

1 **Supplementary Data for: Effects of rare taxa on fish index of biotic integrity**
2 **results in a southeastern US biodiversity hotspot**

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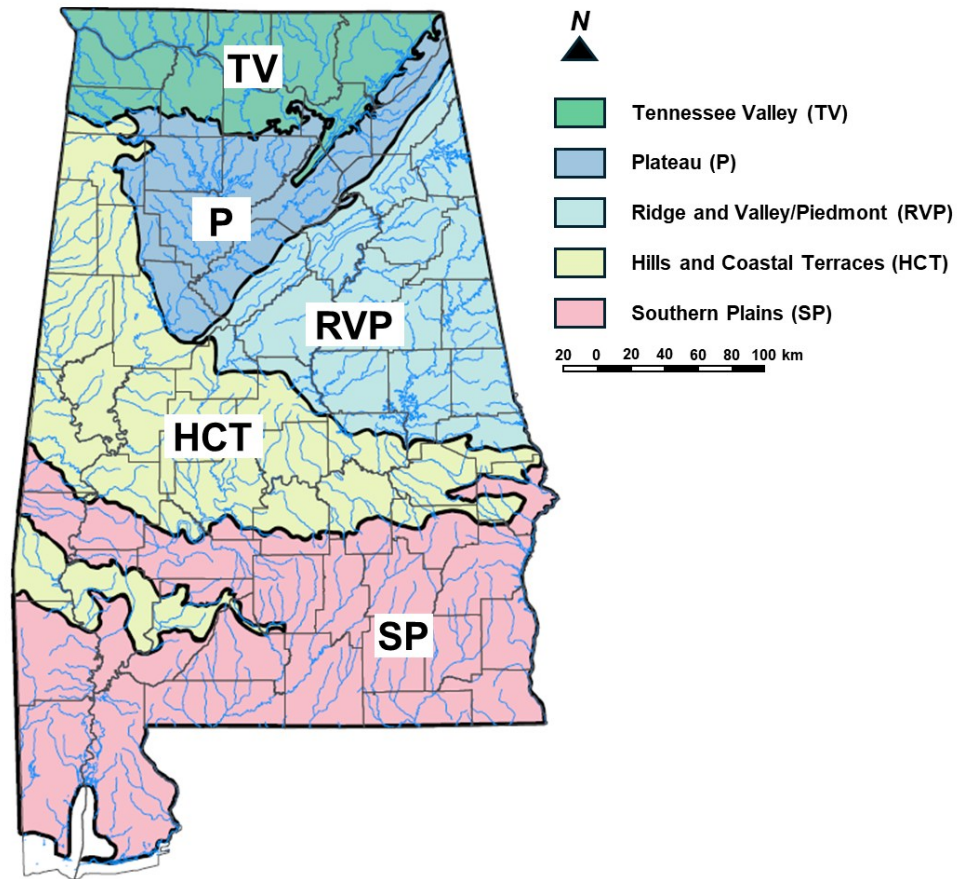
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18 **Data S1. Supplementary Methods, Results, & Discussion**

19 *Note:* references not cited in the main text are presented in the References section of this
20 document; see main text for all other cited works. Abbreviations follow the main text.

21 **Supplementary Methods**

22 As noted in the main text, Alabama currently has five fish biogeographic provinces, or
23 ‘ichthyoregions’. The initial state ichthyoregion classification was developed by O’Neil and
24 Shepard (2007) based on cluster analysis of Alabama fish community survey data, and the
25 classification was later updated in subsequent studies (e.g., O’Neil and Shepard 2010, 2011a,b).
26 The different ichthyoregions of the state generally contain internally cohesive species
27 assemblages, physiographic attributes, and geologic settings, as well as similar stream types
28 (O’Neil and Shepard 2007), and one fish IBI tool has been calibrated for each ichthyoregion
29 (Table 1). A map of Alabama’s ichthyoregions is provided for reference in Fig. S1 *below*.



30

31 **Fig. S1** Map of the five ichthyoregions of Alabama. Ichthyoregions refer to distinct, yet
 32 internally cohesive, fish faunal assemblages. The map *above* was modified and partly redrawn
 33 after O’Neil and Shepard (2011b), while maintaining their color scheme (see legend).

34 Wilcoxon signed-rank tests were conducted to evaluate the overall significance of
 35 differences in metric-level regression parameters, including goodness-of-fit statistics (i.e., R^2)
 36 and slopes, between the SDR and ART treatments, as the data were non-normal (typically left-
 37 skewed) and paired (same metric for each treatment). A valid test was possible when comparing
 38 post-SDR and post-ART R^2 distributions from the regression models; however, comparisons
 39 including SRT R^2 -values would not be valid. The reason for this was that the SRT treatment
 40 matrix that was used to calculate IBI outcomes was a long-format resampling of the original data
 41 matrix with $n = 3,007$ sites/rows, making the observations violate the common statistical
 42 assumption that data are independent and identically distributed. Tests were conducted in the R

43 statistical environment (R Core Team 2023) using the `wilcox.test()` function, and results
44 were considered significant at the $\alpha = 0.05$ level.

45 **Supplementary Results**

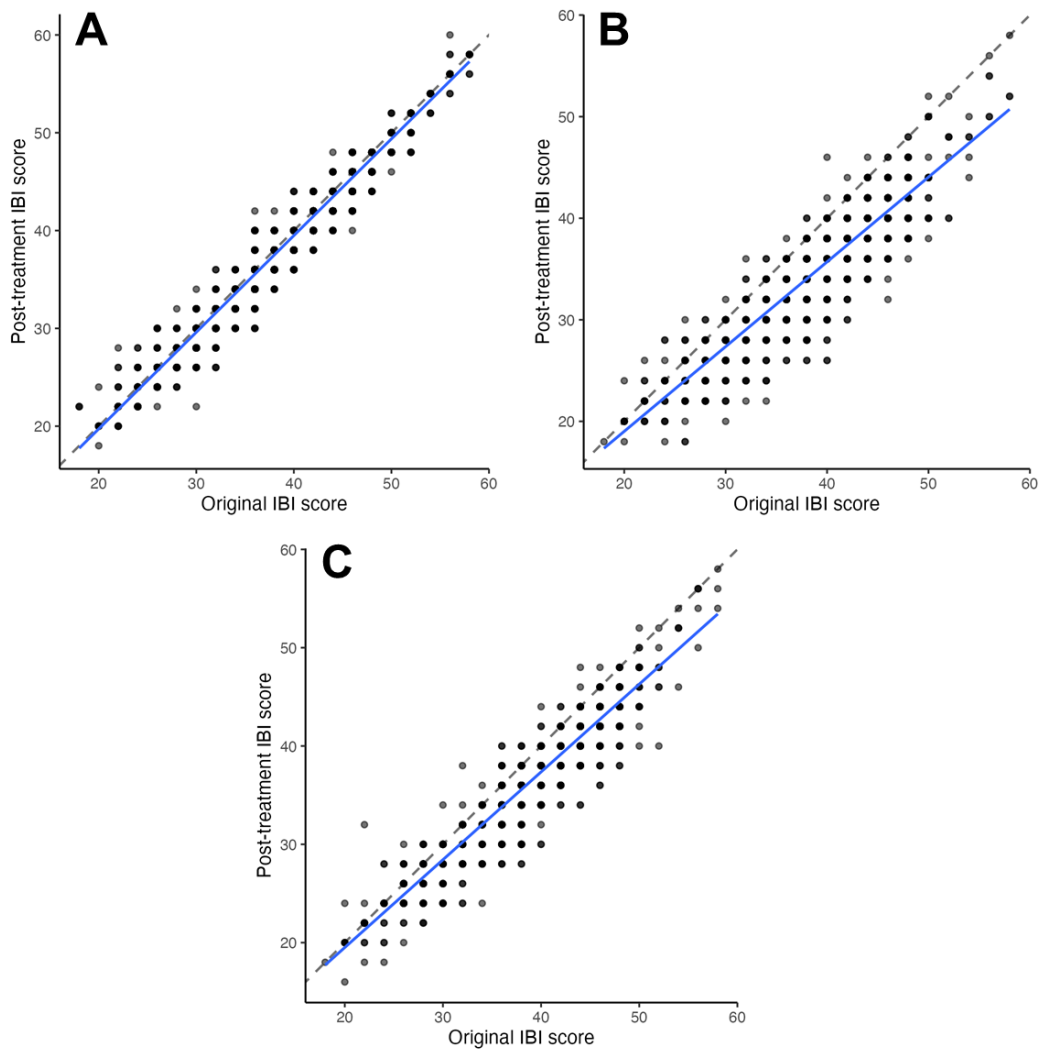
46 ***Data and treatment characteristics***

