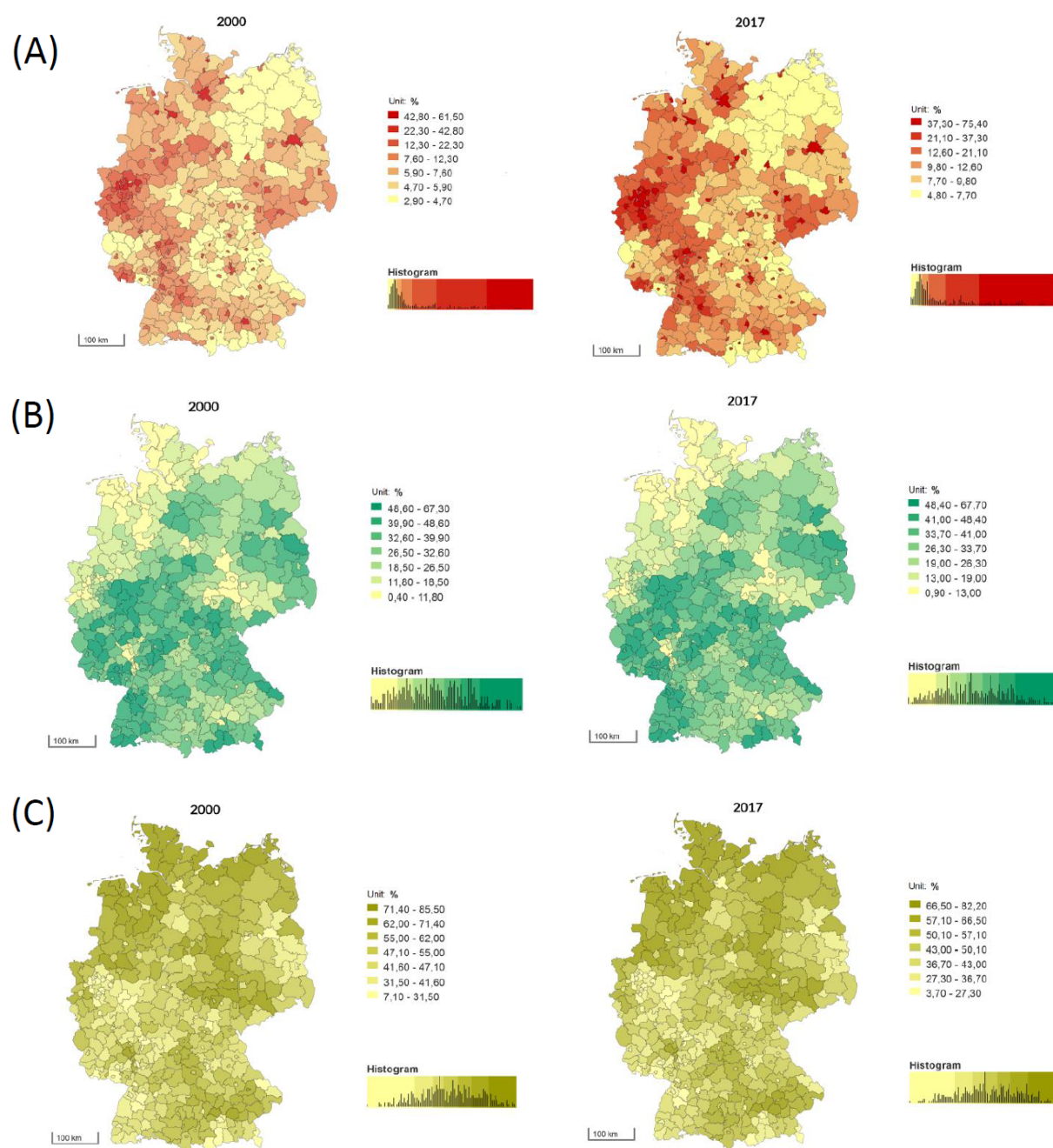
