

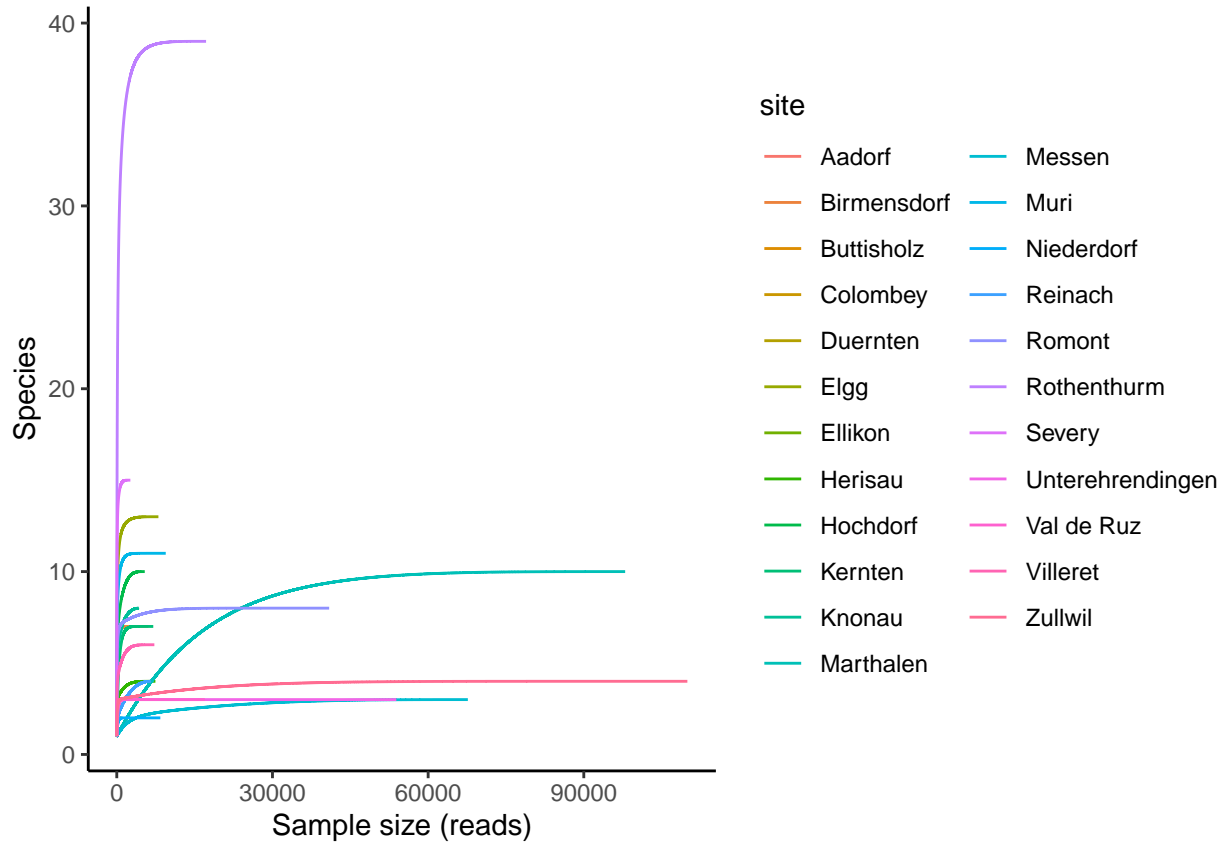
Supplementary Information for:

A triad of kicknet sampling, eDNA metabarcoding, and
predictive modeling to assess aquatic macroinvertebrate
biodiversity

