Electronic Supplementary Material

Prediction of phylogeographic endemism in an environmentally complex biome.

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Supplementary Methods

Overall Approach.

To map phylogeographic endemism across the forest, we build a biome-wide phylogeographic synthesis, the largest to date, in which we combine new and published sequence-level data from 25 vertebrate species or species groups. More than 90% of the data (23 taxa) come from amphibians and reptiles, low-dispersal species for which the impacts of environmental change are expected to be the strongest. To ask whether phylogeographic endemism patterns can be explained by inferred shifts of the forest climate through time, we build correlative models of forest distribution at 4 kyr intervals extending through a full glacial cycle (120 kyrs) into the past, as well as at 1 kyr intervals back to the Last Glacial Maximum (LGM). Our working assumption is that forest models will be more useful for lineage endemism prediction than taxon-based models because of the potential for broader generalization afforded by focusing on habitat shifts, as opposed to shifts in individual species. However, the applicability of these habitat models will depend on how accurately they predict climate-driven shifts of the taxa occupying unique microclimates, eco-regions, or smaller climatic envelopes *within* the biome of interest. This becomes especially relevant in geographically extensive and topographically complex regions that are climatologically heterogeneous, or which host biogeographically distinct assemblages of species, or species pools. The AF is a case in point.

Previous studies attempted to model the historical stability of the AF based on an intersection of habitat models developed under current climate, climatic conditions 6 kyr before present (6 kybp), and 21 kybp [1]. Those results suggested much higher forest stability in the north relative to the south of the AF. While multiple phylogeographic datasets showed that the Carnaval-Moritz model [1] successfully predicted patterns of genetic diversity in lowland and mid-altitude species [2-4], subsequent data from more narrowly distributed (southern) and montane species indicated long-term persistence of unique and narrowly distributed lineages in areas predicted as unstable as per the original model [5,6]. Combined with phylogeographic data from relatively widespread groups, including organisms seemingly able to tolerate colder temperatures [7-9], these results suggest that the simple AF stability model of Carnaval and Moritz [1] is unable to predict diversity and phylogeographic endemism patterns across species pools that occupy distinct climatic envelopes within the extensive (~3000 km) and topographically complex AF. We predict that such limited transferability of a generic habitat model across the entirety of the biome, particularly across sets of taxa with disparate environmental attributes and biogeographical connections, will likely be prevalent in other similarly extensive and complex natural systems. To circumvent this problem, we use ordination-based characterization and independent modeling of distinct forest climate spaces to address major discrepancies across predictive models of regional species pools and improve climate-based stability models for the AF. Our expectation is that the incorporation of subregional differences in predictive mapping of forest persistence will improve overall prediction of phylogeographic endemism and historical demography across taxa with radically different environmental correlates – in Brazil and beyond.

Mapping phylogeographic endemism.

We used *Biodiverse* [10] to estimate phylogeographic endemism based on mtDNA genealogies of 25 AF tetrapod species (table S1). In this calculation, the length of each branch on the genealogy is divided equally across the grid cells in which it or it descendant lineages occur. These adjusted branch lengths are then summed for each cell. High scores therefore are allocated to regions where a large component of phylogenetic variation is restricted to a small area. Data for 13 taxa were obtained from published materials and downloaded from Genbank; mtDNA genealogies for the remaining species were generated through standard extraction, amplification and Sanger sequencing protocols (table S2). Filling a previous sampling gap, we focused on southern montane sites and mid-montane northern localities.

To estimate phylogeographic endemism, *Biodiverse* [10] requires species presence data for all grid cells in the region of study. In lieu of this information, which is unavailable, we used geo-referenced information from each taxon (dataset S1), thinned at a 5km threshold to minimize sampling bias, to generate 2.5'-resolution (4km x 4 km) models of current species distribution in MaxEnt [11]. Species model outputs were carefully checked against the reported distribution of the focal species to ensure that they provided the most accurate measure of endemism possible. Models were then converted to binary presence/absence data using a moderately conservative "equal training sensitivity & specificity" threshold [12], and upscaled to more computationally feasible grid sizes of 5'. To estimate phylogeographic endemism, we used geo-referenced haplotype data and the species-level trees to subdivide the range of each species into lineage-specific ranges. After superimposing the tree on the distribution model of each species, we drew a minimum area polygon around each well-supported lineage. If samples were lacking from areas located in-between polygons, we used the midpoint between their adjacent borders to arbitrarily set the geographical limits of the lineages.

Given our interest in pooled phylogeographic datasets, we focused on recent evolutionary history by aggregating available within-species genetic information into a composite mtDNA phylogeny, yet removing higher-level phylogenetic information (fig. S1). This was done by incorporating only those well-supported clades identified for each species (> 80% Maximum Likelihood Bootstrap Support). The independent history of these major mtDNA clades is broadly supported by evidence from nuclear data sets, which are available for 19 of the 25 target taxa (2 widespread, 10 in the south, 7 in the north). Analyses performed within species complexes were able to detect well-supported nuclear clades that match several, if not all, mtDNA lineages used here [7, 8, 13, unpublished data]. Private nuclear alleles, significant differences in nuclear haplotype frequencies, and cytogenetic differences detected through intra-specific studies [4, 15, unpublished data] further support the notion that these mtDNA lineages represent independently evolving organismal lineages.

Branch lengths were calculated through maximum-likelihood GTR+G distances in Geneious, ver. 5 (Biomatters). Eighty-one percent of the data sets corresponded to protein-coding mitochondrial gene sequences and were pooled in a composite phylogenetic tree without branch-length corrections. To incorporate five additional data sets consisting of 16s ribosomal DNA sequences, which are known to evolve at a different rate relative to protein-coding mtDNA, we rescaled the branch lengths of the 16S genealogies by a factor of 1.5 before combining them with the remaining data sets (as per [15]).

Identifying climatic spaces within the AF.

Because phylogeographic data gathered from AF species with distinct environmental requirements (e.g. lowland vs. montane specialists) indicate that preliminary habitat models [1] were inefficient at explaining differential historical responses to climate change, we sought to identify and independently model distinct environmental envelopes occupied by the biome. For that, we used simple ordination methods to delimit unique climate spaces within the forest. First, we extracted values of mean temperature, mean precipitation, and annual temperature seasonality [16] from 14,000 random points throughout the pre-clearing extent of the forest as per Fundação Instituto Brasileiro de Geografia e Estatística [17]. We then used a Principal Component Analysis (PCA) implemented in R ver. 2.14 to examine climate variation within the forest. Because studies of humid air circulation in the AF suggest that the forest should be treated as two distinct climatological units (a northern forest characterized by rainy winters, a southern forest with rainy summers [18]), we implemented a k-means cluster analysis to our PCA plots and set the algorithm to identify two distinct climatic spaces within the biome. After noticing that the PCA-inferred climatic spaces matched the northern (lowland and mid-altitude dominated, $PC1<0$) and the southern (cooler and more montane, $PC1>0$) portions of the forest, in broad agreement with the circulation-based data, we performed identity and background tests [19] with 100 replicates, to test for niche similarity. Once the climatic uniqueness of these two forest spaces was verified, we proceeded to generate separate correlative models of forest distribution based on randomly extracted points from each of the two climatic regions.

To verify whether the climate-based division of the forest environmental space was biologically meaningful, we performed a separate PCA based on climatic values extracted from the locality data of all target species. If the proposed distinction of forest climatic spaces is biologically relevant, which is desirable for accurate biodiversity prediction purposes, then we expect that the detected break in forest environmental space will roughly match a turnover in species composition. Because the majority of variation in species-specific PC scores occurred along the first axis, similar to the PC analysis of the forest, we used the species PC1 scores as a guide to tentatively classify each taxon as either southern (cooler, more montane), northern (warmer, mostly lowland and mid-altitude), or widespread. Species for which the median PC1 value was greater than 0.5 were grouped together and tentatively classified as "southern", matching the forest classification; species with median value lower than -0.5 were categorized as "northern". The remaining taxa (median value between -0.5 and 0.5) were categorized as 'widespread' and used only for overall phylogeographic endemism calculations (see table S1).

Estimating historical climatic stability based on snapshot paleoclimate simulations.

To estimate historical forest stability, we used MaxEnt to develop present-day models of the distribution of the entire forest, as well as of each PCA-delimited forest space. The former were developed from 1,200 sites randomly sampled from the pre-clearing extent of the forest, using points located 25 km of each other or more to avoid spatial autocorrelation. Models of the two PCA-delimited spaces were generated from 600 random points each. We then projected these models to paleoclimatic simulations dating every 1 kyr from 1 kybp to 21 kybp (the last glacial maximum), as well as every 4 kyr from 4 kybp to 120 kybp (the last interglacial), providing a more continuous view into the past, as per recent studies [20]. Models were run with default regularization at a 2.5’ spatial resolution through the ‘crossvalidate’ replicate option, each averaging five runs with a different 80% - 20% set of localities for training and testing, respectively. Eight WorldClim bioclimatic variables [16] were used for modeling, representing biologically relevant summaries of means and variation in temperature and precipitation: annual mean temperature, temperature seasonality, mean temperature of warmest and coldest quarters, annual precipitation, precipitation seasonality, and precipitation of wettest and driest quarters. Past climates were based on snapshot simulations covering the last 120,000 years using the Hadley Centre Climate model (HadCM3 [20, 21]). Using this circulation model [21], for which climatic reconstructions are available at small (1 or 4kyr) time intervals, we were able to provide a more continuous and dynamic view of forest shifts through time. All paleobioclimate layers are available for download at Dryad (doi:10.5061/dryad.8kc1v). We used Viterbi’s algorithm [22] to combine predictions of past distributions of the forest across time intervals and estimated historical forest stability per pixel while allowing for 0 m, 5 m, and 10 m forest dispersal per year, as per published protocols [23]. Original grid files of all maps can be downloaded from Dryad (doi:10.5061/dryad.8kc1v). By comparing our results under a maximally restrictive, static refugia model (forest dispersal = 0 m per year) to more biologically plausible dynamic refugia models (forest dispersal 5 m and 10 m per year), we were able to evaluate the sensitivity of our analyses to forest dispersal ability. Forest stability values were then extracted from the entire forest space, as well as northern and southern forest climatic subsets defined through the PCA procedure. These maps are henceforth referred to as shifting refugia maps, and the stability values obtained per grid cell were used as proxies for historical potential for lineage maintenance in our predictive model.

