

Supplementary Materials: Next-Generation Sequencing of Two Mitochondrial Genomes from Family Pompilidae (Hymenoptera: Vespoidea) Reveal Novel Patterns of Gene Arrangement

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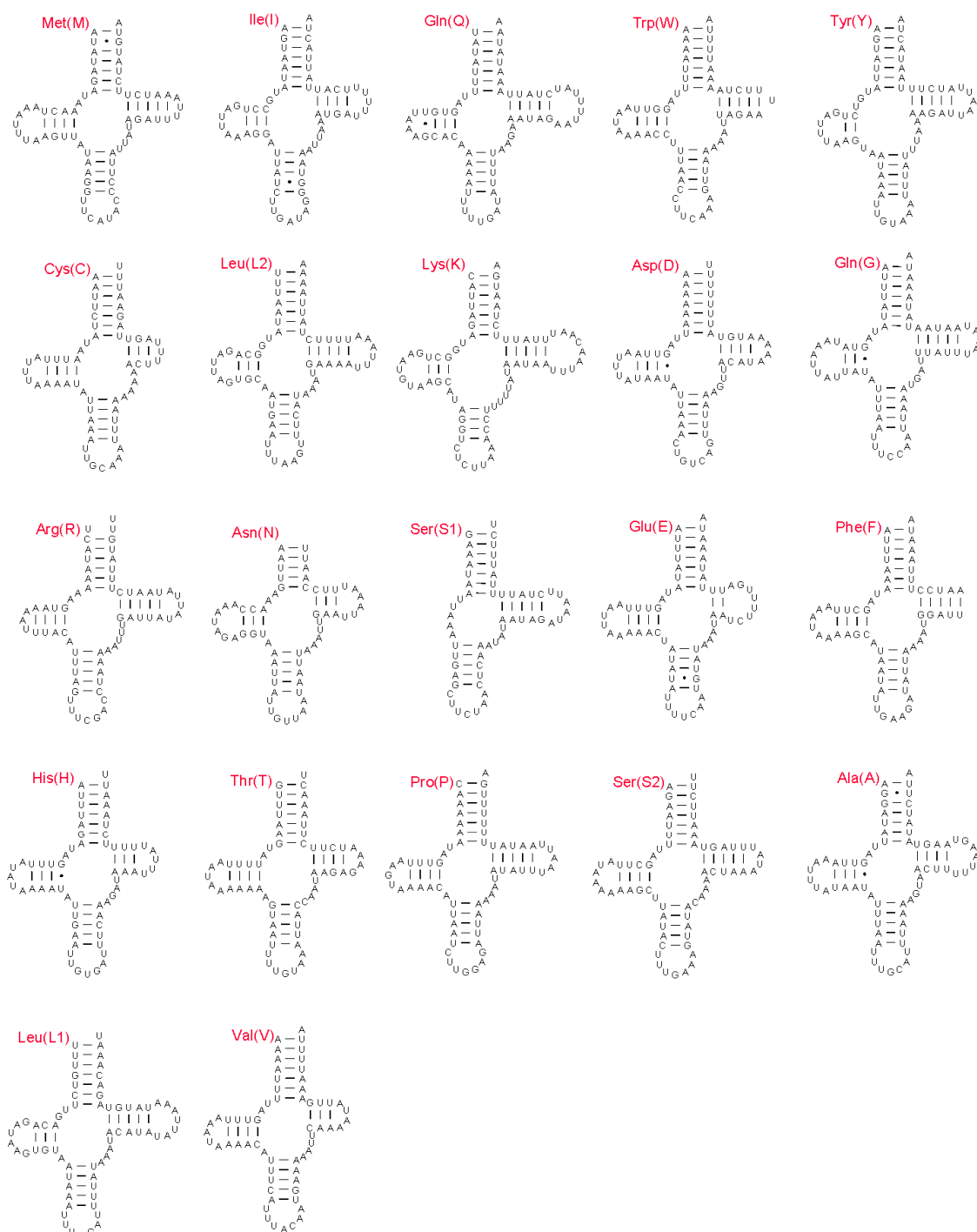


Figure S1. Predicted secondary structures for the 22 typical tRNA genes of *Auplopus* mitochondrial genome. Base-pairing is indicated as follows: Watson–Crick pairs by lines, wobble GU pairs by dots and other noncanonical pairs by circles.

