SUPPLEMENTARY MATERIAL

Rare species contribute disproportionately to the functional structure of species assemblages

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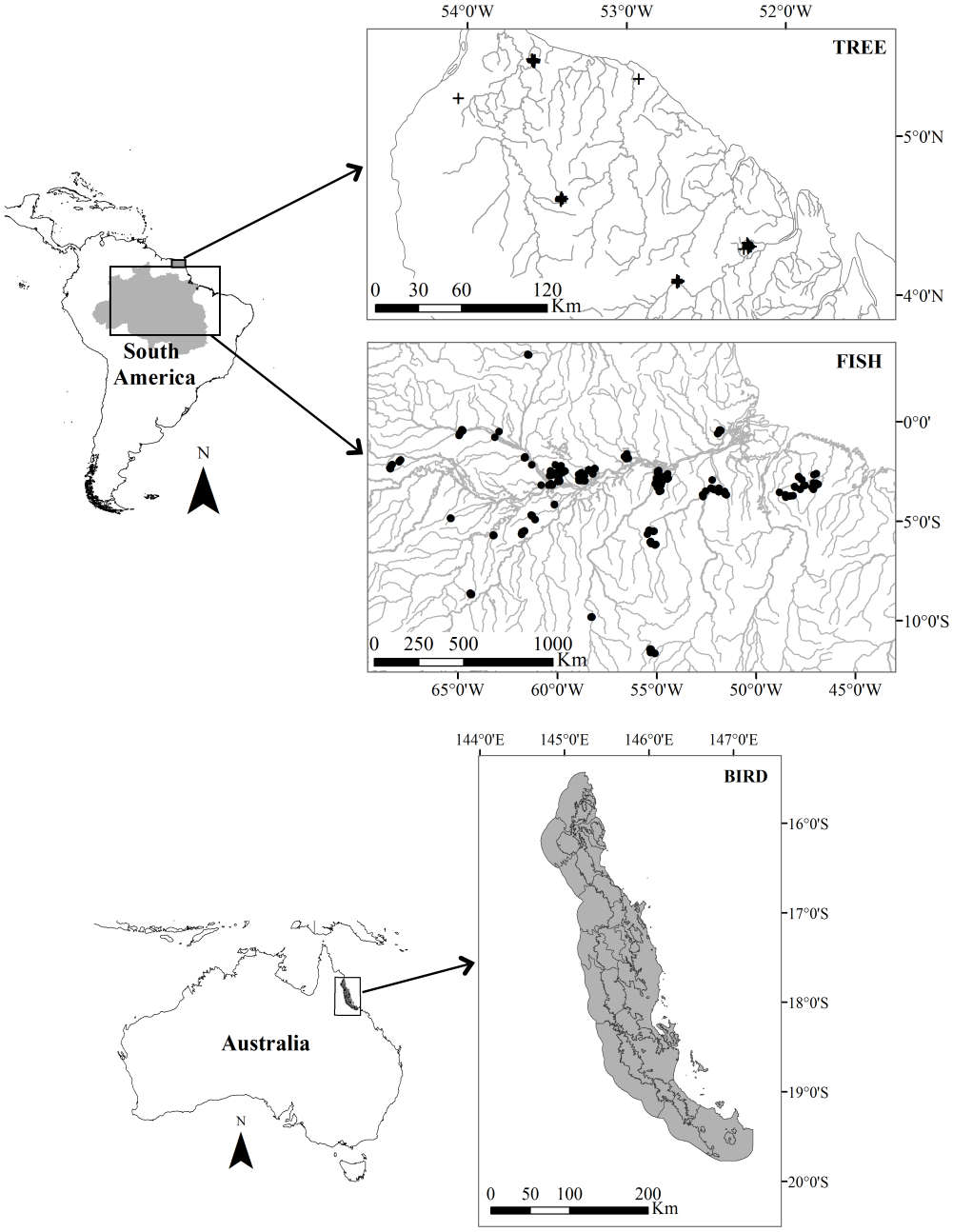

Figure S1. Geographic locations sampled for rainforest trees in French Guiana (36 plots represented by black cross), stream fish in the Brazilian Amazon (320 sites represented by black dots; grey polygon in South America map delimiting the Brazilian Amazon Basin), and birds in the Australian Wet Tropics (47 sub-regions).

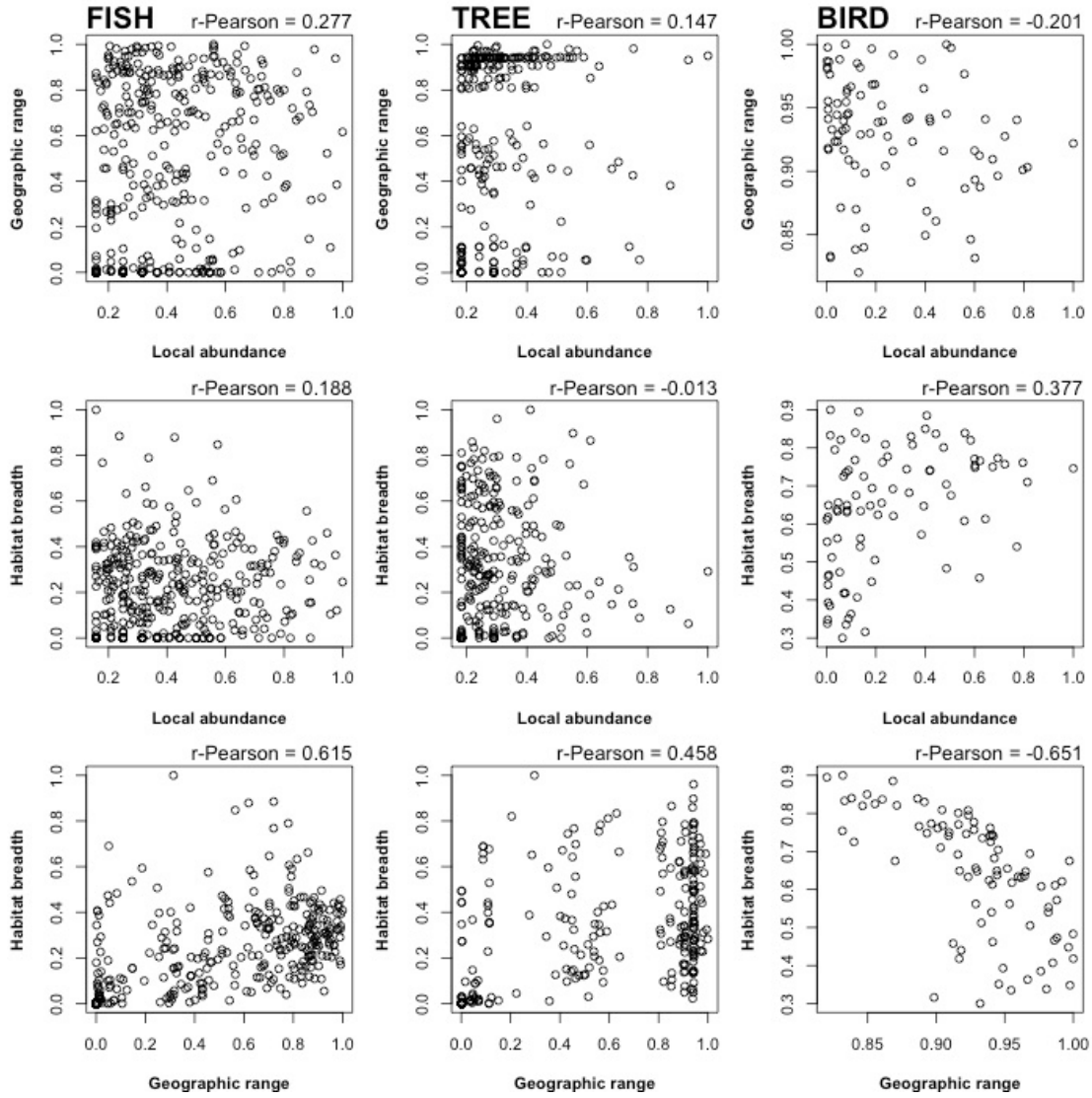

Figure S2. Correlations between the three metrics (local abundance, geographic range, and habitat breadth) used to build an integrative measure of rarity vs. commonness (i.e. Rarity Index – RI_i) for each species of: stream fish from the Brazilian Amazon (395 species; left plots), rainforest trees from French Guiana (262 species; middle plots), and birds from the Australian Wet Tropics (86 species; right plots). Each metric was log-transformed and standardized between 0 and 1.

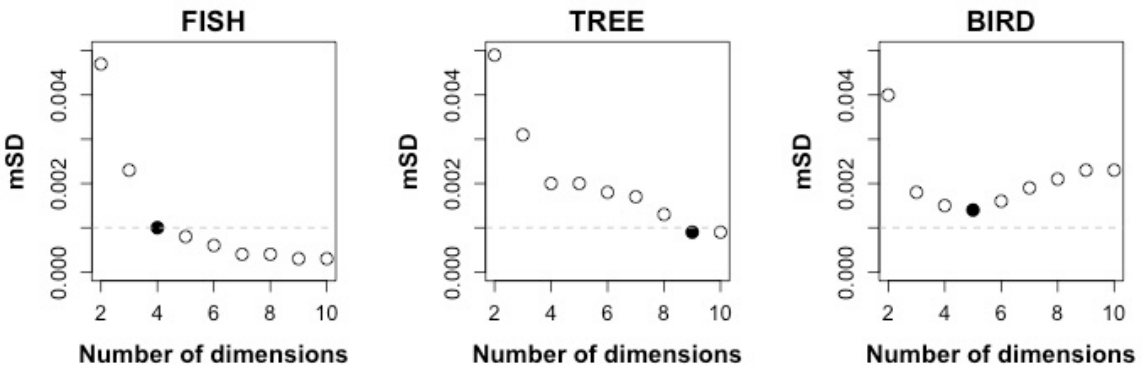

Figure S3. Evaluation of the quality of the functional spaces. Plots show the Mean Squared-Deviation index (mSD) when using different numbers of dimensions (i.e. PCoA axes) to build functional spaces. The chosen number of axes for each taxonomic group (i.e. fish = 4; trees = 9; birds = 5) is represented by a black dot. mSD values <0.001 (grey dashed line) indicate functional spaces with high quality according to Maire *et al.* [1]. Although the functional space with four dimensions for fish dataset is not the best one, it has high quality and does not demand removing many samples to compute functional indices (i.e. most local assemblages have at least five species).

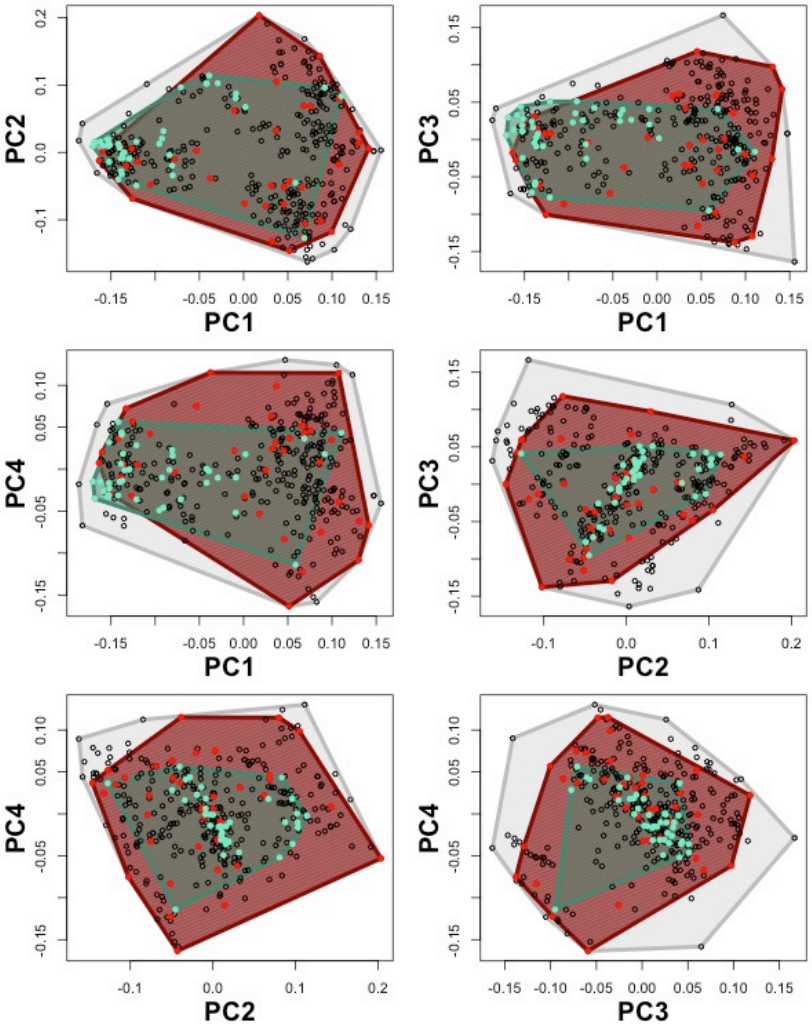

Figure S4. Four-dimensional functional space of the regional pool of stream fish from the Brazilian Amazon (395 species). Each plot represents two axes of a Principal Coordinate Analysis (PC), where species are plotted with circles according to their respective trait values. The 10% rarest and 10% commonest species are filled with red and green, respectively. Projections of the convex hull volumes are illustrated by the polygons embedding: all species (grey), the 10% rarest (red), and the 10% commonest (green) species.

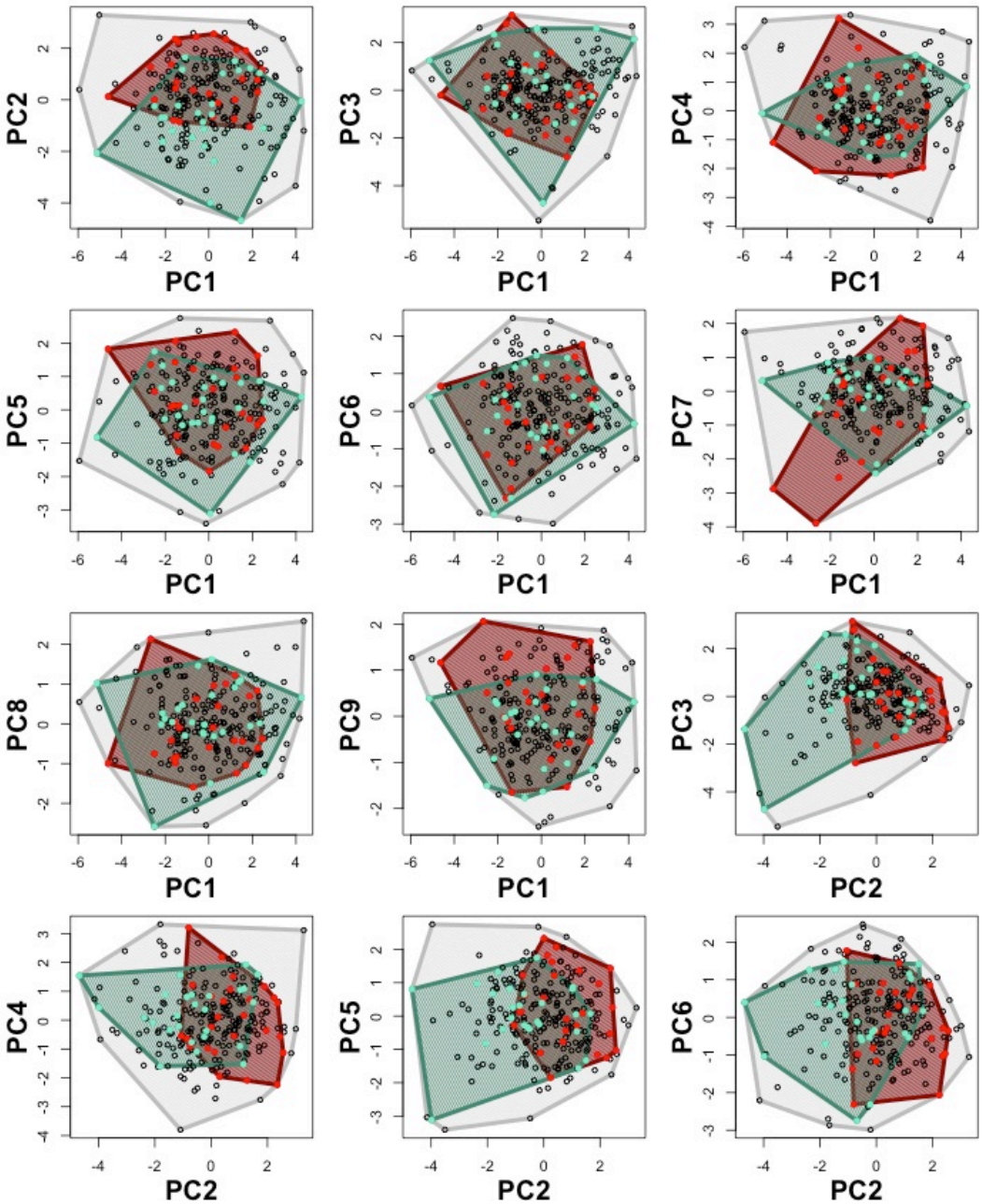

Figure S5. Nine-dimensional functional space of the regional pool of rainforest trees from French Guiana (262 species). Each plot represents two axes of a Principal Coordinate Analysis (PC), where species are plotted with circles according to their respective trait values. The 10% rarest and 10% commonest species are filled with red and green, respectively. Projections of the convex hull volumes are illustrated by the polygons embedding: all species (grey), the 10% rarest (red), and the 10% commonest (green) species.

