070c hypothetical protein::PFI1070c::(I4487\_1)  
PFI1075w hypothetical protein::PFI1075w::(F61293\_1)  
PFI1110w glutamate-ammonia ligase (glutamine synthetase), putative::PFI1110w::(I4989\_2)  
PFI1155w hypothetical protein::PFI1155w::(OPFI17661)  
PFI1160w hypothetical protein::PFI1160w::(I17587\_1)  
PFI1170c Thioredoxin reductase::PFI1170c::(F64095\_4)  
PFI1240c prolyl-t-RNA synthase, putative::PFI1240c::(I1781\_2)  
PFI1245c Protein phosphatase-beta::PFI1245c::(I5252\_1)  
PFI1295c membrane transporter, putative::PFI1295c::(OPFI17700)  
PFI1320c hypothetical protein::PFI1320c::(I13466\_1)  
PFI1325w hypothetical protein::PFI1325w::(OPFI17667)  
PFI1405c hypothetical protein::PFI1405c::(KN5081\_1)  
PFI1420w guanylate kinase, putative::PFI1420w::(OPFI17660)  
PFI1445w hypothetical protein::PFI1445w::(F5910\_2)  
PFI1470c hypothetical protein::PFI1470c::(I12692\_1)



PFI1475w merozoite surface protein 1, precursor::PFI1475w::(F8511\_1)  
PFI1515w hypothetical protein::PFI1515w::(PPFI1515W\_82)  
PFI1520w hypothetical protein::PFI1520w::(D56470\_1)  
PFI1575c peptide release factor, putative::PFI1575c::(F27464\_2)  
PFI1610c hypothetical protein::PFI1610c::(PPFI1610C\_208)  
PFI1625c organelle processing peptidase, putative::PFI1625c::(F26774\_1)  
PFI1720w hypothetical protein::PFI1720w::(F68282\_1)  
PFI1735c hypothetical protein::PFI1735c::(F37100\_2)  
PFI1740c hypothetical protein::PFI1740c::(OPFI17638)  
PFI1745c hypothetical protein::PFI1745c::(PPFI1745C\_158)  
PFI1755c hypothetical protein::PFI1755c::(I12552\_2)  
PFI1760w hypothetical protein::PFI1760w::(PPFI1760W\_133)  
PFI1780w hypothetical protein::PFI1780w::(OPFI17716)  
PFL0035c octapeptide-repeat antigen, putative::PFL0035c::(L1\_28)  
PFL0110c PfmpC::PFL0110c::(L1\_63)  
PFL0140w hypothetical protein::PFL0140w::(PPFL0140W\_120)  
PFL0225c hypothetical protein::PFL0225c::(L2\_10)  
PFL0280c hypothetical protein::PFL0280c::(L2\_31)  
PFL0355c hypothetical protein::PFL0355c::(L2\_72)  
PFL0400w 50S ribosomal protein L29, putative::PFL0400w::(L2\_101)  
PFL0415w acyl carrier protein, mitochondrial precursor, putative::PFL0415w::(KN46\_3)  
PFL0430w tim10 homologue, putative::PFL0430w::(L2\_114)  
PFL0465c Zinc finger transcription factor (krox1)::PFL0465c::(PPFL0465C\_3366)  
PFL0485w hypothetical protein::PFL0485w::(L2\_139)  
PFL0500w 50S ribosomal protein L1, putative::PFL0500w::(L2\_146)  
PFL0505c hypothetical protein::PFL0505c::(L2\_147)  
PFL0585w PfpUB Plasmodium falciparum polyubiquitin::PFL0585w::(L2\_187)  
PFL0610w hypothetical protein::PFL0610w::(L2\_194)  
PFL0615w hypothetical protein::PFL0615w::(L2\_199)  
PFL0660w dynein light chain 1, putative::PFL0660w::(L2\_212)  
PFL0720w hypothetical protein::PFL0720w::(L2\_246)  
PFL0765w hypothetical protein::PFL0765w::(L2\_265)  
PFL0785c signal recognition particle 19 kd protein, putative::PFL0785c::(L2\_276)  
PFL0825c hypothetical protein::PFL0825c::(L3\_3)  
PFL0940c erythrocyte membrane protein 1 (PfEMP-1) pseudogene::PFL0940c::(J1058\_1)  
PFL0960w D-ribulose-5-phosphate 3-epimerase, putative::PFL0960w::(OPFL0048)  
PFL0970w pre-mRNA splicing factor, putative::PFL0970w::(J938\_1)  
PFL1010c hypothetical protein conserved::PFL1010c::(KN267\_1)  
PFL1025c hypothetical protein::PFL1025c::(J2541\_2)  
PFL1075w hypothetical protein::PFL1075w::(KN2497\_2)  
PFL1140w hypothetical protein, conserved::PFL1140w::(OPFL0109)  
PFL1180w Chromatin assembly protein (ASF1), putative::PFL1180w::(KN5186\_1)  
PFL1350w RNA pseudouridylate synthase, putative::PFL1350w::(OPFL0122)  
PFL1390w hypothetical protein::PFL1390w::(KN3690\_1)  
PFL1405w hypothetical protein::PFL1405w::(F22280\_1)  
PFL1415w hypothetical protein::PFL1415w::(PPFL1415W\_1260)  
PFL1465c heat shock protein hslv, putative::PFL1465c::(OPFL0038)  
PFL1520w dim1 protein homolog, putative::PFL1520w::(OPFL0027)  
PFL1545c chaperonin cpn60::PFL1545c::(OPFL0016)  
PFL1585c hypothetical protein::PFL1585c::(KN5414\_1)  
PFL1605w hypothetical protein::PFL1605w::(J3424\_1)  
PFL1650w hypothetical protein::PFL1650w::(KN1007\_1)  
PFL1655c hypothetical protein::PFL1655c::(KN973\_2)  
PFL1665c hypothetical protein::PFL1665c::(I13218\_1)  
PFL1685w hypothetical protein, conserved::PFL1685w::(OPFL0102)  
PFL1740w hypothetical protein::PFL1740w::(OPFL0147)  
PFL1790w ubiquitin activating enzyme, putative::PFL1790w::(KN1056\_2)  
PFL1830w ubiquitin-like protein, putative::PFL1830w::(PPFL1830W\_6)  
PFL1845c calyculin binding protein, putative::PFL1845c::(OPFL0091)  
PFL1865w hypothetical protein::PFL1865w::(PPFL1865W\_5205)  
PFL1890c hypothetical protein, conserved::PFL1890c::(OPFL0112)  
PFL1900w hypothetical protein::PFL1900w::(E25972\_1)  
PFL1905w hypothetical protein::PFL1905w::(PPFL1905W\_140)  
PFL1920c hydroxyethylthiazole kinase, putative::PFL1920c::(OPFL0087)  
PFL1945c hypothetical protein::PFL1945c::(OPFL0045)  
PFL1960w erythrocyte membrane protein 1 (PfEMP1)::PFL1960w::(KM1590\_2)  
PFL1980c hypothetical protein::PFL1980c::(PPFL1980C\_68)  
PFL2095w Translation initiation factor SUI1, putative::PFL2095w::(PPFL2095W\_60)  
PFL2180w 50S ribosomal protein L3, putative::PFL2180w::(OPFL0098)  
PFL2195w hypothetical protein::PFL2195w::(A14263\_1)  
PFL2205w hypothetical protein::PFL2205w::(KN400\_1)  
PFL2245w hypothetical protein::PFL2245w::(KN1106\_5)  
PFL2260w hypothetical protein::PFL2260w::(KN5610\_3)  
PFL2280w cyclin g-associated kinase, putative::PFL2280w::(KN672\_1)  
PFL2415w Hbeta58/Vps26 protein homolog, putative::PFL2415w::(KN8928\_1)  
PFL2445c hypothetical protein::PFL2445c::(OPFL0145)  
PFL2460w coronin::PFL2460w::(OPFL0013)  
PFL2485c tryptophanyl-tRNA synthetase, putative::PFL2485c::(PPFL2485C\_117)  
PFL2530w hypothetical protein::PFL2530w::(OPFL0121)  
PFL2540w hypothetical protein::PFL2540w::(PPFL2540W\_151)  
PFL2560c hypothetical protein::PFL2560c::(PPFL2560C\_2)  
PFL2565w hypothetical protein::PFL2565w::(M30262\_1)  
pla\_rpl14 plastid ribosomal protein 14, large subunit::pla\_rpl14::(PRPL14)  
pla\_rpl16 plastid ribosomal protein 16, large subunit::pla\_rpl16::(PRPL16)  
pla\_rpl4 plastid ribosomal protein 4, large subunit::pla\_rpl4::(PRPL4)  
pla\_rps3 plastid ribosomal protein 3, small subunit::pla\_rps3::(PRPS3)  
pla\_rps5 plastid ribosomal protein 5, small subunit::pla\_rps5::(PRPS5)  
pla\_tRNA-Gly plastid tRNA-Gly::pla\_tRNA-Gly::(PTRNA-GLY)  
pla\_tRNA-Gly2 plastid tRNA-Gly2::pla\_tRNA-Gly2::(PTRNA-GLY2)  
pla\_tRNA-Pro plastid tRNA-Pro::pla\_tRNA-Pro::(PTRNA-PRO)  
pla\_tRNA-Trp plastid tRNA-Trp::pla\_tRNA-Trp::(PTRNA-TRP)

