

Description of additional supplementary files

Supplementary data 1: Putative lncRNAs identified and investigated in this study. Chromosome, coordinates, and expression profile for all lncRNAs identified along with probe and primer sequences used to investigate several stage-specific lncRNAs.

1a: Mapping statistic for Nuclear and Cytoplasmic RNA-seq data.

1b: Putative lncRNAs identified in this study.

1c: Sequences of primers used for RT-PCR and the generation of RNA-FISH probes. The oligonucleotides were synthesized by IDT at 25 nmole scale.

1d: Number of foci detected by RNA-FISH.

1e: lncRNAs used for ChIRP-seq analysis.

1f: ChIRP-seq probes and sequences used for identifying lncRNA-chromatin interactions. The oligonucleotides were synthesized by Sigma at 100 nmole scale.

1g: lncRNA-TARE4 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1h: lncRNA-13 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1i: lncRNA-178 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1j: lncRNA-271 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1k: lncRNA-ch9 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1l: lncRNA-ch14 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1 : lncRNA-1494 ChIRP-seq peak calling results. P-values (pval) were determined by negative binomial with local variance estimation⁸¹.

1m: List of primers used for lncRNA-14 KO. The oligonucleotides were synthesized by IDT at 25 nmole scale.

Supplementary data 2: Whole genome sequencing results showing identified mutations in NF54 control and Δ lncRNA-ch14 transfected lines. The mutation in the *gdv1* gene essential for gametocyte formation exists only in the parental NF54 parasites highlighted in red.

Supplementary data 3: DEseq2 analysis of Δ IncRNA-ch14 clone compared to WT controls. Results for schizont and gametocyte stages are presented in two different sheets. The p-values were obtained by two-tailed Wald test and corrected for multiple testing using the Benjamini-Hochberg correction.