# Appendix A

The models used in this study incorporate a dataset consisting of seven environmental variables related to oceanography, hydrography, and granulometry obtenained from Boyé *et al.* (2017). The oceanographic variables include the standard deviation of salinity, surface water temperature, mean velocity of currents, and fetch, which were obtained from the PREVIMER database based on the MARS3D model. The variables were averaged by extracting daily data for the sampled year at the site coordinates and the eight adjacent cells. The fetch was calculated as the average length of nine radiating fetch segments with a maximum distance of 300km. The granulometry variables were derived from sediment cores that were taken along with associated fauna. The cores were dried, separated into 15 fractions, and the Trask index was calculated as the ratio of the 25th to 75th percentile of the grain distribution. Organic matter mass was estimated through the loss of mass after combustion in an oven.

# Appendix B

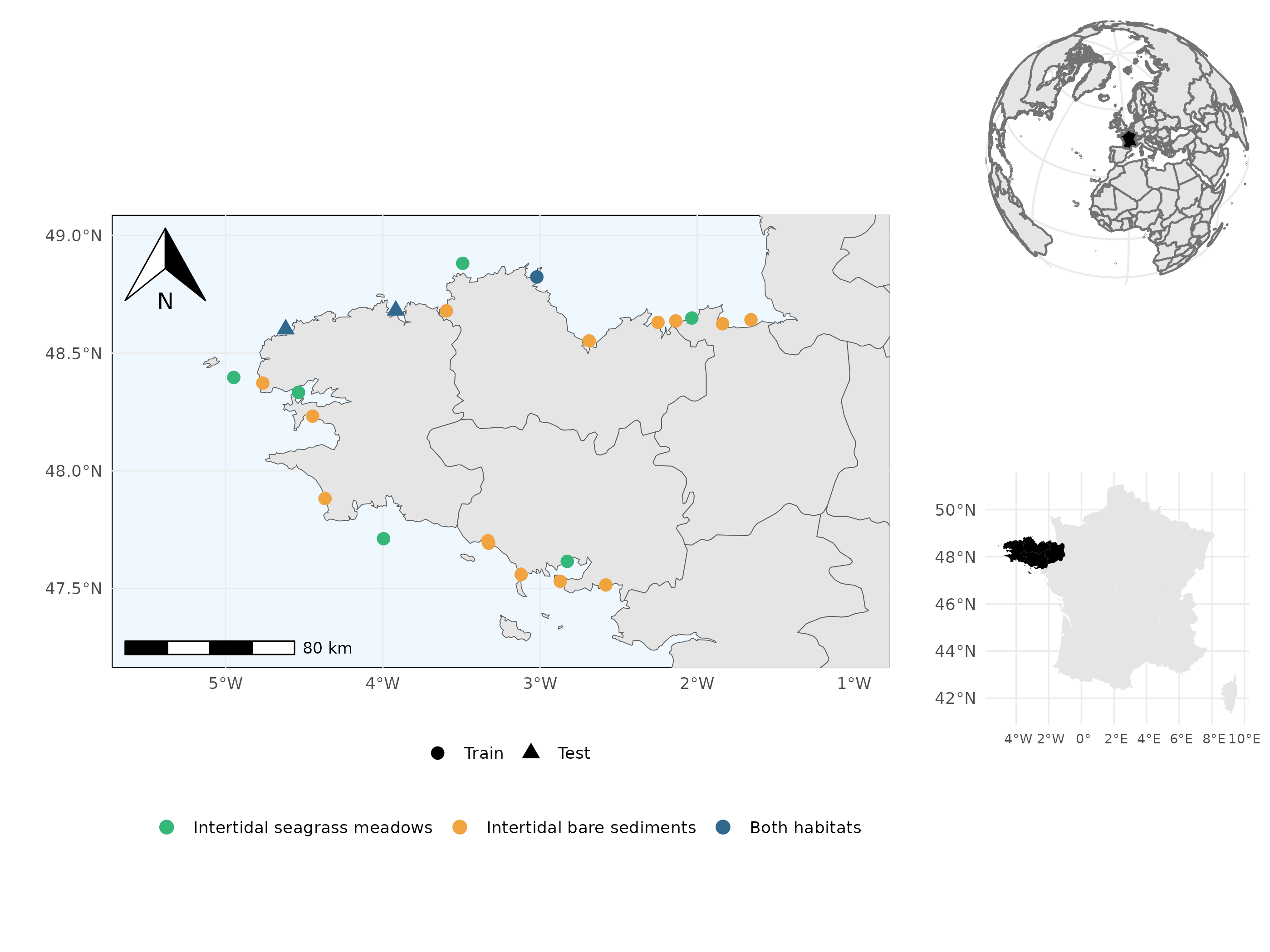


Figure S 1: Map of the sampled sites. Point shapes vary according to their contribution to model training set (circles ; used to evaluate model explanatory power) as opposed to the two sites retained for independent model testing (triangles ; used to evaluate model predictive power). Point colors vary according to the presence or absence of the two habitats in each site. The two test sites include the two habitats (i.e. seagrass and bare sand) and were chosen because they occur in environmental conditions that can be considered average at the scale of the region (thereby limiting extrapolation of the model) but still harbour different communities, representative of the known diversity gradient across the region.

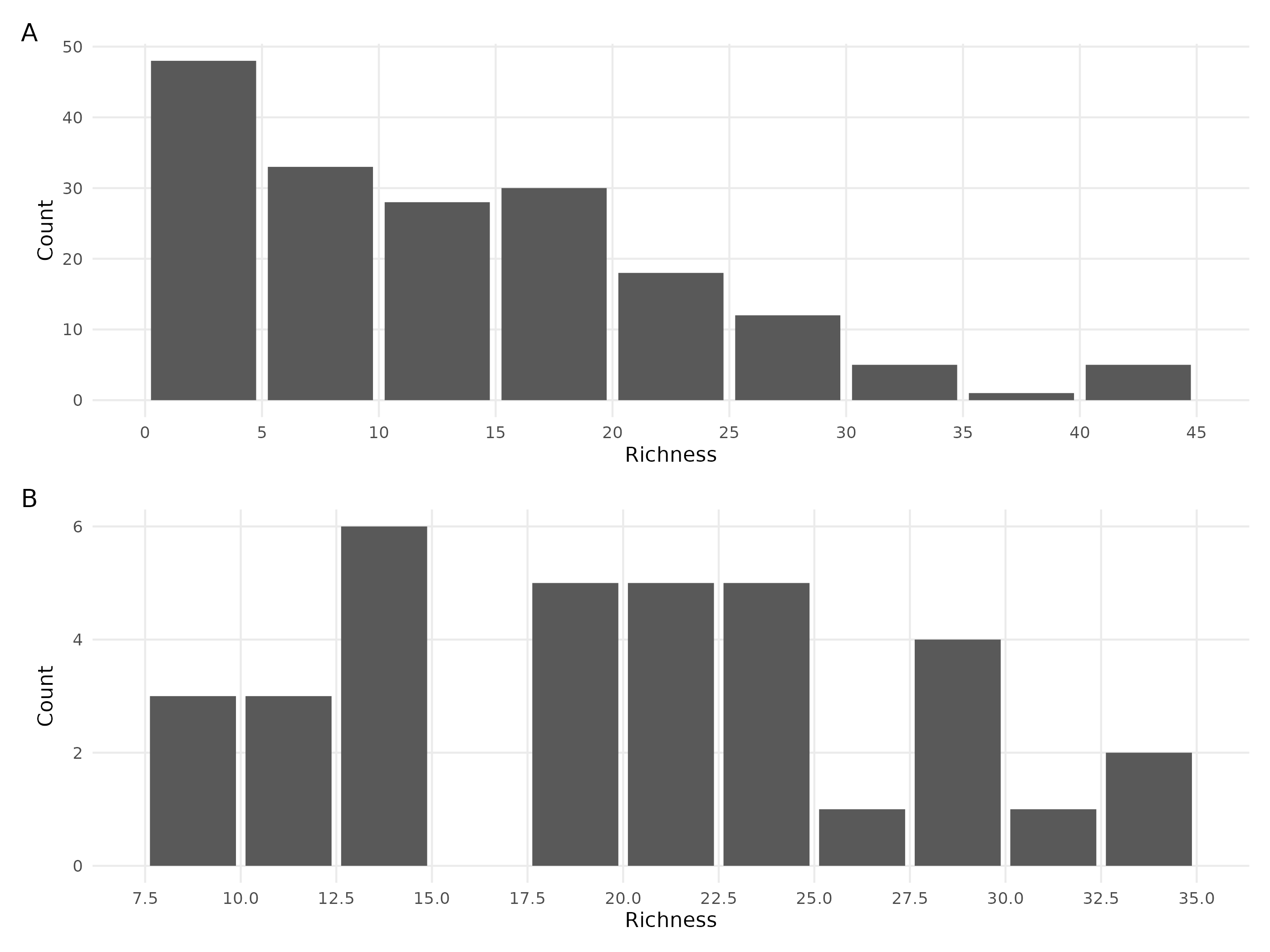


Figure S 2: A. Distribution of the richness in the sites of the train dataset. B. Distribution of the richness in the sites of the test dataset.

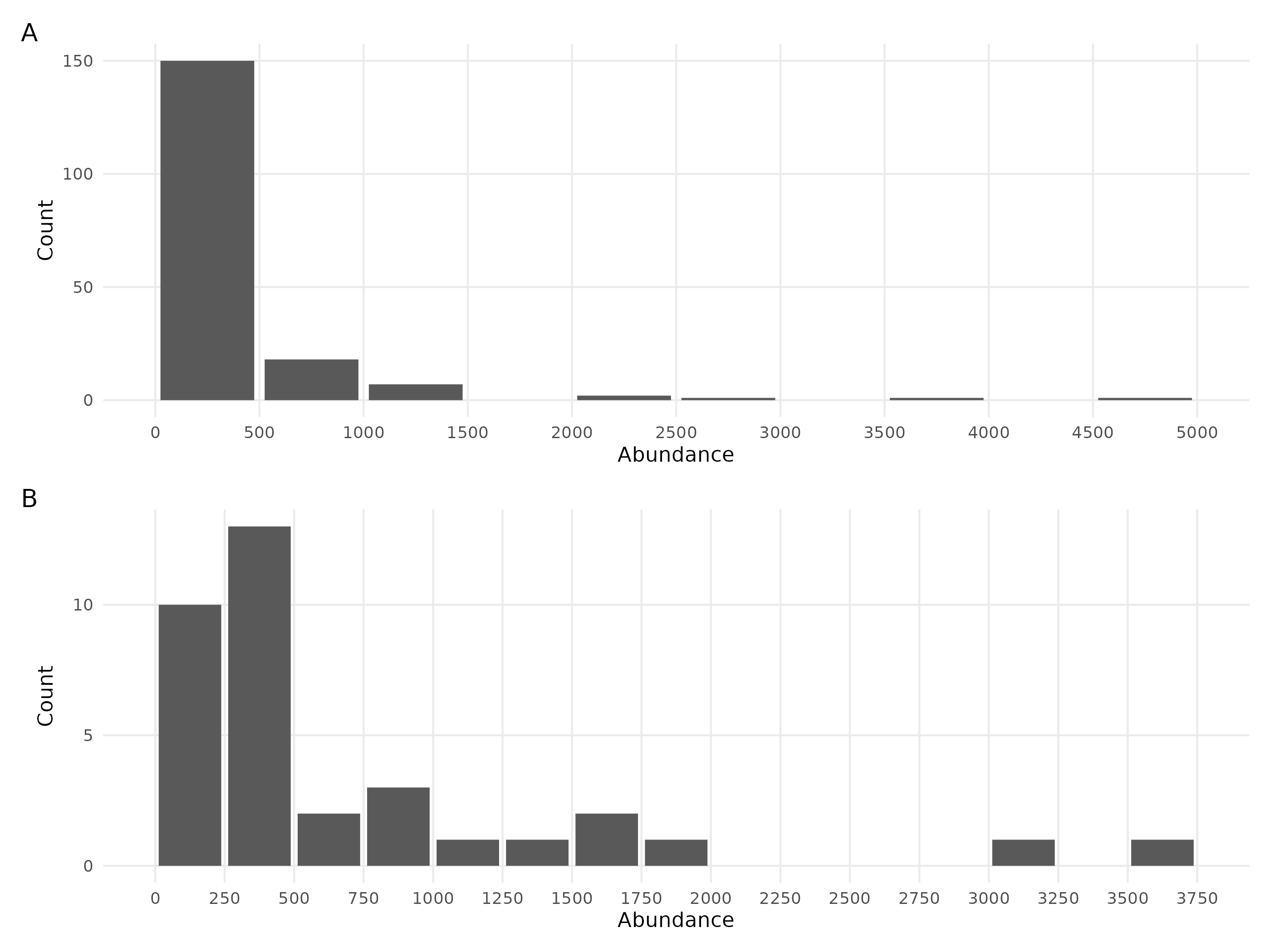


Figure S 3: A. Distribution of the abundance in the sites of the train dataset. B. Distribution of the abundance in the sites of the test dataset.