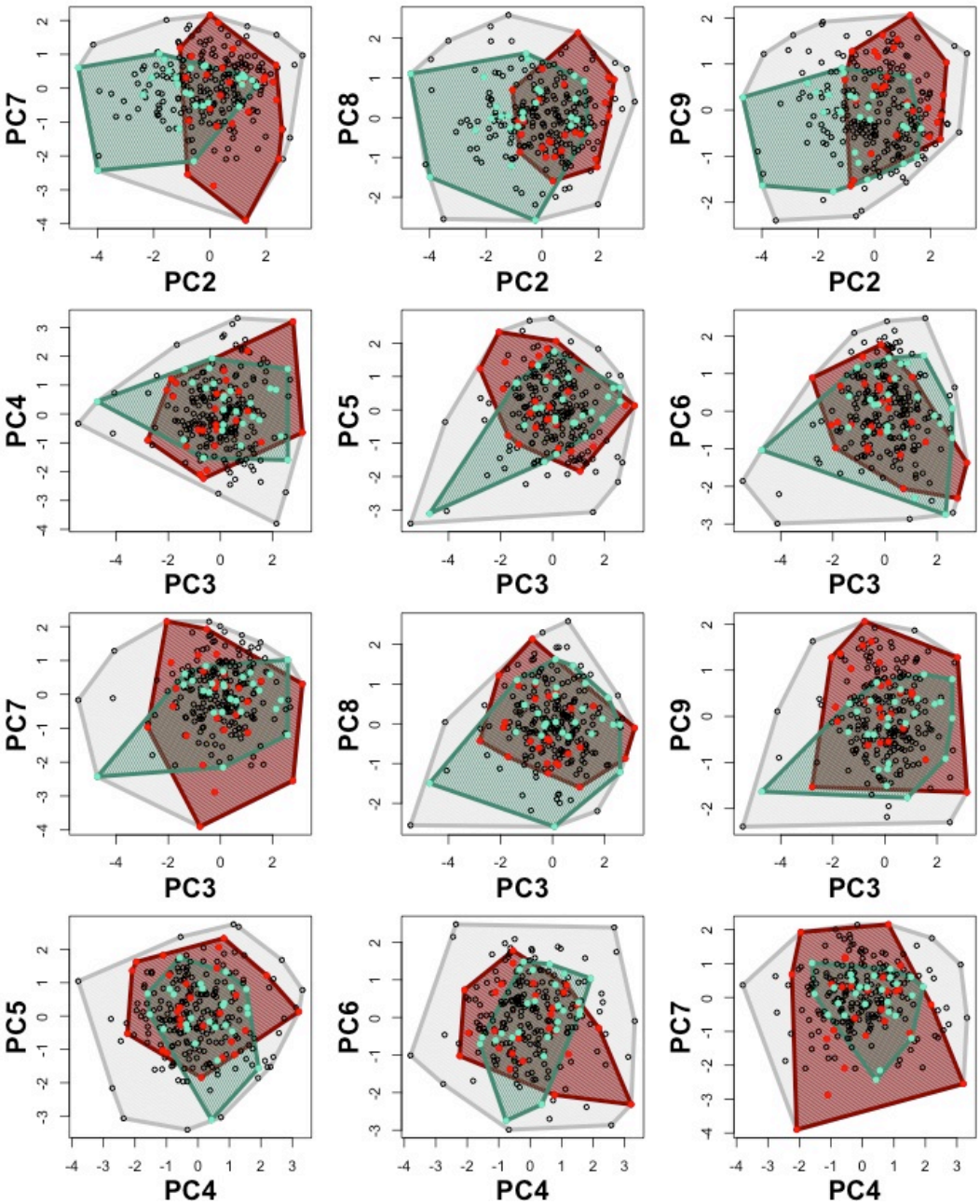

Figure S5 (continuation)

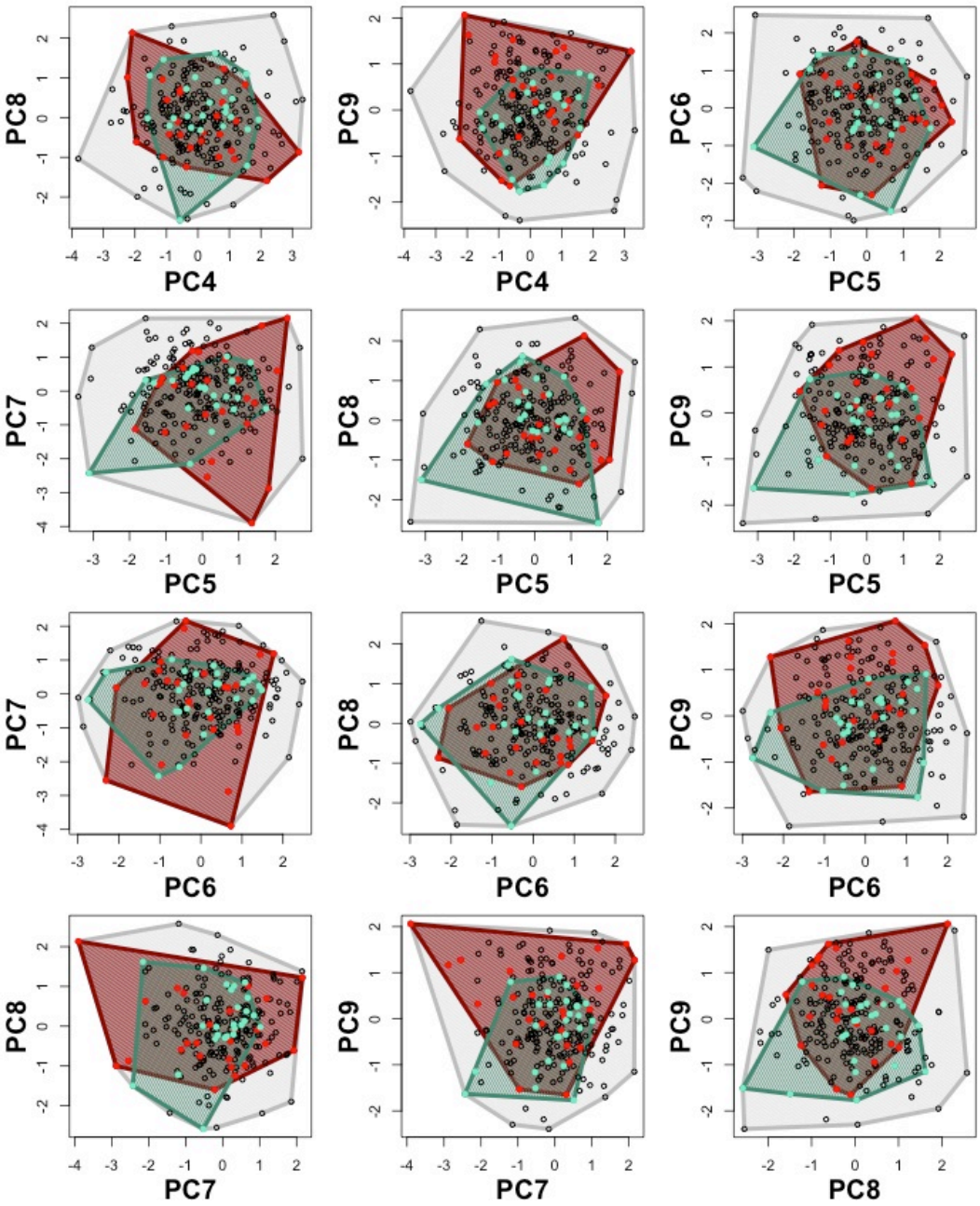

Figure S5 (continuation)

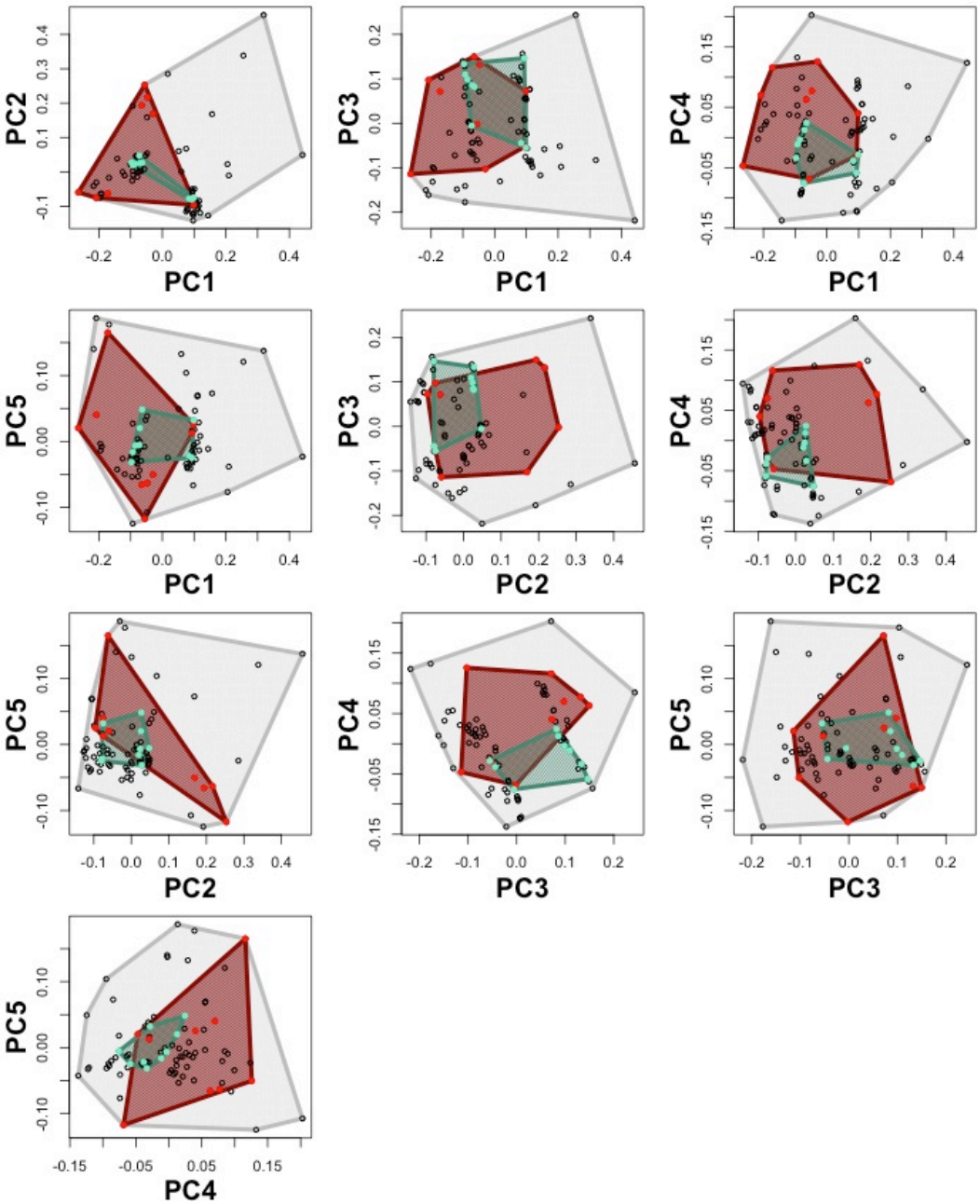

Figure S6. Five-dimensional functional space of the regional pool of birds from the Australian Wet Tropics (86 species). Each plot represents two axes of a Principal Coordinate Analysis (PC), where species are plotted with circles according to their respective trait values. The 10% rarest and 10% commonest species are filled with red and green, respectively. Projections of the convex hull volumes are illustrated by the polygons embedding: all species (grey), the 10% rarest (red), and the 10% commonest (green) species.

SUPPLEMENTARY TABLES

Table S1. Eigenvalues and explained variance (%) of each PCoA axis used to build the multidimensional functional spaces for fish, tree, and bird assemblages. The low variance values for fish and bird datasets should be considered with caution, as in PCoA based on Gower distances the maximal number of axes possible is the number of species minus one. See detailed criteria to select the number of dimensions in Material and Methods.

PCoA	FISH		TREE		BIRD	
axis	Eigenvalue	%ExpVariance	Eigenvalue	%ExpVariance	Eigenvalue	%ExpVariance
1	12.69	12.78	3.41	22.77	5.46	16.64
2	7.19	7.23	1.96	13.10	3.51	10.71
3	4.45	4.45	1.45	9.68	2.85	8.69
4	3.69	3.71	1.30	8.66	1.57	4.80
5	-	-	1.16	7.75	1.16	3.55
6	-	-	1.03	6.87	-	-
7	-	-	0.88	5.87	-	-
8	-	-	0.75	5.02	-	-
9	-	-	0.74	4.96	-	-

Table S2. Friedman paired test (χ^2; p-value) comparing the functional structure – FS (functional richness – FRic, specialization – FSpe, and originality – FOri) of local assemblages (stream fish from the Brazilian Amazon, rainforest trees from French Guiana, and birds from the Australian Wet Tropics) after species-loss simulations (from 10 to 90% of local richness) on three different scenarios: lose rarest species first; lose commonest species first; and lose species randomly (sampled in each local pool 1,000 times). N: number of local assemblages used for each level of species loss.

FS index	Species loss (%)	FISH			TREE			BIRD		
		χ^2	p	N	χ^2	p	N	χ^2	p	N
FRic	**10**	54.8	< 0.001	294	2.3	0.311	6	71.4	< 0.001	47
	20	80.3	< 0.001	294	4.0	0.135	6	94.0	< 0.001	47
	30	64.1	< 0.001	264	7.0	0.030	6	94.0	< 0.001	47
	40	79.3	< 0.001	246	12.0	0.002	6	94.0	< 0.001	47
	50	86.3	< 0.001	218	10.3	0.006	6	94.0	< 0.001	47
	60	104.6	< 0.001	149	12.0	0.002	6	94.0	< 0.001	47
	70	92.6	< 0.001	104	7.0	0.030	6	94.0	< 0.001	47
	80	48.2	< 0.001	39	1.5	0.472	4	94.0	< 0.001	47
	90	6.0	0.049	4	-	-	1	92.0	< 0.001	47
FSpe	**10**	49.4	< 0.001	319	1.0	0.607	6	94.0	< 0.001	47
	20	79.5	< 0.001	319	2.3	0.311	6	94.0	< 0.001	47
	30	66.9	< 0.001	319	9.3	0.009	6	94.0	< 0.001	47
	40	57.0	< 0.001	319	12.0	0.002	6	94.0	< 0.001	47
	50	67.2	< 0.001	319	12.0	0.002	6	94.0	< 0.001	47
	60	60.8	< 0.001	319	12.0	0.002	6	94.0	< 0.001	47
	70	63.8	< 0.001	319	10.3	0.006	6	94.0	< 0.001	47
	80	79.5	< 0.001	317	2.3	0.310	6	94.0	< 0.001	47
	90	49.5	< 0.001	306	1.0	0.607	6	94.0	< 0.001	47
FOri	**10**	110.2	< 0.001	319	1.3	0.513	6	94.0	< 0.001	47
	20	99.7	< 0.001	319	4.3	0.115	6	94.0	< 0.001	47
	30	40.4	< 0.001	319	10.3	0.006	6	94.0	< 0.001	47
	40	15.7	< 0.001	319	7.0	0.030	6	94.0	< 0.001	47
	50	3.3	0.193	319	10.3	0.006	6	94.0	< 0.001	47
	60	16.0	< 0.001	319	7.0	0.030	6	94.0	< 0.001	47
	70	42.7	< 0.001	319	8.3	0.016	6	94.0	< 0.001	47
	80	103.8	< 0.001	317	4.3	0.115	6	94.0	< 0.001	47
	90	116.7	< 0.001	306	1.3	0.513	6	94.0	< 0.001	47

Table S3. List of functions and R-packages for computations.

Main goal	Specific action	Function	Library
Rarity index	Geographic range (Extend of Occurrence – EOO)	SpatialPoints projection spTransform gArea	sp raster rgdal rgeos
Rarity index	Geographic distance	spDists	sp
Rarity index	Habitat breadth (Outlying Mean Index – OMI)	niche	ade4
Rarity index	Correlations among rarity facets	cor	stats
Functional structure	Dissimilarity matrix (Gower or Euclidean distance)	daisy	cluster
Functional structure	Synthetic axes for multidimensional functional space	pcoa	ape
Functional structure	Sensitivity analysis *ii*	mantel	vegan
Functional structure	Functional richness – FRic	convhulln	geometry
Functional structure	Functional specialization – FSpe Functional originality – FOri	* adapted from FDind	ape geometry
Data analysis	Randomizations for null models	sample	base

* http://esapubs.org/archive/appl/A020/056/suppl-1.htm

APPENDICES

Appendix S1. Local habitat assessment

Fishes

A set of 15 environmental parameters describing stream channel structure, substrate and water quality was taken at each sampled site (320 streams) in the Brazilian Amazon (table A1.1; figure A1.1). These variables were used to estimate the habitat breadth of each fish species in this study. Detailed description of measurements is found in Mendonça *et al.* [2].

Table A1.1. Environmental parameters measured in each of the 320 streams sampled for fish in the Brazilian Amazon.

Group	Variable	Unit	Mean	Min	Max
Channel structure	Mean width	m	2.28	0.44	10.78
	Mean depth	m	0.21	0.02	0.87
	Mean current velocity	cm s^{-1}	18.56	0.00	100.68
Substrate	Sand	%	24.99	0.00	88.89
	Clay	%	5.76	0.00	91.43
	Coarse litter	%	33.48	0.00	97.22
	Organic silt	%	12.40	0.00	64.44
	Trunk	%	5.89	0.00	38.00
	Fine roots	%	11.69	0.00	58.33
	Macrophytes	%	1.24	0.00	75.24
	Gravel	%	2.60	0.00	56.19
	Boulder	%	1.97	0.00	88.89
Water quality	Temperature	° C	24.82	20.40	29.40
	O2	mg L^{-1}	5.18	0.62	8.81
	pH	N/A	5.00	3.02	8.70

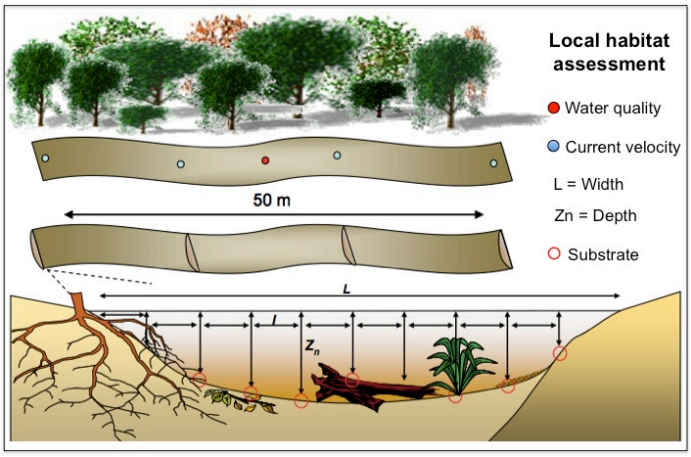

Figure A1.1. Schema of local habitat assessment for Amazonian fishes showing where each environmental parameter was measured at the streams.

