**Supplementary Figure 1. AIC scores and Moran's I values for spatial autoregressive (SAR) models. a-d,** AIC values for increasing neighbourhood sizes and weighting regimes show that inverse weighting by distance performed the best across analyses and that all SAR models were a much better fit than simple linear models. The dependent variable and whether grid cells with no coral snakes present were included is given in panel titles and correspond to E-H below. **e-h,** Moran's I values for linear and SAR models show that the best fit SAR models removed most of the spatial autocorrelation present in the data. Best fit neighbourhood size and *P* values (full model above, coral snake effect below) are given at the top of each panel.
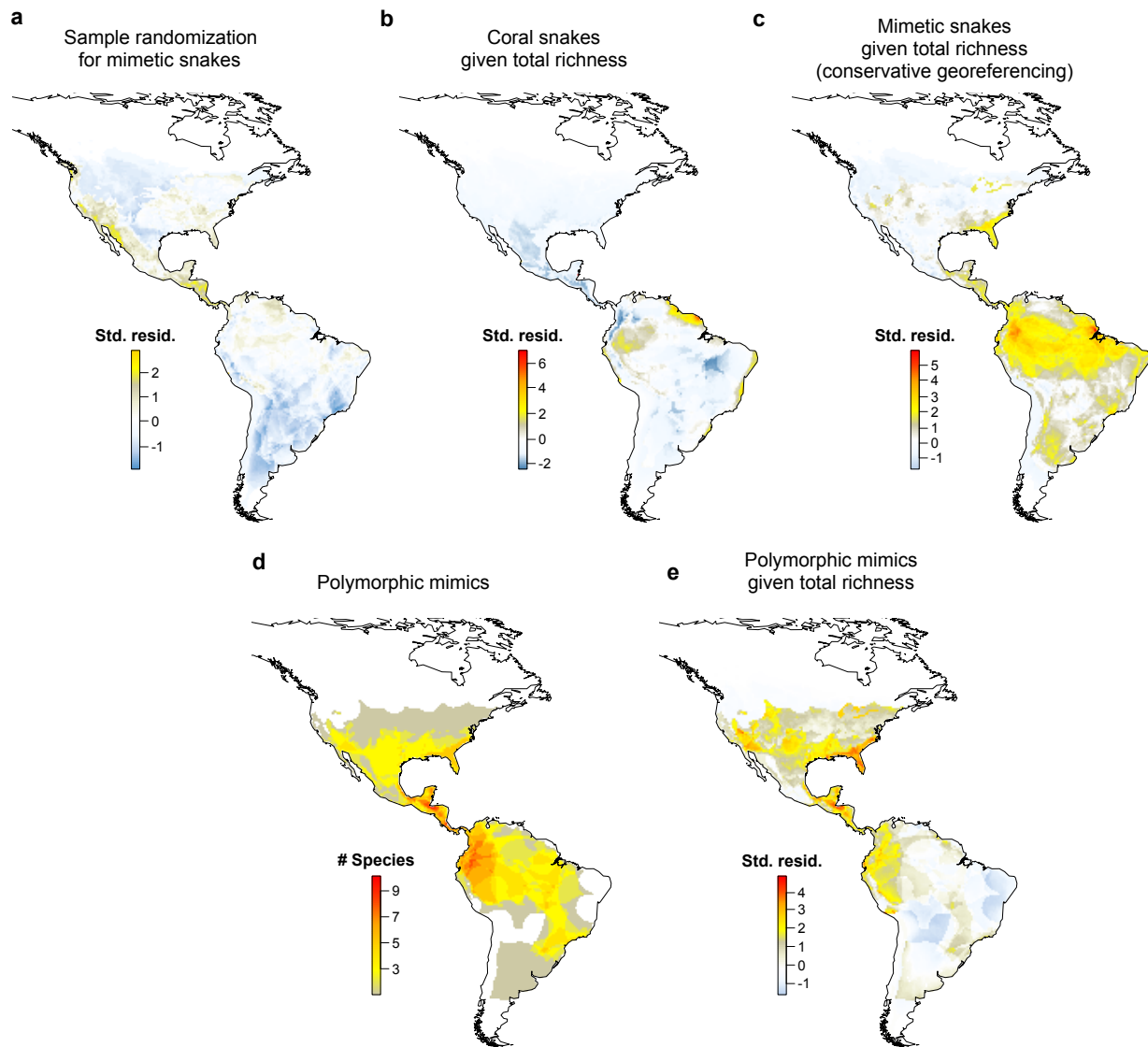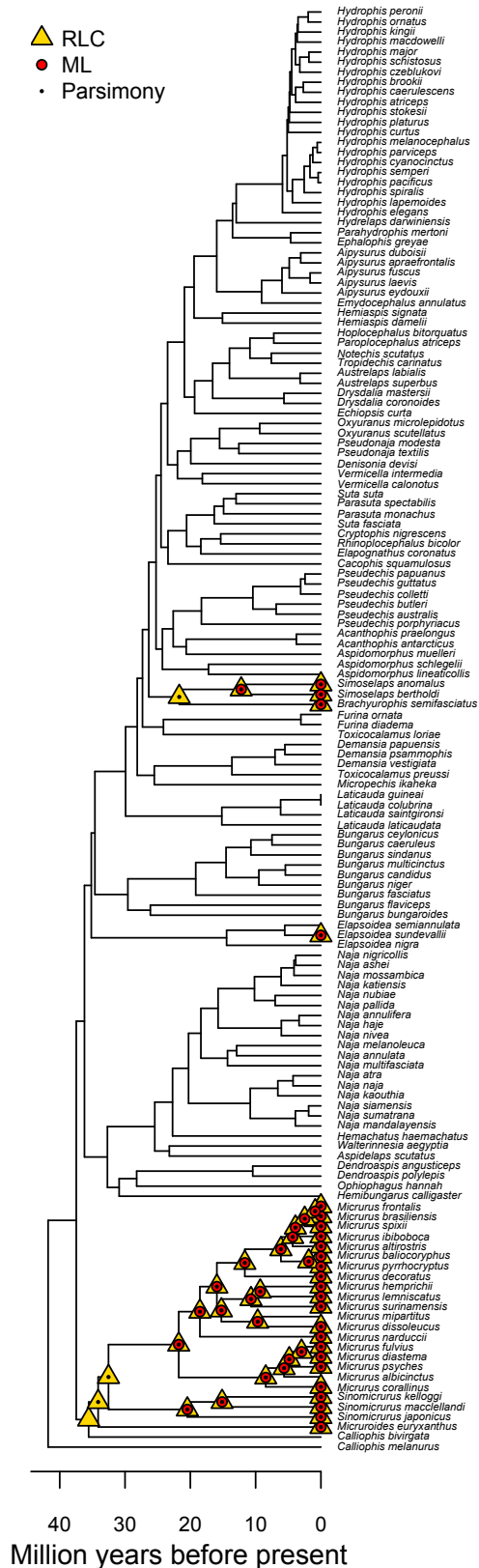
