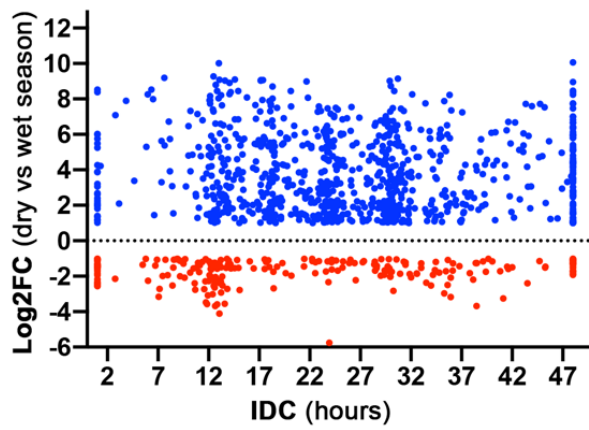


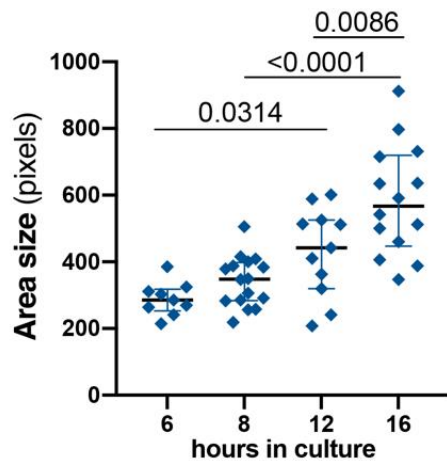
Supplementary Information File

***P. falciparum* transcription in different clinical presentations of malaria associates with circulation time of infected erythrocytes**

Richard Thomson-Luque¹, Lasse Votborg-Novél^{1,2}, Wanangwa Ndovie³, Carolina M. Andrade¹, Moussa Niangaly^{2,4}, Charalampos Attipa^{3,5}, Nathalia F Lima¹, Drissa Coulibaly⁴, Didier Doumtabe⁴, Bouréima Guindo⁴, Bourama Tangara⁴, Fayçal Maiga⁴, Abdoulaye Kassoum Kone⁴, Karim Traore⁴, Kassoum Kayentao⁴, Aissata Ongoiba⁴, Safiatou Doumbo⁴, Mahamadou A. Thera⁴, Boubacar Traoré⁴, Karl Seydel^{6,7}, Nuno S. Osório⁸, Silvia Portugal^{1,2*}



Supplementary Fig. 1 | Log_2 expression reported by Andrade et al. of 568 (50.22% of the total 1131) DEGs upregulated in low parasitaemias at the end of the dry season (blue), and 216 (45.38% of the total 476) DEGs upregulated in higher parasitaemias in malaria cases in the wet season (red), shown along the *X* axis according to Bozdech et al. peak timing of transcription.



Supplementary Fig. 2 | 3D7 *P. falciparum* area measured from Giemsa-stained thick smears after 6, 8, 12 and 16 h in culture following merozoite invasion (n= 9, 16, 11 and 14 parasite measured respectively) . Data indicate median \pm IQR; one-way ANOVA.