47 The sampled fish taxa included 78 North American minnow species (Leuciscidae) including 50
48 ‘shiners’ from genera *Alburnops*, *Coccotis*, *Cyprinella*, *Ericymba*, *Luxilus*, *Lythrurus*, *Miniellus*,
49 *Notropis*, *Paranotropis*, and *Pteronotropis*; 18 sucker species (Catostomidae); ~18–22 sunfish
50 and black basses (Centrarchidae); 68 darter species (Percidae: Etheostomatinae); and 8 madtom
51 species (Ictaluridae: *Noturus*; Bagley et al. 2023). The 11 species that were globally rare in the
52 fish community data matrix analyzed in this study included one lamprey (*Lethenteron appendix*;
53 Petromyzontidae), one herring (*Alosa chrysochloris*; Dorosomatidae), two minnows (*Cyprinella*
54 *callitaenia*, *Hybognathus hayi*; Leuciscidae), one sucker (*Carpionodes carpio*; Catostomidae), one
55 madtom (*Noturus* sp. cf. *flavus*; Ictaluridae), four darters—*Etheostoma boschungii*, *Etheostoma*
56 *trisella*, *Nothonotus (Etheostoma) wapiti*, and *Percina phoxocephala* (Percidae), and the
57 introduced Asian pond loach (*Misgurnus anguillicaudatus*; Cobitidae; Bagley et al. 2023). The
58 leuciscid minnows of Alabama were all formerly lumped within Cyprinidae, and these taxa are
59 still referred to informally as ‘cyprinids’ by some biologists as well as in our Alabama fish IBI
60 metric names (e.g., Tables 1 and S1; O’Neil et al. 2006; O’Neil and Shepard 2010), which were
61 published before the taxonomic changes placing North American minnows in Leuciscidae took
62 effect (Tan and Armbruster 2018; Stout et al. 2022; Bagley et al. 2023).

63 ***Effects of rare taxon removal on IBI scores and condition ratings***

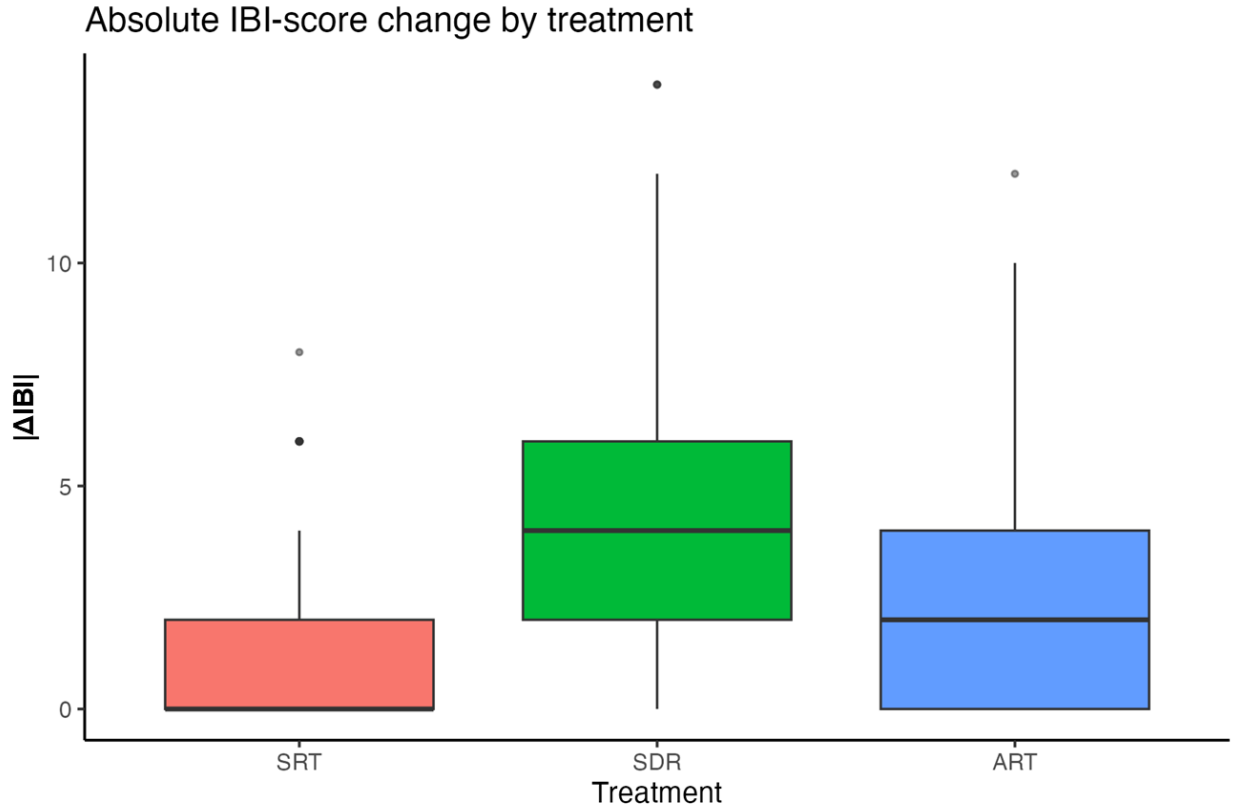
64 Regarding treatment effects on site IBI scores, a feature presented in the text but not expanded
65 upon precisely was that the IQR of scores increased with treatment intensity, from SRT to ART

66 and SDR (Table 2). Likewise, the ranges of changes in IBI scores varied with treatment intensity.
67 While these changes are visualized in Figs 2A-C of the main text and supplementary Fig. S2
68 *below*, the raw ranges were from -8 to $+6$ points around the original IBI scores following the
69 SRT treatment, from -14 to $+6$ points around the original scores for SDR, and from -12 to $+10$
70 points around the original scores for ART. The near-unity regression of post-treatment on



71
72 **Fig. S2** Scatterplots of post-treatment (y -axis) vs. original site IBI scores (x -axis). Results are
73 shown for each of the three treatments discussed in the main text, including the (A) SRT, (B)
74 SDR, and (C) ART removal treatments. Site results (*transparent gray dots*) are shown alongside
75 the corresponding fitted regression lines (*blue lines*) and a unit (1:1) line for reference (*dashed*
76 *line*).

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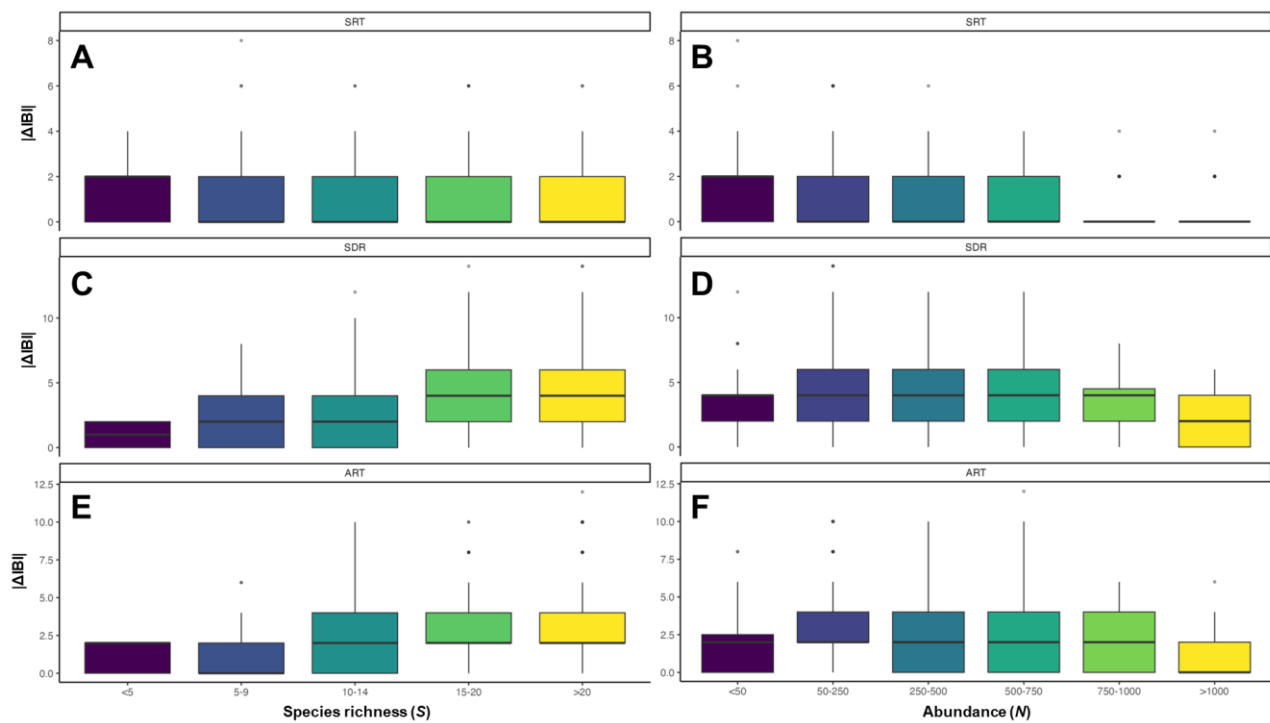
79 **Fig. S3** Box plot summaries of the absolute value of change in IBI score ($|\Delta\text{IBI}|$) across sites,
 80 presented for each treatment. Here, the raw response variable was calculated as $\Delta\text{IBI} = \text{IBI}_{R,i}$
 81 $- \text{IBI}_{O,i}$, as discussed in the main text. *Vertical lines and dots* represent the range of values, *top*
 82 *and bottom of boxes* indicate the third and first quartiles (75% and 25%), respectively, and the
 83 *dark lines* represent median values.