Supplementary Figure 2. Supplementary spatial plots for mimicry and polymorphism. a, Standardised residuals of mimetic snakes for a single randomisation compared to the simulated means for each grid cell confirm that the null distributions perform well (nearly all grid cell values between ±2 s.d. and minimal spatial pattern to outlier cells). Yellow and warmer colours denote significant positive deviation in all panels. **b,** Standardised residuals of observed coral snakes to simulated means confirm no complex interaction effect between coral snake and overall species richness. **c,** Standardised residuals of observed mimicry data under a conservative georeferencing regime are qualitatively similar to results with non-georeferenced records placed randomly within collection state (Fig. 1d). **d,** Observed species richness distribution of mimetic species with colour polymorphism (*n* = 46 species). **e,** Standardised residuals of polymorphic mimics show a more complicated geographic pattern in which polymorphism is high both in areas with many coral snake species (western Amazon, Central America) as well as in allopatry to coral snakes (western United States).
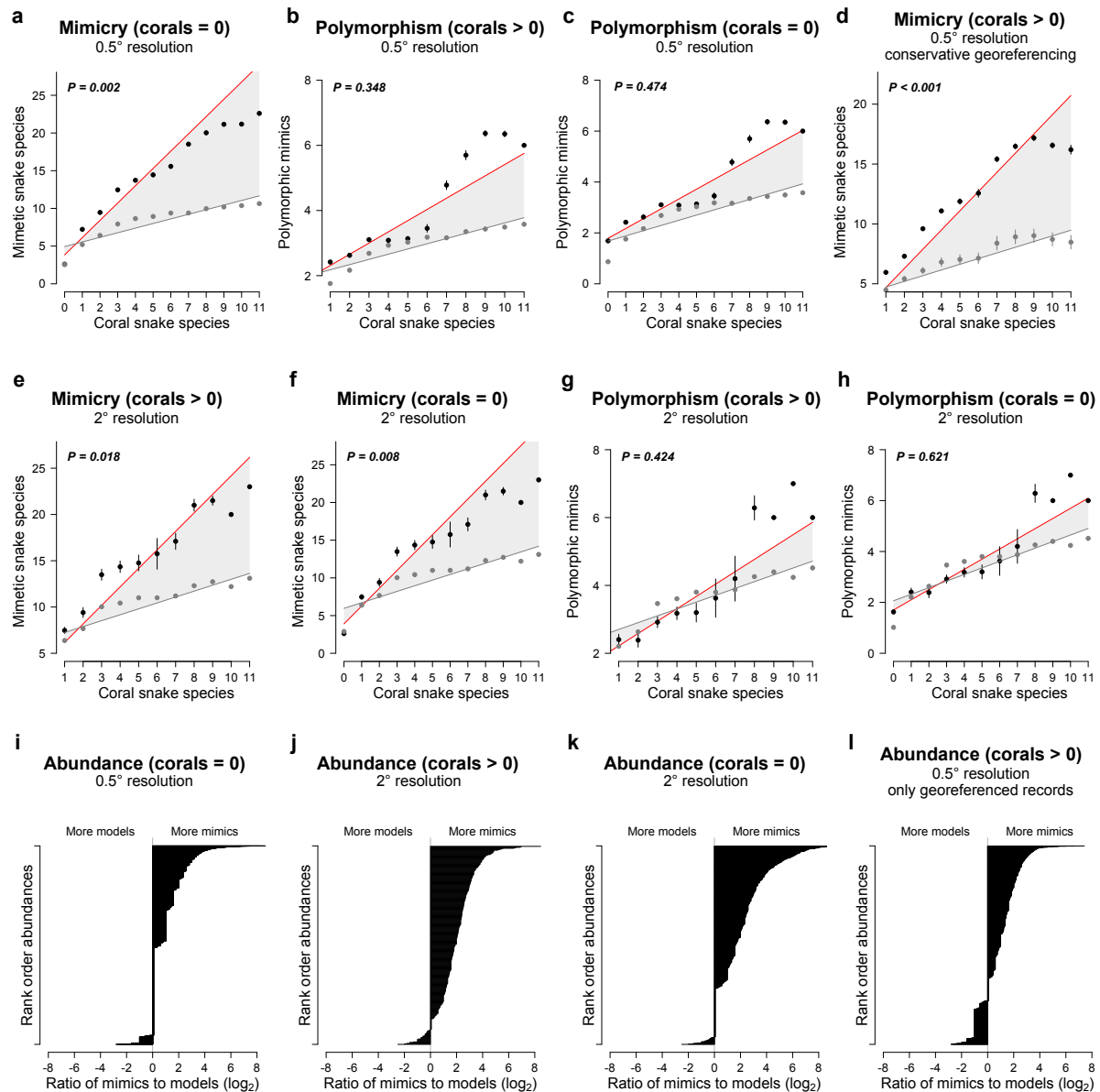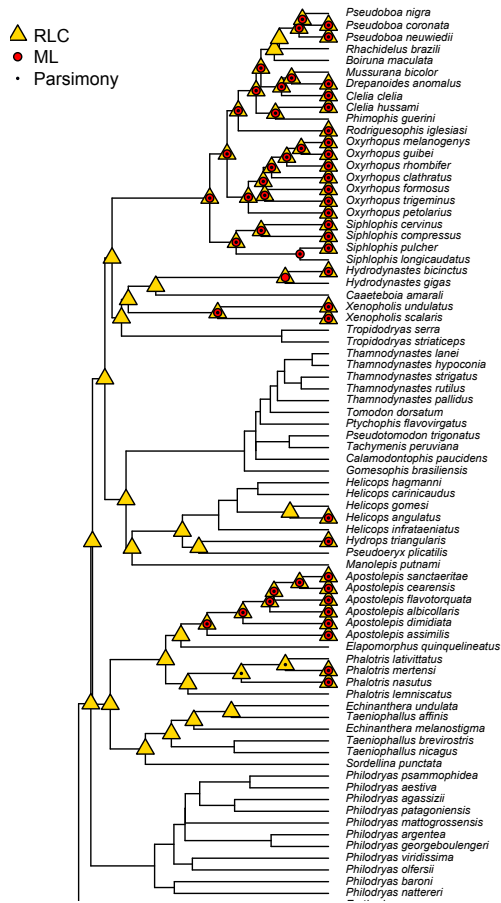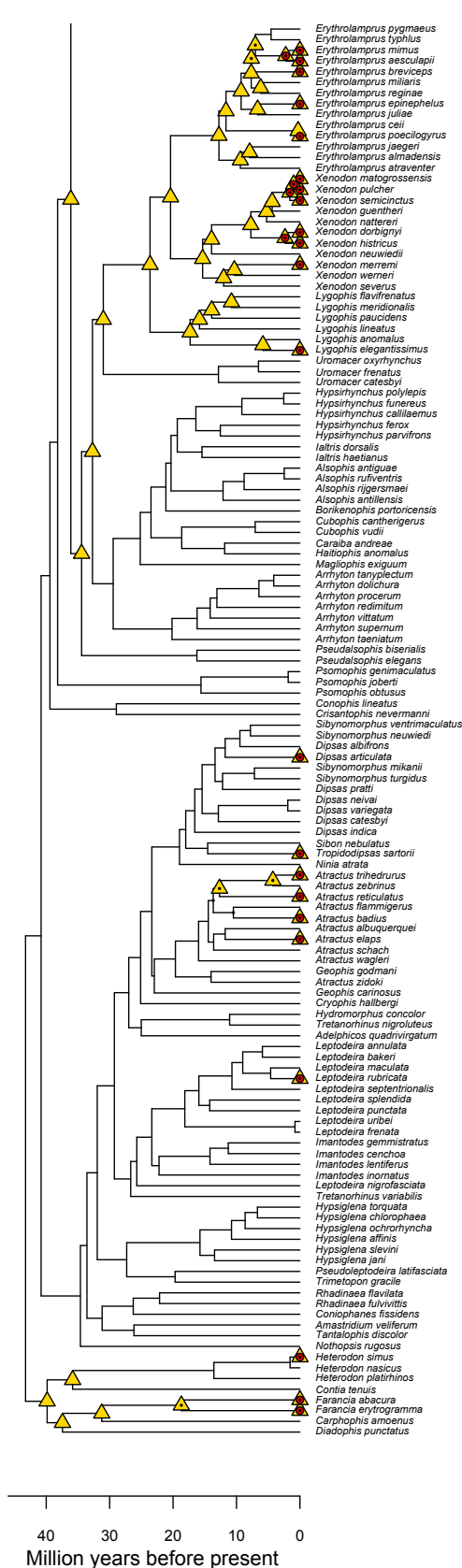
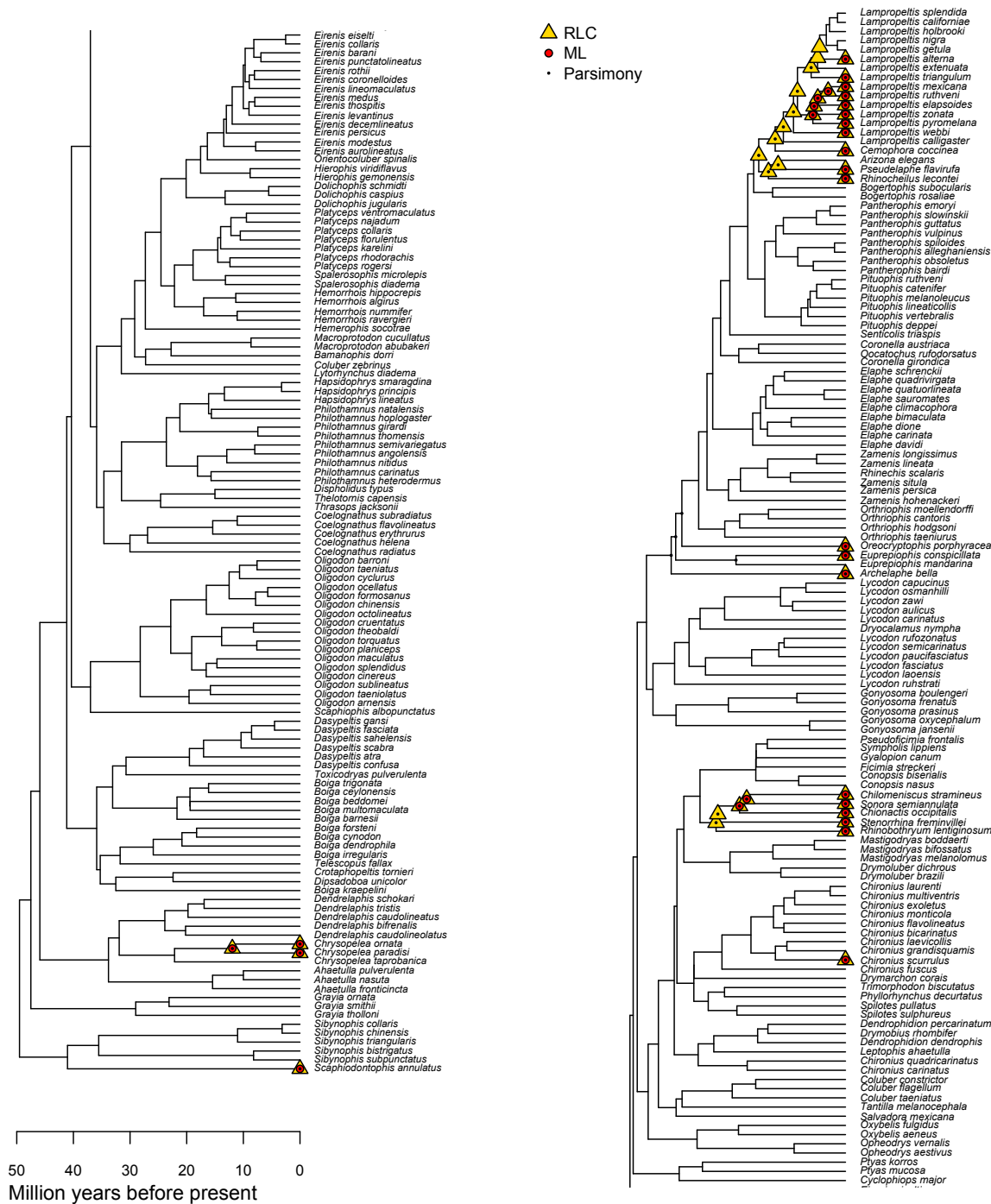**Supplementary Figure 3. Supplementary regression and abundance plots.**
a, Regression models including grid cells containing no coral snakes show the same result as regressions with only cells where coral snakes are present (Fig. 2a). For all regression plots, black points are observed data and grey dots are expected values from simulation. **b,** Weak but nonsignificant positive correlation between the number of polymorphic mimics and number of coral snakes, excluding cells with no coral snakes. **c,** Weak but nonsignificant positive correlation between polymorphism and coral snakes when including cells with no coral snakes. **d,** More conservative placement of non-georeferenced occurrences shows the same result as our original georeferencing pipeline (Fig. 2a). **e-h,** Repeated richness analyses at a 2° grid cell resolution. **i,** Abundance plot including grid cells with no coral snakes show increased ratios of 0 but do not change the overall conclusion that mimetic snakes are often more abundant than coral snakes. **j-k,** Repeated abundance analyses at a 2° grid cell resolution. **l,** Using only georeferenced occurrence records show the same pattern as the full record set (Fig. 2b).

