S15 Figure: Transcripts in rhesus macaque IGS. Transcriptome assemblies were performed using unstranded polyA(+) RNA-seq data from the rhesus macaque tissues indicated to the left. The first row represents consensus transcripts (dark green boxes) obtained by merging the individual IGS transcripts (light green boxes) from the different tissues (rows beneath). The names of the consensus transcripts are indicated next to them. The scale above shows the position in the rhesus macaque rDNA IGS.

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S15 Figure