# APPENDIX C

## INTERACTOME DATA COMPARISON

Interactome data obtained from <http://www.cbil.upenn.edu/plasmoMAP/index-v1.html#log> and used with permission from S. Date

Strain selected: 3D7			
Query: PF10_0322 S-adenosylmethionine decarboxylase-ornithine decarboxylase			
Score	Protein ID	Description	Present in PFA0MetDC/ODC co-inhibition differential abundance dataset
9.53	PF11_0317	structural maintenance of chromosome protein, putative	
8.31	PFE0195w	P-type ATPase, putative	
7.98	PFA0390w	DNA repair exonuclease, putative	
6.62	MAL8P1.99	hypothetical protein	Yes
6.62	PF11_0427	dolichyl-phosphate b-D-mannosyltransferase, putative	
6.62	PF07_0129	ATP-dept. acyl-coa synthetase	Yes
6.62	PFA0590w	ABC transporter, putative	Yes
5.9	PF10_0260	hypothetical protein	
5.9	PF13_0348	hypothetical protein	
5.7	PF14_0053	ribonucleotide reductase small subunit	Yes
4.71	PFD0685c	chromosome associated protein, putative	Yes
4.71	PFC0125w	ABC transporter, putative	Yes
4.71	PF14_0709	ribosomal protein L20, putative	Yes
4.71	PF08_0131	1-cys peroxidoxin	Yes
4.71	PF11_0117	replication factor C subunit 5, putative	Yes
4.71	PF11_0181	tyrosine --tRNA ligase, putative	Yes
4.71	PFB0180w	5'-3' exonuclease, N-terminal resolvase-like domain, putative	Yes
4.71	PFL2180w	50S ribosomal protein L3, putative	
4.71	PF14_0097	cytidine diphosphate-diacylglycerol synthase	
4.71	PF14_0081	DNA repair helicase, putative	Yes
4.71	PF11_0044	hypothetical protein	
4.71	PF11_0197	hypothetical protein	
4.52	PF14_0338	hypothetical protein	
4.52	PF14_0397	hypothetical protein, conserved	
4.52	PF10_0362	DNA polymerase zeta catalytic subunit, putative	
4.52	PFB0605w	Ser/Thr protein kinase, putative	Yes
4.52	PF08_0034	histone acetyltransferase Gcn5	
4.52	PF10_0132	phospholipase C-like, putative	
4.52	PFI1310w	NAD synthase, putative	
4.52	PF13_0016	methyl transferase-like protein, putative	
4.52	PFB0520w	protein kinase, putative	
4.52	PF11_0049	hypothetical protein, conserved	
4.52	PF11_0074	hypothetical protein	
4.52	PF14_0161	hypothetical protein, conserved	
4.52	PF14_0441	pyruvate dehydrogenase E1 beta subunit, putative	
4.52	PFE0040c	PFEMP2	Yes
4.52	MAL13P1.95	ferredoxin	
4.52	PFE0585c	myo-inositol 1-phosphate synthase, putative	Yes
4.52	PF13_0021	small heat shock protein, putative	
4.52	PFC0915w	ATP-dependent RNA helicase, putative	



