

Supplemental Information for

“No link between population isolation and speciation rate in squamate reptiles”

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Range map reconstruction

To infer range maps for *Bothrops moojeni* and *Micrablepharus atticolus*, we used an approach based on cropping an alpha-hull model of all occurrence points by an ecological niche model (ENM) (1). Here, we used expert datasets on occurrence points of these two species (2, 3). We first constructed an alpha hull polygon around these points using the alphahull package in R (4). We then used MaxEnt (5) to construct ENMs for each of these species using the 18 BioClim variables at 2.5m resolution (6). We converted ENMs to ENM range maps with a threshold set at 3%. Finally, we clipped the alpha hull polygon to the extent of the ENM inferred range.

Forward Genetic Simulations

To test how sample size influences error in IBD estimates, we conducted a series of forward, individual-based simulations using the program SLiM v3.6 (7). These simulations are extensively borrowed from similar simulations of genetic differentiation across space (8, 9). At time 0, we initialized a population of hermaphroditic individuals across a square space that was 50 by 50 units. Each unit had a carrying capacity of 5 individuals for a total carrying capacity of 12,500 individuals. We simulated 5,000 loci of 3,000 base pairs each, with mutation rate of 1×10^{-8} and recombination rate of 1×10^{-8} . Three aspects of individual behavior are set by the parameter σ , which we treat here as the dispersal parameter: the distance individuals disperse from its parent and the distance that determines mate choice and competitive interactions among individuals. In each generation, individuals disperse, reproduce with individuals within 3σ distance, and die as a function of local population density (local population size here is defined as 3σ). We ran five simulations across 4 values of sigma: 0.25, 0.5, 1.0, and 2.0. Simulations were run for 1e6 generations, at which point we recorded individual locations and output individual genotypes for segregating sites. We randomly sampled either 5, 10, 15 or 20 individuals to use for IBD estimation.

Supplemental Figures

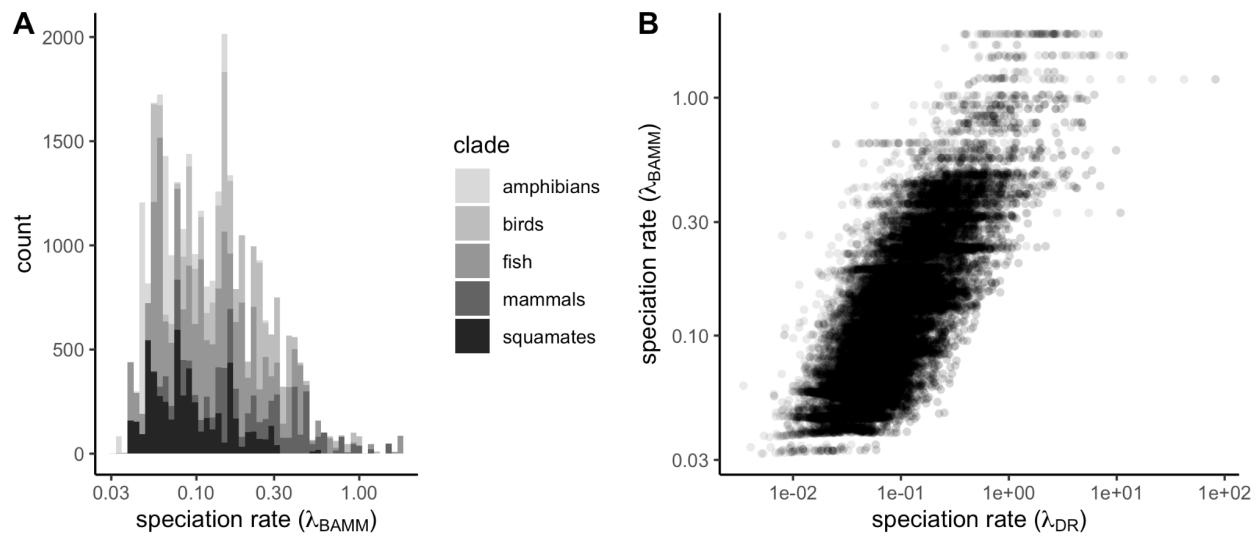


Figure S1: (A) Speciation rates across vertebrates; rates are estimated using the BAMM (10). The data are from Cooney & Thomas (2020; 11). Speciation rate distributions are highly skewed and are thus presented on a log10 scale. BAMM rates are known for being conservative (12); still, speciation rates across the fastest 1% and slowest 1% vary anywhere from 5-fold to 31-fold. Whether measured using the DR statistic (Fig. 1) or BAMM, speciation rates are highly variable across clades. (B) Speciation rates measured using the DR statistic and BAMM are highly correlated (non-phylogenetic $r = 0.78$).

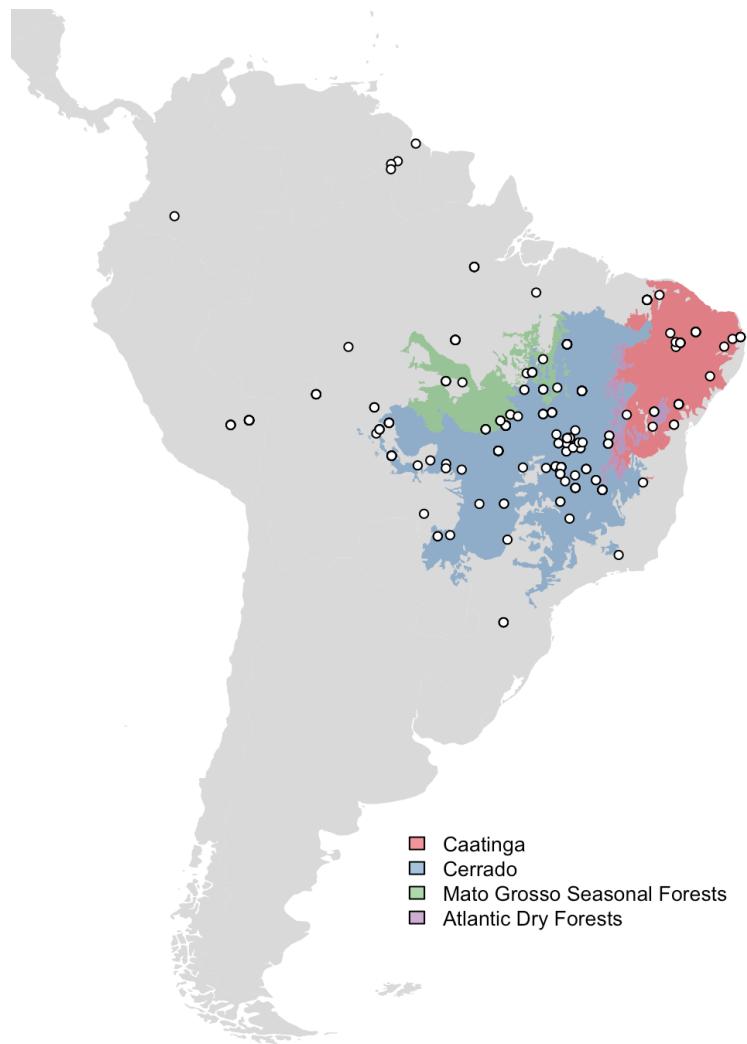


Figure S2: Map of the samples included in this study ($n = 375$). Seventy percent of samples fall in one of four eco-regions that collectively make up South America's "Dry Diagonal" biogeographic region: the Caatinga, Cerrado, Mato Grosso Seasonal Forests, and Atlantic Dry Forests. This focused sampling helps control for some of the ecological and geographic factors that might also influence diversification rates.

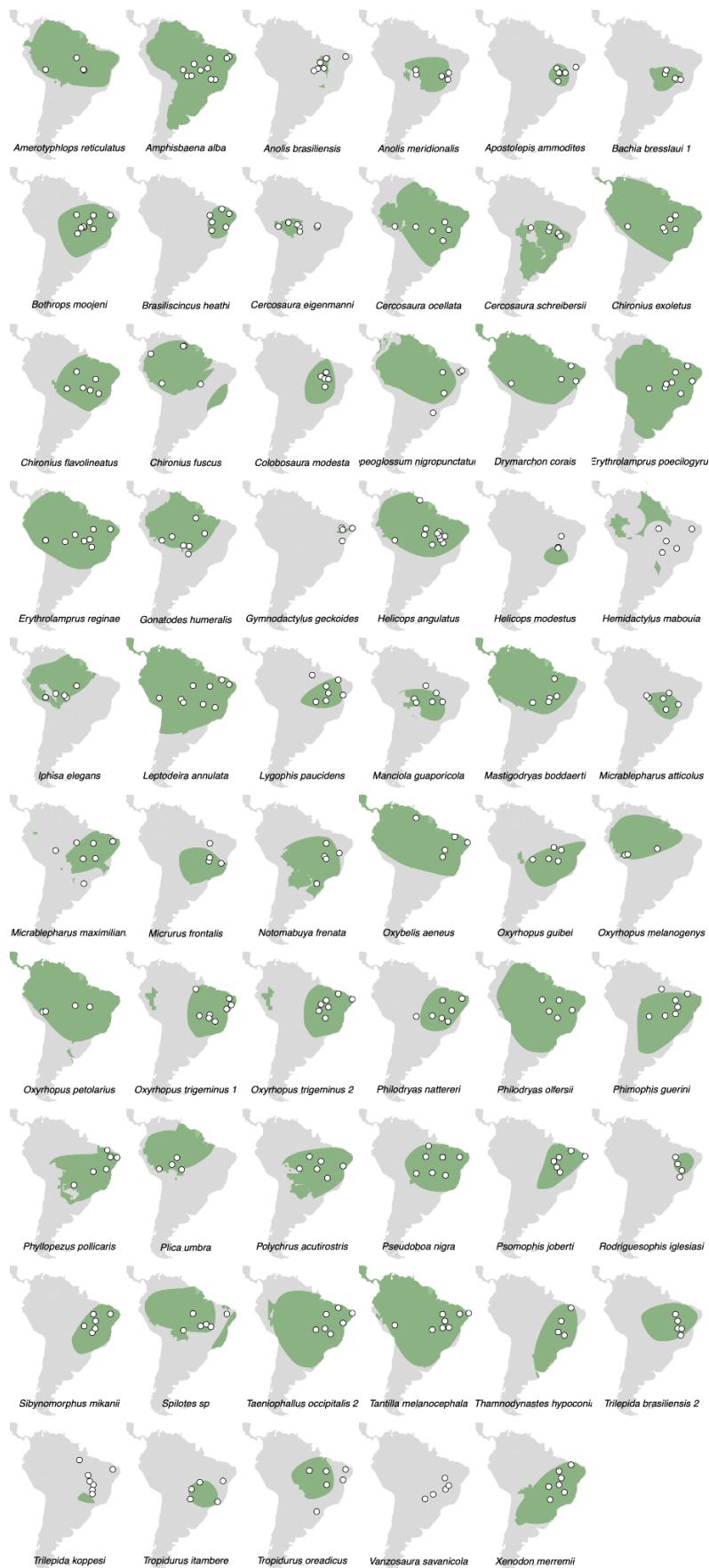


Figure S3: Geographic maps and sampling points shown for each operational taxonomic unit (OTU) included in this study. Geographic maps are from (13). Note that some geographic ranges do not encompass all points; geographic distributions are not well-circumscribed for many Neotropical species (2). Given uncertainty in geographic limits, our sampling (while relatively limited in number of individuals) spans most of the geographic range of most taxa.

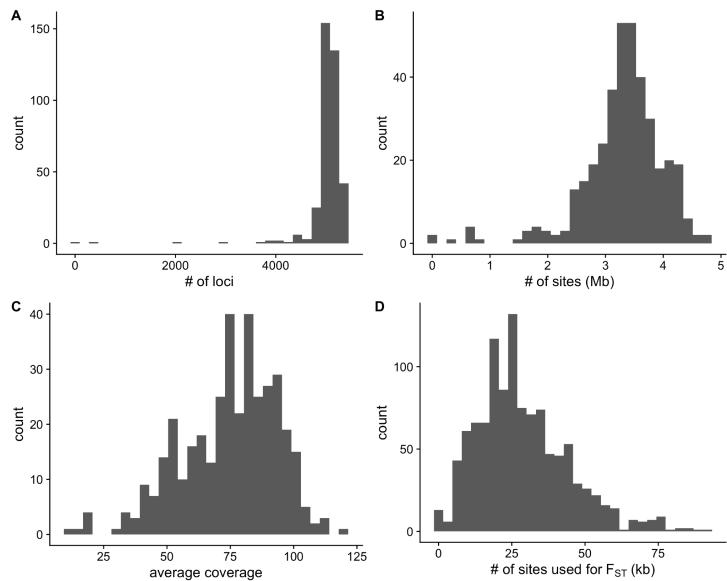


Figure S4: Data quality for the individuals ($n = 375$) included in this study: (A) number of loci sampled (mean = 5019), (B) number of high-quality (≥ 20) and high-coverage (≥ 10) invariant and variant sites sampled (mean = 3.3 Megabases [Mb]), (C) average coverage across these sites (mean = 74.6), and (D) number of variable sites used for F_{ST} estimation (mean = 28.5 kilobases [kb]). Our genomic inferences were based on a high-quality, locus-rich dataset.

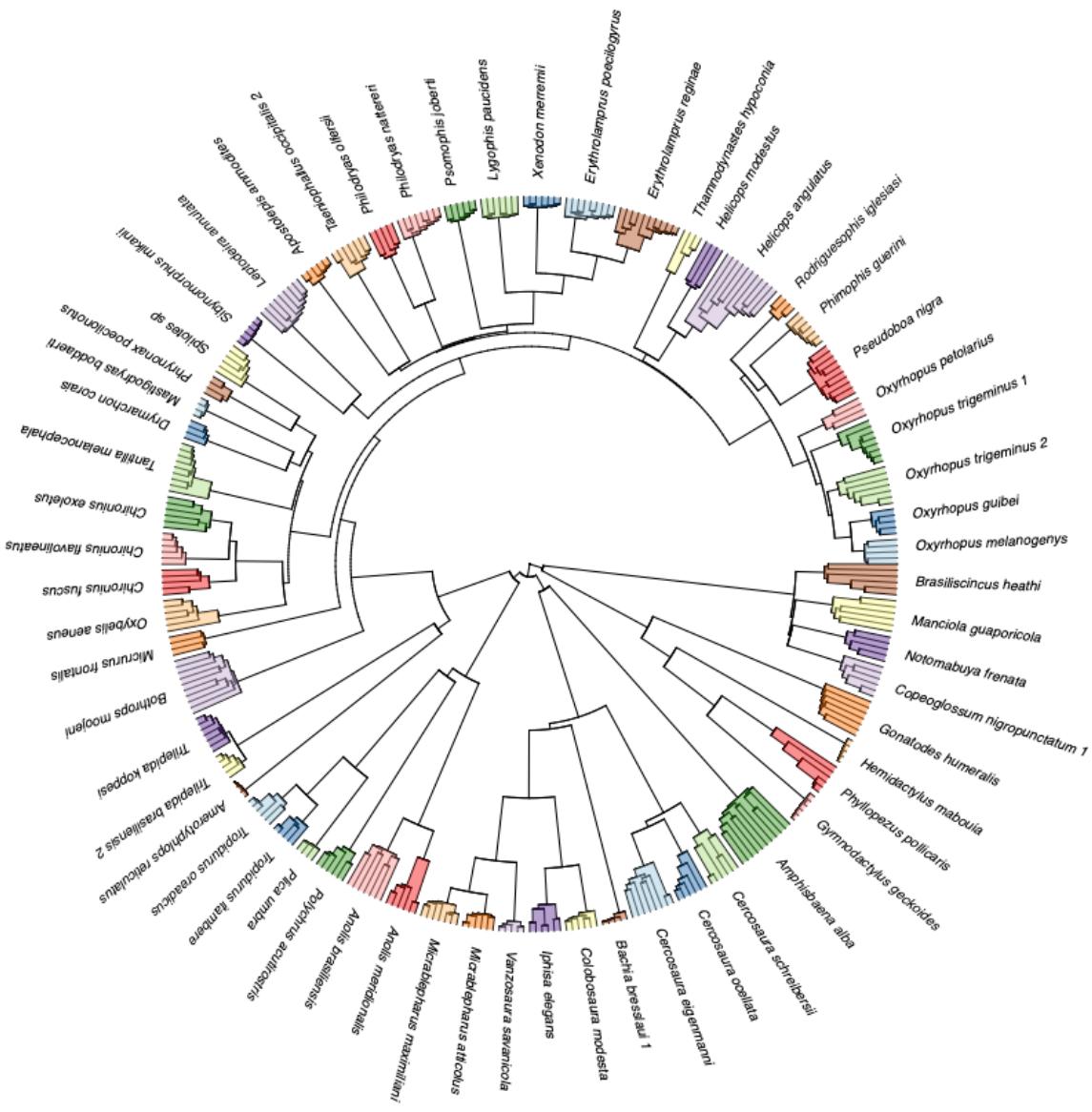
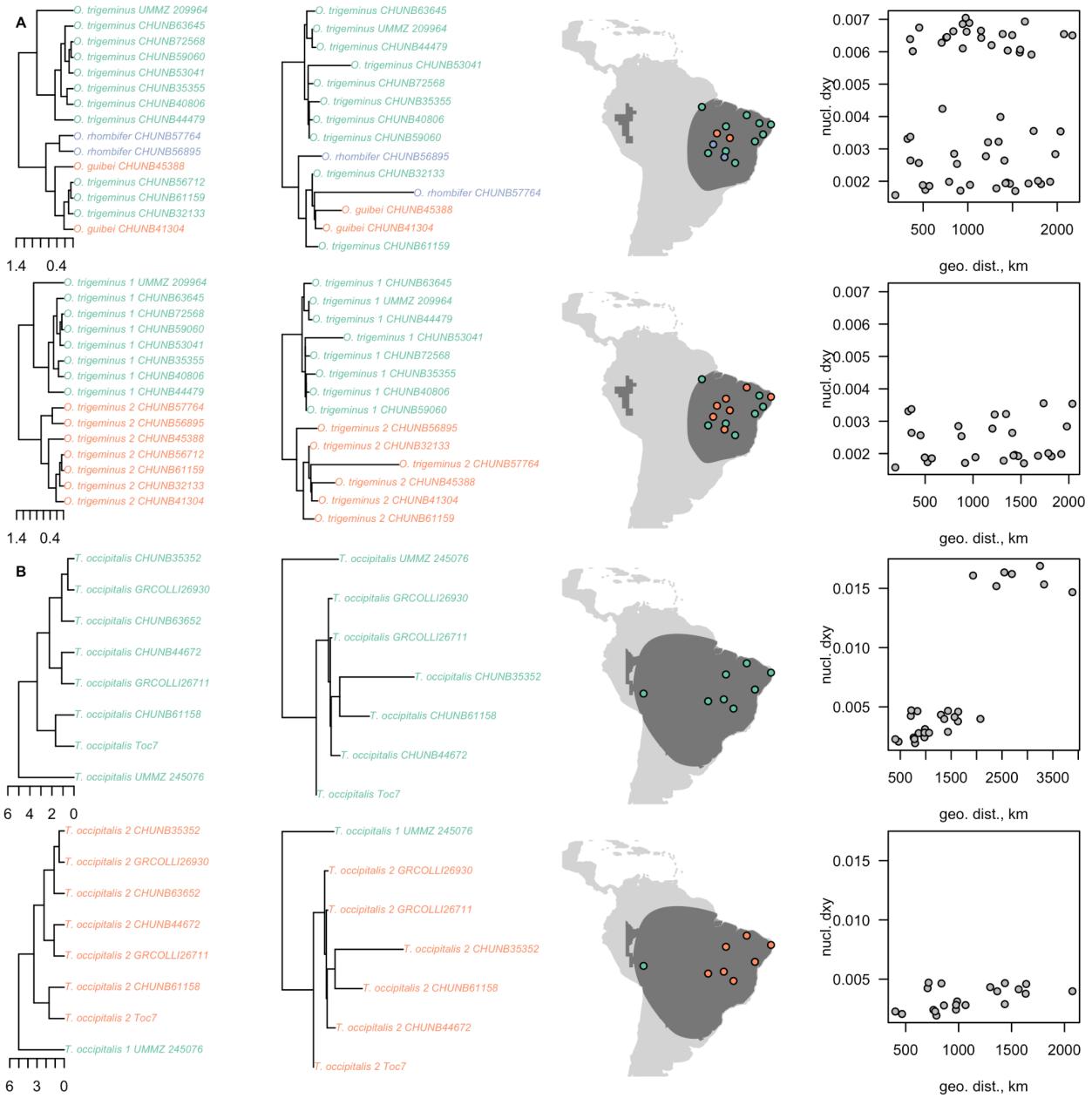


