



Figure 1. *F. tularensis* ribosomes are heterogenous with respect to bS21. **A.** Chart demonstrating purity of wild-type ribosomes. Categories represent classification of proteins identified by mass spectrometry of ribosomes purified from wild-type *F. tularensis* LVS cells. Numbers represent the percentage of spectral counts corresponding to proteins in each category, combined from quadruplicate samples. **B.** Wild-type *F. tularensis* LVS ribosomes contain more than one bS21 homolog. Table detailing the number of spectral counts corresponding to bS21 homologs identified from individual ribosome purifications (A – D) from wild-type cells. Spectral counts corresponding to bS21-1 and/or bS21-3 cannot be unambiguously assigned due to complete sequence identity of detected peptides. ND: not detected. **C.** Each bS21 homolog can be incorporated into ribosomes. Top: Sucrose gradient sedimentation profile from actively-translating wild-type cells containing an empty vector. Nucleic acid content was monitored by A260 (y-axis). Peaks corresponding to the 30S, 50S, 70S, and polysomes are indicated. Fractions collected are indicated on the x-axis. Bottom: Immunoblot analysis of fractions from sucrose gradient sedimentation performed on actively-translating cells ectopically expressing indicated bS21 homolog with VSV-G epitope tag. Wells correspond to fractions 1 – 21 from profile above.