Table S9: Genes conserved in primate parasites but absent in rodent parasites.

PfGene (PvPID/OG)	Product	RNA-seq expr. (IDC)	Protein expr.	GO biological process	Additional information
MAL13P1.214 (64/VIRI)	phosphoethanolamine N-methyltransferase	5 0 20 20 40	MZ;GC;SC; SZ;RU;TZ	Phosphatidylchol- ine biosynth. pr.	methionine and polyamine metabolism
MAL8P1.202 (53/ALVE)	apicoplast phosphate- idic acid phosphatase	5 0 10 10 10 10 10 10 10 10 10 10 10 10 10	-	-	dolichol metabolism; SP
PF14_0565 (44/)	unknown function	5 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MZ	-	WD40 repeat-like
PF14_0036 (69/ALVE)	acid phosphatase, putative	S 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MZ;GC;SC; TZ;RU	-	hydrolase activity
PF11_0186 (65/)	unknown function	5 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GC;SZ	-	-
PF14_0662 (50/ALVE)	nucleoside transporter, putative	5 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	-	-	nucleoside transmem- brane transporter
PFF0680c (40/FIRM)	thiamin-phosphate pyrophosphorylase	5 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MZ	thiamine bio- synthetic process	-
PFE1030c (67/PROT)	phosphomethylpyrimi dine kinase, putative	5 0 10 10 40	SC;SZ; RU	thiamine bio- synthetic process	-
PFL1920c (76/FIRM)	hydroxyethylthiazole kinase, putative	0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	MZ;GC;TZ; SC;RU	thiamine bio- synthetic process	-
MAL7P1.339 (46/ALVE)	Ca++ chelating serine protease, putative	5 0 10 20 40	-	-	SCP/Tpx-1/Ag5/PR-1/Sc7 family; SP
PFI0405w (46/)	unknown function	5 5 5 5 40		-	1 TM; AP
MAL8P1.111 (42/ALVE)	JmjC domain containing protein	5 0 20 20 40	GC	-	[Histone H3]-lysine-36 demethylase
PFL2255w (69/ALVE)	unknown function	5 0 10 20 40	-	ubiquitin cycle	-
PFL1840w (66/ALVE)	unknown function	5 0 20 20 40	GC;SZ	-	SP; 4 TM; COPI associated
PFL0305c (85/ALVE)	IMP-specific 5'- nucleotidase, putative	5 0 20 30 42	GC; oocyst SZ	nucleotide metabolic process	magnesium ion binding; phosphatase activity
PFI1220w (47/ALVE)	unknown function	5 0 20 30 40	-	-	acyl-CoA N-acyltransfer- ase; upregul. in GC/SZ

Same genes as in Table 1 but including graphical RNA-seq expression profiles taken from PlasmoDB 7.1. RNA-seq expression values represent scaled expression values from the intraerythrocytic developmental cycle (IDC) as reported by Bartfai R *et al.* (2010). Diagram tick marks represent hours post infection along the x-axis (10, 20, 30, and 40 h post infection) and normalized coverage (log2) on the y-axis. For remaining legend please refer to legend of Table 1.