Mapping present-day environmental heterogeneity.

To evaluate how present-day climatic heterogeneity potentially restricts the distribution of our target lineages and affects endemism, we applied K-means clustering to a PCA analysis based on values of mean temperature, mean precipitation, and annual temperature seasonality from random forest localities. With this, we delimited the largest possible number of uniquely different, diagnosable climatic spaces within the forest. After multiple iterations of the PCAs, each time applying a different K value, we found the upper limit of K that allows for the recognition of the largest number of climatically discrete spaces to be 14 (fig. S3). We then calculated the area of each polygon, or uniquely recognized climatic space under contemporary conditions, and applied this value to all grid cells within each respective polygon as a proxy for contemporary lineage dispersal potential.

Examining the predictive power of historical and contemporary variables in predictions of phylogeographic endemism.

To examine the relative effects of historical and present-day climate on phylogeographic endemism, we examined correlations between per grid cell values of phylogeographic endemism and 120 kyr forest stability, 21 kyr forest stability, the total area of the contemporary climatic space occupied by each cell, and net primary productivity (NPP) per cell. The NPP data (ftp://ftp.ntsg.umt.edu/pub/MODIS/NTSG_Products/MOD17/MOD17A3/, U. of Montana) correspond to averages across 2000-2011 yearly NPP means estimated at a 1 km resolution [24].

For the correlation analysis, we used the software Spatial Analyses in Macroecology (SAM, [25]) to calculate correlation coefficients (r, measuring the strength and the direction of the relationship between two variables) and to test for significance after correcting for spatial autocorrelation. SAM uses Dutilleul's method [26] to estimate the effective number of degrees of freedom. Additionally, we used SAM's partial least squares regression analysis to determine coefficients of determination, r^2, and therefore understand which proportion of the variance (fluctuation) of one variable that is predictable from another variable. Specifically, we used r^2 to examine the relative explanatory power of historical vs. contemporary climate in predicting phylogeographic endemism. Regressions were run on phylogeographic endemism values estimated from all species (overall phylogeographic endemism), and on estimates of southern or northern species only. Overall regression analyses were run on the 420 grid cells for which phylogeographic data were available. Independent analyses of northern and southern taxa were based on 93 and 176 points, accordingly.

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II. Supplementary Tables:

Table S1. Table of molecular datasets used in the present study, including mtDNA marker utilized, number of sequenced specimens (N), and categorization of the species range (northern, southern, or widespread) as explained in Methods. References are provided whenever DNA datasets were obtained from published GenBank records. Novel datasets are indicated by respective GenBank accession numbers.

Species	Order, Family	marker utilized	N	Range Category	Source of mtDNA data
Anolis punctatus	Squamata, Polychrotidae	ND2	20	North	KM204350 - KM204354
Bothrops jararaca	Squamata, Viperidae	Cyt b	159	South	[1]
Brachycephalus spp. complex	Anura, Brachycephalidae	16s	53	South	KM204365 - KM204369
Chiasmocleis carvalhoi	Anura, Microhylidae	ND2	50	North	[2]
Coleodactylus meridionalis	Squamata, Sphaerodactylidae	16s	138	North	DQ110494.1, KM204325 - KM204333
Colobdactylus taunayi	Squamata, Gymnophthalmidae	16s	18	South	KM204372 - KM204373
Dendropsophus elegans	Anura, Hylidae	ND2	172	Widespread	[2]
Enyalius catenatus	Squamata, Leiosauridae	ND4	161	North	KM204334 - KM204336
Gymnodactylus darwinii	Squamata, Gekkonidae	Cyt b	47	North	[3]
Heterodactylus imbricatus	Squamata, Gymnophthalmidae	16s	8	South	KM204374 - KM204375
Hypsiboas albomarginatus	Squamata, Hylidae	ND2	130	North	[4]
Hypsiboas faber	Squamata, Hylidae	ND2	137	Widespread	[4]
Hypsiboas semilineatus	Squamata, Hylidae	ND2	112	North	[4]
Leposoma scincoides complex	Squamata, Gymnophthalmidae	ND4	91	North	[5] and KM204337 - KM204344
Mabuya dorsivittata	Squamata, Scincidae	Cyt b	25	South	KM204355 - KM204358
Melanophryinscus spp. complex	Anura, Bufonidae	16s	10	South	KM204370 - KM204371

Phyllomedusa burmeisteri complex	Anura, Hylidae	ND2	35	South	[6]
Placosoma glabellum	Squamata, Gymnophthalmidae	ND4	16	South	KM204345 - KM204349
Proceratophrys boiei	Anura, Leptodactylidae	Cyt b	169	South	[7]
Proceratophrys renalis	Anura, Leptodactylidae	Cyt b	42	North	[8]
Pyriglena complex	Passeriformes, Thamnophilidae	ND2	245	Widespread	[9]
Rhinella crucifer complex	Anura, Bufonidae	ND1	78	South	[10]
Vitreorana eurygnatha	Anura, Centrolenidae	ND1	31	South	KM204320 - KM204324
Vitreorana uranoscopa	Anura, Centrolenidae	ND1	57	South	KM204359 - KM204364
Xiphorhynchus fuscus	Passeriformes, Furnariidae	Cyt b	22	Widespread	[11]

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Table S2. Primers and amplification protocols utilized for newly generated data.

Species	primer pair	PCR profile
Anolis punctatus	LVT_Metf.6_AnCr, LVT_5617_AnCr [1].	94°C (3 min); 35 cycles at 94°C (45 s), 60°C (45 s), and 72°C (1:30 min); 72°C (7 min).
Brachycephalus spp.	16SA-L, 16SB-H [2].	96°C (1 min); 35 cycles at 96°C (15s), 56°C (50s) and 60°C (4 min).
Coleodactylus meridionalis	16SF, 16SR [3].	94°C (5 min); 35 cycles at 94°C (40 s), 60°C (40 s), 72°C (40 s); 72°C (7 min).
Colobdactylus taunayi	MVZ117, MVZ 98 [4].	95°C (10 min); 35 cycles at 94°C (30 s), 50°C (45 s), 72°C (1 min); 72°C (10 min).
Enyalius catenatus	ND4, LEU [5].	95°C (3 min); 40 cycles at 95°C (25 s), 52°C (60 s), 72°C (2 min); 72°C (5 min).
Heterodactylus imbricatus	MVZ117, MVZ 98 [4].	95°C (10 min); 35 cycles at 94°C (30 s), 50°C (45 s), 72°C (1 min); 72°C (10 min).
Leposoma scincoides	ND4, LEU [5].	95°C (3 min); 35 cycles at 95°C (30 s), 52°C (30 s), 72°C (30s); 72°C (5 min).
Mabuya dorsivittata	L15146, H15915sh [6].	94°C (3 min); 35 cycles at 94°C (45 s), 53°C (45 s), 72°C (1:30 min); 72°C (7 min).
Melanophryinscus	16SA-L, 16SB-H [2].	96°C (1 min); 35 cycles at 96°C (15s), 56°C (50s) and 60°C (4 min).
Placosoma glabellum	ND4F, ND4R [7].	94°C (3 min); 37 cycles at 94°C (45 s), 48°C (45 s), 72°C (1 min); 72°C (7 min).
Vitreorana eurygnatha	16S-frog, tMet-frog [8].	95°C (2 min); 6 cycles at 95°C (30 s), 56-50°C (-1.0°C /cycle, 30 s), 72°C (1:45 min); 30 cycles at 95°C (30 s), 52°C (30 s), 72°C (1:45 min); 72°C (5 min).
Vitreorana uranoscopa	16S-frog, tMet-frog [8].	95°C (2 min); 6 cycles at 95°C (30 s), 56-50°C (-1.0°C /cycle, 30 s), 72°C (1:45 min); 30 cycles at 95°C (30 s), 52°C (30 s), 72°C (1:45 min); 72°C (5 min).

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Table S3. Spatially-corrected correlation analyses between phylogeographic endemism and their potential contemporary and historical determinants. Present-day variables include the geographic extent (area) of unique contemporary climatic spaces (as proxy for present-day range restriction), and net primary productivity (NPP). Historical determinants correspond to forest stability over the last 21 and 120 kyr (as proxies for lineage maintenance through time), using zero and non-zero dispersal distances for the forest (5m forest dispersal/year, and 10m forest dispersal/ year, respectively). Correlations are examined across A) the entire Atlantic Forest, B) the northern climatic space of the forest, and C) the southern climatic space of the forest. Correlation coefficients (r) are provided for each comparison, alongside corrected p-values.