# Appendix C

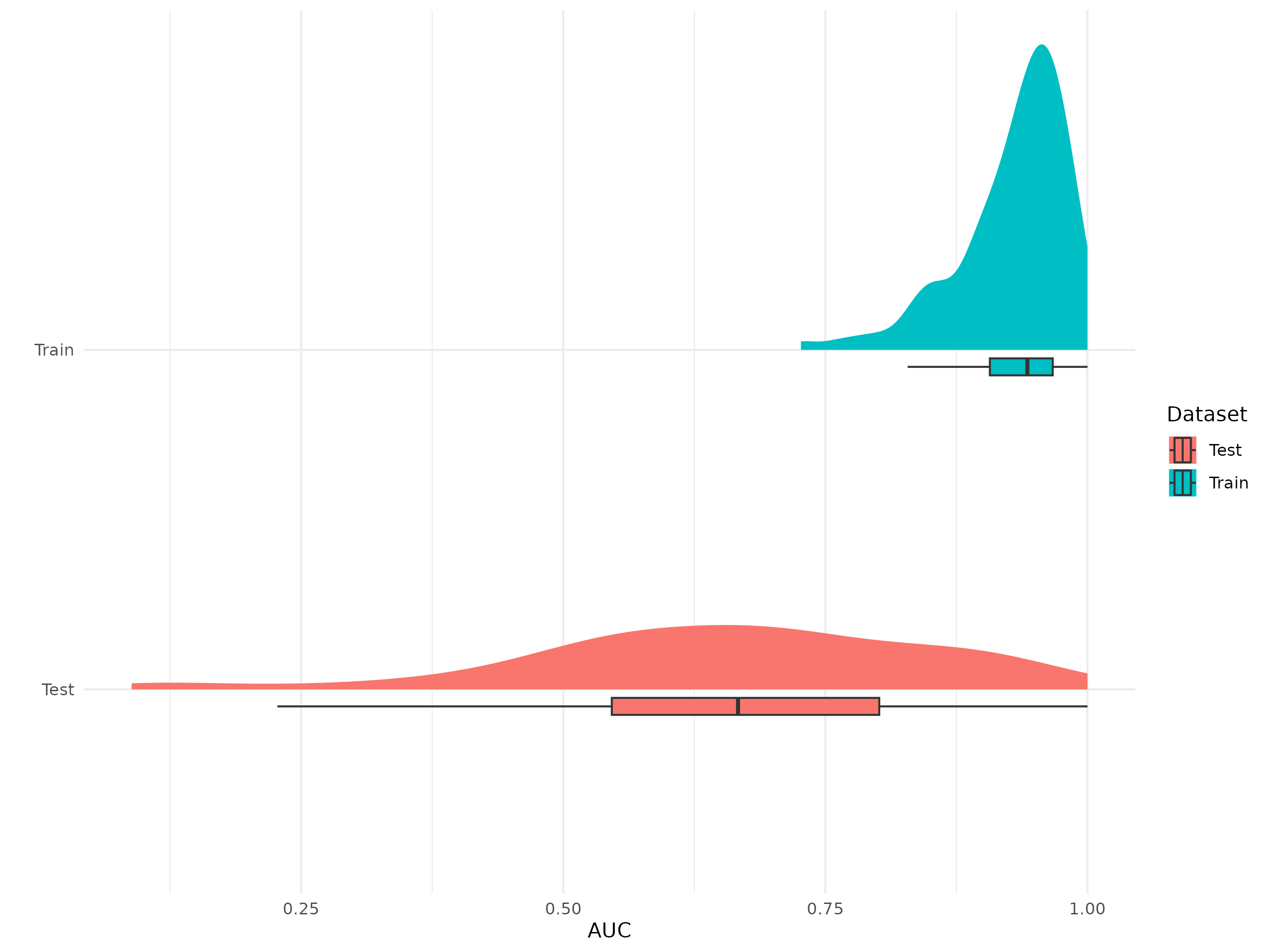


Figure S 4: Distribution of species-specific AUC estimates that characterise explanatory (predictions Vs train set observations; top panel) and predictive power (prediction versus test dataset observations; bottom panel) for the benchmark model fitted on presence/absence data.

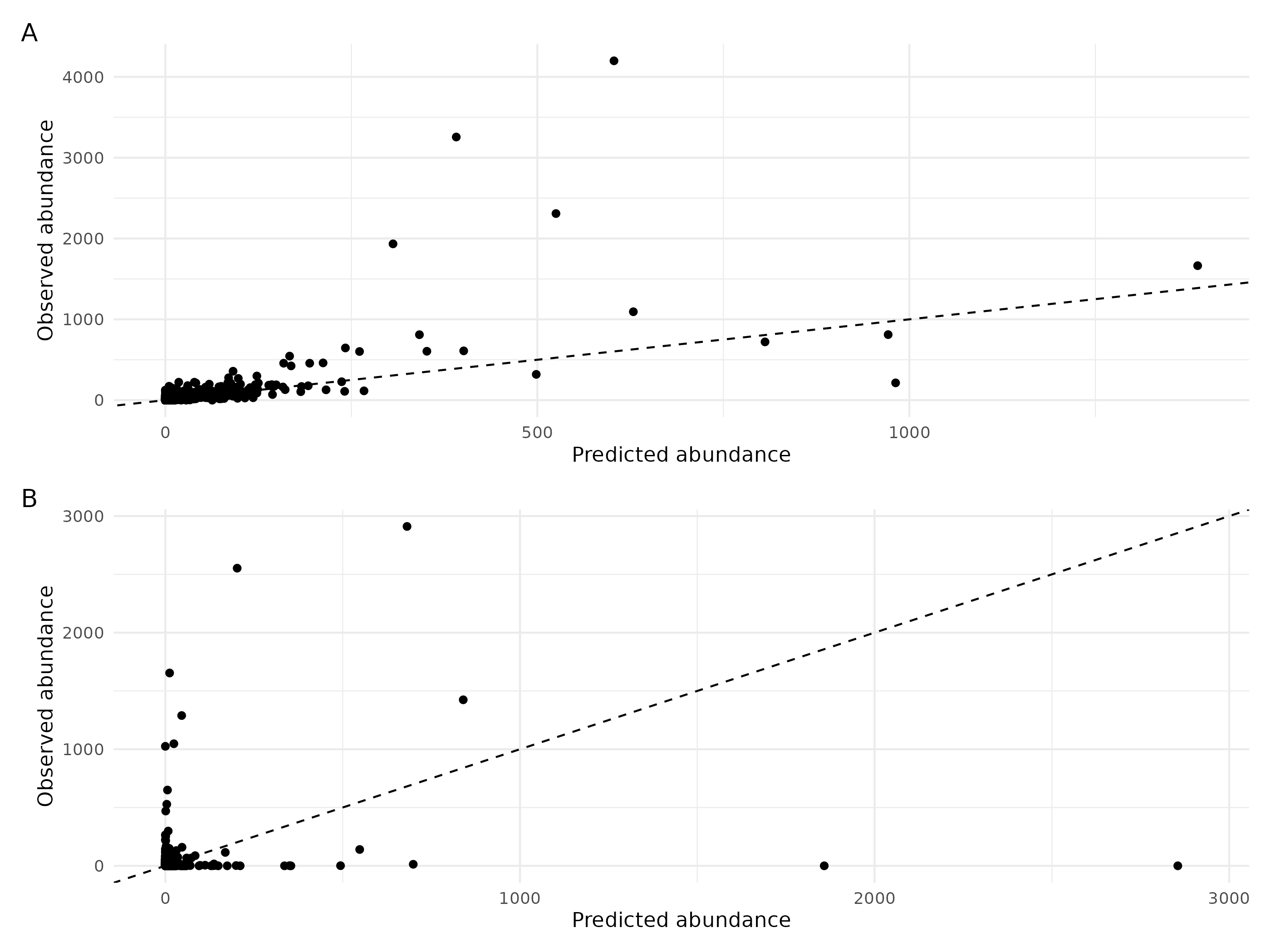


Figure S 5: Explanatory (A) and predictive (B) power of the benchmark model for abundance data. Each dot is a species predicted for one observational unit (i.e. one habitat in one site for a given year). The y-axis represents the number of individuals observed for each species in each observational unit. The x-axis shows the number of individuals predicted by the model for each observational unit. The dotted line represents the theoretical line of perfect fit of the model to the data (1:1).

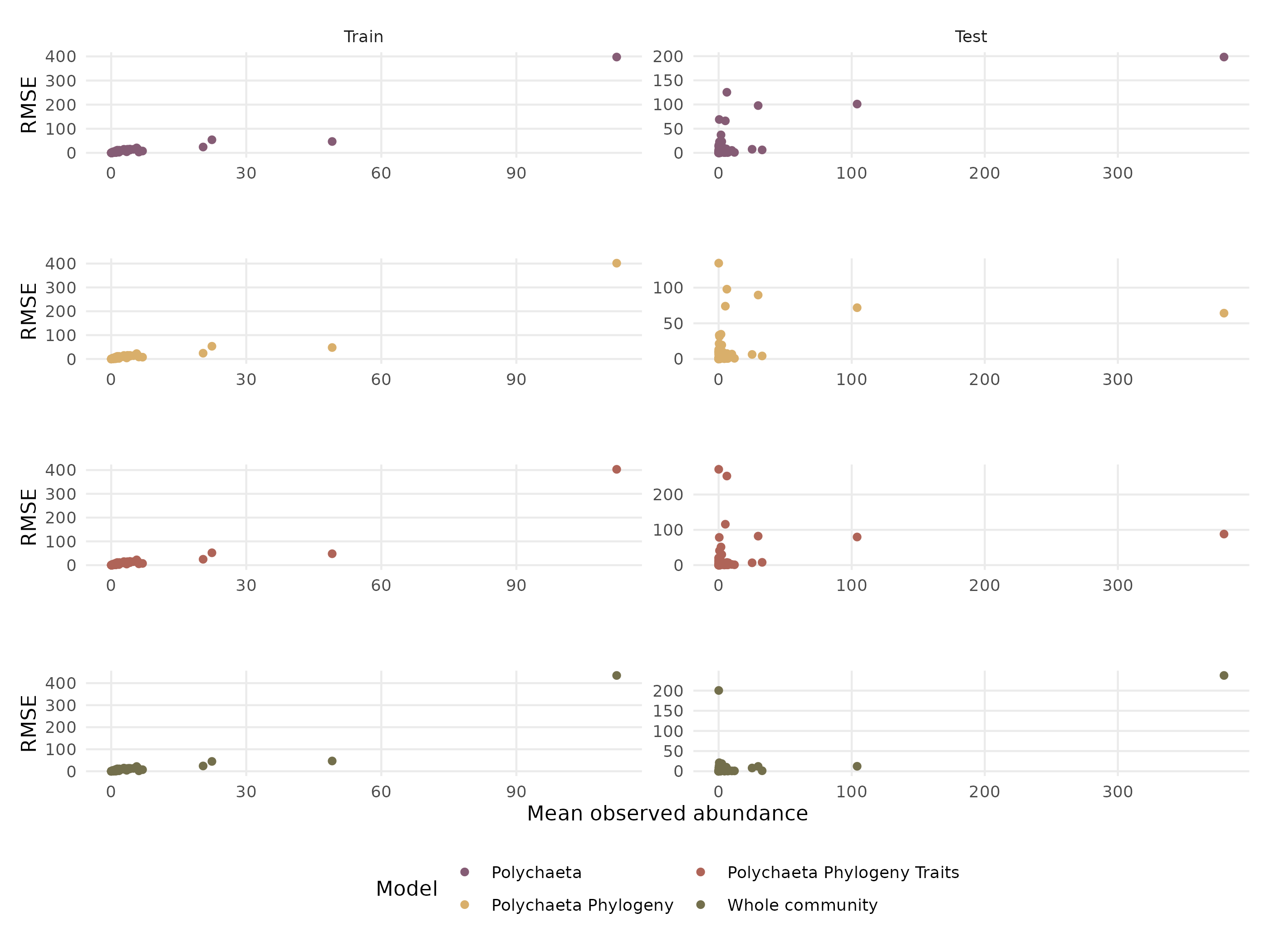


Figure S 6: RMSE of the abundance as a function of the mean observed abundance.