Figure S5: Concatenated phylogeny of 4796 loci across the 375 individuals included in this study. Phylogeny was dated using penalized likelihood (14) as implemented in the “chronos” function in the R package ape(15). The root age was set to 180 million years (16). Clades are colored by operational taxonomic unit (OTU) identity. While most taxa in our study correspond directly to accepted, nominal taxa, some taxa (23%) required taxonomic revision to reflect cryptic species or taxonomic uncertainties. This phylogeny was used solely to help guide OTU delimitation; inferences on speciation rate and other interspecific comparative analyses used the time-calibrated published phylogeny of Tonini et al. 2016.



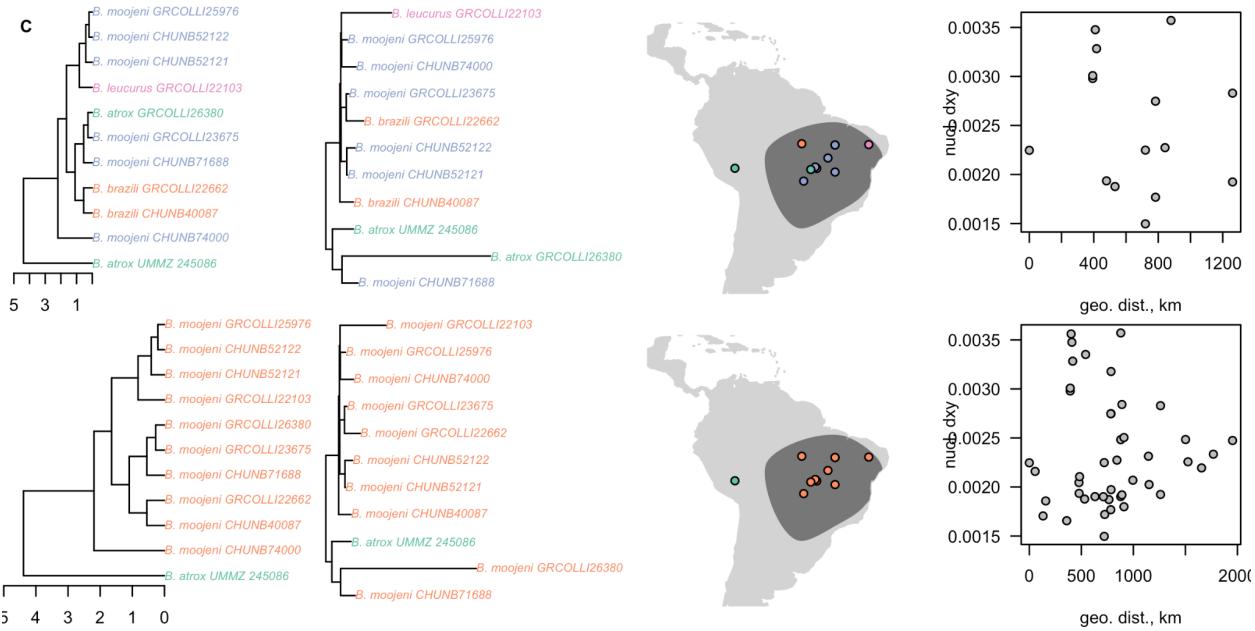


Figure S6: Phylogenetic data for three exemplar taxa that required subsequent refinement of operational taxonomic unit (OTU) boundaries based on phylogenetic data. (A) *Oxyrhopus trigeminus*, where samples were assigned to multiple nominate taxa that show paraphyletic relationships, (B) *Taeniophallus occipitalis*, where one individual provided evidence for a deep split within the nominal species, and (C) *Bothrops moojeni*, a species complex known to have messy taxonomic boundaries that were clarified using genetic data. The top row shows (L → R) concatenated nuclear phylogeny, concatenated mtDNA phylogeny, range maps with tips and points colored by nominal species identity, and genetic divergence across geographic space. The bottom row shows the same data for revised taxon identities. Phylogeny was dated using penalized likelihood(14) as implemented in the “chronos” function in the R package ape(15). The root age was set to 180 million years(16); scale bars reflect million years of evolution. Range maps were taken from Roll et al. 2017(13). In total, we provisionally modified 15 nominal species.

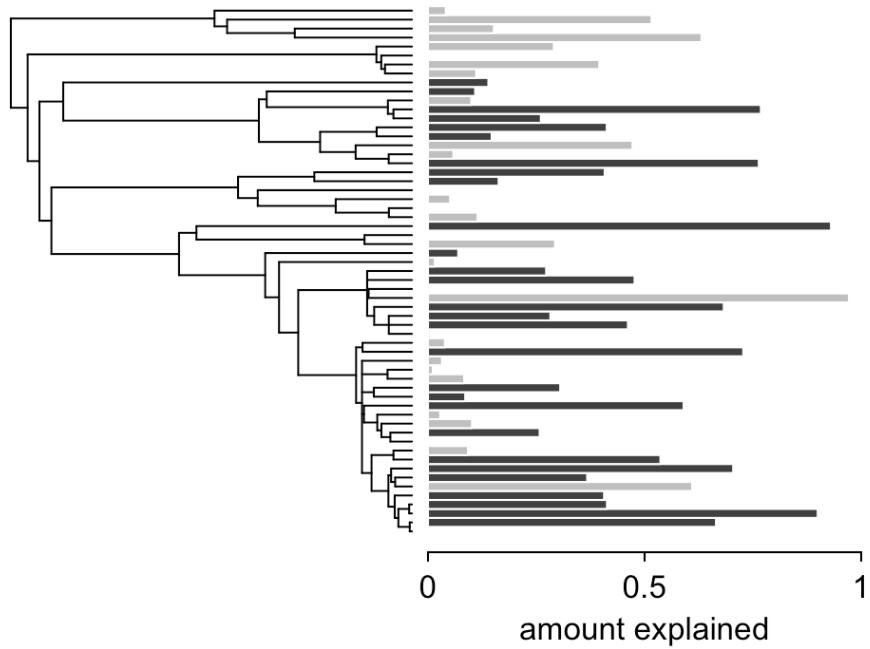
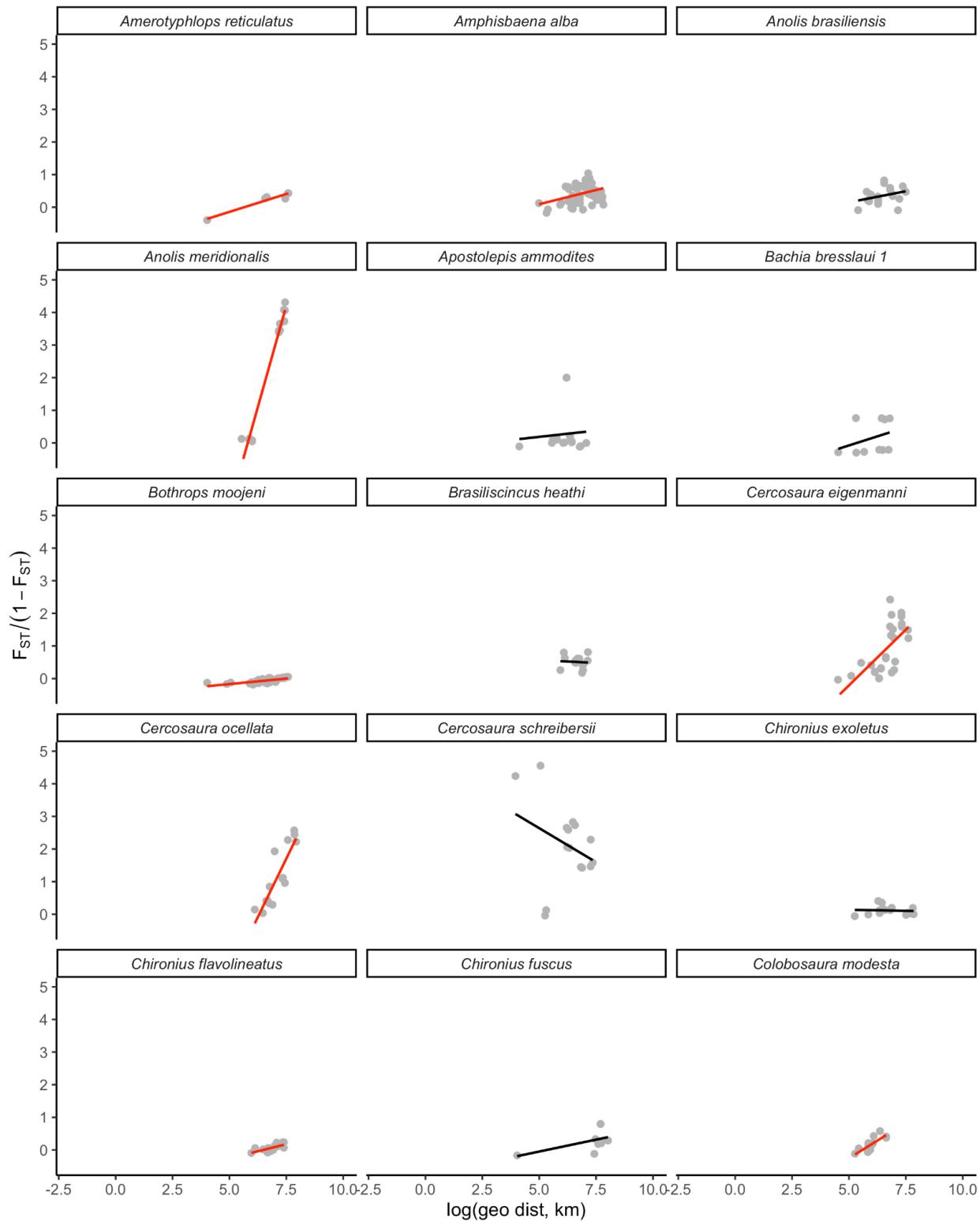
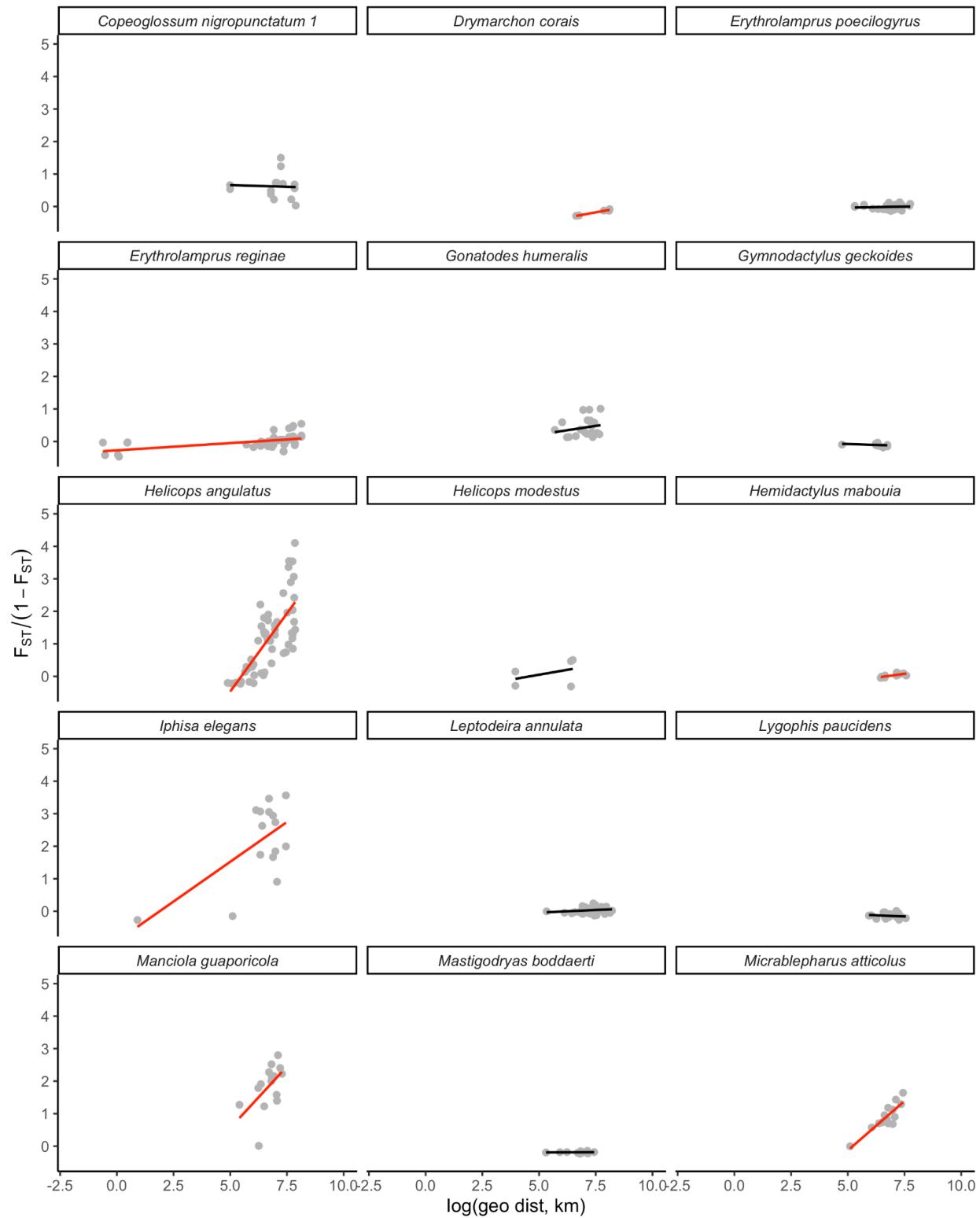
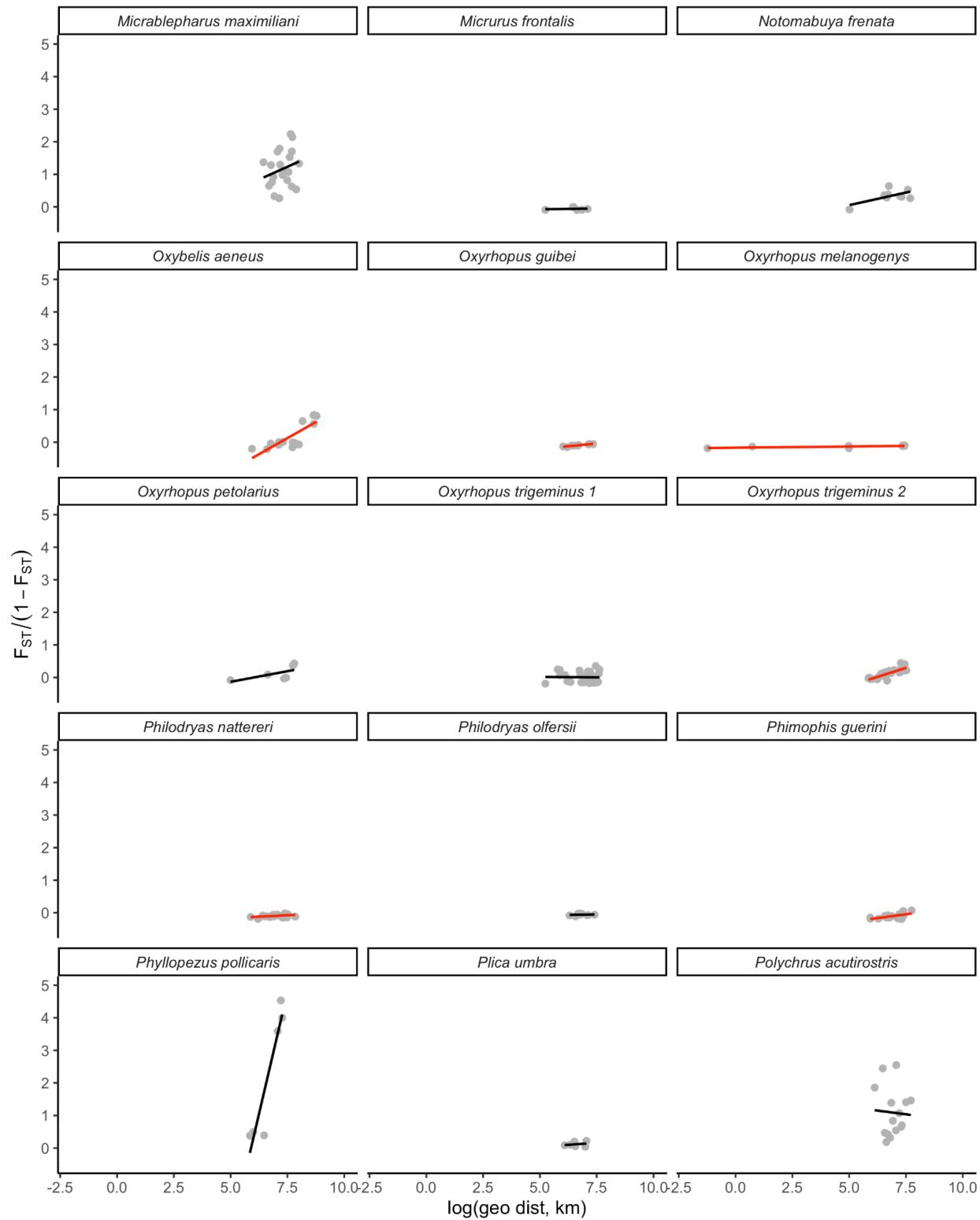


