**Fig S1. Species-wise grid with the frequency of the major prey types identified from the metabarcoding data and the average prey-type selectivity.** Gut content cells in white indicate absence, and cells in grey indicate presence in one specimen, or more than one specimen if labeled with a number. Selectivity colors mapped to Strauss’ L.I. values.

**Table S1. Read abundances assigned to each DNA source interpretation category for each siphonophore species.**

**Table S2. Read abundances assigned to each DNA source interpretation category for each siphonophore species by barcode.**

**Table S3. Read abundances assigned to each DNA source interpretation category for each siphonophore specimen.**

**Table S4. Read abundances assigned to each DNA source interpretation category for each siphonophore specimen by barcode.**

**Table S5. Read abundances assigned to each OTU broad taxon for each siphonophore species.**

**Table S6. Read abundances assigned to each OTU broad taxon for each siphonophore species by barcode.**

**Table S7. Read abundances assigned to each OTU broad taxon for each siphonophore specimen.**

**Table S8. Read abundances assigned to each OTU broad taxon for each siphonophore specimen by barcode.**

**Table S9. Read abundances assigned to each prey OTU broad taxon for each siphonophore species.**

**Table S10. Read abundances assigned to each prey OTU broad taxon for each siphonophore specimen.**

**Table S11. Read abundances assigned to each prey OTU broad taxon for each siphonophore species by barcode.**

**Table S12. Read abundances assigned to each prey OTU broad taxon for each siphonophore specimen by barcode.**

**Table S13. Number of unique sequences assigned to each barcode in each DNA source interpretation category.**

**Table S14. Number of unique sequences assigned to each OTU broad taxon.**

**Table S15. Specimen collection metadata and Yale Peabody Museum catalog numbers for voucher specimens.**