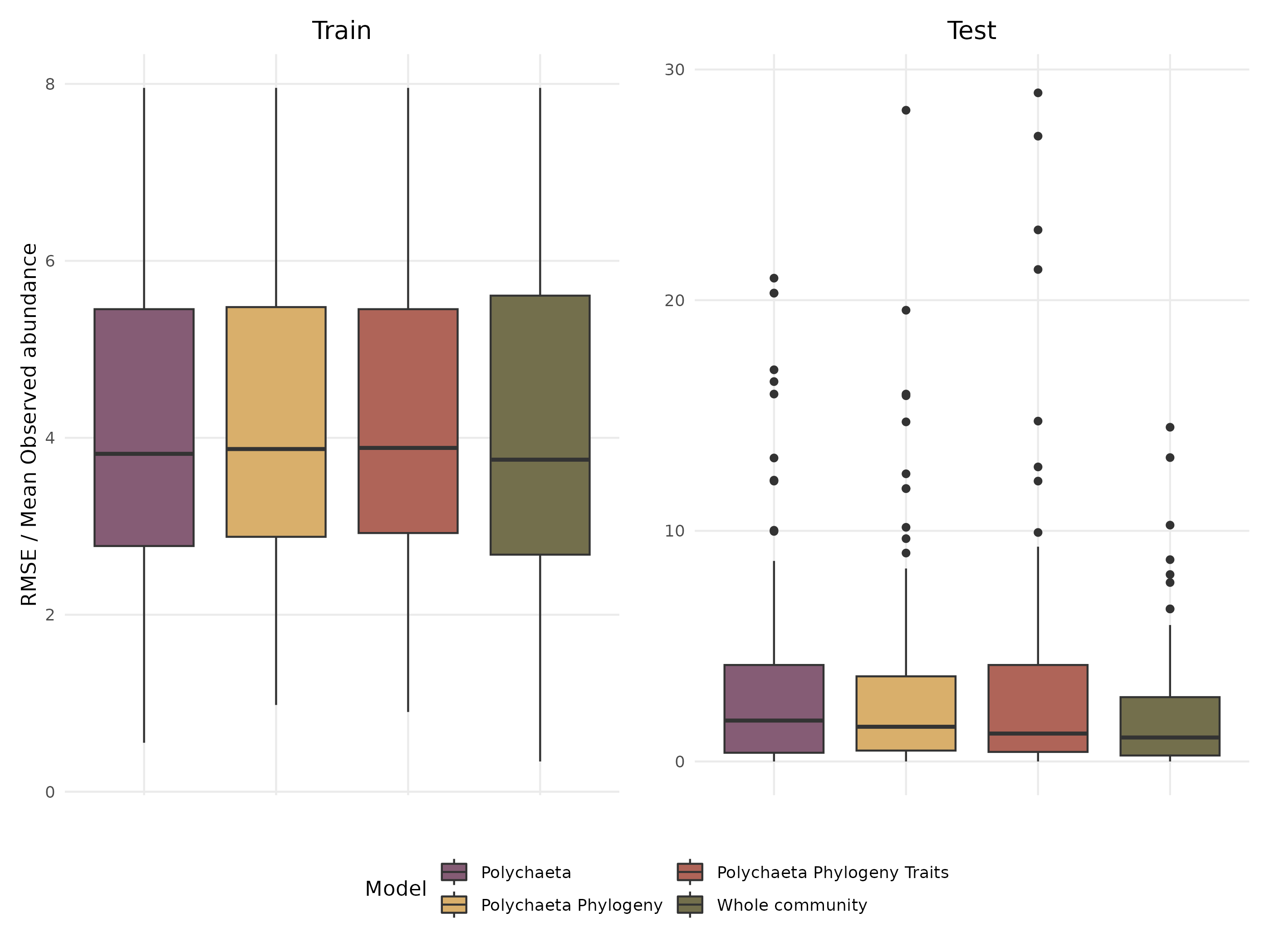


Figure S 7: Ratio between RMSE and observed abundance for the traing dataset (left column) and test dataset (right column)

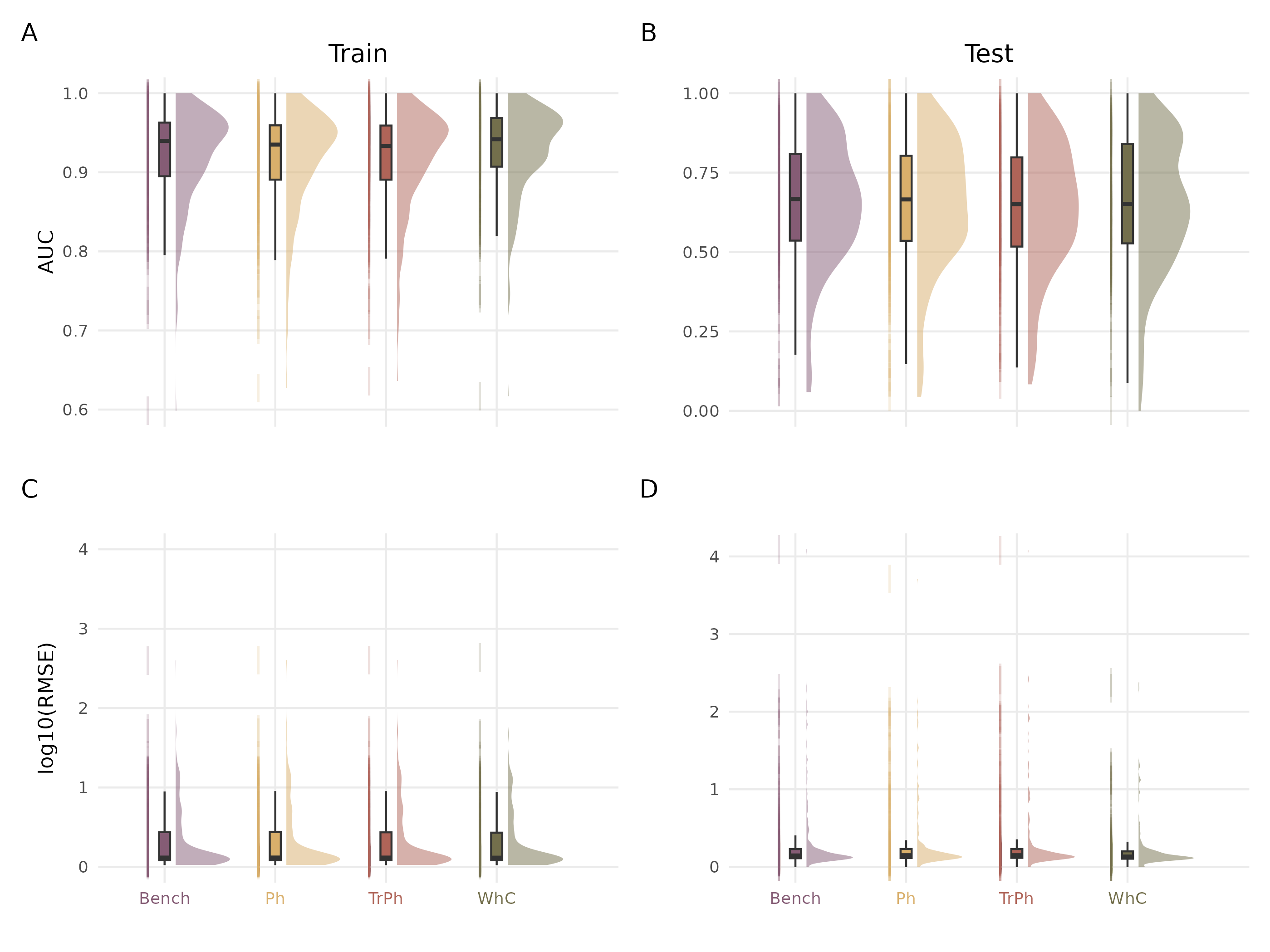


Figure S 8: Comparison of explanatory (left column; Train set) and predictive (right column; Test set) capacities of the different model structures fitted on presence/absence (top panels) or abundance (bottom panels) data

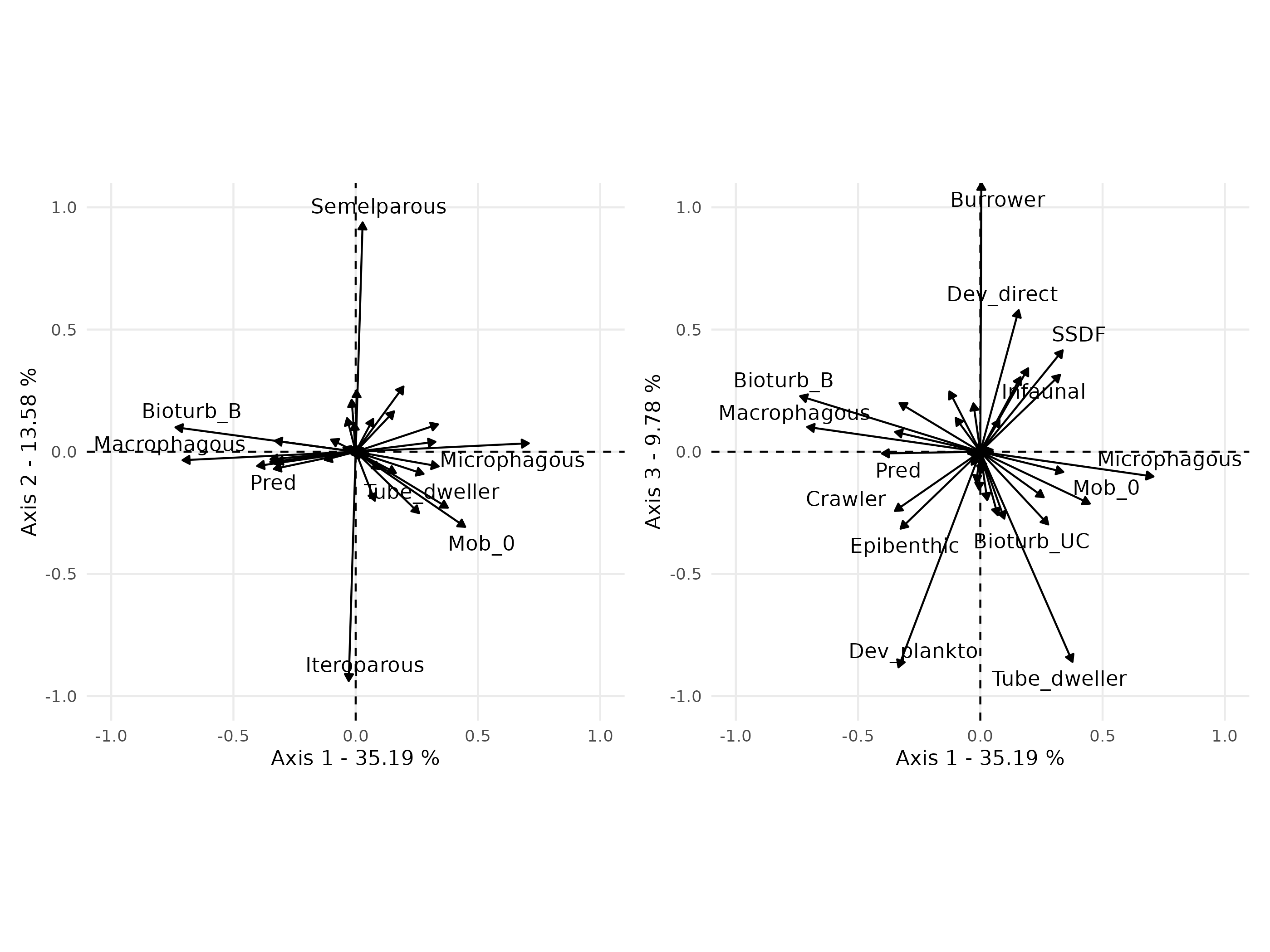


Figure S 9: Fuzzy PCA of the species-by-trait matrix. The first three axes represent 58.55% of the total variance. The first axis distinguishes sessile microphagous species (top positive values) from mobile macrophages predatory species (bottom negative values). The second axis is a gradient of reproductive strategies (semelparous Vs. iteroparous). The third axis distinguishes burrowers with direct development from tube-dwellers with planktonic development. For abbreviations and meaning of the trait modalities, see Boyé *et al.* (2019).

