

Supplementary Materials: Environmental DNA and Video Surveys of Seamounts and Coral Reefs Reveal Biomass Oases on Shallow Seamounts

Supplementary Section S1: General data description

Table S1: BRUVS and eDNA samples collected on 5 different environments: coral reefs (15 m), seamounts (50 m), continental slopes (150 m), seamounts (250 m) and seamounts (500 m).

Environment	Site name	Latitude	Longitude	Summit depth (m)	Summit height (m)	eDNA	BRUVS		
						Sample size	Sample depth range (m)	Sample size	Sample depth range (m)
Coral reef	Noumea	-22.29341	166.2149	-	-	6	10.6 - 14.3	13	8.8 - 14
	St Vincent	-22.05113	165.9717	-	-	6	10.9 - 13.9	14	5.5 - 15
	Bourail	-21.68457	165.4693	-	-	6	2.5 - 19.5	15	1.9 - 23.4
	Nepoui	-21.39059	164.928	-	-	6	4.6 - 18.9	16	3.2 - 19.8
	Gatope	-20.9797	164.5894	-	-	6	6.7 - 19.7	15	4.4 - 22
	Poum	-20.36597	163.9297	-	-	6	7.7 - 16.6	16	7.1 - 20
	Grand Lagon Nord	-19.41589	163.2245	-	-	6	20 - 22.5	14	18 - 28
Seamount_50	Torche	-22.87503	167.6631	45	1318	10	45 - 58	5	47 - 62
	Antigonia	-23.42824	168.0752	54	1330	10	54 - 70	8	56 - 66
	Capel	-25.03758	159.5323	60	3054	10	60 - 70	10	65 - 69
	Fairway	-21.04964	162.255	62	2964	10	62 - 67	10	63 - 67
Deep slope_150	St Vincent	-22.12531	166.0376	-	-	10	80 - 219	7	120 - 180
	Nepoui	-21.42488	164.9774	-	-	10	88 - 218	10	105 - 150
	Poum	-20.15007	163.7853	-	-	10	100 - 185	8	100 - 220
	Grand Lagon Nord	-19.45239	163.2159	-	-	10	85 - 235	10	118 - 150
Seamount_250	Crypthelia	-23.3078	168.2498	195	1627	10	201 - 236	9	200 - 244
	Kaimon Maru	-24.74137	168.1411	236	1799	10	238 - 325	8	238 - 340
	Jumeau Ouest	-23.68215	168.0081	239	1119	10	242 - 313	8	245 - 339
	Argo	-23.09286	159.463	299	2251	10	299 - 313	8	301 - 312
Seamount_500	Stylaster	-23.6461	167.7134	434	801	10	439 - 488	8	444 - 491
	Ile Des Pins	-22.38325	167.407	470	818	10	469 - 488	5	480 - 506
	Eponge	-24.91183	168.363	511	1932	10	518 - 570	7	520 - 552

Table S2: Environmental variables used in the BRT modelling of species richness, fish biomass and large predator biomass for BRUVS, and eDNA MOTU richness. BRUVS micro-habitat variables were extracted through a semi-quantitative scale. Micro-habitat covers were evaluated on a 0-100% at a 5% precision. Substrate complexity and topography were evaluated on a scale of 0 to 5 and transformed in percentages. These variables were then used to calculate the Shannon diversity indices used in the boosted regression tree modelling.

Variable name	Description	Use in BRTs	Reference	Source
Depth	Depth value taken on the ship's echo sounder	Used	(Priede et al. 2013; Letessier et al. 2019)	Ship
Habitat diversity (BRUVS only)	Shannon diversity indice on percentages of visually evaluated habitat features (Bare substrate, vegetation, filter feeders, coral, indetermined, sand, gravel, rubbles, rocks, reef structure, substrate complexity, topography)	Used	(Eduardo et al. 2018; Sih et al. 2019)	BRUVS still images
Turbidity	Visually evaluated in four categories (Clear, Particulate, Turbid, Very turbid)	Used	(Baletaud et al. 2022)	BRUVS still images
Travel time	Time to travel from Noumea's center using the shortest path	Used	(Maire et al. 2016)	(Maire et al. 2016)
Chl-a concentration	Chlorophyll concentration in milligram.m3	Removed (correlated)	(Leitner et al. 2020)	https://resources.marine.copernicus.eu/product-detail/OCEANCOLOUR_GLO_CHL_L4_REP_OBSERVATIONS_009_082/INFORMATION
Seafloor temperature	Seafloor potential temperature (degree C)	Used	(Tittensor et al. 2010; Woolley et al. 2016)	https://resources.marine.copernicus.eu/product-detail/GLOBAL_REANALYSIS_PHY_001_030/INFORMATION
Minimal SST	Average sea surface temperature of the coldest month of each year over the last 10 years (degrees C).	Removed (correlated)	(Tittensor et al. 2010)	https://podaac.jpl.nasa.gov/dataset/MUR-JPL-L4-GLOB-v4.1

