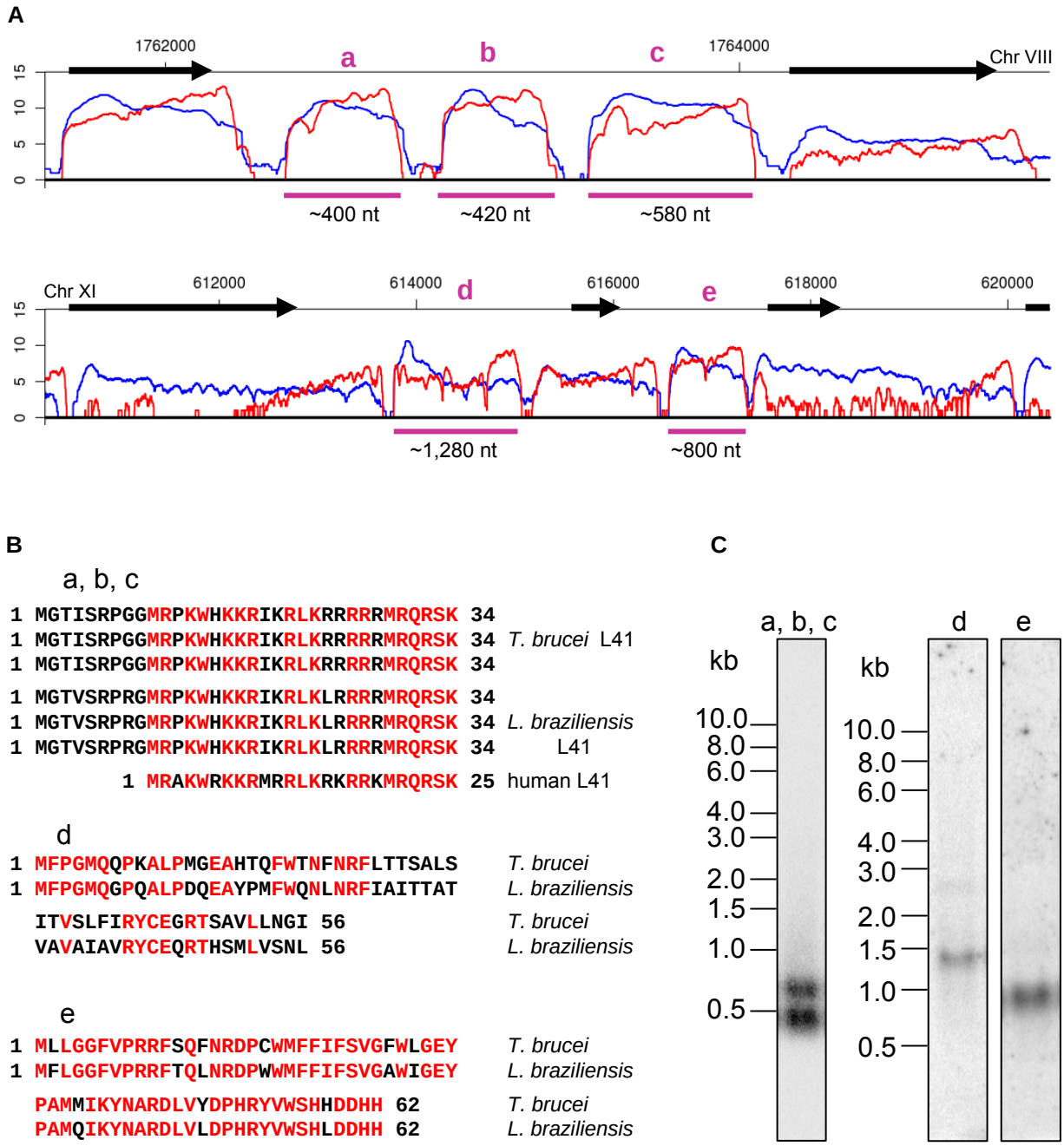

Figure S9. Experimental validation of transcripts for novel *T. brucei* genes. (*A*) Overlay of the number of reads ($\log_2$) from 5′-end- (blue) and 3′-end-enriched (red) libraries aligning to the shown regions of chromosomes VIII and XI. Transcripts for novel genes (purple bars) are labeled a through e and their approximate sizes indicated [excluding the poly(A) tail]. (*B*) Sequence of the polypeptides encoded by putative ORFs in the indicated (a – e) transcripts. a, b, and c encode the *T. brucei* ribosomal protein L41. Also shown are the sequences for the three *Leishmania braziliensis* L41 polypeptides (encoded by three unannotated, tandemly arranged genes) and the human L41 sequence. Identical amino acids between the sequences from the three species are colored red. d and e encode 56 AA and 62 AA proteins respectively that are conserved but not annotated in *L. braziliensis*. (*C*) Northern blots of total RNA fractionated on denaturing agarose gels with probes against the indicated (a – e) transcripts. The (a, b, c) blot was performed with a probe against the short ORF present in all three transcripts. Transcripts a and b have almost identical size and they co-migrate during electrophoretic separation of the RNA sample. Positions of marker RNA bands are indicated on the left.