Trees

A set of 14 environmental parameters describing climate and soil characteristics was taken at each sampled site (36 forest plots) in lowland rainforests from French Guiana (table A1.2). These variables were used to estimate the habitat breadth of each tree species in this study. The plots covered common lowland forest habitats of tropical South America (seasonally flooded, non-flooded and white-sand forests). Detailed description of measurements is found in Baraloto *et al.* [3,4] and Fortunel *et al.* [5,6].

Table A1.2. Environmental parameters measured in each of the 36 rainforest plots sampled for trees in French Guiana.

Group	Variable	Unit	Mean	Min	Max
Climate	Rainfall	mm yr^{-1}	3208.53	2471.00	4421.00
	Dry season index	days	27.91	23.70	36.80
Soil	N	%	0.21	0.02	0.76
	C	%	3.08	0.51	13.62
	C : N	N/A	16.40	1.94	26.41
	NO_3 – N	ppm	8.14	0.10	55.22
	Olsen P	ppm	3.19	1.00	12.20
	K	mEq/100g	0.09	0.01	0.22
	Na	mEq/100g	0.06	0.01	0.16
	Ca	mEq/100g	0.41	0.03	4.15
	Mg	mEq/100g	0.36	0.06	1.83
	Sand	%	72.07	18.00	99.00
	Silt	%	8.42	1.00	36.00
	Clay	%	19.54	0.43	69.00

Appendix S2. Functional trait assessment

Fishes

We conducted an ecomorphological analysis to evaluate functional structure in fish assemblages by characterizing all the 395 species for three key functions: food acquisition, locomotion, and habitat preferences. Body mass and morphometric measures (figure A2.1) were taken on 1,965 specimens (up to 12 individuals per species), preferably from different sites, and then combined into 15 ecomorphological traits (table A2.1). To scale at the species level we used the mean values for each trait measured across individuals. These traits, except the log-transformed mass, are expressed as unitless ratios, reducing body-size effects. We also assessed the number and shape of teeth and gill rakers on one individual per species. These 18 traits have been previously used in studies on functional morphology and ecomorphology of fish (table A2.1).

Specimens were weighted using electronic balance (0.001 g). Body width, mouth width, mouth depth, snout length and protrusion length were measured using digital caliper (0.1 mm). The other morphological measures were taken by the use of digital pictures analyzed in Image J software (0.1 mm). The evaluation of gill-raker and teeth characteristics was made under binocular microscope.

Although this standard protocol was designed to cover a broad range of morphologies among fish groups [7], we had to use some particular conventions. Synbranchiformes and Gymnotiformes (except Apteronotidae) have no caudal fin, so the *Aspect ratio of the caudal fin*, *Fins surface ratio*, and *Caudal peduncle throttling* were fixed to 0. Synbranchiformes also have no pectoral fins, so *Pectoral fin position*, *Aspect ratio of the pectoral fin*, and *Fins surface to body size ratio* were fixed to 0.

Voucher specimens are deposited in the fish collection of National Institute for Amazonian Research – INPA, Manaus, Brazil.

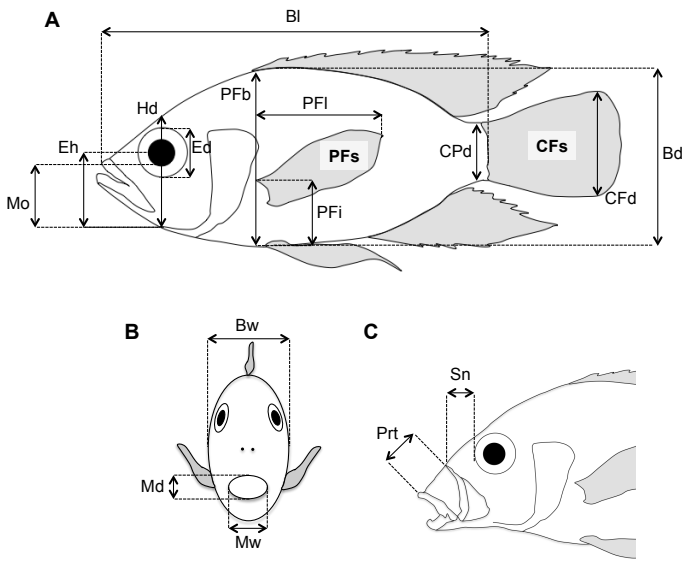

Figure A2.1. Morphological traits measured for fish on digital pictures (A): *Bd* body depth, *CPd* caudal-peduncle minimal depth, *CFd* caudal-fin depth, *CFs* caudal-fin surface, *PFi* distance between the insertion of pectoral fin to the bottom of the body, *PFb* body depth at the level of the pectoral-fin insertion, *PFl* pectoral-fin length, *PFs* pectoral-fin surface, *Hd* head depth along the vertical axis of the eye, *Ed* eye diameter, *Eh* distance between the center of the eye to the bottom of the head, *Mo* distance from the top of the mouth to the bottom of the head along the head depth axis; and with digital caliper (B, C): *Bw* body width, *Md* mouth depth, *Mw* mouth width, *Sn* snout length, *Prt* protrusion length.

Table A2.1. List of the 18 functional traits measured for stream fish from the Brazilian Amazon. Codes for morphological measures are showed in figure A2.1.

Functional trait	Calculation/ Class	Nature	Ecological meaning	References
Teeth shape (Tsh)	Absent Canine Comb-shaped Conic Incisiform Molariform Aliasing multicuspid Spoon-shaped Tricuspid Viliform	Nominal	Nature of food items captured and feeding method	adapted from [8,9,10]
Number of teeth (Tnu)	Mean number of teeth between upper and lower jaws	Continuous	Nature of food items captured and feeding method	adapted from [8]

Gill-raker shape (Rsh)	Absent Short/ sparse Intermediate Long/ numerous	Ordinal	Filtering ability and gill protection	adapted from [11]
Mouth-protrusion length (Prt)	$\frac{Prt}{Sn}$	Continuous	Nature of food items captured and feeding method	adapted from [8]
Oral-gape surface (Osf)	$\frac{Mw \times Md}{Bw \times Bd}$	Continuous	Nature/Size of food items captured	adapted from [12]
Oral-gape shape (Osh)	$\frac{Md}{Mw}$	Continuous	Method to capture food items	[12]
Oral-gape position (Ops)	$\frac{Mo}{Hd}$	Continuous	Feeding method in the water column	adapted from [11]
Eye size (Edst)	$\frac{Ed}{Hd}$	Continuous	Prey detection	adapted from [13]
Eye position (Eps)	$\frac{Eh}{Hd}$	Continuous	Vertical position in the water column	[8]
Body transversal shape (Bsh)	$\frac{Bd}{Bw}$	Continuous	Vertical position in the water column and hydrodynamism	[11]
Body transversal surface (Bsf)	$\frac{\ln\left[\left(\frac{\pi}{4} \times Bw \times Bd\right) + 1\right]}{ln\ (\text{Mass} + 1)}$	Continuous	Mass distribution along the body for hydrodynamism	[7]
Pectoral-fin position (PFps)	$\frac{PFi}{PFb}$	Continuous	Pectoral fin use for maneuverability	[14]
Aspect ratio of the pectoral fin (PFar)	$\frac{PFl^2}{PFs}$	Continuous	Pectoral fin use for propulsion	adapted from [15]
Caudal-peduncle throttling (CPt)	$\frac{CFd}{CPd}$	Continuous	Caudal propulsion efficiency through reduction of drag	[16]
Aspect ratio of the caudal fin (CFar)	$\frac{CFd^2}{CFs}$	Continuous	Caudal fin use for propulsion and/or direction	[16]
Fins surface ratio (Frt)	$\frac{2 \times PFs}{CFs}$	Continuous	Main type of propulsion between caudal and pectoral fins	[7]
Fins surface to body size ratio (Fsf)	$\frac{(2 \times PFs) + CFs}{\frac{\pi}{4} \times Bw \times Bd}$	Continuous	Acceleration and/or maneuverability efficiency	[7]
Body mass (logM)	log (Mass +1)	Continuous	Metabolism, endurance and swimming ability	[7]

Trees

We measured 15 leaf and wood traits (table A2.2) for 262 tree species (at least one individual per species in each sampled plot). We used standardized protocols to measure traits on trees [5], controlling for tree size and light environment (e.g. all trees measured were found in the understory). Palm species were excluded because of the unfeasibility to measure stem wood specific gravity. To scale at the species level we use the mean values for each trait measured across individuals. Detailed methods are found in Fortunel *et al.* [5].

Table A2.2. List of the 15 functional traits measured for trees from French Guiana.

Functional trait	Unit	Nature	Ecological meaning	References
Laminar thickness (L_thick)	Mm	Continuous	Resource capture and defence	[17]
Laminar toughness (L_tough)	N	Continuous	Resource capture and defence	[18,19]
Leaf tissue density (LTD)	$g\ cm^{-3}$	Continuous	Resource capture and defence	[17,20]
Specific leaf area (SLA)	$m^2\ kg^{-1}$	Continuous	Resource capture and defence	[21,22]
Leaf area (LA)	cm^2	Continuous	Resource capture	[23]
Foliar carbon (LCC)	$cg\ g^{-1}$	Continuous	Resource capture and defence	[24]
Foliar nitrogen (LNC)	$cg\ g^{-1}$	Continuous	Resource capture	[21]
Foliar phosphorus (LPC)	$\mu g\ g^{-1}$	Continuous	Resource capture	[24]
Foliar potassium (LKC)	$\mu g\ g^{-1}$	Continuous	Resource capture	[25]
Foliar C : N ratio (LC.N)	$cg\ g^{-1}$	Continuous	Resource capture and defence	[18]
Foliar ^{13}C composition (L13C)	‰	Continuous	Resource capture	[26]
Laminar total chlorophyll (L_chl)	$\mu g\ mm^{-2}$	Continuous	Resource capture	[24]
Trunk bark thickness (Bark_thick)	Mm	Continuous	Transport, structure, defence	[27,28]
Stem wood specific gravity (S_wood_iD)	N/A	Continuous	Transport, structure, defence	[29]
Root wood specific gravity (R_wood_iD)	N/A	Continuous	Transport, structure, defence	[29]

Birds

To assess the functional structure of bird assemblages, seven traits describing aspects of the species life history and behaviour (table A2.3) were obtained for 86 species. Full description of trait measurements is found in Williams *et al.* [30], a data paper that compiled distributional and functional trait information for vertebrates from the Australian Wet Tropics (AWT).

Table A2.3. List of the seven functional traits (life history and behaviour) assessed for birds from the Australian Wet Tropics (AWT).

Functional trait	Calculation/ Class	Unit	Nature
Body mass	Average log-transformed body mass of adult individuals	g	Continuous
Clutch size	Average number of offspring produced in a single reproductive event	Number of individuals	Continuous
Reproductive seasonality	Seasonality of reproductive events: highly seasonal = all births ≤ 2 months moderately seasonal = all births ≤ 6 months aseasonal = births occurring over > 6 months	N/A	Ordinal
Diet	Broad dietary preferences: A = seeds B = nectar or fruit with invertebrates C = > 50 % invertebrates or vertebrates	N/A	Nominal
Activity period	Primary time of activity: A = diurnal B = nocturnal C = crepuscular	N/A	Nominal
Shelter type	Primary type of shelter recorded: protected = constructed nest, tree hollow intermediate = tree canopy, hollow log, nest on ground open = under shrubs, in grass	N/A	Nominal
Vertical strata used	Primary type of strata of habitat used: A = terrestrial B = volant C = arboreal/terrestrial	N/A	Nominal

Appendix S3. R-Script to run simulations of species loss

```
##1) INPUT MATRICES
#OBS: Adjust ".txt" files according to each dataset (Fish, Tree, Bird)

#Rarity matrix (species (rows) X rarity estimators (columns))
Rarity<-read.table("Rarity_.txt",header=T,row.names=1)
RI<-Rarity["RI"]#Rarity index values

#Local-assemblage matrix (species (rows) X sites (columns))
Local<-read.table("Local_.txt",header=T,row.names=1)

#Trait matrix (species (rows) X traits (columns))
traits<-read.table("Trait_.txt",header=T,row.names=1)
traits[,"T1"]<-as.ordered(traits[,"T1"])#Inform that trait "T1" is ordinal (e.g. Gill-raker
shape for fish; see appendix S2)
traits[,"T2"]<-as.factor(traits[,"T2"])#Inform that trait "T2" is nominal (e.g. Teeth shape
for fish; see appendix S2)
#########################################
#########################################

##2) FUNCTIONAL SPACE
library(cluster)
#Gower distance between species (not all traits continous; e.g. Fish and Birds)
distance<-daisy(traits, metric="gower")

#Euclidean distance between species (all traits continous; e.g. Trees)
traits_Scaled<-scale(traits)#Scaling and centering trait matrix
distance<-daisy(traits_Scaled, metric="euclidean")

#PCoA based on Gower/Euclidean distance between species
library(ape)
PCOA<-pcoa(distance, correction="cailliez")

#Number of dimensions of the functional space
NoD<-4
#OBS: Adjust "NoD" acording to the number of dimensions (PCoA axes) for each
taxonimic group
#(Fish=4; Trees=9; Birds=5; see M&M)
Axes<-PCOA$vectors[,1:NoD]
#########################################
#########################################

##3) SIMULATIONS OF REGIONAL SPECIES LOSS
```

```
##3.1) FUNCTIONAL RICHNESS (FRic)
library(geometry)

#Input: PCoA axes + RI
ERS<-cbind(Axes,RI)

NoS<-389
#OBS: Adjust "NoS" acording to the maximum possible number of species in each
dataset for the analysis!
#(Fish=389; Tree=252; Bird=80)
#OBS: This maximum possible number of species is due to the impossibility to compute
FRic with few species in null models

#Scenario losing rarest species first
###############Run for################
Simulat_rare<-ERS[order(ERS[,"RI"]),]
tr_rare<-Simulat_rare[,1:NoD]
FRic_Simulat_rare=matrix(NA,nrow=NoS,ncol=1)
for (i in 1:NoS)
{
  tr_rare=tr_rare[-1,]
  FRic_Simulat_rare[i]<-convhulln(tr_rare,"FA")$vol
}
###############End of for#############

#Scenario losing commonest species first
###############Run for################
Simulat_comm<-ERS[order(ERS[,"RI"],decreasing=T),]
tr_comm<-Simulat_comm[,1:NoD]
FRic_Simulat_comm=matrix(NA,nrow=NoS,ncol=1)
for (i in 1:NoS)
{
  tr_comm=tr_comm[-1,]
  FRic_Simulat_comm[i]<-convhulln(tr_comm,"FA")$vol
}
###############End of for#############

#Scenario losing species randomly (null model)
###############Run for################
dataperm=ERS
randFRic=matrix(NA,nrow=NoS,ncol=1000)#ncol= #randomizations
for (j in 1:1000)
{
  dataperm[,"RI"]=sample(dataperm[,"RI"])
  Null_Simulat<-dataperm[order(dataperm[,"RI"]),]
  Null_tr<-Null_Simulat[,1:NoD]
  for (i in 1:NoS)
  {
    Null_tr=Null_tr[-1,]
    randFRic[i,j]<-convhulln(Null_tr,"FA")$vol
  }
```

```
}
##Calculating median and quantiles from the null models
Null_FRic= matrix(NA,nrow=NoS,ncol=3)
for (i in 1:NoS)
{
  Null_FRic[i,1]=median(randFRic[i,])
  Null_FRic[i,2]=quantile(randFRic[i,],probs=0.025)
  Null_FRic[i,3]=quantile(randFRic[i,],probs=0.975)
}
##############End of for#############

#Plot regional species loss scenarios - FRic
Spp_erosion<-c(1:NoS)
plot(Spp_erosion,Null_FRic[,1]/max(Null_FRic[,1]),type="l",xlim=c(0,NoS),xlab="Region
al Species loss
(%)",ylab="FRic",font.lab=2,cex.lab=1.4,cex.axis=1.2,col="gray",pch=16,cex=1.5,xaxt="n
")
axis(side=1, at=c(0,NoS/4,NoS/2,NoS/1.333,NoS),
labels=c(0,25,50,75,100),line=F,tick=-0.3,cex.axis=1.2,mgp=c(3,1,0))
polygon(c(1:NoS,rev(1:NoS)),c(Null_FRic[,2]/max(Null_FRic[,2]),rev(Null_FRic[,3]/max
(Null_FRic[,3]))),col="grey88",border=F)
points(Null_FRic[,1]/max(Null_FRic[,1]),col="gray",cex=1.6,type="l",lty=1,lwd=4)
points(FRic_Simulat_rare/max(FRic_Simulat_rare),col="black",cex=1.6,type="l",lwd=4)
points(FRic_Simulat_comm/max(FRic_Simulat_comm),col="black",cex=1.6,type="l",lwd
=4,lty=3)
##########################################


##3.2) FUNCTIONAL SPECIALIZATION (FSpe)
#Computing functional specialization for each species (speS)
O<-apply(Axes, 2, mean)
speS<-apply(Axes, 1, function(x) { (sum((x-O)^2) )^0.5} )
speS<-speS/max(speS)

ERS<-cbind(RI,speS)

#Scenario losing rarest species first
##############Run for################
Simulat_rare<-ERS[order(ERS[,"RI"]),]
FSpe_Simulat_rare=matrix(NA,nrow=NoS,ncol=1)
for (i in 1:NoS)
{
  Simulat_rare=Simulat_rare[-1,]
  FSpe_Simulat_rare[i]<-mean(Simulat_rare[,"speS"])
}
##############End of for#############

#Scenario losing commonest species first
##############Run for################
Simulat_comm<-ERS[order(ERS[,"RI"],decreasing=T),]
FSpe_Simulat_comm=matrix(NA,nrow=NoS,ncol=1)
```

```
for (i in 1:NoS)
{
  Simulat_comm=Simulat_comm[-1,]
  FSpe_Simulat_comm[i]<-mean(Simulat_comm[,"speS"])
}
##############End of for#############

#Scenario losing species randomly (null model)
##############Run for################
dataperm=ERS
randSPE=matrix(NA,nrow=NoS,ncol=1000)#ncol= #randomizations
for (j in 1:1000)
{
  dataperm[,1]=sample(dataperm[,1])
  Null_Simulat_rare<-dataperm[order(dataperm[,"RI"]),]
  for (i in 1:NoS)
  {
    Null_Simulat_rare=Null_Simulat_rare[-1,]
    randSPE[i,j]<-mean(Null_Simulat_rare[,"speS"])
  }
}
##Calculating median and quantiles from the null models
Null_FSpe= matrix(NA,nrow=NoS,ncol=3)
for (i in 1:NoS)
{
  Null_FSpe[i,1]=median(randSPE[i,])
  Null_FSpe[i,2]=quantile(randSPE[i,],probs=0.025)
  Null_FSpe[i,3]=quantile(randSPE[i,],probs=0.975)
}
##############End of for#############

#Plot regional species loss scenarios - FSpe
Spp_erosion<-c(1:NoS)
plot(Spp_erosion,Null_FSpe[,1],type="l",xlim=c(0,NoS),xlab="Regional Species loss
(%)",ylab="FSpe",font.lab=2,cex.lab=1.4,cex.axis=1.2,col="gray",pch=16,cex=1.5,xaxt="n
",ylim=c(min(Null_FSpe),max(Null_FSpe)))
axis(side=1, at=c(0,NoS/4,NoS/2,NoS/1.333,NoS),
labels=c(0,25,50,75,100),line=F,tick=-0.3,cex.axis=1.2,mgp=c(3,1,0))
polygon(c(1:NoS,rev(1:NoS)),c(Null_FSpe[,2],rev(Null_FSpe[,3])),col="grey88",border=
F)
points(Null_FSpe[,1],col="gray",cex=1.6,type="l",lty=1,lwd=4)
points(FSpe_Simulat_rare,col="black",type="l",lty=1,lwd=4)
points(FSpe_Simulat_comm,col="black",type="l",lty=3,lwd=4)
#########################################


##3.3) FUNCTIONAL ORIGINALITY (FOri)
#Computing functional originality for each species (oriS)
dist_F<-as.matrix(dist(Axes,method="euclidean")) ; dist_F[which(dist_F==0)]<-NA
oriS<-apply(dist_F, 1, min, na.rm=T )
oriS<-oriS/max(oriS)
```

```
ERS<-cbind(RI,oriS)

#Scenario losing rarest species first
###############Run for################
Simulat_rare<-ERS[order(ERS[,"RI"]),]
FOri_Simulat_rare=matrix(NA,nrow=NoS,ncol=1)
for (i in 1:NoS)
{
  Simulat_rare=Simulat_rare[-1,]
  FOri_Simulat_rare[i]<-mean(Simulat_rare[,"oriS"])
}
###############End of for##############

#Scenario losing commonest species first
###############Run for################
Simulat_comm<-ERS[order(ERS[,"RI"],decreasing=T),]
FOri_Simulat_comm=matrix(NA,nrow=NoS,ncol=1)
for (i in 1:NoS)
{
  Simulat_comm=Simulat_comm[-1,]
  FOri_Simulat_comm[i]<-mean(Simulat_comm[,"oriS"])
}
###############End of for##############

#Scenario losing species randomly (null model)
###############Run for################
dataperm=ERS
randORI=matrix(NA,nrow=NoS,ncol=1000)#ncol= #randomizations
for (j in 1:1000)
{
  dataperm[,1]=sample(dataperm[,1])
  Null_Simulat_rare<-dataperm[order(dataperm[,"RI"]),]
  for (i in 1:NoS)
  {
    Null_Simulat_rare=Null_Simulat_rare[-1,]
    randORI[i,j]<-mean(Null_Simulat_rare[,"oriS"])
  }
}
##Calculating median and quantiles from the null models
Null_FOri= matrix(NA,nrow=NoS,ncol=3)
for (i in 1:NoS)
{
  Null_FOri[i,1]=median(randORI[i,])
  Null_FOri[i,2]=quantile(randORI[i,],probs=0.025)
  Null_FOri[i,3]=quantile(randORI[i,],probs=0.975)
}
###############End of for##############

#Plot regional species loss scenarios - FOri
Spp_erosion<-c(1:NoS)
```

```
plot(Spp_erosion,Null_FOri[,1],type="l",xlim=c(0,NoS),xlab="Regional Species loss
(%)",ylab="FOri",font.lab=2,cex.lab=1.4,cex.axis=1.2,col="gray",pch=16,cex=1.5,xaxt="n
",ylim=c(min(Null_FOri),max(Null_FOri)))
axis(side=1, at=c(0,NoS/4,NoS/2,NoS/1.333,NoS),
labels=c(0,25,50,75,100),line=F,tick=-0.3,cex.axis=1.2,mgp=c(3,1,0))
polygon(c(1:NoS,rev(1:NoS)),c(Null_FOri[,2],rev(Null_FOri[,3])),col = "grey88", border
= F)
points(Null_FOri[,1],col="gray",cex=1.6,type="l",lty=1,lwd=4)
points(FOri_Simulat_rare,col="black",type="l",lty=1,lwd=4)
points(FOri_Simulat_comm,col="black",type="l",lty=3,lwd=4)
#########################################
#########################################
```