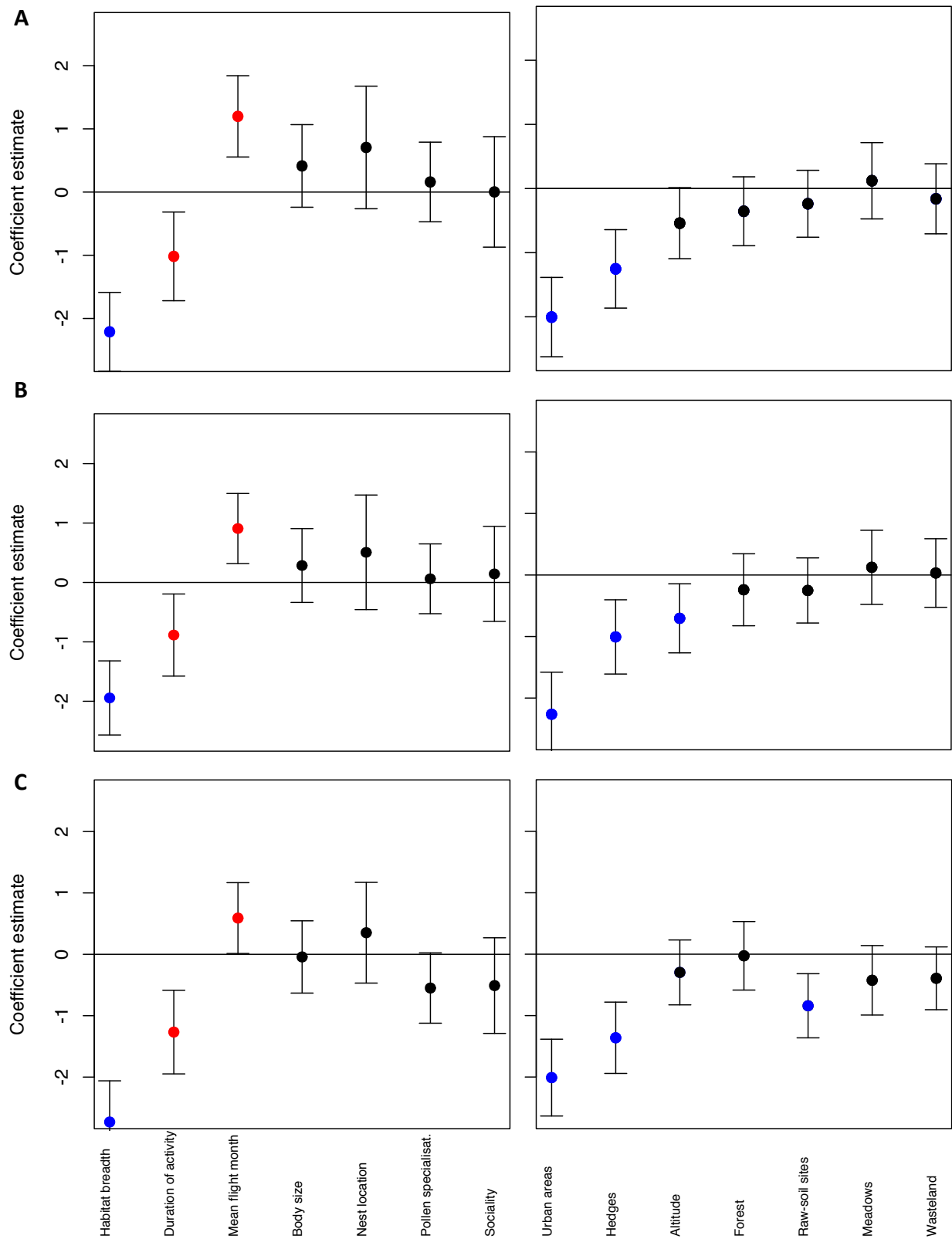


