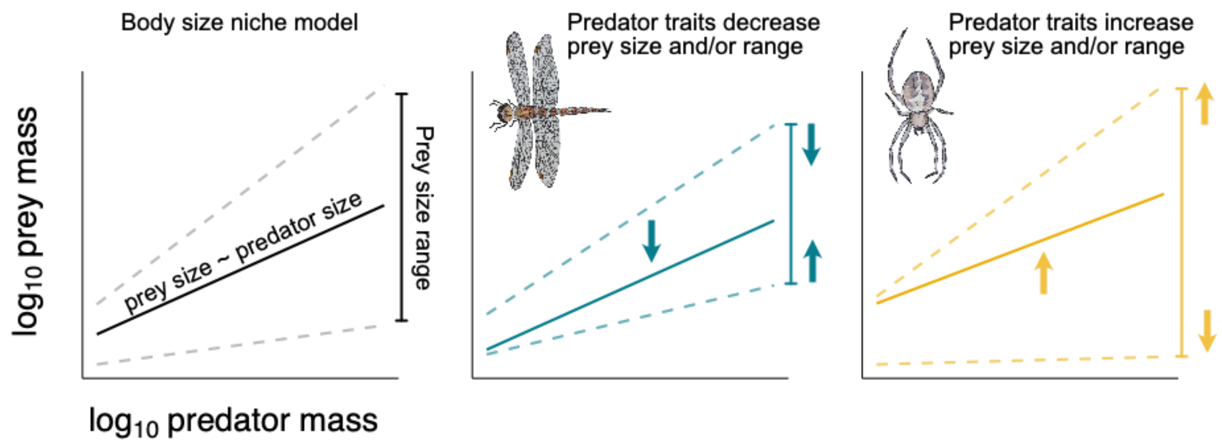
Supplementary Figures

Figure 1: conceptual of the niche model



Predator traits can lower or raise the linear relationship between predator size and prey size. These traits may also increase or decrease the range of prey sizes available to a predator. These traits may include: gape limitation, tool use (e.g. webs or venom), hunting strategy, and locomotion, among others (e.g. Brose et al. 2019, Laigle et al.)

Table 1: Table: samples and sequencing run

Species and sample sizes by sequencing run		
Species	Individuals	Run
Heteropoda venatoria	39	a
Neoscona theisi	24	a
Scytodes longipes	7	a
Geophilomorpha	12	b
Phisis holdhausi	42	b
Smeringopus pallidus	13	b
Euborellia annulipes	18	c
Oonopidae	4	c
Pantala flavescens	9	c
Heteropoda venatoria	14	d

Table 2: Prey Class, Order, and Family taxonomies.

Class	**Order**	**Family**
Arachnida	Araneae	Araneidae
Arachnida	Araneae	Oxyopidae
Arachnida	Araneae	Pholcidae
Arachnida	Araneae	Salticidae
Arachnida	Araneae	Theridiidae
Arachnida	Sarcoptiformes	Acaridae
Arachnida	Sarcoptiformes	Pyroglyphidae
Arachnida	Sarcoptiformes	Suidasiidae
Chilopoda	Geophilomorpha	Mecistocephalidae
Collembola	Entomobryomorpha	Entomobryidae
Collembola	Entomobryomorpha	Isotomidae
Collembola	Symphypleona	Bourletiellidae
Collembola	Symphypleona	Sminthuridae
Insecta	Blattodea	Blaberidae
Insecta	Blattodea	Blattidae
Insecta	Blattodea	Ectobiidae
Insecta	Coleoptera	Coccinellidae
Insecta	Coleoptera	Curculionidae
Insecta	Coleoptera	Elateridae
Insecta	Coleoptera	Hydrophilidae
Insecta	Coleoptera	Staphylinidae
Insecta	Dermaptera	Anisolabididae
Insecta	Diptera	Agromyzidae
Insecta	Diptera	Calliphoridae
Insecta	Diptera	Cecidomyiidae
Insecta	Diptera	Ceratopogonidae
Insecta	Diptera	Chloropidae
Insecta	Diptera	Culicidae
Insecta	Diptera	Dolichopodidae
Insecta	Diptera	Limoniidae
Insecta	Diptera	Lonchaeidae
Insecta	Diptera	Phoridae
Insecta	Diptera	Platystomatidae
Insecta	Diptera	Psychodidae
Insecta	Diptera	Sciaridae
Insecta	Diptera	Stratiomyidae

Insecta	Hemiptera	Aleyrodidae
Insecta	Hemiptera	Coccidae
Insecta	Hemiptera	Pseudococcidae
Insecta	Hymenoptera	Eulophidae
Insecta	Hymenoptera	Evaniidae
Insecta	Hymenoptera	Formicidae
Insecta	Lepidoptera	Agonoxenidae
Insecta	Lepidoptera	Crambidae
Insecta	Lepidoptera	Erebidae
Insecta	Lepidoptera	Tineidae
Insecta	Odonata	Libellulidae
Insecta	Orthoptera	Acrididae
Insecta	Orthoptera	Mogoplistidae
Insecta	Orthoptera	Tettigoniidae
Insecta	Psocoptera	Ectopsocidae
Insecta	Psocoptera	Lepidopsocidae
Insecta	Psocoptera	Liposcelididae
Insecta	Psocoptera	Myopsocidae
Insecta	Thysanoptera	Thripidae
Malacostraca	Isopoda	Philosciidae

