

1 **Supporting information: Appendix**

2 **Tests for robustness of the richness-biomass relationship.** Because our results are based on
3 observational data, establishing causality of the diversity-biomass relationship faces the
4 challenge that richness estimates depend inherently on sample size (number of individuals). We
5 took several measures to evaluate the importance of this effect and minimize it. Most
6 importantly, our estimates of species richness based on sample coverage (1) rigorously account
7 for this dependence, allowing comparisons among samples with different numbers of
8 individuals. To test whether any residual correlation between abundance and richness estimate
9 remained after this correction we conducted three additional analyses. First, we asked whether
10 the richness-biomass relationship was unduly influenced by small samples (surveys with few
11 fish). We created a new data subset by removing all surveys with fewer than 100 individual fish
12 observed, and reran the global analysis on this subset. Fitting the global hierarchical model to
13 this subset (3873 surveys of 4556 in the complete data set) produced slightly smaller estimates of
14 the effects of species richness (standardized $\beta = 0.172 \pm 0.034$) and functional diversity ($0.178 \pm$
15 0.023) on fish biomass, but these diversity components remained among the strongest predictors.
16 Removal of surveys with fewer than 500 individuals (leaving 2466 surveys) produced a slightly
17 larger estimate of the effect of species richness (0.200 ± 0.042) and a smaller estimate of
18 functional diversity (0.165 ± 0.030). For all of these estimates, $P < 0.001$.

19 A second analysis similarly supported the robustness of the richness effect on biomass.
20 Comparison of the slope of the richness-biomass relationship estimated separately for each
21 ecoregion showed a stronger relationship in ecoregions with fewer individuals but the effect of
22 estimated richness on biomass nevertheless remained positive even where mean abundance per
23 survey approached 10,000 individuals (Fig. 4a).

24 Third, we partially decoupled the influence of survey-level abundance on richness
25 estimates by using regional species pool size as the estimate of richness in predicting biomass.
26 As an estimate of species pool size we used the observed richness within the surrounding
27 ecoregion. Because the validity of this approach depends on a robust estimate of regional
28 richness, we restricted the analysis to a subset of ecoregions with at least 20 surveys each and
29 included only surveys with >50 individual fish. These criteria ensured that the estimated species
30 pool for each ecoregion in the analysis was based on a minimum of 1000 individuals (i.e.,
31 minima of 20 surveys x 50 individuals per survey). Applying these criteria produced a data
32 subset of 1374 surveys (of 4556 total) from 26 ecoregions (of 75 total). Fitting the global model
33 to this data subset produced a standardized estimate of the partial effect of log ecoregion richness
34 on log survey biomass of $\beta = 0.404 \pm 0.130$ ($P = 0.012$). Thus, the estimated effect of ecoregion-
35 level richness on biomass was even stronger than that based on survey-level richness, although
36 the P-value was larger due in part to the 70% reduction in sample size compared with the full
37 data set.

38 Finally, there is some evidence that the relationship between species richness and
39 biomass production differs among scales, with stronger relationships at the regional than local
40 scales (2, 3). To explore this possibility we fit parallel models (same set of predictor variables)
41 using survey data aggregated at site and ecoregion scales. Results were generally quite similar
42 among scales, qualitatively and quantitatively (Fig. 2a-d): fish biomass was affected similarly at
43 both scales by diversity, human population, temperature, and depth.

44 A different challenge in testing the diversity-biomass relationships with observational
45 data stems from the possibility that the relationship reflects a shared correlation with some
46 unmeasured variable. We tested for such spurious correlations in two ways. First, we tested

47 whether the diversity effect on biomass was robust to shared correlations by conducting a
48 random forest analysis with species richness, functional diversity, and 25 other predictors, and
49 found that (coverage-corrected) species richness and functional diversity were the top two
50 predictors (SI Appendix, Fig. S2). Second, our use of hierarchical mixed models accounted for
51 shared correlations by measuring environmental and human-impact variables as well as
52 unexplained spatial variation in biomass by including random terms for marine realm, province,
53 and ecoregion. For example, if a bivariate correlation between richness and biomass was actually
54 driven by effects of temperature on both, then including all three variables in a model should
55 return a strong partial effect of temperature on biomass with no partial effect of richness. As a
56 final check on the robustness of our model we tested whether our final selection of variables
57 influenced the estimated richness effect on biomass by refitting the global model with 0-8
58 environmental predictors (functional diversity was left out to simplify the model interpretation),
59 and each time calculated the partial effect of estimated richness. The number of other predictors
60 had almost no effect on the estimated effect of richness (SI Appendix, Fig. S5a). In summary,
61 one or both components of biodiversity were consistently strong predictors of fish community
62 biomass across latitudes, regions, and trophic levels in all our analyses.

63 Finally, diversity can be modeled as a predictor only for sites where fish are present. All
64 surveys used in our analyses recorded fish, but not all trophic groups and size classes were
65 present on all surveys. Therefore, analyses of specific trophic levels and of large fishes used only
66 subsets of the data. To check whether use of such subsets changed our estimates of the effects of
67 predictors, we fit a second set of models for each trophic level, and for large fishes, that excluded
68 diversity as predictors. This ensured that all surveys were included (even those with no
69 individuals of the group in question); the regression coefficients produced by these models (SI

70 Appendix, Figs. S3b, S6) can be interpreted as quantifying the importance of human population
71 and environmental drivers in influencing both presence/absence and abundance of the focal
72 group. The results show that exclusion of diversity in this way generally had little influence on
73 estimates of human and environmental drivers (compare SI Appendix, Figs. S3a,b, S6). The
74 exceptions were top carnivores and planktivores, which showed stronger forcing by temperature
75 when diversity was excluded (compare Figs. 3a,d; SI Appendix, S6a,d); this can be interpreted to
76 mean that top carnivores and planktivores were present primarily at warmer sites.