Figure S7: Amount of variation in genetic divergence explained by isolation-by-distance, as measured by r^2 of a Mantel test comparing an inverse F_{ST} matrix to a matrix of log of geographic distance. Dark gray bars indicate significant relationships. Of the 59 species tested, 28 species returned significant isolation-by-distance models; overall, these models explained an average of 31% of the variation in genetic divergence. In our robustness analyses, we demonstrate that our overall results are unaffected by restricting our inferences to only those taxa showing strong / significant IBD relationships (Fig. S14, Table S3). In fact, the overall direction of the effect becomes negative ($r = -0.004$; non-significant) when restricted to taxa with significant IBD relationships.







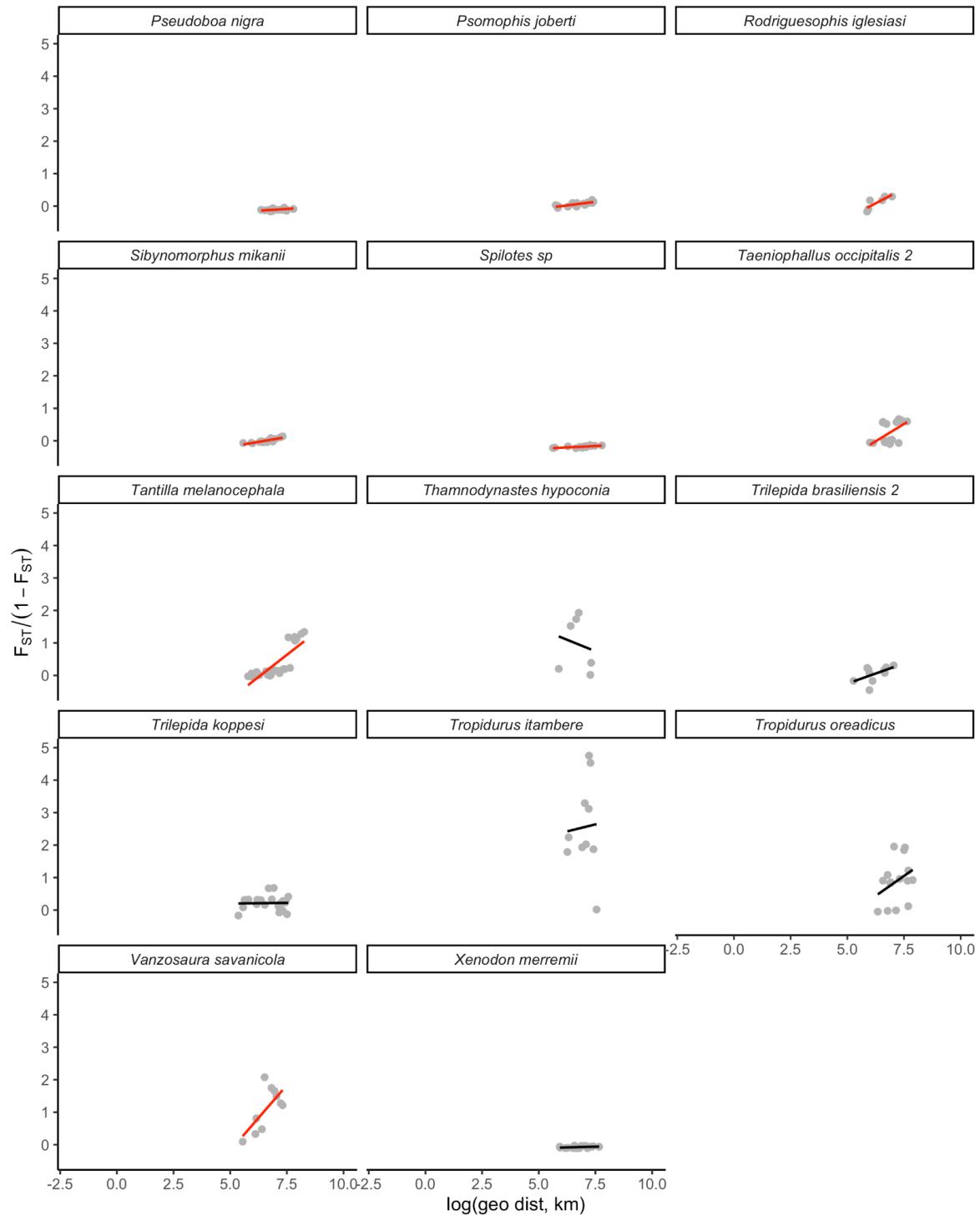


Figure S8: Isolation-by-distance relationships for all taxa ($n = 59$) included in this study. Shown is inverse F_{ST} along the natural log of geographic distance for pairwise individual comparisons within taxa. β_{IBD} – our study's key metric for measuring the rate at which population isolation accumulates – is the slope of the regression line through these points. Significant β_{IBD} relationships are shown in red.

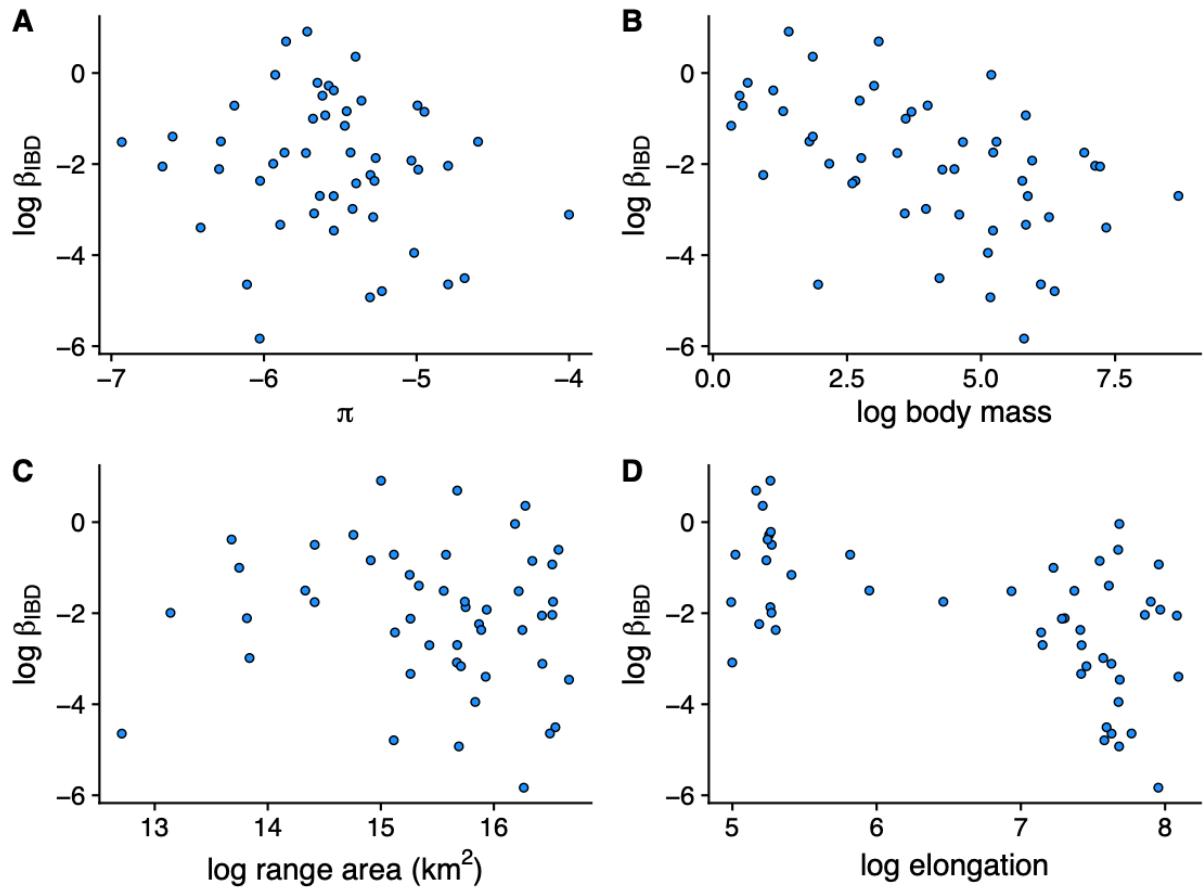


Figure S9: The correlation between organismal traits and slope of isolation-by-distance (β_{IBD}): (A) average genetic diversity (π), (B) body mass of species, (C) geographic range area, and (D) the elongation index which captures how elongated a species is. These four traits are thought to influence both population density and organismal dispersal, two factors that affect levels of isolation-by-distance. Log elongation was the only significant predictor of β_{IBD} (Table S2).

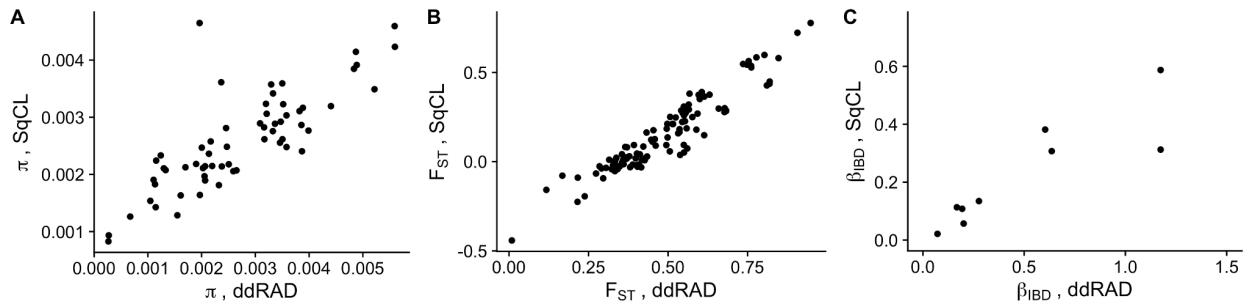


Figure S10: Concordance between population genetic metrics calculated using ddRAD vs. SqCL markers: (A) nucleotide diversity (π), (B) genetic differentiation (F_{ST}), and (C) slope of isolation-by-distance (β_{IBD}). Estimates of genetic diversity and differentiation inferred from SqCL markers are consistently lower than those inferred from ddRAD loci, as expected given that SqCL markers are likely under stronger purifying selection than ddRAD loci. Despite this, metrics are highly correlated across both markers; Pearson correlations are (A) $r = 0.81$, $p = 3.4e-15$, $n = 61$, (B) $r = 0.94$, $p < 3e-16$, $n = 110$, and (C) $r = 0.97$, $p = 4.9e-6$, $n = 10$.

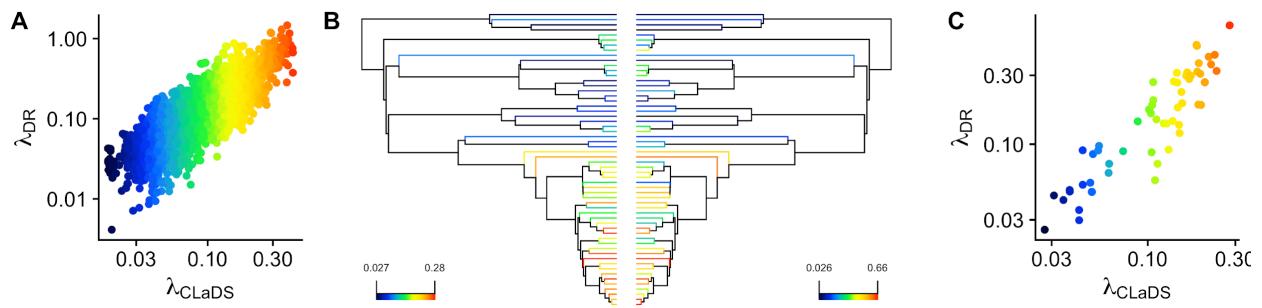


Figure S11: Comparison of speciation rates as estimated via a model-based approach (CLaDS, λ_{CLaDS}) and a semi-parametric approach (DR statistic, λ_{DR}). (A) Correlation of rates across all squamate species ($n = 9755$, $r = 0.87$, $p < 2e-16$). (B) Comparison of speciation rates across the taxa included in this analysis; the left phylogeny shows λ_{CLaDS} and the right phylogeny shows λ_{DR} . (C) Correlation between λ_{DR} and λ_{CLaDS} across all species included in this analysis ($n = 59$, $r = 0.87$, $p < 2e-16$). Speciation rates are highly correlated across inference methods.