84

85 original IBI scores ($R^2 = 0.969$, $a = 0.988$, $b = -0.04$) and a low nRMSE of 2.86% under the SRT
 86 treatment confirmed that removing a single rare taxon rarely disrupts the Alabama fish IBIs,
 87 overall (e.g., Fig. S2A). In contrast, the IBI score regression following the SDR treatment
 88 showed clear compression bias ($R^2 = 0.809$, $a = 0.834$, $b = 2.33$; Fig. S2B), and nRMSE for
 89 metric scores after this treatment reached 10.73%. And, last, under the ART treatment, the IBI
 90 score regression indicated a modest but consistent downward bias ($R^2 = 0.874$, $a = 0.893$, $b =$
 91 1.65 ; Fig. S2C), and nRMSE was 7.51%.

92 Our analyses of the absolute value of changes in IBI scores for sites ($|\Delta\text{IBI}|$) provided

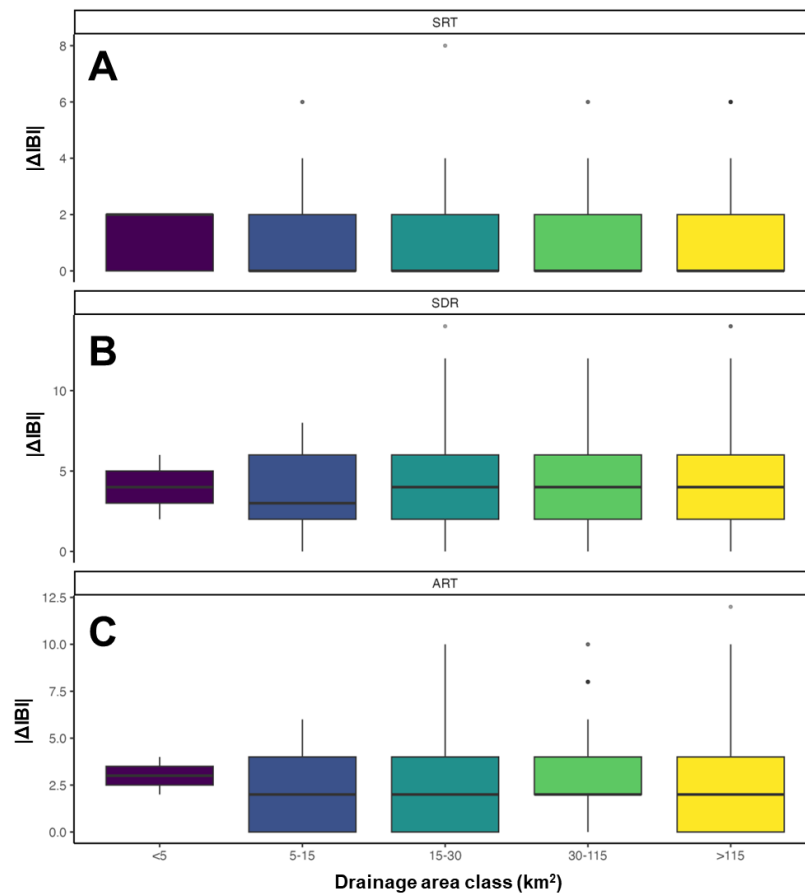
93 additional evidence on the effects of rare taxon removal on fish IBI scores and condition ratings.
 94 For example, box plots of $|\Delta\text{IBI}|$ as a function of treatment showed that, as with raw IBI changes
 95 and R^2 above, the resulting median $|\Delta\text{IBI}|$ values tracked treatment intensity, increasing from
 96 SRT to ART to SDR, and also showed the greatest variance under the SDR treatment (Fig. S3).
 97 Furthermore, box plots evaluating $|\Delta\text{IBI}|$ as a function of our five species richness classes (S), six
 98 abundance classes (N), and five drainage area classes revealed that changes in IBI scores were
 99 relatively invariant under the SRT treatment (Figs. S4A,B and S5A), had higher medians and
 100 variance under the ART treatment (Figs. S4E,F and S5C), and showed roughly the highest
 101 medians and variance under the SDR treatment (Figs. S4C,D and S5B). Within treatments, $|\Delta\text{IBI}|$



102

103 **Fig. S4** Summaries of the absolute value of change in IBI score ($|\Delta\text{IBI}|$) across sites as a function
 104 of sampling intensity classes discussed in the main text (which are the same classes as those
 105 shown in Fig. 4). Results are presented as box plots stratified by sample species richness (S) and
 106 abundance (N) for each of the three treatments, including (A, B) SRT removal, (C, D) SDR
 107 removal, and (E, F) ART removal. Stratification was based on five species richness classes ($S =$
 108 $\leq 5, 5-9, 10-14, 15-20,$ and > 20) and six abundance classes ($N = < 50, 50-250, 250-500, 500-$
 109 $750, 750-1000,$ and > 1000). Box representations are the same as those described in the caption
 110 to Fig. S3 above, except each box is assigned a *different color* by class.

111 results were particularly robust to variation in drainage area, with little to no change in medians
 112 across drainage size classes (Fig. S5). Yet, comparing the S and N analyses, median $|\Delta\text{IBI}|$
 113 increased the most for the $S = 15\text{--}20$ and $S > 20$ species-richness classes under the SDR
 114 treatment (Fig. S4C,D). Compared with the smallest abundance class, median $|\Delta\text{IBI}|$ rose
 115 similarly for the four N classes ranging from 50 to 1000 individuals (i.e., $N = 50\text{--}250$, $250\text{--}500$,
 116 $500\text{--}750$, and $750\text{--}1000$ individuals) under the SDR and ART treatments (Fig. S4D,F). and
 117 dropped back to lower levels in the largest abundance class ($N > 1000$).



118
 119 **Fig. S5** Summaries of the absolute value of change in IBI score ($|\Delta\text{IBI}|$) across sites, presented as
 120 a function of drainage area classes discussed in the text (which are the same classes as those
 121 shown in plots of nRMSE in Fig. S9 below). Results are presented as box plots stratified by site
 122 drainage areas for each of the three treatments, including (A) SRT removal, (B) SDR removal,
 123 and (C) ART removal. Box representations are the same as those described in the caption to Fig.
 124 S3 above, except each box is assigned a *different color* based on x -axis class.

125 ***Per-metric responses and treatment intensity***

126 The full results of linear regression analyses of post-treatment IBI metric scores as a function of
127 original scores are presented in Figs S6–S8 and Table S1 *below*. Linear modeling of metric
128 scores provided additional evidence that the SDR treatment had the greatest effect on IBI metric
129 scores, and the regression results agreed well with the per-metric κ results (Table S2 *below*).

130 Iteratively removing each rare taxon within each sample in the SRT treatment to create
131 replicate samples ($n = 3,007$) caused marginal decreases in IBI metric scores, with regression
132 slope parameters and R^2 goodness-of-fit statistics generally falling near 1.0 (mean \pm s.d. $a = 0.95$
133 ± 0.07 , mean \pm s.d. $R^2 = 0.92 \pm 0.08$; Fig. S6; Table S1). In line with our a priori expectations,
134 post-SRT removal IBI metric scores more frequently deviated from the original scores for
135 metrics representing measures of species richness (mean \pm s.d. $R^2 = 0.89 \pm 0.06$; see metric types
136 in Table 1) when compared with metrics based on species relative abundances (mean \pm s.d. $R^2 =$
137 0.95 ± 0.09). However, given R^2 -values for abundance metric models after SRT were left-
138 skewed, a Welch's t -test was applied (because it allows comparison of means without assuming
139 equal variances) and showed the R^2 distribution for richness metrics was not significantly
140 different than that for abundance-based metrics under this treatment ($t = -1.70$, $df = 15.54$, $p =$
141 0.11). Post-treatment metrics with the greatest deviations from the original scores based on R^2
142 values were '% DELT + hybrids' followed by several richness measures, including 'Number of
143 centrarchid species', 'Total native species', 'Number of *Lepomis* species', and 'Number of
144 sucker species' (Fig. S6; Table S1). Intercepts, b , for all SRT regressions were close to zero but
145 positive, indicating post-treatment IBI metric scores increased slightly after removals.

146 After removing singleton/doubleton taxa in the SDR treatment, IBI metric scores
147 decreased to a greater extent than for SRT, causing the regression slope and R^2 statistics to reach

148 **Table S1** Linear regression results showing the fit between post-treatment and original IBI metric scores, following three removal
 149 treatments. Regressions were performed separately on results from 1) removing single rare taxa within each sample, 2) removing
 150 singleton/doubleton taxa, and 3) removing all rare taxa. The “Metric label” column gives abbreviated names matching Figs S6–S8
 151 *below* (for full names, see Table 1, main text).