		0m dispersal		5m dispersal		10m dispersal	
response variable	predictor variables	R	corrected p	R	corrected p	R	corrected p
overall phylogeographic endemism (Atlantic forest-wide, all species pooled)	**area**	**-0.243**	**0.033**	**-0.243**	**0.033**	**-0.243**	**0.033**
	npp	**0.415**	**0.001**	**0.415**	**0.001**	**0.415**	**0.001**
	120k stability of entire forest	**0.387**	**0.007**	**0.562**	**0.002**	**0.571**	**0.003**
	21k stability of entire forest	**0.265**	**0.033**	**0.262**	**0.031**	**0.327**	**0.017**
phylogeographic endemism, northern species only	area	0.097	0.595	0.097	0.595	0.097	0.595
	npp	0.076	0.670	0.076	0.670	0.076	0.670
	120k stability of northern forest	**0.677**	**0.019**	0.700	0.117	0.670	0.171
	21k stability of northern forest	**0.642**	**0.040**	0.640	0.064	0.657	0.096
phylogeographic endemism, southern species only	**area**	**-0.397**	**0.01**	**-0.397**	**0.01**	**-0.397**	**0.01**
	npp	**0.467**	**0.001**	**0.467**	**0.001**	**0.467**	**0.001**
	120k stability of southern forest	0.069	0.733	0.244	0.257	0.077	0.759
	21k stability of southern forest	-0.001	0.995	<0.001	1.000	0.146	0.492

Table S4. Partial Least Squares Regressions[1] of phylogeographic endemism against potential contemporary[2] and historical[3] predictor variables. Regressions are examined across A) the entire Atlantic Forest, B) the northern climatic space of the forest, and C) the southern climatic space of the forest.

response variable	predictor variables	r^2	AIC weights	predictor variables	r^2	AIC weights
A. overall phylogeographic endemism (forest-wide, all species pooled)	**120k stability + area + NPP**	**0.303**	**0.706**			
	120k stability	0.150	<0.001	120k stability + area	0.208	<0.001
	area	0.059	<0.001	120k stability + NPP	0.295	0.294
	NPP	0.172	<0.001	area + NPP	0.178	<0.001
	21k stability + area + NPP	**0.258**	**0.757**			
	21k stability	0.070	<0.001	21k stability + area	0.141	<0.001
	area	0.059	<0.001	21k stability + NPP	0.248	0.243
	NPP	0.172	<0.001	area + NPP	0.178	<0.001
B. phylogeographic endemism, northern species only	120k stability + area + NPP	0.468	0.133			
	120k stability	**0.458**	**0.459**	120k stability + area	0.459	0.173
	area	0.009	<0.001	120k stability + NPP	0.462	0.236
	NPP	0.006	<0.001	area + NPP	0.029	<0.001
	21k stability + area + NPP	0.415	0.080			
	21k stability	**0.412**	**0.528**	21k stability + area	0.414	0.211
	area	0.009	<0.001	21k stability + NPP	0.412	0.181
	NPP	0.006	<0.001	area + NPP	0.029	<0.001
C. phylogeographic endemism, southern species only	120k stability + area + NPP	0.264	0.261			
	120k stability	0.005	<0.001	120k stability + area	0.162	<0.001
	area	0.157	<0.001	120k stability + NPP	0.218	<0.001
	NPP	0.218	0.002	**area + NPP**	**0.264**	**0.736**
	21k stability + area + NPP	0.267	0.343			
	21k stability	<0.001	<0.001	21k stability + area	0.158	<0.001
	area	0.157	<0.001	21k stability + NPP	0.221	0.001
	NPP	0.218	0.002	**area + NPP**	**0.264**	**0.654**

[1] Coefficients of determination (r^2) are provided alongside corrected AIC weights, which indicate the relative importance of forest stability, current climate, and combined stability and current climate as predictors of phylogeographic endemism. Variables with highest predictive power in bold.

[2] Present-day variables include the geographic extent (area) of unique contemporary climatic spaces (as proxy for present-day range restriction), and net primary productivity (NPP).

[3] Historical predictors correspond to forest stability over the last 21 and 120 kyr (as proxies for lineage maintenance through time).

Table S5. Partial Least Squares Regressions of phylogeographic endemism against potential contemporary and historical predictor variables. Present-day variables include the geographic extent (area) of unique contemporary climatic spaces (as proxy for present-day range restriction), and net primary productivity (NPP). Historical predictors correspond to forest stability over the last 21 and 120 kyr (as proxies for lineage maintenance through time), estimated under an assumption of non-zero dispersal distances for the forest (5m forest dispersal/year, and 10m forest dispersal/ year, respectively). Regressions are examined across A) the entire Atlantic Forest, B) the northern climatic space of the forest, and C) the southern climatic space of the forest. Coefficients of determination (r^2) are provided alongside corrected AIC weights, which indicate the relative importance of forest stability, current climate, and combined stability and current climate as predictors of phylogeographic endemism. Most predictive variables in bold.

	5m forest dispersal per year					
response variable	predictor variables	r^2	AIC weight	predictor variables	r^2	AIC weight
A. overall phylogeographic endemism (Atlantic forest-wide, all species pooled)	**120k stability + area + NPP**	**0.402**	**0.759**			
	120k stability	0.316	<0.001	120k stability + area	0.354	<0.001
	area	0.059	<0.001	120k stability + NPP	0.394	0.241
	NPP	0.172	<0.001	area + NPP	0.178	<0.001
	21k stability + area + NPP	**0.255**	**0.748**			
	21k stability	0.068	<0.001	21k stability + area	0.138	<0.001
	area	0.059	<0.001	21k stability + NPP	0.245	0.252
	NPP	0.172	<0.001	area + NPP	0.178	<0.001
B. phylogeographic endemism, northern species only	120k stability + area + NPP	0.505	0.146			
	120k stability	0.490	0.263	120k stability + area	0.497	0.185
	area	0.009	<0.001	**120k stability + NPP**	**0.505**	**0.407**
	NPP	0.006	<0.001	area + NPP	0.029	<0.001
	21k stability + area + NPP	0.414	0.081			
	21k stability	**0.410**	**0.525**	21k stability + area	0.412	0.214
	area	0.009	<0.001	21k stability + NPP	0.410	0.080
	NPP	0.006	<0.001	area + NPP	0.029	<0.001
	120k stability + area + NPP	0.268	0.399			

c. Phylogeographic endemism, southern species only	120k stability	0.060	<0.001	120k stability + area	0.180	<0.001
	area	0.157	<0.001	120k stability + NPP	0.226	0.002
	NPP	0.218	0.002	**area + NPP**	**0.264**	**0.597**
	21k stability + area + NPP	0.267	0.353			
	21k stability	<0.001	<0.001	21k stability + area	0.158	<0.001
	area	0.157	<0.001	21k stability + NPP	0.221	0.001
	NPP	0.218	0.002	**area + NPP**	**0.264**	**0.644**

	10m forest dispersal per year					
response variable	predictor variables	r^2	AIC weight	Predictor variables	r^2	AIC weight
A. overall phylogeographic endemism (Atlantic forest-wide, all species pooled)	**120k stability + area + NPP**	**0.391**	**0.518**			
	120k stability	0.326	<0.001	120k stability + area	0.350	<0.001
	area	0.059	<0.001	120k stability + NPP	0.387	0.482
	NPP	0.172	<0.001	area + NPP	0.178	<0.001
	21k stability + area + NPP	**0.298**	**0.818**			
	21k stability	0.107	<0.001	21k stability + area	0.181	<0.001
	area	0.059	<0.001	21k stability + NPP	0.287	0.182
	NPP	0.172	<0.001	area + NPP	0.178	<0.001
B. phylogeographic endemism, northern species only	120k stability + area + NPP	0.485	0.133			
	120k stability	0.449	0.271	120k stability + area	0.472	0.214
	area	0.009	0.067	**120k stability + NPP**	**0.479**	**0.447**
	NPP	0.006	<0.001	area + NPP	0.029	<0.001
	21k stability + area + NPP	0.433	0.068			
	21k stability	**0.432**	**0.543**	21k stability + area	0.433	0.204
	area	0.009	<0.001	21k stability + NPP	0.432	0.185
	NPP	0.006	<0.001	area + NPP	0.029	<0.001

C. phylogeographic endemism, southern species only	**120k stability + area + NPP**	**0.273**	**0.568**			
	120k stability	0.006	<0.001	120k stability + area	0.158	<0.001
	area	0.157	<0.001	120k stability + NPP	0.222	<0.001
	NPP	0.218	0.001	area + NPP	0.264	0.430
	21k stability + current climate + NPP	0.264	0.261			
	21k stability	<0.001	0.021	21k stability + area	0.163	<0.001
	area	0.157	<0.001	21k stability + NPP	0.216	<0.001
	NPP	0.218	0.002	**area + NPP**	**0.264**	**0.736**

Supplementary Figures:

Fig. S1. Pruned phylogenetic tree used in PE estimations. Basal branch lengths (equal across sampled groups) are exaggerated for visualization only. Unique lineages within species are given distinct identifier numbers.

Fig. S2. Dynamic forest refuge models over the last 21 kyr (above) and 120 kyr (below), assuming low (5m/year, left) and medium (10m/year, right) forest dispersal. Within each dispersal treatment, the left panel depicts predictions of forest stability when the AF is modeled as a whole. Central and right panels portray predictions of forest stability of the northern and southern climatic spaces, respectively. Suitability values represent the sum of negative log probabilities.