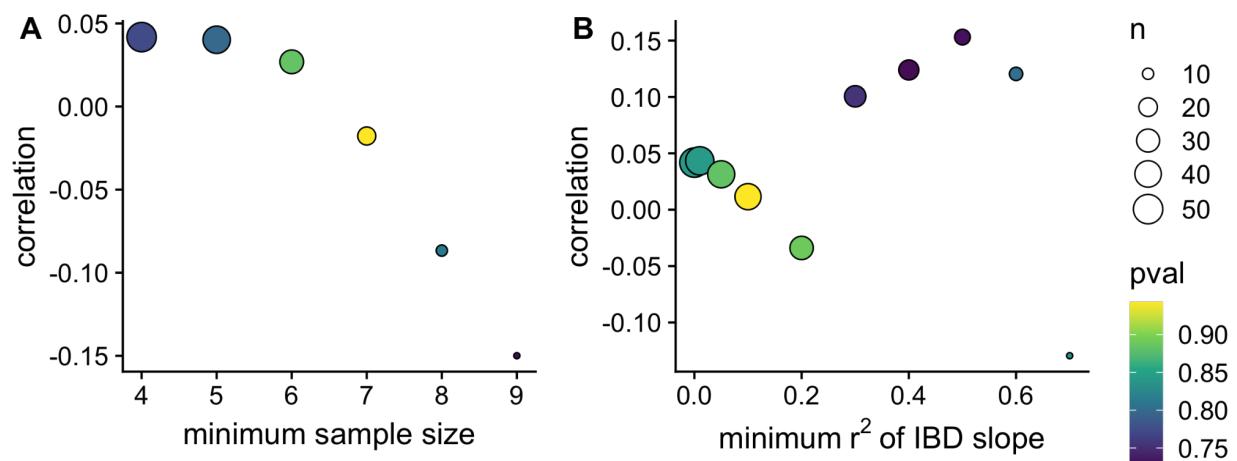


Figure S12: Effects of (A) sample size and (B) estimation error on correlation between isolation-by-distance (IBD) slope and speciation rate. We subsetted the dataset by filtering out taxa with (A) minimum sample sizes or (B) minimum r^2 for the IBD slope estimate. For each filtered dataset, we tested the correlation between IBD slope and speciation rate. Even after removing IBD slopes with low sample size or high error, we still find no relationship between population isolation and speciation rate.

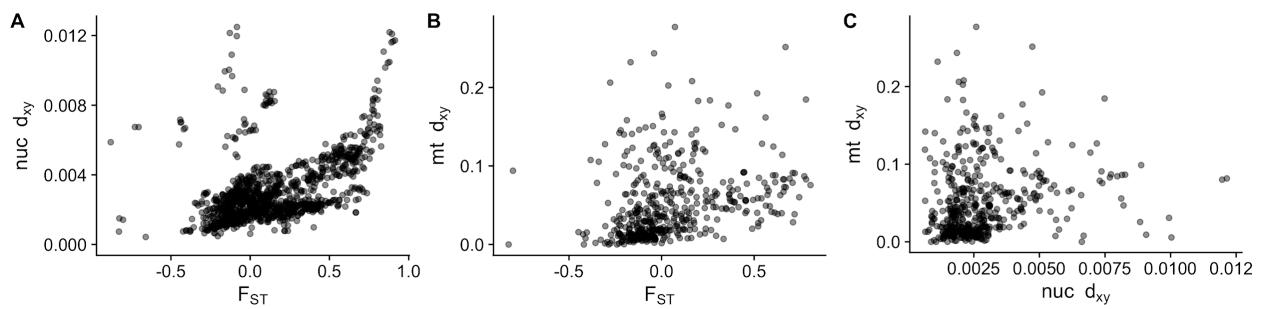


Figure S13: Correlation in estimates of genetic divergence across different metrics for divergence (A) nuclear F_{ST} versus nuclear d_{xy} , (B) nuclear F_{ST} versus mitochondrial d_{xy} , and (C) nuclear vs. mitochondrial d_{xy} . For (B) and (C), only pairwise comparisons where ≥ 500 bp of mitochondrial sequence was sampled are shown. Estimates of genetic divergence are highly correlated between nuclear estimates of divergence and more weakly between nuclear and mitochondrial divergence; Pearson correlations are (A) $r = 0.47$, $p < 3e-16$, $n = 1100$, (B) $r = 0.30$, $p = 6.9e-11$, $n = 462$, and (C) $r = 0.16$, $p = 4e-4$, $n = 462$.

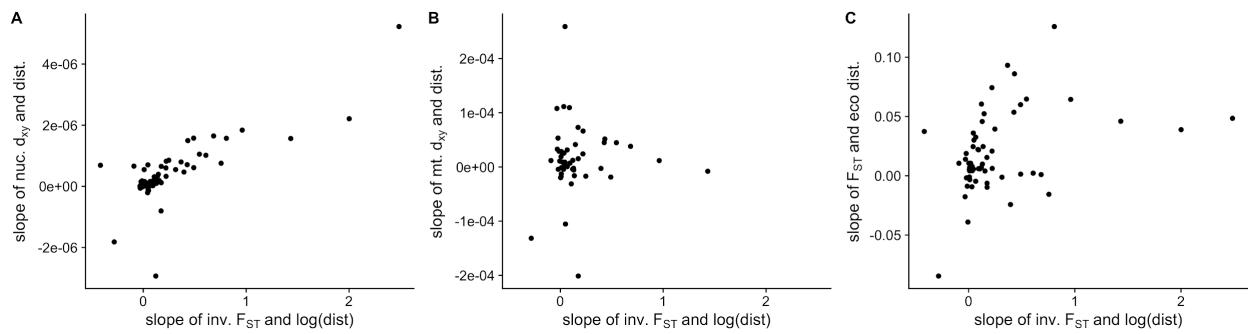


Figure S14: Correlations between isolation-by-distance (IBD) slopes measured using alternate metrics of genetic differentiation and distance; IBD slope between inverse F_{ST} and log geographic distance compared to (A) IBD slope between nuclear d_{xy} and geographic distance, (B) IBD slope between mitochondrial d_{xy} and geographic distance, and (C) IBD slope between F_{ST} and ecological distance. Correlations across different types of slopes vary greatly; Pearson correlations are (A) $r = 0.79$, $p = 1e-13$, $n = 59$, (B) $r = 0.03$, $p = 0.86$, $n = 47$, and (C) $r = 0.37$, $p = 0.003$, $n = 59$. However, across all alternate measures of IBD slope, we find no correlation between IBD slope and speciation rate (Table S3).

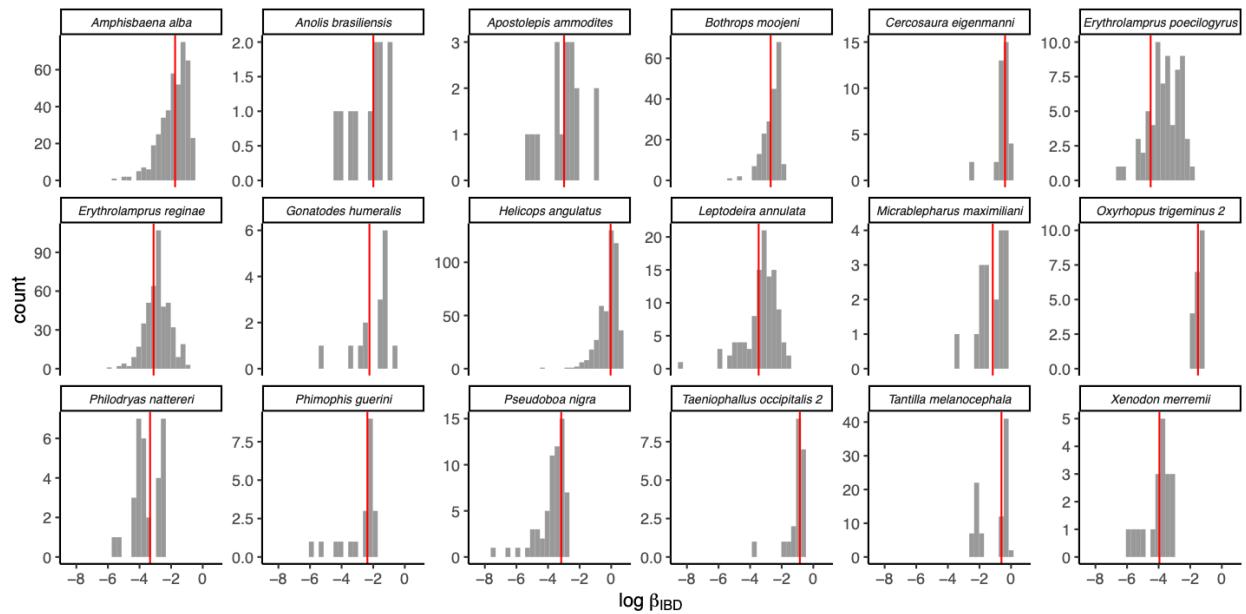


Figure S15: For the taxa that were sampled at ≥ 5 individuals, we sampled all possible combinations of 4 individuals and calculated IBD slopes (β_{IBD}) for subsampled datasets. We depict here only those taxa with 10 or more subsampled datasets. Shown in gray are the subsampled slope values; shown in red is the value estimated for the complete dataset. Although some subsamples are noticeably different from those estimated with the full dataset, most subsampled datasets recover similar IBD slopes seen with the full dataset.

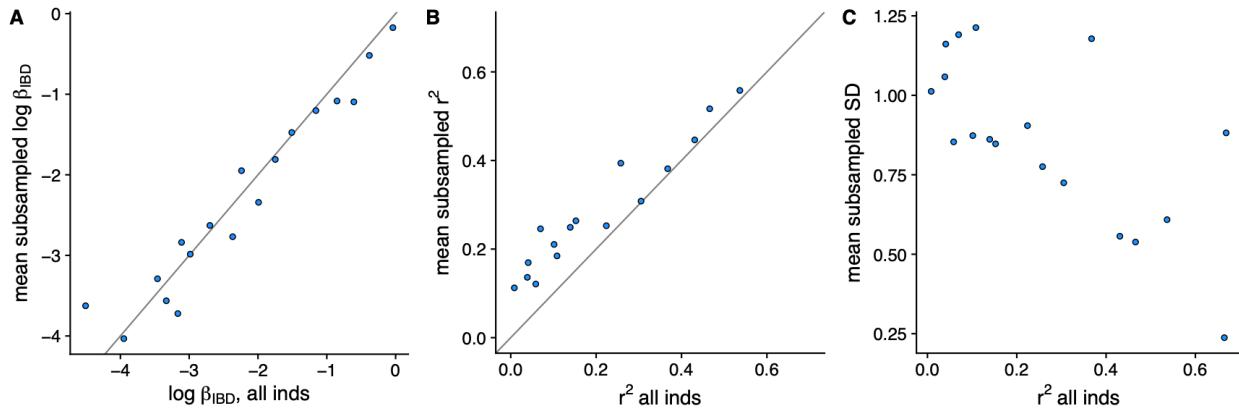


Figure S16: For the taxa that were sampled at >5 individuals, we sampled all possible combinations of 4 individuals and calculated IBD slopes (β_{IBD}) for subsampled datasets. Shown here is (A) $\log \beta_{IBD}$ measured across the complete sampling for a taxa versus the mean subsampled $\log \beta_{IBD}$, (B) r^2 for β_{IBD} calculated across all individuals versus the mean subsampled r^2 , and (C) the r^2 for β_{IBD} calculated across all individuals versus the mean subsampled β_{IBD} standard deviation (SD). Gray lines in (A) and (B) are the lines of unity. Subsampled datasets have similar means and model fit as the full dataset. Further, the greater the model fit for the full dataset, the less variation we see in subsampled datasets. This suggests dropping OTUs with low model fits (see Fig. S14) is an effective way to account for limited sampling.

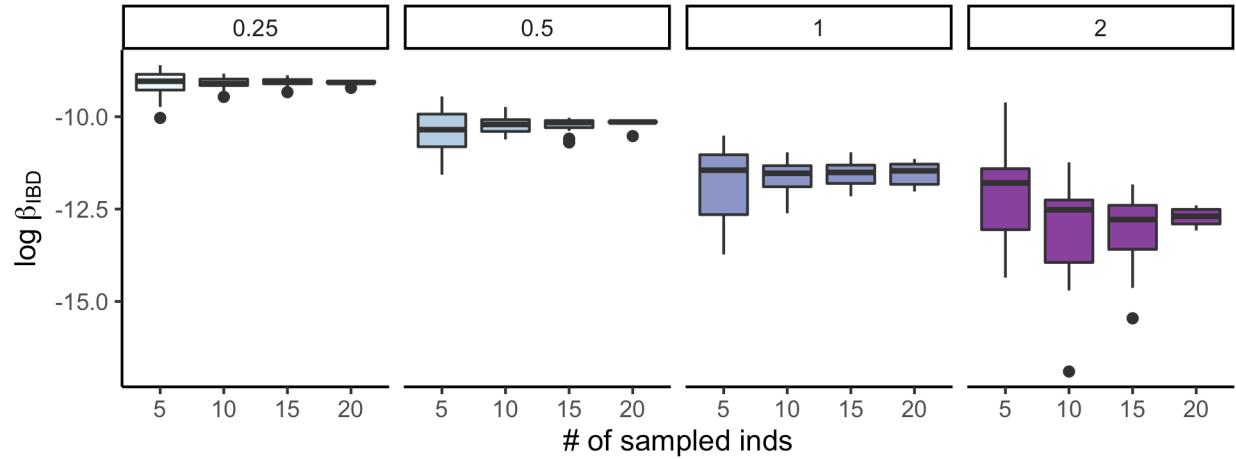


Figure S17: Accuracy of IBD slope estimation (β_{IBD}) in forward genetic simulations. Individuals were simulated at varying levels of dispersal ($\sigma = 0.25, 0.5, 1$, and 2 ; shown by panel). We then sampled either 5, 10, 15 or 20 individuals and estimated β_{IBD} . Each simulation was run across 5 replicates. Even with small sample sizes, we can accurately estimate β_{IBD} and capture varying dispersal across populations.

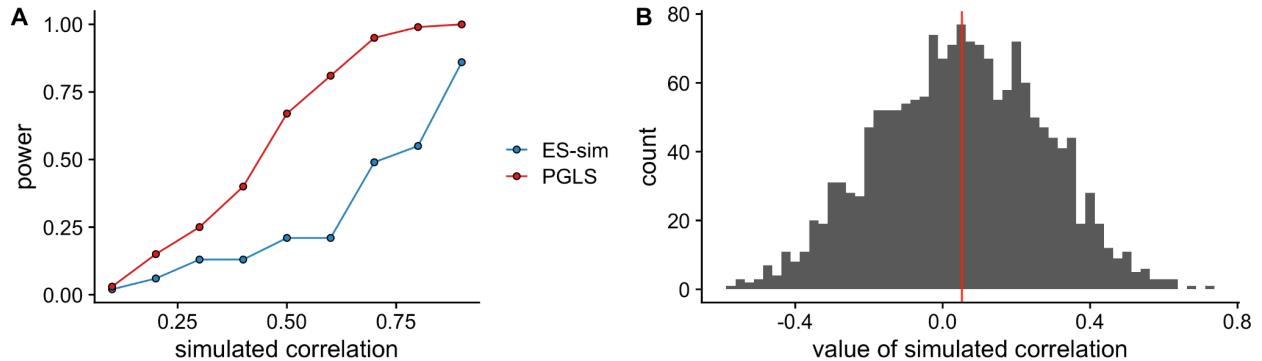


Figure S18: Power in our study design to recover a significant correlation between log-transformed speciation rate and IBD slopes (β_{IBD}) if one existed and quasi-posterior distribution of the true correlation as inferred from rejection sampling. (A) For a range of simulated correlations ($r = 0.1$ to 0.9), for 100 simulations each, we simulated our trait of interest (here, β_{IBD}) following Brownian motion under a given correlation to empirical speciation rates. We then used two methods (phylogenetic generalized least squares; PGLS) and ES-SIM to test both significance of the trait to speciation rates. PGLS had greater power to detect a correlation than ES-SIM. (B) Quasi-posterior distribution on the correlation between log-transformed speciation rate and β_{IBD} conditional on the phylogeny and the observed speciation rate variation, estimated using rejection sampling. Distribution was estimated using our observed correlation ($r = 0.04$) as a summary statistic; correlations were sampled from a uniform (-1, 1) prior distribution and accepted if a given true correlation yielded a summary statistic that deviated by less than 0.01 from the observed value. Posterior distribution is centered approximately on zero, with a median of $r = 0.05$ (red line). Given our estimated correlation, it is unlikely that the true correlation between population isolation and speciation rate is substantial, and it is nearly as likely to be negative as positive.