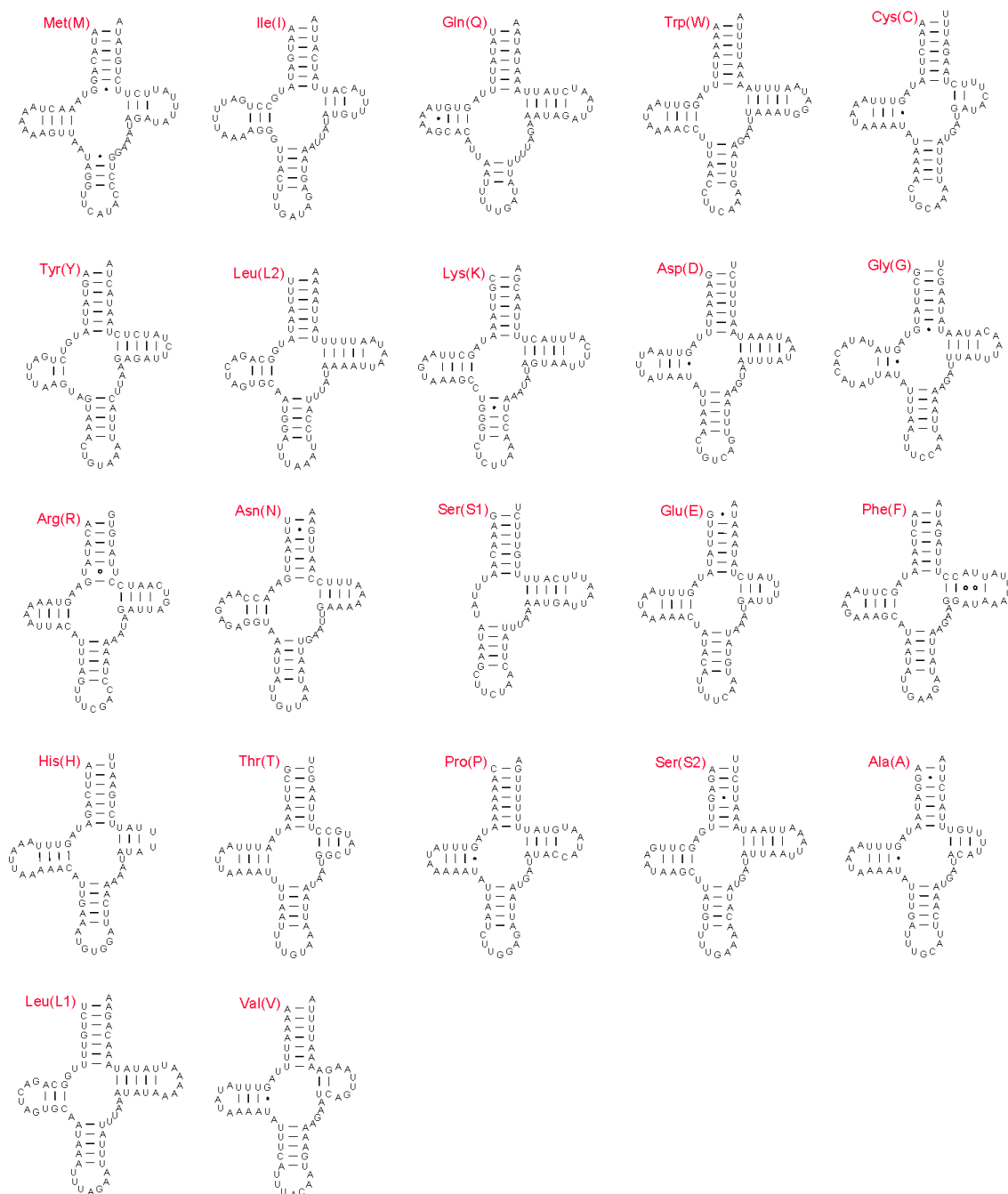


Figure S2. Predicted secondary structures for the 22 typical tRNA genes of *Ageoioideus* mitochondrial genome. Symbols are as in Figure S1.