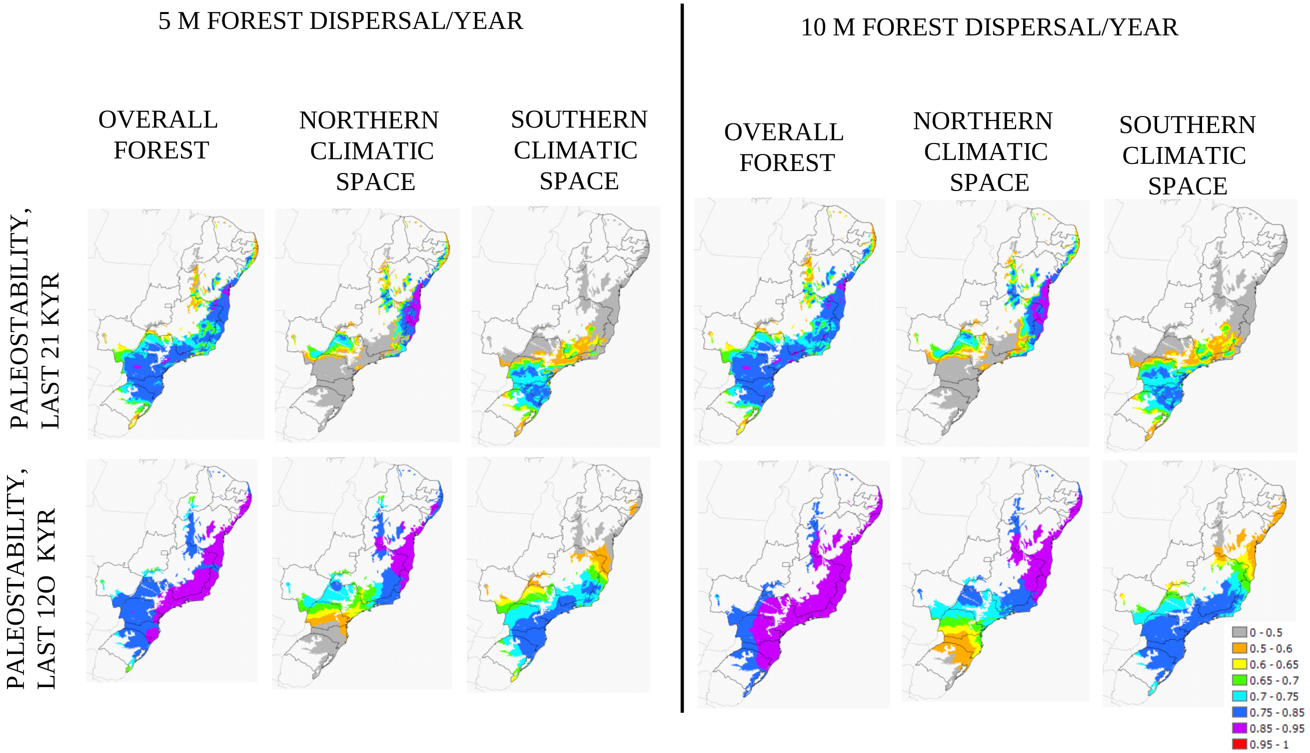


Fig. S3. Discrete climatic spaces within the Atlantic Forest under present-day climates given K-clustering analysis (K = 14). Boundaries delineate the northern (black) and southern (red) climatic spaces of the forest.

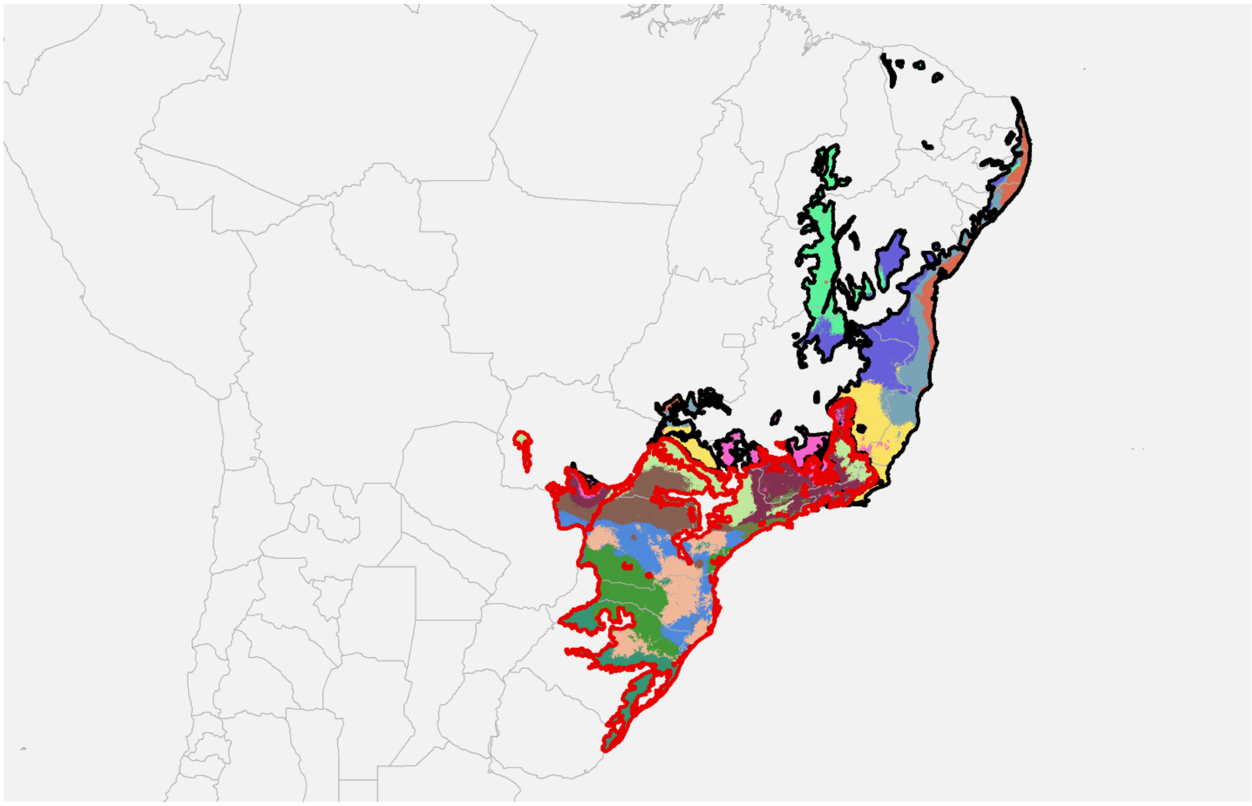
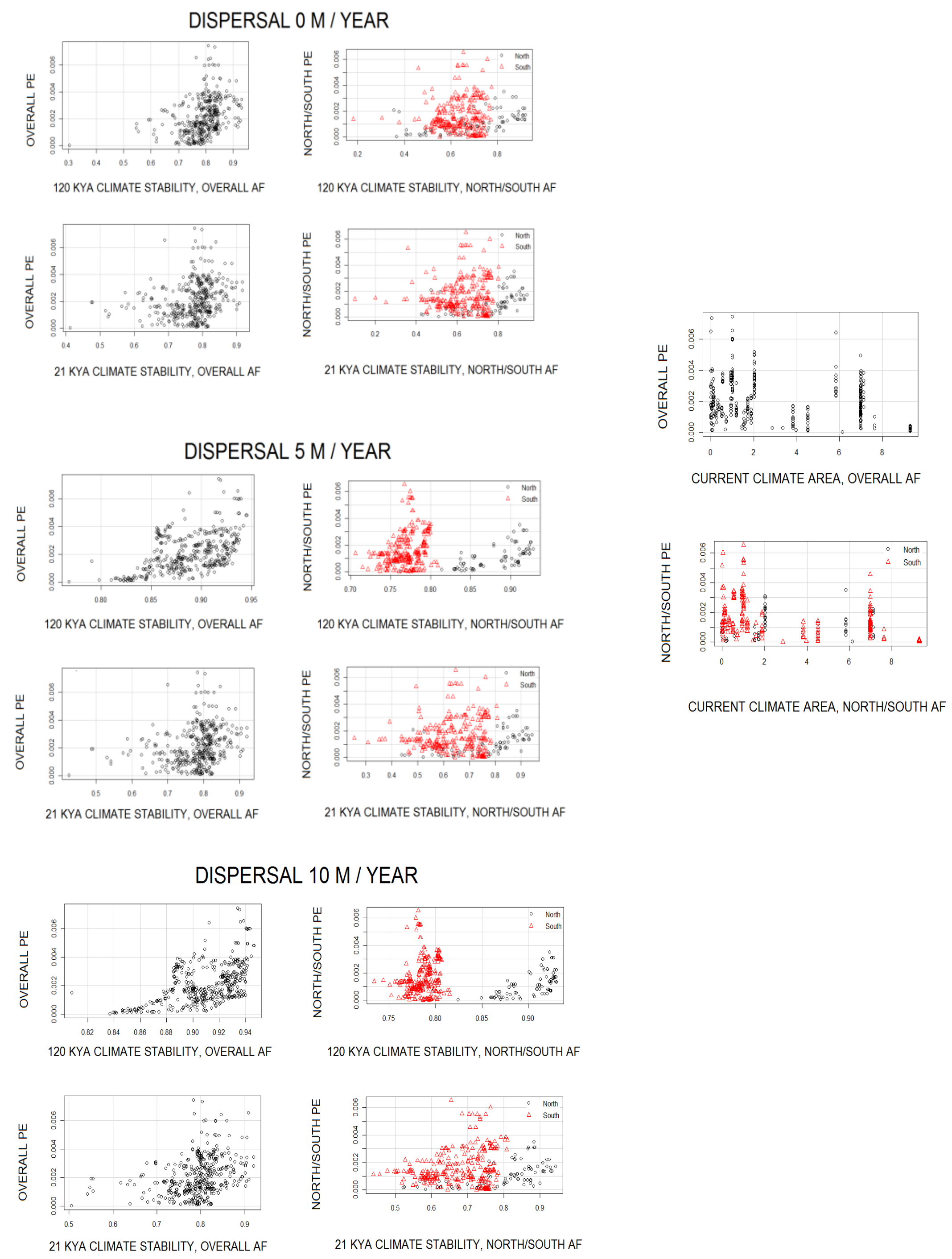


Fig. S4. Phylogeographic endemism vs. 120 kyr and 21 kyr forest stability values (proxy for historical lineage persistence) for three different forest dispersal scenarios (0m/yr, 5m/yr & 10m/yr; left panel) and inferred area of current climatic envelopes (proxy for current range restriction; right panel). Red triangles depict sites in the northern forests, black circles denote southern forest spaces.



Supplementary Dataset:

Dataset S1. Locality data utilized to build correlative models of species distribution for all target taxa. Species names are in alphabetical order, followed by longitude and latitude.