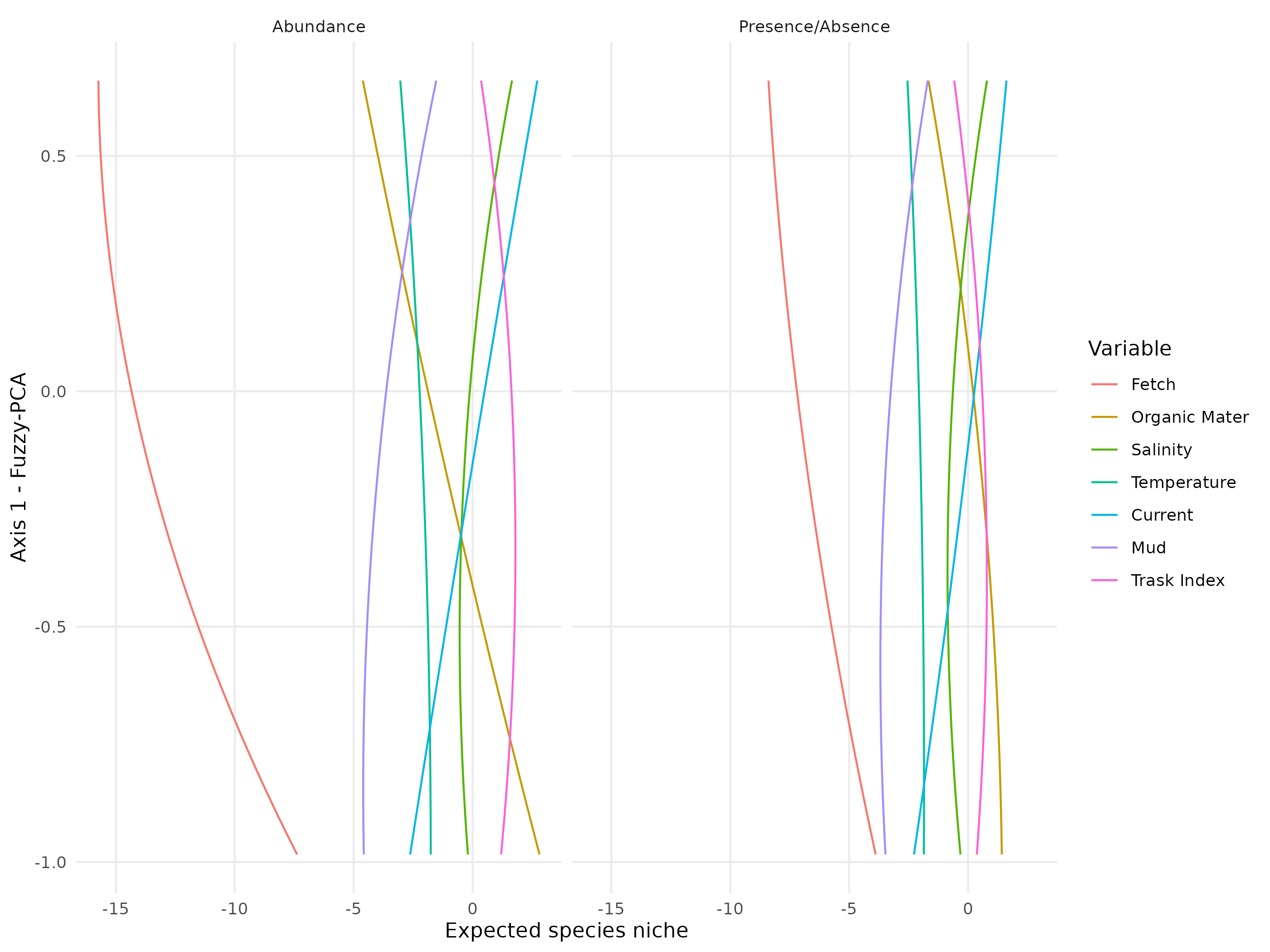


Figure S 10: Relationship between species’ position along the first axis of the fuzzy PCA (sessile microphagous-mobile macrophagous gradient) and the different environmental variables used in the models (fitted with abundance data in the left panel, and with presence/absence data in the right panel). Relationships are derived from the regression coefficients estimated for the PhTr model (γ coefficients in HMSC; Ovaskainen & Abrego (2020)).The lines are fitted loess/gam representing the average response across the different species. As an example of interpretation, the red lines in both graphs indicate that sessile microphagous species are more negatively influenced (lower abundance, low probability for presence) by fetch than macrophagous mobile species.

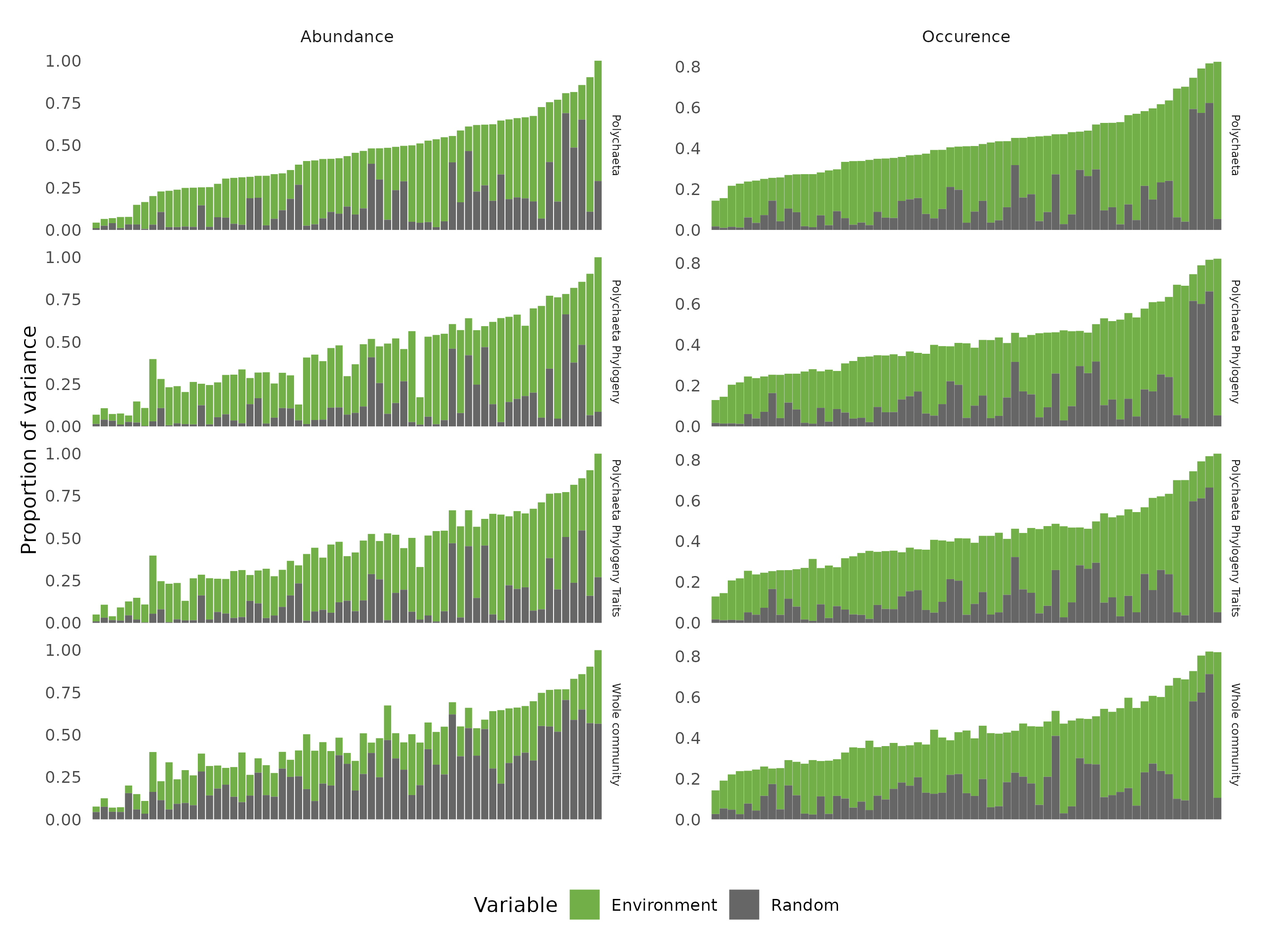


Figure S 11: Comparison across alternative models of explained variance partitioning for each species (along the x-axis) attributed to all environmental variables (Environment) or to the three random effects (Random) or the unexplained variance (white) for the models fitted with abundance (left) and presence/absence (right) data. Species are ordered by decreasing order of variance explained by the environment for the benchmark model.

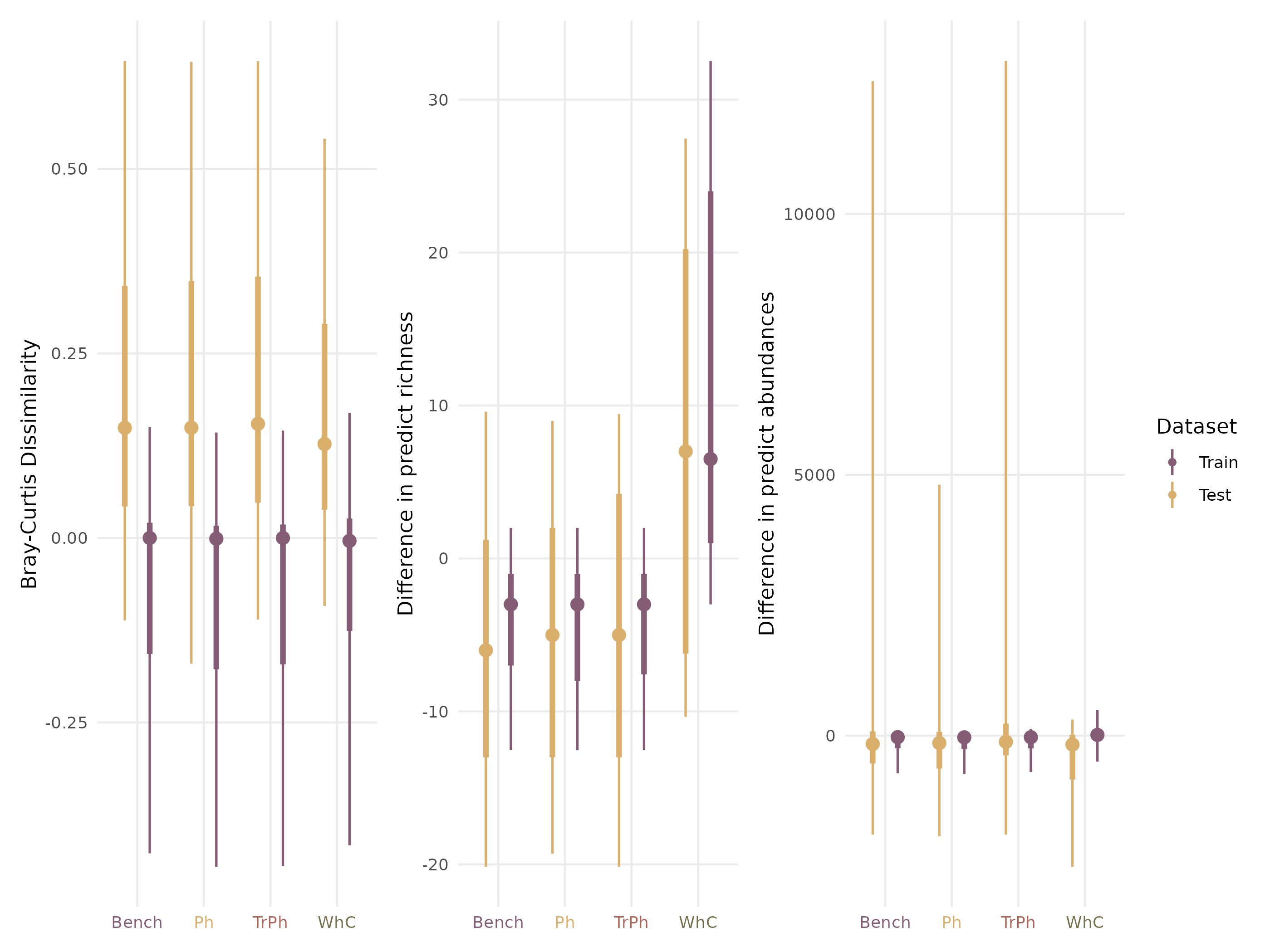


Figure S 12: Comparison of the model performances to predict the community structes for the models fitted with abundance data for the train (purple) and test (yellow) dataset. The left column indicate for each model the difference in dissimilarity between the observed community and the predict one. The middle column presents the differences in richness prediction between the observed and predict community. The right column presents the differences in abundances between the observed and predict community.

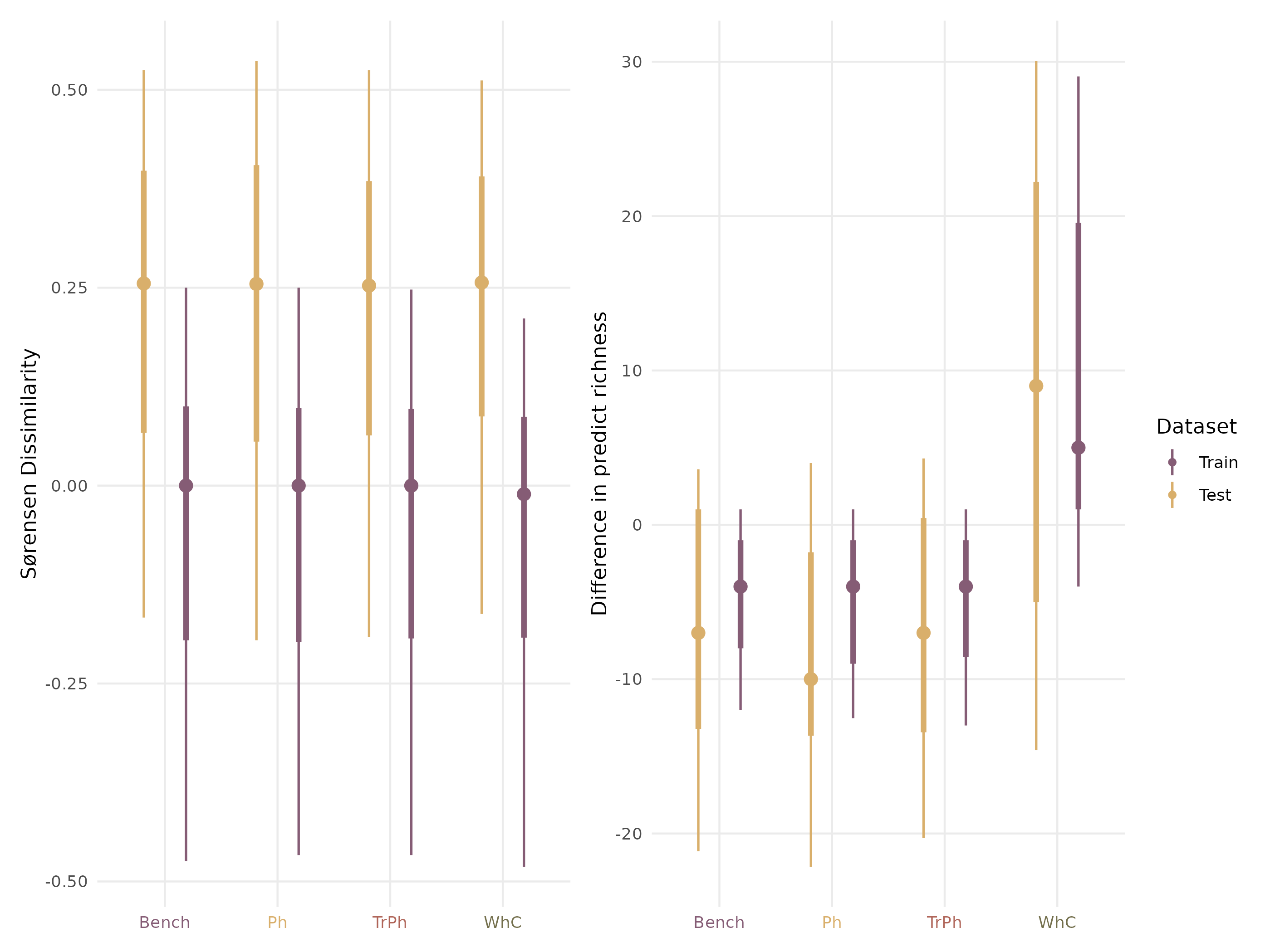


Figure S 13: Comparison of the model performances to predict the community structes for the models fitted with presence/absence data for the train (purple) and test (yellow) dataset. The left column indicate for each model the difference in dissimilarity between the observed community and the predict one. The right column presents the differences in richness prediction between the observed and predict community.