RLC
ML
Parsimony

Hydrophis peronii
Hydrophis ornatus
Hydrophis kingii
Hydrophis macdowelli
Hydrophis major
Hydrophis schistosus
Hydrophis czeblukovi
Hydrophis brookii
Hydrophis caerulescens
Hydrophis atriceps
Hydrophis stokesii
Hydrophis platurus
Hydrophis curtus
Hydrophis melanocephalus
Hydrophis parviceps
Hydrophis cyanocinctus
Hydrophis semperi
Hydrophis pacificus
Hydrophis spiralis
Hydrophis lapemoides
Hydrophis elegans
Hydrelaps darwiniensis
Parahydrophis mertoni
Ephalophis greyae
Aipysurus duboisii
Aipysurus apraefrontalis
Aipysurus fuscus
Aipysurus laevis
Aipysurus eydouxii
Emydocephalus annulatus
Hemiaspis signata
Hemiaspis damelii
Hoplocephalus bitorquatus
Paroplocephalus atriceps
Notechis scutatus
Tropidechis carinatus
Austrelaps labialis
Austrelaps superbus
Drysdalia mastersii
Drysdalia coronoides
Echiopsis curta
Oxyuranus microlepidotus
Oxyuranus scutellatus
Pseudonaja modesta
Pseudonaja textilis
Denisonia devisi
Vermicella intermedia
Vermicella calonotus
Suta suta
Parasuta spectabilis
Parasuta monachus
Suta fasciata
Cryptophis nigrescens
Rhinoplocephalus bicolor
Elapognathus coronatus
Cacophis squamulosus
Pseudechis papuanus
Pseudechis guttatus
Pseudechis colletti
Pseudechis butleri
Pseudechis australis
Pseudechis porphyriacus
Acanthophis praelongus
Acanthophis antarcticus
Aspidomorphus muelleri
Aspidomorphus schlegelii
Aspidomorphus lineaticollis
Simoselaps anomalus
Simoselaps bertholdi
Brachyurophis semifasciatus
Furina ornata
Furina diadema
Toxicocalamus loriae
Demansia papuensis
Demansia psammophis
Demansia vestigiata
Toxicocalamus preussi
Micropechis ikaheka
Laticauda guineai
Laticauda colubrina
Laticauda saintgironsi
Laticauda laticaudata
Bungarus ceylonicus
Bungarus caeruleus
Bungarus sindanus
Bungarus multicinctus
Bungarus candidus
Bungarus niger
Bungarus fasciatus
Bungarus flaviceps
Bungarus bungaroides
Elapsoidea semiannulata
Elapsoidea sundevallii
Elapsoidea nigra
Naja nigricollis
Naja ashei
Naja mossambica
Naja katiensis
Naja nubiae
Naja pallida
Naja annulifera
Naja haje
Naja nivea
Naja melanoleuca
Naja annulata
Naja multifasciata
Naja atra
Naja naja
Naja kaouthia
Naja siamensis
Naja sumatrana
Naja mandalayensis
Hemachatus haemachatus
Walterinnesia aegyptia
Aspidelaps scutatus
Dendroaspis angusticeps
Dendroaspis polylepis
Ophiophagus hannah
Hemibungarus calligaster
Micrurus frontalis
Micrurus brasiliensis
Micrurus spixii
Micrurus ibiboboca
Micrurus altirostris
Micrurus baliocoryphus
Micrurus pyrrhocryptus
Micrurus decoratus
Micrurus hemprichii
Micrurus lemniscatus
Micrurus surinamensis
Micrurus mipartitus
Micrurus dissoleucus
Micrurus narducii
Micrurus fulvius
Micrurus diastema
Micrurus psyches
Micrurus albicinctus
Micrurus corallinus
Sinomicrurus kelloggi
Sinomicrurus macclellandi
Sinomicrurus japonicus
Micruroides euryxanthus
Calliophis bivirgata
Calliophis melanurus