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78 **Interactions of diversity with stressors.** We tested whether species richness stabilized reef fish
79 biomass against stressors by fitting separate models that included interactions of species richness
80 with rising temperature, temperature variability, or human impact (population index) (SI
81 Appendix, Table S2). To explore visually the findings (see Results) that high species richness
82 stabilized biomass against rising and variable temperatures, we divided the dataset into sites
83 below (low-richness) and above (high-richness) the median richness value, and fit separate
84 regressions of biomass against mean annual temperature (Fig. 2e,f) and annual temperature range
85 (Fig. 2g,h).

86 A possible alternative hypothesis for the steeper decline in biomass with temperature
87 range in low-richness communities is that sites with higher temperature variability have lower
88 coral cover, and therefore lower fish biomass. To explore this hypothesis we first fit the global
89 model described above with addition of log coral cover, using only tropical sites since coral is
90 absent or low at temperate sites. Log coral cover had no significant partial effect on fish biomass
91 ($\beta = 0. -0.041 \pm 0.039$, $P = 0.291$) when the other predictors were included in the model. We then
92 fit the same model with an interaction between log coral cover and temperature range, to test

93 whether higher temperature range and low coral cover might explain the difference in biomass
94 between low- and high-richness tropical sites. There was no significant interaction between log
95 coral cover and temperature range ($P = 0.660$). Nor was coral cover lower in more thermally
96 variable tropical environments ($P = 0.232$).

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98 **References cited**

- 99 1. Chao A, Jost L (2012) Coverage-based rarefaction and extrapolation: standardizing samples
100 by completeness rather than size. *Ecology* 93(12):2533–2547.
- 101 2. Bond EM, Chase JM (2002) Biodiversity and ecosystem functioning at local and regional
102 spatial scales. *Ecol Letters* 5:467–470.
- 103 3. Chase JM, Leibold MA (2002) Spatial scale dictates the productivity-biodiversity
104 relationship. *Nature* 416(6879):427–430.

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107 **Table S1:** SEM coefficients, standard errors, and P-values for the hierarchical model fit
 108 separately for the global data set, temperate and tropical data sets, individual trophic levels, for
 109 large (> 35 cm) fishes, and using observed rather than estimated richness.

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111 **Table S1a:** Standardized coefficients (scaled by mean and variance) from the global structural
 112 equation model including all fishes. Coefficients correspond to arrow widths in Figure 1a and
 113 Extended Data Figure 1.

Response	Predictor	Estimate	Standard error	P-value
Biomass	Functional diversity	0.230	0.019	0.000
Biomass	log ₁₀ (Estimated richness)	0.189	0.027	0.000
Biomass	Temperature (range)	-0.252	0.037	0.000
Biomass	Depth	0.101	0.015	0.000
Biomass	log ₁₀ (Population index)	-0.164	0.042	0.000
Biomass	Temperature (mean)	0.296	0.090	0.001
Biomass	Salinity	-0.117	0.057	0.041
Biomass	log ₁₀ (Chlorophyll)	0.043	0.033	0.198
Biomass	log ₁₀ (Nitrate)	0.028	0.053	0.589
Biomass	log ₁₀ (PAR)	-0.027	0.073	0.708
Biomass	log ₁₀ (Phosphate)	-0.001	0.058	0.985
Functional diversity	log ₁₀ (Estimated richness)	0.221	0.034	0.000
Functional diversity	Temperature (range)	0.263	0.047	0.000
Functional diversity	Temperature (mean)	0.494	0.133	0.000
Functional diversity	log ₁₀ (Nitrate)	-0.169	0.069	0.014
Functional diversity	log ₁₀ (Phosphate)	0.162	0.074	0.028
Functional diversity	Salinity	0.132	0.076	0.080
Functional diversity	log ₁₀ (Chlorophyll)	0.022	0.043	0.603
Functional diversity	log ₁₀ (Population index)	0.021	0.055	0.704

Functional diversity	Depth	0.005	0.019	0.779
Functional diversity	log ₁₀ (PAR)	0.021	0.094	0.823
log ₁₀ (Estimated richness)	Temperature (mean)	0.489	0.089	0.000
log ₁₀ (Estimated richness)	Temperature (range)	-0.143	0.033	0.000
log ₁₀ (Estimated richness)	log ₁₀ (Chlorophyll)	-0.092	0.030	0.002
log ₁₀ (Estimated richness)	log ₁₀ (Population index)	0.081	0.038	0.036
log ₁₀ (Estimated richness)	log ₁₀ (PAR)	-0.130	0.064	0.043
log ₁₀ (Estimated richness)	Depth	-0.020	0.014	0.159
log ₁₀ (Estimated richness)	Salinity	0.053	0.051	0.301
log ₁₀ (Estimated richness)	log ₁₀ (Phosphate)	-0.023	0.052	0.658
log ₁₀ (Estimated richness)	log ₁₀ (Nitrate)	-0.006	0.047	0.905
log ₁₀ (Chlorophyll)	Temperature (range)	0.348	0.026	0.000
log ₁₀ (Chlorophyll)	log ₁₀ (Population index)	0.198	0.036	0.000
log ₁₀ (Chlorophyll)	Salinity	-0.292	0.060	0.000
log ₁₀ (Chlorophyll)	Temperature (mean)	-0.367	0.085	0.000
log ₁₀ (Chlorophyll)	Depth	-0.036	0.010	0.001
log ₁₀ (Chlorophyll)	log ₁₀ (PAR)	0.185	0.059	0.002
log ₁₀ (Chlorophyll)	log ₁₀ (Phosphate)	0.141	0.046	0.002
log ₁₀ (Chlorophyll)	log ₁₀ (Nitrate)	0.089	0.041	0.031
log ₁₀ (Phosphate)	Salinity	-0.681	0.049	0.000
log ₁₀ (Phosphate)	Temperature (mean)	-0.853	0.067	0.000
log ₁₀ (Phosphate)	log ₁₀ (PAR)	-0.290	0.040	0.000
log ₁₀ (Phosphate)	Temperature (range)	-0.036	0.019	0.061
log ₁₀ (Phosphate)	log ₁₀ (Population index)	-0.035	0.027	0.197
log ₁₀ (Phosphate)	Depth	0.000	0.008	0.992
log ₁₀ (Nitrate)	log ₁₀ (PAR)	-0.884	0.044	0.000
log ₁₀ (Nitrate)	Salinity	-0.638	0.055	0.000