Metric label	Single-rare-taxon removal				Singleton/doubleton removal				All-rare-taxa removal			
	<i>N</i>	<i>R</i> ²	<i>a</i>	<i>b</i>	<i>N</i>	<i>R</i> ²	<i>a</i>	<i>b</i>	<i>N</i>	<i>R</i> ²	<i>a</i>	<i>b</i>
Total native spp.	3007	0.82	0.93	0.082	719	0.34	0.55	0.28	719	0.44	0.66	0.35
No. shiner spp.	1885	0.95	0.97	0.045	444	0.64	0.76	0.26	444	0.79	0.87	0.17
No. cyprinid spp.	1122	0.91	0.95	0.050	274	0.58	0.65	0.33	273	0.70	0.78	0.19
No. sucker spp.	2252	0.90	0.92	0.067	546	0.42	0.47	0.51	545	0.58	0.63	0.34
No. darter+madtom spp.	3007	0.90	0.96	0.037	719	0.53	0.64	0.26	719	0.65	0.77	0.19
No. Lepomis spp.	1877	0.87	0.94	0.16	447	0.32	0.61	0.89	447	0.53	0.75	0.62
No. centrarchid spp.	618	0.78	0.87	0.20	146	0.33	0.48	0.33	146	0.40	0.59	0.33
No. intolerant spp.	1267	0.95	0.96	0.054	298	0.69	0.75	0.31	298	0.79	0.83	0.24
% tolerant spp.	2997	0.98	0.99	0.012	716	0.94	0.98	0.11	717	0.97	0.99	0.04
% dominant spp.	1122	0.99	1.00	-0.001	274	0.90	0.96	0.14	273	0.95	0.98	0.07
% Lepomis	2389	0.98	0.99	0.033	573	0.96	0.99	0.05	573	0.98	1.00	0.03
% GSF+YB	618	0.92	0.95	0.25	145	0.55	0.70	1.61	146	0.72	0.84	0.93
% invertivores	1130	0.99	0.99	0.004	270	0.95	0.99	0.07	271	0.98	0.99	0.02
% omnivores	1695	0.99	1.00	-0.010	433	0.98	1.00	-0.04	433	1.00	1.00	-0.01
% insect. cyprinids	2067	0.98	1.00	0.016	457	0.91	0.99	0.12	458	0.96	1.00	0.05
% top carnivores	3007	0.93	0.98	-0.006	718	0.61	0.82	-0.01	719	0.77	0.92	-0.03
% DELT+hybrids	3007	0.71	0.72	1.39	718	0.19	0.20	4.01	719	0.39	0.42	2.92
No. lithophilic spawners	1885	0.93	0.96	0.037	444	0.61	0.73	0.24	444	0.73	0.83	0.14
% simple lithophils	1122	0.99	0.99	0.008	274	0.97	0.99	0.04	273	0.99	1.00	0.01

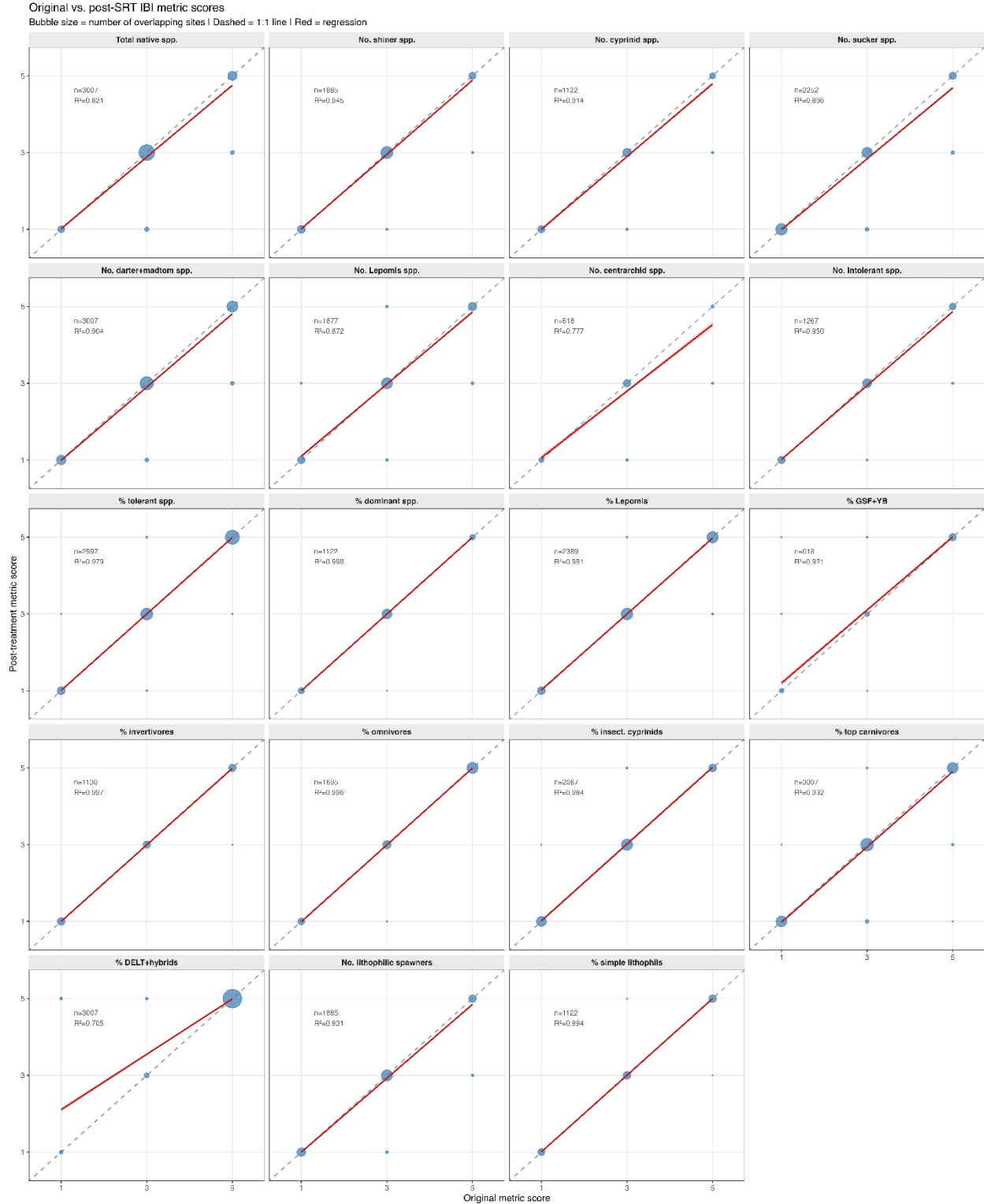
152 Regression abbreviations: *a*, slope; *b*, intercept; *N*, number of samples where metric was applied; *R*², coefficient of determination

153 (goodness-of-fit statistic). Other abbreviation definitions follow the text and Table 1.

154

155 their lowest values among any removal treatment results (mean \pm s.d. $a = 0.75 \pm 0.23$, mean \pm
156 s.d. $R^2 = 0.65 \pm 0.26$; Fig. S7; Table S1). Post-treatment IBI metric scores deviated more
157 frequently from the original scores for richness-based metrics (mean \pm s.d. $R^2 = 0.50 \pm 0.15$) as
158 compared to relative abundance metrics (mean \pm s.d. $R^2 = 0.80 \pm 0.26$) for this second treatment.
159 Again Welch's t -test was appropriate, but in this case differences in R^2 values between these two
160 metric types were statistically significant ($t = -3.13$, $df = 14.28$, $p < 0.01$). The post-treatment
161 IBI metrics with the greatest deviations from original metric scores after the SDR treatment were
162 the same five listed above for the SRT treatment. Intercept parameters for regressions
163 corresponding to this second treatment were ~ 1.4 -fold to ~ 99 -fold higher than those for the SRT
164 removal treatment, consistent with a greater depression of IBI metric scores for larger original
165 IBI metric scores and/or an increase in post-treatment IBI metric scores for lower original IBI
166 metric scores. Two exceptional cases, with negative regression intercepts, were the '%
167 omnivores' metric ($b = -0.04$) and the '% top carnivores' metric ($b = -0.01$; Fig. S7; Table S1).
168 The highest intercept value was $b = 4.01$ for the '% DELT+ hybrids' metric, indicating a greater
169 decline in post-treatment IBI metric scores for this metric, as compared with other metrics.