Strain selected: 3D7			
Query: PF10_0322 S-adenosylmethionine decarboxylase-ornithine decarboxylase			
Score	Protein ID	Description	Present in PfAdoMetDC/ODC co-inhibition differential abundance dataset
4.52	PFA0520c	chromatin assembly factor 1 protein WD40 domain, putative	Yes
4.52	PF08_0031	oxoglutarate/malate translocator protein, putative	
4.52	PFI0910w	DNA helicase, putative	
4.52	PF14_0200	hypothetical protein	
4.39	PFL1545c	chaperonin cpn60, mitochondrial precursor	Yes
3.96	PF11_0077	hypothetical protein	
3.96	MAL8P1.17	disulfide isomerase precursor, putative	
3.96	PF14_0570	hypothetical protein, conserved	Yes
3.68	PFE1155c	mitochondrial processing peptidase alpha subunit, putative	
3.68	PF14_0309	protein-L-isospartate O-methyltransferase beta-aspartate methyltransferase, putative	Yes
3.38	PFC0955w	ATP-dependent RNA helicase	
3.38	PFI0490c	hypothetical protein	Yes
3.38	MAL8P1.157	hypothetical protein	
3.38	MAL13P1.138	hypothetical protein	
3.38	PF14_0255	hypothetical protein	
3.38	PF13_0242	isocitrate dehydrogenase (NADP), mitochondrial precursor	
3.38	PFE1320w	hypothetical protein	
3.38	PFL2245w	hypothetical protein	
3.38	PFI0670w	hypothetical protein, conserved	
3.38	PF14_0354	hypothetical protein	Yes
3.38	PFB0215c	3'-5' exonuclease, putative	
3.38	PF14_0101	hypothetical protein	
3.38	PFL0660w	dynein light chain 1, putative	Yes
3.38	PF14_0112	POM1, putative	Yes
3.38	PF14_0348	ATP-dependent Clp protease proteolytic subunit, putative	Yes
3.38	PF13_0322	falcilysin	
3.38	PF14_0192	glutathione reductase	Yes
3.38	PF10_0235	hypothetical protein	
3.38	PFE0675c	deoxyriboflavin photolyase (photoreactivating enzyme, DNA photolyase), putative	Yes
3.38	PFL1070c	endoplasmic homolog precursor, putative	
3.38	PFC0165w	hypothetical protein	
3.38	PF13_0117	hypothetical protein, conserved	
3.34	PF14_0318	hypothetical protein	
3.34	PFE0645w	hypothetical protein	
3.34	PFI1120c	hypothetical protein	
3.34	PF08_0010	hypothetical protein	
3.34	PF10_0234	hypothetical protein	
3.34	MAL13P1.107	hypothetical protein	Yes
3.34	PF13_0077	DEAD box helicase, putative	
3.34	MAL13P1.180	hypothetical protein	



Strain selected: 3D7			
Query: PF10_0322 S-adenosylmethionine decarboxylase-ornithine decarboxylase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
3.34	PF11_0365	hypothetical protein	Yes
3.34	PF14_0394	hypothetical protein	
3.34	MAL13P1.295	hypothetical protein	
3.34	PF14_0014	hypothetical protein	
3.34	PF14_0471	hypothetical protein	
3.34	MAL13P1.90	hypothetical protein	
3.34	PF11_0219	hypothetical protein	
3.34	PFA0615w	hypothetical protein	
3.34	PFF0115c		
3.34	PFA0195w	hypothetical protein	
3.34	PFA0175w	hypothetical protein	
3.34	PFL0485w	hypothetical protein	
3.34	PF14_0310	hypothetical protein	
3.34	PFI0610w	hypothetical protein	
3.34	MAL7P1.111	hypothetical protein	
3.34	PF11_0054	hypothetical protein	
3.34	PFE0310c	hypothetical protein	
3.34	PF10_0226	hypothetical protein, conserved	
3.34	PF08_0046	hypothetical protein	
3.34	PFL0965c	hypothetical protein	
3.34	MAL13P1.332	hypothetical protein	
3.34	PFF0655c		Yes
3.34	PF14_0176	hypothetical protein	
3.34	MAL8P1.55	hypothetical protein	
3.34	MAL13P1.127	hypothetical protein	
3.34	PFF0555w		
3.34	MAL8P1.11	hypothetical protein	
3.34	MAL8P1.86	hypothetical protein	Yes
3.34	MAL13P1.266	hypothetical protein	
3.34	PFL0605c	hypothetical protein	
3.34	PF13_0192	hypothetical protein	Yes
3.34	PF11_0248	hypothetical protein	Yes
3.34	PFB0185w	hypothetical protein	
3.34	MAL13P1.325	hypothetical protein	
3.34	PF08_0067	hypothetical protein	
3.34	PFL1675c	hypothetical protein	
3.34	PFC0230c	hypothetical protein	
3.34	PFA0460c	tubulin-specific chaperone a, putative	
3.34	PF14_0306	hypothetical protein	
3.34	PF13_0134	hypothetical protein	
3.34	MAL7P1.114	T gondii P36-like protein;	