##4) SIMULATIONS OF LOCAL SPECIES LOSS

##4.1) FUNCTIONAL RICHNESS (FRic)

```
#RUN FUNCTION "calcFRic" (see AppendixS4_R_Functions.R file)!!!
library(geometry)

#Input: Local-assemblage matrix + RI + PCoA axes
fullMat<-cbind(Local,RI,Axes)

taxa="FISH"
#Adjust "taxa" according to taxonomic group ("FISH", "TREE", "BIRD")

#Scenarios of losing rarest or commonest species first
rule="rare"
#Adjust "rule" according to removal scenario ("rare", "common")
#####################################
FRic_Local<-c(mean(calcFRic(fullMat,taxa,.1,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.2,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.3,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.4,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.5,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.6,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.7,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.8,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.9,rule),na.rm=T))
#####################################
FRic_Local_RARE<-FRic_Local#When rule="rare"
FRic_Local_COMM<-FRic_Local#When rule="common"

#Scenario losing species randomly (null model)
###############Run for################
rule="random"
FRic_Local=matrix(NA,nrow=9,ncol=1000)#ncol= #randomizations
for (i in 1:1000)
{
FRic_Local[,i]<- c(
```

```
mean(calcFRic(fullMat,taxa,.1,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.2,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.3,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.4,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.5,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.6,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.7,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.8,rule),na.rm=T),
mean(calcFRic(fullMat,taxa,.9,rule),na.rm=T))
}
##############End of for#############
FRic_Local_NULL<-rowMeans(FRic_Local)#When rule="random"

#Plot local species loss scenarios - FRic
erosion1<-seq(0,100,10)
plot(erosion1,c(1,FRic_Local_NULL,0),type="l",ylim=c(0,1),xlim=c(0,100),col="gray",pc
h=16,cex=1.5,xlab="Local species loss
(%)",ylab="FRic",font.lab=2,cex.lab=1.4,cex.axis=1)
points(erosion1[-
c(1,11)],FRic_Local_NULL,type="p",col="black",pch=21,bg="gray",cex=1)
points(erosion1,c(1,FRic_Local_RARE,0),type="l",ylim=c(0,1),col="black")
points(erosion1[-
c(1,11)],FRic_Local_RARE,type="p",col="black",pch=21,bg="black",cex=1)
points(erosion1,c(1,FRic_Local_COMM,0),type="l",ylim=c(0,1),col="black",lty=2)
points(erosion1[-
c(1,11)],FRic_Local_COMM,type="p",col="black",pch=21,bg="white",cex=1)
legend(60,max(FRic_Local_COMM)/1.1,legend=c("common","random","rare"),col=c("bl
ack","gray","black"),cex=1,lty=c(3,1,1),lwd=1.3,xjust=-
0.01,yjust=0.5,horiz=F,text.font=0.5,x.intersp=0,bty="n")
########################################


## 4.2) FUNCTIONAL SPECIALIZATION (FSpe)

#RUN FUNCTION "calcSPE" (see AppendixS4_R_Functions.R file)!!!

#Computing functional specialization for each species (speS)
O<-apply(Axes, 2, mean)
speS<-apply(Axes, 1, function(x) { (sum((x-O)^2) )^0.5} )
speS<-speS/max(speS)

#Input: Local-assemblage matrix + RI + speS
fullMat<-cbind(Local,RI,speS)

taxa="FISH"
#Adjust "taxa" according to taxonomic group ("FISH", "TREE", "BIRD")

#Scenarios of losing rarest or commonest first
rule="rare"
#Adjust "rule" according to removal scenario ("rare", "common")
#####################################
```

```
FSpe_Local<- c(mean(calcSPE_total(fullMat),na.rm=T),
mean(calcSPE(fullMat,taxa,.1,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.2,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.3,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.4,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.5,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.6,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.7,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.8,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.9,rule),na.rm=T))
####################################
FSpe_Local_RARE<-FSpe_Local#When rule="rare"
FSpe_Local_COMM<-FSpe_Local#When rule="common"

#Scenario losing species randomly (null model)
###############Run for################
rule="random"
FSpe_Local=matrix(NA,nrow=10,ncol=1000)#ncol= #randomizations
for (i in 1:1000)
{
FSpe_Local[,i]<- c(mean(calcSPE_total(fullMat),na.rm=T),
mean(calcSPE(fullMat,taxa,.1,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.2,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.3,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.4,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.5,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.6,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.7,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.8,rule),na.rm=T),
mean(calcSPE(fullMat,taxa,.9,rule),na.rm=T))}
###############End of for##############
FSpe_Local_NULL<-rowMeans(FSpe_Local)

#Plot local species loss scenarios - FSpe
erosion<-seq(0,90,10)
plot(erosion,FSpe_Local_NULL,type="l",ylim=c(min(FSpe_Local_RARE),max(FSpe_Local
_COMM)),xlim=c(0,100),col="gray",pch=16,cex=1.5,xlab="Local species loss
(%)",ylab="FSpe",font.lab=2,cex.lab=1.4,cex.axis=1)
points(erosion[-1],FSpe_Local_NULL[-1],type="p",col="gray",pch=21,bg="gray",cex=1)
points(erosion,FSpe_Local_RARE,type="l",ylim=c(0,1),col="black")
points(erosion[-1],FSpe_Local_RARE[-
1],type="p",col="black",pch=21,bg="black",cex=1)
points(erosion,FSpe_Local_COMM,type="l",ylim=c(0,1),col="black",lty=2)
points(erosion[-1],FSpe_Local_COMM[-
1],type="p",col="black",pch=21,bg="white",cex=1)
legend(0,max(FSpe_Local_COMM)/1.05,legend=c("common","random","rare"),col=c("bl
ack","gray","black"),cex=1,lty=c(3,1,1),lwd=1.3,xjust=-
0.01,yjust=0.5,horiz=F,text.font=0.5,x.intersp=0,bty="n")
#########################################

## 4.3) FUNCTIONAL ORIGINALITY (FOri)
```

```
#RUN FUNCTION "calcORI" (see AppendixS4_R_Functions.R file)!!!

#Computing functional originality for each species (oriS)
dist_F<-as.matrix(dist(Axes,method="euclidean")) ; dist_F[which(dist_F==0)]<-NA
oriS<-apply(dist_F, 1, min, na.rm=T )
oriS<-oriS/max(oriS)

#Input: Local-assemblage matrix + RI + oriS
fullMat<-cbind(Local,RI,oriS)

taxa="FISH"
#Adjust "taxa" according to taxonomic group ("FISH", "TREE", "BIRD")

#Scenarios of losing rarest or commonest first
rule="rare"
#Adjust "rule" according to removal scenario ("rare", "common")
#####################################
FOri_Local<- c(mean(calcORI_total(fullMat),na.rm=T),
mean(calcORI(fullMat,taxa,.1,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.2,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.3,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.4,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.5,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.6,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.7,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.8,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.9,rule),na.rm=T))
#####################################
FOri_Local_RARE<-FOri_Local#When rule="rare"
FOri_Local_COMM<-FOri_Local#When rule="common"

#Scenario losing species randomly (null model)
###############Run for################
rule="random"
FOri_Local=matrix(NA,nrow=10,ncol=1000)#ncol= #randomizations
for (i in 1:1000)
{
FOri_Local[,i]<- c(mean(calcORI_total(fullMat),na.rm=T),
mean(calcORI(fullMat,taxa,.1,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.2,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.3,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.4,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.5,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.6,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.7,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.8,rule),na.rm=T),
mean(calcORI(fullMat,taxa,.9,rule),na.rm=T))}
###############End of for##############
FOri_Local_NULL<-rowMeans(FOri_Local)
```

```
#Plot local species loss scenarios - FOri
erosion<-seq(0,90,10)
plot(erosion,FOri_Local_NULL,type="l",ylim=c(min(FOri_Local_RARE),max(FOri_Local_C
OMM)),xlim=c(0,100),col="gray",pch=16,cex=1.5,xlab="Local species loss
(%)",ylab="FOri",font.lab=2,cex.lab=1.4,cex.axis=1)
points(erosion[-1],FOri_Local_NULL[-1],type="p",col="gray",pch=21,bg="gray",cex=1)
points(erosion,FOri_Local_RARE,type="l",ylim=c(0,1),col="black")
points(erosion[-1],FOri_Local_RARE[-1],type="p",col="black",pch=21,bg="black",cex=1)
points(erosion,FOri_Local_COMM,type="l",ylim=c(0,1),col="black",lty=2)
points(erosion[-1],FOri_Local_COMM[-
1],type="p",col="black",pch=21,bg="white",cex=1)
legend(0,max(FOri_Local_COMM)/1.05,legend=c("common","random","rare"),col=c("bl
ack","gray","black"),cex=1,lty=c(3,1,1),lwd=1.3,xjust=-
0.01,yjust=0.5,horiz=F,text.font=0.5,x.intersp=0,bty="n")
#########################################
#########################################
```

Appendix S4. R-Functions to compute functional structure of local assemblages on simulations of species loss

#1)#Function to compute Functional Richness (FRic)

```
###############RUN FUNCTION calcFRic##########################
calcFRic <- function(fullMat,taxa,prob,rule){
 if(taxa=="FISH"){
  colCom <- 1:294
  fullMat<-fullMat[,-c(1:26)]
  if(prob==.1) {colCom<-1:294
          fullMat<-fullMat}
  if(prob==.2) {colCom<-1:294
          fullMat<-fullMat}
  if(prob==.3) {colCom<-1:264
          fullMat<-fullMat[,-c(1:30)]}
  if(prob==.4) {colCom<-1:246
          fullMat<-fullMat[,-c(1:48)]}
  if(prob==.5) {colCom<-1:218
          fullMat<-fullMat[,-c(1:76)]}
  if(prob==.6) {colCom<-1:149
          fullMat<-fullMat[,-c(1:145)]}
  if(prob==.7) {colCom<-1:104
          fullMat<-fullMat[,-c(1:190)]}
  if(prob==.8) {colCom<-1:39
          fullMat<-fullMat[,-c(1:255)]}
  if(prob==.9) {colCom<-1:4
          fullMat<-fullMat[,-c(1:290)]}
 }
 if(taxa=="TREE"){
  colCom <- 1:6
  if(prob==.8) {colCom<-1:4
          fullMat<-fullMat[,-c(1:2)]}
  if(prob==.9) {colCom<-1
          fullMat<-fullMat[,-c(1:5)]}
 }
 if(taxa=="BIRD"){
  colCom <- 1:47
 }
 colPCOA <- grep("Axis",names(fullMat))
 siteNames <- names(fullMat)[colCom]
 FRic_sites <- sapply(siteNames,function(s,rule){
  cat(s,"\n")
  site <- fullMat[,s]
  pcoaMat <- fullMat[(c(FALSE,TRUE)[site+1]),colPCOA]
  if(rule=="common"){
```

```
    riSite <- fullMat$RI * site
    names(riSite) <- rownames(fullMat)
    riSite <-riSite[riSite!=0]
    nRem <- round(length(riSite) * prob)
    if(nRem==0) nRem <- 1
    riSiteSorted <- riSite
    riSiteSorted <- sort(riSiteSorted,decreasing = TRUE)
    vecRem <- 1:nRem
    riSiteSorted <- riSiteSorted[-vecRem]
    matFinal <- pcoaMat[names(riSiteSorted),]
   }
   if(rule=="rare"){
    riSite <- fullMat$RI * site
    names(riSite) <- rownames(fullMat)
    riSite <-riSite[riSite!=0]
    nRem <- round(length(riSite) * prob)
    if(nRem==0) nRem <- 1
    riSiteSorted <- riSite
    riSiteSorted <- sort(riSiteSorted)
    vecRem <- 1:nRem
    riSiteSorted <- riSiteSorted[-vecRem]
    matFinal <- pcoaMat[names(riSiteSorted),]
   }
   if(rule=="random"){
    riSite <- fullMat$RI * site
    names(riSite) <- rownames(fullMat)
    riSite <- riSite[riSite!=0]
    nRem <- round(length(riSite) * prob)
    if(nRem==0) nRem <- 1
    toRem <- sample(1:length(riSite),nRem)
    matFinal <- pcoaMat[-toRem,]
   }
   hullSub <- convhulln(matFinal,"FA")$vol
   hullCom <- convhulln(pcoaMat,"FA")$vol
   prop <- hullSub / hullCom
  },rule=rule)
  return(FRic_sites)
}
##########END OF FUNCTION calcFRic##########################
```

