Supplementary Table 1. Genomic coordinates and detection probes for *P.falciparum* structural RNAs.

Supplementary Table 2. Features and genomic location of ribosomal RNAs (rRNAs) and transfer RNAs (tRNAs) in *P.falciparum*.

Supplementary Figure 1.

(a.) Schematic representation of the location of individual probes for detection and mapping of *P.falciparum* telomerase RNA. The template region of the RNA is shown as an open box on the large and small transcripts (grey). Individual probes (underlined) and their locations are shown with respect to nucleotide positions on chromosome 9. These probes were used for both northern and RNase Protection Assays (RPA). **(b.)** RNAse protection assay with cRNA Probe 4-14 (chr9:763,162-763,441) used to map the 3' end if telomerase RNA transcript. Lane 1, probe alone (digested with RNAse); lane 2, probe alone (no RNAse) and lane 3, RNA with probe (digested with RNAse). **(c.)** Probe-16-17 (chr9:761,052-761,328) was used to map the 5' end of telomerase RNA. Lane 1, RNA with probe (digested with RNAse); lane 2, probe alone (digested with RNAse) and lane 3, probe alone (no RNAse). RNAse undigested probe is shown as input. Protected fragments shown as 'P' on the blots.

Supplementary Figure 2.

Sequence Alignment of *P.falciparum* U1 snRNA. ss: Splice site. SM corresponds to putative Sm Protein binding motif. Pf: *P. falciparum*, Pr: *P. reichenowi*, Pv: *P. vivax*, Pk: *P. knowlesi*, Pg: *P. gallinaceum*, Pc: *P. chabaudi*, Pb: *P. berghei*, Py: *P. yoelii yoelii,* Hu and Mu are human and mouse sequences respectively (same abbreviations used in all snRNA alignments).

Supplementary Figure 3.

Sequence Alignment of *P.falciparum* U2 snRNA. BP: Branchpoint sequence. Helix 2a terminal loop sequence and its conserved complementarity marked in 'x'. SM corresponds to putative Sm Protein binding motif. U2-U6 helices and branchpoint (BP) sequences are shown as [::].

Supplementary Figure 4.

Sequence Alignment of *P.falciparum* U4 snRNA. Non-canonical pairing in terminal loop of U4 helix I is shown by 'x'. SM corresponds to putative Sm Protein binding motif.

Supplementary Figure 5.

Sequence Alignment of *P.falciparum* **U5** snRNA

Supplementary Figure 6.

Sequence Alignment of *P.falciparum* **U6** snRNA. U4-U6 and U2-U6 pairings are shown at the bottom of alignments.

Supplementary Figure 7.

(a.) Primer extension reaction on 6% denaturing polyacryalamide-urea gel : Lane M-100 is a 100 bp ladder marker , Lane 1 - RNAse MRP, Lane 2 - RNAse P, Lane 3 - U3 snoRNA, Lane 4 - SRP-RNA and Lane M - 10 is a 10bp ladder marker. **(b.)** U3 RNA alignment shown in dot-bracket structure. Pf: *P. falciparum*, Pv: *P. vivax*, Pr: *P. reichenowi*, Pk: *P. knowlesi*, Pg: *P.*

gallinaceum, Pc: *P. chabaudi* and Pb: *P. berghei*. U3 structural elements are shown on the top of alignments and helices are shown at the bottom of the alignment.

Supplementary Figure 8.

Sequence alignment of the upstream SNPE element for all U RNAs from various species of malaria parasite. Pf: *P. falciparum*, Pr: *P. reichenowi*, Pv: *P. vivax*, Pk: *P. knowlesi*, Pg: *P. gallinaceum*, Pc: *P. chabaudi*, Pb: *P. berghei*, Py: *P. yoelii yoelii*

Supplementary Figure 9. (a.) *P.falciparum* SRP-RNA detected on the Northern blot **(b.)**. Multiple sequence alignment of SRP RNA. Helices denoted by 'H' with corresponding number from published structure model (see text) . Pf: *P. falciparum*, Pv: *P. vivax*, Pr: *P. reichenowi*, Pk: *P. knowlesi*, Pg: *P. gallinaceum*, Pc: *P. chabaudi*, Pb: *P. berghei*, and Py: *P. yoelii yoelii.*