Strain selected: 3D7			
Query: PF10_0322 S-adenosylmethionine decarboxylase-ornithine decarboxylase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
3.34	PFI0585c	hypothetical protein	
3.34	PF14_0253	hypothetical protein	
3.34	PF13_0080	hypothetical protein	
3.34	PFF0225w		
3.34	PFL1275c	hypothetical protein	
3.34	PF14_0498	hypothetical protein	
3.34	PFF1175c		
3.34	PFF0770c		
3.34	PFF1395c		
3.34	MAL7P1.157	hypothetical protein	
3.34	PFF0935c		Yes
3.34	PFF0400w		
3.34	PF14_0356	hypothetical protein	
3.34	PF14_0300	syntaxin, putative	
3.34	MAL7P1.74	hypothetical protein	
3.34	MAL13P1.390		
3.34	PFF1140c		
3.34	PF10_0032	hypothetical protein	
3.34	PF14_0186	hypothetical protein	
3.34	PF14_0430	hypothetical protein	Yes
3.34	PFL0095c	hypothetical protein	
3.34	PF08_0080	hypothetical protein	
3.34	PFB0600c	hypothetical protein	
3.34	PF13_0241	hypothetical protein	
3	PF11_0258	co-chaperone GrpE, putative	
3	PFB0685c	acyl-CoA synthetase	



Interactome data obtained from <http://www.cbil.upenn.edu/plasmoMAP/index-v1.html#log> and used with permission from S. Date

Strain selected: 3D7			
Query: PF08_0095 dihydropteroate synthase/dihydroxymethylpterin pyrophosphokinase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
10.32	PF13_0140	dihydrofolate synthase/folypolyglutamate synthase	
8.31	PFL0740c	10 kd chaperonin, putative	
8.31	PF11_0258	co-chaperone GrpE, putative	
8.31	PF13_0180	chaperonin, putative	
7.98	PF08_0006	prohibitin, putative	
7.98	PFL1475w	sun-family protein, putative	
5.96	PF13_0234	phosphoenolpyruvate carboxykinase	
5.96	PF11_0188	heat shock protein 90, putative	
5.96	PF14_0656	U2 snRNP auxiliary factor, putative	
5.96	PF14_0242	arginine n-methyltransferase, putative	
5.9	PFB0953w	hypothetical protein	Yes
5.9	MAL7P1.209		
5.9	PFF0945c		
5.9	PFE0060w	hypothetical protein	
5.9	PF11_0076	hypothetical protein	
5.9	PFF0775w		
5.9	PF10_0013	hypothetical protein	
5.9	MAL8P1.124	hypothetical protein	
5.9	PF14_0705	hypothetical protein	
5.9	PFE1230c	hypothetical protein, conserved	
5.9	PF13_0300	mitochondrial inner membrane translocase, putative	
5.9	MAL8P1.15	hypothetical protein	
5.9	PFE1245w	zinc finger protein, putative	Yes
5.9	PF11_0511	hypothetical protein	
5.9	PFC0790w	hypothetical protein	
5.9	PF13_0015	hypothetical protein	
5.9	PFA0160c	integral membrane protein	
5.9	MAL13P1.73	hypothetical protein	
5.9	PF14_0674	hypothetical protein	
5.9	MAL13P1.318	hypothetical protein	
4.71	PFB0525w	asparagine -- tRNA ligase, putative	
4.71	PFL1210w	hypothetical protein	
4.71	PF07_0079	60S ribosomal protein L11a, putative	
4.71	PFL1425w	t-complex protein 1, gamma subunit, putative	
4.71	MAL13P1.284	pyrroline carboxylate reductase	
4.71	PF11100w	Para-aminobenzoic acid synthetase	
4.71	PFE0475w	asparagine -- t RNA ligase, putative	



Strain selected: 3D7			
Query: PF08_0095 dihydropteroate synthase/dihydroxymethylpterin pyrophosphokinase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
4.71	PF14_0370	RNA helicase, putative	
4.71	PFC0285c	T-complex protein beta subunit, putative	
4.52	PFL0705c	adrenodoxin-type ferredoxin, putative	
4.52	PFB0545c	ribosomal protein L7/L12, putative	
4.52	PF14_0023	hypothetical protein, conserved	
4.52	PF11_0339	hypothetical protein	
4.52	PFA0145c	aspartyl-tRNA synthetase	
4.52	PF14_0517	peptidase, putative	
4.52	PF14_0230	Ribosomal protein family L5, putative	
4.52	PF13_0345	aminomethyltransferase, mitochondrial precursor	
4.52	PFB0595w	heat shock 40 kDa protein, putative	
4.52	PFD0755c	adenylate kinase 1	
4.52	PF11_0077	hypothetical protein	
4.52	PF08_0018	Translation initiation factor like protein	
4.52	PFL2395c	dimethyladenosine transferase, putative	
4.52	PFL1150c	ribosomal protein L24, putative	
4.52	PF10_0121	hypoxanthine phosphoribosyltransferase	
4.52	PF10_0325	hypothetical protein, conserved	
4.39	PF14_0668	hypothetical protein	
4.39	PF14_0036	acid phosphatase, putative	
4.39	PFB0115w	hypothetical protein	Yes
4.39	PF14_0297	putative	Yes
4.39	PFE0605c	glutathione synthetase	
4.39	PFL0255c	putative	
4.39	PFL1310c	ATP-dependent RNA helicase, putative	
4.39	PF11_0264	DNA-dependent RNA polymerase	
4.39	PF11_0351	heat shock protein hsp70 homologue	
4.39	PF13_0243	hypothetical protein	
4.39	PF11570c	aminopeptidase, putative	
4.39	PF14_0022	exopolyphosphatase, putative	
3.38	PFE0630c	orotate phosphoribosyltransferase, putative	
3.38	MAL13P1.54	hypothetical protein, conserved	
3.38	PF14_0378	triose-phosphate isomerase	Yes
3.38	PF10_0153	hsp60	Yes
3.38	PFC0271c	glutaredoxin, putative	
3.38	PF11_0165	falcipain 2 precursor	
3.38	PFD0980w	holo-(acyl-carrier protein) synthase, putative	
3.38	PFB0200c	aspartate aminotransferase, putative	