40   30   20   10   0
Million years before present

Supplementary Figure 4. Red-black banded (RBB) warning coloration in Elapidae. Character reconstructions for the snake family Elapidae using three different methods show multiple independent origins of RBB coloration. Marked nodes are those reconstructed as red-black banded.

4

Supplementary Figure 5. Red-black banded (RBB) mimetic coloration in Dipsadines. Character reconstructions for the subfamily Dipsadinae (family Colubridae) using three different methods show multiple independent origins of RBB coloration. Marked nodes are those reconstructed as red-black banded. Tree fragment on the right follows from the top of the tree fragment on the left.
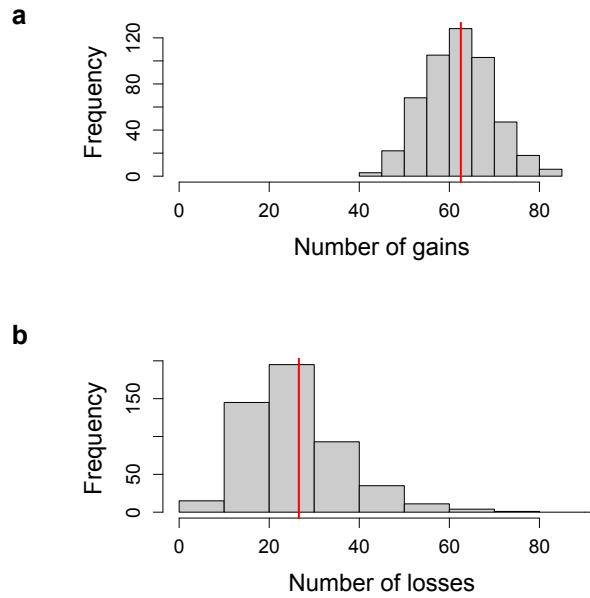
**Supplementary Figure 6. Red-black banded (RBB) mimetic coloration in Colubrines.**
Character reconstructions for the subfamily Colubrinae (family Colubridae) using three different methods show multiple independent origins of RBB coloration. Marked nodes are those reconstructed as red-black banded. Tree fragment on the right follows from the top of the tree fragment on the left.
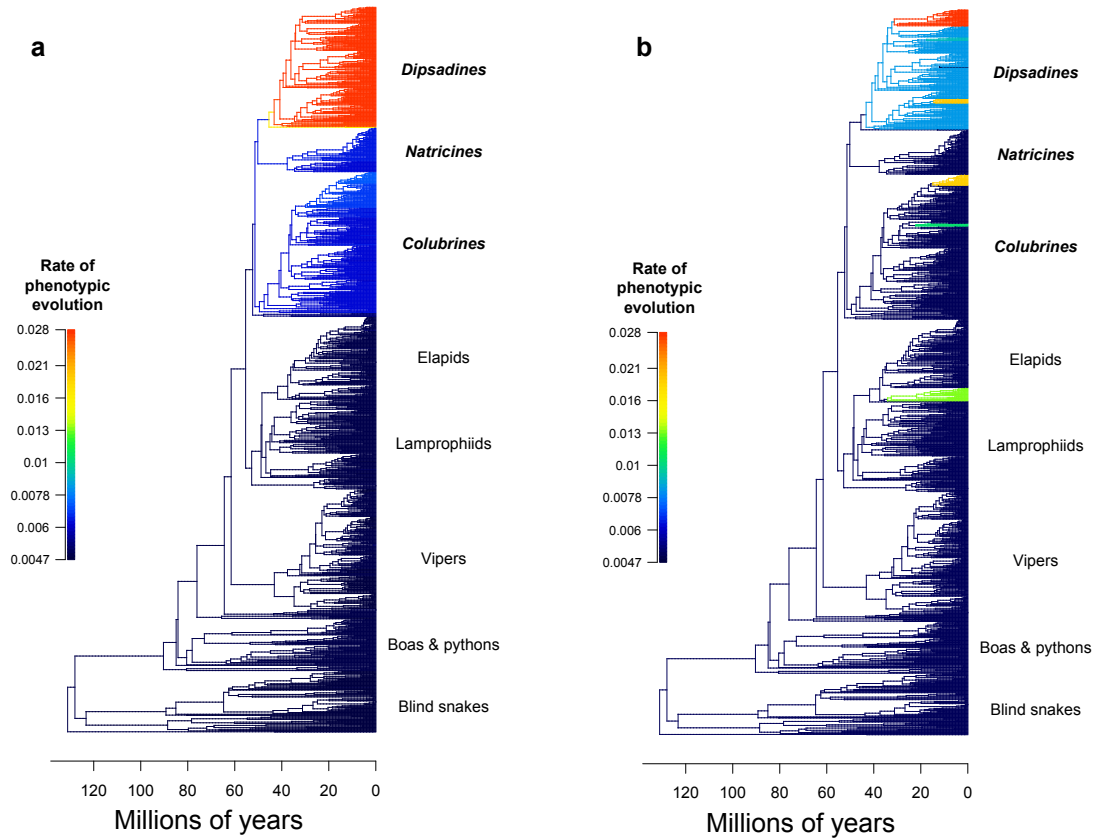
Supplementary Figure 7. Rates of phenotypic evolution. a, Phylogenetic tree with branches coloured by rate of colour pattern evolution (number of changes per million years) from the random local clock (RLC) model show a much higher rate in the subfamily Dipsadinae. Units correspond to number of changes per million years. **b,** Rate estimation under the maximum likelihood (ML) model shows greater rate heterogeneity than the RLC model.