#2)#Function to compute Functional Specialization (FSpe)

```
################RUN FUNCTION calcSPE##########################
calcSPE <- function(fullMat,taxa,prob,rule){
  if(taxa=="FISH"){
   colCom <- 1:320
  }
  if(taxa=="TREE"){
   colCom <- 1:6
  }
```

```
  if(taxa=="BIRD"){
    colCom <- 1:47
  }
  siteNames <- names(fullMat)[colCom]
  SPE_sites <- sapply(siteNames,function(s,rule){
    cat(s,"\n")
    site <- fullMat[,s]
    SPE <- fullMat[(c(FALSE,TRUE)[site+1]),"speS"]
    names(SPE) <- rownames(fullMat[(c(FALSE,TRUE)[site+1]),])
    if(rule=="common"){
      riSite <- fullMat$RI * site
      names(riSite) <- rownames(fullMat)
      riSite <-riSite[riSite!=0]
      nRem <- round(length(riSite) * prob)
      if(nRem==0) nRem <- 1
      riSiteSorted <- riSite
      riSiteSorted <- sort(riSiteSorted,decreasing = TRUE)
      vecRem <- 1:nRem
      riSiteSorted <- riSiteSorted[-vecRem]
      vecFinal <- SPE[names(riSiteSorted)]
    }
    if(rule=="rare"){
      riSite <- fullMat$RI * site
      names(riSite) <- rownames(fullMat)
      riSite <-riSite[riSite!=0]
      nRem <- round(length(riSite) * prob)
      if(nRem==0) nRem <- 1
      riSiteSorted <- riSite
      riSiteSorted <- sort(riSiteSorted)
      vecRem <- 1:nRem
      riSiteSorted <- riSiteSorted[-vecRem]
      vecFinal <- SPE[names(riSiteSorted)]
    }
    if(rule=="random"){
      riSite <- fullMat$RI * site
      names(riSite) <- rownames(fullMat)
      riSite <- riSite[riSite!=0]
      nRem <- round(length(riSite) * prob)
      if(nRem==0) nRem <- 1
      toRem <- sample(1:length(riSite),nRem)
      riSite <- riSite[-toRem]
      vecFinal<-SPE[names(riSite)]
    }
    mean(vecFinal)
  },rule=rule)
  return(SPE_sites)
}
#Computing total FSpe#
calcSPE_total <- function(fullMat){
  if(taxa=="FISH"){
    colCom <- 1:320
```

```
  }
  if(taxa=="TREE"){
    colCom <- 1:6
  }
  if(taxa=="BIRD"){
    colCom <- 1:47
  }
  siteNames <- names(fullMat)[colCom]
  SPE_sites <- sapply(siteNames,function(s){
    cat(s,"\n")
    site <- fullMat[,s]
    SPE <- fullMat[(c(FALSE,TRUE)[site+1]),"speS"]
    names(SPE) <- rownames(fullMat[(c(FALSE,TRUE)[site+1]),])
    vecFinal <- SPE[names(SPE)]
    mean(vecFinal)
  })
  return(SPE_sites)
}
#############END OF FUNCTION calcSPE##########################
```

#3)#Function to compute Functional Originality (FOri)

```
##################RUN FUNCTION calcORI#######################
calcORI <- function(fullMat,taxa,prob,rule){
  if(taxa=="FISH"){
    colCom <- 1:320
  }
  if(taxa=="TREE"){
    colCom <- 1:6
  }
  if(taxa=="BIRD"){
    colCom <- 1:47
  }
  siteNames <- names(fullMat)[colCom]
  ORI_sites <- sapply(siteNames,function(s,rule){
    cat(s,"\n")
    site <- fullMat[,s]
    ORI <- fullMat[(c(FALSE,TRUE)[site+1]),"oriS"]
    names(ORI) <- rownames(fullMat[(c(FALSE,TRUE)[site+1]),])
    if(rule=="common"){
      riSite <- fullMat$RI * site
      names(riSite) <- rownames(fullMat)
      riSite <-riSite[riSite!=0]
      nRem <- round(length(riSite) * prob)
      if(nRem==0) nRem <- 1
      riSiteSorted <- riSite
      riSiteSorted <- sort(riSiteSorted,decreasing = TRUE)
      vecRem <- 1:nRem
      riSiteSorted <- riSiteSorted[-vecRem]
      vecFinal <- ORI[names(riSiteSorted)]
```

```
    }
    if(rule=="rare"){
      riSite <- fullMat$RI * site
      names(riSite) <- rownames(fullMat)
      riSite <-riSite[riSite!=0]
      nRem <- round(length(riSite) * prob)
      if(nRem==0) nRem <- 1
      riSiteSorted <- riSite
      riSiteSorted <- sort(riSiteSorted)
      vecRem <- 1:nRem
      riSiteSorted <- riSiteSorted[-vecRem]
      vecFinal <- ORI[names(riSiteSorted)]
    }
    if(rule=="random"){
      riSite <- fullMat$RI * site
      names(riSite) <- rownames(fullMat)
      riSite <- riSite[riSite!=0]
      nRem <- round(length(riSite) * prob)
      if(nRem==0) nRem <- 1
      toRem <- sample(1:length(riSite),nRem)
      riSite <- riSite[-toRem]
      vecFinal<- ORI[names(riSite)]
    }
    mean(vecFinal)
  },rule=rule)
  return(ORI_sites)
}
#Computing total FOri#
calcORI_total <- function(fullMat){
  if(taxa=="FISH"){
    colCom <- 1:320
  }
  if(taxa=="TREE"){
    colCom <- 1:6
  }
  if(taxa=="BIRD"){
    colCom <- 1:47
  }
  siteNames <- names(fullMat)[colCom]
  ORI_sites <- sapply(siteNames,function(s){
    cat(s,"\n")
    site <- fullMat[,s]
    ORI <- fullMat[(c(FALSE,TRUE)[site+1]),"oriS"]
    names(ORI) <- rownames(fullMat[(c(FALSE,TRUE)[site+1]),])
    vecFinal <- ORI[names(ORI)]
    mean(vecFinal)
  })
  return(ORI_sites)
}
############END OF FUNCTION calcORI##########################
#############################################################
```

Appendix S5. Sensitivity analyses

We conducted a set of sensitivity analyses to assess the robustness of our findings to three methodological aspects:

(*i*) To assess the potential effects of the uneven number of traits, for fish and trees datasets we randomly selected 7 traits (i.e. the minimum number among the three groups, observed for birds) and built a pairwise distance matrix for each of 1,000 replicates. We then compared each of these matrices with the initial one using a Mantel test. This analysis showed high congruence between the matrices of functional distances for both fish (Mantel $r = 0.78 \pm 0.06$) and trees ($r = 0.78 \pm 0.03$), indicating that the number of traits did not modify functional distances between species pairs.

(*ii*) To evaluate the influence of one particular trait we fully reran the species loss simulations using all sub-combinations of traits where one is removed. This analysis indicated that no one trait drives the patterns alone (figures A5.1–18).

(*iii*) To assess the influence of the chosen number of dimensions (i.e. PCoA axes) for each study case, we contrasted our results with the ones obtained when adding or removing one axis at a time. We firstly ordered the species according to their commonness (i.e. RI_i values) and equally divided them into 10 classes. We then computed the functional indices for each class and calculated Pearson's correlation between values obtained with the initial vs. the alternative number of dimensions. This analysis showed strong correlations between the results obtained with the chosen number of dimensions and with an alternative number (+/- one), indicating that adding or removing one axis to functional spaces did not affect the results (figure A5.19).

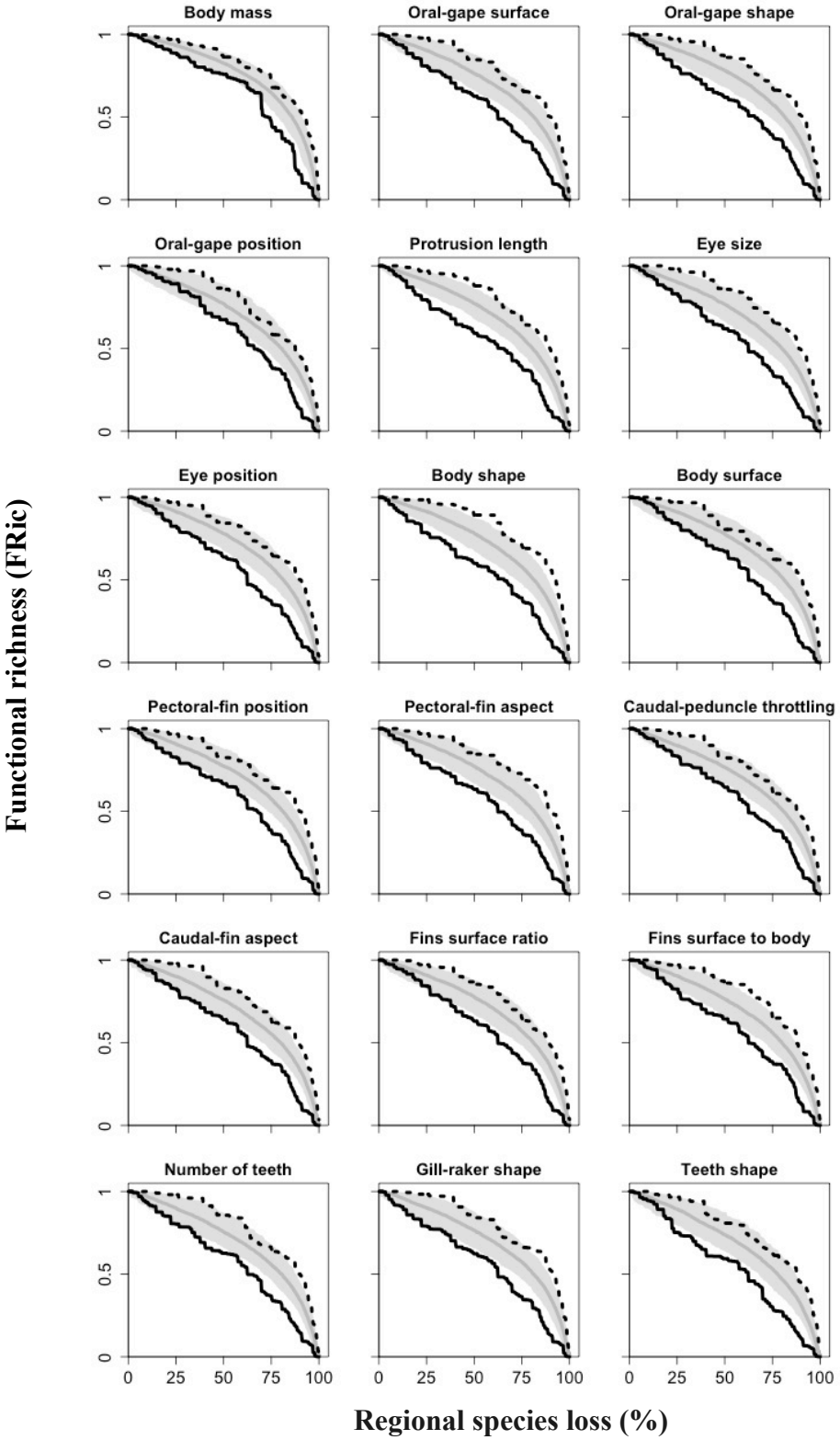

Figure A5.1. Sensitivity of functional richness loss to the set of traits used to describe fish assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

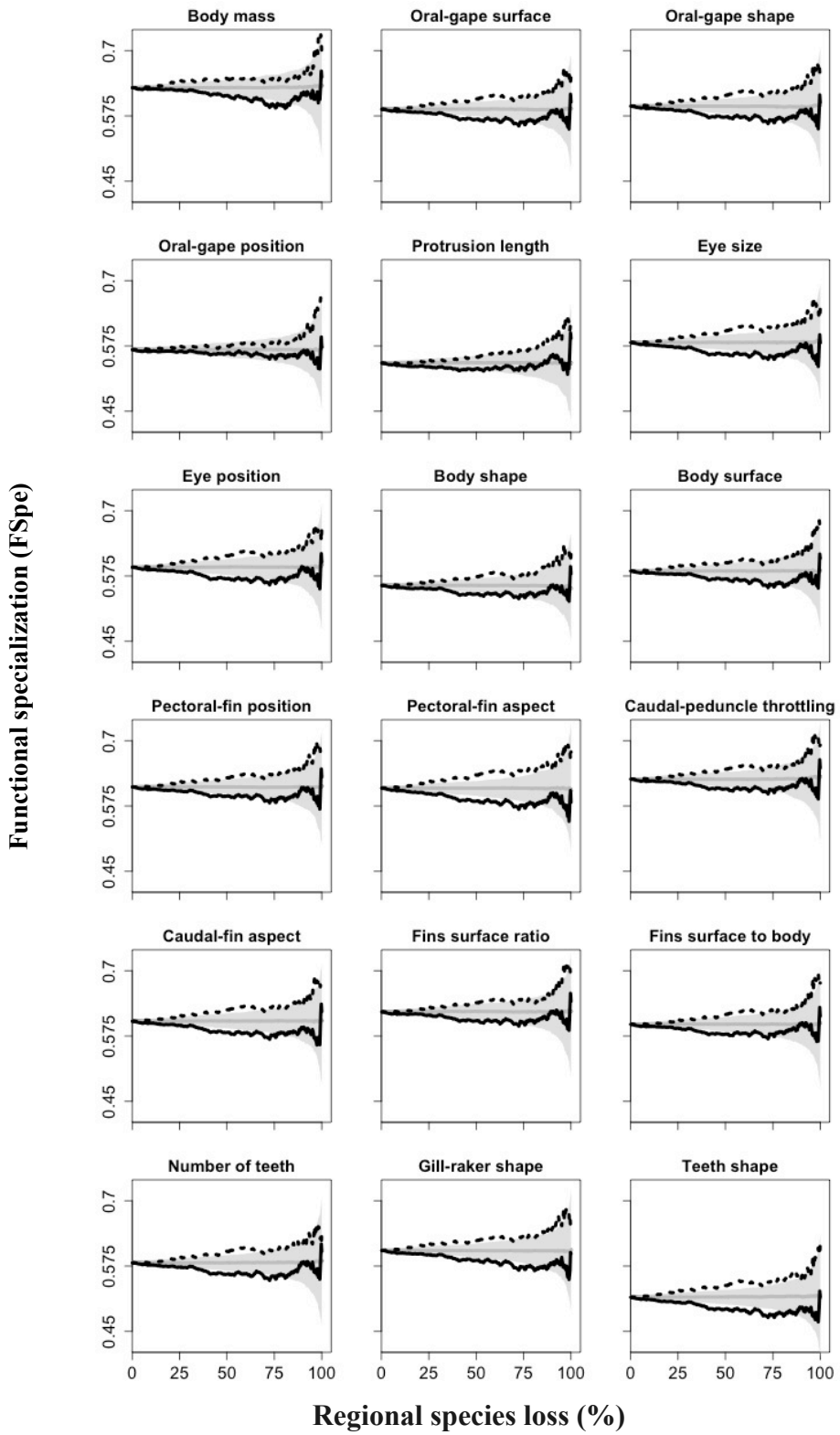

Figure A5.2. Sensitivity of functional specialization changes to the set of traits used to describe fish assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

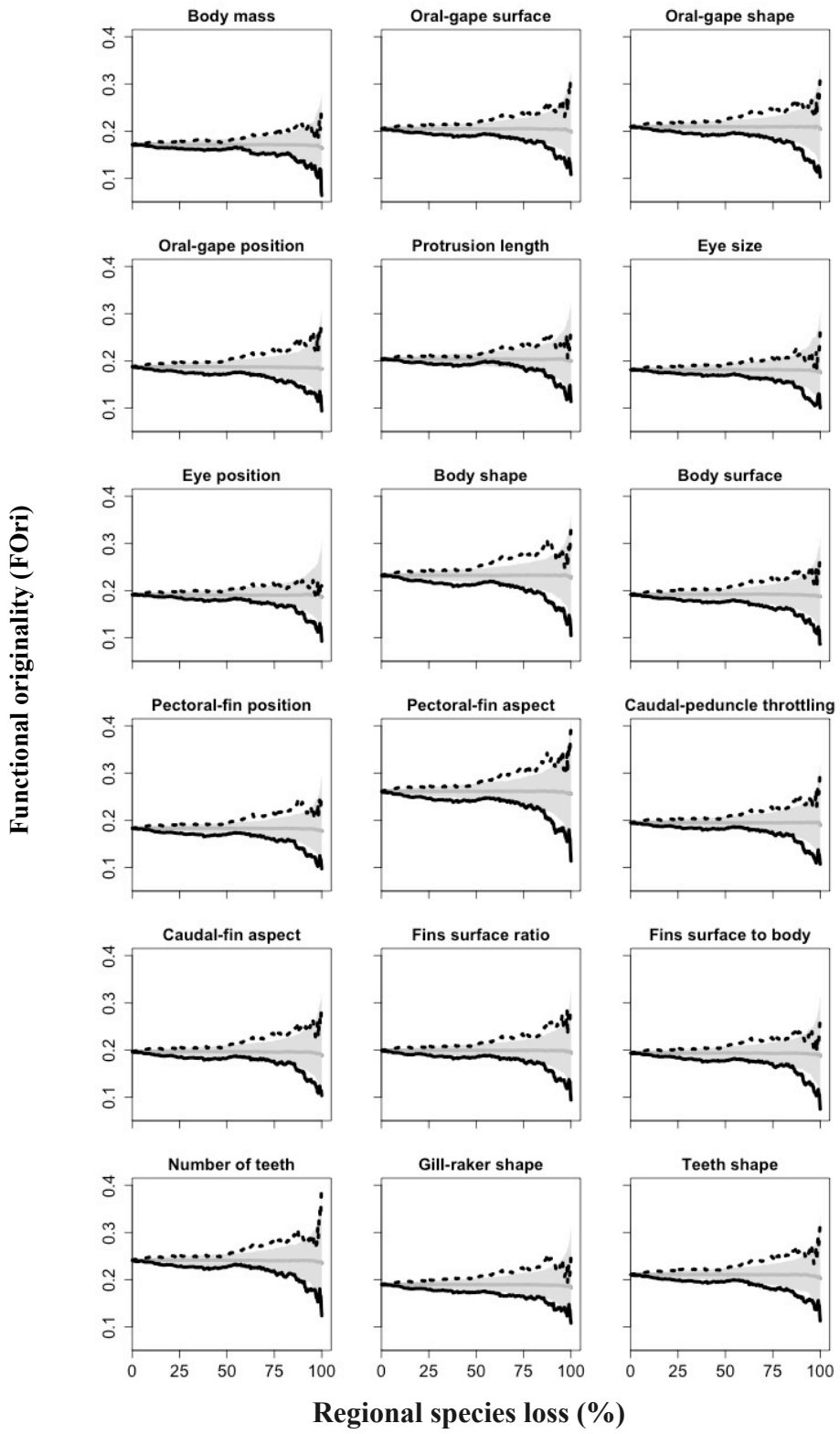

Figure A5.3. Sensitivity of functional originality changes to the set of traits used to describe fish assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