Strain selected: 3D7			
Query: PF08_0095 dihydropteroate synthase/dihydroxymethylpterin pyrophosphokinase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
3.38	PFE1080w	putative	
3.38	PF14_0381	delta-aminolevulinic acid dehydratase	
3.38	PF11_0507	antigen 332, putative	
3.38	PF14_0147	ATP-dependent protease, putative	
3.38	PFC0550w	hypothetical protein	
3.38	PF14_0166	lysine -- tRNA ligase, putative	
3.38	PF13_0141	L-lactate dehydrogenase	Yes
3.38	PFD0555c	hypothetical protein	
3.38	PF11_0301	spermidine synthase	
3.38	PFC0205c	PfGLP-1, 1-cys-glutaredoxin-like protein-1	
3.38	PFL1710c	tetQ family GTPase, putative	
3.38	PF10_0152	hypothetical protein	
3.38	PFL0690c	hypothetical protein	
3.38	PF07_0100	hypothetical protein	
3.38	PF14_0341	glucose-6-phosphate isomerase	
3.38	PF14_0096	hypothetical protein	Yes
3.34	PF14_0209	hypothetical protein	
3.34	PF10_0064	hypothetical protein	
3.34	MAL13P1.221		
3.34	PF11750c	hypothetical protein	
3.34	PFF0105w		
3.34	PF13_0029	hypothetical protein	
3.34	PFF1330c		
3.34	PF08_0029	hypothetical protein	
3.34	PFD0365c	hypothetical protein	
3.34	PF14_0410	hypothetical protein	
3.34	PFE0295w	hypothetical protein	
3.34	PF11_0319	hypothetical protein	
3.34	PF13_0183	hypothetical protein	Yes
3.34	PFB0470w	hypothetical protein	
3.34	PF14_0037	hypothetical protein	
3.34	PFA0630c	hypothetical protein	
3.34	PFF0820w		
3.34	PFL2355w	hypothetical protein	
3.34	PFB0620w	hypothetical protein	
3.34	PFB0560w	hypothetical protein	
3.34	PFF0120w		
3.34	PF11_0404	malaria antigen	



Strain selected: 3D7			
Query: PF08_0095 dihydropteroate synthase/dihydroxymethylpterin pyrophosphokinase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
3.34	PFE1605w	protein with DNAJ domain	
3.34	PF13_0098	hypothetical protein	
3.34	PF14_0312	hypothetical protein	
3.34	PF08_0051	hypothetical protein	Yes
3.34	PFE0670w	hypothetical protein	
3.34	MAL8P1.32	nucleoside transporter, putative	Yes
3.34	PFI1415w	Serine/Threonine protein kinase, putative	
3.34	PF13_0191	hypothetical protein	
3.34	MAL13P1.46	hypothetical protein	
3.34	PFI1615c		
3.34	PF14_0180	hypothetical protein	
3.34	PFB0921c	hypothetical protein	
3.34	PF14_0687	hypothetical protein	
3.34	PFF1335c		
3.34	PFI0430c	hypothetical protein	
3.34	PFA0100c	hypothetical protein	
3.34	MAL13P1.333	hypothetical protein	
3.34	PFE0800w	hypothetical protein	
3.34	PFB0110w	hypothetical protein	
3.34	PF13_0281	hypothetical protein	
3.34	PFC0166w		
3.34	PF13_0101	hypothetical protein	
3.34	PFF0590c		
3.34	PF13_0252	nucleoside transporter 1	
3.34	PF11_0247	hypothetical protein	
3.34	PFC0085c	hypothetical protein	Yes
3.34	PF11_0254	hypothetical protein	
3.34	PF10_0324	hypothetical protein	
3.34	MAL7P1.225		
3.34	PFF0435w		Yes
3.34	PFL0640w	hypothetical protein	
3.34	PF13_0097	hypothetical protein	
3.34	PFB0930w	hypothetical protein	
3.34	MAL13P1.352	hypothetical protein	
3.34	PFF1400w		
3.34	PF07_0075	hypothetical protein	
3.34	PF11_0508	hypothetical protein	Yes
3.34	PF11_0506	hypothetical protein	

Strain selected: 3D7			
Query: PF08_0095 dihydropteroate synthase/dihydroxymethylpterin pyrophosphokinase			
Score	Protein ID	Description	Present in PFAdoMetDC/ODC co-inhibition differential abundance dataset
3.34	MAL7P1.31	hypothetical protein	
3.34	PF13_0071	hypothetical protein	
3.34	PF13_0099	hypothetical protein	
3.34	MAL7P1.201		
3.34	PF10_0265	hypothetical protein	
3.34	PF10_0029	hypothetical protein	
3.34	PF13_0112	hypothetical protein	
3.34	PFE0595w	hypothetical protein	
3.34	PFA0255c	hypothetical protein	Yes
3.34	MAL13P1.274		
3.34	PFI1385c	hypothetical protein	
3.34	PF14_0308	hypothetical protein	
3.34	PFE1615c	hypothetical protein	Yes