Figure: Phylogenetic tree of prey items

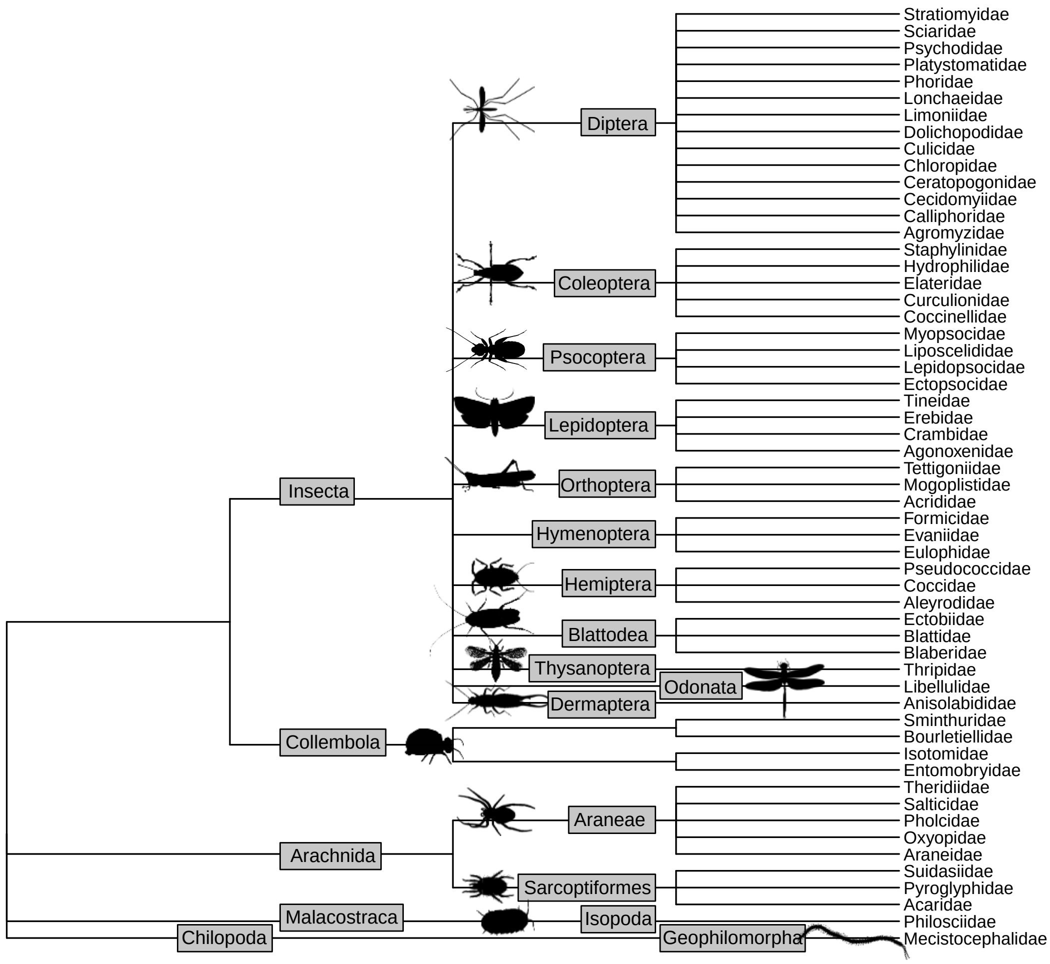
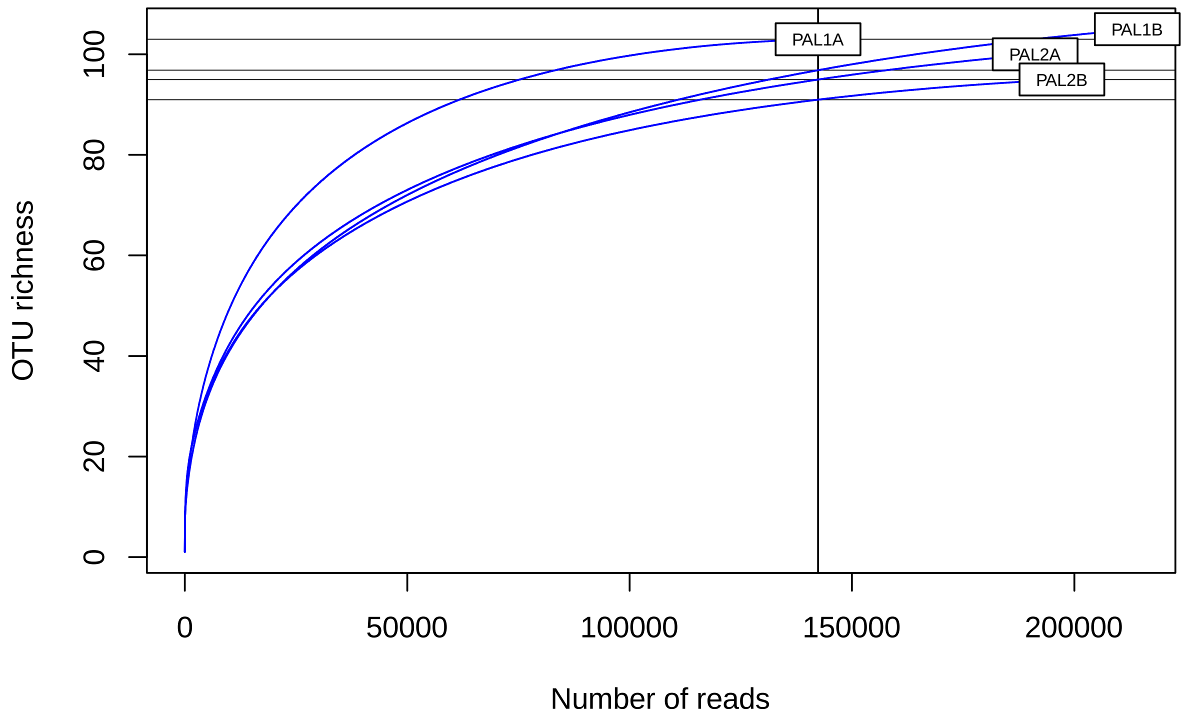