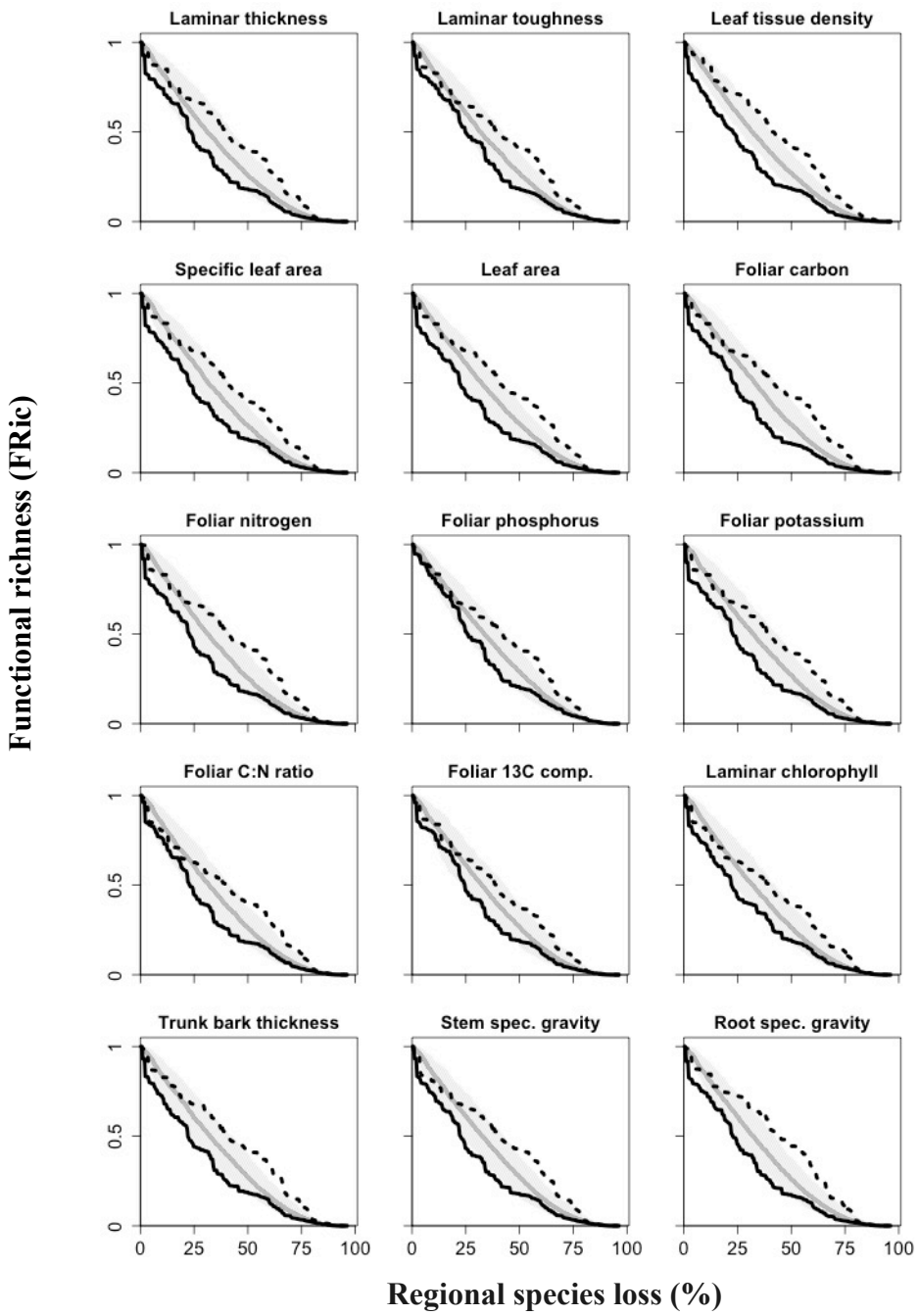

Figure A5.4. Sensitivity of functional richness loss to the set of traits used to describe tree assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

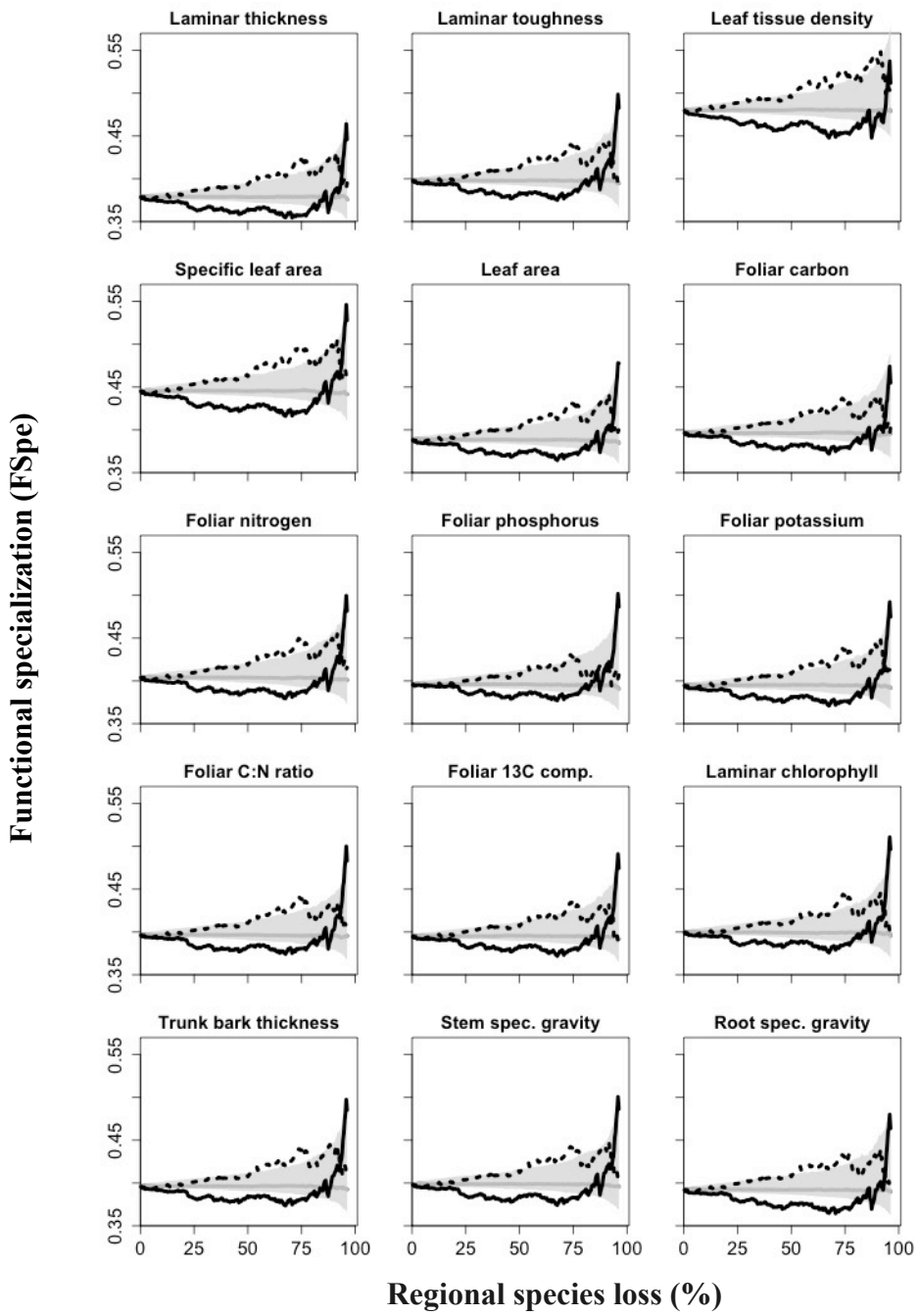

Figure A5.5. Sensitivity of functional specialization changes to the set of traits used to describe tree assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

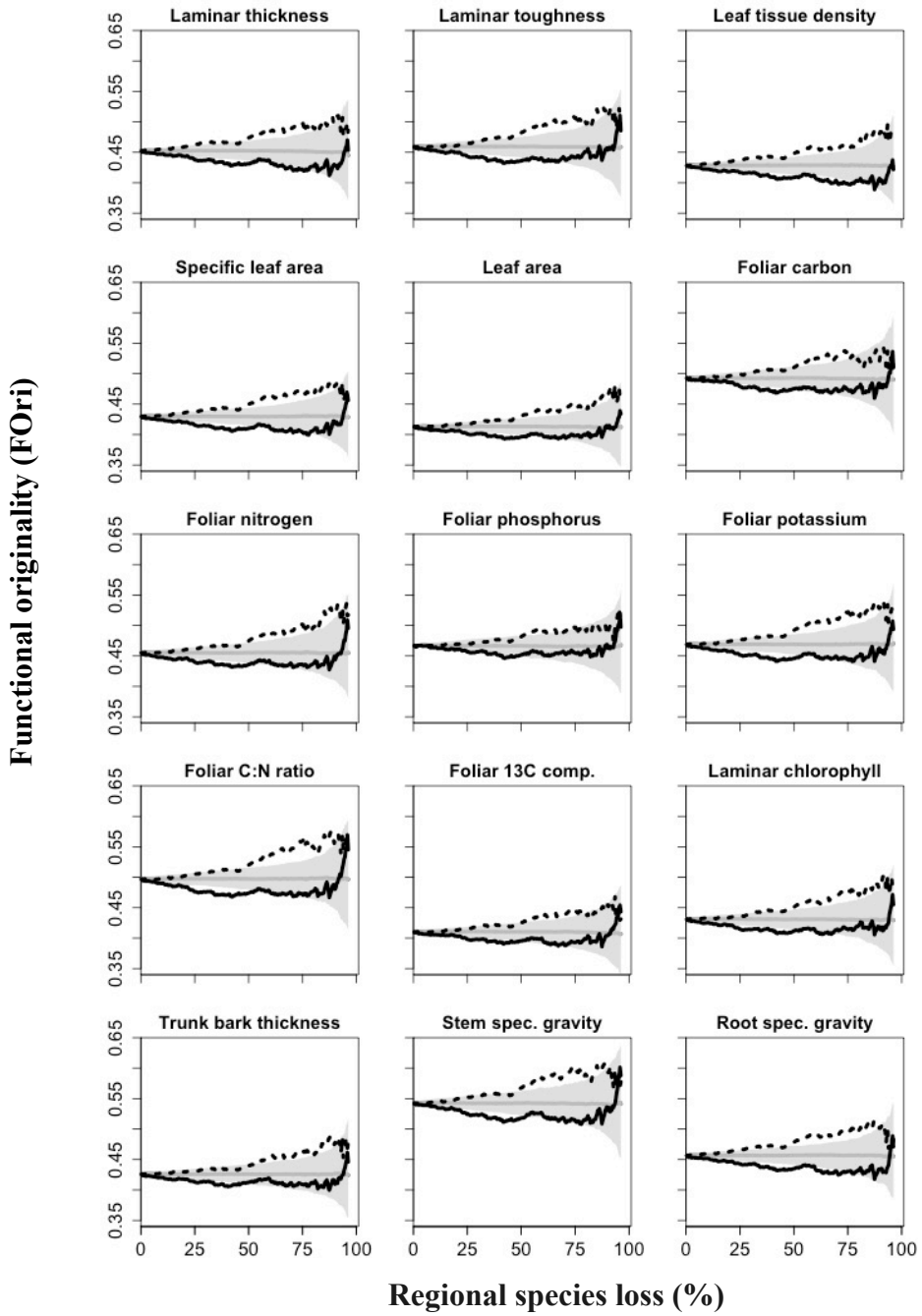

Figure A5.6. Sensitivity of functional originality changes to the set of traits used to describe tree assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

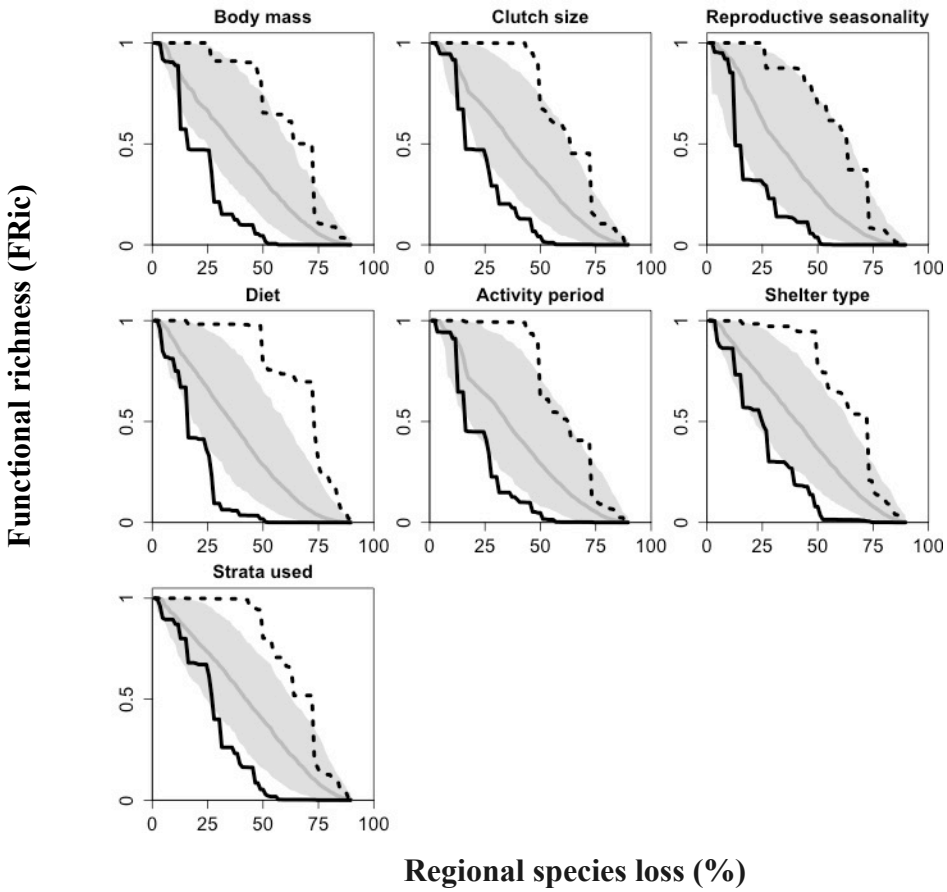

Figure A5.7. Sensitivity of functional richness loss to the set of traits used to describe bird assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

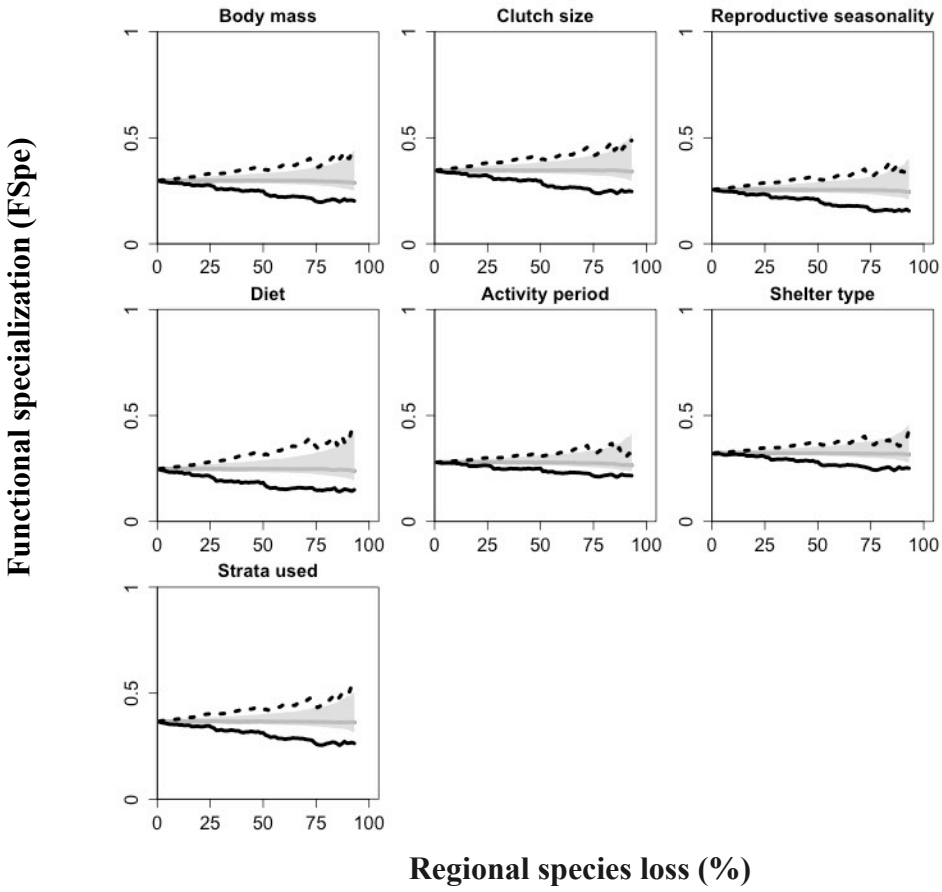

Figure A5.8. Sensitivity of functional specialization changes to the set of traits used to describe bird assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

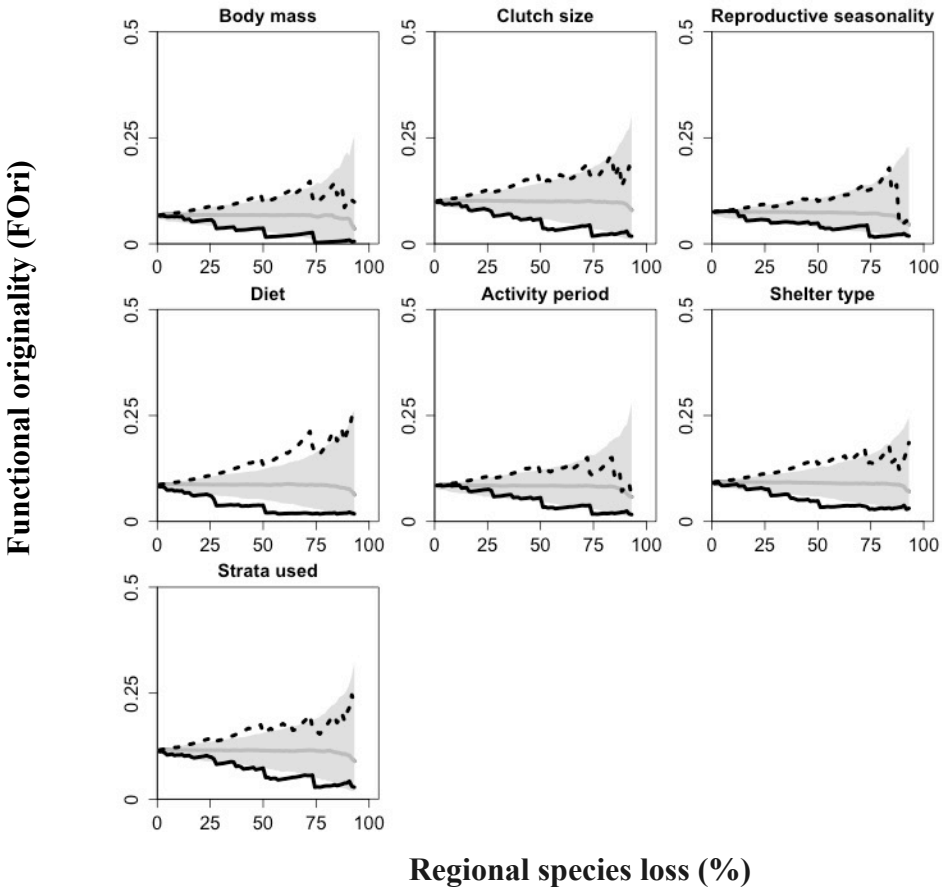

Figure A5.9. Sensitivity of functional originality changes to the set of traits used to describe bird assemblages. See figure 2 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the regional scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey line indicating the median and shaded area representing the 95% confidence interval).

