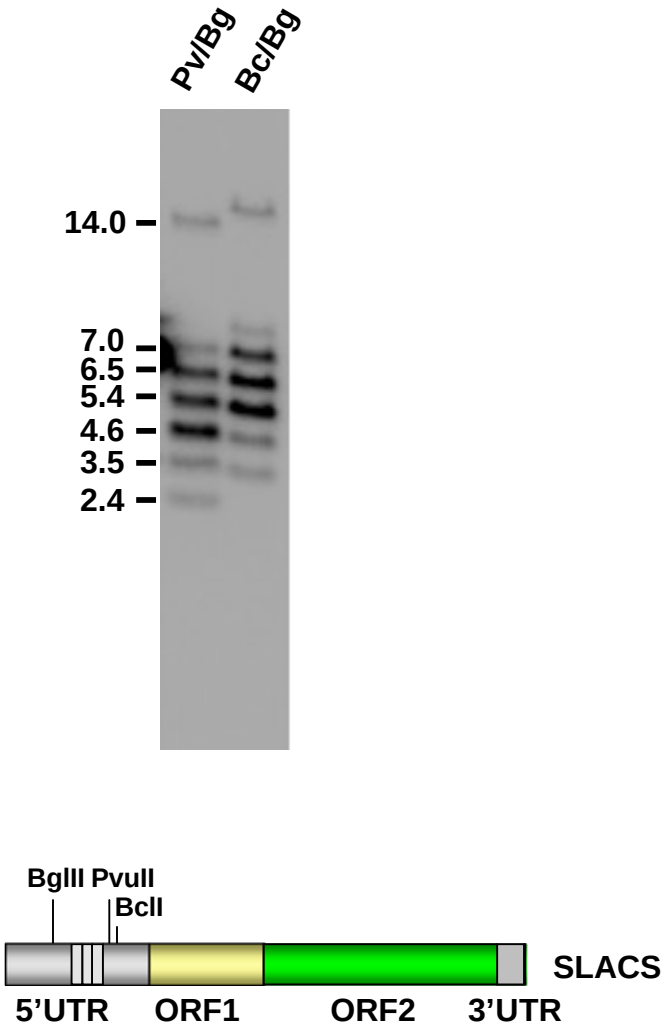
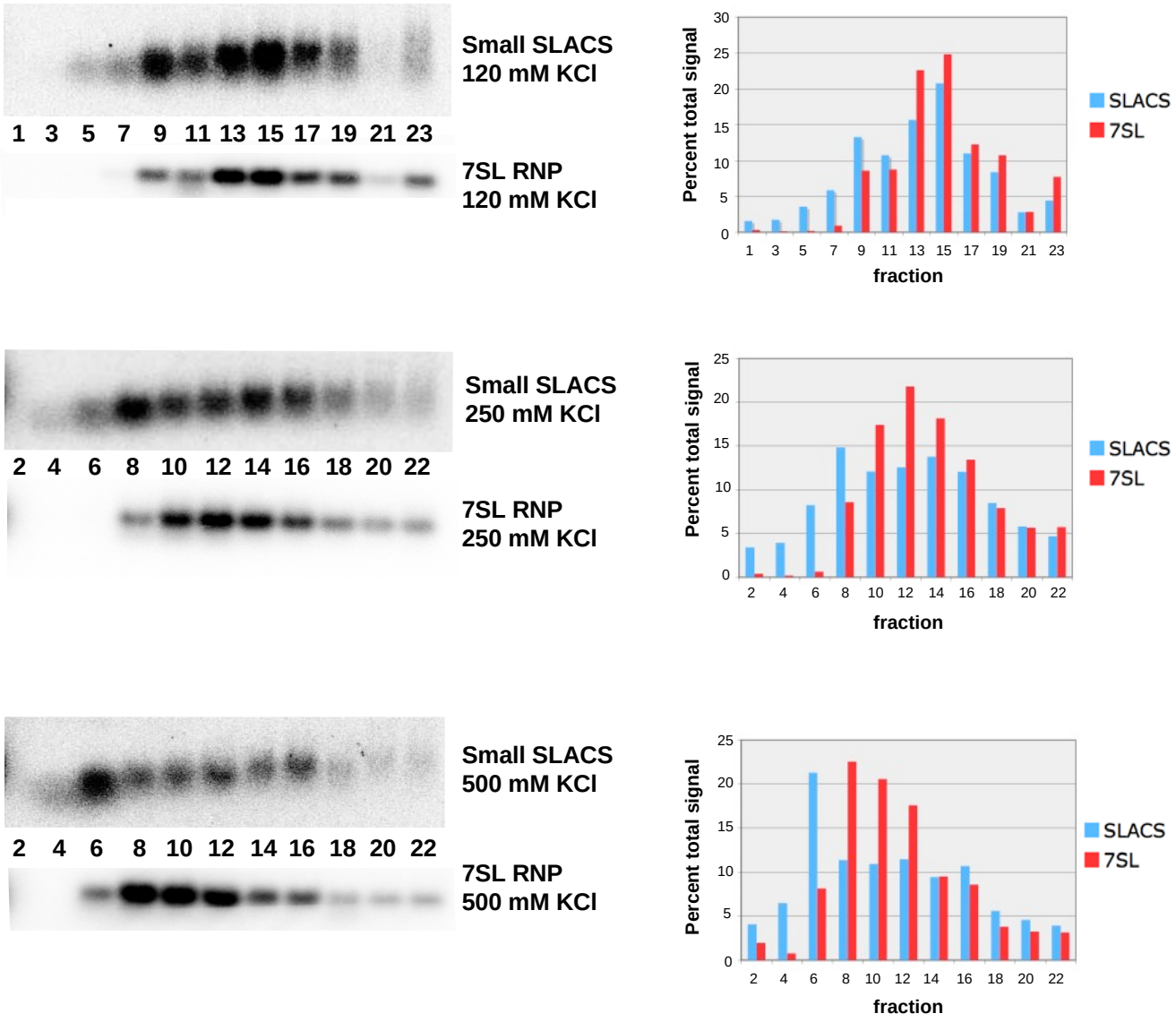
Fig. S1