Mean SST	Average temperature over the last 10 years (degrees C)	Used	(Tittensor et al. 2010)	https://podaac.jpl.nasa.gov/dataset/MUR-JPL-L4-GLOB-v4.1
Maximal SST	Average temperature of the hottest month of each year over the last 10 years (degrees C).	Removed (correlated)	(Tittensor et al. 2010)	https://podaac.jpl.nasa.gov/dataset/MUR-JPL-L4-GLOB-v4.1
Suspended particulate matter	Inorganic suspended particulate matter (g/m3)	Removed (correlated)	(Capblancq 1990)	https://resources.marine.copernicus.eu/product-download/OCEANCOLOUR_GLO_OPTICS_L4_REP_OBSERVATIONS_009_081
Salinity	Salinity (10 ⁻³)	Removed (correlated)	(Barletta et al. 2005)	https://resources.marine.copernicus.eu/product-detail/GLOBAL_REANALYSIS_PHY_001_030/INFORMATION
Eastward velocity	Eastward velocity (m.s-1)	Used	(Rogers 2018)	https://resources.marine.copernicus.eu/product-detail/GLOBAL_REANALYSIS_PHY_001_030/INFORMATION
Northward velocity	Northward velocity (m.s-1)	Used	(Rogers 2018)	https://resources.marine.copernicus.eu/product-detail/GLOBAL_REANALYSIS_PHY_001_030/INFORMATION
Environnemental stratum	Coral reef, continental slope (150 m), seamount (50 m), seamount (250 m), seamount (500 m)	Used	This study	Method

Supplementary Section S2: Imputing missing length data on BRUVS

Due to the random nature of fish behavior, all individually counted fish could not be measured. When possible, each species on each BRUVS was measured up to its abundance level to a limit of ten individuals to optimize processing time. A total of 3369 individual measures were used, from 281 out of the 443 (63%) species. Averaging the individual measures per species per BRUVS yielded 1315 averaged lengths. 2009 remaining lengths of species on different BRUVS were therefore imputed using the random forest algorithm and the *missForest* v1.4 R (Stekhoven & Buhlmann 2012) package with 999 trees. Lengths were estimated based on measured lengths when the species presented other records, but also family, genus, and maximum size and size type from FishBase (<https://www.fishbase.se>). Latitude and longitude of available lengths of species were also used to account for geographic proximity of existing lengths. The *missForest* accuracy was tested with a k-fold cross validation procedure by predicting 5% of the lengths each time by training the *missForest* on the 95% left of the data and look at the linear fit between the original and predicted value. Results showed a mean R^2 of 0.82 (SD ± 0.07) between the measured and predicted lengths of the *missForest* model (Fig. S2).

As we did not seek highly accurate length structure among replicates but rather the general pattern of lengths and then biomass between assemblages among our stratum, we considered the imputed values exploitable with an average r^2 of 0.84. We also ensured that imputed length did not exceed Fishbase's max reported length.