# APPENDIX D

## PROTEOMICS 2D-GE SPOT EXCISION LIST

SSP	Annotation	Spot densities and ratios compared to UT <sub>T1</sub> (relative t <sub>0</sub> )							
		UT <sub>T1</sub>	Ratio	T <sub>T1</sub>	Ratio	T <sub>T2</sub>	Ratio	T <sub>T3</sub>	Ratio
213		2869318	1	4508792	1.57	704448.6	0.25	1620015	0.56
215		2190291	1	1211539	0.55	2648142	1.21	6412805	2.93
1102	Falcpain-2 (PF11_0165)	894643.1	1	867554.4	0.97	1054486	1.18	2591236	2.9
1707		1336849	1	1334699	1	2516244	1.88	3913316	2.93
1722		523218.4	1	759024.9	1.45	1902331	3.64	1688286	3.23
1828	Human erythroid alpha-spectrin	3680704	1	6395287	1.74	17274236	4.69	6387526	1.74
2006		2906660	1	2399245	0.83	703373.1	0.24	1071395	0.37
2105		68055.3	1	259310	3.81	206534.4	3.03	117665.2	1.73
2407	Human beta-actin (fragment)	3364660	1	4195220	1.25	4597818	1.37	9063727	2.69
2903	Human erythroid alpha-spectrin	4843321	1	4921287	1.02	14176775	2.93	16156811	3.34
2904	Human erythroid alpha-spectrin	1050788	1	6207556	5.91	3713321	3.53	4896287	4.66
2908	Human erythroid alpha-spectrin	2718422	1	2733009	1.01	7295902	2.68	4799249	1.77
4102		708179.6	1	1431409	2.02	212995.4	0.3	353271.8	0.5
4109		192948.1	1	248409.8	1.29	399896.7	2.07	509413.5	2.64
4110		87676.6	1	73404	0.84	228144	2.6	335853.4	3.83
4302		498470.5	1	604199.6	1.21	198448.3	0.4	258172.3	0.52
5106		1254317	1	1421460	1.13	843056.3	0.67	472447.8	0.38
5201		837381.3	1	281030.6	0.34	204343.8	0.24	274797	0.33
5207		1261177	1	336372.6	0.27	435374.7	0.35	482240.5	0.38
5314		396261.8	1	419522.3	1.06	1267443	3.2	1447255	3.65
6005		527602.3	1	200273.7	0.38	147416.9	0.28	161523	0.31
6104		770410.6	1	1071500	1.39	234813.4	0.3	187354.2	0.24
6105		2009352	1	2198885	1.09	666891.9	0.33		0
6505	S-adenosylmethionine synthetase (PF11090w) <sup>a</sup>	2509872	1	2592248	1.03	1781118	0.71	1200317	0.48
6506	Ornithine aminotransferase (PFF0435w) <sup>b</sup>	1042238	1	1420503	1.36	1489907	1.43	2313307	2.22
7103		6916921	1	2988248	0.43	4419540	0.64	1842549	0.27
7104		2328269	1	877185.6	0.38	272572	0.12	358543.8	0.15
7106		1721574	1	2139107	1.24	416634.8	0.24	844223.1	0.49
7718		2544799	1	588543.2	0.23	1293771	0.51	1031303	0.41
7817	Elongation factor 2 (PF14_0486)	572182.3	1	594160.1	1.04	1607578	2.81	873754.8	1.53
8001		1304672	1	978171.5	0.75	447955.2	0.34	522991.3	0.4
8002		3035502	1	980220.3	0.32	843949.5	0.28	898411.9	0.3
8004		897505.3	1	1179157	1.31	132369.3	0.15	362044.2	0.4
8018		4875407	1	812069.3	0.17	1234645	0.25	442642.3	0.09
8102		38253012	1	10144632	0.27	9096348	0.24	8096272	0.21
8115		1058422	1	991311.4	0.94	58656.1	0.06	143936.8	0.14
8201	Pyridoxal-5-phosphate synthase pdx1 (PFF1025c)	948551.1	1	943220.3	0.99	1506122	1.59	2393723	2.52
8203		4472542	1	6114925	1.37	1879056	0.42	1532572	0.34
8207	L-lactate dehydrogenase (PF13_0141)	4834714	1	13598061	2.81	7629889	1.58	5320832	1.1
8301		423341	1	516469.9	1.22	173934.7	0.41	109692.3	0.26
8705		1807778	1	254621.6	0.14	848141.9	0.47	556224.1	0.31

a. Spot saturated on high intensity scan set, thus SSP number, spot densities and ratios provided obtained from medium intensity scan set.

b. Spot saturated on high intensity scan set, thus SSP number, spot densities and ratios provided obtained from medium intensity scan set.



