Supplemental Figure 1 - Analysis of the size distribution of *H. somni* RNA molecules produced with the RNA Isolation and Ribodepletion Combination 2 method. a) capillary electrophoretic separation pattern of total RNA from *H. somni* USDA-ARS-USMARC-63250 grown in BHI-TT. The electropherogram is on the left and its corresponding digital gel image is on the right. LM designates the lane marker standard at 15 nt; these runs were calibrated with known standards according to vendors directions. A prominent 23S band in the vicinity of 3.1 kB was not observed, instead 1.38 and 1.86 kB peaks were observed, consistent with 23S rRNA fragmentation. b) After ribodepletion using Ribo-Zero, the peaks at 1.38 and 1.86 are greatly diminished, suggesting their association with rRNA.
**H. somni** fragmented 23S RNA

**Supplemental Figure 2**: Discontiguous megablast result using USDA-ARS-USMARC-63250 CP018802-23S-1 query sequence against all Gammaproteobacteria (taxid 1236) in the RefSeq RNA database. Results sorted by Geneious grade.
**H. somni** fragmented 23S RNA

**Supplemental Figure 3** – Discontiguous megablast results using USDA-ARS-USMARC-63250 CP018802-23S-1 query sequence (top) against all Gammaproteobacteria (taxid 1236) in the RefSeq RNA database. Results sorted by Geneious grade, zoomed in view of gap region. Bases in subject sequences that are different than the query sequence are colored, those that are the same are grey.

**Supplemental Figure 4** - RNAfold predicted minimum free energy (MFE) rRNA stem-loop structure of 109 bp IVS region of NR_076444 (**H. somni** strain 129PT with a MFE predicted to be --43.05 kcal/mol constituting 5.81% of the ensemble of structures predicted. Colored arrows point to changes in predicted secondary structure relative to USDA-ARS-USMARC-63250 IVS in Figure 4 b. Grey arrows point to predicted excision site.