Table 3: Samples and body sizes

Species size statistics			
Species	Min Size (mg)	Max Size (mg)	Mean Size (mg)
Oonopidae	0.2	0.5	0.4
Neoscona theisi	0.5	24.2	9.4
Geophilomorpha	2.6	28.4	11.3
Scytodes longipes	1.1	40.7	13.2
Euborellia annulipes	0.4	53.4	15.4
Smeringopus pallidus	8.5	28.2	16.2
Phisis holdhausi	4.1	78.5	33.1
Pantala flavescens	151.1	259.8	205.7
Heteropoda venatoria	1.3	929.0	280.8

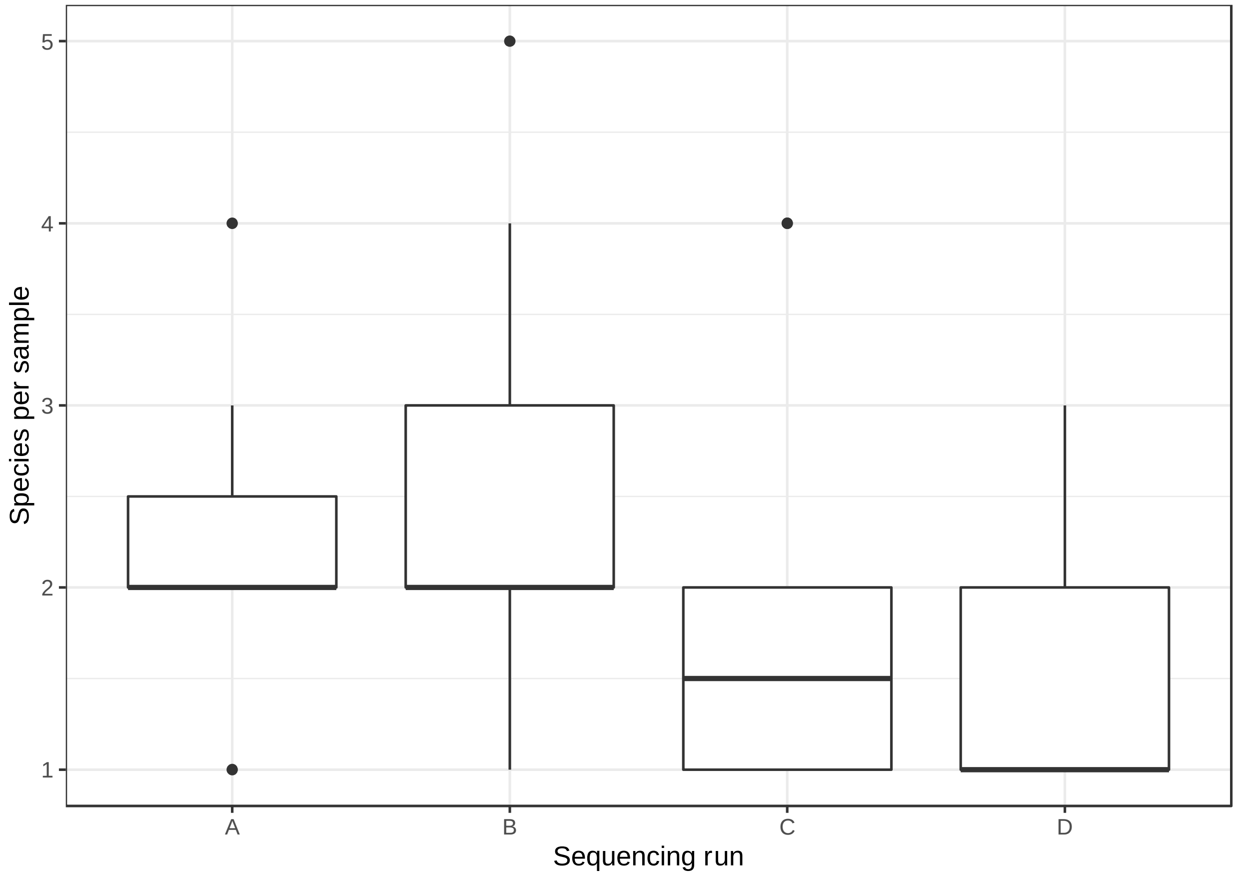
Figure 2: Sequencing depth of initial four samples rarefaction