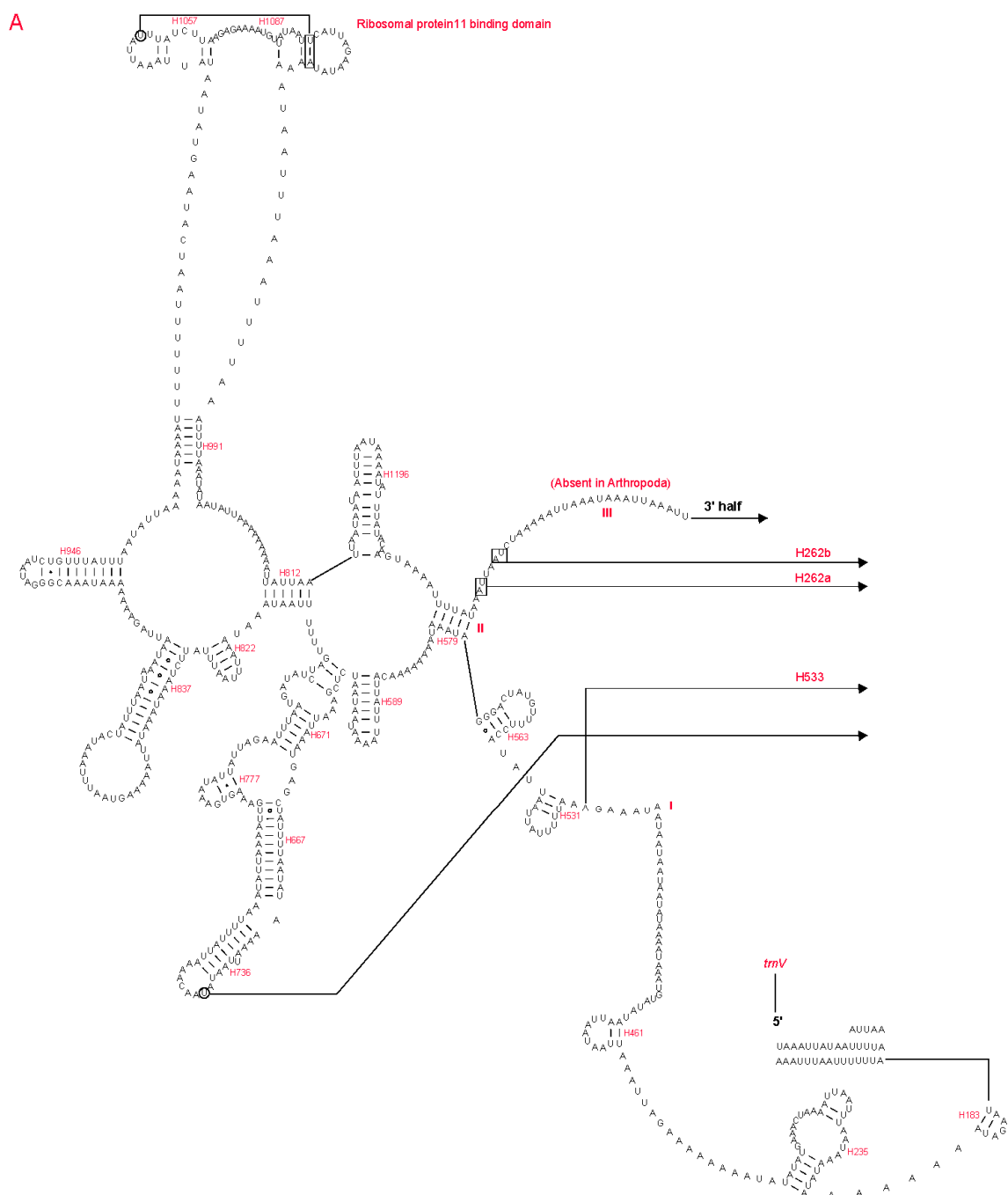
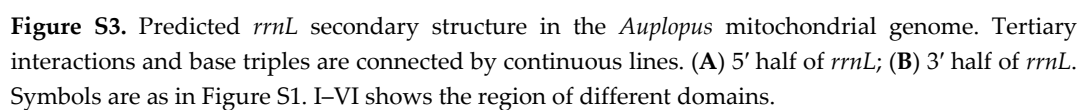


Figure S3. Cont.