## Supplementary figures S1-S5

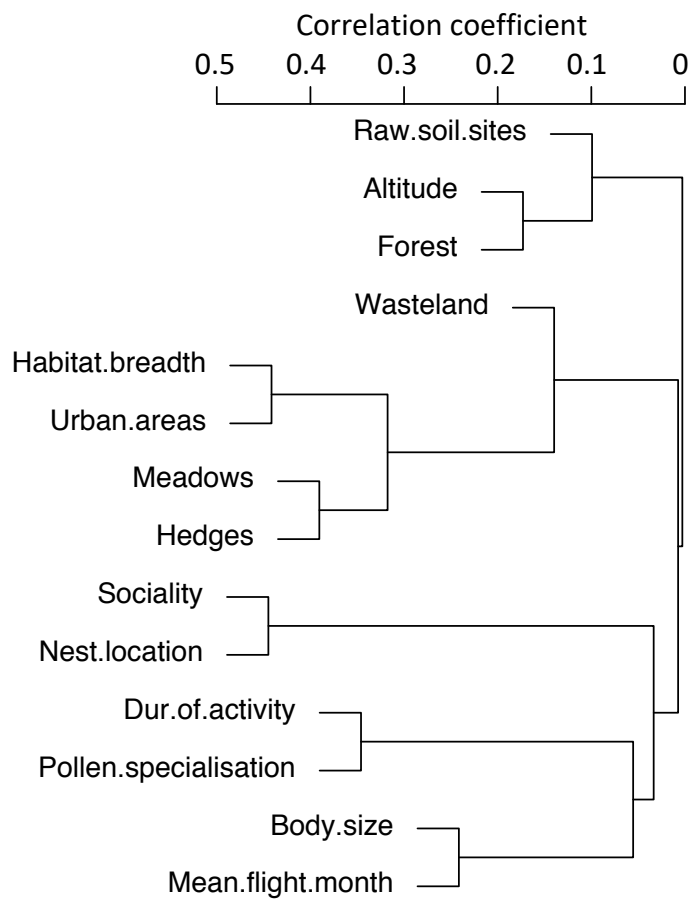


**Figure S1 | Percentages of (A) human settlements and the transport infrastructure, (B) woodland, and (C) arable land in 2000 and 2017.**