log ₁₀ (Nitrate)	Temperature (mean)	-0.842	0.075	0.000
log ₁₀ (Nitrate)	Temperature (range)	-0.156	0.021	0.000
log ₁₀ (Nitrate)	Depth	0.030	0.008	0.000
log ₁₀ (Nitrate)	log ₁₀ (Population index)	-0.086	0.030	0.004

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116 **Table S1b:** Standardized coefficients (scaled by mean and variance) from the global model
 117 predicting fish biomass including only fishes >35 cm in total length.

Predictor	Estimate	Standard error	P-value
log ₁₀ (Estimated richness)	0.357	0.040	0.000
Depth	0.153	0.024	0.000
Functional diversity	0.142	0.029	0.000
log ₁₀ (Population index)	-0.280	0.057	0.000
Temperature (mean)	-0.250	0.108	0.021
Temperature (range)	-0.102	0.049	0.038
log ₁₀ (PAR)	0.144	0.089	0.106
Salinity	-0.091	0.071	0.204
log ₁₀ (Chlorophyll)	0.040	0.050	0.418
log ₁₀ (Nitrate)	0.045	0.068	0.507
log ₁₀ (Phosphate)	0.008	0.074	0.916

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120 **Table S1c:** Standardized coefficients (scaled by mean and variance) from the global model
 121 predicting fish biomass including only temperate sites.

Predictor	Estimate	Standard error	P-value
Functional diversity	0.234	0.025	0.000
Temperature (range)	-0.257	0.038	0.000
log ₁₀ (Estimated richness)	0.155	0.029	0.000
Depth	0.110	0.021	0.000
Temperature (mean)	0.431	0.090	0.000
Salinity	-0.156	0.061	0.011
log ₁₀ (Population index)	-0.083	0.035	0.020
log ₁₀ (Nitrate)	0.170	0.075	0.023
log ₁₀ (Chlorophyll)	0.053	0.035	0.132
log ₁₀ (Phosphate)	-0.049	0.079	0.532
log ₁₀ (PAR)	0.044	0.083	0.597

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124 **Table S1d:** Standardized coefficients (scaled by mean and variance) from the global model
 125 predicting fish biomass including only tropical sites.

Predictor	Estimate	Standard error	P-value
Functional diversity	0.301	0.041	0.000
log ₁₀ (Estimated richness)	0.166	0.041	0.000
log ₁₀ (Population index)	-0.292	0.076	0.000
Depth	0.074	0.031	0.016
Salinity	-0.233	0.110	0.035
log ₁₀ (Chlorophyll)	-0.131	0.067	0.051
Temperature (mean)	0.105	0.104	0.313
log ₁₀ (PAR)	0.048	0.073	0.512
log ₁₀ (Nitrate)	-0.051	0.107	0.635
log ₁₀ (Phosphate)	-0.020	0.109	0.858
Temperature (range)	0.015	0.084	0.861

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128 **Table S1e:** Standardized coefficients (scaled by mean and variance) from the global model
 129 predicting fish biomass including only top carnivores.

Predictor	Estimate	Standard error	P-value
Functional diversity	0.206	0.022	0.000
log ₁₀ (Population index)	-0.128	0.038	0.001
log ₁₀ (Chlorophyll)	0.118	0.036	0.001
Depth	0.047	0.017	0.007
Salinity	-0.098	0.045	0.032
log ₁₀ (Nitrate)	0.101	0.050	0.045
log ₁₀ (Estimated richness)	0.041	0.029	0.159
log ₁₀ (PAR)	0.080	0.066	0.230
Temperature (range)	-0.034	0.041	0.404
Temperature (mean)	0.052	0.077	0.495
log ₁₀ (Phosphate)	-0.036	0.054	0.502

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132 **Table S1f:** Standardized coefficients (scaled by mean and variance) from the global model
 133 predicting fish biomass including only benthic carnivores.

Predictor	Estimate	Standard error	P-value
Functional diversity	0.128	0.024	0.000
Depth	0.096	0.020	0.000
Temperature (range)	-0.207	0.046	0.000
log ₁₀ (Population index)	-0.172	0.053	0.001
log ₁₀ (Chlorophyll)	0.081	0.043	0.060
Salinity	-0.115	0.070	0.100
Temperature (mean)	-0.155	0.104	0.135
log ₁₀ (Nitrate)	0.086	0.063	0.173
log ₁₀ (Estimated richness)	-0.044	0.034	0.188
log ₁₀ (PAR)	0.093	0.090	0.305
log ₁₀ (Phosphate)	-0.042	0.074	0.571

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136 **Table S1g:** Standardized coefficients (scaled by mean and variance) from the global model
 137 predicting fish biomass including only herbivores.