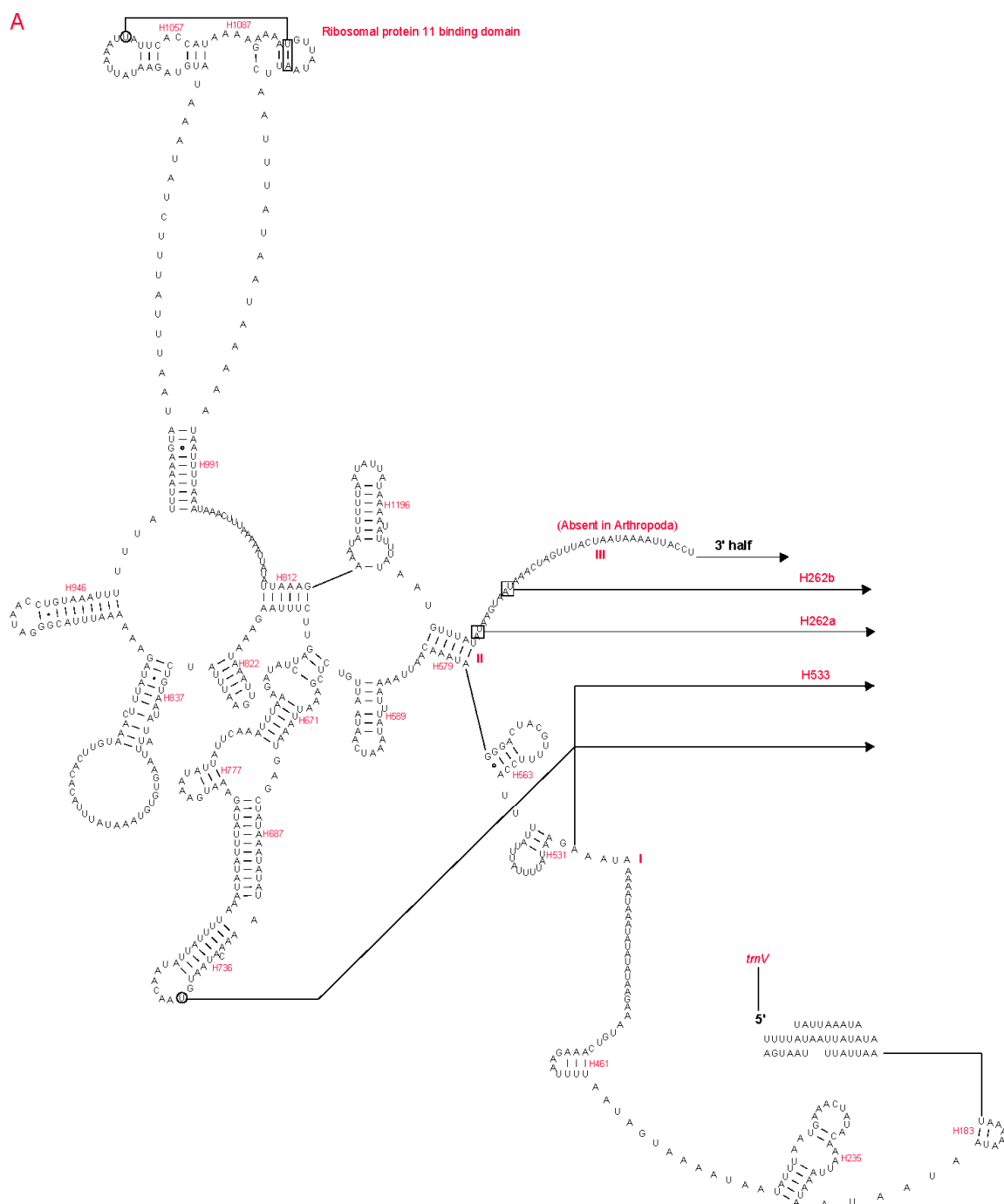
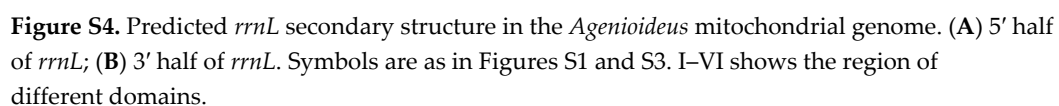


Figure S4. Cont.