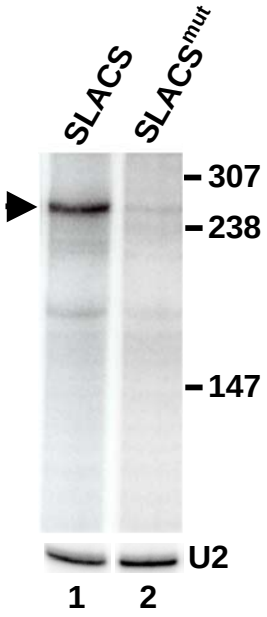
Supplementary Figure 1. Southern blot analysis of SLACS repeat regions. YTat 1.1 genomic DNA was digested with either PvuII and BglII (Pv/Bg) or BclI and BglII (Bc/Bg), separated on a .7% agarose gel, and hybridized to a probe complementary to the 185 bp SLACS repeat sequence. The size of each band indicates the number of SLACS repeats in various elements found in the *T. brucei rhodesiense* genome. The numbers alongside the blot estimate the number of 185-bp repeats contained in each band of the PvuII/BglII digest (the SLACS reference sequence (accession #X17078) contains 3.5 185-bp repeats).

Fig. S2



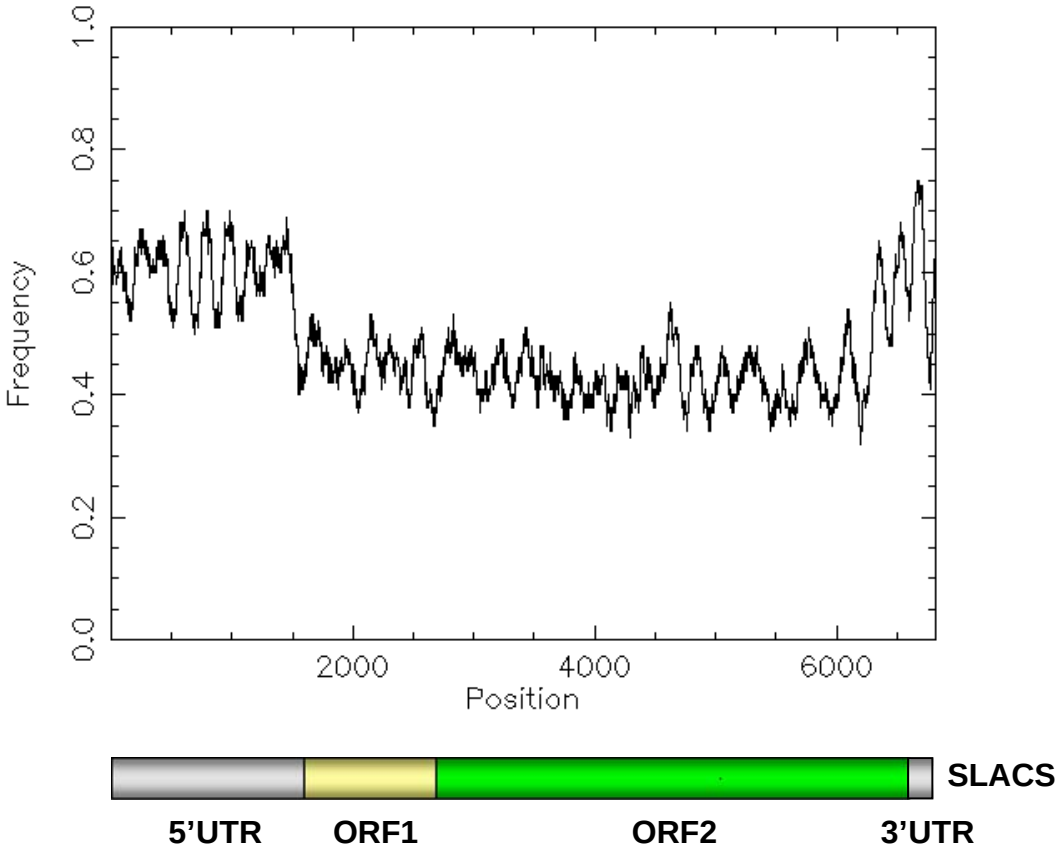
Supplementary Figure 2. sSLACS RNP stability in different salt concentrations. A post-nuclear supernatant from *ago1*$^{-/-}$ cells (S14) was separated by high speed centrifugation in a soluble (S100) and pellet fraction (P100) and the S100 was applied to a 10-30% glycerol density gradient containing 120 mM KCl, 250 mM KCl, or 500 mM KCl. Selected fractions were Northern blotted with a probe complementary to SLACS ORF1 and subsequently hybridized with a probe complementary to the 7SL RNA. The intensity of signal in each fraction was quantitated using OptiQuant software (Perkin Elmer) and expressed as a percent of the total hybridization signal in the graphs on the right.

Fig. S3



Supplementary Figure 3. *In vitro* transcription of pSLACS and pSLACS^{mut} vectors. Both pSLACS and pSLACS^{mut} were digested with BglI and added to transcription reactions containing [α-^{32}P]GTP. Transcription of pSLACS produced an ~250 nt radiolabeled RNA.

Fig. S4



Supplementary Figure 4. FREAK program analysis of SLACS A+T content.