Anolis punctatus	-39.0333	-14.8167
Anolis punctatus	-39.5167	-15.1500
Anolis punctatus	-39.5192	-15.4445
Anolis punctatus	-40.0650	-19.1516
Anolis punctatus	-40.0714	-19.4344
Anolis punctatus	-40.5219	-20.2811
Anolis punctatus	-41.7114	-20.9803
Anolis punctatus	-42.5254	-19.6844
Anolis punctatus	-42.6611	-22.4506
Anolis punctatus	-43.2347	-22.9392
Anolis punctatus	-43.3316	-20.3292
Anolis punctatus	-43.5833	-22.4000
Anolis punctatus	-46.0033	-23.7839
Bothrops jararaca	-40.3069	-20.3058
Bothrops jararaca	-40.5822	-19.9364
Bothrops jararaca	-40.6681	-20.3664
Bothrops jararaca	-40.7333	-20.0333
Bothrops jararaca	-41.8833	-22.7511
Bothrops jararaca	-42.0272	-21.9581
Bothrops jararaca	-42.1492	-20.3842
Bothrops jararaca	-42.2667	-20.7994
Bothrops jararaca	-42.2678	-20.1672
Bothrops jararaca	-42.2844	-21.5500
Bothrops jararaca	-42.3636	-22.0350
Bothrops jararaca	-42.5275	-22.2636
Bothrops jararaca	-42.6525	-22.4872
Bothrops jararaca	-42.8181	-22.9164
Bothrops jararaca	-42.9178	-22.0075
Bothrops jararaca	-42.9750	-22.4158
Bothrops jararaca	-43.0397	-22.6606
Bothrops jararaca	-43.0728	-22.8353
Bothrops jararaca	-43.1567	-19.8358
Bothrops jararaca	-43.1856	-22.5203
Bothrops jararaca	-43.2081	-22.1158
Bothrops jararaca	-43.2925	-22.1603
Bothrops jararaca	-43.3553	-21.7531
Bothrops jararaca	-43.4108	-19.9728

Bothrops jararaca	-43.4847	-20.8492
Bothrops jararaca	-43.6678	-22.4103
Bothrops jararaca	-43.6828	-22.5528
Bothrops jararaca	-43.6842	-20.7831
Bothrops jararaca	-43.7044	-22.2456
Bothrops jararaca	-43.8253	-22.4711
Bothrops jararaca	-44.4017	-22.1672
Bothrops jararaca	-45.0761	-23.4525
Bothrops jararaca	-45.4508	-22.7994
Bothrops jararaca	-45.9664	-19.2172
Bothrops jararaca	-46.5133	-18.5892
Bothrops jararaca	-46.5442	-23.7125
Bothrops jararaca	-46.5569	-23.1239
Bothrops jararaca	-46.6283	-23.5336
Bothrops jararaca	-46.6842	-22.6653
Bothrops jararaca	-46.7467	-23.4131
Bothrops jararaca	-46.7689	-23.6031
Bothrops jararaca	-46.8033	-23.5197
Bothrops jararaca	-46.8733	-23.1994
Bothrops jararaca	-46.9181	-23.4497
Bothrops jararaca	-46.9911	-22.9742
Bothrops jararaca	-47.0333	-23.6825
Bothrops jararaca	-47.0511	-23.9500
Bothrops jararaca	-47.0692	-23.4333
Bothrops jararaca	-47.2183	-23.6506
Bothrops jararaca	-47.4114	-23.7122
Bothrops jararaca	-47.4831	-23.9514
Bothrops jararaca	-47.5206	-23.2119
Bothrops jararaca	-48.5378	-24.1867
Bothrops jararaca	-49.0647	-25.4525
Bothrops jararaca	-49.0967	-26.9181
Bothrops jararaca	-49.0972	-26.4836
Bothrops jararaca	-49.1739	-26.7544
Bothrops jararaca	-49.1789	-25.5775
Bothrops jararaca	-49.2203	-26.4464
Bothrops jararaca	-49.2842	-25.4306
Bothrops jararaca	-49.4100	-26.2183
Bothrops jararaca	-49.7172	-23.0333
Bothrops jararaca	-49.7311	-25.7647
Bothrops jararaca	-49.7333	-23.1678
Bothrops jararaca	-49.8492	-29.3497

Bothrops jararaca	-49.8625	-28.8214
Bothrops jararaca	-50.0594	-27.0556
Bothrops jararaca	-50.0683	-29.5833
Bothrops jararaca	-50.3939	-26.1811
Bothrops jararaca	-50.4008	-28.6994
Bothrops jararaca	-50.5792	-29.4431
Bothrops jararaca	-50.6172	-24.3375
Bothrops jararaca	-50.6547	-28.9331
Bothrops jararaca	-50.7939	-29.5792
Bothrops jararaca	-50.8094	-29.3633
Bothrops jararaca	-51.0675	-26.2333
Bothrops jararaca	-51.0836	-29.5325
Bothrops jararaca	-51.2169	-30.0397
Bothrops jararaca	-51.5167	-29.4511
Bothrops jararaca	-51.5486	-28.9386
Bothrops jararaca	-51.6014	-28.7844
Bothrops jararaca	-51.6169	-27.1167
Bothrops jararaca	-51.6647	-23.2394
Bothrops jararaca	-51.6667	-27.5736
Bothrops jararaca	-51.8025	-27.4197
Bothrops jararaca	-52.0183	-28.9839
Bothrops jararaca	-53.4522	-24.9672
Bothrops jararaca	-53.8961	-30.0394
Bothrops jararaca	-54.4497	-27.6506
Brachycephalus	-48.6256	-24.3925
Brachycephalus	-48.6907	-25.6248
Brachycephalus	-48.8378	-25.2664
Brachycephalus	-48.8561	-25.6111
Brachycephalus	-48.9086	-25.3408
Brachycephalus	-48.9164	-25.4508
Brachycephalus	-48.9236	-26.0058
Brachycephalus	-48.9303	-26.7997
Brachycephalus	-48.9580	-26.2122
Brachycephalus	-48.9821	-25.5153
Brachycephalus	-48.9957	-25.9016
Brachycephalus	-49.0042	-25.3886
Brachycephalus	-49.0533	-26.2331
Brachycephalus	-49.0622	-26.1142
Brachycephalus	-49.6701	-25.5162
BrachycephalusB	-41.0100	-20.4733
BrachycephalusB	-41.1142	-20.5281

BrachycephalusB	-42.2972	-22.3603
BrachycephalusB	-43.0011	-22.4511
BrachycephalusB	-43.2439	-22.4731
BrachycephalusB	-43.4433	-22.9322
BrachycephalusB	-43.6050	-22.4864
BrachycephalusB	-44.1922	-22.8336
BrachycephalusB	-44.6094	-22.4564
BrachycephalusB	-44.7803	-23.3119
BrachycephalusB	-44.7886	-23.1772
BrachycephalusB	-45.0736	-23.3917
BrachycephalusB	-45.1375	-23.3444
BrachycephalusB	-45.1969	-23.4556
BrachycephalusB	-45.3486	-23.8719
BrachycephalusB	-45.5278	-22.8656
BrachycephalusB	-45.8667	-23.6333
BrachycephalusB	-45.9678	-22.8956
BrachycephalusB	-46.5167	-23.1819
BrachycephalusB	-46.6364	-23.4536
BrachycephalusB	-46.6458	-23.7864
BrachycephalusB	-46.8169	-22.8983
BrachycephalusB	-46.9433	-22.2367
BrachycephalusB	-46.9728	-23.7022
Chiasmocleis carvalhoi	-39.1247	-16.5366
Chiasmocleis carvalhoi	-39.8442	-18.3553
Chiasmocleis carvalhoi	-39.9928	-19.1606
Chiasmocleis carvalhoi	-40.1833	-20.1025
Chiasmocleis carvalhoi	-40.5219	-20.2811
Chiasmocleis carvalhoi	-41.0194	-20.9823
Chiasmocleis carvalhoi	-41.2814	-21.2100
Chiasmocleis carvalhoi	-42.7641	-22.4457
Chiasmocleis carvalhoi	-43.2385	-22.5994
Chiasmocleis carvalhoi	-44.8333	-23.3667
Coleodactylus meridionalis	-34.8500	-7.7500
Coleodactylus meridionalis	-34.8670	-7.1170
Coleodactylus meridionalis	-35.0749	-7.8706
Coleodactylus meridionalis	-35.1417	-8.6680
Coleodactylus meridionalis	-35.1792	-6.7209
Coleodactylus meridionalis	-35.2223	-5.7221
Coleodactylus meridionalis	-35.3300	-7.6670
Coleodactylus meridionalis	-35.3359	-7.5043
Coleodactylus meridionalis	-35.3840	-7.2520

Coleodactylus meridionalis	-35.4830	-9.2330
Coleodactylus meridionalis	-35.5170	-8.7000
Coleodactylus meridionalis	-35.7038	-6.9675
Coleodactylus meridionalis	-35.8039	-9.5656
Coleodactylus meridionalis	-35.9303	-9.2639
Coleodactylus meridionalis	-35.9550	-9.5800
Coleodactylus meridionalis	-35.9639	-8.2883
Coleodactylus meridionalis	-36.0830	-9.7830
Coleodactylus meridionalis	-36.9072	-10.6510
Coleodactylus meridionalis	-37.5181	-11.5201
Coleodactylus meridionalis	-37.5314	-11.3155
Coleodactylus meridionalis	-37.7670	-9.6450
Coleodactylus meridionalis	-38.0062	-12.5691
Coleodactylus meridionalis	-38.0333	-8.6330
Coleodactylus meridionalis	-38.1290	-12.6370
Coleodactylus meridionalis	-38.1670	-12.7500
Coleodactylus meridionalis	-38.4489	-12.9713
Coleodactylus meridionalis	-38.4790	-12.4113
Coleodactylus meridionalis	-38.7500	-8.5167
Coleodactylus meridionalis	-38.8634	-12.8591
Coleodactylus meridionalis	-38.9172	-4.2303
Coleodactylus meridionalis	-38.9330	-15.6830
Coleodactylus meridionalis	-38.9354	-13.0445
Coleodactylus meridionalis	-39.0160	-14.9500
Coleodactylus meridionalis	-39.0164	-15.2814
Coleodactylus meridionalis	-39.0330	-14.2630
Coleodactylus meridionalis	-39.0704	-14.4152
Coleodactylus meridionalis	-39.0839	-13.3614
Coleodactylus meridionalis	-39.0892	-7.3491
Coleodactylus meridionalis	-39.1552	-14.0248
Coleodactylus meridionalis	-39.2833	-14.5833
Coleodactylus meridionalis	-39.3927	-12.9704
Coleodactylus meridionalis	-39.4686	-16.9723
Coleodactylus meridionalis	-39.6140	-13.9044
Coleodactylus meridionalis	-39.7047	-13.5806
Coleodactylus meridionalis	-39.7240	-7.5120
Coleodactylus meridionalis	-40.4775	-14.8387
Coleodactylus meridionalis	-40.5207	-11.3676
Coleodactylus meridionalis	-41.0825	-11.9212
Coleodactylus meridionalis	-41.2085	-11.5920
Coleodactylus meridionalis	-41.3237	-12.7646