Predictor	Estimate	Standard error	P-value
Functional diversity	0.123	0.019	0.000
Temperature (range)	-0.168	0.034	0.000
log ₁₀ (Chlorophyll)	-0.095	0.031	0.002
Depth	0.037	0.014	0.008
log ₁₀ (Estimated richness)	0.063	0.024	0.010
log ₁₀ (Phosphate)	-0.118	0.050	0.018
log ₁₀ (PAR)	0.125	0.060	0.036
log ₁₀ (Population index)	-0.059	0.035	0.095
Temperature (mean)	-0.078	0.083	0.348
log ₁₀ (Nitrate)	-0.037	0.044	0.401
Salinity	-0.024	0.056	0.669

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140 **Table S1h:** Standardized coefficients (scaled by mean and variance) from the global model
 141 predicting fish biomass including only planktivores.

Predictor	Estimate	Standard error	P-value
Depth	0.168	0.015	0.000
log ₁₀ (Estimated richness)	0.159	0.024	0.000
Functional diversity	0.053	0.018	0.003
log ₁₀ (Population index)	-0.070	0.038	0.063
Temperature (range)	-0.058	0.037	0.123
log ₁₀ (Nitrate)	-0.052	0.050	0.302
Temperature (mean)	0.090	0.088	0.305
log ₁₀ (Phosphate)	0.054	0.054	0.317
log ₁₀ (PAR)	0.039	0.068	0.566
log ₁₀ (Chlorophyll)	-0.015	0.034	0.662
Salinity	0.014	0.051	0.792

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144 **Table S1i:** Standardized coefficients (scaled by mean and variance) from the global model
 145 predicting fish biomass including only invertivores.

Predictor	Estimate	Standard error	P-value
Functional diversity	0.128	0.024	0.000
Depth	0.096	0.020	0.000
Temperature (range)	-0.207	0.046	0.000
log ₁₀ (Population index)	-0.172	0.053	0.001
log ₁₀ (Chlorophyll)	0.081	0.043	0.060
Salinity	-0.115	0.070	0.100
Temperature (mean)	-0.155	0.104	0.135
log ₁₀ (Nitrate)	0.086	0.063	0.173
log ₁₀ (Estimated richness)	-0.044	0.034	0.188
log ₁₀ (PAR)	0.093	0.090	0.305
log ₁₀ (Phosphate)	-0.042	0.074	0.571

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148 **Table S1j:** Standardized coefficients (scaled by mean and variance) from the global model
 149 predicting fish biomass at the ecoregion level.

Predictor	Estimate	Standard error	P-value
log ₁₀ (Population index)	-0.192	0.054	0.001
Temperature (range)	-0.231	0.075	0.003
Functional diversity	0.168	0.064	0.012
log ₁₀ (Chlorophyll)	0.193	0.079	0.018
Depth	0.156	0.066	0.023
log ₁₀ (Estimated richness)	0.202	0.132	0.132
Temperature (mean)	0.154	0.136	0.264
log ₁₀ (Nitrate)	-0.061	0.095	0.521
log ₁₀ (Phosphate)	-0.063	0.101	0.535
Salinity	0.011	0.064	0.870
log ₁₀ (PAR)	-0.016	0.099	0.871

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151 **Table S1k:** Standardized coefficients (scaled by mean and variance) from the global model
 152 predicting fish biomass at the site level using raw (observed) species richness.

Predictor	Estimate	Standard error	P-value
log ₁₀ (Observed richness)	0.7887	0.0331	0.0000
Depth	0.0933	0.0132	0.0000
Functional diversity	0.0910	0.0176	0.0000
Temperature (range)	-0.1665	0.0329	0.0000
log ₁₀ (Population index)	-0.1575	0.0385	0.0000
Temperature (mean)	-0.2238	0.0795	0.0050
Salinity	-0.1397	0.0519	0.0072
log ₁₀ (Chlorophyll)	0.0576	0.0295	0.0508
log ₁₀ (PAR)	0.0708	0.0643	0.2711
log ₁₀ (Phosphate)	-0.0214	0.0523	0.6830
log ₁₀ (Nitrate)	0.0116	0.0456	0.7995

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154 **Table S2:** Effects of species richness on resistance of fish biomass to changing climate and
 155 human impacts. Cells show standardized partial regression coefficients of interactions between
 156 estimated richness and sea surface temperature (SST, mean and range) and log human population
 157 index from global hierarchical models of reef fish log biomass. Bold black terms indicate
 158 significant ($P < 0.05$) stabilizing effects on biomass, i.e., richness reduces the effect of the
 159 stressor. Gray terms are not significant at $P < 0.05$.

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Response (biomass)	SST mean	SST range	population
all fish (global)	-0.127	0.128	0.014
all fish (temperate)	-0.158	0.075	-0.001
all fish tropical)	-0.031	0.030	0.030
top carnivores (global)	0.012	0.080	-0.022
top carnivores (temperate)	0.007	0.047	0.001
top carnivores (tropical)	-0.107	0.045	-0.050
large fish (global)	0.010	0.040	0.008
large fish (temperate)	0.003	0.000	0.034
large fish (tropical)	-0.093	0.040	-0.022