We initially determined how many samples per sequencing run based on a MiSeq Nano run with four samples. From this, we determined that samples needed to be sequenced to a depth of roughly 140,000 reads to capture full OTU diversity. Thus, we based the number of samples per run (roughly 100) based on this optimal sequencing depth per sample.

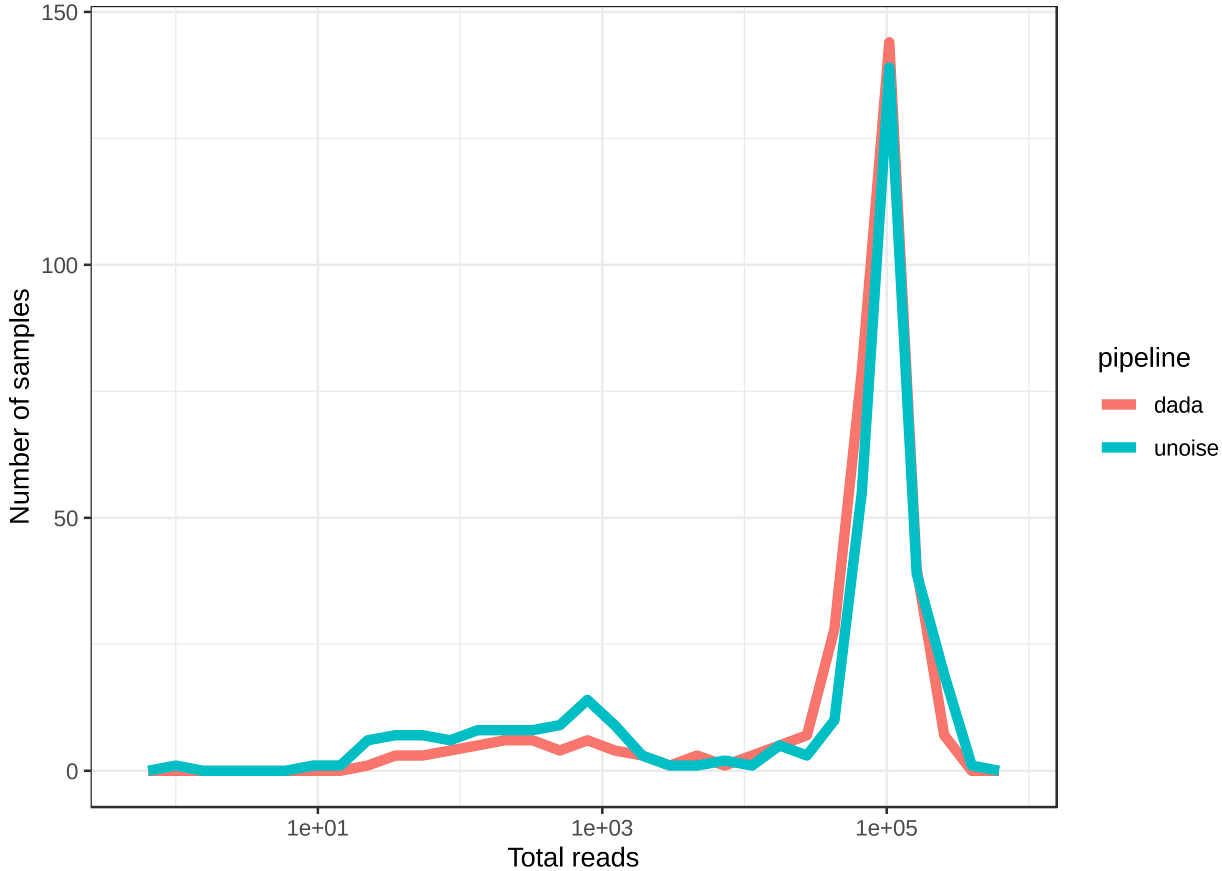
Figure 3: Run-to-run variation in ASV number and diet family number