Coleodactylus meridionalis	-41.3500	-9.4830
Coleodactylus meridionalis	-41.3597	-12.6019
Coleodactylus meridionalis	-41.9045	-11.3544
Coleodactylus meridionalis	-42.1167	-11.0333
Coleodactylus meridionalis	-42.5670	-4.7690
Coleodactylus meridionalis	-42.8556	-2.7576
Coleodactylus meridionalis	-43.6562	-10.7158
Coleodactylus meridionalis	-44.9752	-12.3265
Coleodactylus meridionalis	-46.5360	-7.3510
Coleodactylus meridionalis	-47.3340	-3.0740
Coleodactylus meridionalis	-47.4360	-6.7330
Coleodactylus meridionalis	-47.4900	-7.2860
Coleodactylus meridionalis	-47.5300	-6.6700
Coleodactylus meridionalis	-48.0130	-2.6220
Coleodactylus meridionalis	-48.3867	-9.7310
Colobodactylus taunayi	-46.9601	-23.6745
Colobodactylus taunayi	-47.0200	-23.9500
Colobodactylus taunayi	-47.0333	-23.6833
Colobodactylus taunayi	-47.4831	-23.9514
Colobodactylus taunayi	-47.6100	-23.4200
Colobodactylus taunayi	-47.9500	-25.0200
Colobodactylus taunayi	-48.3583	-24.1883
Colobodactylus taunayi	-48.4022	-24.6500
Colobodactylus taunayi	-48.5749	-23.7513
Colobodactylus taunayi	-49.7994	-23.9327
Dendropsophus elegans	-35.3140	-7.5031
Dendropsophus elegans	-35.7932	-8.7389
Dendropsophus elegans	-35.9667	-8.2667
Dendropsophus elegans	-36.1761	-10.1335
Dendropsophus elegans	-36.3503	-9.7795
Dendropsophus elegans	-37.4253	-10.6850
Dendropsophus elegans	-38.2999	-12.5309
Dendropsophus elegans	-39.0232	-14.9377
Dendropsophus elegans	-39.0365	-14.8015
Dendropsophus elegans	-39.0676	-13.3740
Dendropsophus elegans	-39.0929	-16.5846
Dendropsophus elegans	-39.1505	-13.7325
Dendropsophus elegans	-39.2308	-17.3326
Dendropsophus elegans	-39.2914	-14.5868
Dendropsophus elegans	-39.4086	-14.3608
Dendropsophus elegans	-39.4123	-15.2593

Dendropsophus elegans	-39.4882	-15.1694
Dendropsophus elegans	-39.5012	-15.4145
Dendropsophus elegans	-39.8417	-18.3553
Dendropsophus elegans	-39.9925	-19.1098
Dendropsophus elegans	-40.0715	-19.3909
Dendropsophus elegans	-40.0978	-19.1969
Dendropsophus elegans	-40.1184	-19.0235
Dendropsophus elegans	-40.1833	-20.1025
Dendropsophus elegans	-40.2743	-19.8196
Dendropsophus elegans	-40.4948	-20.3893
Dendropsophus elegans	-40.5219	-20.2811
Dendropsophus elegans	-40.6006	-19.9361
Dendropsophus elegans	-40.6592	-20.3633
Dendropsophus elegans	-41.3684	-21.0664
Dendropsophus elegans	-41.6667	-20.5000
Dendropsophus elegans	-42.1500	-20.7166
Dendropsophus elegans	-42.2796	-20.7269
Dendropsophus elegans	-42.4000	-20.6000
Dendropsophus elegans	-43.0398	-22.6567
Dendropsophus elegans	-43.1786	-22.5050
Dendropsophus elegans	-43.3131	-22.7868
Dendropsophus elegans	-43.4166	-20.3779
Dendropsophus elegans	-44.3284	-22.9050
Dendropsophus elegans	-45.0860	-23.4340
Dendropsophus elegans	-45.4598	-22.9236
Dendropsophus elegans	-45.7624	-23.7571
Dendropsophus elegans	-46.1394	-23.8553
Dendropsophus elegans	-46.6300	-23.5400
Dendropsophus elegans	-47.1733	-24.2946
Dendropsophus elegans	-47.5710	-24.6975
Dendropsophus elegans	-47.8840	-24.7102
Dendropsophus elegans	-47.9323	-25.0244
Dendropsophus elegans	-48.5900	-24.5800
Dendropsophus elegans	-48.7119	-25.4286
Dendropsophus elegans	-48.8317	-25.4790
Enyalius catenatus	-35.3801	-7.6047
Enyalius catenatus	-35.5167	-8.7000
Enyalius catenatus	-35.9074	-8.9817
Enyalius catenatus	-36.0340	-8.9845
Enyalius catenatus	-38.0375	-12.5035
Enyalius catenatus	-38.3778	-12.3783

Enyalius catenatus	-38.4042	-12.7847
Enyalius catenatus	-39.0061	-14.2844
Enyalius catenatus	-39.0073	-13.1819
Enyalius catenatus	-39.0333	-14.7833
Enyalius catenatus	-39.0639	-15.1678
Enyalius catenatus	-39.0647	-16.4500
Enyalius catenatus	-39.0667	-14.4167
Enyalius catenatus	-39.1651	-15.2225
Enyalius catenatus	-39.1674	-13.3509
Enyalius catenatus	-39.1749	-17.0485
Enyalius catenatus	-39.2667	-14.5833
Enyalius catenatus	-39.2833	-15.5500
Enyalius catenatus	-39.3500	-15.0833
Enyalius catenatus	-39.4827	-12.8999
Enyalius catenatus	-39.4974	-15.1320
Enyalius catenatus	-39.5192	-15.4445
Enyalius catenatus	-39.6342	-13.0374
Enyalius catenatus	-39.6897	-13.5686
Enyalius catenatus	-40.5196	-11.3692
Enyalius catenatus	-40.5825	-11.7617
Enyalius catenatus	-40.8383	-11.5500
Enyalius catenatus	-41.3597	-12.6019
Enyalius catenatus	-41.9823	-20.4808
Gymnodactylus darwinii	-35.2000	-7.7833
Gymnodactylus darwinii	-35.7333	-9.6500
Gymnodactylus darwinii	-38.0000	-12.5667
Gymnodactylus darwinii	-38.3000	-12.5333
Gymnodactylus darwinii	-39.0333	-14.7833
Gymnodactylus darwinii	-39.0500	-16.4333
Gymnodactylus darwinii	-39.0667	-15.2833
Gymnodactylus darwinii	-39.8167	-19.6333
Gymnodactylus darwinii	-44.7500	-23.3333
Gymnodactylus darwinii	-45.1500	-23.5667
Gymnodactylus darwinii	-45.4000	-23.7500
Heterodactylus imbricatus	-40.5219	-20.2811
Heterodactylus imbricatus	-40.5219	-20.2811
Heterodactylus imbricatus	-41.4835	-13.0519
Heterodactylus imbricatus	-41.4835	-13.0519
Heterodactylus imbricatus	-43.4993	-19.2082
Heterodactylus imbricatus	-43.5500	-19.2600
Heterodactylus imbricatus	-43.5500	-19.2600

Heterodactylus imbricatus	-46.5356	-21.7933
Heterodactylus imbricatus	-46.5356	-21.7933
Heterodactylus imbricatus	-47.1500	-23.5667
Heterodactylus imbricatus	-47.1500	-23.5667
Hypsiboas albomarginatus	-35.0497	-8.2368
Hypsiboas albomarginatus	-35.3167	-7.5167
Hypsiboas albomarginatus	-35.8642	-8.9822
Hypsiboas albomarginatus	-36.0250	-8.3736
Hypsiboas albomarginatus	-38.1410	-12.4738
Hypsiboas albomarginatus	-38.5167	-12.9833
Hypsiboas albomarginatus	-39.0000	-12.1689
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Hypsiboas albomarginatus	-39.1600	-14.3634
Hypsiboas albomarginatus	-39.4728	-13.7865
Hypsiboas albomarginatus	-39.4974	-15.1320
Hypsiboas albomarginatus	-39.5192	-15.4445
Hypsiboas albomarginatus	-39.6342	-13.0374
Hypsiboas albomarginatus	-40.5307	-19.9482
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Hypsiboas albomarginatus	-41.3000	-21.7500
Hypsiboas albomarginatus	-41.3265	-21.0471
Hypsiboas albomarginatus	-41.7167	-20.3167
Hypsiboas albomarginatus	-41.7225	-17.7451
Hypsiboas albomarginatus	-42.6133	-19.7056
Hypsiboas albomarginatus	-43.1132	-22.6121
Hypsiboas albomarginatus	-43.4331	-22.8775
Hypsiboas albomarginatus	-44.3263	-22.9294
Hypsiboas albomarginatus	-45.0459	-23.1546
Hypsiboas albomarginatus	-46.3167	-23.5200
Hypsiboas albomarginatus	-46.5501	-23.8122
Hypsiboas albomarginatus	-47.0240	-23.9547
Hypsiboas albomarginatus	-47.1489	-24.2997
Hypsiboas albomarginatus	-47.7160	-24.8590
Hypsiboas albomarginatus	-48.0795	-24.5336
Hypsiboas albomarginatus	-48.6163	-27.1731
Hypsiboas albomarginatus	-49.2333	-26.4333
Hypsiboas faber	-35.8448	-8.7132
Hypsiboas faber	-36.2840	-9.8096
Hypsiboas faber	-37.4217	-10.6853
Hypsiboas faber	-39.1167	-16.5542