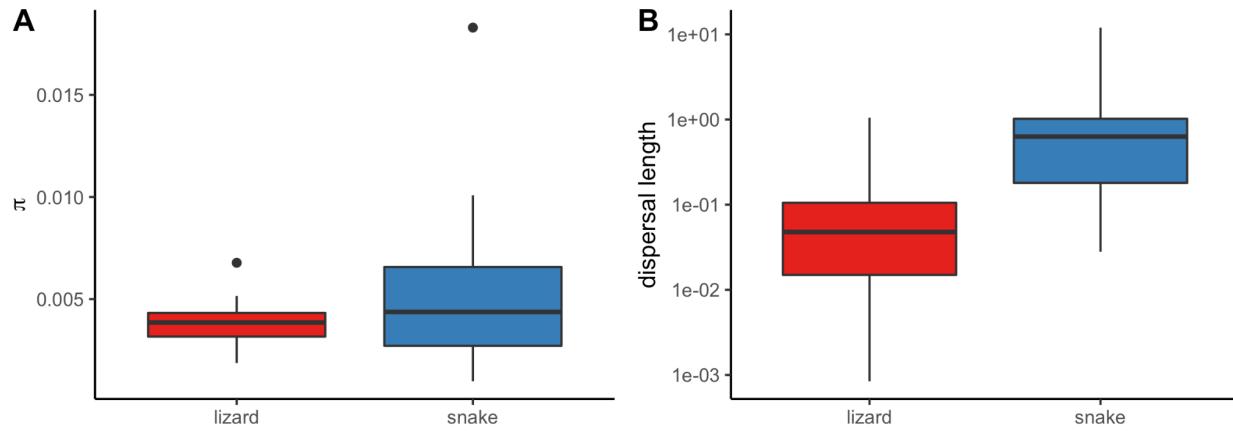


Figure S19: Why do more elongate animals show greater levels of isolation-by-distance? We test two possible reasons: (A) More elongate animals (e.g., snakes) have greater population density than less elongate animals (e.g., lizards), resulting in higher levels of genetic diversity (π). We find no support for this hypothesis across our dataset ($n = 59$; phylogenetic ANOVA $p = 0.78$). (B) Snakes have greater dispersal than lizards. We summarize across 34 published studies of lizard and snake dispersal to find that snakes have $\sim 10x$ greater dispersal than lizards (Table S4). Given that these studies use a diversity of methods and dispersal metrics, we note these results are provisional and thus do not conduct any formal statistical tests.

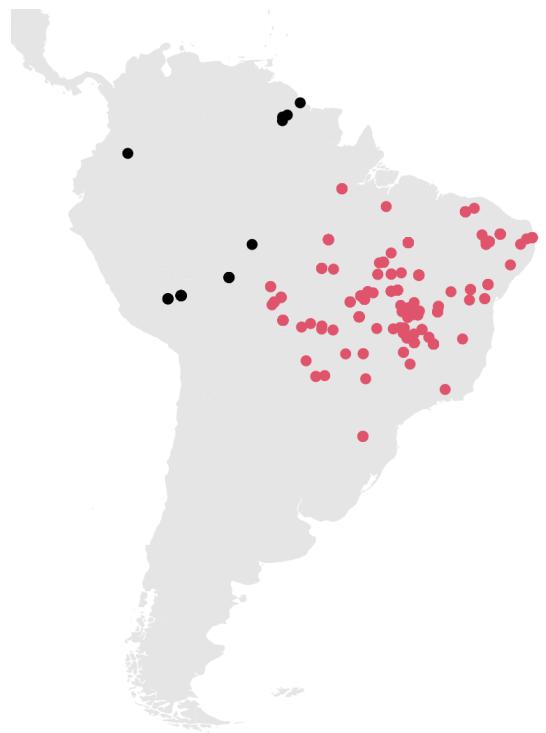


Figure S20: The effects of non-Cerrado individuals. In order to ensure our limited sampling outside of the core Cerrado region did not affect our results, we removed 36 individuals (shown in black) that fall out of the core Cerrado region and then repeated IBD slope estimation with the remaining 339 individuals (shown in pink). Using these IBD slopes, we tested our hypothesis that IBD slope predicts speciation rate, again recovering no relationship (Table S3).

Supplemental Tables

Table S1: Data on the individuals ($n = 375$) included in this study: nominal species designation, revised operational taxonomic unit (OTU) name provisionally used in this study, sample locality, and information on genetic data collected for sample (number of loci captured, number of sites captured in megabase (Mb), average coverage, and SRA accession ID where data can be downloaded).

individual	nominal species	revised taxon name	latitude	longitude	# of loci	# of sites (Mb)	avg. cov.	SRA
CHUNB40084	<i>Amerotyphlops reticulatus</i>	<i>Amerotyphlops reticulatus</i>	-7.034836	-55.41987	4969	3.4	91.9	SAMN23818006
CHUNB68360	<i>Amerotyphlops reticulatus</i>	<i>Amerotyphlops reticulatus</i>	-12.932049	-51.833363	4892	3.5	74.6	SAMN23818007
CHUNB71122	<i>Amerotyphlops reticulatus</i>	<i>Amerotyphlops reticulatus</i>	-12.5923	-52.209892	4843	3.2	52.4	SAMN23818008
RAB_00216	<i>Amerotyphlops reticulatus</i>	<i>Amerotyphlops reticulatus</i>	-12.571939	-70.085827	4510	2.1	42	SAMN23818009
AAGarda02343	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-12.029774	-48.537811	5204	3.6	81.7	SAMN23818010
CHUNB44483	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-17.359421	-44.955194	5200	4.1	77.5	SAMN23818011
CHUNB52145	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-7.330783	-47.470092	5159	3.5	66.2	SAMN06705350
GRCOLLI04518	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-12.741373	-60.138584	5247	3.2	96.1	SAMN23818012
GRCOLLI10442	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-17.219742	-46.875419	5231	3.4	88.9	SAMN23818013
GRCOLLI15744	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-6.485331	-38.311129	5211	3.4	83.4	SAMN23818014
GRCOLLI21850	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-7.231753	-39.40839	5224	4	84	SAMN23818015
GRCOLLI24519	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-12.932049	-51.833363	5221	3.6	93.6	SAMN23818016
TMOTT175	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-9.954073	-54.916057	5203	3.4	76.3	SAMN23818017
TMOTT191	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-15.674071	-58.097904	5188	3.5	69.8	SAMN23818018
TMOTT199	<i>Amphisbaena alba</i>	<i>Amphisbaena alba</i>	-15.569989	-56.073252	5212	3.4	79.7	SAMN23818019
GFHORTA0098	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-12.173598	-51.503639	5333	3.5	74.9	SAMN23818020
GRCOLLI26899	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-7.330783	-47.470092	5283	4.1	84.1	SAMN06705372
CHUNB51972	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-7.330783	-47.470092	5277	4.5	71.9	SAMN06705325
CHUNB58055	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-9.329425	-50.344804	5326	2.5	54	SAMN23818021
GRCOLLI12455	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-12.029774	-48.537811	5338	2.6	79	SAMN23818022

GRCOLLI15938	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-6.485331	-38.311129	5367	3.9	100.9	SAMN23818023
GRCOLLI26418	<i>Anolis brasiliensis</i>	<i>Anolis brasiliensis</i>	-13.188043	-53.261519	5356	3.4	93.9	SAMN23818024
CHUNB60380	<i>Anolis brasiliensis</i>	<i>Anolis meridionalis</i>	-15.794087	-47.887905	5325	3.7	79.8	SAMN23818025
GRCOLLI25188	<i>Anolis meridionalis</i>	<i>Anolis meridionalis</i>	-15.009324	-59.952558	5319	3.4	70.9	SAMN23818026
GRCOLLI04475	<i>Anolis meridionalis</i>	<i>Anolis meridionalis</i>	-12.741373	-60.138584	5326	4.5	83.2	SAMN23818027
CHUNB51197	<i>Anolis meridionalis</i>	<i>Anolis meridionalis</i>	-14.171078	-44.545669	5345	4.3	94.7	SAMN23818028
CHUNB70203	<i>Anolis meridionalis</i>	<i>Anolis meridionalis</i>	-15.794087	-47.887905	5324	3.3	84.8	SAMN23818029
GRCOLLI16776	<i>Anolis meridionalis</i>	<i>Anolis meridionalis</i>	-17.359421	-44.955194	5332	3.7	85.9	SAMN23818030
GRCOLLI12452	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-12.029774	-48.537811	10	0	11.7	SAMN23818031
CHUNB38443	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-14.450174	-47.045083	5065	3.2	92.4	SAMN23818032
CHUNB51360	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-14.17108	-44.54567	5020	3.8	73.3	SAMN23818033
CHUNB59061	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-14.136245	-47.519093	5032	3.3	73.9	SAMN23818034
CHUNB62399	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-18.169573	-47.947703	5108	3.8	120.1	SAMN23818035
GRCOLLI18529	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-14.171078	-44.545669	4970	2.6	50.9	SAMN23818036
LJVITT09444	<i>Apostolepis ammodites</i>	<i>Apostolepis ammodites</i>	-11.463466	-39.526265	5075	3.4	97.4	SAMN23818037
CHUNB25842	<i>Bachia bresslaui</i>	<i>Bachia bresslaui</i>	-17.219742	-46.875419	5135	2.9	78.5	SAMN23818038
CHUNB44521	<i>Bachia bresslaui</i>	<i>Bachia bresslaui</i>	-17.359421	-44.955194	5114	2.8	75.4	SAMN23818039
CHUNB63628	<i>Bachia bresslaui</i>	<i>Bachia bresslaui</i>	-14.66918	-52.361193	5118	2.8	71.9	SAMN23818040
CHUNB74029	<i>Bachia bresslaui</i>	<i>Bachia bresslaui</i>	-16.769434	-47.606818	5145	3.1	83.9	SAMN23818041
GFHORTA0135	<i>Bachia bresslaui</i>	<i>Bachia bresslaui</i>	-12.932049	-51.833363	5142	3	81.1	SAMN23818042
CHUNB40087	<i>Bothrops brazili</i>	<i>Bothrops moojeni</i>	-7.034836	-55.41987	5079	3.3	73.4	SAMN23818043
CHUNB52121	<i>Bothrops moojeni</i>	<i>Bothrops moojeni</i>	-7.330783	-47.470092	4392	2.4	44.8	SAMN06705343
CHUNB52122	<i>Bothrops moojeni</i>	<i>Bothrops moojeni</i>	-7.330783	-47.470092	4819	2.9	47.6	SAMN06705344
CHUNB71688	<i>Bothrops moojeni</i>	<i>Bothrops moojeni</i>	-15.964838	-54.964188	5126	3.7	102.3	SAMN15718137
CHUNB74000	<i>Bothrops moojeni</i>	<i>Bothrops moojeni</i>	-10.440931	-49.166658	4313	2.4	48.4	SAMN06705359
GRCOLLI22103	<i>Bothrops leucurus</i>	<i>Bothrops moojeni</i>	-7.231753	-39.40839	5086	3.4	79.3	SAMN23818044
GRCOLLI22662	<i>Bothrops brazili</i>	<i>Bothrops moojeni</i>	-12.932049	-51.833363	5077	3.7	84.1	SAMN23818045
GRCOLLI23675	<i>Bothrops moojeni</i>	<i>Bothrops moojeni</i>	-12.5923	-52.209892	5006	4.4	102.5	SAMN06705364

GRCOLLI25976	<i>Bothrops moojeni</i>	<i>Bothrops moojeni</i>	-13.799279	-47.463436	4981	4.6	91.8	SAMN06705365
GRCOLLI26380	<i>Bothrops atrox</i>	<i>Bothrops moojeni</i>	-13.188043	-53.261519	5107	3.6	85.8	SAMN23818046
CHUNB40588	<i>Brasiliscincus heathi</i>	<i>Brasiliscincus heathi</i>	-10.544429	-46.412466	5276	4.1	81.4	SAMN23818047
CHUNB37505	<i>Brasiliscincus heathi</i>	<i>Brasiliscincus heathi</i>	-14.482839	-46.515638	5246	4	68.4	SAMN23818048
CHUNB37518	<i>Brasiliscincus heathi</i>	<i>Brasiliscincus heathi</i>	-6.485331	-38.311129	5213	3.2	50.5	SAMN23818049
CHUNB56572	<i>Brasiliscincus heathi</i>	<i>Brasiliscincus heathi</i>	-12.870575	-39.859127	5264	4.2	73.3	SAMN23818050
CHUNB61038	<i>Brasiliscincus heathi</i>	<i>Brasiliscincus heathi</i>	-4.276069	-41.778505	5277	4.1	82.4	SAMN23818051
CN1637	<i>Brasiliscincus heathi</i>	<i>Brasiliscincus heathi</i>	-7.330783	-47.470092	5031	3.3	46.5	SAMN06705362
CHUNB22672	<i>Cercosaura argula</i>	<i>Cercosaura eigenmanni</i>	-10.773884	-65.323952	5131	3.3	94.1	SAMN23818052
CHUNB11467	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-12.741373	-60.138584	5069	3.1	74	SAMN23818053
CHUNB18028	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-11.677537	-61.183666	5122	3.4	98.4	SAMN23818054
CHUNB22468	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-10.773884	-65.323952	5095	3.2	82.1	SAMN23818055
CHUNB68408	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-12.932049	-51.833363	5090	3.1	84.4	SAMN23818056
CHUNB73582	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-12.173598	-51.503639	5119	3.4	96.7	SAMN23818057
GRCOLLI25802	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-15.009324	-59.952558	5059	2.8	73.1	SAMN23818058
UMMZ_245036	<i>Cercosaura eigenmanni</i>	<i>Cercosaura eigenmanni</i>	-12.562486	-70.096652	4457	1.8	53.6	SAMN23818059
GRCOLLI04419	<i>Cercosaura ocellata</i>	<i>Cercosaura ocellata</i>	-12.741373	-60.138584	5111	3.5	84.1	SAMN23818060
GRCOLLI18507	<i>Cercosaura ocellata</i>	<i>Cercosaura ocellata</i>	-14.171078	-44.545669	5103	3.1	80.1	SAMN23818061
GRCOLLI21268	<i>Cercosaura ocellata</i>	<i>Cercosaura ocellata</i>	-14.66918	-52.361193	5144	3.2	94.7	SAMN23818062
LJVITT10185	<i>Cercosaura ocellata</i>	<i>Cercosaura ocellata</i>	-10.544429	-46.412466	5125	3.3	89.2	SAMN23818063
PHV1022	<i>Cercosaura ocellata</i>	<i>Cercosaura ocellata</i>	-19.338658	-47.292008	5142	3.7	101	SAMN23818064
UMMZ_245038	<i>Cercosaura ocellata</i>	<i>Cercosaura ocellata</i>	-12.56208	-70.096524	5134	3.5	94.5	SAMN23818065
CHUNB43410	<i>Cercosaura schreibersii</i>	<i>Cercosaura schreibersii</i>	-16.258541	-47.95572	5083	2.7	82.1	SAMN23818066
CHUNB50667	<i>Cercosaura schreibersii</i>	<i>Cercosaura schreibersii</i>	-13.195033	-60.818426	5111	3.1	89.4	SAMN23818067
CHUNB57518	<i>Cercosaura schreibersii</i>	<i>Cercosaura schreibersii</i>	-15.794087	-47.887905	5093	2.8	77.9	SAMN23818068
CHUNB63866	<i>Cercosaura schreibersii</i>	<i>Cercosaura schreibersii</i>	-14.66918	-52.361193	5103	3	84.5	SAMN23818069
CHUNB73702	<i>Cercosaura schreibersii</i>	<i>Cercosaura schreibersii</i>	-12.932049	-51.833363	5080	3.1	82.2	SAMN23818070
GRCOLLI06659	<i>Cercosaura schreibersii</i>	<i>Cercosaura schreibersii</i>	-17.219742	-46.875419	5091	2.7	88.2	SAMN23818071