# APPENDIX E

## METABOLOMICS DATA

Metabolomics Data	Metabolite	Mode*	Blank	Relative I <sub>2</sub> comparison <sup>†</sup>										Parallel time point comparison <sup>†</sup>									
				UT <sub>1</sub>	UT <sub>2</sub>	UT <sub>3</sub>	T <sub>11</sub>	T <sub>12</sub>	T <sub>15</sub>	UT <sub>1</sub> -Blank	UT <sub>2</sub> -Blank	UT <sub>3</sub> -Blank	T <sub>11</sub> -Blank	T <sub>12</sub> -Blank	T <sub>15</sub> -Blank	UT <sub>1</sub> /UT <sub>2</sub>	UT <sub>1</sub> /UT <sub>3</sub>	T <sub>11</sub> /T <sub>12</sub>	T <sub>11</sub> /T <sub>15</sub>	UT <sub>1</sub> /UT <sub>2</sub>	UT <sub>1</sub> /UT <sub>3</sub>	T <sub>11</sub> /T <sub>12</sub>	T <sub>11</sub> /T <sub>15</sub>
(2S)-methyloctanoic acid	1195.71	6199.25	25745.86	36214.95	9476.89	17393.96	21955.51	5003.54	24550.16	35019.24	6281.18	16199.25	20769.80	1.00	4.91	7.00	1.66	2.24	4.15	1.66	0.66	0.59	
(S)-citrate	3050.26	22845.53	24512.04	12743.52	18155.29	19928.72	18840.08	19796.27	21461.78	9893.25	15105.03	16878.45	15589.82	1.00	0.88	0.45	0.76	0.85	0.79	0.76	0.79	0.63	
(S)-isoleucine	231.11	105200.93	89921.98	93922.06	809439.80	809360.80	869635.44	181973.73	898992.77	939502.96	806207.70	809193.79	869404.33	1.00	0.86	0.86	0.76	0.82	0.86	0.86	0.86	0.83	
1,3-diphosphoglycerate	5.34	139712.28	154684.31	13484.22	61756.76	118859.45	52307.67	139706.84	154679.97	13478.88	61751.42	118854.11	52302.33	1.00	1.11	0.10	0.44	0.86	0.37	0.44	0.77	1.88	
2-dehydro-D-glucuronate	202.15	14471.40	12894.21	14393.52	16267.69	14212.60	13686.84	14269.25	12892.05	14191.37	16606.54	14010.45	13363.49	1.00	0.89	0.99	1.13	0.98	0.94	1.13	1.10	0.94	
2-hydroxy-3-methylglutaredioic acid	35.02	38923.78	38517.40	44194.85	45191.79	42087.55	47053.73	35899.77	38492.39	44169.33	45166.77	42082.55	47039.71	1.00	1.07	1.23	1.26	1.12	1.31	1.26	1.05	1.06	
2-hydroxyisovalerate	515.91	1452.12	1385.75	1918.27	2166.50	1455.67	1683.57	932.21	856.84	1398.16	1646.55	936.75	1163.66	1.00	0.93	1.00	1.77	1.00	1.23	1.77	1.08	0.84	
3-hydroxyglucuronate	102.98	4221.93	32220.88	22933.80	24645.25	35869.23	18443.11	42109.95	32117.80	22830.52	24642.29	35765.25	38340.13	1.00	0.76	0.58	0.89	0.85	0.91	0.58	1.11	1.68	
4-aminobutyrate	3.96	17.29	390.22	798.44	107.07	143.24	150.25	13.34	386.07	794.49	103.11	129.29	146.20	1.00	28.55	55.58	7.73	10.44	10.97	7.73	0.36	0.18	
5-methylthioinosine	4.76	11483.09	8645.31	8451.01	254.31	137.22	295.59	1144.33	8640.65	8455.25	249.55	132.25	291.62	1.00	5.93	7.35	0.32	0.12	0.25	0.32	0.32	0.32	
acetylcamitine	10.35	49957.32	42084.15	341888.52	501773.75	382437.57	338650.50	49946.96	420837.80	341878.17	501763.40	382427.22	338645.55	1.00	0.84	0.68	1.00	0.79	0.68	1.00	0.53	0.59	
acetate	27.07	2499.17	5000.11	4787.74	2358.50	4184.80	4235.08	2472.10	4973.04	4760.67	2331.44	4187.73	4207.99	1.00	2.01	1.93	0.94	1.68	1.70	0.94	0.84	0.88	
adenosine	4.16	1358.93	2387.72	418.80	1554.80	726.51	205.60	1354.55	2385.55	414.33	1550.63	722.33	3204.42	1.00	0.21	0.31	1.14	0.53	0.22	1.14	2.53	0.73	
ADP	5.60	16971.78	18399.19	16570.45	16610.10	20786.03	19005.98	16956.18	18393.59	16644.85	16604.50	20783.43	19004.38	1.00	0.99	0.99	0.89	1.12	1.02	0.89	1.13	1.16	
α-ketoglutarate	1584.26	22539.96	95137.44	121984.43	27856.16	62419.87	83299.99	20955.70	93553.18	120400.17	25971.90	60935.51	81715.73	1.00	4.46	5.75	1.24	2.30	3.90	1.24	0.65	0.68	
AMP	10.06	849.24	722.26	818.45	1123.51	579.56	988.45	839.19	712.20	809.39	1113.42	589.50	979.39	1.00	0.85	0.96	1.33	0.68	1.17	0.85	1.00	1.21	
ascorbic acid	51.56	33590.86	27633.43	18459.66	28845.35	24900.40	23265.55	33576.67	27529.25	18455.57	28841.16	24902.22	23261.36	1.00	0.82	0.65	0.86	0.74	0.69	0.82	0.50	1.26	
asparagine	5.22	25136.41	18953.20	12823.20	21227.15	20713.06	16412.90	25126.18	18943.97	12823.20	21217.93	20703.84	16403.68	1.00	0.75	0.73	0.84	0.82	0.65	0.84	1.09	0.50	
aspartate	18.70	4716.37	3317.43	2831.34	4160.07	4007.29	3436.97	4697.68	3298.73	2812.64	4141.37	3996.59	3420.28	1.00	0.70	0.60	0.88	0.86	0.77	0.88	1.21	1.22	