Hypsiboas faber	-39.3800	-12.9759
Hypsiboas faber	-39.4179	-15.2353
Hypsiboas faber	-40.0716	-19.1506
Hypsiboas faber	-40.5307	-19.9482
Hypsiboas faber	-40.5787	-14.9032
Hypsiboas faber	-41.3265	-21.0471
Hypsiboas faber	-41.4835	-13.0519
Hypsiboas faber	-41.7245	-17.7434
Hypsiboas faber	-42.6133	-19.7056
Hypsiboas faber	-43.1610	-22.4017
Hypsiboas faber	-43.3316	-20.3292
Hypsiboas faber	-44.1990	-19.9471
Hypsiboas faber	-45.0459	-23.1546
Hypsiboas faber	-45.8933	-23.6508
Hypsiboas faber	-47.4378	-23.7865
Hypsiboas faber	-48.5749	-23.7513
Hypsiboas faber	-48.7869	-22.1698
Hypsiboas faber	-48.8748	-25.4334
Hypsiboas faber	-49.2333	-26.4333
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Hypsiboas faber	-49.7840	-23.8540
Hypsiboas faber	-50.9476	-24.1343
Hypsiboas faber	-50.9806	-29.6143
Hypsiboas semilineatus	-39.1242	-16.5350
Hypsiboas semilineatus	-39.4179	-15.2353
Hypsiboas semilineatus	-39.6342	-13.0374
Hypsiboas semilineatus	-39.6433	-13.9712
Hypsiboas semilineatus	-40.0290	-19.1517
Hypsiboas semilineatus	-40.6325	-19.8768
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Hypsiboas semilineatus	-45.0459	-23.1546
Hypsiboas semilineatus	-45.9971	-23.7934
Hypsiboas semilineatus	-47.1489	-24.2997
Leposoma scincoides	-39.0333	-14.7833
Leposoma scincoides	-39.0667	-16.4500
Leposoma scincoides	-39.1167	-16.5333
Leposoma scincoides	-39.1350	-14.3851

Leposoma scincoides	-39.1713	-14.7950
Leposoma scincoides	-39.2667	-14.7833
Leposoma scincoides	-39.3433	-15.1664
Leposoma scincoides	-39.5200	-15.4400
Leposoma scincoides	-39.5250	-16.1555
Leposoma scincoides	-39.5339	-15.9508
Leposoma scincoides	-39.5436	-15.3866
Leposoma scincoides	-39.6535	-15.3865
Leposoma scincoides	-39.6550	-15.1926
Leposoma scincoides	-39.8803	-19.6319
Leposoma scincoides	-40.0667	-19.1500
Leposoma scincoides	-40.1513	-19.2766
Leposoma scincoides	-40.5167	-11.3833
Leposoma scincoides	-40.5200	-19.9600
Leposoma scincoides	-40.5787	-14.8810
Leposoma scincoides	-40.9695	-16.3460
Leposoma scincoides	-41.0117	-16.3333
Mabuya dorsivittata	-41.8006	-20.3936
Mabuya dorsivittata	-41.8650	-20.4585
Mabuya dorsivittata	-43.5315	-19.2591
Mabuya dorsivittata	-43.5907	-19.2891
Mabuya dorsivittata	-44.3928	-22.7286
Mabuya dorsivittata	-44.9416	-23.0522
Mabuya dorsivittata	-46.6474	-23.6497
Mabuya dorsivittata	-46.9150	-23.4490
Mabuya dorsivittata	-46.9601	-23.6745
Mabuya dorsivittata	-47.6064	-23.4380
Mabuya dorsivittata	-47.6284	-23.4039
Mabuya dorsivittata	-48.3583	-24.1883
Mabuya dorsivittata	-48.5749	-23.7513
Mabuya dorsivittata	-52.1727	-21.9096
Melanophryniscus	-48.6911	-25.6253
Melanophryniscus	-48.7194	-24.8550
Melanophryniscus	-48.8208	-25.1303
Melanophryniscus	-48.8358	-25.2442
Melanophryniscus	-48.8586	-25.6119
Melanophryniscus	-48.9319	-26.7986
Melanophryniscus	-48.9897	-26.1644
Melanophryniscus	-48.9964	-26.0217
Melanophryniscus	-49.1786	-26.1467
Melanophryniscus	-50.0044	-25.2475

Phyllomedusa complex	-37.3153	-10.7578
Phyllomedusa complex	-39.0636	-14.7822
Phyllomedusa complex	-39.2844	-14.5931
Phyllomedusa complex	-39.5087	-15.4164
Phyllomedusa complex	-39.5395	-14.5734
Phyllomedusa complex	-40.0722	-19.3911
Phyllomedusa complex	-40.2733	-19.8203
Phyllomedusa complex	-40.4308	-13.4411
Phyllomedusa complex	-42.9024	-16.5909
Phyllomedusa complex	-46.9439	-23.2496
Phyllomedusa complex	-47.6755	-22.3472
Phyllomedusa complex	-47.7164	-23.8131
Phyllomedusa complex	-47.8811	-24.7150
Phyllomedusa complex	-48.5928	-23.7975
Phyllomedusa complex	-48.6324	-25.8694
Phyllomedusa complex	-48.7003	-24.5328
Phyllomedusa complex	-48.7119	-25.4286
Phyllomedusa complex	-48.7430	-24.3586
Phyllomedusa complex	-48.7657	-26.7222
Phyllomedusa complex	-49.3786	-26.2503
Phyllomedusa complex	-49.4575	-28.5156
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Phyllomedusa complex	-52.4550	-26.6314
Phyllomedusa complex	-53.5653	-30.1606
Phyllomedusa complex	-53.6725	-31.5581
Phyllomedusa complex	-53.8069	-29.6842
Placosoma glabellum	-42.9831	-22.4331
Placosoma glabellum	-43.5284	-19.2244
Placosoma glabellum	-44.3928	-22.7286
Placosoma glabellum	-44.8333	-23.3667
Placosoma glabellum	-45.3342	-23.4200
Placosoma glabellum	-45.4167	-23.8000
Placosoma glabellum	-45.8667	-23.6333
Placosoma glabellum	-47.0333	-23.6833
Placosoma glabellum	-47.0700	-23.9272
Placosoma glabellum	-47.5500	-24.7167
Placosoma glabellum	-47.7000	-23.8167

Placosoma glabellum	-48.4022	-24.6500
Placosoma glabellum	-48.5667	-25.9000
Placosoma glabellum	-48.5833	-24.5833
Proceratophrys boiei	-40.6325	-19.8768
Proceratophrys boiei	-41.0027	-20.6450
Proceratophrys boiei	-41.4336	-20.4272
Proceratophrys boiei	-41.7495	-19.7575
Proceratophrys boiei	-41.8489	-20.4192
Proceratophrys boiei	-41.9872	-19.9986
Proceratophrys boiei	-42.0359	-20.7815
Proceratophrys boiei	-42.0359	-22.0348
Proceratophrys boiei	-42.1020	-19.7118
Proceratophrys boiei	-42.2237	-21.0141
Proceratophrys boiei	-42.5013	-22.3194
Proceratophrys boiei	-42.7286	-22.5157
Proceratophrys boiei	-42.8734	-22.3135
Proceratophrys boiei	-42.8858	-20.7401
Proceratophrys boiei	-43.1140	-22.1239
Proceratophrys boiei	-43.1610	-22.4017
Proceratophrys boiei	-43.2600	-20.2600
Proceratophrys boiei	-43.2896	-21.6064
Proceratophrys boiei	-43.2999	-22.6314
Proceratophrys boiei	-43.3216	-19.8176
Proceratophrys boiei	-43.4052	-22.3657
Proceratophrys boiei	-43.4081	-20.0754
Proceratophrys boiei	-43.4690	-21.9856
Proceratophrys boiei	-43.6103	-20.3910
Proceratophrys boiei	-43.6372	-19.8678
Proceratophrys boiei	-43.7183	-19.4407
Proceratophrys boiei	-43.8788	-22.0409
Proceratophrys boiei	-43.9597	-19.9024
Proceratophrys boiei	-44.1248	-21.9467
Proceratophrys boiei	-44.1548	-21.1168
Proceratophrys boiei	-44.1882	-22.5062
Proceratophrys boiei	-44.1990	-19.9471
Proceratophrys boiei	-44.4830	-22.2158
Proceratophrys boiei	-44.5836	-22.4385
Proceratophrys boiei	-44.8200	-22.6200
Proceratophrys boiei	-44.8222	-21.2915
Proceratophrys boiei	-45.0657	-21.0779
Proceratophrys boiei	-45.1800	-23.1100

Proceratophrys boiei	-45.2322	-22.7928
Proceratophrys boiei	-45.3777	-22.0009
Proceratophrys boiei	-45.6300	-22.7200
Proceratophrys boiei	-45.6875	-23.3125
Proceratophrys boiei	-45.9665	-21.3893
Proceratophrys boiei	-46.1100	-22.4800
Proceratophrys boiei	-46.1872	-23.5681
Proceratophrys boiei	-46.3023	-23.0465
Proceratophrys boiei	-46.3045	-22.6319
Proceratophrys boiei	-46.5863	-23.1227
Proceratophrys boiei	-46.6000	-23.3667
Proceratophrys boiei	-46.6220	-20.7190
Proceratophrys boiei	-46.8137	-23.0060
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Proceratophrys boiei	-47.0118	-23.4116
Proceratophrys boiei	-47.0437	-22.8834
Proceratophrys boiei	-47.0625	-23.9375
Proceratophrys boiei	-47.4375	-23.6875
Proceratophrys boiei	-47.6289	-23.4039
Proceratophrys boiei	-47.7280	-23.8560
Proceratophrys boiei	-47.9667	-25.1333
Proceratophrys boiei	-48.0300	-24.3300
Proceratophrys boiei	-48.0531	-24.7757
Proceratophrys boiei	-48.2895	-24.0386
Proceratophrys boiei	-48.4679	-22.8624
Proceratophrys boiei	-48.5458	-24.5119
Proceratophrys boiei	-48.5749	-23.7513
Proceratophrys boiei	-48.5837	-25.5838
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Proceratophrys boiei	-48.7775	-24.2556
Proceratophrys boiei	-48.7869	-22.1698
Proceratophrys boiei	-48.9632	-26.2469
Proceratophrys boiei	-49.0543	-25.4710
Proceratophrys boiei	-49.3275	-26.4387
Proceratophrys boiei	-49.4550	-28.3844
Proceratophrys boiei	-49.5337	-27.0156
Proceratophrys renalis	-35.1833	-8.0167
Proceratophrys renalis	-35.3667	-7.6000
Proceratophrys renalis	-35.8333	-8.7167
Proceratophrys renalis	-36.0167	-8.3667
Proceratophrys renalis	-36.4000	-8.2000

