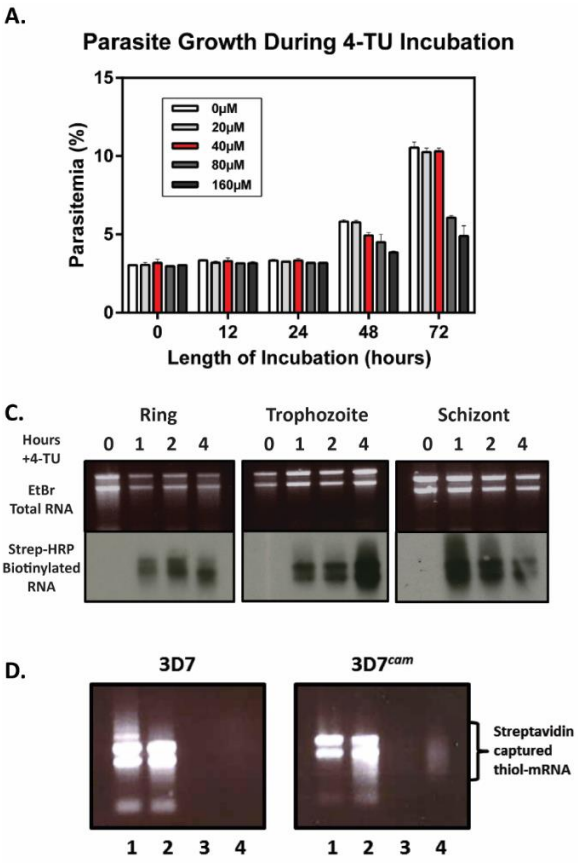

B.

Correlation of Total mRNA Abundance Profiles Between Strains

	3D7 0h	3D7 12h	3D7 24h	3D7 36h	
3D7^{cam} 0h	**0.816**	0.189	-0.501	-0.272	
3D7^{cam} 12h	-0.168	**0.835**	-0.220	-0.388	
3D7^{cam} 24h	-0.470	-0.486	**0.900**	0.435	
3D7^{cam} 36h	-0.057	-0.289	0.176	**0.865**	Median Correlation 0.850

	3D7 0h	3D7 12h	3D7 24h	3D7 36h	
3D7^{pfs16} 0h	**0.865**	-0.096	-0.552	-0.229	
3D7^{pfs16} 12h	0.040	**0.827**	-0.490	-0.538	
3D7^{pfs16} 24h	-0.530	-0.205	**0.807**	0.080	
3D7^{pfs16} 36h	-0.136	-0.407	0.092	**0.897**	Median Correlation 0.846

	3D7^{cam} 0h	3D7^{cam} 12h	3D7^{cam} 24h	3D7^{cam} 36h	
3D7^{pfs16} 0h	**0.823**	-0.072	-0.272	-0.134	
3D7^{pfs16} 12h	0.243	**0.803**	-0.558	-0.423	
3D7^{pfs16} 24h	-0.510	-0.088	**0.806**	-0.004	
3D7^{pfs16} 36h	-0.227	-0.385	0.173	**0.867**	Median Correlation 0.815

Figure S1: The effects of 4-TU incorporation and capture throughout *P. falciparum* 3D7^{cam} development within human erythrocytes. A) 4-TU has a concentration dependent effect on development. *P.f.* 3D7^{cam} growth in the presence of various concentrations of 4-TU (0, 20, 40, 80, 160µM) was monitored every 12hrs for 72hrs by Giemsa-stained thin blood films. Parasitemia percentages (infected/uninfected erythrocytes) are represented as an average of two independent experiments ± s.d. across this timeframe, 40µM (red bars) or less had no effect on parasite growth. B) Transcript abundance profiles during the IDC were not altered by the addition of 40µM 4-TU. Total RNA isolated from 3D7^{cam} and 3D7^{pfs16} incubated for 12h with 40µM 4-TU was compared by DNA microarray. The Pearson correlation (r) of the Log_2(Cy3/Cy5) ratio for each gene across the array at 0, 12, 24, and 36h was calculated. The median correlation of the log_2 ratio of each gene over time in either 3D7^{cam} (top panel) or 3D7^{pfs16} (middle panel) compared to a previously published 3D7 mRNA abundance timecourse (Kafsack et al. 2012) was 0.850 and 0.846, respectively. The median correlation between total RNA abundance of 3D7^{cam} and 3D7^{pfs16} was determined to be 0.815. C) To ensure that 4-TU is efficiently incorporated throughout the IDC, highly synchronized *P.f.* 3D7^{cam} was grown in the presence of 40µM 4-TU for various lengths of time (0, 1, 2, 4 hours) during three major developmental stages during the IDC (ring, trophozoite, and schizont). Following incubation, total RNA was extracted, biotinylated and separated on an agarose gel (2µg/lane) (top panel). Incorporation of 4-TU throughout the IDC was assessed by Northern blot and probed with streptavidin-HRP (bottom panel). D) Thiolated RNA can be separated from the parasite total RNA using streptavidin magnetic beads. Biotinylated RNA from both wild-type 3D7 and 3D7^{cam} eluted from streptavidin magnetic beads was run on an ethidium bromide stained gel as follows: (1) total RNA, (2) flow-through/non-biotinylated RNA, (3) last wash of 4, and (4) β-mercaptoethanol eluted/thiol-tagged RNA.

Kafsack BF, Painter HJ, Llinas M. 2012. New Agilent platform DNA microarrays for transcriptome analysis of *Plasmodium falciparum* and *Plasmodium berghei* for the malaria research community. *Malar J* **11**: 187.