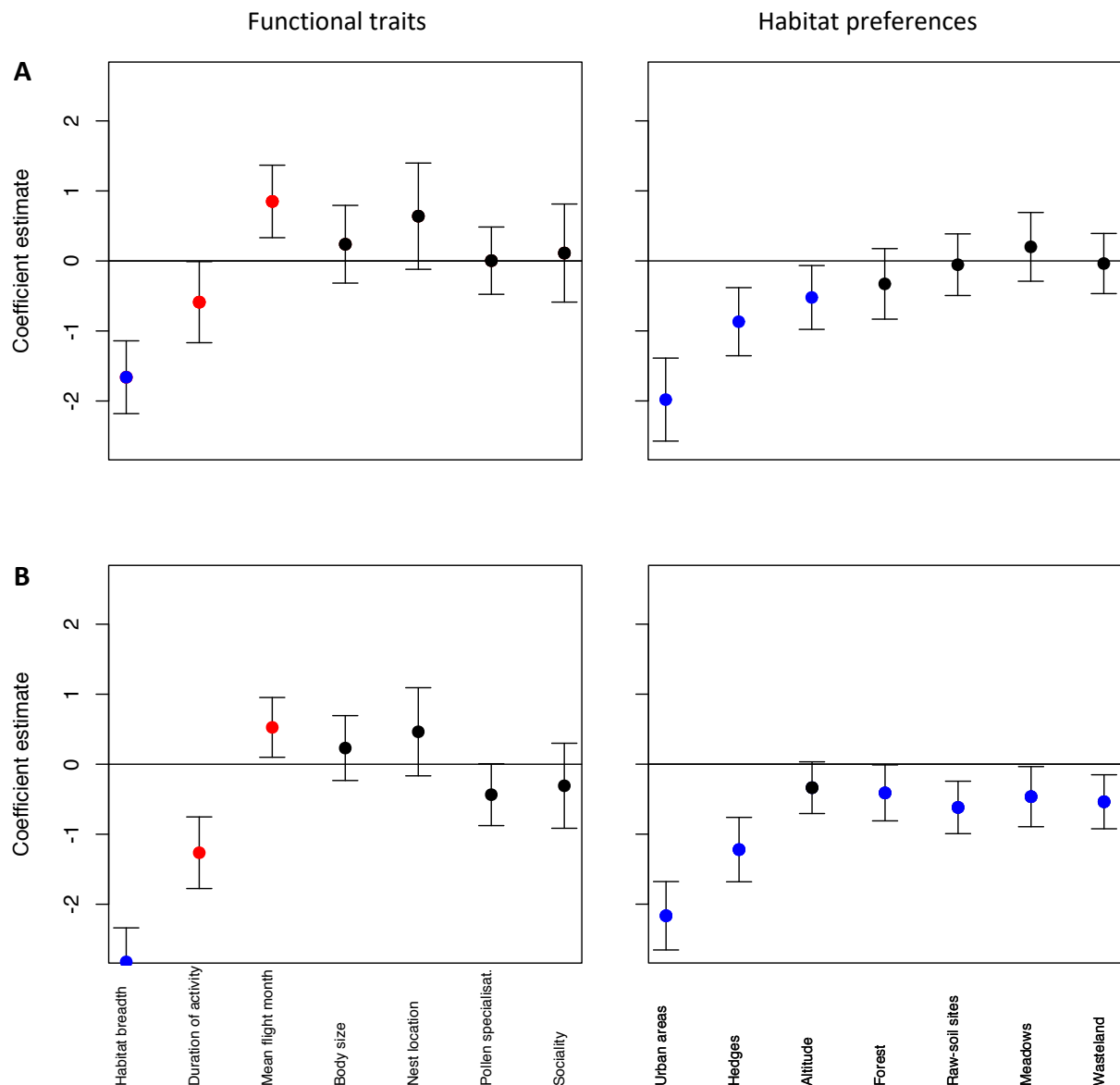


**Figure S2 | Extinction risk (A), population trends (B) and abundance (C) of bee species occurring in Germany modeled as binary characters. a, Coefficient estimates (effective**