Quantifying cross-run variation



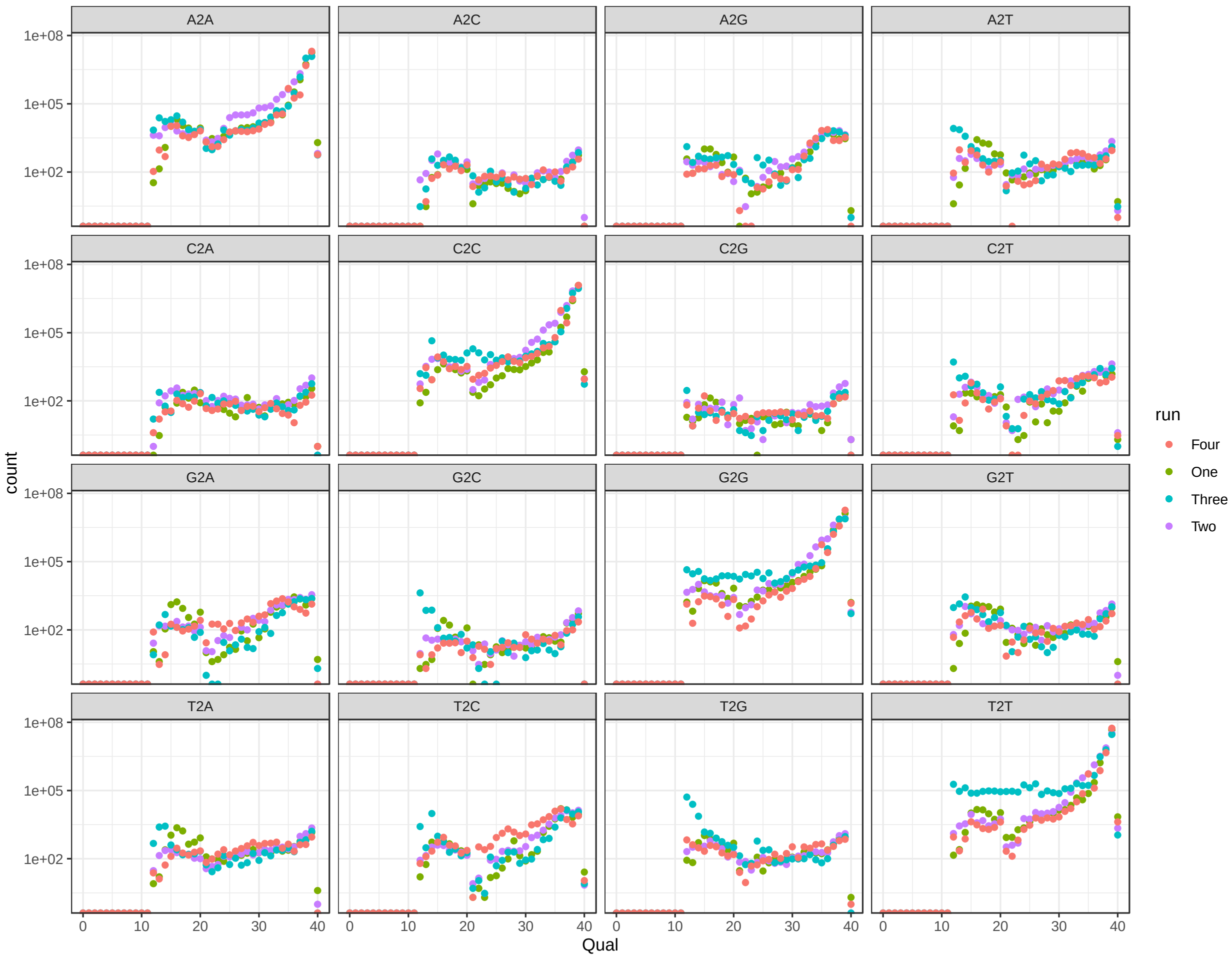
There was significant cross-run variation, with significant differences (pair-wise differences between runs with p-value ≤ 0.05) between run 1-4, 2-3, and 2-4. On average, samples had: A: 2.26 ± 0.15, B: 2.33 ± 0.24, C: 1.72 ± 0.23, and D: 1.44 ± 0.15 species in each sample. Because each species was run on a sequencing run with all other individuals from that species and because we did not compare species richness as a response variable across predator species in this study, we report this as the variation across sequencing runs but do not correct for it in future analyses.