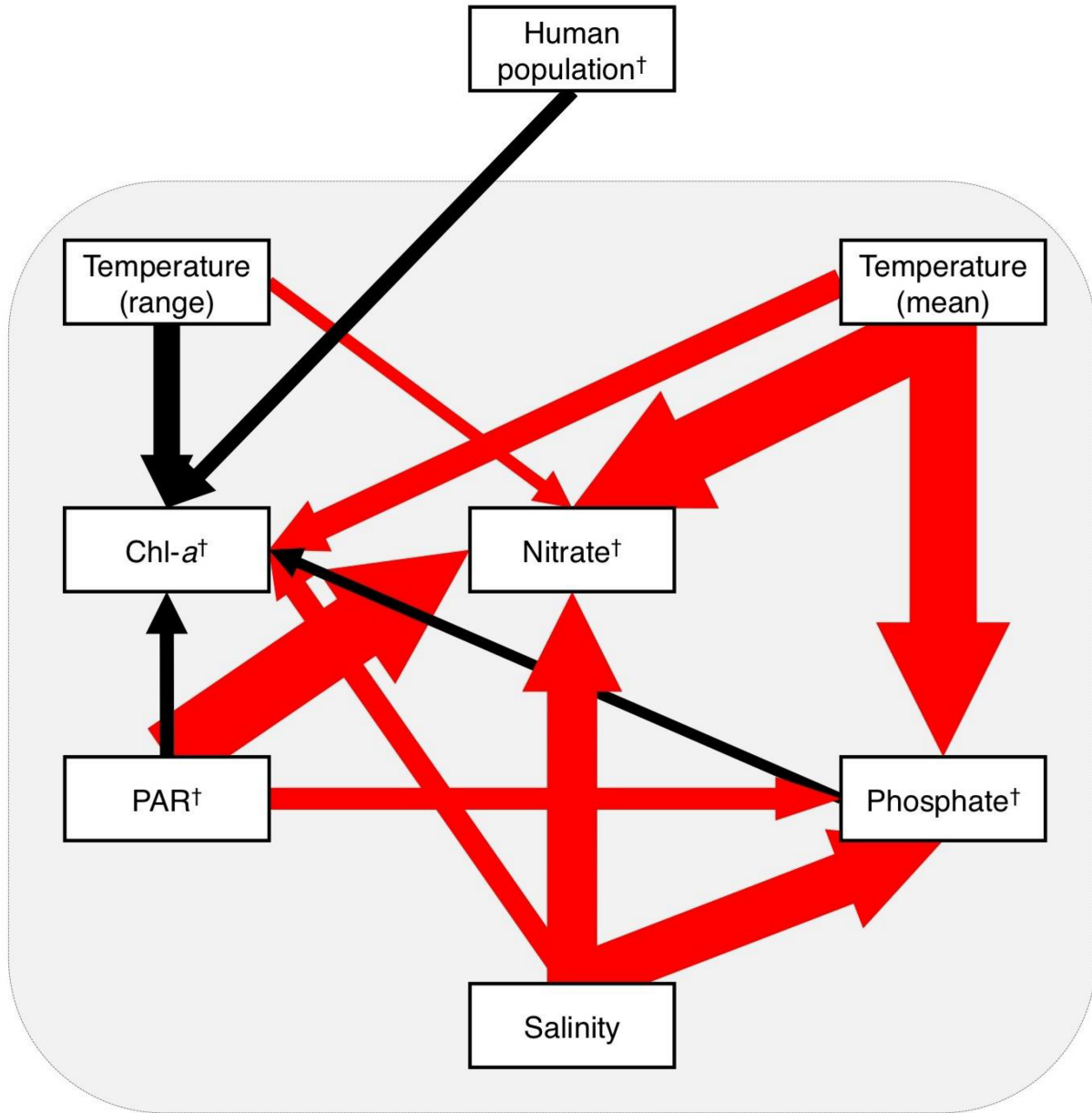
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163 **Table S3:** Functional traits used in the analysis of functional diversity (adopted from ref. 38).

Trait	Category	Units
Maximum length	Body size	Continuous (cm)
Trophic breadth	Trophic niche	Number of prey phyla consumed (1-8)
Trophic group	Trophic niche	Browsing herbivore, scraping herbivore, benthic invertivore, planktivore, higher carnivore
Water column position	Behavior	Benthic, demersal, site-attached pelagic, roaming pelagic
Gregariousness	Behavior	Singleton, paired to forming small schools, always schools
Diel activity pattern	Behavior	Nocturnal, diurnal
Preferred substrate	Habitat use	Hard substrate, soft sediment
Habitat complexity requirements	Habitat use	Low, medium, high