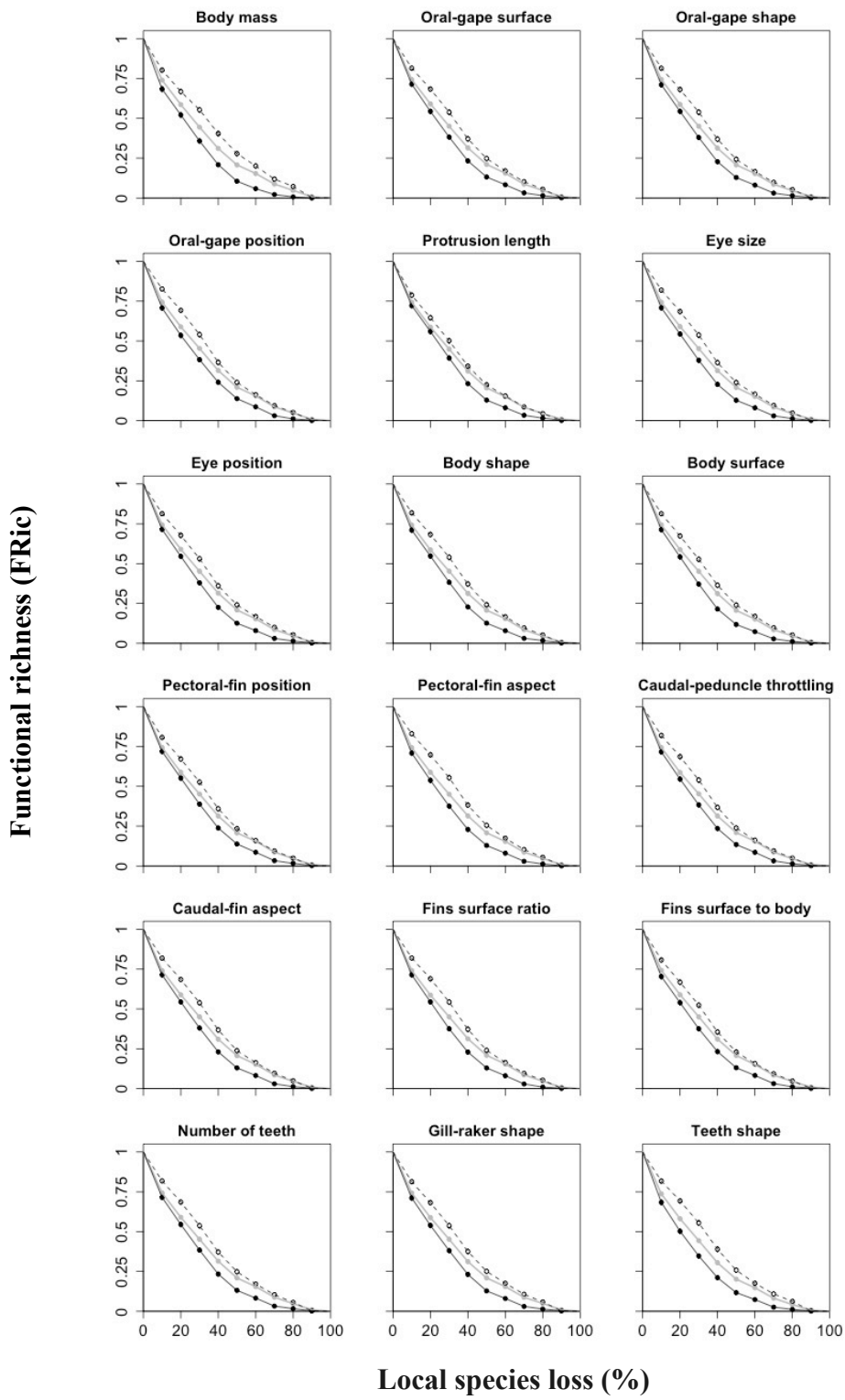

Figure A5.10. Sensitivity of functional richness loss to the set of traits used to describe fish assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

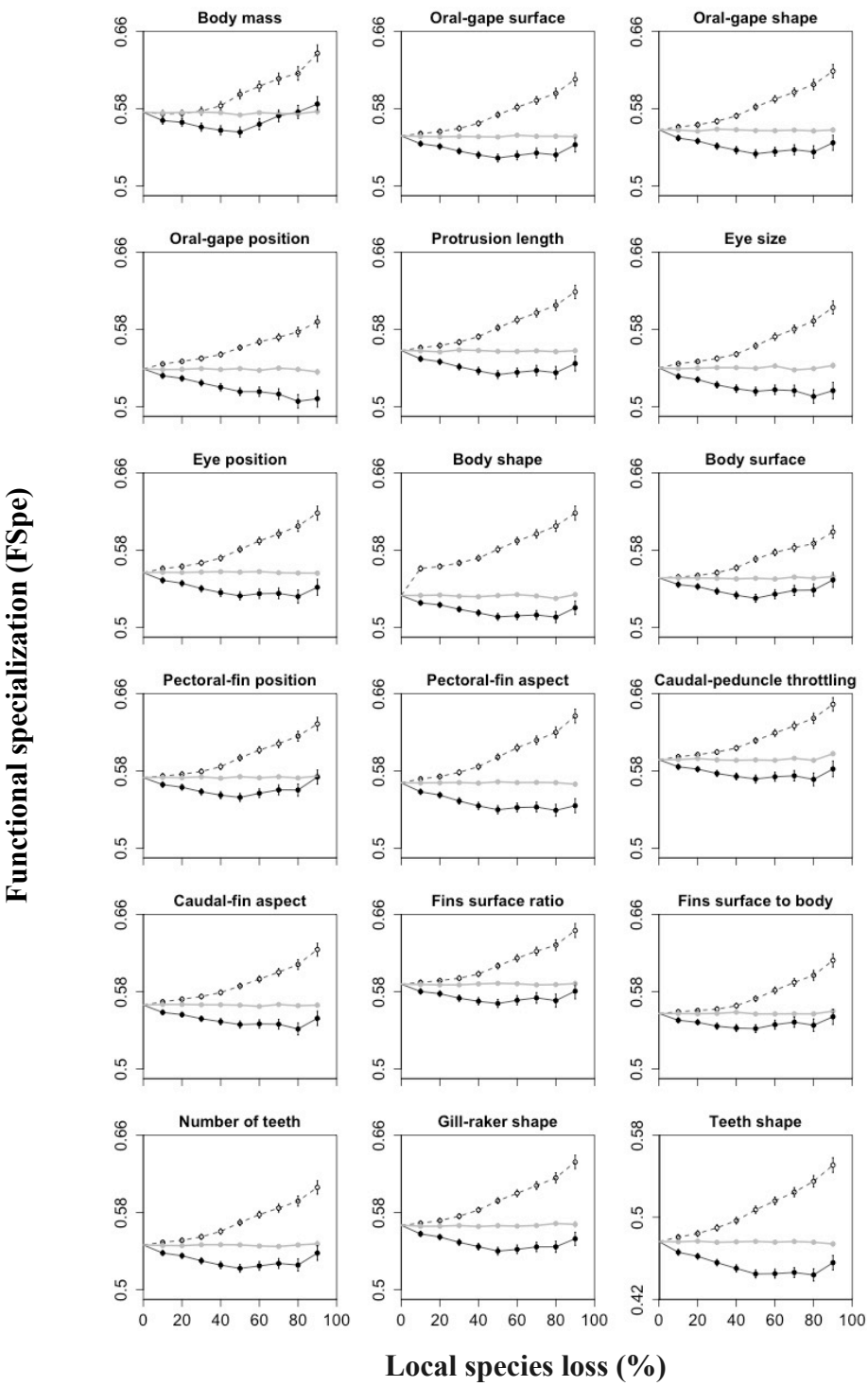

Figure A5.11. Sensitivity of functional specialization changes to the set of traits used to describe fish assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

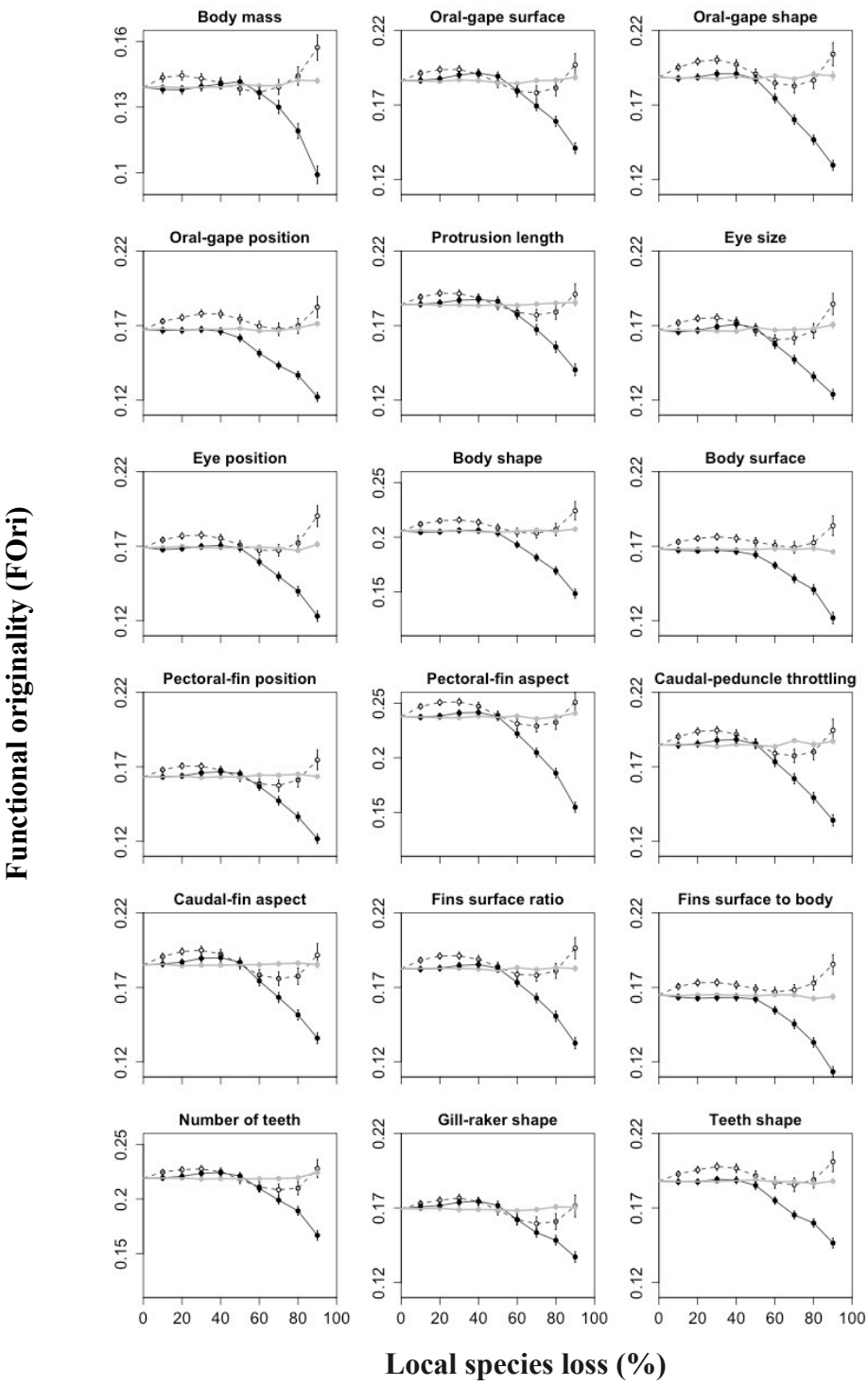

Figure A5.12. Sensitivity of functional originality changes to the set of traits used to describe fish assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

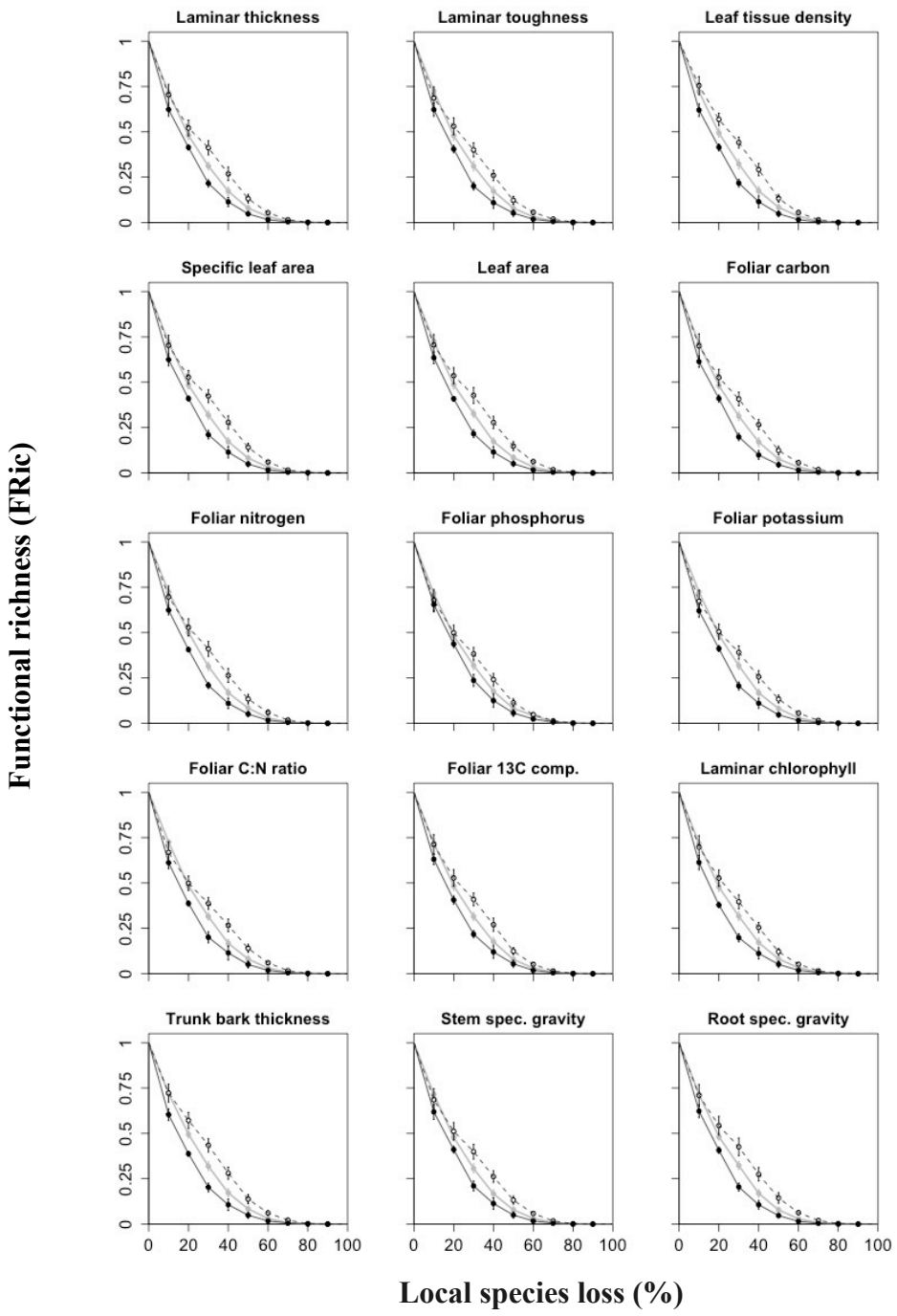

Figure A5.13. Sensitivity of functional richness loss to the set of traits used to describe tree assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

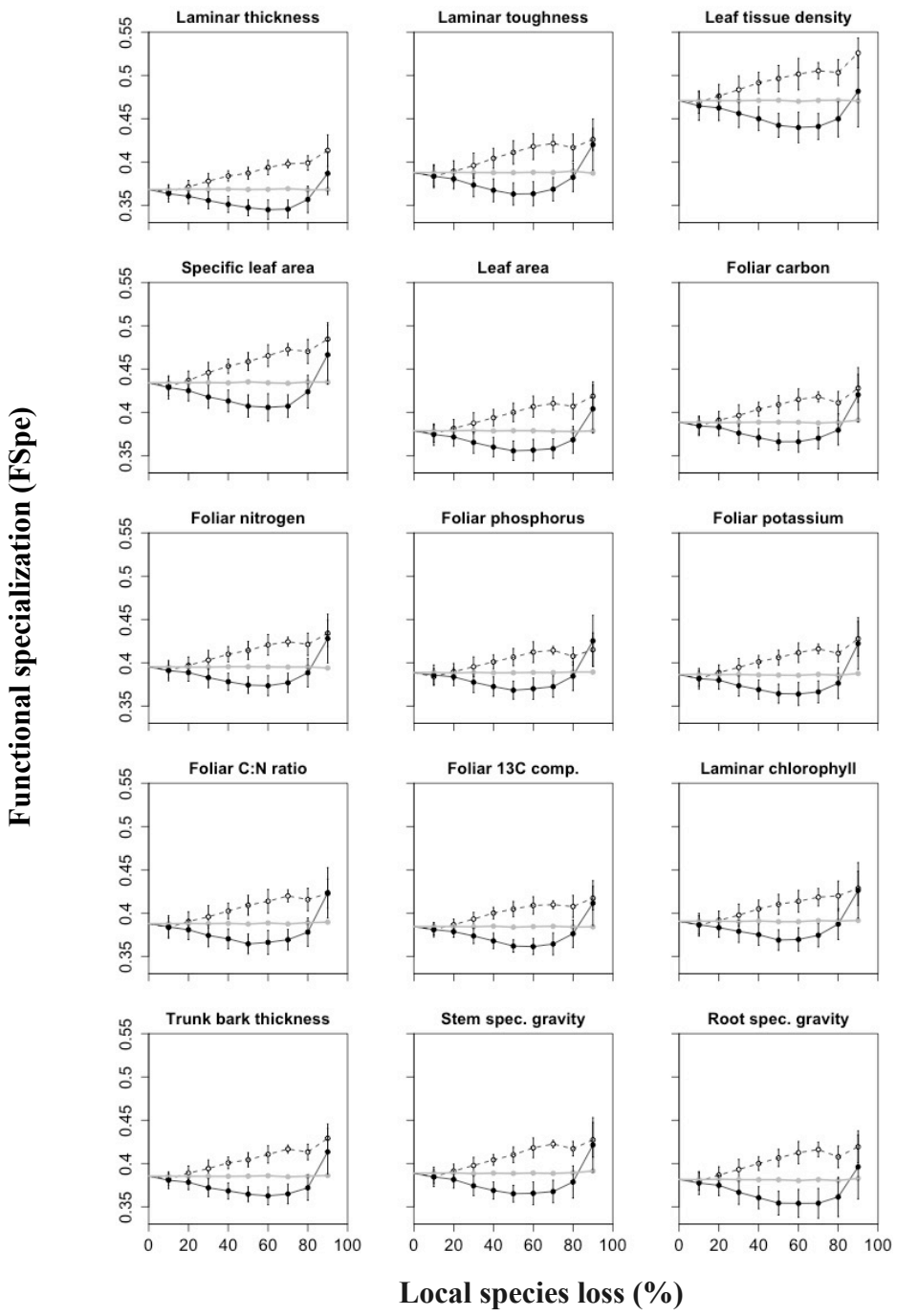

Figure A5.14. Sensitivity of functional specialization changes to the set of traits used to describe tree assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