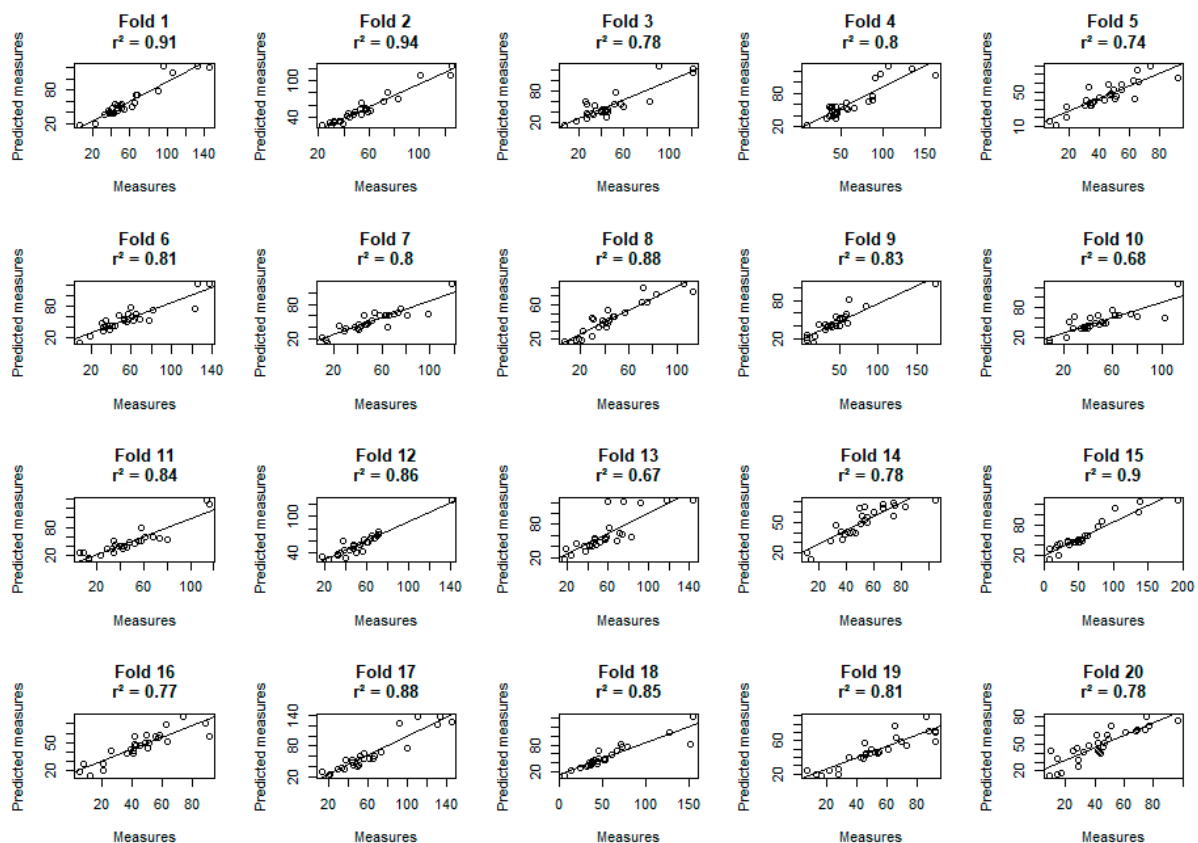


Figure S1: Predicted against true measures of fish for each of the twenty-fold cross-validation results from the 5% artificial imputation using *missForest* out of the 792-measurement data.

Supplementary Section S3: Boosted regression trees on richness, biomass and biomass of large predators

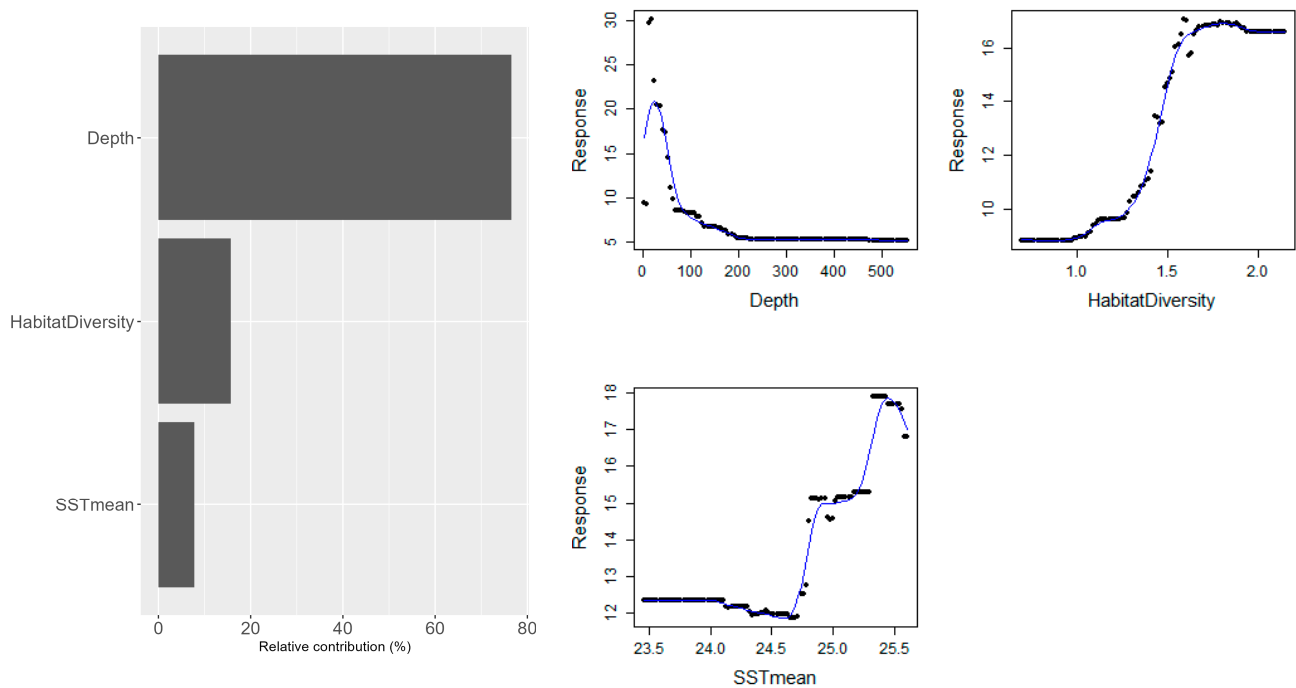


Figure S2: Variable importance and partial dependence plots from boosted regression trees ran on the reduced number of variables on BRUVS data with richness as the predicted value (response). Cross validation correlation value was 0.89 for this model.