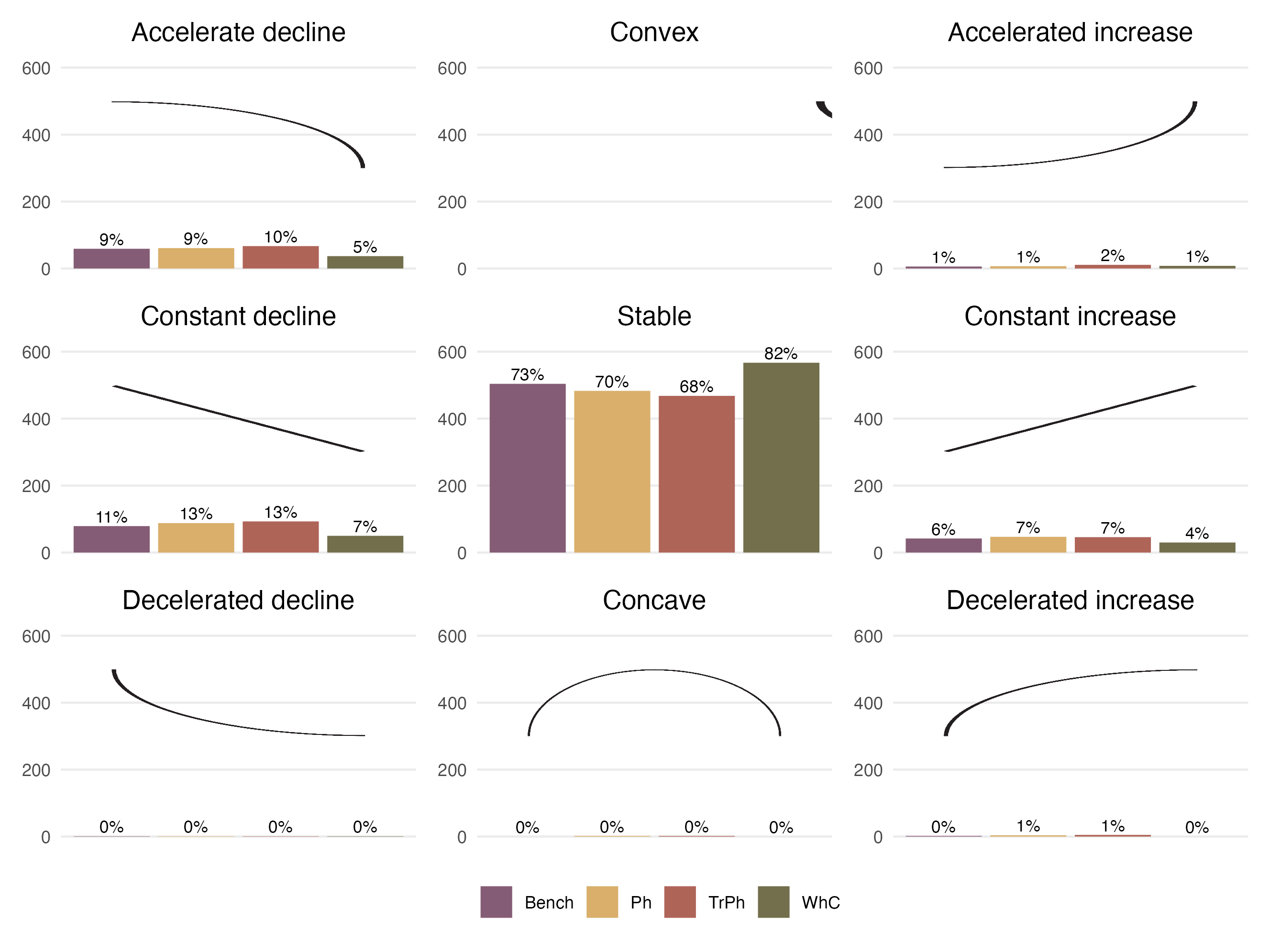


Figure S 14: Same figure as Fig. 4 in main text for presence/absence models. Number (y-axis) and proportion (indicated above individual bars) of response curves (i.e. one for each species-predictor combination) according to the nomenclature (nine shapes highlighted by the black curve in each panel) defined by Rigal *et al.* (2020) for different abundance model structures.

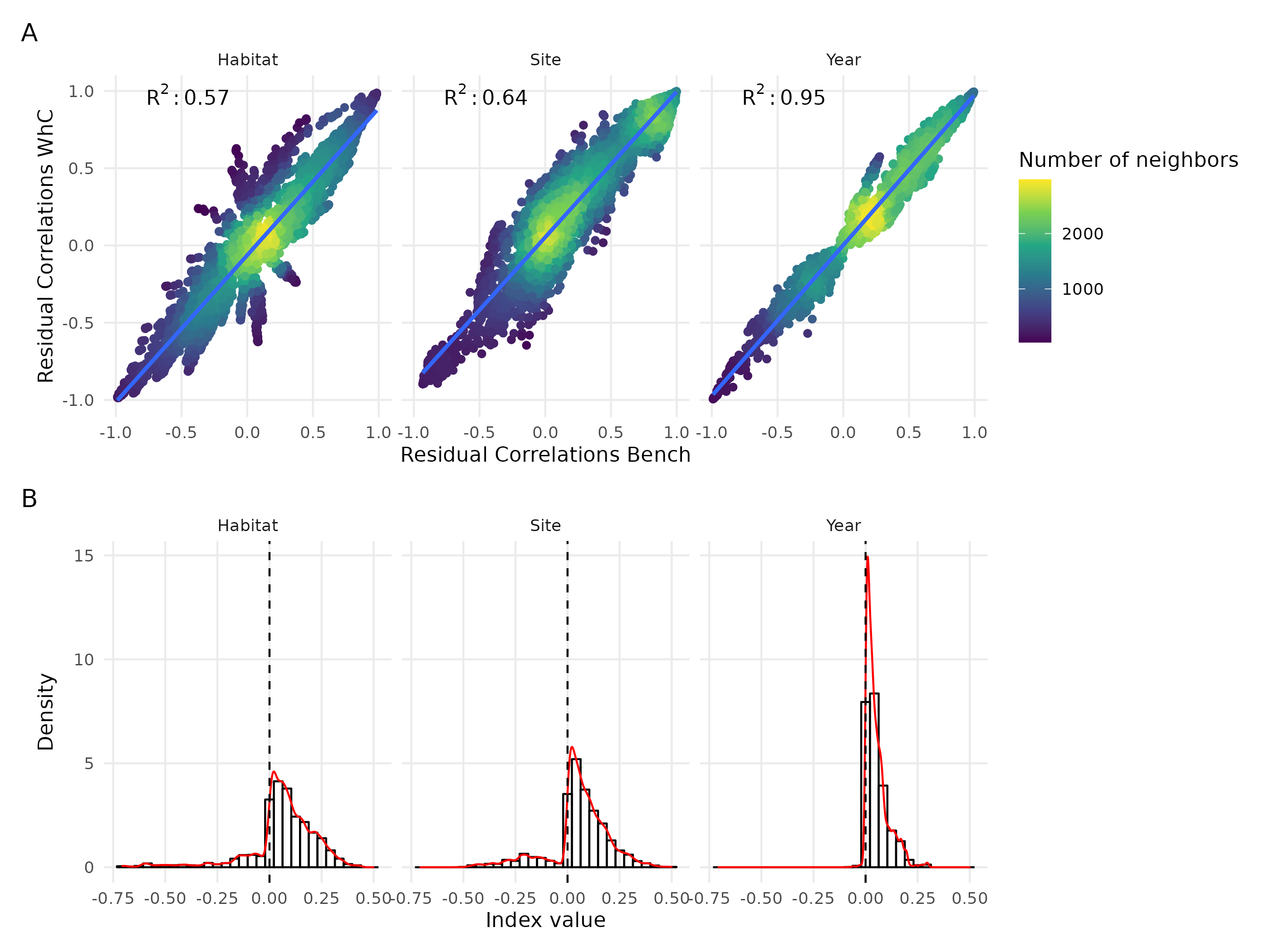


Figure S 15: Same figure as Fig. 5 in the main text for presence/absence-based models. (A) Comparison of residual correlations associated with the three random effects estimated by the Whole Community Model (y-axis) and the Benchmark model (x-axis) fitted on abundance data. The colour scale highlights the density of points in each scatter plot. (B) Distribution of the index measuring change in sign (sign change left to the zero line, no change to the right) and magnitude (higher departure from the zero line indicate higher difference) between residual correlations estimated by the whole community model and the benchmark model adjusted with abundance data for the three random effects (Habitat, Site, Year).

# Appendix D

## MCMC convergence diagnostic

### Environmental coefficients

Table S 1: Potential scale reduction factors (PSRF) and effective sample sizes (ESS) for environmental regression parameters (i.e beta coefficients) estimated for the models including phylogeny data. For further details see Fig. S12 to Fig. S19.

| Model | Number of coefficient | PSRF (mean sd) | ESS (mean sd) |
| --- | --- | --- | --- |
| Polychaeta model - Abundance | 1485 | 1.18 0.267 | 701 576 |
| Polychaeta model - Presence/Absence | 1485 | 1.00 0.002 | 4967 417 |
| Phylogeny model - Abundance | 1485 | 1.18 0.204 | 566 420 |
| Phylogeny - Presence/Absence | 1485 | 1.00 0.001 | 4947 408 |
| Traits & Phylogeny - Abundance | 1485 | 1.21 0.317 | 489 358 |
| Traits & Phylogeny - Presence/Absence | 1485 | 1.00 0.008 | 11459 2649 |
| Whole community - Abundance | 4170 | 1.21 0.287 | 739 631 |
| Whole community - Presence/Absence | 4170 | 1.00 0.002 | 4962 406 |