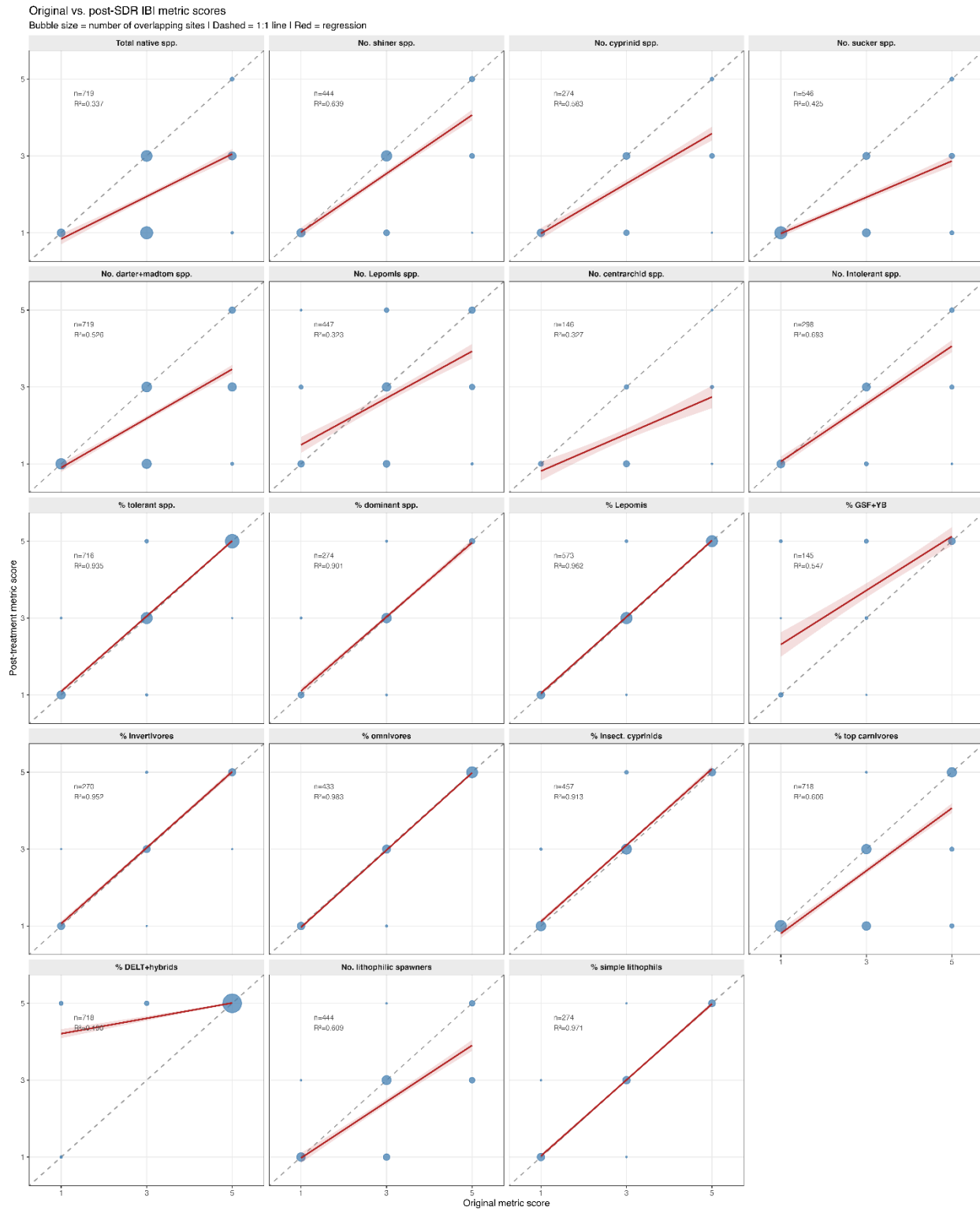
170 After removing all rare taxa in the ART treatment, IBI metric scores decreased such that
171 regression slope and R^2 statistics fell noticeably below 1.0 (mean \pm s.d. $a = 0.83 \pm 0.17$, mean \pm
172 s.d. $R^2 = 0.75 \pm 0.21$; Fig. S8; Table S1). Again, consistent with our expectations based on prior
173 work (Wan et al. 2010), the post-treatment IBI metric scores more frequently deviated from the
174 original scores for species richness metrics (mean \pm s.d. $R^2 = 0.62 \pm 0.15$) as compared with
175 those based on relative abundances (mean \pm s.d. $R^2 = 0.87 \pm 0.20$). A Welch's t -test showed that
176 differences in R^2 values between these two metric types under ART were highly statistically
177 significant ($t = -3.16$, $df = 16.45$, $p < 0.01$). The five post-treatment IBI metrics with the greatest



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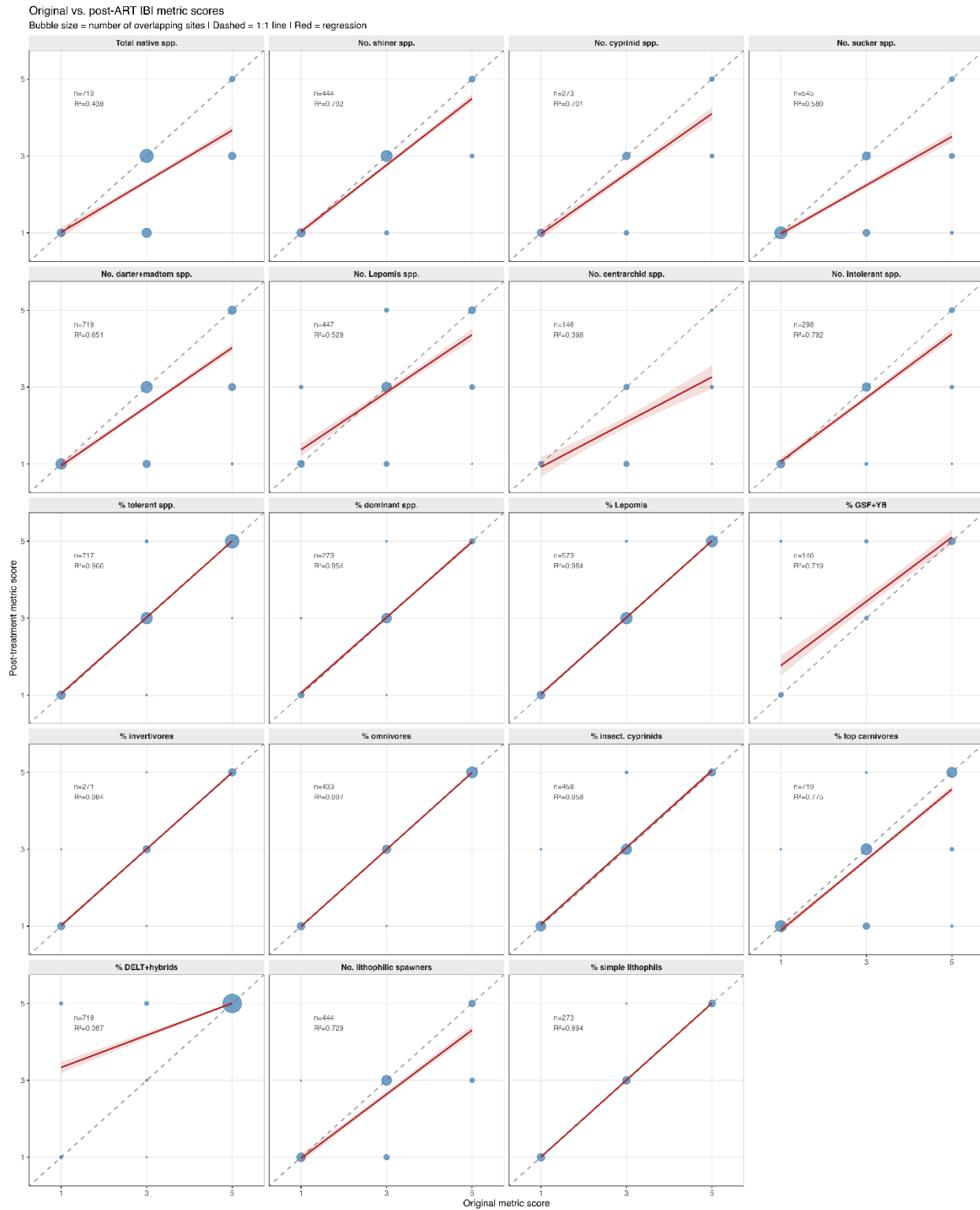
179 **Fig. S6** Plots of post-treatment (y-axis) versus original (x-axis) IBI metric scores following the
 180 single-rare-taxon (SRT) removal treatment. Results are presented as one panel for each of the 19
 181 metrics in this study. Raw values are shown as *transparent blue bubbles*, with bubble size
 182 proportional to the number of overlapping observations (sites), while *red lines* display the fitted

183 regression lines, and a *gray dashed 1:1 line* is shown for reference. Sample sizes and coefficients
 184 of determination (R^2) are inset in the upper left of each panel, and panel headings give the
 185 corresponding metric names.



186
 187 **Fig. S7** Plots of post-treatment versus original IBI metric scores following singleton/doubleton

188 removal (SDR). Panel formatting follows that in Fig. S6 *above* (see caption of that figure for
 189 additional details).