a

b

Supplementary Figure 8. Losses and gains of red-black banded coloration. Frequency histograms of 500 character reconstruction permutations using the maximum likelihood + stochastic character mapping method recover more than twice as many gains (**a**) of RBB coloration as losses (**b**), although losses of mimicry are still quite common. Means are indicated by vertical red lines.
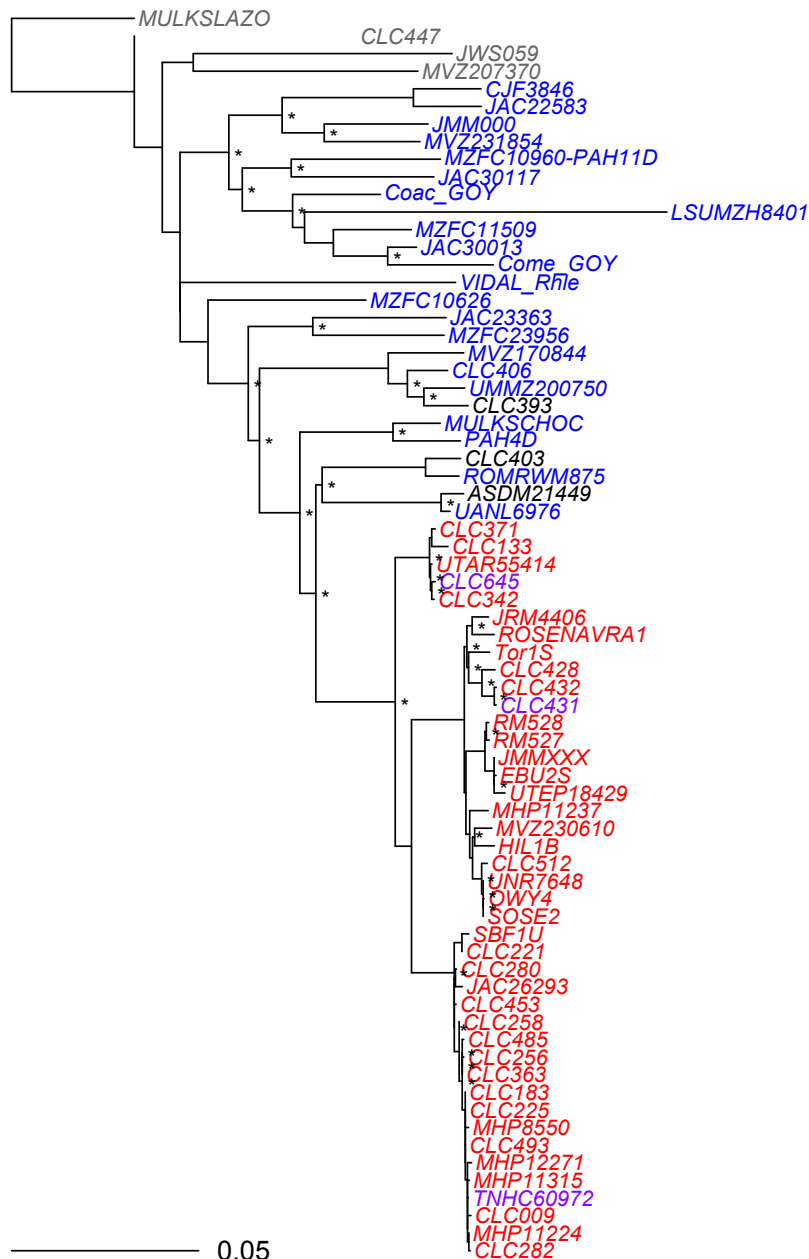
Supplementary Figure 9. Phylogeny of the Sonorini from 6 nuclear and 2 mitochondrial genes. Maximum likelihood reconstruction of the phylogenetic relationships of 22 species within the snake tribe Sonorini, including population-level sampling within the *Sonora semiannulata* species complex. Taxon labels and bootstrapped node support values are provided for comparison to Fig. 3c and Fig. 3d. Blue taxa were included in the species-level phylogeny in Fig. 3c, red taxa in Fig. 3d, and purple taxa in both. Grey taxa are outgroups. Corresponding specimen data and GenBank numbers are in Supplementary Table 5. Asterisks show node support > 50.