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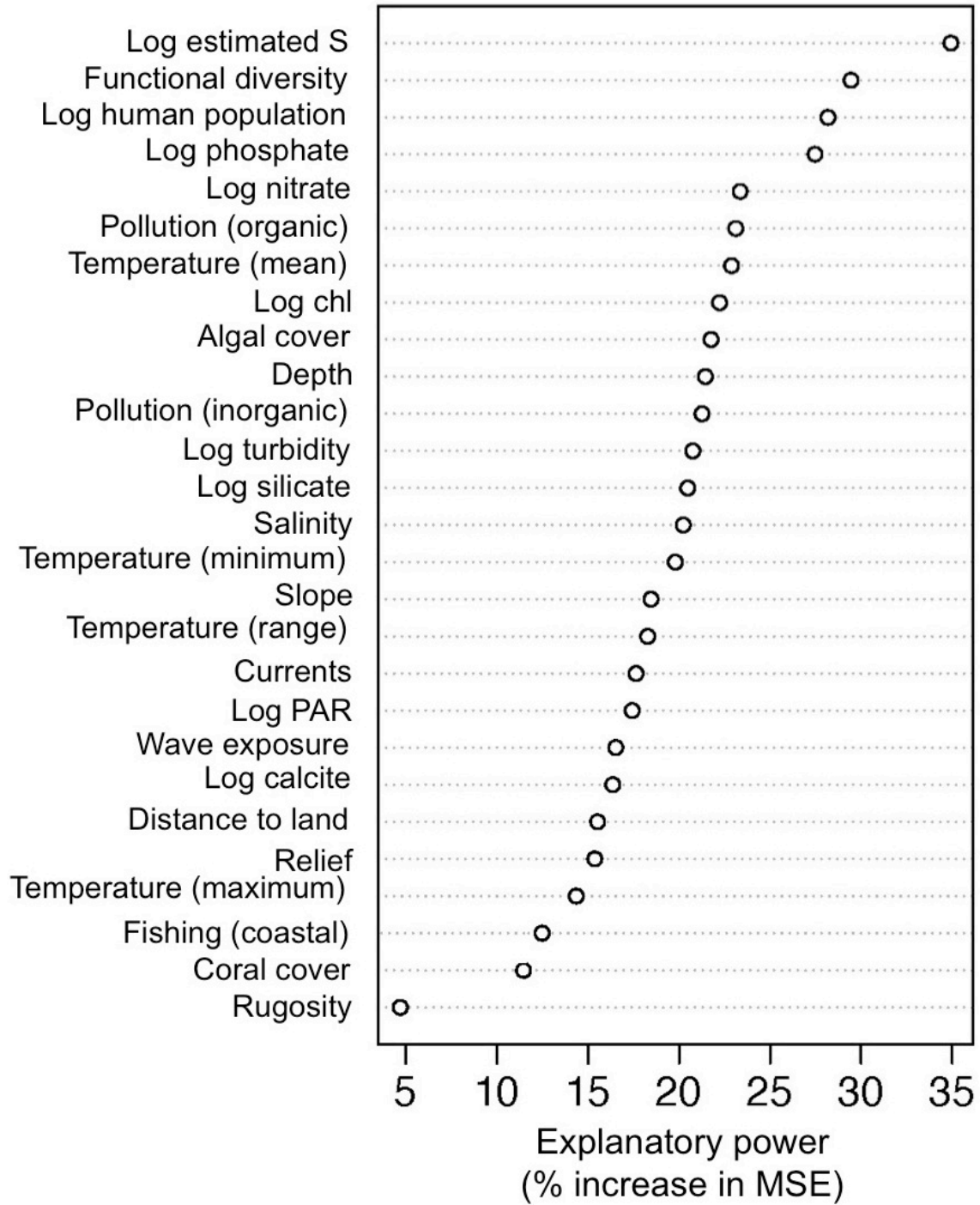
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166 **Figure S1:** Path diagram of relationships among abiotic forcing factors, and human population,

167 influencing fish diversity and biomass (Fig. 1). Paths of $\beta < 0.05$ are not shown. Gray box

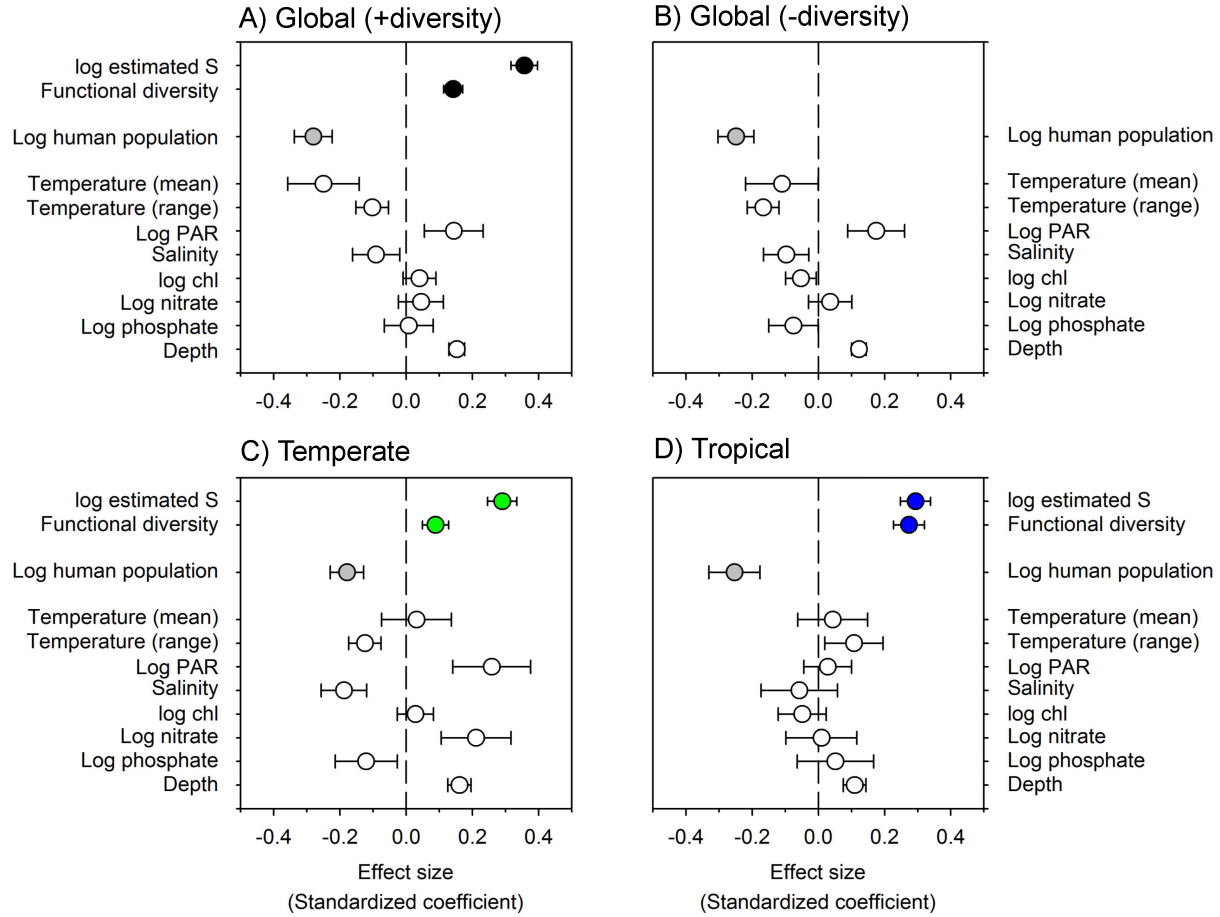
168 surrounds abiotic variables plus phytoplankton (Chl-*a*). [†] = log₁₀-transformed.