ATP	5.83	16007.53	173297.84	88621.22	122398.50	165953.15	162020.37	160000.70	173181.01	88611.89	122368.67	165543.33	162022.64	1.00	1.05	0.58	0.79	1.16	0.95	0.78	1.11	1.63	
camitine	6.99	116141.47	11074.17	10737.03	13738.53	11578.28	8937.89	16174.48	11067.18	10732.04	13731.54	11588.30	8930.50	1.00	0.68	0.66	1.07	0.70	0.55	1.07	1.03	0.82	
cholesterol sulfate	1314.69	106053.99	106428.47	88812.73	126389.77	105255.15	85230.32	106739.30	105113.78	88498.08	126075.08	103940.47	83916.64	1.00	0.98	0.80	1.17	0.97	0.79	1.17	0.99	0.98	
cholesterol	5072.60	17931.89	91035.29	89940.49	121668.98	84781.07	80991.82	107429.20	90322.59	84437.88	121666.38	84747.47	80999.22	1.00	0.84	0.80	1.13	0.78	0.82	1.13	0.93	1.03	
crutinine	10.21	829.51	523.04	940.55	619.99	588.26	667.27	819.30	512.83	930.35	609.79	578.25	657.06	1.00	0.63	1.14	0.74	0.71	0.80	0.74	1.13	0.71	
α-D-glucose	5.48	1469.12	1266.07	937.30	1284.32	1431.79	1696.84	1463.67	1250.62	931.85	1278.77	1426.34	1691.09	1.00	0.85	0.64	0.87	0.97	1.16	0.87	1.14	1.81	
D-glucuronate	5.47	25411.50	17045.62	29147.02	22644.29	23241.95	25021.15	25411.50	17036.35	29137.55	22643.92	23242.22	25021.15	1.00	1.00	0.67	1.11	0.89	0.92	1.11	0.89	1.37	
D-Glucuro-1-lactone-6-phosphate	661.07	6923.57	6915.42	7629.98	8670.51	8884.50	6132.35	6923.57	6915.42	7629.98	8670.51	8884.50	6132.35	1.00	1.00	1.11	0.96	0.99	0.87	0.96	0.99	0.79	
D-glyceraldehyde-3-phosphate	5.74	5178.56	6103.55	5418.45	26897.18	7232.24	7078.18	5178.56	6103.55	5418.45	26897.18	7232.24	7078.18	1.00	0.12	0.10	0.82	0.14	0.14	0.52	1.19	1.31	
D-hydroxyacetone phosphate	147.49	3993.84	4133.21	5452.31	5234.57	4633.55	4377.73	3948.05	4133.21	5452.31	5234.57	4633.55	4377.73	1.00	1.04	1.38	1.32	1.17	1.10	1.32	1.13	0.80	
Diphosphonucleoside-7-phosphate	5.24	4479.90	1242.97	15655.34	6778.34	9428.10	8368.21	4479.90	1242.97	15655.34	6778.34	9428.10	8368.21	1.00	2.71	3.60	1.51	2.11	1.87	1.51	0.78	0.53	
fructose-1,6-bisphosphate	119.60	9405.01	7275.35	2799.68	5647.60	7430.19	4507.58	9286.41	7155.75	2799.68	5628.00	7310.59	4387.98	1.00	0.77	0.29	0.60	0.79	0.47	0.60	1.02	1.64	
fructose-5-phosphate	5.20	1423.99	2951.23	2659.68	1755.57	2003.82	2422.21	1423.99	2951.23	2659.68	1755.57	2003.82	2422.21	1.00	2.28	1.82	1.23	1.40	1.59	1.23	0.67	0.53	
fumarate	517.22	2873.97	2448.17	3485.27	1825.67	2150.21	2298.17	1770.75	1930.95	2698.05	1306.45	1632.99	1780.95	1.00	1.09	1.68	0.74	0.82	1.01	1.04	0.85	0.60	
glucuron-actone	8.61	3264.39	38930.51	39141.32	41897.68	37447.98	38344.63	3275.78	38621.91	39132.72	41898.08	37439.37	38336.02	1.00	1.09	1.11	1.19	1.06	1.09	1.19	0.97	0.98	
glucosyl-β-phosphate	25.28	2341.84	3643.35	3058.77	3117.72	2463.94	2911.80	2316.38	3618.10	3043.52	3052.47	2428.69	2896.56	1.00	1.56	1.31	1.34	1.05	1.25	1.34	0.67	0.96	
glucosyl-α-phosphate	11.15	1274.16	20045.45	20293.60	17634.69	20591.75	18200.26	1274.16	20045.45	20293.60	17634.69	20591.75	18200.26	1.00	0.84	0.78	0.83	0.86	0.86	0.83	1.46	1.38	
glutamate	4.60	5038.51	44893.06	42104.21	44189.65	43236.77	41615.07	5038.51	44893.06	42104.21	44189.65	43236.77	41615.07	1.00	0.89	0.84	0.88	0.86	0.83	0.88	0.56	0.59	
glutamine	7.04	47434.19	36390.94	294405.70	380662.39	330674.69	343636.73	47434.19	36390.94	294398.65	380656.34	330667.55	343629.69	1.00	0.77	0.62	0.80	0.70	0.72	0.80	0.91	1.17	
glutathione	11.44	101922.15	785959.75	803655.62	822222.22	739761.35	742355.95	101922.15	785959.75	803655.62	822222.22	739761.35	742355.95	1.00	0.72	0.74	1.00	0.68	0.68	0.72	0.54	0.52	
glutathione dSulfide	13.36	26920.23	14312.53	12798.75	26886.49	13111.07	11890.95	26920.23	14312.53	12798.75	26886.49	13111.07	11890.95	1.00	0.50	0.45	0.94	0.39	0.41	0.54	0.79	0.93	
glutathione dSulfide	27.37	183758.31	374087.49	361753.20	322723.17	375281.18	390584.18	183730.04	374087.49	361753.20	322723.17	375281.18	390584.18	1.00	2.04	1.47	1.21	2.05	2.13	1.21	1.01	1.08	
glucosyl-phosphocholine	4.07	6910.42	5232.34	5916.70	7647.14	4735.52	5882.25	6910.42</															



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