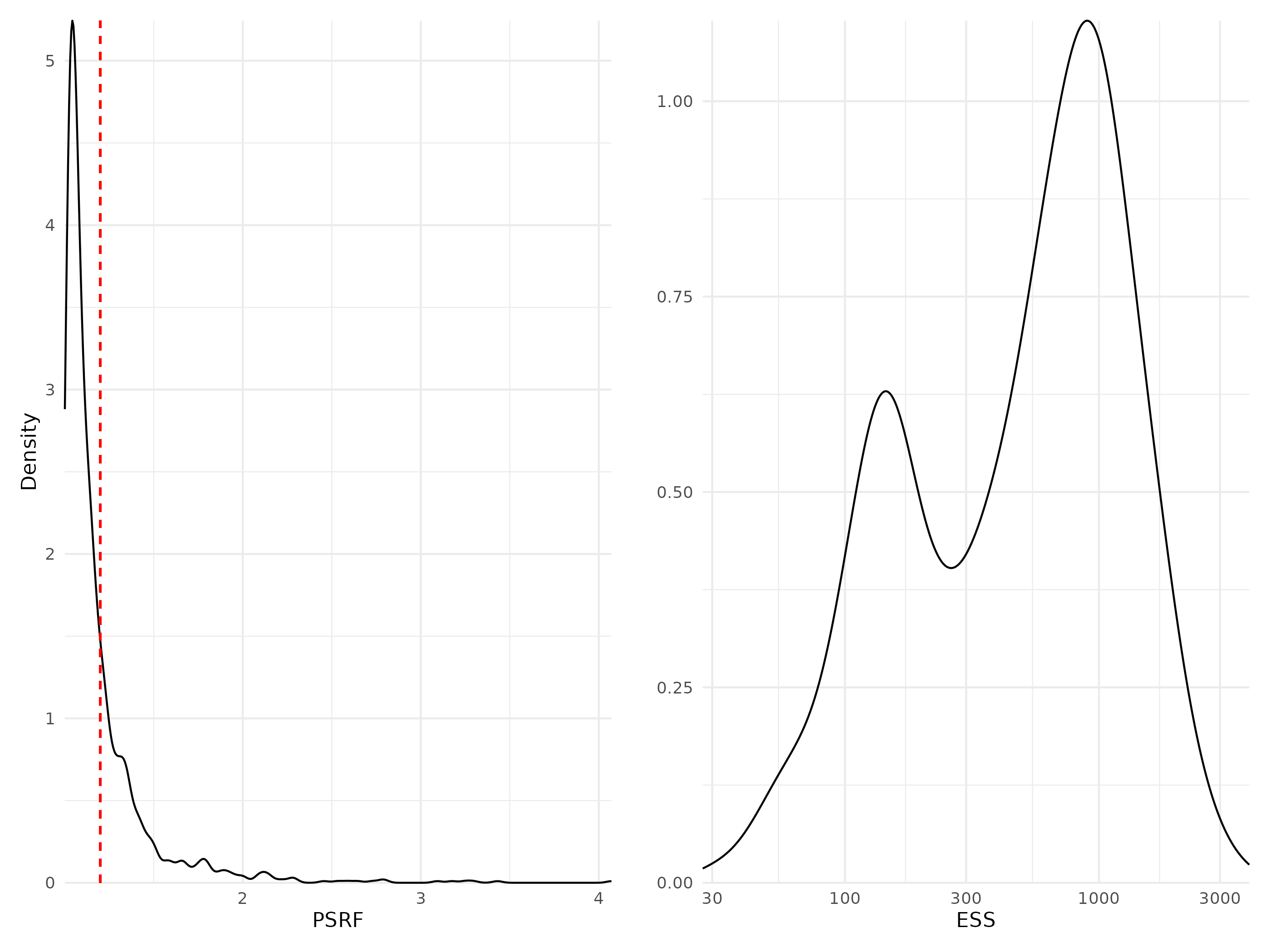


Figure S 16: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the benchmark model fitted with abundance data. For PSRF, values greater than 1.2 (dotted red line) indicate potential convergence issues. ESS estimates the number of independent samples used to estimate each parameter (the more the better).

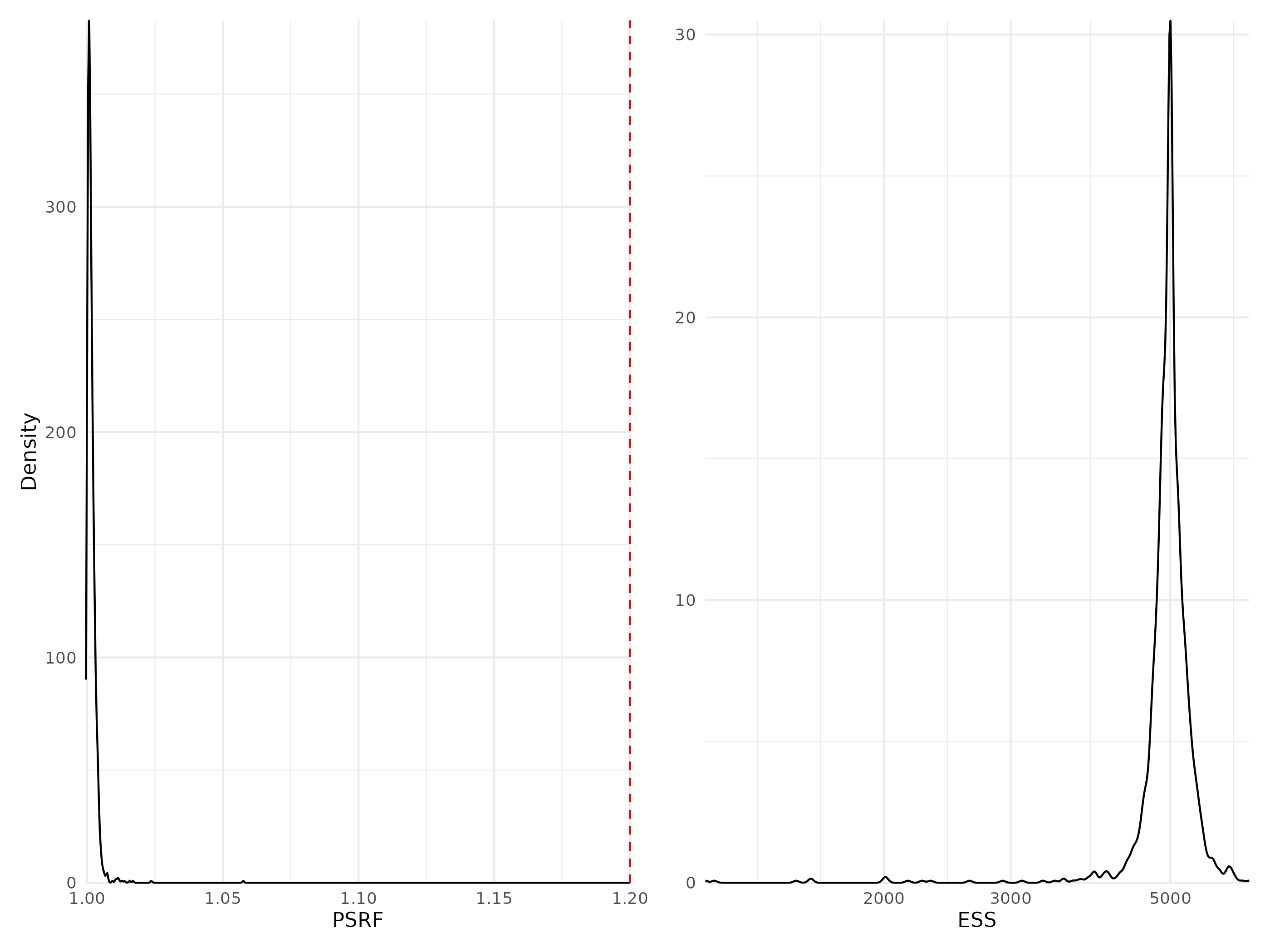


Figure S 17: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the benchmark model fitted with presence/absence data. For further details see Fig. S12.

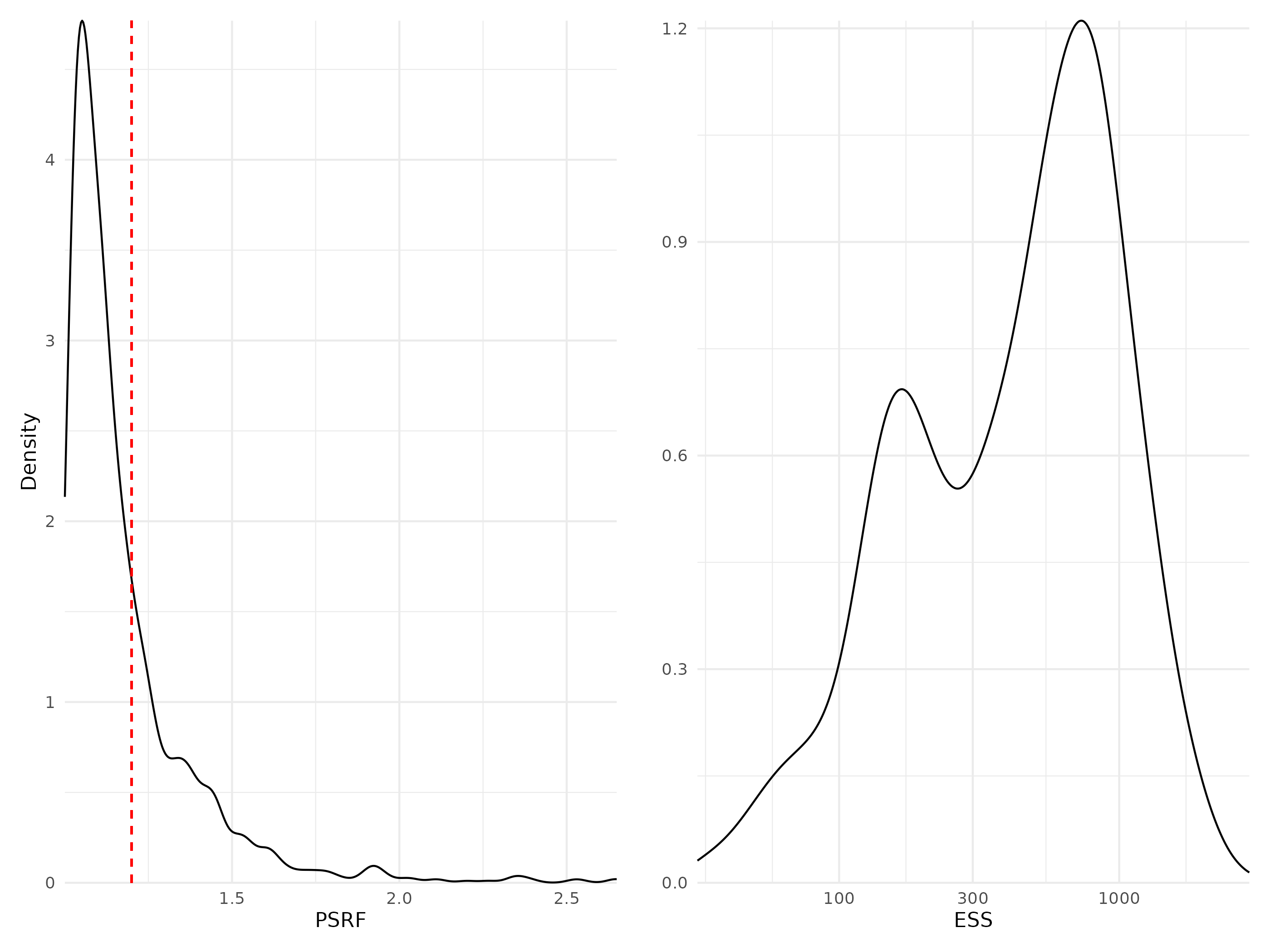


Figure S 18: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the phylogeny model fitted with abundance data. For further details see Fig. S12.

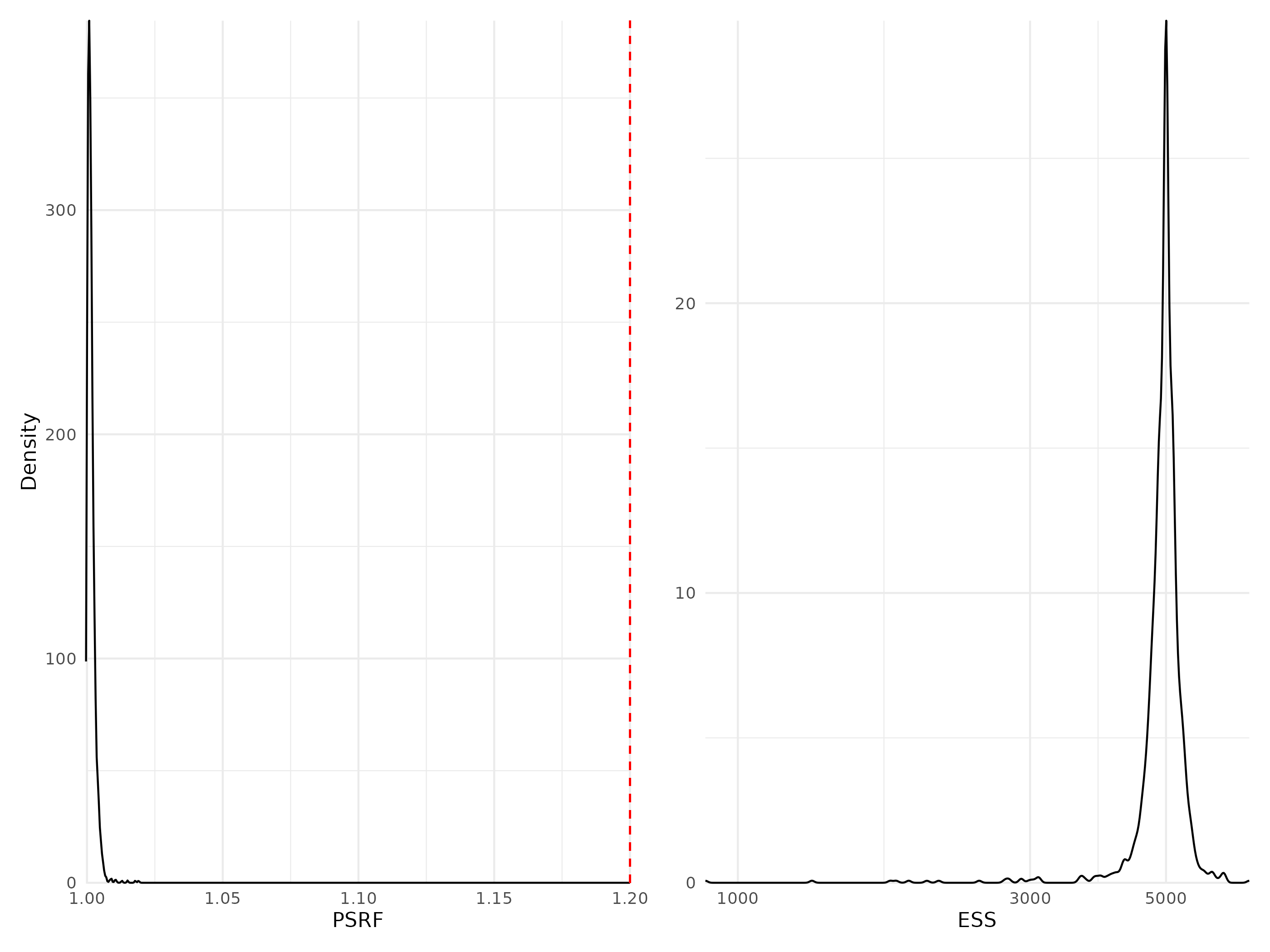


Figure S 19: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the phylogeny model fitted with presence/absence data. For further details see Fig. S12.

