

Figure S1: Maps and histograms for environmental covariates used in occupancy modeling. (a,b) Median elevation. (c,d) Median topographic position index (TPI). (e,f) Median distance to nearest road. (g,h) Median distance to nearest stream. (i,j) Distance from patrol area centroid to nearest reserve boundary.

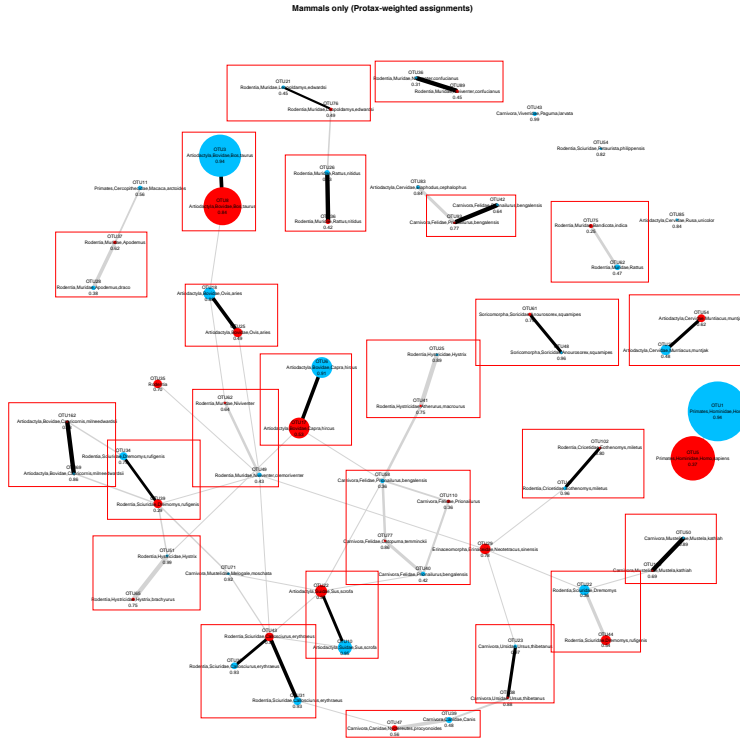


Figure S2: Bipartite network visualization of pairwise Spearman correlations between mammal LSU and SSU pre-OTU across lab replicates. Blue and red nodes represent pre-OTUs from the LSU and SSU datasets respectively. The size of each node is proportional to the square-root transformed occupancy of the pre-OTU calculated across lab replicates (i.e. the fraction of replicates in which the pre-OTU was detected). Each node is labelled with the lowest taxonomic assignment that was not missing or unknown, as well as the PROTAX probability for that assignment. For every pair of LSU and SSU pre-OTUs, we calculated the Spearman correlation of read counts across lab replicates. We discarded any correlations that were < 0.1 , or that were not significant at $\alpha = 0.5$ after false discovery rate correction. We drew a bipartite graph using the package `igraph` [14] with the remaining correlations as edge weights connecting nodes representing the pre-OTUs. Thicker edges thus indicate higher correlation coefficients. Edges are shown in black where they join nodes with the same lowest taxonomic assignment, and are otherwise shown in grey. Red boxes show manually assigned groupings of pre-OTUs that were deemed to be the same taxon. For example, at the bottom of the figure, pre-OTU38 (SSU) and pre-OTU38 (LSU) were both assigned to the Asiatic black bear, *U. thibetanus*, and the thick line indicates that these OTUs were found in (nearly) the same subset of replicates, as expected if the two OTUs were amplified from the same bloodmeals and thus from the same individual mammals. Also at the bottom of the figure, pre-OTU47 (SSU) was assigned to Canidae, *Nyctereutes procyonoides*, but pre-OTU39 (LSU) was assigned to Canidae, *Canis*. Given that these OTUs were also found in nearly the same subset of replicates, we conclude that pre-OTU39 is also *Nyctereutes procyonoides*.