190

191 **Fig. S8** Plots of post-treatment versus original IBI metric scores following the all-rare-taxa

192 (ART) removal treatment. Panel formatting follows that in Fig. S6 *above* (see caption of that
193 figure for additional details).
194

195 deviations from original metric scores were again ‘% DELT + hybrids’, ‘Number of centrarchid
196 species’, ‘Total native species’, ‘Number of *Lepomis* species’, and ‘Number of sucker species’
197 (Table S1). Intercept parameters, b , for regressions corresponding to this third removal treatment
198 were up to ~51-fold higher than those for the first removal experiment (median 3.7-fold higher),
199 consistent with a substantial effect on IBI metric scores in essentially all cases. The only
200 exception to this was the ‘% top carnivores metric’, which had a negative intercept ($b = -0.03$)
201 after removal (Table 2). The highest intercept value, $b = 2.92$, was obtained for the regression
202 corresponding to the ‘% DELT + hybrids’ metric.

203 ***IBI metric agreement and rare taxon removal***

204 As noted in the main text, Cohen’s κ calculations were made overall and for each IBI metric to
205 quantify the agreement between post-treatment versus original IBI metric scores. While Fig. 2D–
206 F of the main text provide visualizations of the distributions of per-metric κ -values, colored by
207 metric type, the full results for each per-metric κ test are presented *below* in Table S2. Only four
208 metrics had $\kappa = 1.00$ indicating perfect agreement with their original values after the SRT
209 treatment, including ‘% dominant species’, ‘% invertivores’, ‘% omnivores’, and ‘% simple
210 lithophils’. Two of these metrics, ‘% omnivores’ and ‘% simple lithophils’, also showed perfect
211 agreement with their original values following the ART removal treatment. ‘Total native species’
212 showed the most reduced agreement with original metric scores across our three treatments
213 (Table S2). Central tendencies of κ under each treatment are given in the main text. The overall
214 pattern of κ -value findings supported the SDR treatment as having the greatest effect on the IBI
215 metrics, and SDR and ART having greater effects on IBI metrics than the SRT treatment.

216 **Table S2** Summary of per-metric weighted Cohen’s κ -values for IBI metric scores. Results are presented for all 19 metrics used in
 217 Alabama fish IBIs, with the “Metric label” column giving abbreviated names matching Fig. 2 (for full names, see Table 1, main text).
 218 The three treatments were: 1) removal of single rare taxa, 2) singleton/doubleton removal, and 3) removal of all rare taxa. P -values are
 219 not presented, as all tests were highly significant ($p < 0.0001$), thus κ -values took precedent for interpretation.

Metric label	Single-rare-taxon removal			Singleton/doubleton removal			All-rare-taxa removal		
	N	Cohen’s κ	z	N	Cohen’s κ	z	N	Cohen’s κ	z
Total native spp.	3007	0.88	66.20	719	0.25	12.74	719	0.45	19.45
No. shiner spp.	1885	0.96	57.07	444	0.70	20.24	444	0.85	23.99
No. cyprinid spp.	1122	0.94	41.70	274	0.59	13.54	273	0.74	16.24
No. sucker spp.	2252	0.92	55.89	546	0.47	15.77	545	0.63	19.56
No. darter+madtom spp.	3007	0.93	67.81	719	0.50	20.19	719	0.68	25.41
No. Lepomis spp.	1877	0.91	53.06	447	0.44	12.93	447	0.64	18.21
No. centrarchid spp.	618	0.85	27.94	146	0.26	5.56	146	0.41	7.49
No. intolerant spp.	1267	0.96	45.57	298	0.76	17.50	298	0.85	19.37
% tolerant spp.	2997	0.99	67.84	716	0.95	32.11	717	0.98	32.94
% dominant spp.	1122	1.00	45.81	274	0.94	21.23	273	0.97	21.95
% Lepomis	2389	0.99	62.39	573	0.97	30.12	573	0.99	30.63
% GSF+YB	618	0.95	28.68	145	0.65	9.65	146	0.80	11.56
% invertivores	1130	1.00	42.20	270	0.96	19.97	271	0.99	20.57
% omnivores	1695	1.00	50.80	433	0.99	25.27	433	1.00	25.60
% insect. cyprinids	2067	0.99	59.09	457	0.93	26.12	458	0.97	27.06
% top carnivores	3007	0.95	68.39	718	0.68	24.48	719	0.83	28.90
% DELT+hybrids	3007	0.85	54.61	718	0.27	11.67	719	0.52	17.69
No. lithophilic spawners	1885	0.95	55.41	444	0.63	18.56	444	0.77	22.00
% simple lithophils	1122	1.00	42.67	274	0.98	20.76	273	1.00	21.09

220 Abbreviations: N , sample size; No., number; spp., species (singular or plural); z , test statistic used to determine statistical significance

221 of weighted Cohen’s κ . All other abbreviations follow the caption information for Table 1.

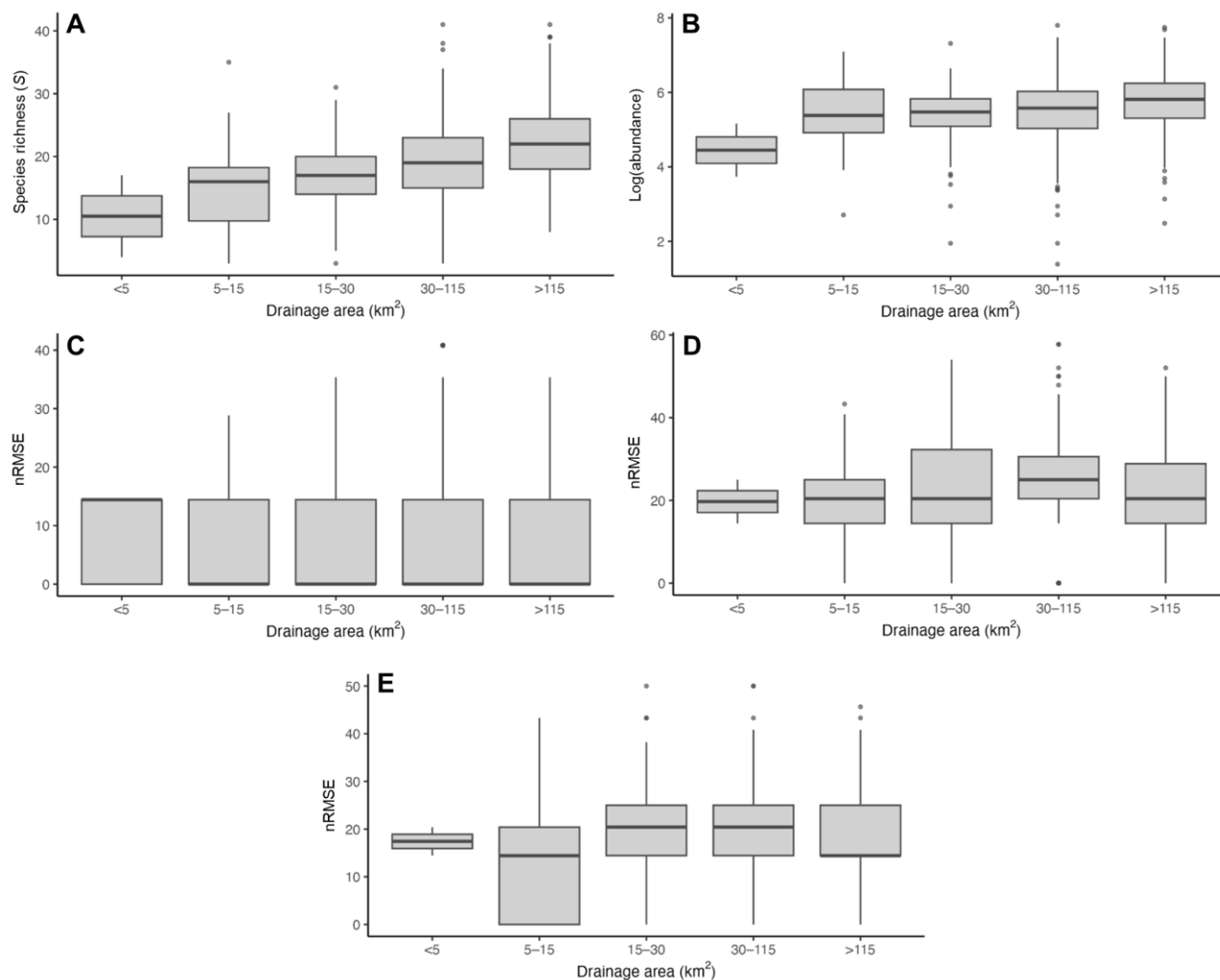
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223 During metric-level analyses, the results of our Wilcoxon signed-rank test on paired SDR
224 vs. ART regression R^2 -values in R showed that these treatments produced significantly different
225 goodness-of-fit statistic distributions across linear regressions of the 19 metrics ($W = 2, z =$
226 $-3.74, p < 0.001$). Additionally, paired Wilcoxon tests on SDR vs. ART slope (a) results also
227 showed significantly different slope distributions across linear regressions, between treatments
228 ($W = 0, z = -3.82, p < 0.001$). Comparisons involving the SRT treatment were not run, even for
229 comparative purposes, due to violations of standard assumptions for statistical tests.