CHUNB63632	<i>Chironius exoletus</i>	<i>Chironius exoletus</i>	-14.66918	-52.361193	5120	3.6	100.3	SAMN23818072
GRCOLLI26431	<i>Chironius multiventris</i>	<i>Chironius exoletus</i>	-13.188043	-53.261519	5023	3.3	57.9	SAMN23818073
RAB_00525	<i>Chironius carinatus</i>	<i>Chironius exoletus</i>	-12.5613	-70.107	4794	2.4	59.9	SAMN23818074
CHUNB45394	<i>Chironius exoletus</i>	<i>Chironius exoletus</i>	-9.267406	-49.948692	5064	2.8	61.6	SAMN23818075
CHUNB52147	<i>Chironius exoletus</i>	<i>Chironius exoletus</i>	-7.330783	-47.470092	4865	3.8	47.5	SAMN06705351
GRCOLLI26131	<i>Chironius exoletus</i>	<i>Chironius exoletus</i>	-13.799279	-47.463436	5113	3.3	91.1	SAMN23818076
CHUNB40091	<i>Chironius flavolineatus</i>	<i>Chironius flavolineatus</i>	-7.034836	-55.41987	5121	4.1	102.5	SAMN23818077
CHUNB41307	<i>Chironius flavolineatus</i>	<i>Chironius flavolineatus</i>	-10.544429	-46.412466	5089	3.6	83.7	SAMN23818078
CHUNB44474	<i>Chironius flavolineatus</i>	<i>Chironius flavolineatus</i>	-17.359421	-44.955194	5110	3.5	88.9	SAMN23818079
CHUNB67435	<i>Chironius flavolineatus</i>	<i>Chironius flavolineatus</i>	-15.853342	-48.962527	5109	3.5	87.6	SAMN23818080
GRCOLLI20917	<i>Chironius flavolineatus</i>	<i>Chironius flavolineatus</i>	-14.66918	-52.361193	4945	2.6	41.5	SAMN23818081
GRCOLLI25508	<i>Chironius flavolineatus</i>	<i>Chironius flavolineatus</i>	-15.009324	-59.952558	5108	3.3	94.1	SAMN23818082
CHUNB68954	<i>Chironius fuscus</i>	<i>Chironius fuscus</i>	-12.932049	-51.833363	5110	3.9	90.1	SAMN23818083
TJC1155	<i>Chironius fuscus</i>	<i>Chironius fuscus</i>	5.27739	-59.5174	5161	4.1	105.5	SAMN23818084
TJC1604	<i>Chironius fuscus</i>	<i>Chironius fuscus</i>	5.08401	-59.98777	5113	4.1	87.3	SAMN23818085
UMMZ_245047	<i>Chironius fuscus</i>	<i>Chironius fuscus</i>	-12.5613	-70.107	5040	3.2	77.4	SAMN23818086
TJC1654	<i>Chironius monticola</i>	<i>Chironius fuscus</i>	1.49087	-75.40594	5130	4.3	96.6	SAMN23818087
CHUNB45243	<i>Colobosaura modesta</i>	<i>Colobosaura modesta</i>	-9.267406	-49.948692	5078	4.3	81.8	SAMN06705321
Cmo4	<i>Colobosaura modesta</i>	<i>Colobosaura modesta</i>	-10.3176	-48.1647	4799	2.7	60.3	SAMN06705360
CN1507	<i>Colobosaura modesta</i>	<i>Colobosaura modesta</i>	-7.330783	-47.470092	5063	3.6	71.9	SAMN06705361
GRCOLLI18297	<i>Colobosaura modesta</i>	<i>Colobosaura modesta</i>	-14.150185	-48.076843	5097	3.7	91.2	SAMN06705363
GRCOLLI26643	<i>Colobosaura modesta</i>	<i>Colobosaura modesta</i>	-7.330783	-47.470092	5057	4.2	68.5	SAMN06705367
LJVITT08623	<i>Colobosaura modesta</i>	<i>Colobosaura modesta</i>	-10.544429	-46.412466	5061	3.4	72.7	SAMN06705374
CHUNB64621	<i>Copeoglossum arajara</i>	<i>Copeoglossum nigropunctatum 1</i>	-7.231753	-39.40839	5259	4.7	74.3	SAMN23818088
CHUNB64623	<i>Copeoglossum arajara</i>	<i>Copeoglossum nigropunctatum 1</i>	-7.231753	-39.40839	5313	4.2	109.6	SAMN23818089
CHUNB26401	<i>Copeoglossum nigropunctatum</i>	<i>Copeoglossum nigropunctatum 1</i>	-17.219742	-46.875419	5281	3.9	86.8	SAMN23818090

CHUNB51999	<i>Copeoglossum nigropunctatum</i>	<i>Copeoglossum nigropunctatum 1</i>	-7.330783	-47.470092	5224	4.2	73.4	SAMN06705327
GRCOLLI04909	<i>Copeoglossum nigropunctatum</i>	<i>Copeoglossum nigropunctatum 1</i>	-26.481473	-51.988774	5276	4.2	81.6	SAMN23818091
GRCOLLI16027	<i>Copeoglossum nigropunctatum</i>	<i>Copeoglossum nigropunctatum 1</i>	-6.485331	-38.311129	5283	4.2	92.4	SAMN23818092
CHUNB35758	<i>Drymarchon corais</i>	<i>Drymarchon corais</i>	-11.463466	-39.526265	5106	3.9	89.7	SAMN23818093
CHUNB41313	<i>Drymarchon corais</i>	<i>Drymarchon corais</i>	-10.544429	-46.412466	4949	2.6	46.4	SAMN23818094
CHUNB61846	<i>Drymarchon corais</i>	<i>Drymarchon corais</i>	-4.276069	-41.778505	5002	2.8	50.3	SAMN23818095
RAB_00246	<i>Drymarchon corais</i>	<i>Drymarchon corais</i>	-12.571939	-70.085827	5106	3.1	83.5	SAMN23818096
GRCOLLI22519	<i>Erythrolamprus typhlus</i>	<i>Erythrolamprus poecilogyrus</i>	-12.932049	-51.833363	5037	4	96.2	SAMN23818097
CHUNB38780	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-17.359421	-44.955194	4995	3.7	74.8	SAMN23818098
CHUNB40825	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-11.463466	-39.526265	4969	3.2	61.8	SAMN23818099
CHUNB52059	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-7.330783	-47.470092	2889	0.7	45.2	SAMN06705331
CHUNB62581	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-12.13678	-49.173847	4929	3.1	55.3	SAMN23818100
GRCOLLI20248	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-4.276069	-41.778505	4922	2.9	52.9	SAMN23818101
GRCOLLI20891	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-14.66918	-52.361193	5032	3.8	94.7	SAMN23818102
GRCOLLI23352	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-12.932049	-51.833363	5024	3.7	92.8	SAMN23818103
GRCOLLI25761	<i>Erythrolamprus poecilogyrus</i>	<i>Erythrolamprus poecilogyrus</i>	-15.009324	-59.952558	5031	3.5	88.6	SAMN23818104
RAB_00226	<i>Liophis sp</i>	<i>Erythrolamprus reginae</i>	-12.56809	-70.09943	5019	3.3	81.3	SAMN23818105
UMMZ_245061	<i>Liophis sp</i>	<i>Erythrolamprus reginae</i>	-12.563182	-70.097307	5004	3	75.5	SAMN23818106
UMMZ_245063	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-12.57	-70.09	4770	2.4	50.2	SAMN23818107
CHUNB47087	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-9.871723	-56.09161	4972	2.3	65.3	SAMN23818108
CHUNB50635	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-13.195033	-60.818426	4979	3.5	77	SAMN23818109
CHUNB52120	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-7.330783	-47.470092	1960	0.4	63.7	SAMN06705342
CHUNB62579	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-12.13678	-49.173847	5020	3.8	92.2	SAMN23818110
CHUNB67484	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-15.737939	-48.283444	5018	3.2	88.1	SAMN23818111
GRCOLLI22198	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-7.231753	-39.40839	5009	3.8	85.4	SAMN23818112
GRCOLLI22766	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-12.932049	-51.833363	4999	3.2	74.1	SAMN23818113

UMMZ_245062	<i>Erythrolamprus reginae</i>	<i>Erythrolamprus reginae</i>	-12.571717	-70.085344	4936	2.7	53.4	SAMN23818114
CHUNB22726	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-10.773884	-65.323952	5285	3.1	95.9	SAMN23818115
CHUNB35169	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-2.003328	-54.073375	5206	2.9	78.9	SAMN23818116
CHUNB58535	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-19.006375	-57.648985	5199	3.1	86.9	SAMN23818117
GRCOLLI24011	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-15.331336	-57.201357	5235	3.3	92.7	SAMN23818118
GRCOLLI25683	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-15.009324	-59.952558	5121	1.9	45.3	SAMN23818119
LJVITT10947	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-9.267406	-49.948692	5230	3.5	94.9	SAMN23818120
UMMZ_245017	<i>Gonatodes humeralis</i>	<i>Gonatodes humeralis</i>	-12.569068	-70.100008	5215	3.4	96.9	SAMN23818121
CHUNB56644	<i>Gymnodactylus darwinii</i>	<i>Gymnodactylus geckoides</i>	-6.833715	-35.123893	5165	3.8	59.1	SAMN23818122
CHUNB56540	<i>Gymnodactylus geckoides</i>	<i>Gymnodactylus geckoides</i>	-12.870575	-39.859127	5190	3.3	67.9	SAMN23818123
CHUNB56697	<i>Gymnodactylus geckoides</i>	<i>Gymnodactylus geckoides</i>	-6.833715	-35.123893	5210	3.7	75.1	SAMN23818124
CHUNB61895	<i>Gymnodactylus geckoides</i>	<i>Gymnodactylus geckoides</i>	-6.563298	-40.12316	5210	4.3	70	SAMN23818125
CHUNB61905	<i>Gymnodactylus geckoides</i>	<i>Gymnodactylus geckoides</i>	-7.516307	-39.722728	5195	4	71.2	SAMN23818126
CHUNB63065	<i>Gymnodactylus geckoides</i>	<i>Gymnodactylus geckoides</i>	-6.833715	-35.123893	5172	3.6	59.9	SAMN23818127
CHUNB71691	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-13.776863	-47.26352	5063	3.3	78.3	SAMN23818128
CHUNB43220	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-8.355118	-49.176572	5078	3.8	89	SAMN23818129
CHUNB47128	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-9.871723	-56.09161	4054	0.7	18	SAMN23818130
CHUNB52467	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-12.029774	-48.537811	4988	1.8	50.6	SAMN23818131
GRCOLLI20703	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-14.66918	-52.361193	5070	3.4	74	SAMN23818132
GRCOLLI26039	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-10.440931	-49.166658	4985	2.5	50.7	SAMN23818133
LJVITT09295	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-10.544429	-46.412466	5029	3.3	64.3	SAMN23818134
LJVITT09759	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-7.034836	-55.41987	5074	3.5	74.8	SAMN23818135
LJVITT10944	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-9.267406	-49.948692	5081	3.7	82.8	SAMN23818136
UMMZ_209972	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	6.489491	-58.23184	5086	3.7	96.8	SAMN23818137
UMMZ_245053	<i>Helicops angulatus</i>	<i>Helicops angulatus</i>	-12.57	-70.09	5064	3.5	70.3	SAMN23818138
CHUNB40620	<i>Helicops leopardinus</i>	<i>Helicops modestus</i>	-10.544429	-46.412466	5027	3.4	76.3	SAMN23818139
CHUNB38641	<i>Helicops modestus</i>	<i>Helicops modestus</i>	-15.794087	-47.887905	5057	3.6	91.6	SAMN23818140
CHUNB43293	<i>Helicops modestus</i>	<i>Helicops modestus</i>	-15.794087	-47.887905	456	0	15.1	SAMN23818141

CHUNB43339	<i>Helicops modestus</i>	<i>Helicops modestus</i>	-16.258541	-47.95572	5006	3.2	68.6	SAMN23818142
CHUNB40063	<i>Hemidactylus mabouia</i>	<i>Hemidactylus mabouia</i>	-7.034836	-55.41987	5209	4.2	74.3	SAMN23818143
CHUNB61902	<i>Hemidactylus mabouia</i>	<i>Hemidactylus mabouia</i>	-7.180898	-39.73798	5179	4.2	69.6	SAMN23818144
CHUNB74101	<i>Hemidactylus mabouia</i>	<i>Hemidactylus mabouia</i>	-18.325034	-53.70809	5071	3.1	39.9	SAMN23818145
CHUNB74103	<i>Hemidactylus mabouia</i>	<i>Hemidactylus mabouia</i>	-16.359008	-46.899957	5210	4.2	75.7	SAMN23818146
GRCOLLI23532	<i>Hemidactylus mabouia</i>	<i>Hemidactylus mabouia</i>	-12.932049	-51.833363	5217	4.2	73	SAMN23818147
RAB_00521	<i>Mabuya sp</i>	<i>Iphisa elegans</i>	-12.5613	-70.107	4538	1.7	50.1	SAMN23818148
CHUNB11457	<i>Iphisa elegans</i>	<i>Iphisa elegans</i>	-12.741373	-60.138584	5040	2.6	47.6	SAMN23818149
CHUNB18022	<i>Iphisa elegans</i>	<i>Iphisa elegans</i>	-11.677537	-61.183666	5188	4.1	88.7	SAMN23818150
CHUNB40060	<i>Iphisa elegans</i>	<i>Iphisa elegans</i>	-7.034836	-55.41987	5151	3.7	73.4	SAMN23818151
GRCOLLI06954	<i>Iphisa elegans</i>	<i>Iphisa elegans</i>	-10.773884	-65.323952	5201	4.5	106.5	SAMN23818152
UMMZ_245039	<i>Iphisa elegans</i>	<i>Iphisa elegans</i>	-12.572305	-70.087174	5185	3.8	99.7	SAMN23818153
CHUNB44544	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-17.359421	-44.955194	5010	3.2	55.4	SAMN23818154
CHUNB52871	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-13.476562	-61.044379	5015	3.2	56	SAMN23818155
CHUNB61157	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-4.276069	-41.778505	5085	3.6	86.8	SAMN23818156
CHUNB69398	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-15.818862	-50.609163	5063	3.3	70.6	SAMN23818157
CHUNB69433	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-6.485331	-38.311129	5073	3.1	74.6	SAMN23818158
GRCOLLI25509	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-15.009324	-59.952558	5084	3.8	84.5	SAMN23818159
GRCOLLI26789	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-7.330783	-47.470092	4454	2	37.4	SAMN06705371
LJVITT09836	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-7.034836	-55.41987	5098	3.9	92.9	SAMN23818160
UMMZ_245058	<i>Leptodeira annulata</i>	<i>Leptodeira annulata</i>	-12.870167	-71.407601	5080	3.4	75.3	SAMN23818161
CHUNB35356	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-11.463466	-39.526265	4772	2.6	39.9	SAMN23818162
CHUNB41281	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-10.544429	-46.412466	4930	3.1	67.8	SAMN23818163
CHUNB62394	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-2.003328	-54.073375	4837	3.1	44.7	SAMN23818164
CHUNB74027	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-14.136245	-47.519093	4985	3.6	92.2	SAMN23818165
GRCOLLI19670	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-4.276069	-41.778505	4874	3.3	58.7	SAMN23818166
GRCOLLI21198	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-14.66918	-52.361193	3634	0.8	19.6	SAMN23818167
GRCOLLI26916	<i>Lygophis paucidens</i>	<i>Lygophis paucidens</i>	-7.330783	-47.470092	4521	2.5	37.1	SAMN06705373

CHUNB50707	<i>Manciola guaporicola</i>	<i>Manciola guaporicola</i>	-13.195033	-60.818426	5130	3.4	41.1	SAMN23818168
CHUNB10472	<i>Manciola guaporicola</i>	<i>Manciola guaporicola</i>	-10.466112	-50.506266	5266	4.3	76.1	SAMN23818169
CHUNB38741	<i>Manciola guaporicola</i>	<i>Manciola guaporicola</i>	-14.708216	-47.518802	5231	3.4	66.7	SAMN23818170
CHUNB40065	<i>Manciola guaporicola</i>	<i>Manciola guaporicola</i>	-7.034836	-55.41987	5254	3.3	74.5	SAMN23818171
CHUNB64036	<i>Manciola guaporicola</i>	<i>Manciola guaporicola</i>	-14.66918	-52.361193	5273	3.6	84.2	SAMN23818172
GRCOLLI25705	<i>Manciola guaporicola</i>	<i>Manciola guaporicola</i>	-15.009324	-59.952558	5200	3.8	59.7	SAMN23818173
CHUNB52567	<i>Mastigodryas boddaerti</i>	<i>Mastigodryas boddaerti</i>	-12.029774	-48.537811	3866	0.7	18.7	SAMN23818174
CHUNB68915	<i>Mastigodryas boddaerti</i>	<i>Mastigodryas boddaerti</i>	-12.932049	-51.833363	5142	4	105.5	SAMN23818175
GRCOLLI21125	<i>Mastigodryas boddaerti</i>	<i>Mastigodryas boddaerti</i>	-14.66918	-52.361193	5124	3.8	96.4	SAMN23818176
GRCOLLI25707	<i>Mastigodryas boddaerti</i>	<i>Mastigodryas boddaerti</i>	-15.009324	-59.952558	5073	3	63.4	SAMN23818177
GRCOLLI25914	<i>Mastigodryas boddaerti</i>	<i>Mastigodryas boddaerti</i>	-3.766889	-49.667184	5062	3	67.8	SAMN23818178
CHUNB10584	<i>Micrablepharus atticolus</i>	<i>Micrablepharus atticolus</i>	-10.466112	-50.506266	5038	3	58	SAMN23818179
CHUNB37312	<i>Micrablepharus atticolus</i>	<i>Micrablepharus atticolus</i>	-15.921772	-46.107752	5124	3.4	86.2	SAMN23818180
CHUNB58523	<i>Micrablepharus atticolus</i>	<i>Micrablepharus atticolus</i>	-18.307724	-51.957778	5117	3.6	81.8	SAMN23818181
GRCOLLI04216	<i>Micrablepharus atticolus</i>	<i>Micrablepharus atticolus</i>	-12.741373	-60.138584	5057	3.1	61.9	SAMN23818182
GRCOLLI05508	<i>Micrablepharus atticolus</i>	<i>Micrablepharus atticolus</i>	-11.677537	-61.183666	5131	4.2	88.5	SAMN23818183
GRCOLLI26401	<i>Micrablepharus atticolus</i>	<i>Micrablepharus atticolus</i>	-13.188043	-53.261519	5107	3.1	76.7	SAMN23818184
CHUNB14562	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-26.481473	-51.988774	5094	3.5	70.2	SAMN23818185
CHUNB22676	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-10.773884	-65.323952	5055	3.3	63.2	SAMN23818186
CHUNB34982	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-7.034836	-55.41987	5029	3	63.7	SAMN23818187
CHUNB37170	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-14.482839	-46.515638	5070	3.5	71	SAMN23818188
CHUNB37204	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-6.485331	-38.311129	5122	3.4	81.2	SAMN23818189
CHUNB52077	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-7.330783	-47.470092	4996	2.5	52	SAMN06705339
CHUNB63132	<i>Micrablepharus maximiliani</i>	<i>Micrablepharus maximiliani</i>	-14.66918	-52.361193	5119	3.3	83.7	SAMN23818190
CHUNB52143	<i>Micrurus brasiliensis</i>	<i>Micrurus frontalis</i>	-7.330783	-47.470092	4002	1.5	35.1	SAMN06705348
CHUNB35989	<i>Micrurus frontalis</i>	<i>Micrurus frontalis</i>	-15.794087	-47.887905	5025	3.6	67.8	SAMN23818191
CHUNB42648	<i>Micrurus frontalis</i>	<i>Micrurus frontalis</i>	-16.851781	-42.064207	5044	3.7	76.9	SAMN23818192
NOID1	<i>Micrurus frontalis</i>	<i>Micrurus frontalis</i>	-14.136245	-47.519093	5054	4.2	79.9	SAMN23818193