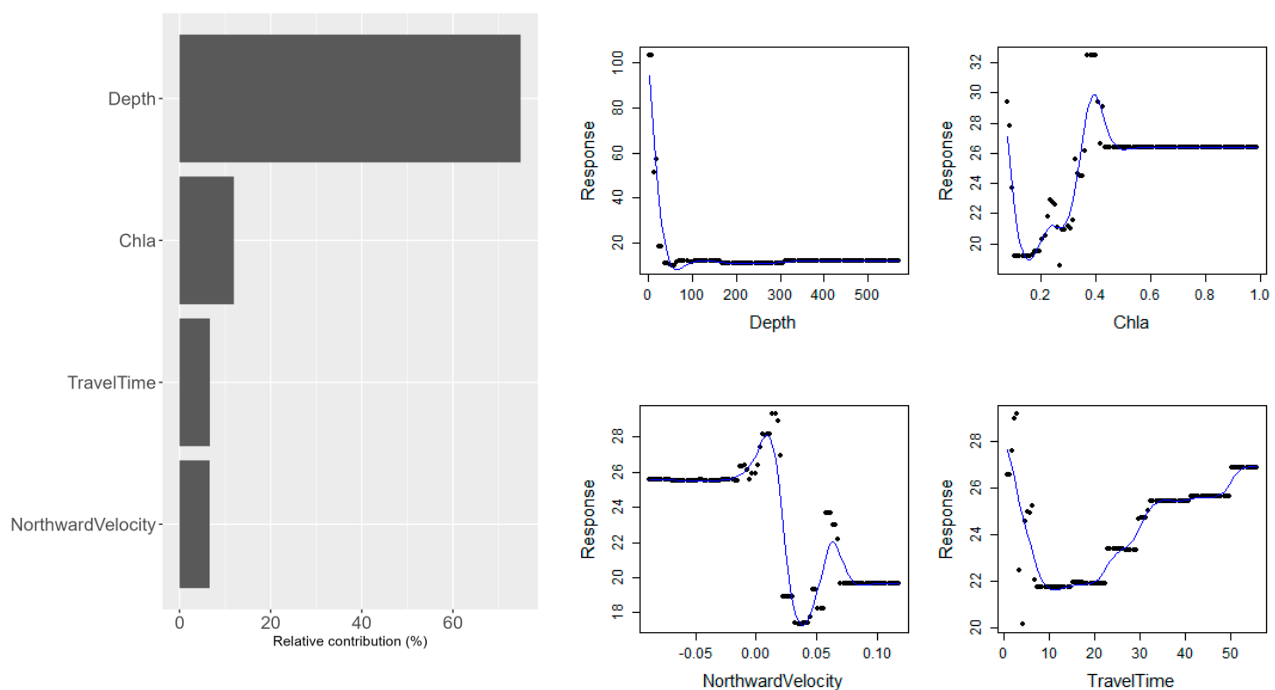


Figure S3: Variable importance and partial dependence plots from boosted regression trees ran on the reduced number of variables through previous boosted trees run on eDNA data with MOTU richness as the predicted value (response). Cross validation correlation value was 0.86 for this model.

Figure S4: Variable importance and partial dependance plots from boosted regression trees ran on the reduced number of variables through previous boosted trees run on BRUVS data with biomass as the predicted value (response). Cross validation correlation value was 0.71 for this model