230 *Species composition and drainage area effects*

231 Consistent with Wan et al. (2010), evaluating impacts of upstream drainage area on S , N , and
232 nRMSE values revealed that S and N scaled weakly linearly with drainage area (especially in
233 log–log space; JCB, unpublished results), increasing with each sequential S and N class (Fig
234 S9A, B). However, S showed a slightly more pronounced positive correlation than N , the latter of
235 which was more upwardly skewed for small numbers of samples. Median S increased over our
236 drainage area classes, ranging from ~11 species for the smallest headwater streams ($< 5 \text{ km}^2$) to
237 22 species in the largest streams and rivers ($> 115 \text{ km}^2$). Median N also increased with increasing
238 sample abundance, from ~85 for the smallest drainage class ($< 5 \text{ km}^2$), to ~215 for the second
239 drainage area class ($5\text{--}15 \text{ km}^2$) representing large headwater or headwater-adjacent streams, to
240 ~330 for the largest drainage class. Consistent with our a priori hypothesis, and similar to the box
241 plots examining stratification by species richness and abundance (Figs 4A, B), box plots of
242 nRMSE values from the first removal treatment showed essentially no relationship between
243 effects of SRT removal on IBI metric scores and our five drainage area classes (Fig. S9C).
244 Impacts of removing singleton/doubleton taxa on IBI metrics were roughly similar across
245 drainage sizes, but lower quantile and median nRMSE values were higher than for the SRT

246 removal and they also decreased slightly for the third drainage area class but increased in the
 247 fourth drainage area class (Fig. S9D), and median values ranged from 14.4 to 20.4 for the SDR
 248 removal treatment. By contrast, median values were noticeably higher for both the third and
 249 fourth drainage area classes following the ART removal, and median and quantile values of



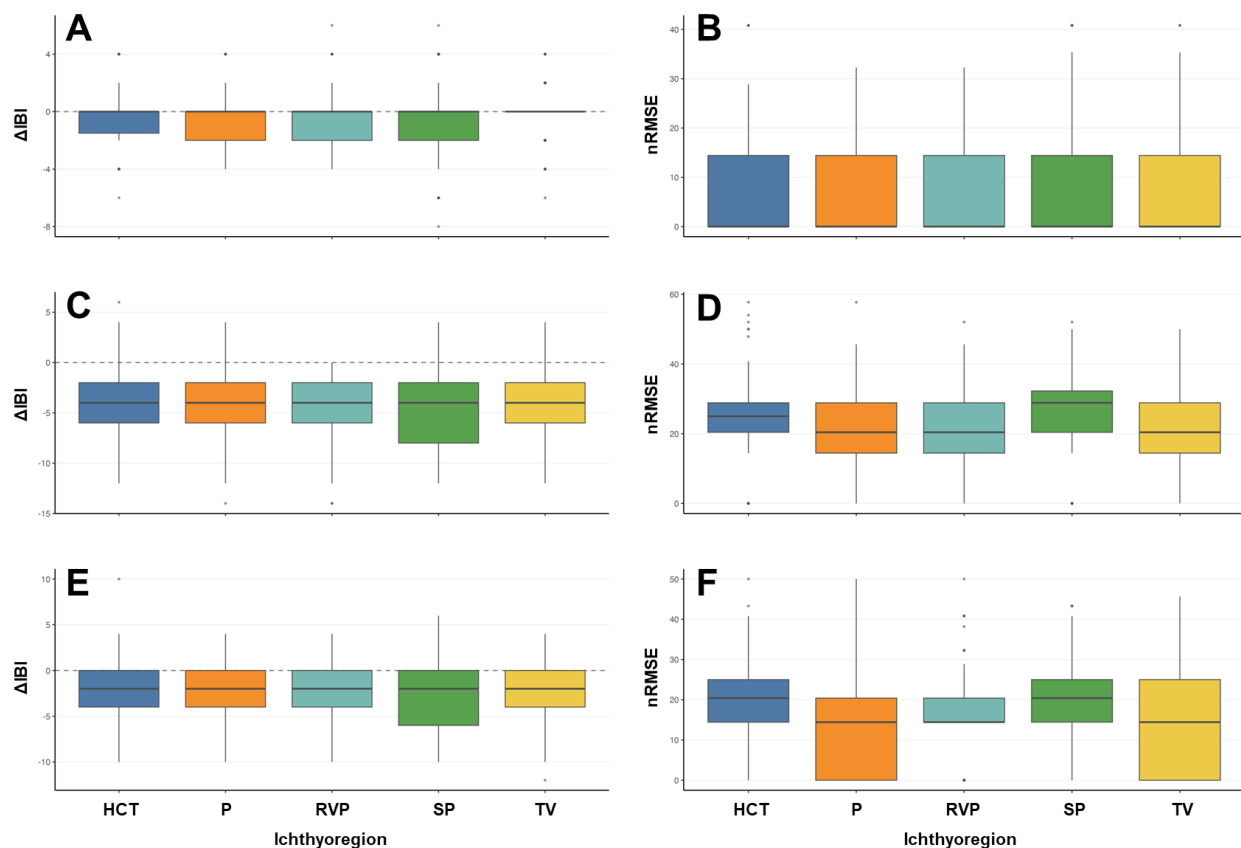
250
 251 **Fig. S9** Box plots evaluating the effects of upstream drainage area on fish community
 252 characteristics and IBI metric sensitivity to rare taxon removals in this study. Plotted along the y-
 253 axis, the panels show (A) species richness (S), (B) total abundance (N , number of individuals),
 254 (C) IBI metric nRMSE values after removal of individual rare taxa within each site (SRT), (D)
 255 IBI metric nRMSE values after removal of singleton/doubleton taxa (SDR), and (E) IBI metric
 256 nRMSE values after removal of all rare taxa from within each site (ART treatment). Box
 257 representations are the same as those described in the caption to Fig. S3 above, except each box
 258 is filled with *gray shading* and separate boxes are plotted for each drainage area class.

259 nRMSE from the ART treatment ranged from 20.4 to 22.7 and essentially showed no overall
260 relationship with increasing drainage size (Fig. S9E).

261 *Ichthyoregion-specific effects of rare taxon removal*

262 Ichthyoregion-specific results are discussed in the main text while referencing the supplementary
263 Fig. S10 *below*, which shows effects of our treatments on site IBI metrics and IBI scores, as
264 judged by Δ IBIs and nRMSEs, respectively, plotted as a function of ichthyoregion. The Δ IBIs
265 and nRMSEs had median values at/near zero under the SRT treatment (Fig. S10A,B), indicating
266 limited effects of single rare taxon removals, as well as similar effects of this treatment across
267 space and biogeographic context, as represented by Alabama's ichthyoregions. By contrast, the
268 greatest effects were witnessed in the SP and HCT ichthyoregions, which are located below the
269 Fall Line (O'Neil and Shepard 2007, 2009, 2010), under the SDR and ART treatments. Stronger
270 effects in these regions were primarily registered as effects on metric scores, i.e., higher median
271 nRMSE values, for these treatments, and the significance of differences in nRMSE between
272 ichthyoregions within treatments was evaluated using Kruskal–Wallis omnibus tests discussed in
273 the text. Kruskal–Wallis tests pool all response variable values across groups, sort them from
274 smallest to largest, and substitute them with ranks; ranks belonging to each group are averaged to
275 yield a mean rank; and the null hypothesis, that the difference between the mean ranks of all
276 groups is zero, is tested. Since we obtained significant results in analyses of each treatment, post-
277 hoc Dunn tests with Holm correction were used to see which pairwise relationships between
278 groups (i.e., ichthyoregions) showed significant differences, and thus contributed to the
279 significant test results. Post-hoc Dunn tests (Table S3) indicated that the SP ichthyoregion
280 exhibited significantly higher nRMSE than the P ichthyoregion (ART: $p_{\text{Holm-adjusted}} < 0.001$; SDR:
281 $p_{\text{Holm-adjusted}} < 0.0001$), RVP ichthyoregion (ART: $p_{\text{Holm-adjusted}} = 0.0014$; SDR: $p_{\text{Holm-adjusted}} = <$

282 0.0001), and TV ichthyoregion (SRT: $p_{\text{Holm-adjusted}} = 0.0073$; SDR: $p_{\text{Holm-adjusted}} < 0.0001$; ART:
 283 $p_{\text{Holm-adjusted}} = 0.0022$) under two or more treatments. The HCT ichthyoregion showed
 284 significantly higher nRMSE than the P ichthyoregion (ART: $p_{\text{Holm-adjusted}} = 0.0056$; SDR: $p_{\text{Holm-}}$
 285 $p_{\text{Holm-adjusted}} = 0.0146$), RVP ichthyoregion (ART: $p_{\text{Holm-adjusted}} = 0.0115$; SDR: $p_{\text{Holm-adjusted}} = 0.0260$),
 286 and TV ichthyoregion (ART: $p_{\text{Holm-adjusted}} = 0.0125$) under the ART and SDR treatments. By



287
 288 **Fig. S10** Summaries of changes in IBI score (ΔIBI) across sites (left column) and IBI metric
 289 nRMSE (right column) as a function of ichthyoregion ($n = 5$; Fig. S1). Results are presented as
 290 box plots stratified ichthyoregion for our three treatments, including (A, B) SRT removal, (C, D)
 291 SDR removal, and (E, F) ART removal. Box representations are the same as those described in
 292 the caption to Fig. S3 *above*, except each box is assigned a different *color* based on
 293 ichthyoregion (*x*-axis labels; abbreviations: HCT, Hills and Coastal Terraces; P, Plateau; RVP,
 294 Ridge and Valley/Piedmont; SP, Southern Plains; TV, Tennessee Valley).