CHUNB09350	<i>Notomabuya frenata</i>	<i>Notomabuya frenata</i>	-13.535094	-48.223908	5118	3.1	47.4	SAMN23818194
CHUNB14575	<i>Notomabuya frenata</i>	<i>Notomabuya frenata</i>	-26.481473	-51.988774	5237	3.3	62.7	SAMN23818195
CHUNB38752	<i>Notomabuya frenata</i>	<i>Notomabuya frenata</i>	-14.708216	-47.518802	5236	2.8	59.3	SAMN23818196
CHUNB58541	<i>Notomabuya frenata</i>	<i>Notomabuya frenata</i>	-11.969573	-41.268403	5223	3.5	55.8	SAMN23818197
GRCOLLI26598	<i>Notomabuya frenata</i>	<i>Notomabuya frenata</i>	-7.330783	-47.470092	5251	4.4	99.6	SAMN06705366
CHUNB33809	<i>Oxybelis aeneus</i>	<i>Oxybelis aeneus</i>	-10.544429	-46.412466	5118	3.1	82.5	SAMN23818198
CHUNB52413	<i>Oxybelis aeneus</i>	<i>Oxybelis aeneus</i>	-13.799279	-47.463436	5124	3.6	93.2	SAMN23818199
CHUNB61164	<i>Oxybelis aeneus</i>	<i>Oxybelis aeneus</i>	-4.276069	-41.778505	4985	2.4	48.1	SAMN23818200
CHUNB63125	<i>Oxybelis aeneus</i>	<i>Oxybelis aeneus</i>	-6.9633	-35.6917	5003	2.7	50.1	SAMN23818201
TJC1032	<i>Oxybelis aeneus</i>	<i>Oxybelis aeneus</i>	17.96901	-89.36086	5033	3.7	53.8	SAMN23818202
TJC1554	<i>Oxybelis aeneus</i>	<i>Oxybelis aeneus</i>	4.72239	-60.0028	5098	4.1	87.3	SAMN23818203
CHUNB38893	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus guibei</i>	-15.794087	-47.887905	5019	2.9	69.4	SAMN23818204
CHUNB41310	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus guibei</i>	-10.544429	-46.412466	5029	3.4	73.2	SAMN23818205
CHUNB45390	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus guibei</i>	-9.267406	-49.948692	5073	3.8	99.3	SAMN23818206
CHUNB55902	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus guibei</i>	-14.66918	-52.361193	5063	3.6	95.9	SAMN23818207
GRCOLLI25679	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus guibei</i>	-15.009324	-59.952558	5024	3.1	71.6	SAMN23818208
CHUNB47098	<i>Oxyrhopus melanogenys</i>	<i>Oxyrhopus melanogenys</i>	-9.871723	-56.09161	4878	1.6	52.4	SAMN23818209
RAB_00002	<i>Oxyrhopus melanogenys</i>	<i>Oxyrhopus melanogenys</i>	-12.893383	-71.403367	4989	3.1	66.8	SAMN23818210
RAB_00269	<i>Oxyrhopus melanogenys</i>	<i>Oxyrhopus melanogenys</i>	-12.5613	-70.107	4933	3	54.1	SAMN23818211
UMMZ_245065	<i>Oxyrhopus melanogenys</i>	<i>Oxyrhopus melanogenys</i>	-12.893046	-71.406034	5036	3.3	74.7	SAMN23818212
UMMZ_245071	<i>Oxyrhopus melanogenys</i>	<i>Oxyrhopus melanogenys</i>	-12.57	-70.09	5015	2.8	62.5	SAMN23818213
CHUNB47113	<i>Oxyrhopus petolarius</i>	<i>Oxyrhopus petolarius</i>	-9.871723	-56.09161	5072	2.6	90	SAMN23818214
CHUNB73994	<i>Oxyrhopus petolarius</i>	<i>Oxyrhopus petolarius</i>	-10.440931	-49.166658	5058	3.2	91.2	SAMN23818215
UMFS_23133	<i>Oxyrhopus petolarius</i>	<i>Oxyrhopus petolarius</i>	-12.867732	-71.406327	5110	3.5	110.9	SAMN23818216
UMMZ_245072	<i>Oxyrhopus petolarius</i>	<i>Oxyrhopus petolarius</i>	-12.571391	-70.085075	5034	3.1	69.8	SAMN23818217
CHUNB59060	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus 1</i>	-14.136245	-47.519093	4961	3	57	SAMN23818218
UMMZ_209964	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus 1</i>	-9.533244	-37.295973	5054	4	75.3	SAMN23818219
CHUNB35355	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus 1</i>	-11.463466	-39.526265	5061	3.4	83.1	SAMN23818220

CHUNB40806	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 1	-6.485331	-38.311129	5070	3.4	85.6	SAMN23818221
CHUNB44479	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 1	-17.359421	-44.955194	5054	3.6	82.8	SAMN23818222
CHUNB53041	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 1	-2.003328	-54.073375	5064	3.6	84.6	SAMN23818223
CHUNB63645	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 1	-14.66918	-52.361193	5076	3.6	86.8	SAMN23818224
CHUNB72568	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 1	-15.794087	-47.887905	5068	2.8	80.7	SAMN23818225
CHUNB41304	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus trigeminus</i> 2	-10.544429	-46.412466	5087	3.4	91.1	SAMN23818226
CHUNB45388	<i>Oxyrhopus guibei</i>	<i>Oxyrhopus trigeminus</i> 2	-9.267406	-49.948692	4996	3	53.3	SAMN23818227
CHUNB56895	<i>Oxyrhopus rhombifer</i>	<i>Oxyrhopus trigeminus</i> 2	-15.794087	-47.887905	5114	3.5	97	SAMN23818228
CHUNB57764	<i>Oxyrhopus rhombifer</i>	<i>Oxyrhopus trigeminus</i> 2	-12.294693	-50.969173	4772	1.7	33.9	SAMN23818229
CHUNB56712	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 2	-6.833715	-35.123893	5094	3.2	92.7	SAMN23818230
CHUNB61159	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 2	-4.276069	-41.778505	5104	3.8	101.7	SAMN23818231
CHUNB32133	<i>Oxyrhopus trigeminus</i>	<i>Oxyrhopus trigeminus</i> 2	-7.330783	-47.470092	4743	3.1	57.4	SAMN06705320
CHUNB52073	<i>Thamnodynastes hypoconia</i>	<i>Philodryas nattereri</i>	-7.330783	-47.470092	4913	3.9	59.5	SAMN06705337
CHUNB38779	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-15.794087	-47.887905	5121	3.4	99.6	SAMN23818232
CHUNB40804	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-6.485331	-38.311129	5119	3.5	94.9	SAMN23818233
CHUNB44543	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-17.359421	-44.955194	5049	3	52	SAMN23818234
CHUNB52154	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-7.330783	-47.470092	4961	3.5	58.6	SAMN06705355
CHUNB63647	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-14.66918	-52.361193	5132	3.8	103.6	SAMN23818235
CHUNB74026	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-12.184014	-43.218696	5119	3.3	94.5	SAMN23818236
GRCOLLI25662	<i>Philodryas nattereri</i>	<i>Philodryas nattereri</i>	-15.009324	-59.952558	5120	3	89.3	SAMN23818237
CHUNB40094	<i>Philodryas olfersii</i>	<i>Philodryas olfersii</i>	-7.034836	-55.41987	5135	3.5	105.8	SAMN23818238
CHUNB52116	<i>Philodryas olfersii</i>	<i>Philodryas olfersii</i>	-7.330783	-47.470092	5017	3.9	92.8	SAMN06705340
CHUNB58538	<i>Philodryas olfersii</i>	<i>Philodryas olfersii</i>	-11.969573	-41.268403	5126	3.3	101.2	SAMN23818239
CHUNB69323	<i>Philodryas olfersii</i>	<i>Philodryas olfersii</i>	-15.737939	-48.283444	5139	3.7	110.1	SAMN23818240
CHUNB71127	<i>Philodryas olfersii</i>	<i>Philodryas olfersii</i>	-12.5923	-52.209892	5064	3.1	64.3	SAMN23818241
CHUNB41117	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-10.544429	-46.412466	5079	3.5	88	SAMN23818242
CHUNB52151	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-7.330783	-47.470092	4822	3.7	58	SAMN06705354
CHUNB56911	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-13.799279	-47.463436	5056	3	80.6	SAMN23818243

CHUNB61151	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-4.276069	-41.778505	5068	3.6	82.5	SAMN23818244
CHUNB61948	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-2.003328	-54.073375	5055	3.5	74.5	SAMN23818245
GFHORTA009	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-14.66918	-52.361193	5064	3.1	76	SAMN23818246
GRCOLLI25770	<i>Phimophis guerini</i>	<i>Phimophis guerini</i>	-15.009324	-59.952558	5018	2.8	61.7	SAMN23818247
CHUNB50457	<i>Phyllopezus pollicaris</i>	<i>Phyllopezus pollicaris</i>	-13.003894	-41.373213	5175	3.3	48.4	SAMN23818248
CHUNB57417	<i>Phyllopezus pollicaris</i>	<i>Phyllopezus pollicaris</i>	-3.936131	-40.893929	5070	3.4	42.3	SAMN23818249
CHUNB58671	<i>Phyllopezus pollicaris</i>	<i>Phyllopezus pollicaris</i>	-20.554843	-56.673567	5255	4.2	79	SAMN23818250
CHUNB59068	<i>Phyllopezus pollicaris</i>	<i>Phyllopezus pollicaris</i>	-14.136245	-47.519093	5198	3.7	64.2	SAMN23818251
CHUNB64617	<i>Phyllopezus pollicaris</i>	<i>Phyllopezus pollicaris</i>	-7.231753	-39.40839	5271	3.8	83.9	SAMN23818252
Ppo6	<i>Phyllopezus pollicaris</i>	<i>Phyllopezus pollicaris</i>	-7.49067	-36.284342	5179	3.3	52.5	SAMN23818253
CHUNB22536	<i>Plica umbra</i>	<i>Plica umbra</i>	-10.773884	-65.323952	5314	4.8	87.2	SAMN23818254
CHUNB32324	<i>Plica umbra</i>	<i>Plica umbra</i>	-7.512225	-63.026698	5320	4.2	86.1	SAMN23818255
CHUNB50638	<i>Plica umbra</i>	<i>Plica umbra</i>	-13.195033	-60.818426	5185	2.9	48.9	SAMN23818256
UMMZ_245045	<i>Plica umbra</i>	<i>Plica umbra</i>	-12.890633	-71.410833	5030	2.4	61.3	SAMN23818257
CHUNB11470	<i>Polychrus acutirostris</i>	<i>Polychrus acutirostris</i>	-12.741373	-60.138584	5304	4	81.2	SAMN15718129
CHUNB26658	<i>Polychrus acutirostris</i>	<i>Polychrus acutirostris</i>	-17.219742	-46.875419	5303	4.4	81.2	SAMN23818258
CHUNB38230	<i>Polychrus acutirostris</i>	<i>Polychrus acutirostris</i>	-11.463466	-39.526265	5283	4.1	70.3	SAMN23818259
CHUNB38260	<i>Polychrus acutirostris</i>	<i>Polychrus acutirostris</i>	-7.034836	-55.41987	5280	4.2	70.9	SAMN23818260
CHUNB45209	<i>Polychrus acutirostris</i>	<i>Polychrus acutirostris</i>	-9.267406	-49.948692	5298	4	77.1	SAMN23818261
CHUNB68399	<i>Polychrus acutirostris</i>	<i>Polychrus acutirostris</i>	-12.932049	-51.833363	5270	3.4	67.6	SAMN23818262
CHUNB52134	<i>Pseudoboa neuwiedii</i>	<i>Pseudoboa nigra</i>	-7.330783	-47.470092	4673	2.5	47.9	SAMN06705347
GRCOLLI26733	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-7.330783	-47.470092	4870	3.6	63.4	SAMN06705369
CHUNB37261	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-15.921772	-46.107752	5054	3.1	74.5	SAMN23818263
CHUNB40096	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-7.034836	-55.41987	5024	2.7	62.2	SAMN23818264
CHUNB50856	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-2.003328	-54.073375	5055	3.1	74.1	SAMN23818265
CHUNB52149	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-7.330783	-47.470092	4567	2.3	40.7	SAMN06705352
CHUNB52150	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-7.330783	-47.470092	4822	3.3	45.2	SAMN06705353
CHUNB63678	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-14.66918	-52.361193	5057	3.2	74.8	SAMN23818266

CHUNB64756	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-7.231753	-39.40839	5052	3.3	72.4	SAMN23818267
GRCOLLI25194	<i>Pseudoboa nigra</i>	<i>Pseudoboa nigra</i>	-15.009324	-59.952558	4744	1.9	29.4	SAMN23818268
CHUNB38372	<i>Psomophis joberti</i>	<i>Psomophis joberti</i>	-14.450174	-47.045083	5016	2.9	78.9	SAMN23818269
CHUNB45421	<i>Psomophis joberti</i>	<i>Psomophis joberti</i>	-9.267406	-49.948692	5041	3.2	100.3	SAMN23818270
CHUNB52071	<i>Psomophis joberti</i>	<i>Psomophis joberti</i>	-7.330783	-47.470092	4820	3.6	49.1	SAMN06705336
CHUNB52752	<i>Psomophis joberti</i>	<i>Psomophis joberti</i>	-12.029774	-48.537811	4907	1.8	50.9	SAMN23818271
CHUNB61140	<i>Psomophis joberti</i>	<i>Psomophis joberti</i>	-4.276069	-41.778505	5014	3.2	88.4	SAMN23818272
Pjo8	<i>Psomophis joberti</i>	<i>Psomophis joberti</i>	-6.833715	-35.123893	4894	2.3	41.8	SAMN23818273
CHUNB41112	<i>Rodriguesophis iglesiasi</i>	<i>Rodriguesophis iglesiasi</i>	-10.544429	-46.412466	5087	3.6	101.6	SAMN23818274
CHUNB52066	<i>Rodriguesophis iglesiasi</i>	<i>Rodriguesophis iglesiasi</i>	-7.330783	-47.470092	5077	3.2	97.5	SAMN23818275
CHUNB62398	<i>Rodriguesophis iglesiasi</i>	<i>Rodriguesophis iglesiasi</i>	-13.625934	-44.46597	5060	3.4	90.9	SAMN23818276
GRCOLLI26951	<i>Rodriguesophis iglesiasi</i>	<i>Rodriguesophis iglesiasi</i>	-16.687373	-45.413633	5046	2.7	73.4	SAMN23818277
CHUNB33806	<i>Sibynomorphus mikanii</i>	<i>Sibynomorphus mikanii</i>	-10.544429	-46.412466	5050	3.2	83.4	SAMN23818278
CHUNB50252	<i>Sibynomorphus mikanii</i>	<i>Sibynomorphus mikanii</i>	-16.069575	-47.984111	5042	3.2	73.8	SAMN23818279
CHUNB52075	<i>Sibynomorphus mikanii</i>	<i>Sibynomorphus mikanii</i>	-7.330783	-47.470092	4808	3	51.7	SAMN06705338
CHUNB64778	<i>Sibynomorphus mikanii</i>	<i>Sibynomorphus mikanii</i>	-7.231753	-39.40839	5059	3.6	88.4	SAMN23818280
CHUNB68936	<i>Sibynomorphus mikanii</i>	<i>Sibynomorphus mikanii</i>	-12.932049	-51.833363	5060	3.1	80.2	SAMN23818281
CHUNB71461	<i>Sibynomorphus mikanii</i>	<i>Sibynomorphus mikanii</i>	-14.100818	-46.631968	5029	2.8	70.8	SAMN23818282
CHUNB44202	<i>Spilotes sp</i>	<i>Spilotes sp</i>	-7.034836	-55.41987	5108	2.2	76.9	SAMN23818283
CHUNB62580	<i>Spilotes sp</i>	<i>Spilotes sp</i>	-12.13678	-49.173847	5125	4.1	93	SAMN23818284
CHUNB64758	<i>Spilotes sp</i>	<i>Spilotes sp</i>	-7.231753	-39.40839	5069	3.2	70.4	SAMN23818285
CHUNB68916	<i>Spilotes sp</i>	<i>Spilotes sp</i>	-12.932049	-51.833363	5099	3.9	81.2	SAMN23818286
CHUNB69456	<i>Spilotes sp</i>	<i>Spilotes sp</i>	-13.257326	-46.885799	5113	4	92.6	SAMN23818287
GRCOLLI25665	<i>Spilotes sp</i>	<i>Spilotes sp</i>	-15.009324	-59.952558	5100	4	83.9	SAMN23818288
CHUNB35352	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis 2</i>	-11.463466	-39.526265	5051	2.7	56.1	SAMN23818289
CHUNB44672	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis 2</i>	-14.150185	-48.076843	5047	3	68.4	SAMN23818290
CHUNB61158	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis 2</i>	-4.276069	-41.778505	5077	3.2	85	SAMN23818291
CHUNB63652	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis 2</i>	-14.66918	-52.361193	5092	3.4	85.3	SAMN23818292