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171 **Figure S2:** Results of random forest analysis of the relative importance of two diversity
 172 components (functional diversity and estimated species richness), human population density, and
 173 25 environmental variables to global reef fish biomass.



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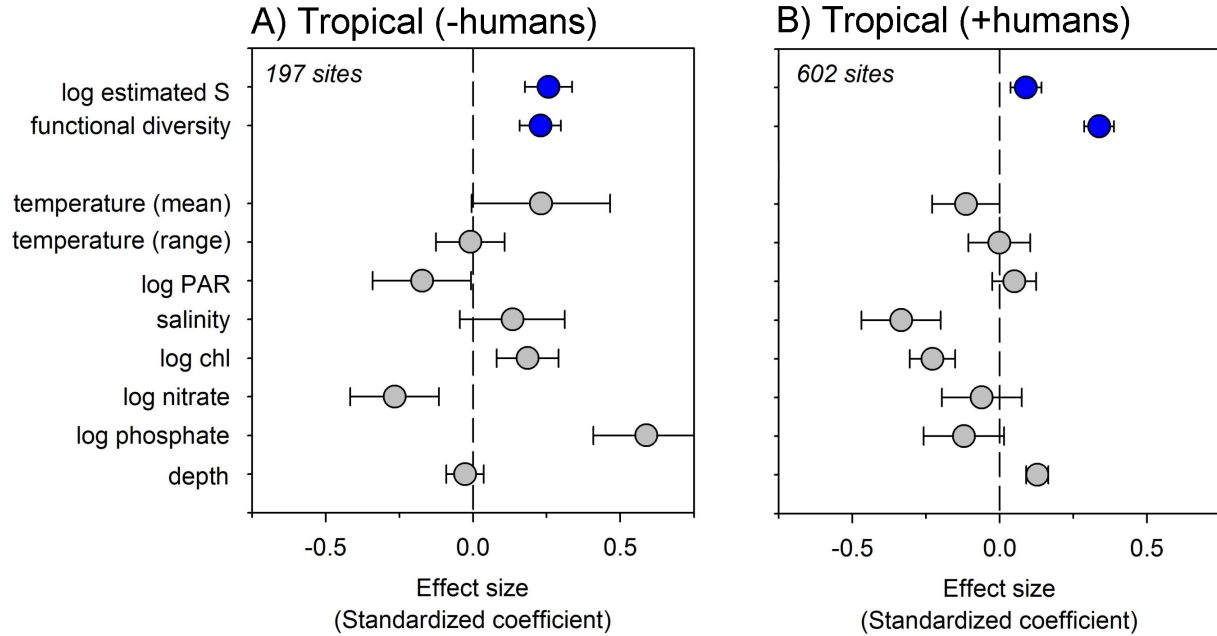
175 **Figure S3:** Relative influence of biodiversity and environmental factors on log biomass of large

176 (> 35 cm) reef fishes. Effect size estimated as standardized partial regression coefficients from

177 hierarchical linear models at the global level (A) with and (B) without diversity as predictors, and

178 separately for (C) temperate and (D) tropical sites.

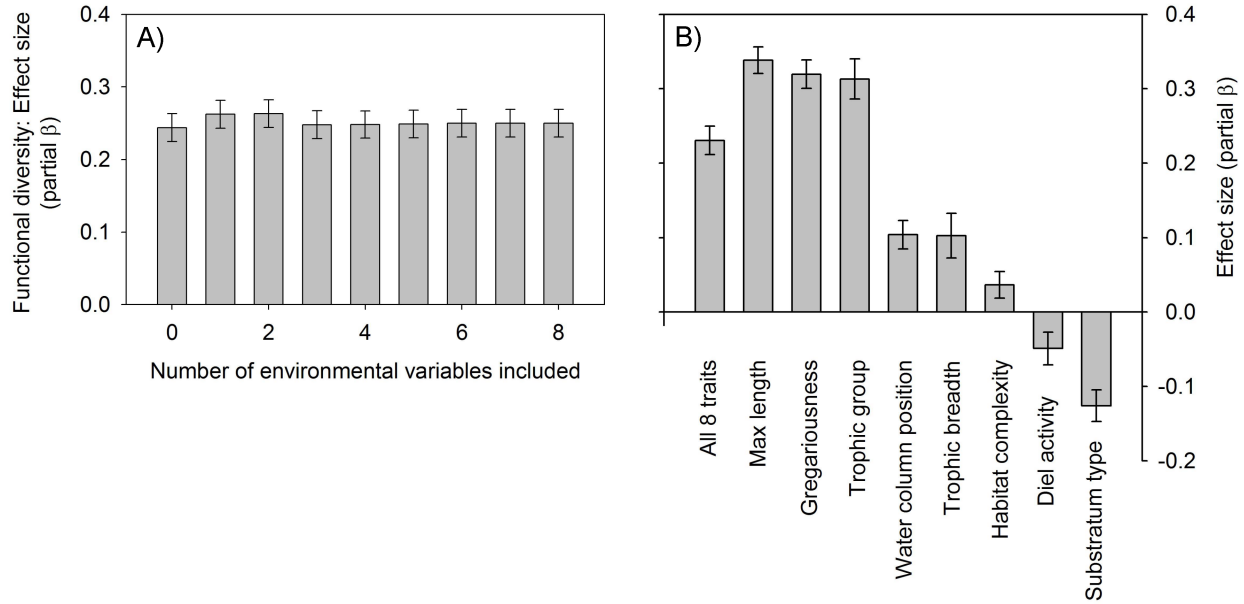
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181 **Figure S4:** Relative influence of biodiversity and environmental factors on log biomass of
 182 tropical reef fishes in the (A) absence and (B) presence of human population. Effects sizes are
 183 standardized partial regression coefficients from hierarchical linear models estimated separately
 184 for tropical sites without vs with human influence.