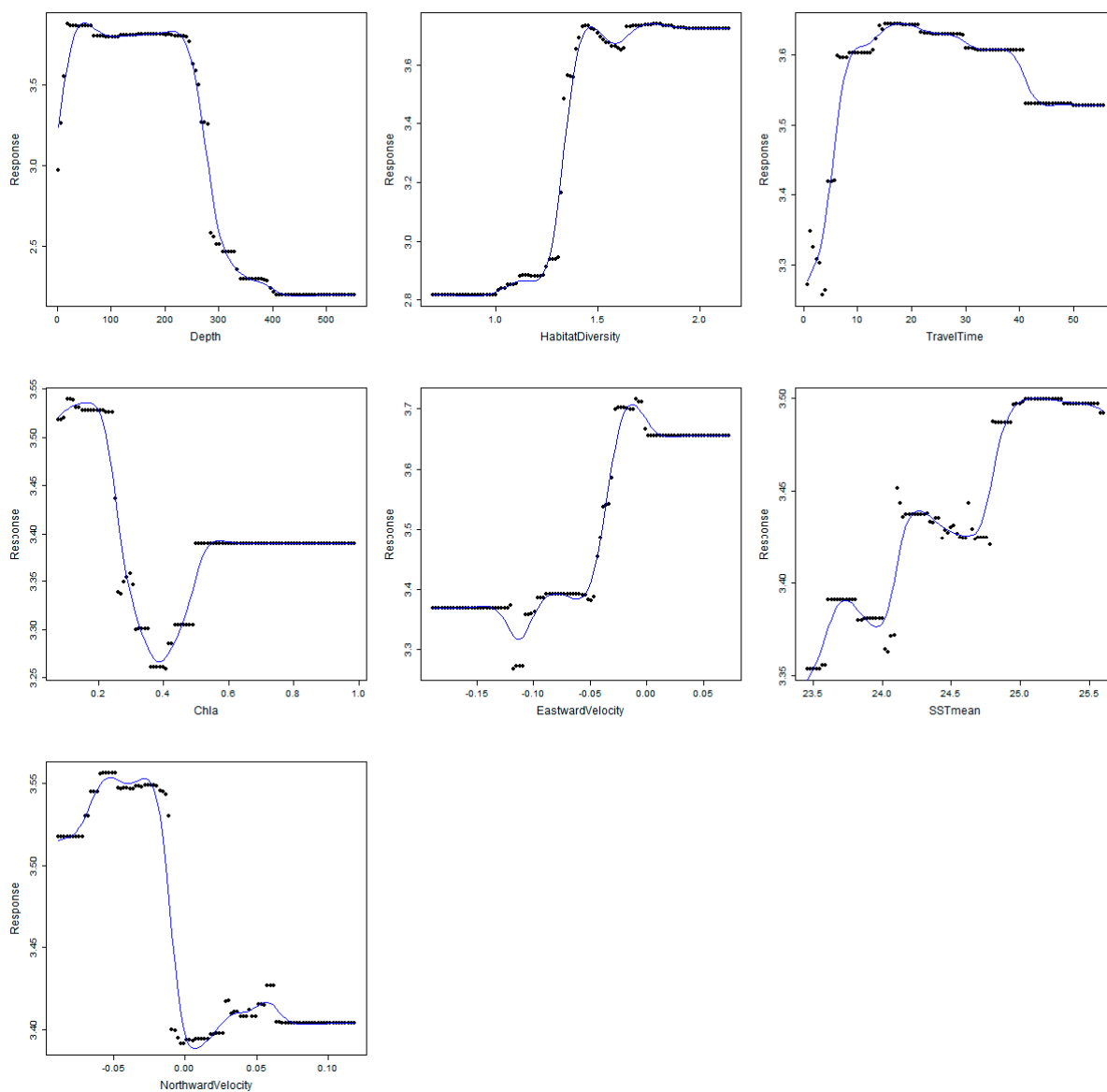
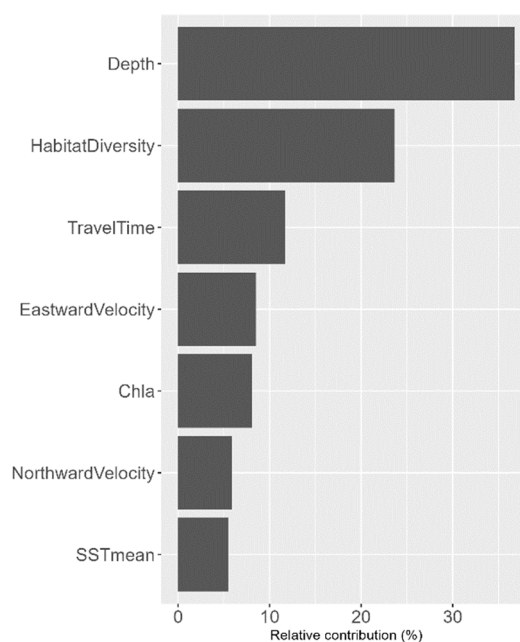
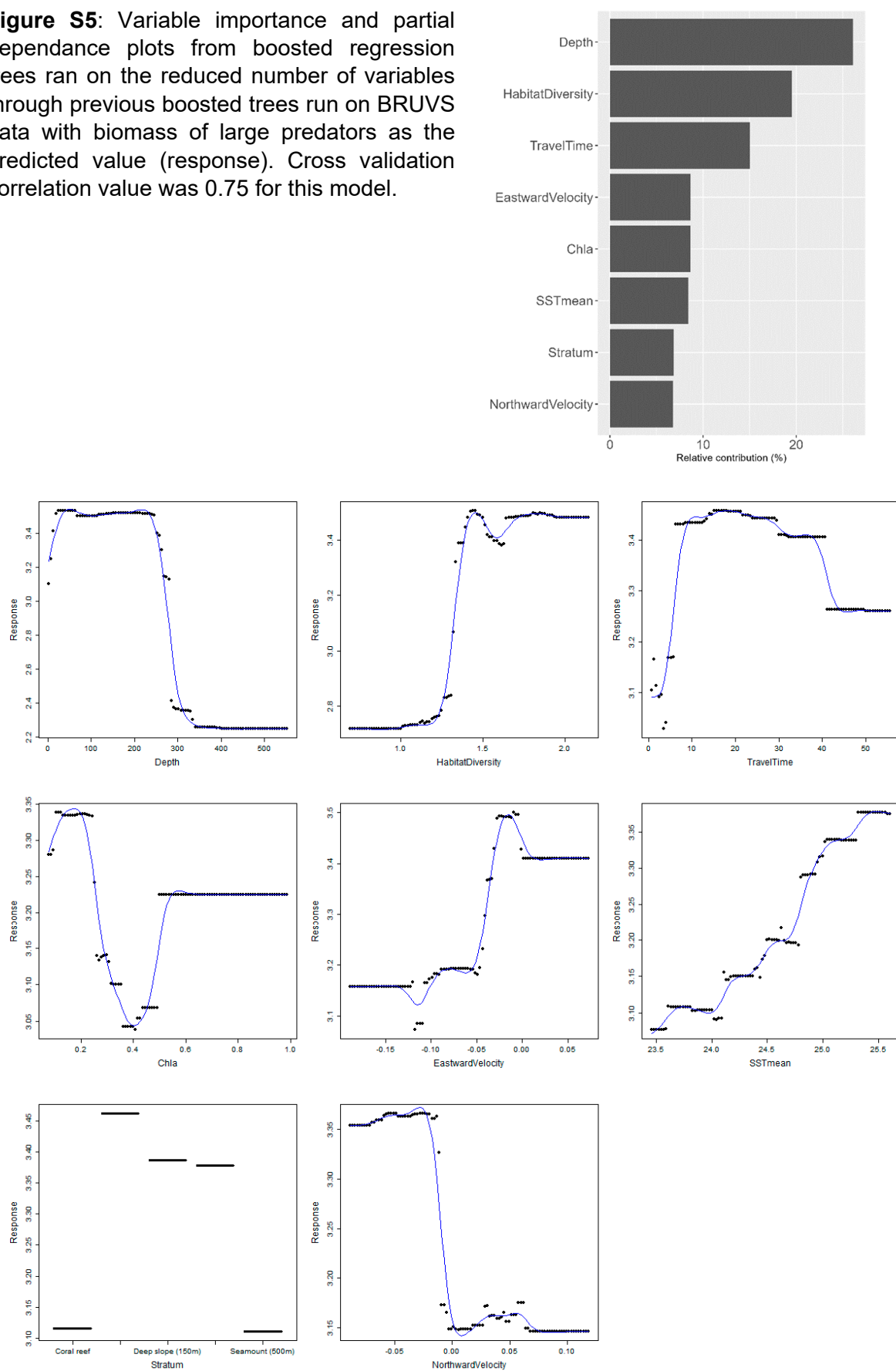