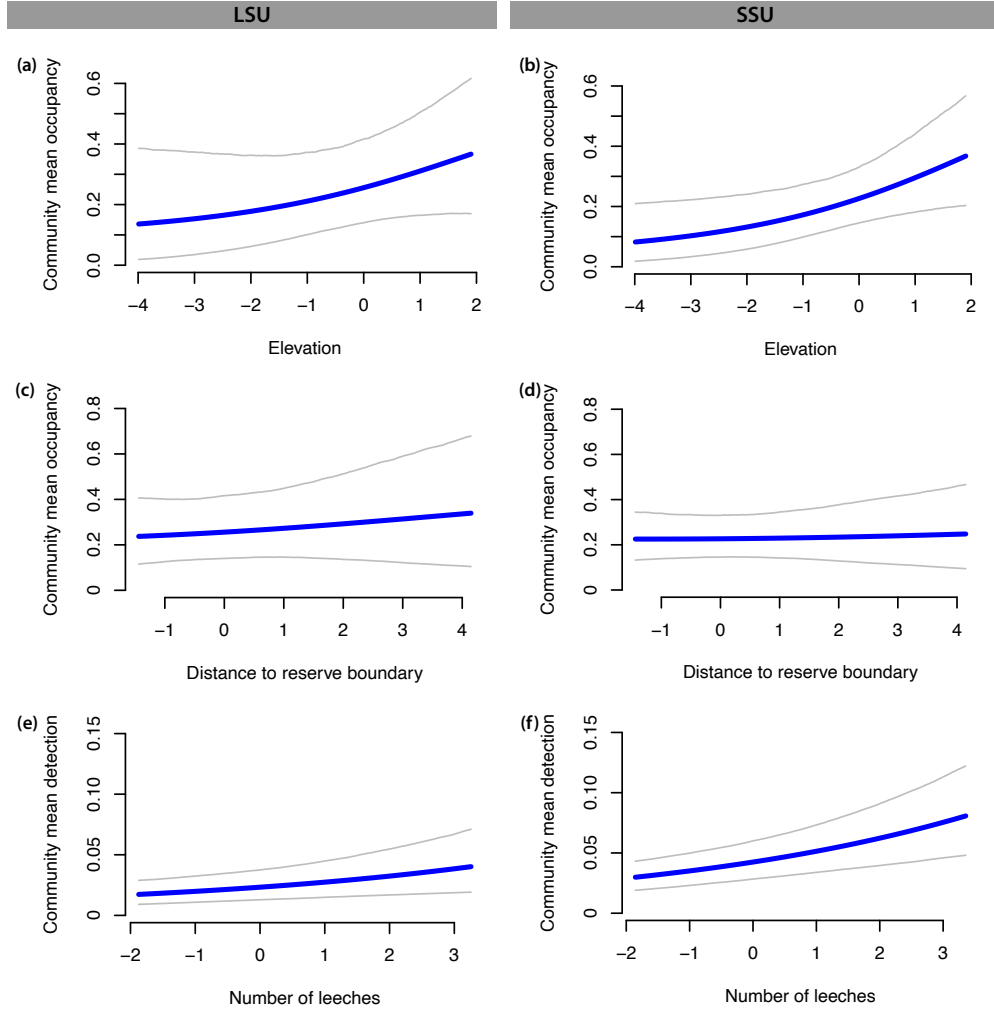


Figure S3: (a) to (d) Community mean occupancy as estimated by the LSU and SSU occupancy models as a function of elevation and distance to reserve boundary. Thick blue curves show the posterior mean community occupancy probability as captured by the hyperparameters μ_{β_0} , μ_{β_1} and μ_{β_2} . The thinner grey curves show 95% Bayesian confidence interval as derived from the 2.5% and 97.5% percentiles of the posterior distributions. (e),(f) Community mean detection probability as estimated by the LSU and SSU occupancy models as a function of number of leeches per replicate. Thick blue curves show the posterior mean community detection probability as captured by the hyperparameters μ_{γ_0} and μ_{γ_1} . The thinner grey curves show 95% Bayesian confidence interval as derived from the 2.5% and 97.5% percentiles of the posterior distributions.