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187 **Figure S5:** Effects of model construction on robustness of estimated diversity effects on reef fish

188 community biomass. (A) Estimated effect of functional diversity in hierarchical mixed models

189 including functional diversity alone (0) versus 1-8 environmental variables, added in decreasing

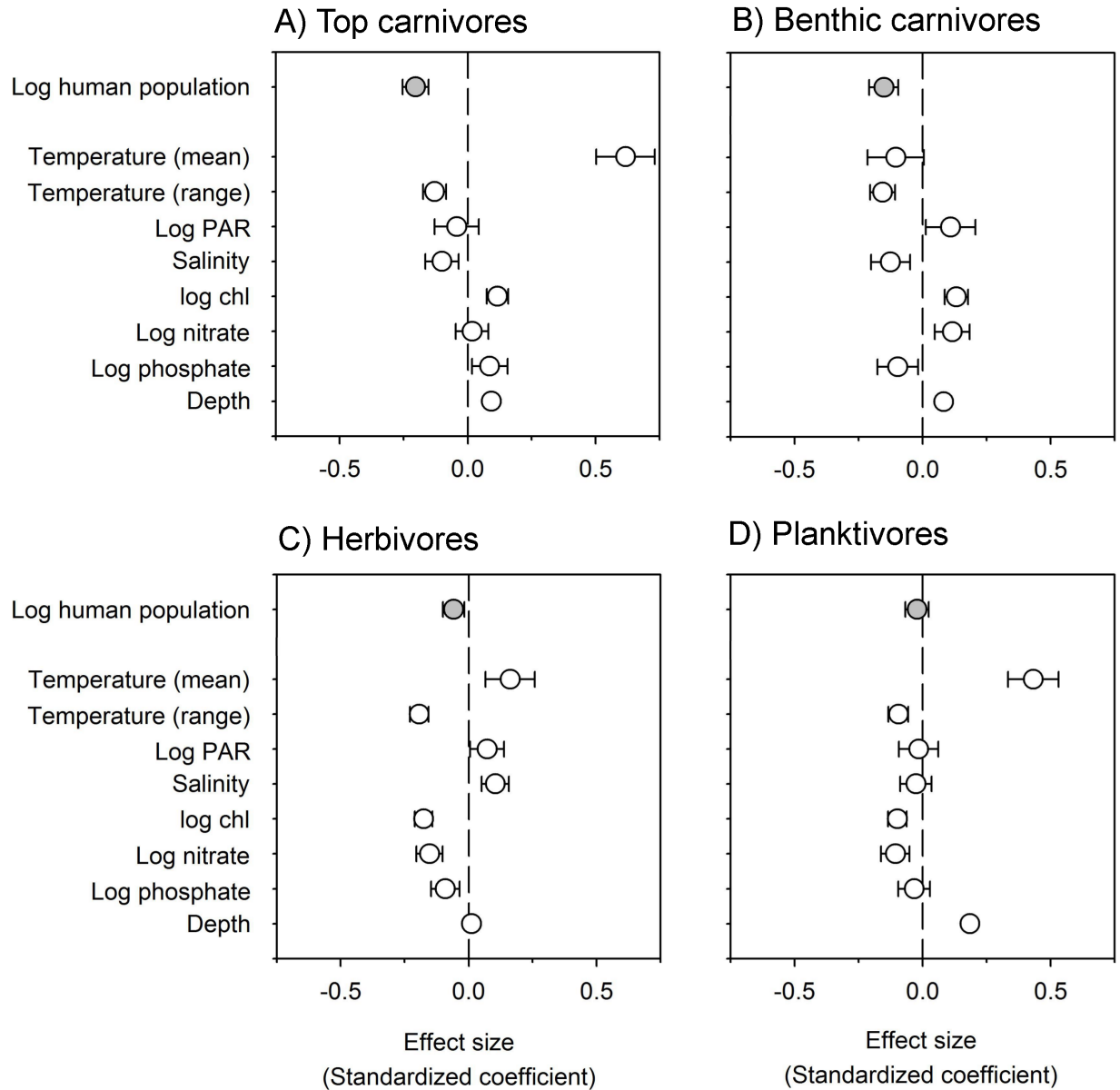
190 order of effect size. (B) Relative importance of component traits to estimated effect of functional

191 diversity on fish community biomass; effect size of functional diversity is calculated from all

192 eight traits versus from each individual component trait in the context of the global hierarchical

193 model.

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196 **Figure S6:** Relative influence of human population and environmental factors on log biomass of

197 different trophic groups of reef fishes. Effects sizes are standardized partial regression

198 coefficients from hierarchical linear models estimated separately by trophic level. This analysis

199 omits diversity as a predictor in order to include all sites, including those with no fishes at that

200 trophic level.

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