Supplementary Note 1

It should be noted that although our spatial dataset is only ~83% complete due to lack of recorded observations in museums, we do not expect these missing species to fundamentally alter our conclusions. The species missing from the richness dataset are generally endemics with very small ranges (as widespread species are most likely to be represented in collections) and the species missing from the abundance dataset are generally quite rare. Thus, the numerical impact of missing data in our analyses is expected to be minimal, as both species richness and abundance grid cell totals would only be negligibly increased by the inclusion of sparsely distributed data given the large overall size of both datasets.

We note that our main temporal tests do not explicitly include full ancestral range reconstructions to validate "ensured historical sympatry" between coral snakes and their mimics. Rather, our temporal correlation simply tests for the *earliest opportunity* in which these clades could have been in sympatry in the New World. Because the fossil record for New World snakes is patchy and sparse (although coral snake vertebrae are known from the Miocene of Nebraska, USA, so coral snakes were historically distributed further north than their current distribution), we originally assumed nothing about the historical distribution of coral snakes other than the timing of their earliest possible arrival to the New World from the molecular split with Asian coral snakes. Although the absolute values of all divergences times may be skewed, that bias should not systematically affect the relative position of these values to each other, which is the metric of interest in our assessment of the timing of RBB origin in coral snakes versus New World colubrids. Although we then reconstructed latitudinal midpoints of geographic ranges as continuous variables across the tree to generate a profile of the geographic distribution of

coloration changes, we note that these are not "full range" constructions - they are are only latitudinal midpoints. Thus, we urge that this analysis should be interpreted conservatively. Because there is considerable geographic conservatism to clade distributions (*e.g.*, there is a large Dipsadine clade that does not expand out of the tropics), we think that this analysis is informative about the relative rate of gain and loss in the tropics and near the margins of the present-day coral snake distribution. Beyond this coarse generalisation, though, we encourage caution in making anything more significant out of this finding.

Additionally, although many taxa are missing from the tree due to lack of DNA sequence information, the overall rarity of the RBB coloration suggests that the future addition of missing taxa will mainly serve to confirm or increase - rather than decrease - the number of transitions recovered here. Transitions could be pushed further back in time by the fortuitous, balanced placement of missing taxa specifically spanning transition points, but numbers of reconstructed origins are far more likely to increase rather than decrease without any changes to the timing of the origin of mimicry within clades (as we found by adding taxa to the Sonorini clade).

We also note that there are two New World mimetic species each on single, long branches (Colubridae: Neckband snakes, *Scaphiodontophis annulatus*; and Aniliidae: South American pipe snakes, *Anilius scytale*) for which we have no information to reliably date the RBB origin. The branch lengths for these species are ~40 and ~80my respectively, and our stochastic character mapping simulations produce essentially uniform distributions of the timing of the RBB origin across each branch. Thus, we do not consider either taxon to be an exception to our finding that RBB coloration in non-venomous snakes arose after the earliest possible arrival of coral snakes

in the New World, but rather that due to their unique topology, we have no information about the

timing in these two lineages to reconstruct these origins with any confidence.

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