Figure S5: Variable importance and partial dependance plots from boosted regression trees ran on the reduced number of variables through previous boosted trees run on BRUVS data with biomass of large predators as the predicted value (response). Cross validation correlation value was 0.75 for this model.



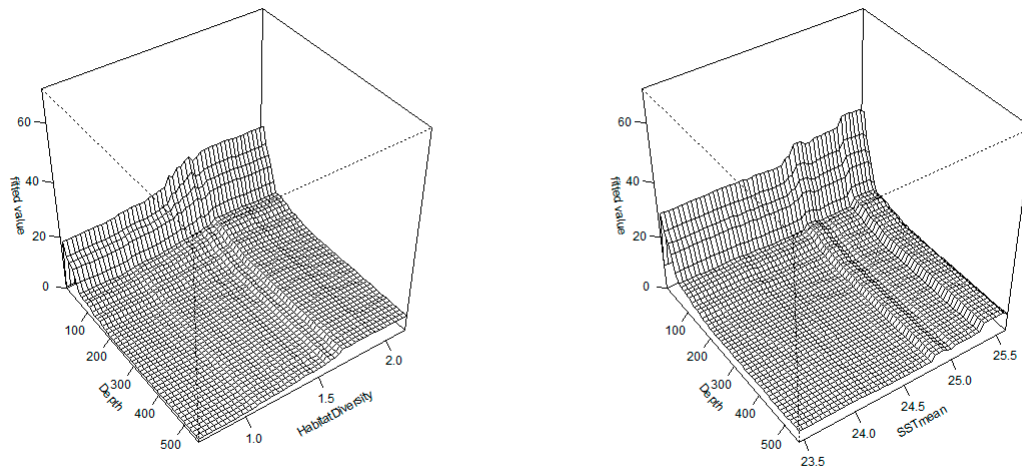


Figure S6: Interaction plots found from boosted regression trees run on the reduced number of variables on BRUVS data with richness as the predicted value (fitted value). Cross validation correlation value was 0.89 for this model.

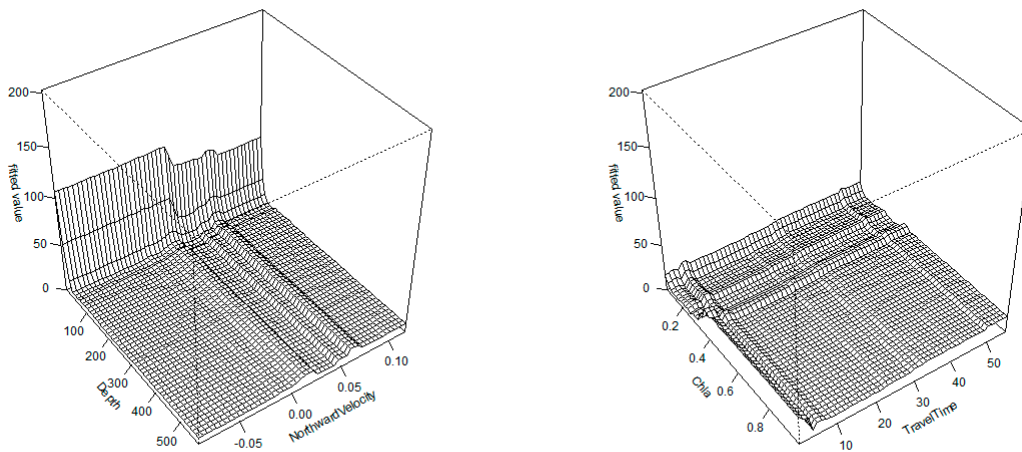


Figure S7: Interaction plots found from boosted regression trees run on the reduced number of variables through previous boosted trees run on eDNA data with MOTU richness as the predicted value (response). Cross validation correlation value was 0.86 for this model.