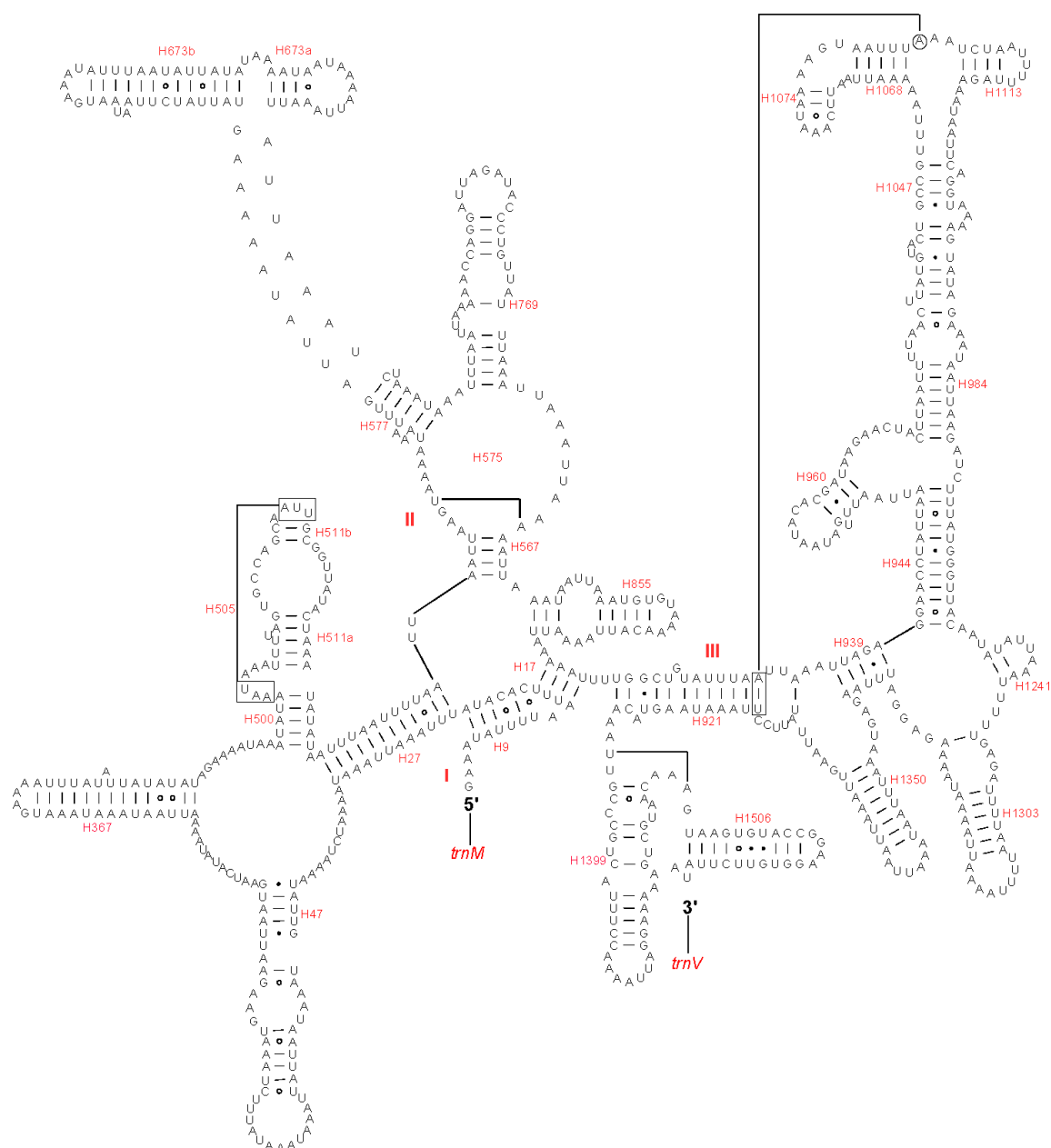


Figure S5. Predicted *rrnS* secondary structure in the *Auplopus* mitochondrial genome. Symbols are as in Figures S1 and S3. I–VI shows the region of different domains.