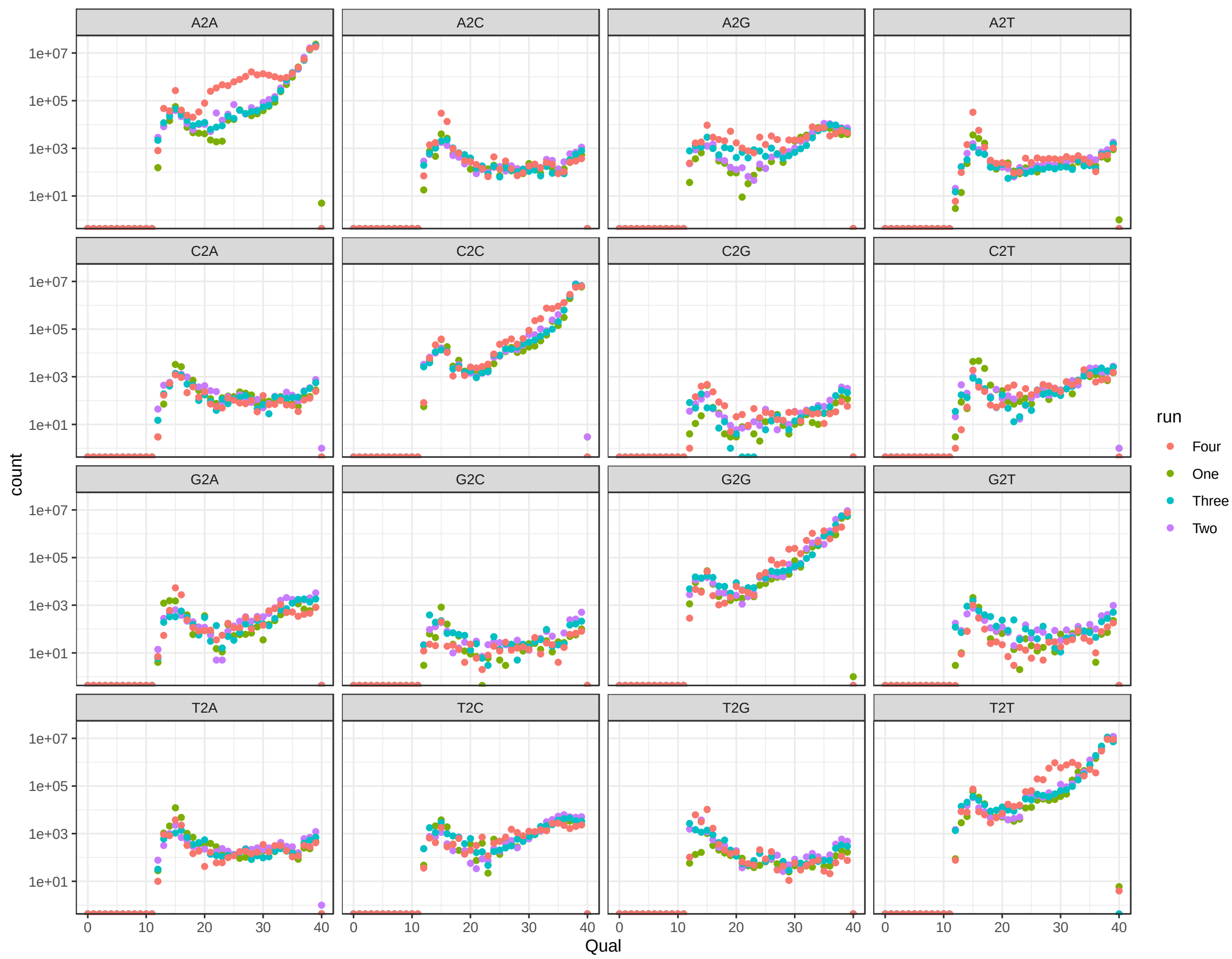
Figure 4: Dada2 vs UNOISE3 – histogram



We compared the reads assigned using both the DADA2 and UNOISE3 algorithms. DADA2 produced more samples with high read abundances than UNOISE3 and so we used this denoising algorithm for this study.

