| 5' enriched motif | z-score | *p*-value | Potential Interacting Protein |
|---|---|---|---|
|  | 191.0 | 1.33e-55 | N/A |
|  | 47.8 | 6.89e-16 | PF3D7_1350900[α] |
|  | 28.7 | 3.69e-10 | PF3D7_1139300[α] |
|  | 26.4 | 9.57e-10 | PF3D7_0420300, PF3D7_0802100,<br>PF3D7_1305200, PF3D7_1456000[α] |
|  | 24.1 | 5.51e-9 | PF3D7_1222600 (AP2-G)[α, β] |

| 3' enriched motif | z-score | *p*-value | Potential Interacting Protein |
|---|---|---|---|
|  | 18.6 | 1.25e-6 | PF3D7_0417100 (PUF2)[γ] |
|  | 13.9 | 8.38e-6 | N/A |

**Figure S7 related to Figure 5: Gametocyte-specific genes are enriched for potential regulatory motifs.** Genes identified as gametocyte-specific identified in 3D7 were analyzed for DNA sequence motif enrichment within their 5' and 3' UTRs (Elemento et al. 2007). Known *trans*-regulatory factors or RNA-binding proteins previously demonstrated to interact with each enriched motif are noted in red. [α] (Campbell et al. 2010); [β] (Kafsack et al. 2014); [γ] (Cui et al. 2002)

Campbell TL, De Silva EK, Olszewski KL, Elemento O, Llinas M. 2010. Identification and genome-wide prediction of DNA binding specificities for the ApiAP2 family of regulators from the malaria parasite. *PLoS Pathog* **6**: e1001165.

Cui L, Fan Q, Li J. 2002. The malaria parasite *Plasmodium falciparum* encodes members of the Puf RNA-binding protein family with conserved RNA binding activity. *Nucleic Acids Research* **30**: 4607-4617.

Elemento O, Slonim N, Tavazoie S. 2007. A universal framework for regulatory element discovery across all genomes and data types. *Mol Cell* **28**: 337-350.

Kafsack BF, Rovira-Graells N, Clark TG, Bancells C, Crowley VM, Campino SG, Williams AE, Drought LG, Kwiatkowski DP, Baker DA et al. 2014. A transcriptional switch underlies commitment to sexual development in malaria parasites. *Nature* **507**: 248-252.