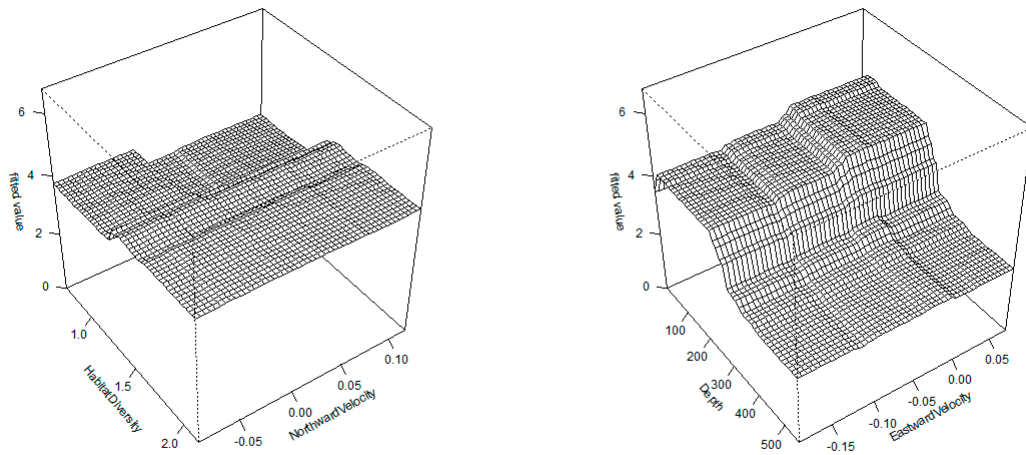


Figure S8: Interaction plots found from boosted regression trees run on the reduced number of variables through previous boosted trees run on BRUVS data with biomass as the predicted value (response). Cross validation correlation value was 0.71 for this model.

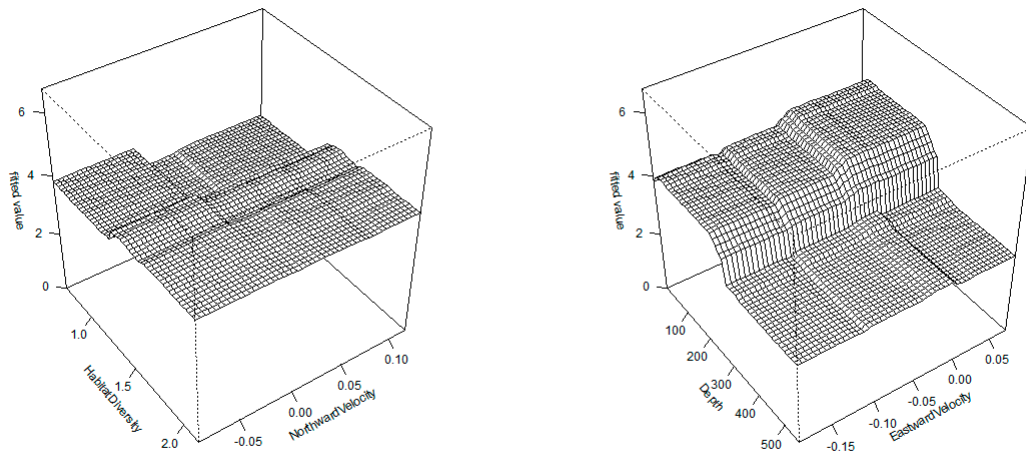


Figure S9: Interaction plots found from boosted regression trees run on the reduced number of variables through previous boosted trees run on BRUVS data with biomass of large predators as the predicted value (response). Cross validation correlation value was 0.75 for this model.