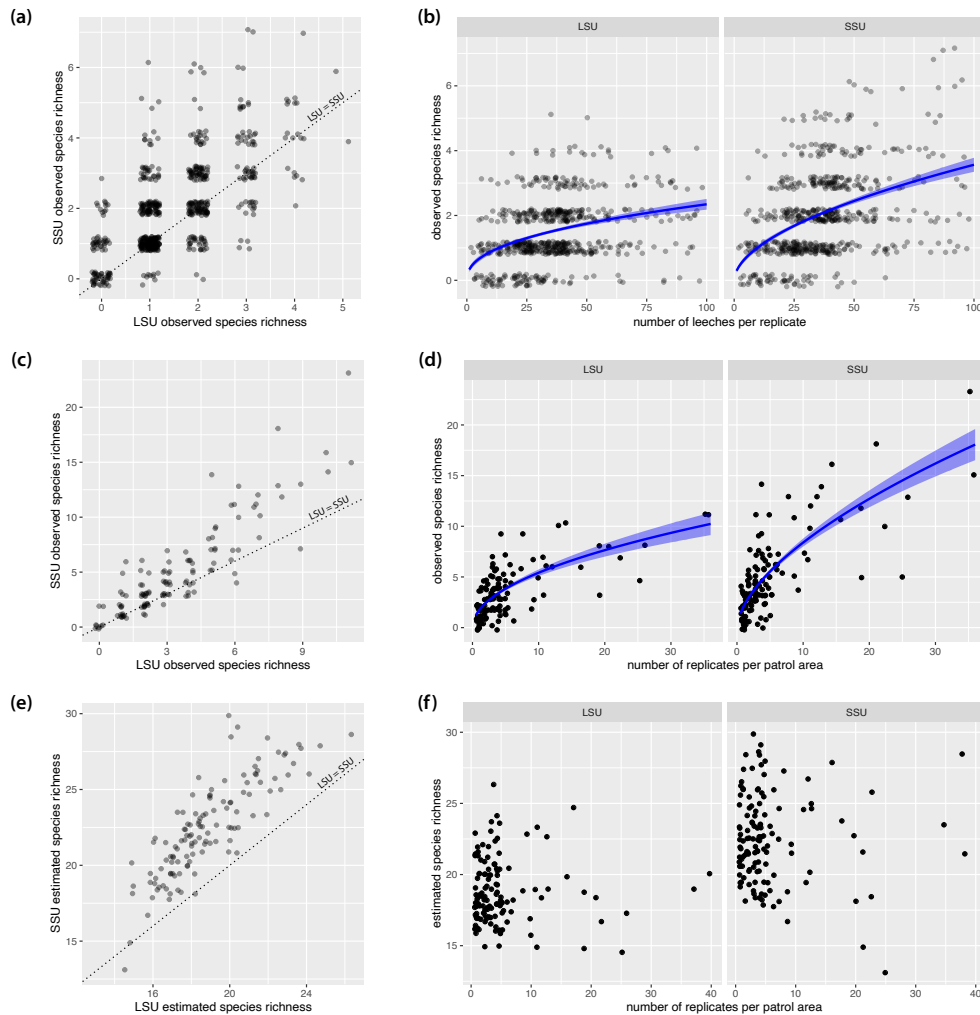


Figure S4: (a,b) Observed species richness per replicate. Note that more species tend to be detected in replicates with more leeches. Blue curves in (b) show predicted values from Poisson GLMs of species richness against log-transformed number of leeches per replicate (slopes: $z = 6.9$, $p < 0.001$ for LSU and $z = 10.0$, $p < 0.001$ for SSU); shaded areas show \pm standard error. (c,d) Observed species richness per patrol area. Note that more species tend to be detected in patrol areas with more replicates. Blue curves in (d) show predicted values from Poisson GLMs of species richness against log-transformed replicate count per patrol area (slopes: $z = 10.2$, $p < 0.001$ for LSU and $z = 14.9$, $p < 0.001$ for SSU); shaded areas show \pm standard error. (e,f) Estimated species richness per patrol area. Note that model corrects for variation in sampling effort so that estimated species richness no longer increases with number of replicates per patrol area. Slope coefficients for least-squares regressions of estimated species richness against log-transformed replicate count per patrol area were non-significant. Points in all plots are jittered to allow overlapping points to be visualized.