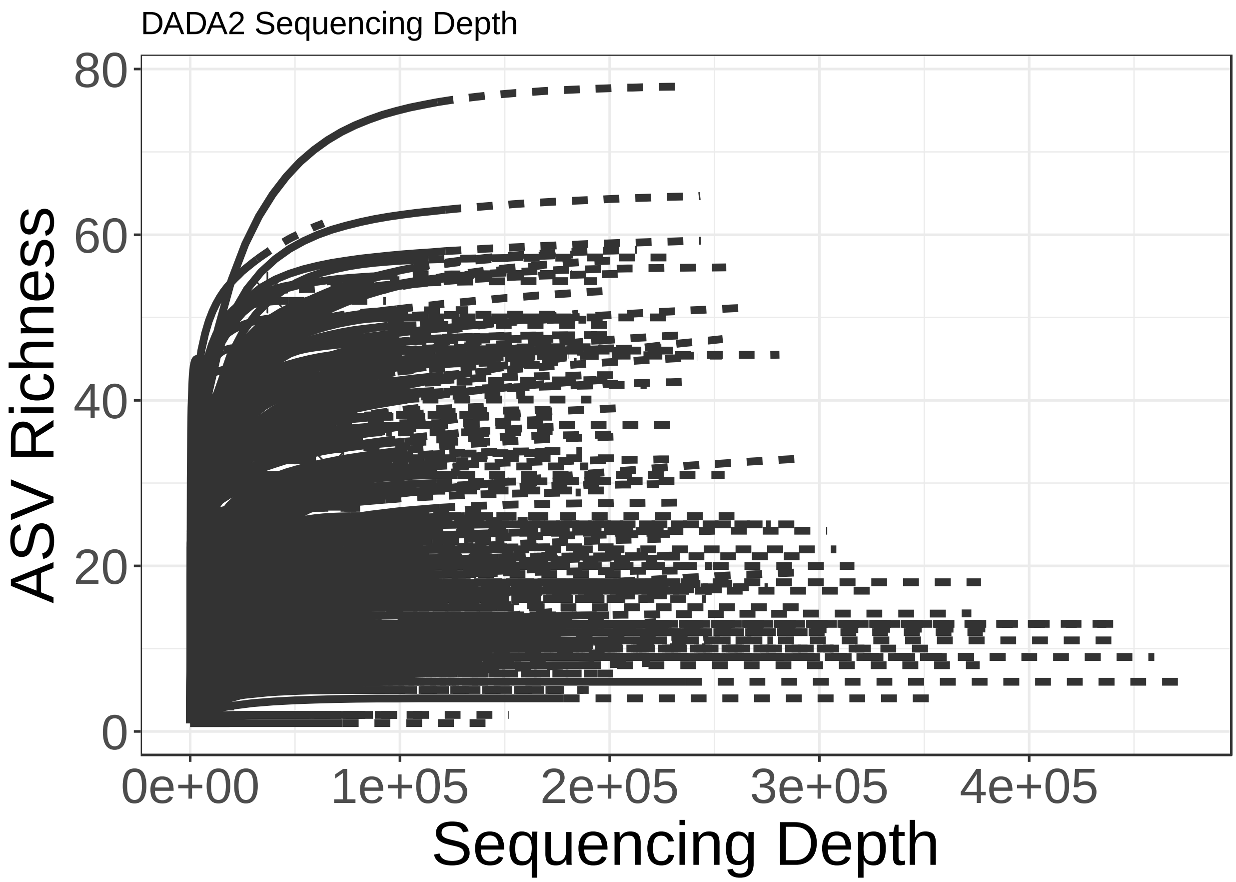
Figure 5: DADA2 – cross-run errors





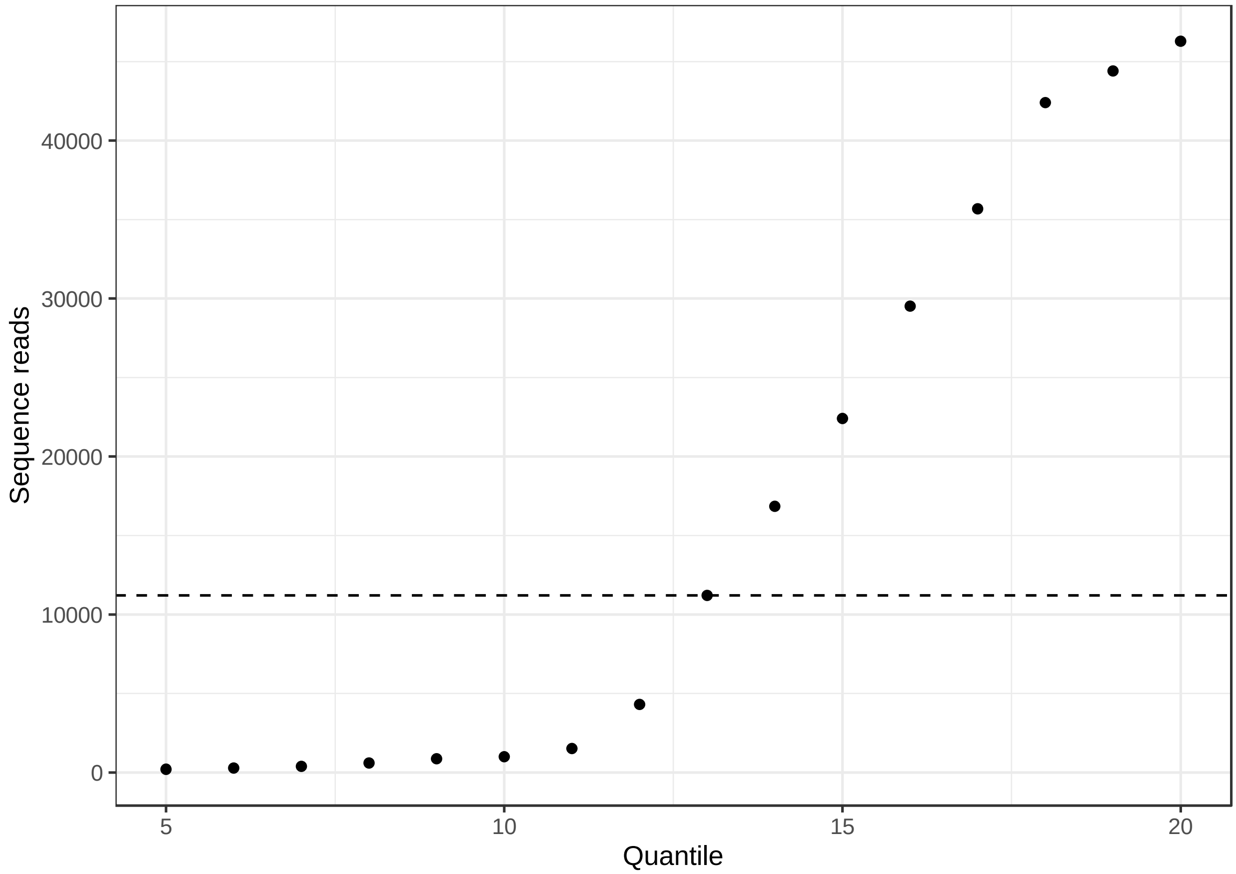
We ran DADA2 on samples across all four runs simultaneously and verified that error rates were similar (above figures) across all runs before doing so.