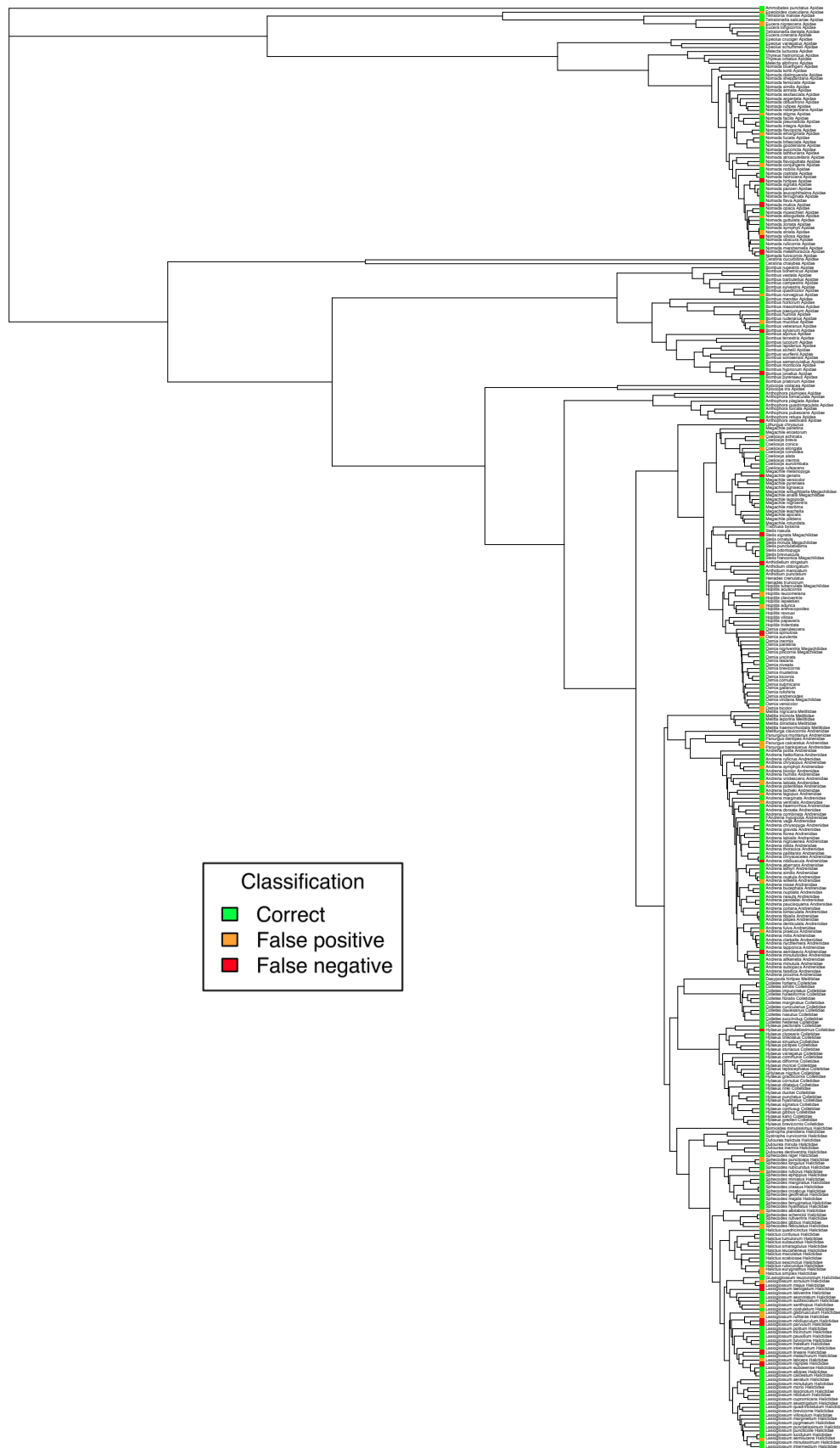
posterior means  $\pm$  95% credible intervals) for the effects of species-specific functional traits (duration of activity, mean flight month, body size, pollen specialization, sociality, nest location) and habitat requirements (habitat breadth, urban areas, hedgerows, altitude, wasteland, meadows, raw-soil sites, forest) on Red List status (A), population trends (B), and abundance (C) (coded as binary variables). Hierarchical Bayesian linear models were applied, including genus and family random effects to account for phylogenetic signal in the data. All variables were standardized to allow for direct effect size comparisons.  $N = 428$  (A), 404 (B), and 445 (C) species.



**Figure S3 | Correlation dendrogram for the 14 variables used to predict extinction risk.** Pearson's correlation coefficients were calculated. All correlation coefficients are  $< 0.5$ , indicating sufficient independence among predictor variables.



**Figure S4 | Population trends (A) and abundance (B) of Germany's bee species are linked to habitat breadth, occurrence in urban areas, and flight time (duration and month of year).** a, Coefficient estimates (effective posterior means  $\pm$  95% credible intervals) for the effects of species-specific functional traits (duration of activity, mean flight month, body size, pollen specialization, sociality, nest location) and habitat requirements (habitat breadth, urban areas, hedgerows, altitude, wasteland, meadows, raw-soil sites, forest) on population trends (A) and abundance (B) (coded as ordinal variables). Hierarchical Bayesian linear models were applied, including genus and family random effects to account for phylogenetic signal in the data. All variables were standardized to allow for direct effect size comparisons.  $N = 404$  (A) and  $445$  (B) species.



**Figure S5 | Phylogeny of 367 bee species occurring in Germany showing for which species, Red List status was misclassified by the generalized linear model.** False positives (Type 1 error): species erroneously predicted endangered (see Table 1). False negatives (Type 2 error): species erroneously predicted to be not endangered. For both false positives and false negatives  $\Lambda < 0.01$ .