GRCOLLI26711	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis</i> 2	-7.330783	-47.470092	4881	3.4	55.2	SAMN06705368
GRCOLLI26930	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis</i> 2	-16.687373	-45.413633	5100	3.4	88.1	SAMN23818293
Toc7	<i>Taeniophallus occipitalis</i>	<i>Taeniophallus occipitalis</i> 2	-6.833715	-35.123893	5077	2.7	78.1	SAMN23818294
CHUNB41316	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-10.544429	-46.412466	4842	2.4	36.8	SAMN23818295
Tsp9	<i>Tantilla sp</i>	<i>Tantilla melanocephala</i>	-6.833715	-35.123893	5047	3.4	64.5	SAMN23818296
CHUNB41284	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-10.544429	-46.412466	5068	3.4	76.6	SAMN23818297
CHUNB52118	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-7.330783	-47.470092	4888	3.6	54.2	SAMN06705341
CHUNB57516	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-13.625934	-44.46597	4949	2.8	41	SAMN23818298
CHUNB63659	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-14.66918	-52.361193	4890	2.4	35.5	SAMN23818299
CHUNB64755	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-7.231753	-39.40839	5045	2.9	53.3	SAMN23818300
GRCOLLI25951	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-13.799279	-47.463436	5079	4.1	88.6	SAMN23818301
UMMZ_245075	<i>Tantilla melanocephala</i>	<i>Tantilla melanocephala</i>	-12.560789	-70.095962	4900	2.7	50.7	SAMN23818302
CHUNB38789	<i>Tantilla melanocephala</i>	<i>Thamnodynastes hypoconia</i>	-17.359421	-44.955194	5087	4.2	98.4	SAMN23818303
CHUNB41315	<i>Thamnodynastes hypoconia</i>	<i>Thamnodynastes hypoconia</i>	-10.544429	-46.412466	5087	3.4	89.2	SAMN23818304
CHUNB61133	<i>Thamnodynastes hypoconia</i>	<i>Thamnodynastes hypoconia</i>	-4.276069	-41.778505	5065	3.5	84.8	SAMN23818305
NOID2	<i>Thamnodynastes hypoconia</i>	<i>Thamnodynastes hypoconia</i>	-15.794087	-47.887905	5087	3.5	95.6	SAMN23818306
CHUNB44545	<i>Trilepida brasiliensis</i>	<i>Trilepida brasiliensis</i> 2	-17.359421	-44.955194	5015	4	84	SAMN23818307
CHUNB50870	<i>Trilepida brasiliensis</i>	<i>Trilepida brasiliensis</i> 2	-14.087734	-46.36201	4996	2.9	70.5	SAMN23818308
CHUNB51368	<i>Trilepida brasiliensis</i>	<i>Trilepida brasiliensis</i> 2	-14.171078	-44.545669	4978	3.6	66.6	SAMN23818309
CHUNB52064	<i>Trilepida brasiliensis</i>	<i>Trilepida brasiliensis</i> 2	-7.330783	-47.470092	4363	1.7	33.9	SAMN06705334
LJVITT10447	<i>Trilepida brasiliensis</i>	<i>Trilepida brasiliensis</i> 2	-10.544429	-46.412466	5014	3.2	79.9	SAMN23818310
GRCOLLI26120	<i>Trilepida brasiliensis</i>	<i>Trilepida koppesi</i>	-13.799279	-47.463436	5051	3.6	85.2	SAMN23818311
CHUNB62577	<i>Leptotyphlops fuliginosus</i>	<i>Trilepida koppesi</i>	-12.13678	-49.173847	4931	2.7	59.3	SAMN23818312
CHUNB46211	<i>Trilepida dimidiata</i>	<i>Trilepida koppesi</i>	-9.267406	-49.948692	5006	3.3	83.3	SAMN23818313
CHUNB40750	<i>Trilepida koppesi</i>	<i>Trilepida koppesi</i>	-16.258541	-47.95572	3809	0.7	19.5	SAMN23818314
CHUNB40813	<i>Trilepida koppesi</i>	<i>Trilepida koppesi</i>	-6.485331	-38.311129	4896	3	55.1	SAMN23818315
CHUNB50869	<i>Trilepida koppesi</i>	<i>Trilepida koppesi</i>	-2.003328	-54.073375	5001	4.3	80.5	SAMN23818316
CHUNB62461	<i>Trilepida koppesi</i>	<i>Trilepida koppesi</i>	-18.169573	-47.947703	5033	4	95.5	SAMN23818317

CHUNB74239	<i>Tropidurus oreadicus</i>	<i>Tropidurus itambere</i>	-15.869179	-56.094162	5332	4.2	86.3	SAMN23818318
CHUNB58560	<i>Tropidurus itambere</i>	<i>Tropidurus itambere</i>	-11.969573	-41.268403	5303	3.1	74	SAMN23818319
CHUNB58565	<i>Tropidurus itambere</i>	<i>Tropidurus itambere</i>	-20.554843	-56.673567	5277	3	64	SAMN23818320
CHUNB71109	<i>Tropidurus itambere</i>	<i>Tropidurus itambere</i>	-12.5923	-52.209892	5325	3.3	79.4	SAMN23818321
CHUNB74201	<i>Tropidurus itambere</i>	<i>Tropidurus itambere</i>	-21.841096	-43.796383	5327	3.9	96.7	SAMN23818322
CHUNB30749	<i>Tropidurus insulanus</i>	<i>Tropidurus oreadicus</i>	-7.034836	-55.41987	5341	3.4	95	SAMN23818323
CHUNB11305	<i>Tropidurus oreadicus</i>	<i>Tropidurus oreadicus</i>	-26.481473	-51.988774	5320	3.5	88.7	SAMN23818324
CHUNB35364	<i>Tropidurus oreadicus</i>	<i>Tropidurus oreadicus</i>	-11.463466	-39.526265	5328	3.4	96.2	SAMN23818325
CHUNB37577	<i>Tropidurus oreadicus</i>	<i>Tropidurus oreadicus</i>	-6.485331	-38.311129	5339	3.5	94.8	SAMN23818326
CHUNB52022	<i>Tropidurus oreadicus</i>	<i>Tropidurus oreadicus</i>	-7.330783	-47.470092	5265	4.4	83.7	SAMN06705329
CHUNB69429	<i>Tropidurus oreadicus</i>	<i>Tropidurus oreadicus</i>	-13.776863	-47.26352	5329	4.3	91.9	SAMN23818327
CHUNB28189	<i>Vanzosaura savanicola</i>	<i>Vanzosaura savanicola</i>	-10.544429	-46.412466	5090	3.2	69.6	SAMN23818328
CHUNB37303	<i>Vanzosaura savanicola</i>	<i>Vanzosaura savanicola</i>	-15.921772	-46.107752	5116	3.3	82.4	SAMN23818329
CHUNB51300	<i>Vanzosaura savanicola</i>	<i>Vanzosaura savanicola</i>	-14.171078	-44.545669	5077	2.9	65.4	SAMN23818330
CHUNB58572	<i>Vanzosaura savanicola</i>	<i>Vanzosaura savanicola</i>	-20.474654	-55.790616	5082	2.6	72	SAMN23818331
CHUNB58587	<i>Vanzosaura savanicola</i>	<i>Vanzosaura savanicola</i>	-18.307724	-51.957778	5072	2.7	61.9	SAMN23818332
CHUNB38942	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-10.544429	-46.412466	5063	3.8	112.9	SAMN23818333
CHUNB44477	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-17.359421	-44.955194	5042	3.5	100.1	SAMN23818334
CHUNB52144	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-7.330783	-47.470092	4849	3.7	59.2	SAMN06705349
CHUNB61173	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-4.276069	-41.778505	5057	3.8	110.4	SAMN23818335
CHUNB63662	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-14.66918	-52.361193	5025	3.5	92.3	SAMN23818336
GRCOLLI24148	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-20.788679	-51.710001	5043	3.3	98	SAMN23818337
GRCOLLI26105	<i>Xenodon merremii</i>	<i>Xenodon merremii</i>	-13.799279	-47.463436	5000	3.1	71.1	SAMN23818338

Table S2: Predictors of isolation-by-distance (β_{IBD}). Using phylogenetic generalized least squares (PGLS), we tested if four organismal traits predict β_{IBD} : average genetic diversity (π), body mass of species, geographic range area, and the elongation index which captures how elongated a species is. These four traits are thought to influence both effective population size and organismal dispersal, two factors that affect levels of isolation-by-distance. Only elongation index significantly predicted β_{IBD} .

Organismal Trait	<i>n</i>	PGLS P-value
Genetic diversity	50	0.81
Body mass	50	0.82
Geographic range area	49	0.87
Elongation index	50	0.004

Table S3: Robustness results testing the correlation between rates of population isolation and speciation rate. We tested five possible sources of error. First, we tested the role of limited sampling by removing OTUs sampled for few individuals (see full results in Fig. S14). Second, we tested the role of measurement error by (1) removing IBD slopes with low r^2 values (see full results in Fig. S14), (2) removing taxa with non-significant IBD slopes (β_{IBD}), and (3) using a phylogenetic mixed model in which the squared standard error of IBD slope is included as a weight. Third, we explored alternate measures of genetic differentiation across space. Fourth, we repeated analyses using nominal species designations in case our revised taxonomy is inaccurate. Fifth, we removed the few individuals sampled outside of the core Cerrado region (Fig. S20) to further control for the effects of biogeography. For each robustness analysis, we report our sample size, the estimate of phylogenetic signal for β_{IBD} as measured by Pagel's lambda and its p-value, and the direction of the phylogenetic generalized least squares (PGLS) correlation between β_{IBD} and speciation rate and its p-value.

Type of robustness analysis	Description	n	Pagel's lambda for included tips	P-val for Pagel's lambda	PGLS correlation direction	PGLS p-val
Primary analysis in main text	All taxa with 4 or more sampled individuals	50	0.24	0.009	+	0.77
Limited sampling	keep taxa with >4 individuals	43	0.27	0.006	+	0.79
Measurement error	keep taxa with $r^2 > 0.2$	31	0.31	0.04	-	0.85
	keep taxa with significant β_{IBD}	29	0.33	0.033	-	0.98
	Using a phylogenetic mixed model in which the squared standard error of IBD slope is included as a weight	50	0.24	0.009	+	0.71
	measure IBD using nuclear d_{xy} across geographic distance	51	0.25	0.02	+	0.57
Alternate measures of differentiation	measure IBD using mtDNA d_{xy} across geographic distance	29	0.17	0.786	-	0.18
	measure IBD using F_{ST} across environmental distance	45	0	1	+	0.76
	Using inverse F_{ST} at 1000 km	43	0.3	0.004	+	0.83
	measure β_{IBD} using nominal species designations	46	0.37	0.004	+	0.87
Biogeography	Remove any individuals sampled outside of general Cerrado region	39	0.29	0.014	+	0.81

Table S4: Literature review on dispersal length in lizard and snake species. From 10 September to 14 September 2021, two searches were done in Google Scholar for “lizard AND dispersal” and “snake AND dispersal”. This was a non-exhaustive search, and the first ~50 citations under each search were reviewed to extract information on dispersal length, units, and approach used to measure dispersal.

species	dispersal	dispersal units	citation	dispersal type	Taxa type
<i>Ameiva chrysoloma</i>	0.0352	km/sqrt(gen)	Dessauer et al. 2000	value for whiptail species (in the same family)	lizards
<i>Amphibolurus muricatus</i>	0.0674	km	Warner and Shine 2007	mean distance traveled of hatchlings	lizards
<i>Anolis sagrei</i>	0.0106	km/gen	Calsbeek et al. 2014	mark-recapture field estimate for congener <i>Anolis sagrei</i> (juveniles); averaged across sexes	lizards
<i>Boa constrictor</i>	1.5	km	Bertona 2003	upper end of dispersal seen across a few months	snakes
<i>Carlia rubrigularis</i>	0.123	km/sqrt(gen)	Phillips et al. 2004	Rousset method (though limited by estimates of D from the center) - 112 to 133 m / sqrt(gen) under mixed model	lizards
<i>Chlamydosaurus kingii</i>	1.05	km	Ujvari et al. 2008	middle point of recapture distance in male juveniles	lizards
<i>Cnemidophorus punctulinealis</i>	0.0352	km/sqrt(gen)	Dessauer et al. 2000	based on unpublished capture-recapture data included in paper	lizards
<i>Coluber constrictor</i>	0.781	km	Brown and Parker 1976	mean male dispersal	snakes
<i>Crotaphytus collaris</i>	0.3	km	Templeton et al. 2011	median dispersal for juvenile (estimated from graph)	lizards
<i>Egernia cunninghami</i>	0.477	km	Stow et al. 2001	distance of adults from natal site to recapture site in reserve	lizards
<i>Elgaria coerulea</i>	0.0161	km	Rutherford and Gregory 2001	recapture distance of adults	lizards
<i>Eumeces skiltonianus</i>	0.008	km	Rutherford and Gregory 2001	recapture distance of adults	lizards
<i>Eunectes murinus</i>	3	km	Munoz and Rivas 1994		snakes
<i>Gnypetoscincus queenslandiae</i>	0.000843	km2 /gen	Sumner et al. 2001	mark-recapture	lizards
<i>Hoplocephalus bungaroides</i>	0.161	km	Webb & Shine 1997	dispersal of juveniles	snakes
<i>Hoplodactylus maculatus</i>	0.05	km/gen	Fitness et al. 2011	upper bound as estimated from mark-recapture	lizards
<i>Lacerta vivipara</i>	0.1	km/gen	Vercken et al. 2012	field-estimate for congener; max dispersal estimated at 100m for <i>Lacerta vivipara</i> , modes at 10-15m (primary) and 30-40m (secondary)	lizards
<i>Liasis fuscus</i>	12	km	Madsen and Shine 1996	(max) movement across wet season	snakes
<i>Natrix maura</i>	0.18	km	Hailey and Davies 1987	distance between recaptures in females	snakes
<i>Natrix natrix</i>	0.63	km	Kindler et al. 2017	sqrt of measure of female home range size (40 ha)	snakes
<i>Niveoscincus microlepidotus</i>	0.012	km	Olsson and Shine 2003	natal dispersal in females	lizards

<i>Opheodrys aestivus</i>	0.028	km	Plummer 1997	distance between captures	snakes
<i>Pantherophis obsoletus</i>	1.02	km	Blouin-Demers and Weatherhead 2002; Blouin-Demers and Weatherhead pers. comm.	"we bound this from 1.02 to 4.03 km given mean and maximum distances of nesting sites to hibernaculum"	snakes
<i>Podarcis muralis</i>	0.5	km	Scaletool website: http://scales.ckff.si/scaletool/index.php?menu=6&submenu=0&sid=113	maximal dispersal (as cited Stumpel 2004)	lizards
<i>Pseudechis porphyriacus</i>	0.3	km	Shine 1987	sqrt of male home range (9.6 ha)	snakes
<i>Rhinoplocephalus nigrescens</i>	0.99	km	Keogh et al. 2007	distance between capture sites over 10 years in males	snakes
<i>Sceloporus grammicus</i>	0.08	km/gen	Sites et al. 1995	mark-recapture (in hybrid zone)	lizards
<i>Sceloporus occidentalis</i>	0.0456	km	Massot et al. 2003	field estimate for congener	lizards
<i>Stegonotus cucullatus</i>	0.285	km/month	Dubey et al. 2008	mark-recapture over one month in males	snakes
<i>Thamnophis atratus</i>	0.0729	km	Welsh et al. 2010	juvenile male dispersal	snakes
<i>Tiliqua adelaidensis</i>	0.011	km	Schofield et al. 2012	seasonal movement from burrows	lizards
<i>Uta stansburiana</i>	0.02	km	Doughty and Sinervo 1994	hatching dispersal, LB	lizards
<i>Uta stansburiana</i>	0.1	km	Doughty and Sinervo 1994	hatching dispersal, DP	lizards

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