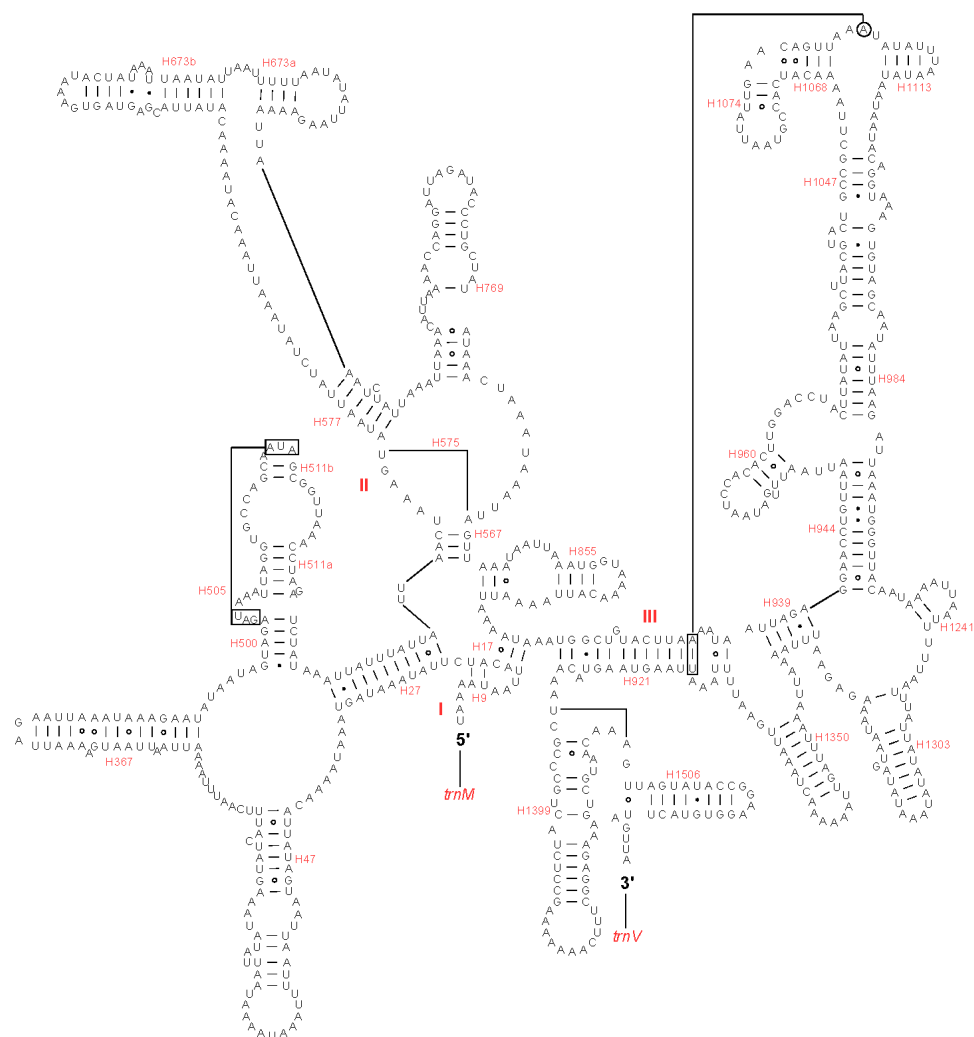


Figure S6. Predicted *rrnS* secondary structure in the *Agenioideus* mitochondrial genome. Symbols are as in Figures S1 and S3. I–VI shows the region of different domains.