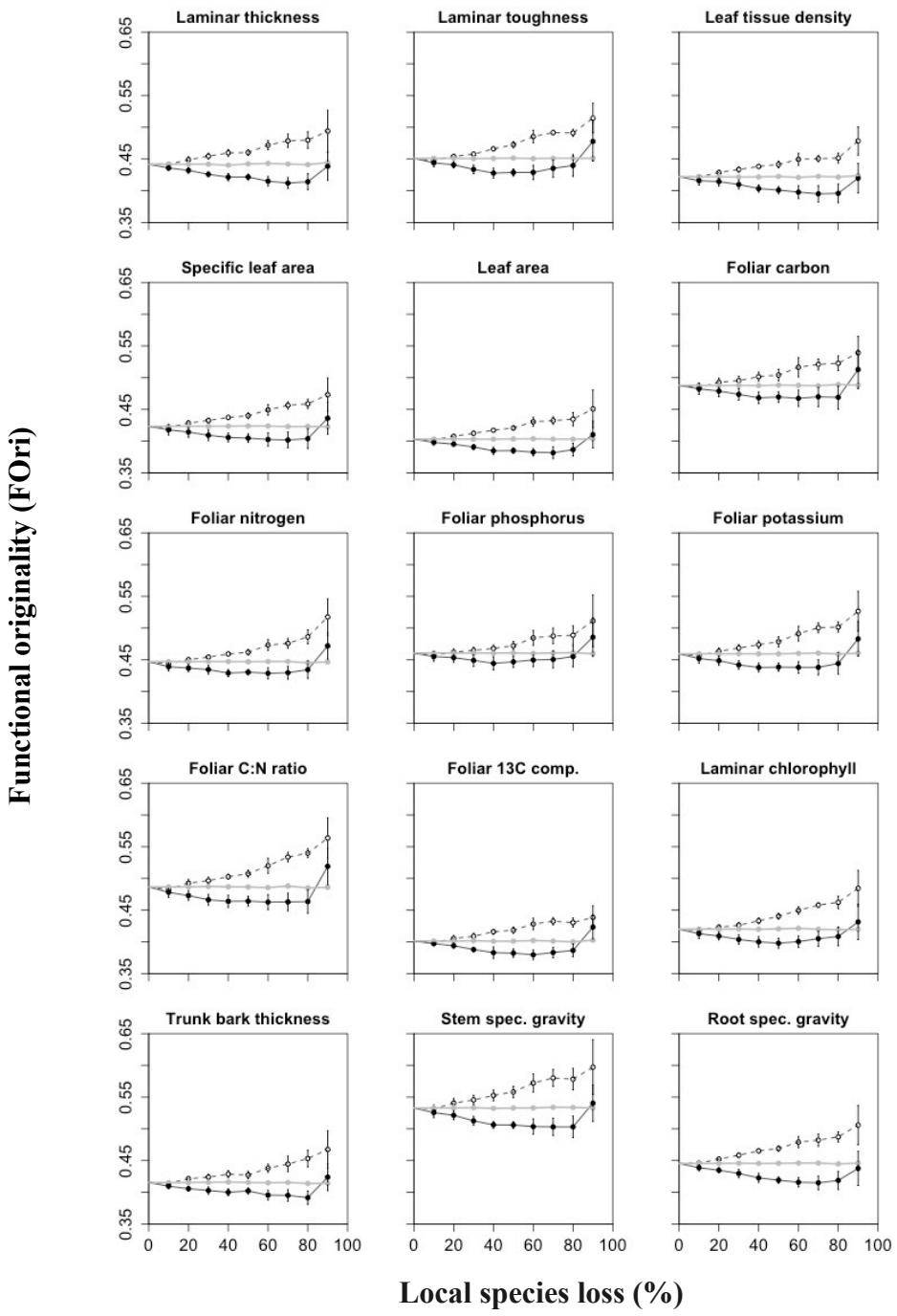

Figure A5.15. Sensitivity of functional originality changes to the set of traits used to describe tree assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

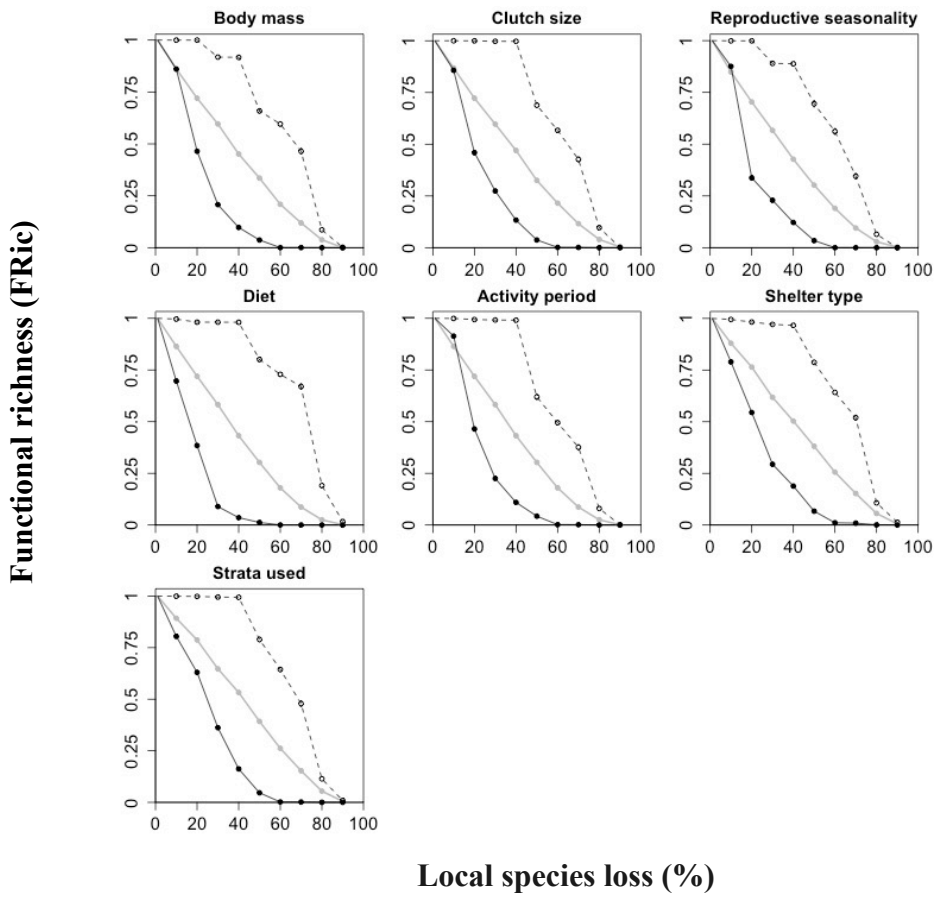

Figure A5.16. Sensitivity of functional richness loss to the set of traits used to describe bird assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

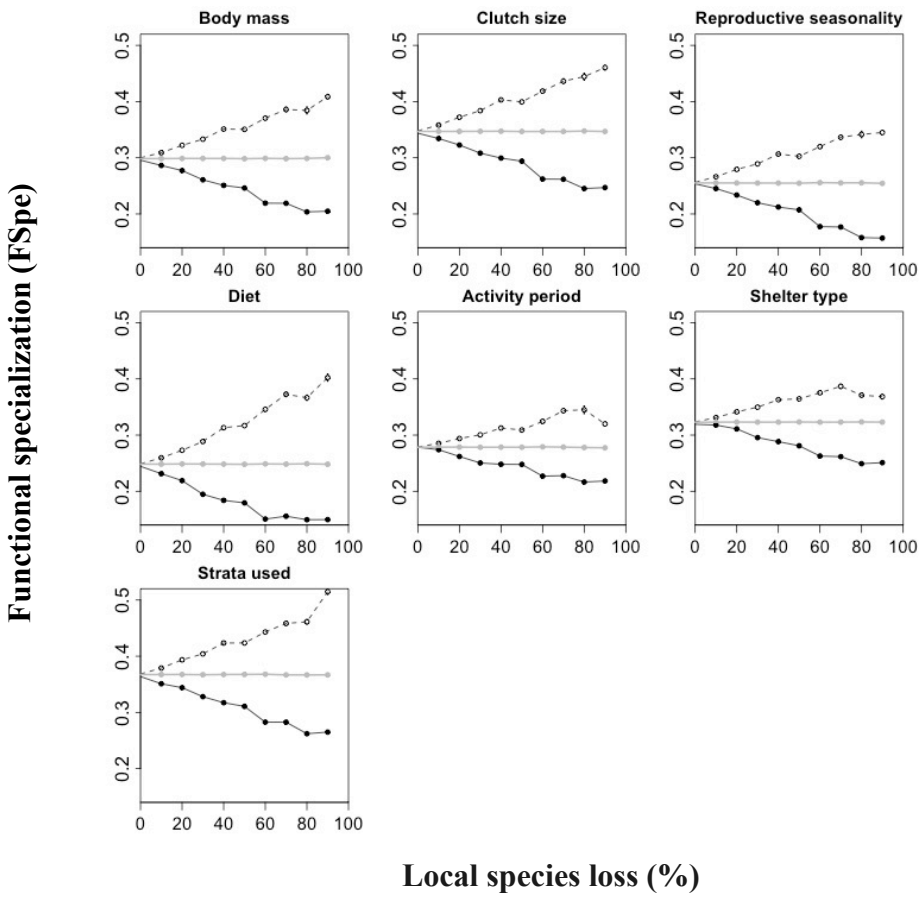

Figure A5.17. Sensitivity of functional specialization changes to the set of traits used to describe bird assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

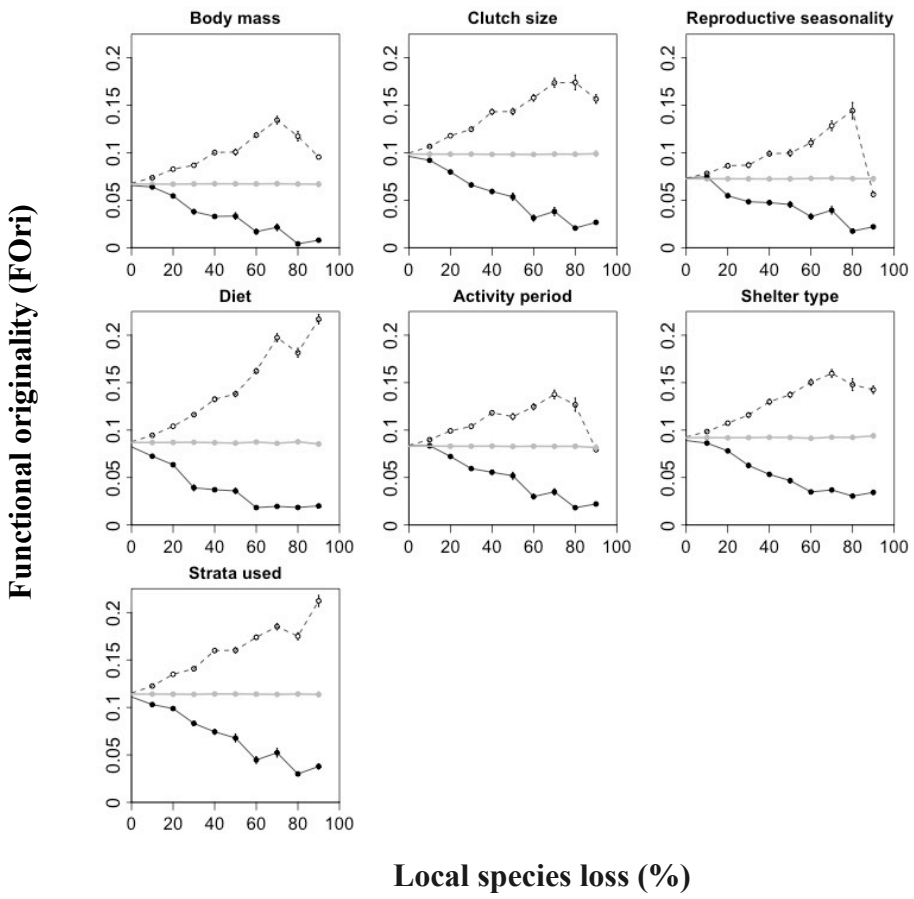

Figure A5.18. Sensitivity of functional originality changes to the set of traits used to describe bird assemblages. See figure 3 for patterns with all traits considered. Name of the removed trait is shown above each plot. Impacts of three species-loss scenarios at the local scale are shown for each plot: rarest species are lost first (black solid line), commonest species are lost first (dashed line), and random species loss (grey solid line). Dots and vertical bars represent mean values and standard error at the species-removal level among all local assemblages.

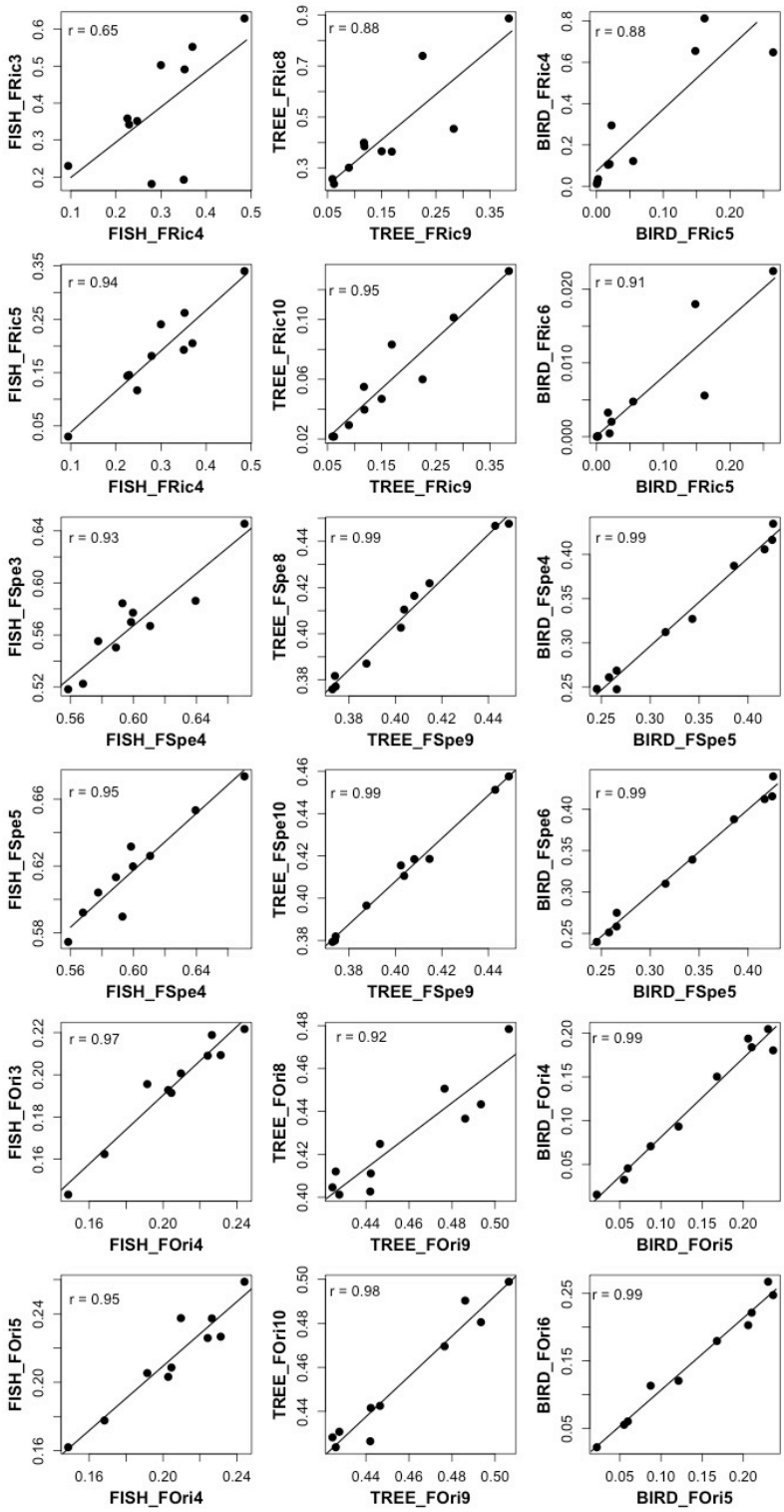

Figure A5.19. Correlation between indices of functional structure (functional richness – FRic, specialization – FSpe, and originality – FOri) when the functional space was built with the optimized number of PCoA axes (abscissas) and with one more or less PCoA axis (ordinates). Taxonomic group, functional index, and number of dimensions are indicated at axis labels.

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