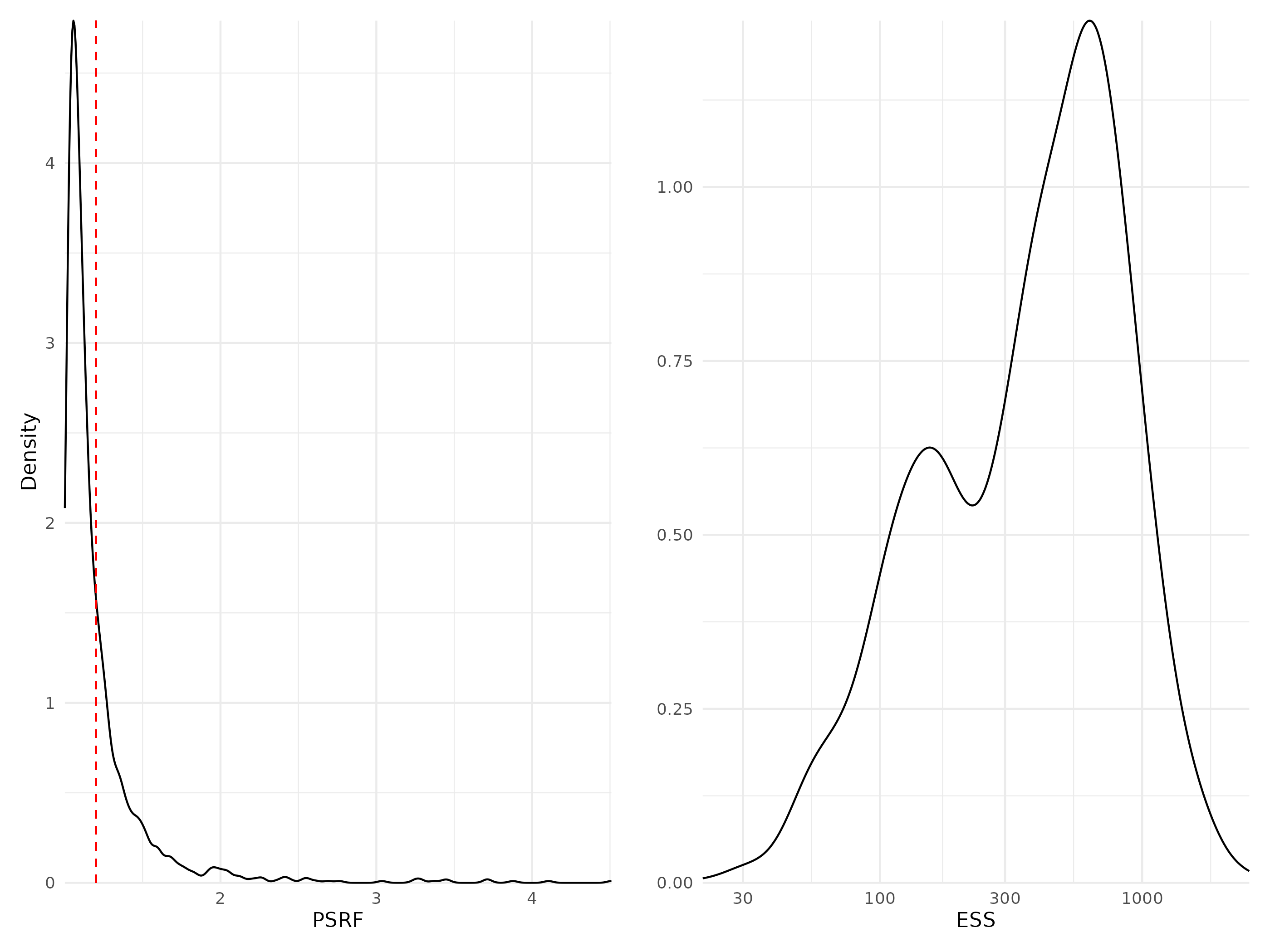


Figure S 20: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the traits & phylogeny model fitted with abundance data. For further details see Fig. S12.

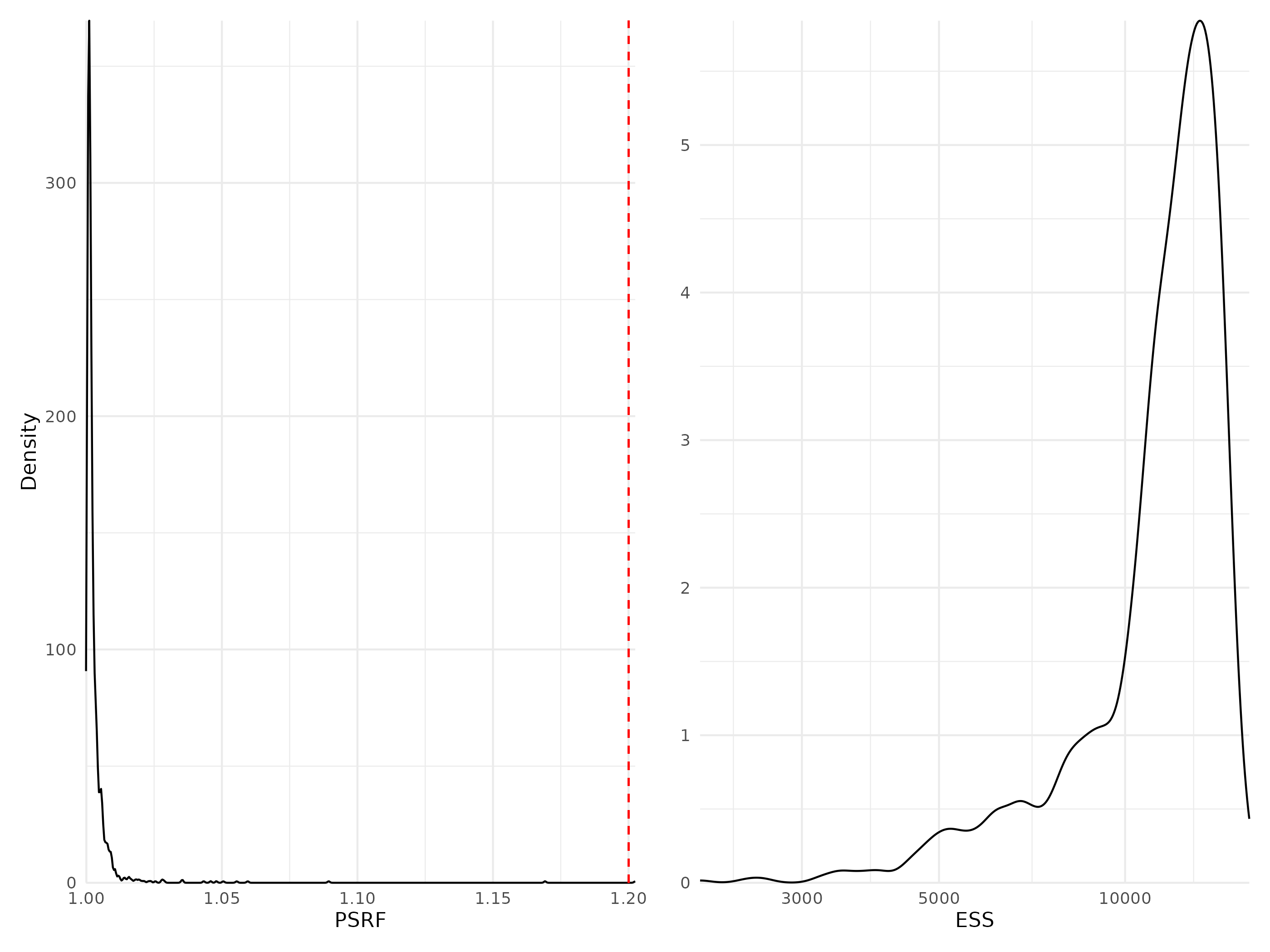


Figure S 21: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the traits & phylogeny model fitted with presence/absence data. For further details see Fig. S12.

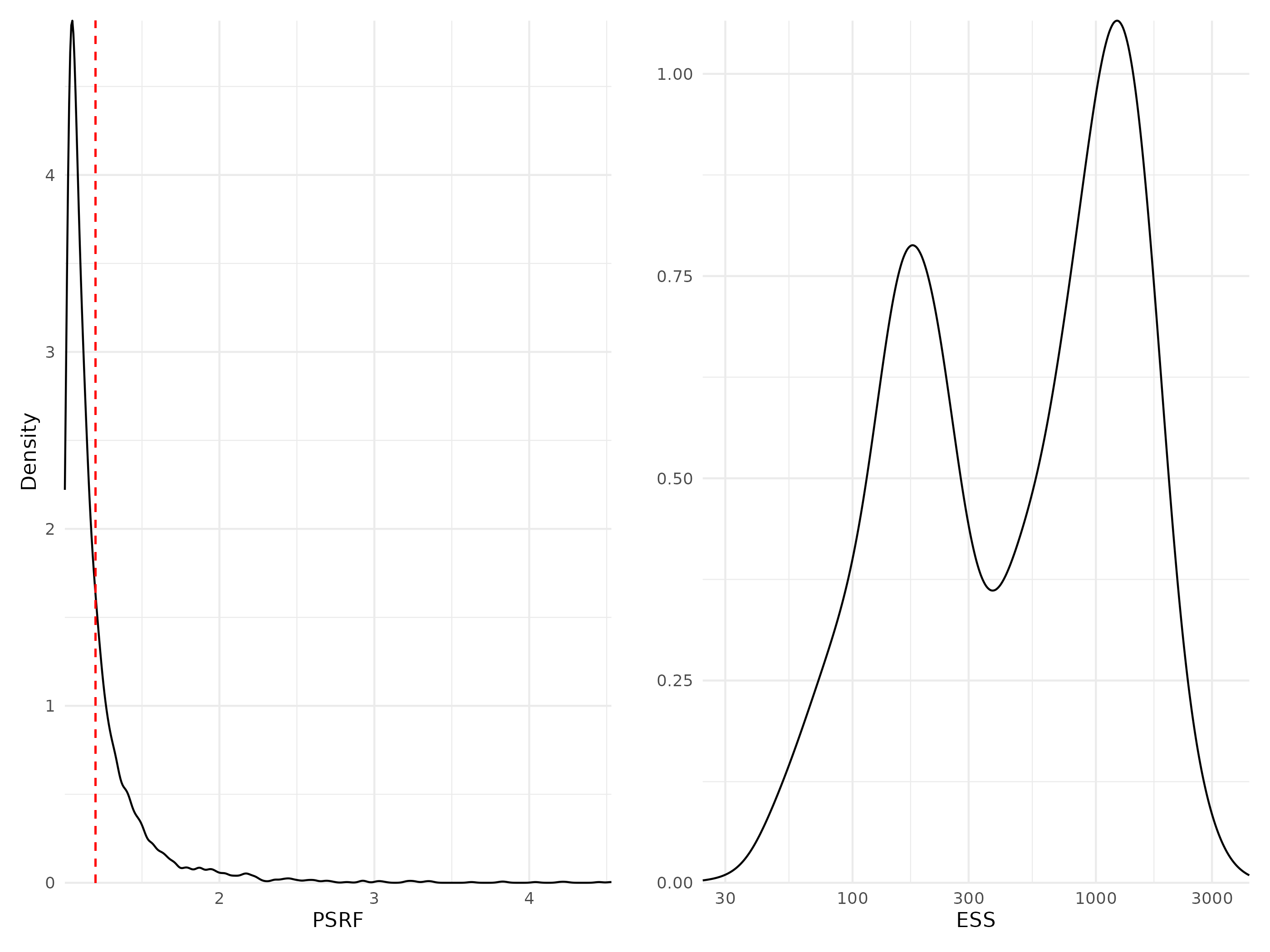


Figure S 22: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the whole community model fitted with abundance data. For further details see Fig. S12.