Proceratophrys renalis	-38.7167	-3.8833
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Pyriglena complex	-37.9710	-12.2550
Pyriglena complex	-38.4080	-12.4480
Pyriglena complex	-38.4610	-12.5110
Pyriglena complex	-39.0980	-13.0230
Pyriglena complex	-39.2830	-16.5030
Pyriglena complex	-39.5330	-16.7450
Pyriglena complex	-39.8720	-16.1560
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Pyriglena complex	-40.0690	-16.4210
Pyriglena complex	-40.1160	-19.0090
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Pyriglena complex	-40.6070	-12.6630
Pyriglena complex	-40.6130	-19.9250
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Pyriglena complex	-41.0030	-16.4340
Pyriglena complex	-41.2150	-11.9130
Pyriglena complex	-41.3630	-12.4330
Pyriglena complex	-41.5390	-12.9500
Pyriglena complex	-42.3020	-22.0340
Pyriglena complex	-42.5020	-17.0650
Pyriglena complex	-42.6620	-22.0570
Pyriglena complex	-43.0100	-22.5210
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Pyriglena complex	-43.6780	-19.8150
Pyriglena complex	-43.7640	-20.4350
Pyriglena complex	-44.7260	-22.4890
Pyriglena complex	-44.7830	-21.2170
Pyriglena complex	-45.0700	-23.4350
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Pyriglena complex	-45.8670	-23.6330
Pyriglena complex	-46.7430	-23.9850
Pyriglena complex	-46.9830	-23.7000
Pyriglena complex	-47.0870	-23.9320
Pyriglena complex	-47.4190	-23.7110
Pyriglena complex	-48.1000	-20.6830
Pyriglena complex	-48.5670	-23.7170
Pyriglena complex	-48.5950	-24.5870
Pyriglena complex	-49.1310	-25.3330

Pyriglena complex	-50.0500	-23.9670
Pyriglena complex	-50.6930	-24.0560
Pyriglena complex	-52.2470	-22.6990
Pyriglena complex	-54.4780	-25.9340
Pyriglena complex	-55.5400	-27.2500
Pyriglena complex	-55.7330	-26.1170
Rhinella crucifer group	-34.9478	-7.8242
Rhinella crucifer group	-39.1470	-16.8002
Rhinella crucifer group	-39.2897	-14.5867
Rhinella crucifer group	-39.3222	-14.3384
Rhinella crucifer group	-39.8170	-19.5507
Rhinella crucifer group	-40.3277	-20.4186
Rhinella crucifer group	-40.5400	-19.9589
Rhinella crucifer group	-41.0100	-20.4733
Rhinella crucifer group	-41.8537	-20.4214
Rhinella crucifer group	-42.9866	-22.4491
Rhinella crucifer group	-43.7123	-22.7256
Rhinella crucifer group	-44.2417	-15.1225
Rhinella crucifer group	-44.5945	-23.0440
Rhinella crucifer group	-44.8253	-23.3646
Rhinella crucifer group	-45.1216	-23.3449
Rhinella crucifer group	-45.2333	-22.2500
Rhinella crucifer group	-45.4097	-23.6075
Rhinella crucifer group	-45.7274	-23.7021
Rhinella crucifer group	-46.2998	-23.8162
Rhinella crucifer group	-46.6036	-21.6774
Rhinella crucifer group	-46.7456	-23.9962
Rhinella crucifer group	-46.9357	-23.5955
Rhinella crucifer group	-46.9669	-23.2169
Rhinella crucifer group	-47.2263	-24.5661
Rhinella crucifer group	-47.3277	-23.7750
Rhinella crucifer group	-47.5229	-22.4119
Rhinella crucifer group	-47.6290	-21.6295
Rhinella crucifer group	-47.8314	-22.2367
Rhinella crucifer group	-48.4647	-24.2201
Rhinella crucifer group	-48.5408	-25.7856
Rhinella crucifer group	-48.6218	-27.0902
Rhinella crucifer group	-49.0101	-25.3107
Rhinella crucifer group	-49.0217	-27.6725
Rhinella crucifer group	-49.0273	-26.7443
Rhinella crucifer group	-49.0916	-22.2355

Rhinella crucifer group	-49.5175	-28.4704
Rhinella crucifer group	-50.0809	-29.0332
Rhinella crucifer group	-50.0989	-25.5717
Rhinella crucifer group	-51.0565	-30.0709
Rhinella crucifer group	-51.2625	-29.1416
Rhinella crucifer group	-51.6119	-27.3436
Rhinella crucifer group	-51.8122	-30.8511
Rhinella crucifer group	-52.1917	-28.2783
Rhinella crucifer group	-52.3013	-22.6057
Rhinella crucifer group	-52.4102	-27.0386
Rhinella crucifer group	-53.8431	-29.7939
Rhinella crucifer group	-54.9520	-27.0888
Vitreorana eurygnatha	-39.5436	-15.4199
Vitreorana eurygnatha	-40.9920	-16.3491
Vitreorana eurygnatha	-41.8425	-20.5750
Vitreorana eurygnatha	-41.9823	-20.4808
Vitreorana eurygnatha	-43.6214	-19.3333
Vitreorana eurygnatha	-44.4779	-22.8864
Vitreorana eurygnatha	-44.5628	-22.4958
Vitreorana eurygnatha	-44.7319	-22.3728
Vitreorana eurygnatha	-45.4586	-22.7006
Vitreorana eurygnatha	-45.5900	-22.7300
Vitreorana eurygnatha	-45.8736	-23.7564
Vitreorana eurygnatha	-46.5356	-21.7933
Vitreorana eurygnatha	-46.5667	-21.9167
Vitreorana eurygnatha	-46.6333	-23.8667
Vitreorana eurygnatha	-47.0250	-23.8682
Vitreorana eurygnatha	-53.2845	-28.3709
Vitreorana uranoscopa	-39.5501	-15.3803
Vitreorana uranoscopa	-41.7922	-20.5894
Vitreorana uranoscopa	-41.8431	-20.4086
Vitreorana uranoscopa	-43.1571	-22.7730
Vitreorana uranoscopa	-43.2999	-22.6314
Vitreorana uranoscopa	-43.8589	-20.5314
Vitreorana uranoscopa	-43.8908	-20.0694
Vitreorana uranoscopa	-44.0663	-22.9320
Vitreorana uranoscopa	-44.4775	-22.8861
Vitreorana uranoscopa	-44.5628	-22.4958
Vitreorana uranoscopa	-45.3100	-23.2217
Vitreorana uranoscopa	-45.4117	-21.5656
Vitreorana uranoscopa	-45.4422	-22.6808

Vitreorana uranoscopa	-45.9351	-23.5869
Vitreorana uranoscopa	-46.3117	-23.7765
Vitreorana uranoscopa	-46.6333	-23.8667
Vitreorana uranoscopa	-46.6474	-23.6497
Vitreorana uranoscopa	-46.8348	-24.0907
Vitreorana uranoscopa	-46.9971	-23.8795
Vitreorana uranoscopa	-47.4086	-23.7167
Vitreorana uranoscopa	-47.9667	-25.1336
Vitreorana uranoscopa	-48.5914	-24.5850
Vitreorana uranoscopa	-49.3831	-26.3119
Vitreorana uranoscopa	-49.5033	-28.4992
Vitreorana uranoscopa	-49.5364	-28.5628
Vitreorana uranoscopa	-49.7994	-23.9327
Vitreorana uranoscopa	-51.0874	-24.1581
Vitreorana uranoscopa	-51.2414	-27.3772
Vitreorana uranoscopa	-52.0222	-25.5131
Vitreorana uranoscopa	-52.4147	-26.8667
Vitreorana uranoscopa	-52.4489	-27.0689
Vitreorana uranoscopa	-52.5569	-26.5642
Xiphorhynchus fuscus	-35.8667	-8.9833
Xiphorhynchus fuscus	-38.9167	-4.2958
Xiphorhynchus fuscus	-38.9333	-4.2333
Xiphorhynchus fuscus	-39.9167	-19.0500
Xiphorhynchus fuscus	-40.0333	-16.0833
Xiphorhynchus fuscus	-40.2833	-17.3667
Xiphorhynchus fuscus	-40.5667	-19.9333
Xiphorhynchus fuscus	-41.0000	-16.3330
Xiphorhynchus fuscus	-41.2000	-11.9000
Xiphorhynchus fuscus	-41.3500	-12.4167
Xiphorhynchus fuscus	-42.0833	-20.8333
Xiphorhynchus fuscus	-42.5500	-22.0000
Xiphorhynchus fuscus	-43.8167	-19.9833
Xiphorhynchus fuscus	-44.3167	-22.6833
Xiphorhynchus fuscus	-44.6333	-22.4000
Xiphorhynchus fuscus	-46.9833	-23.7000
Xiphorhynchus fuscus	-47.1500	-23.5667
Xiphorhynchus fuscus	-48.2167	-22.6333
Xiphorhynchus fuscus	-49.0333	-27.6833
Xiphorhynchus fuscus	-49.7833	-22.8500
Xiphorhynchus fuscus	-52.3000	-22.5000
Xiphorhynchus fuscus	-55.6500	-27.3660