Figure 6: Sequencing depth across samples



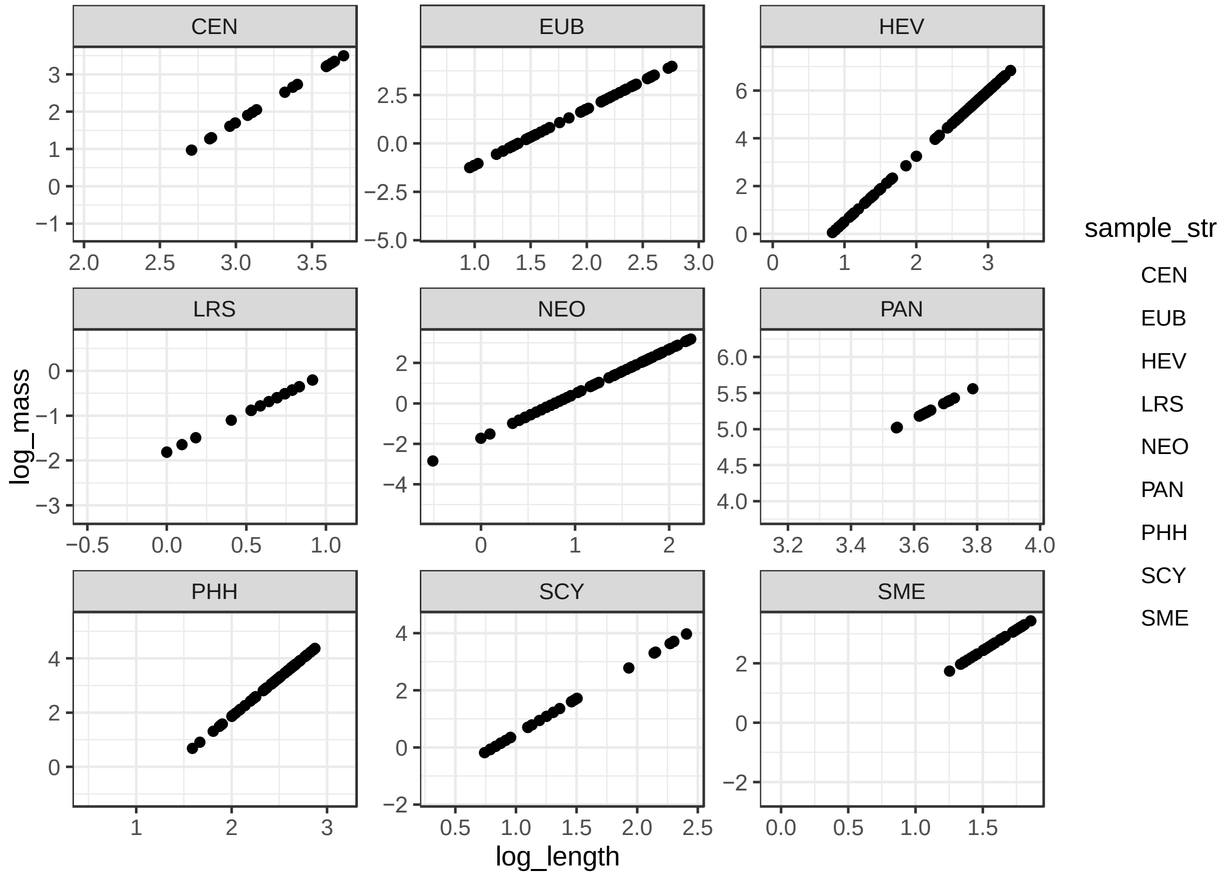
Samples can be sequenced at wide ranges of sequencing depths (10,000 – 100,000 for the current study). We used these sequencing depths to determine which samples had been sequenced below a threshold after which the data from them was incomplete compared to samples that had been sequenced with greater depth.

Figure 7: Inflection point of quantiles of sequencing depth graph



Based on varying sequencing depths from above, we determined the quantiles of sequencing depths and removed all samples from analyses below the lowest quantile with the highest difference between it and the next quantile (at increments of 0.01). This was determined to be the 13th quantile and a sequencing depth below 11,211. All samples with sequencing depths below this threshold were removed from further analyses.

Figure 8: Mass-length relationships by species table and graph



We predicted the mass of predators in this study based on mass-length relationships from predators from Palmyra Atoll and the literature. Plotted are each species' log_{10}-log_{10} mass-length relationships, with the lines and black dots indicating predicted values for predator individuals in this study and the grey background dots the distributions of those predators used to build those models. This model had a significant by-species slope and R^2_m = 0.62 and R^2_c = 0.95.

Table 3: Model outputs for size model

Model selection of predator-prey size linear model						
log10 Predator mass	Predator species	log10 Predator mass*Predator species	df	logLik	AICc	delta
0.41	+	NA	12	−710.04	1,445.04	0.00
−0.46	+	+	20	−702.38	1,447.41	2.37
NA	+	NA	11	−719.36	1,461.52	16.49
0.27	NA	NA	4	−758.61	1,525.34	80.30
NA	NA	NA	3	−764.52	1,535.12	90.08

SI Figure: Size distribution for predators in CCA analysis