295

296 **Table S3** Summary of Dunn post-hoc test results evaluating the magnitude and significance of differences in nRMSEs for all pairs of
 297 ichthyoregions, within each treatment. For each treatment, the groups compared are listed along with the resulting *Z* statistic, raw *p*-
 298 value of the test, Holm-adjusted *p*-value, and significance level (see inset caption details in text box).

Treatment	Group 1	Group 2	<i>Z</i>	<i>p</i> (raw)	<i>p</i> (Holm-adjusted)	Significance
SRT	HCT	P	-0.871	0.384	1.000	
SRT	HCT	RVP	2.037	0.042	0.250	
SRT	P	RVP	2.937	0.003	0.027	*
SRT	HCT	SP	-1.599	0.110	0.439	
SRT	P	SP	-0.706	0.480	0.961	
SRT	RVP	SP	-3.751	<i>p</i> < 0.001	0.002	**
SRT	HCT	TV	1.770	0.077	0.383	
SRT	P	TV	2.607	0.009	0.064	
SRT	RVP	TV	-0.122	0.903	0.903	
SRT	SP	TV	3.349	<i>p</i> < 0.001	0.007	**
SDR	HCT	P	3.077	0.002	0.015	*
SDR	HCT	RVP	2.853	0.004	0.026	*
SDR	P	RVP	-0.409	0.683	1.000	
SDR	HCT	SP	-1.662	0.097	0.386	
SDR	P	SP	-4.764	<i>p</i> < 0.0001	<i>p</i> < 0.0001	***
SDR	RVP	SP	-4.644	<i>p</i> < 0.0001	<i>p</i> < 0.0001	***
SDR	HCT	TV	2.340	0.019	0.096	
SDR	P	TV	-0.678	0.498	1.000	
SDR	RVP	TV	-0.317	0.751	0.751	
SDR	SP	TV	3.987	<i>p</i> < 0.0001	<i>p</i> < 0.0001	***
ART	HCT	P	3.352	<i>p</i> < 0.001	0.006	**
ART	HCT	RVP	3.102	0.002	0.012	*
ART	P	RVP	-0.450	0.652	1.000	
ART	HCT	SP	-0.601	0.548	1.000	
ART	P	SP	-3.989	<i>p</i> < 0.0001	<i>p</i> < 0.001	***
ART	RVP	SP	-3.778	<i>p</i> < 0.001	0.001	**
ART	HCT	TV	3.022	0.003	0.013	*
ART	P	TV	-0.269	0.788	1.000	
ART	RVP	TV	0.158	0.875	0.875	
ART	SP	TV	3.643	<i>p</i> < 0.001	0.002	**

In Table S3, ichthyoregion abbreviation definitions follow the main text and Fig. S1. Significance: * *p* < 0.05; ** *p* < 0.01; *** *p* < 0.001 (all Holm-adjusted). Also, positive *Z*-values indicate that Group 1 had a higher nRMSE rank than Group 2.

300 contrast, no pairwise contrast involving the two least sensitive ichthyoregions, i.e., the TV and P
301 ichthyoregions located above the Fall Line, was statistically significant at the $\alpha = 0.05$ level
302 under any treatment. Taken together, the Kruskal–Wallis and Dunn post-hoc test results indicate
303 that the elevated nRMSE values observed in HCT and SP (Fig. S10) reflect a statistically robust,
304 ichthyoregion-level pattern rather than a sampling artifact, and that this pattern persists across
305 multiple treatments and multiple pairwise comparisons after correction for multiple testing
306 (Table S3).

307 **Supplementary Discussion**

308 Multimetric indices such as the IBI integrate information from biological surveys and drainage
309 characteristics to reveal the structure of local aquatic ecosystems and their responses to human-
310 induced stressors and environmental degradation (Karr 1981; Karr et al. 1986). One key aspect
311 of MMI and IBI applications is component metric selection. Effective metrics must be sensitive,
312 repeatable, capable of distinguishing natural variability in biological condition from human
313 influences, and limited in sensitivity to sampling error (Herricks and Shaefer 1985; Karr et al.
314 1986; Karr and Chu 1997; Vadas et al. 2022). To date, however, studies of IBI sensitivity to
315 errors and variation in component metrics have been sporadic, leaving the topic understudied.
316 Available studies have also used different methods to analyze widely varying datasets, making
317 comparisons difficult. For example, evaluations of the sensitivity of IBI metrics and outcomes to
318 subsampling ($n = 9$ lakes; Barbour and Gerritsen 1996), repeat sampling ($n = 12$ – 37 sites; Fore et
319 al. 1994; Hughes et al. 1998), IBI metrics ($n = 46$ – 84 sites; Angermeier and Karr 1986), rare taxa
320 ($n = 378$ sites; Wan et al. 2010), and DELTs/anomalies and hybrids ($n = 646$ sites; Bagley et al.
321 2025) have used macroinvertebrate or fish datasets varying over ~ 70 -fold in sample size. We
322 recently showed that fish IBIs for Alabama streams were robust to errors in detecting

323 DELTs/anomalies and hybridization, but artificial errors altered 13.2% of IBI scores and ~6% of
324 condition ratings, with important management implications (Bagley et al. 2025). While Bagley et
325 al. (2025) focused on the effects of a single metric—the ‘% DELT + hybrids’ metric, they also
326 highlighted the need for broader sensitivity analyses evaluating multiple IBI metrics and
327 outcomes and further exploring the space of IBI responses to sampling errors. In the present
328 study, we took steps towards meeting this need, and our results demonstrate that Alabama fish
329 IBI metrics and outcomes are consistently and significantly disrupted by simulated non-detection
330 of rare taxa, extending the core findings of Wan et al. (2010) to a state with among the most
331 diverse aquatic faunas in the contiguous United States and validating the generality of their
332 findings for Midwestern US fishes across sharply contrasting ecological and biogeographical
333 regions in the southeastern US.

334 The fact that we found a congruent pattern between our results for Alabama fish IBIs and
335 those that Wan et al. (2010) reported for Minnesota, with species richness-based metrics being
336 more sensitive to rare taxon removal than abundance-based metrics, is particularly noteworthy
337 given that metrics showed only ~44% similarity between our two studies. For example, our
338 dataset containing eight similar IBI metrics (‘Total native species’, ‘Number of darter + madtom
339 species’, ‘Number of intolerant species’, ‘% dominant species’, ‘% DELT + hybrids’, ‘%
340 omnivores’, ‘% simple lithophils’, and ‘% of tolerant species’; Table 1) as compared with those
341 of Wan et al. (2010), plus 11 metrics that differed from the metrics that they used. Such higher-
342 level congruence despite lower-level methodological differences suggests that this trend has
343 generality across space and time and is likely to translate well to other warmwater stream IBI
344 tools and systems in other areas of North America, if not other regions.

345 Our inferences that singletons/doubletons are commonly encountered during Alabama

346 fish IBI surveys and that singleton/doubleton removal had the greatest effects on IBI metrics and
347 outcomes add important insights to our understanding of fish community ecology and surface
348 water bioassessment in the state. Singleton/doubleton observations are often viewed as indicative
349 of scarce local populations (e.g., Maciel and Arlé 2020), but systematists have shown that
350 singletons are very common in nature and in taxonomic treatments (e.g., Lim et al. 2011). Even
351 so, we do not assume that taxa appearing in our dataset as singleton or doubleton observations
352 are intrinsically rare in nature—only that they were *sampled* in very low numbers during the time
353 and at the location of the corresponding field survey, since 1) detection probabilities vary widely
354 among species and 2) fish species were not exhaustively sampled to determine their true
355 abundances (instead, all observations reflect relative abundances; *cf.* Bayley and Peterson 2001;
356 Kanno et al. 2009). Reasons that singleton/doubleton observations during fish IBI surveys might
357 not reflect fish species true abundances within streams include failures to observe individuals
358 due to depth or turbidity, as well as interspecific variation in susceptibility to electrofishing (e.g.,
359 ictalurids vs. other taxa; Kanno et al. 2009).

360

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