Supplementary Section S4: Assemblage ordination

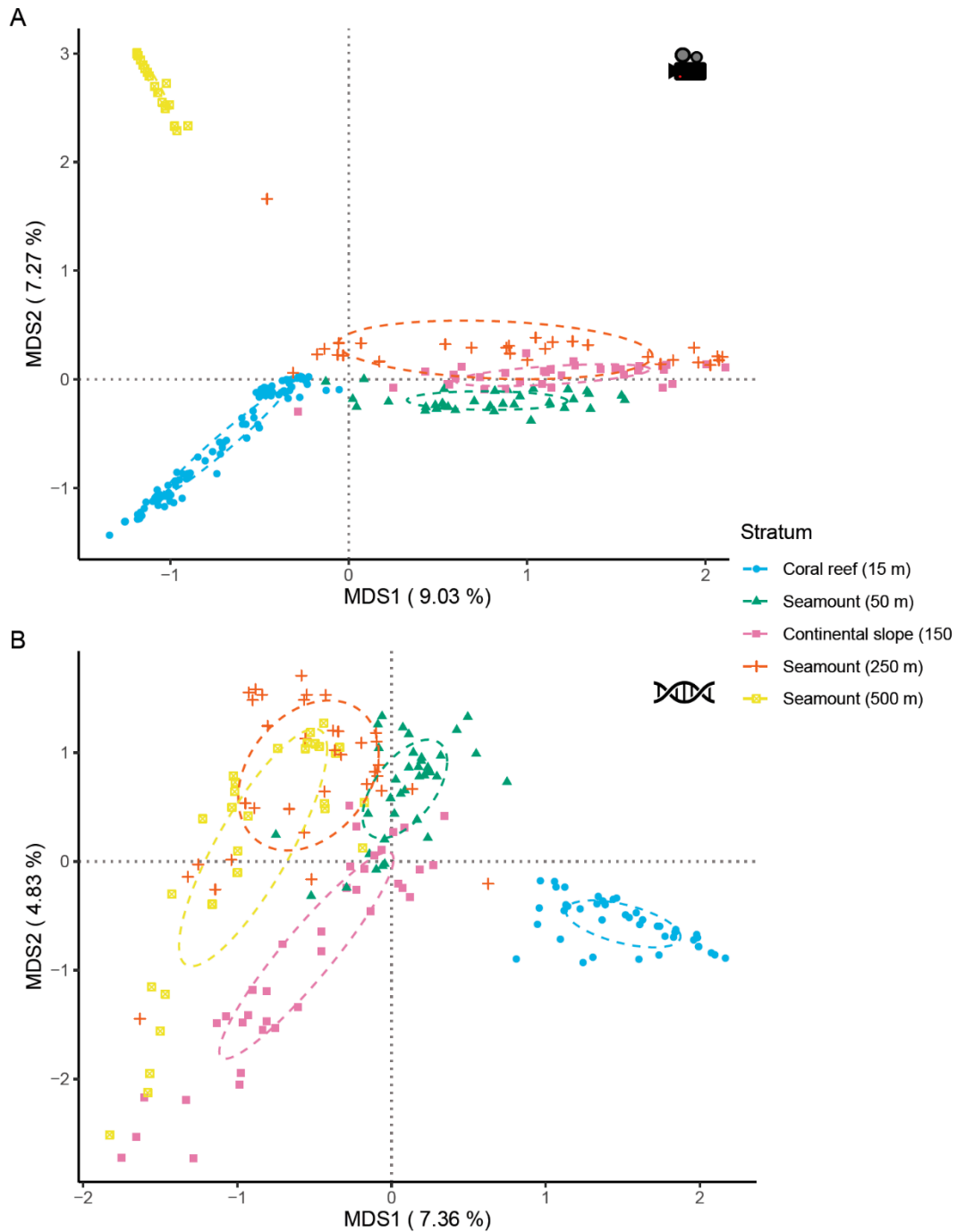


Figure S10: Ordination using Principal Coordinate Analysis (PCoA) on the Hellinger transformed distance matrix of baited remote underwater video stations (BRUVS) abundance data (A) and presence-absence environmental DNA (eDNA) data (B). Ellipses were calculated from the covavariance matrix of each stratum weighted by the number of points.

Supplementary Section S5: sharing of eDNA sequences among the environmental strata

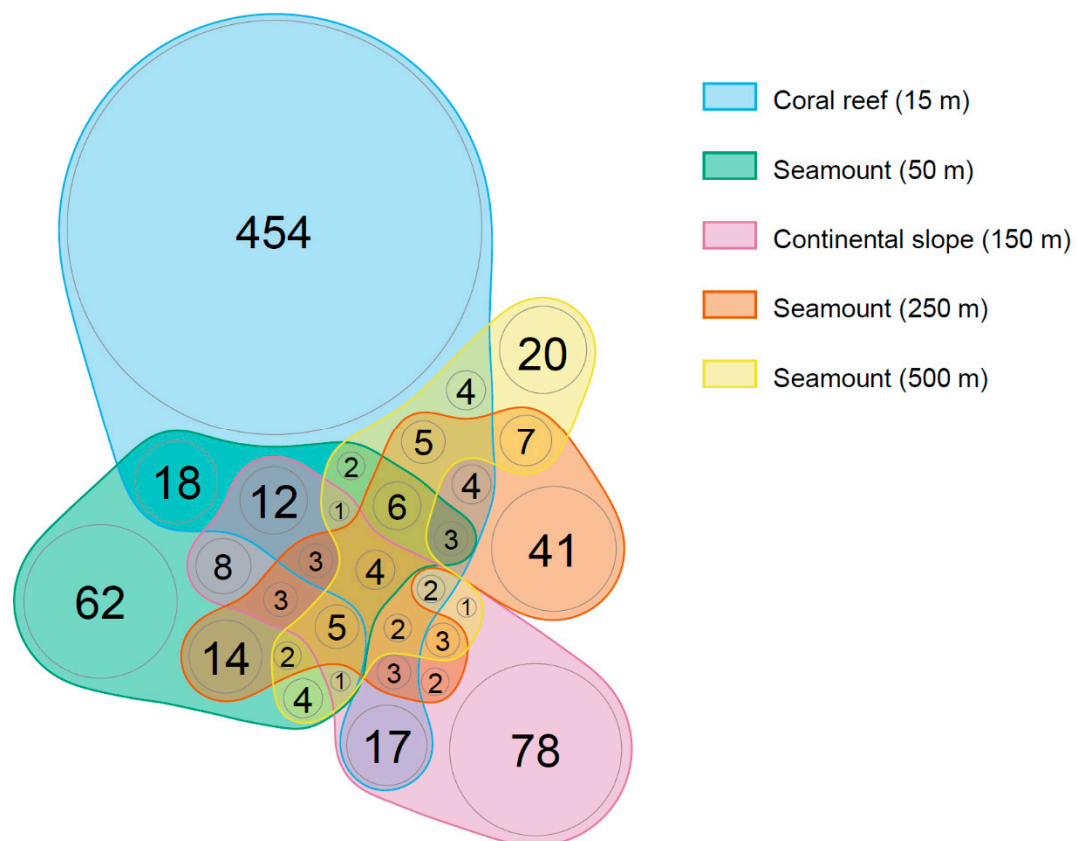


Figure S11: Euler diagram of identified MOTUs from eDNA metabarcoding along 5 environmental strata: coral reefs, seamounts of variable summit depths and continental slopes.

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