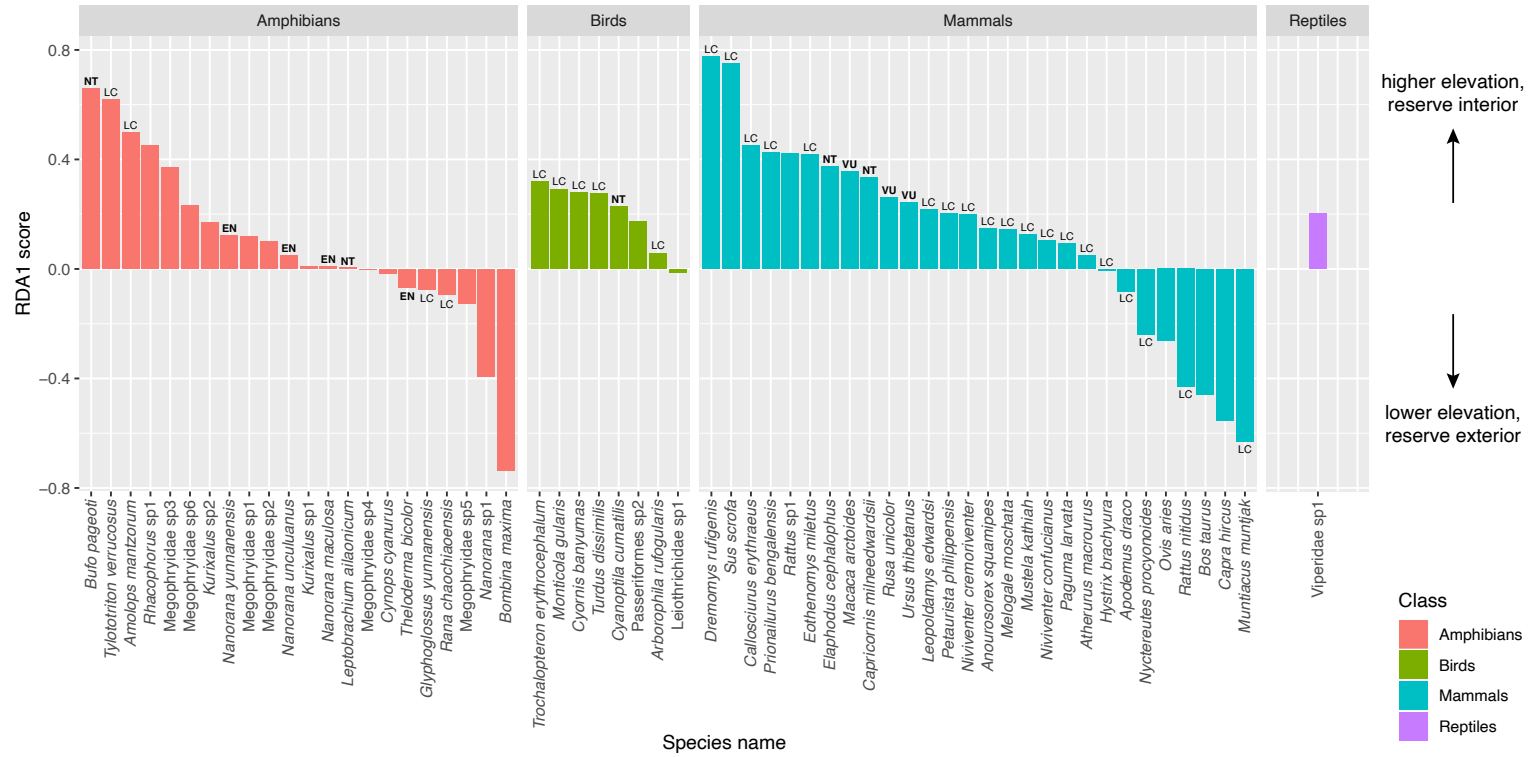


Figure S5: Scores for each species on first redundancy analysis axis ('RDA1') in LSU dataset. Annotations at ends of bars denote IUCN categories: LC = Least Concern; NT = Near Threatened; VU = Vulnerable; EN = Endangered; CR = Critically Endangered. Categories NT and above are shown in bold. Taxa without annotations have not been assigned a category by the IUCN.