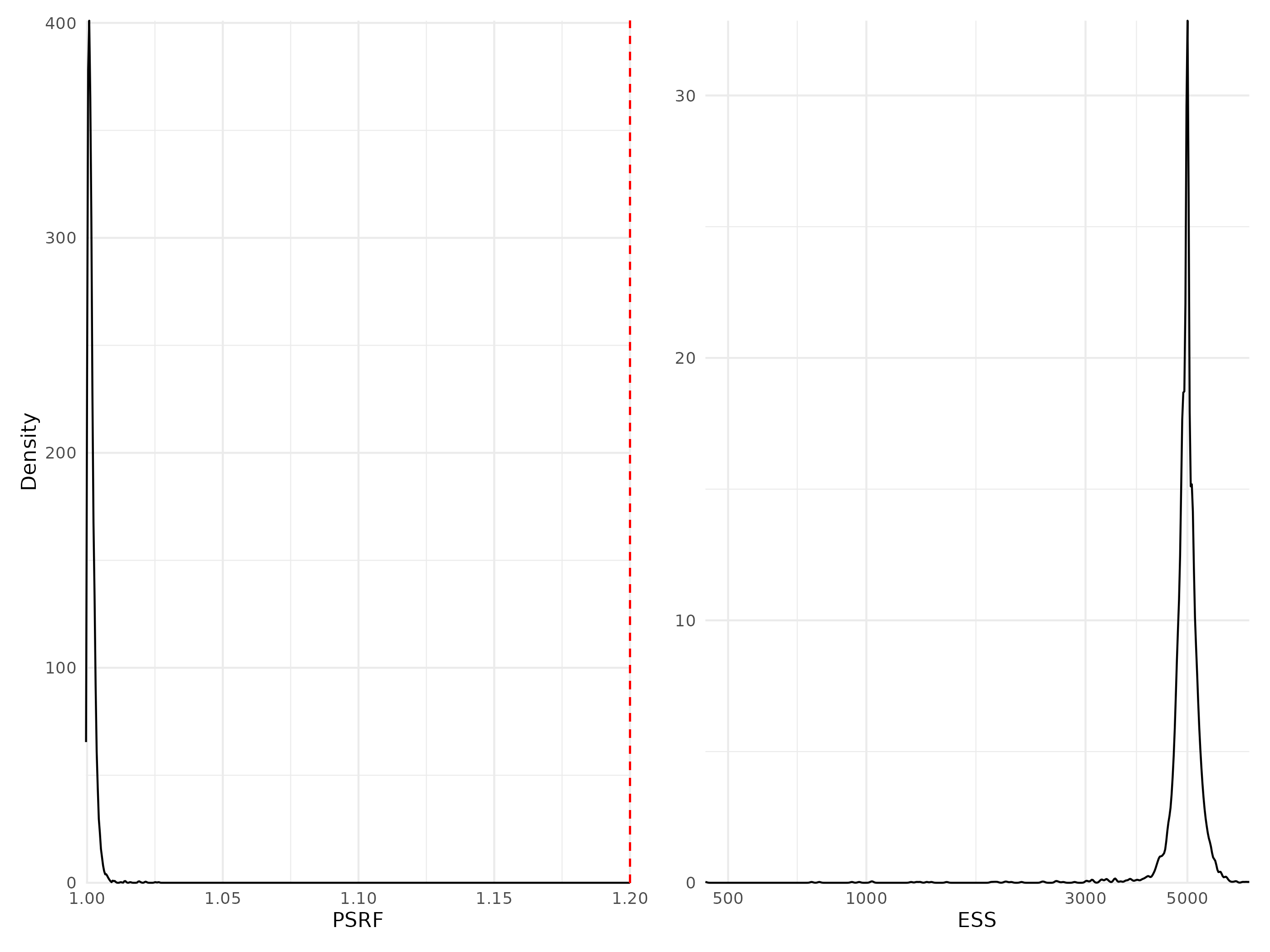


Figure S 23: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Beta regression parameters (i.e environmental coefficients) estimated for the whole community model fitted with presence/absence data. For further details see Fig. S12.

### Traits coefficients

Table S 2: Potential scale reduction factors (PSRF) and effective sample sizes (ESS) for traits regression parameters (i.e gamma coefficients) estimated for the models including phylogeny data. For further details see Fig. S20 to Fig. S21.

| Model | Number of coefficient | PSRF (mean sd) | ESS (mean sd) |
| --- | --- | --- | --- |
| Traits & Phylogeny - Abundance | 60 | 1.08 0.092 | 1232 1209 |
| Traits & Phylogeny - Presence/Absence | 60 | 1.00 0.001 | 13227 1897 |

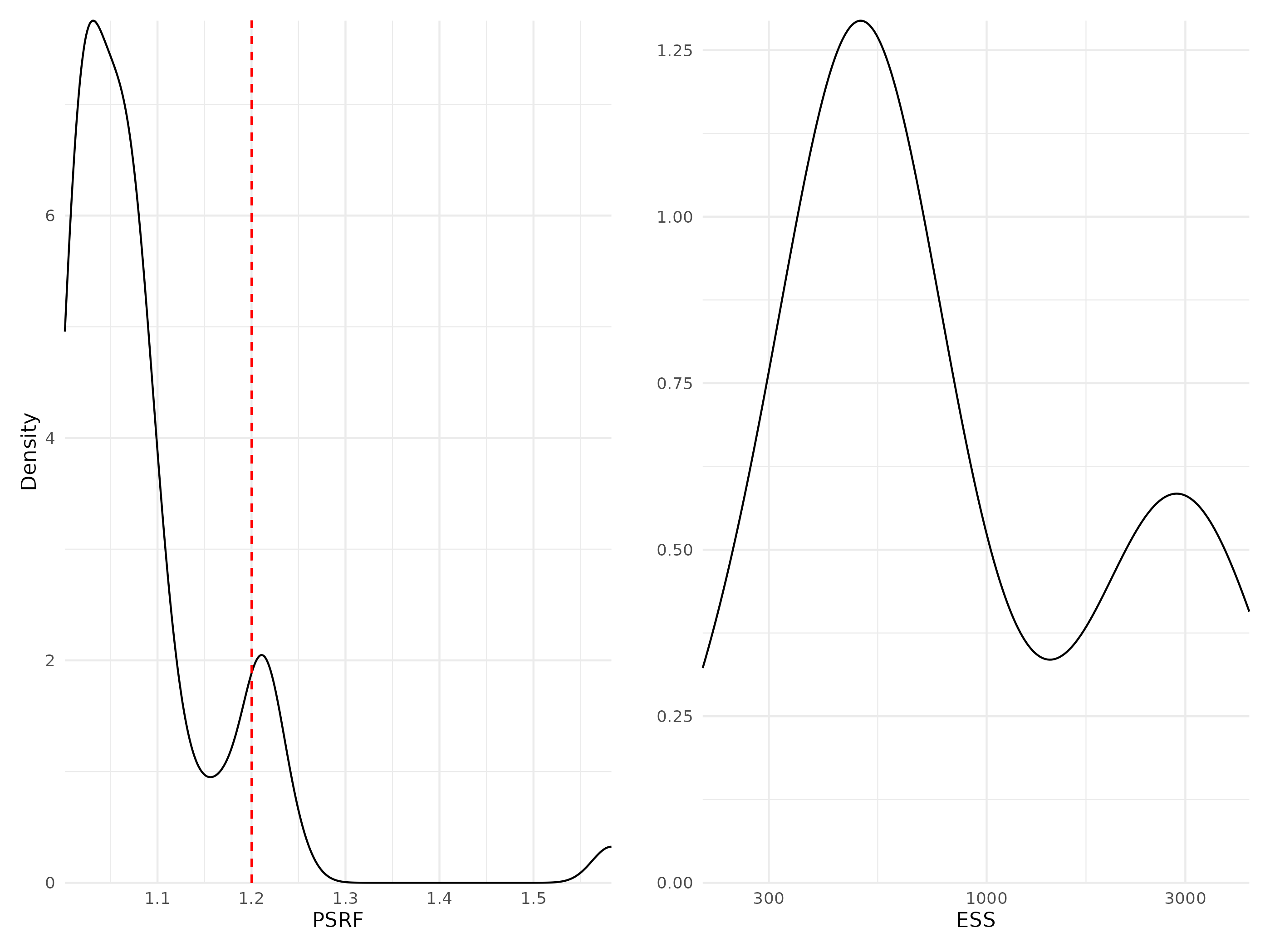


Figure S 24: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Gamma regression parameters (i.e environmental coefficients) estimated for the traits & phylogeny model fitted with abundance data. For further details see Fig. S12.

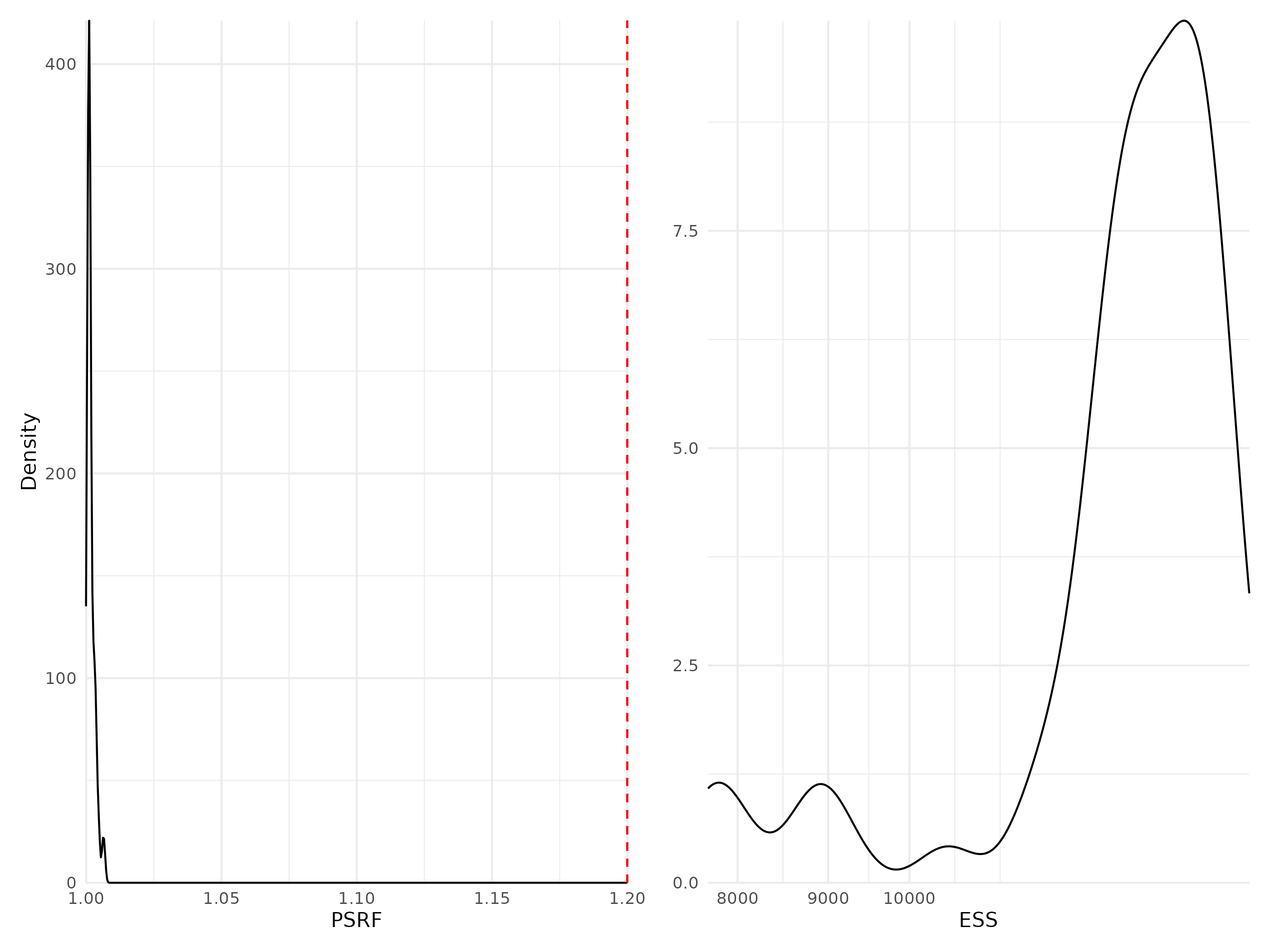


Figure S 25: Density curve of potential scale reduction factors (PSRF see Brooks & Gelman (1998); left panel) and effective sample sizes (ESS; right panel) for Gamma regression parameters (i.e environmental coefficients) estimated for the traits & phylogeny model fitted with presence/absence data. For further details see Fig. S12.

### Phylogeny coefficients

Table S 3: Potential scale reduction factors (PSRF) and effective sample sizes (ESS) for rho regression parameters (i.e phylogeny coefficient) estimated for the models including phylogeny data. For further details see Fig. S12.

| Model PSRF | ESS |  |
| --- | --- | --- |
| Phylogeny model - Abundance | 1.07 | 649 |
| Phylogeny - Presence/Absence | 1.00 | 9349 |
| Traits & Phylogeny - Abundance | 1.15 | 757 |
| Traits & Phylogeny - Presence/Absence | 1.00 | 11291 |

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