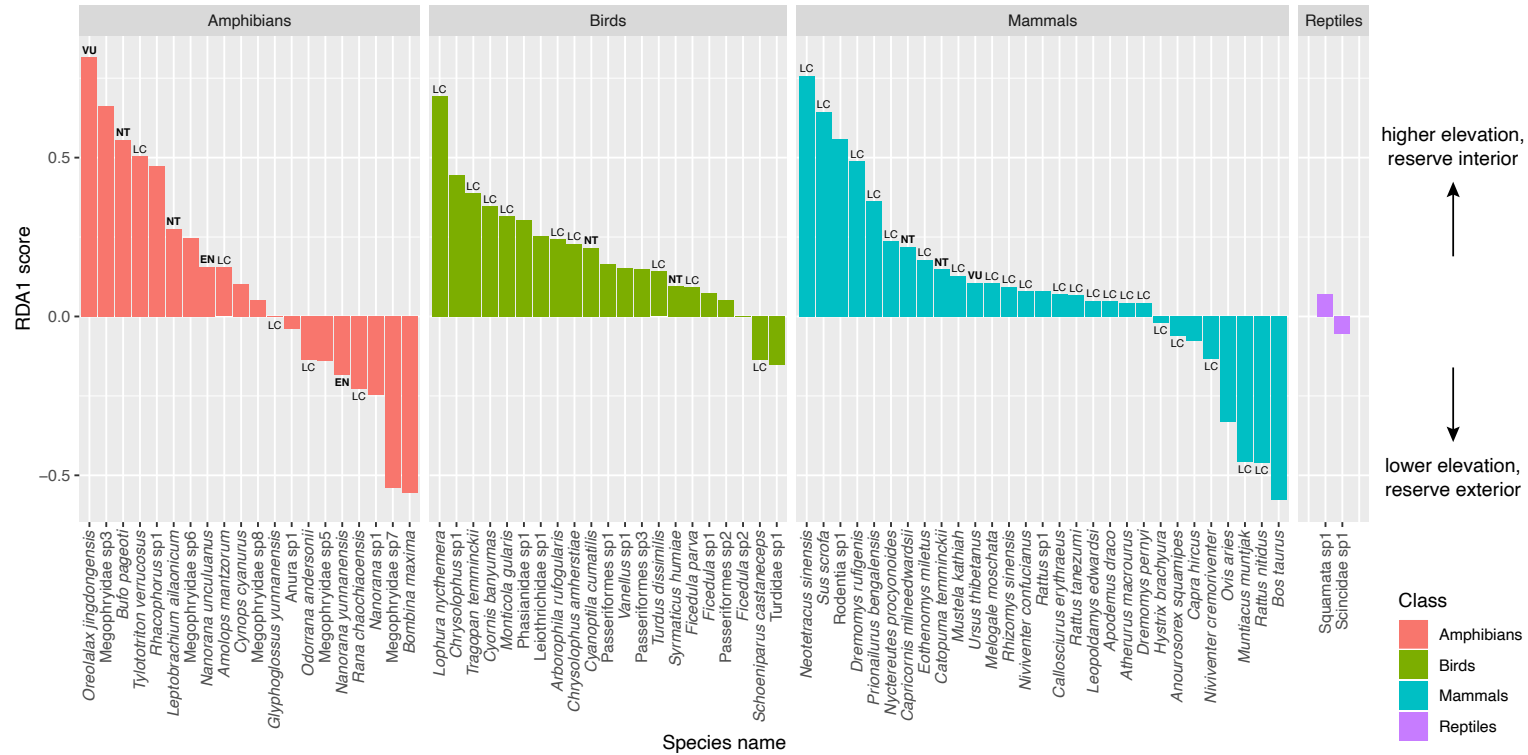


Figure S6: Scores for each species on first redundancy analysis axis ('RDA1') in SSU dataset. Annotations at ends of bars denote IUCN categories: LC = Least Concern; NT = Near Threatened; VU = Vulnerable; EN = Endangered; CR = Critically Endangered. Categories NT and above are shown in bold. Taxa without annotations have not been assigned a category by the IUCN.