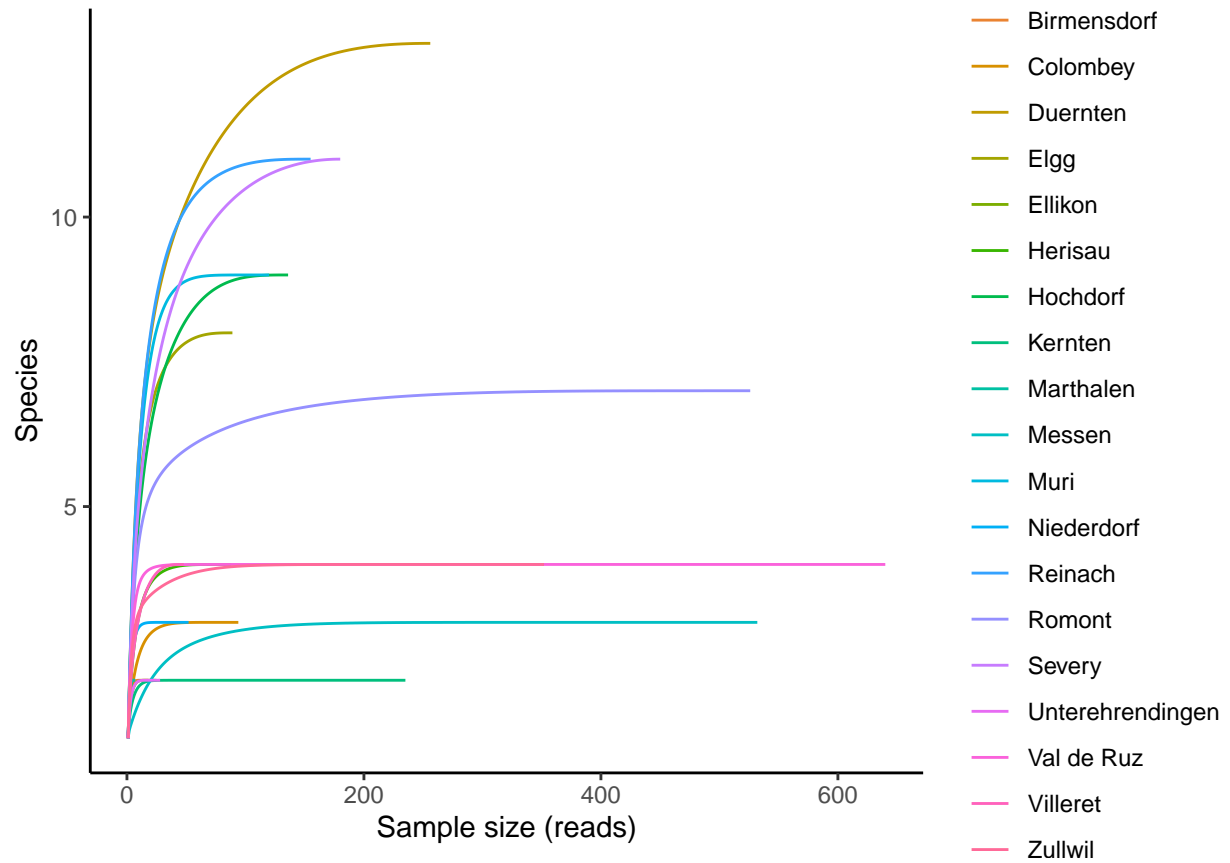
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Christian Stamm, Kristy Deiner and Florian Altermatt

Supplementary Information

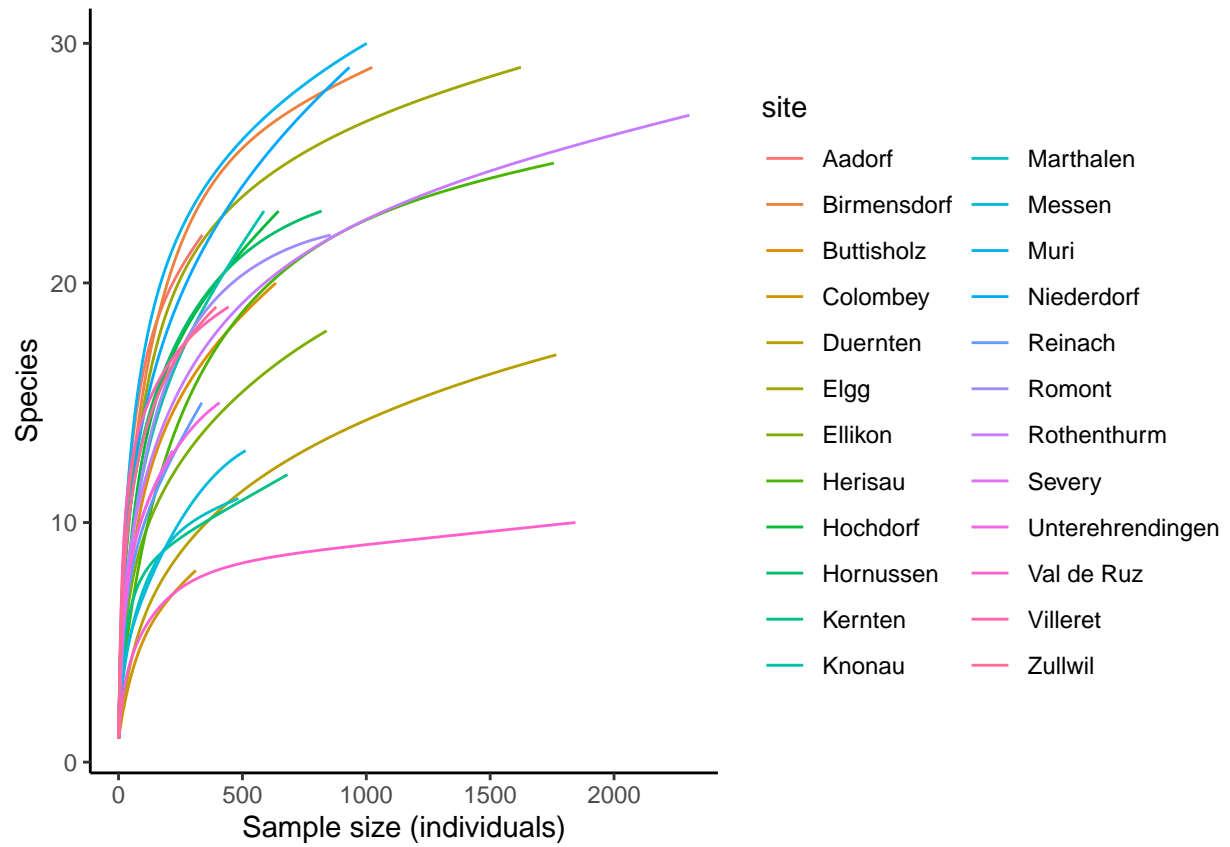
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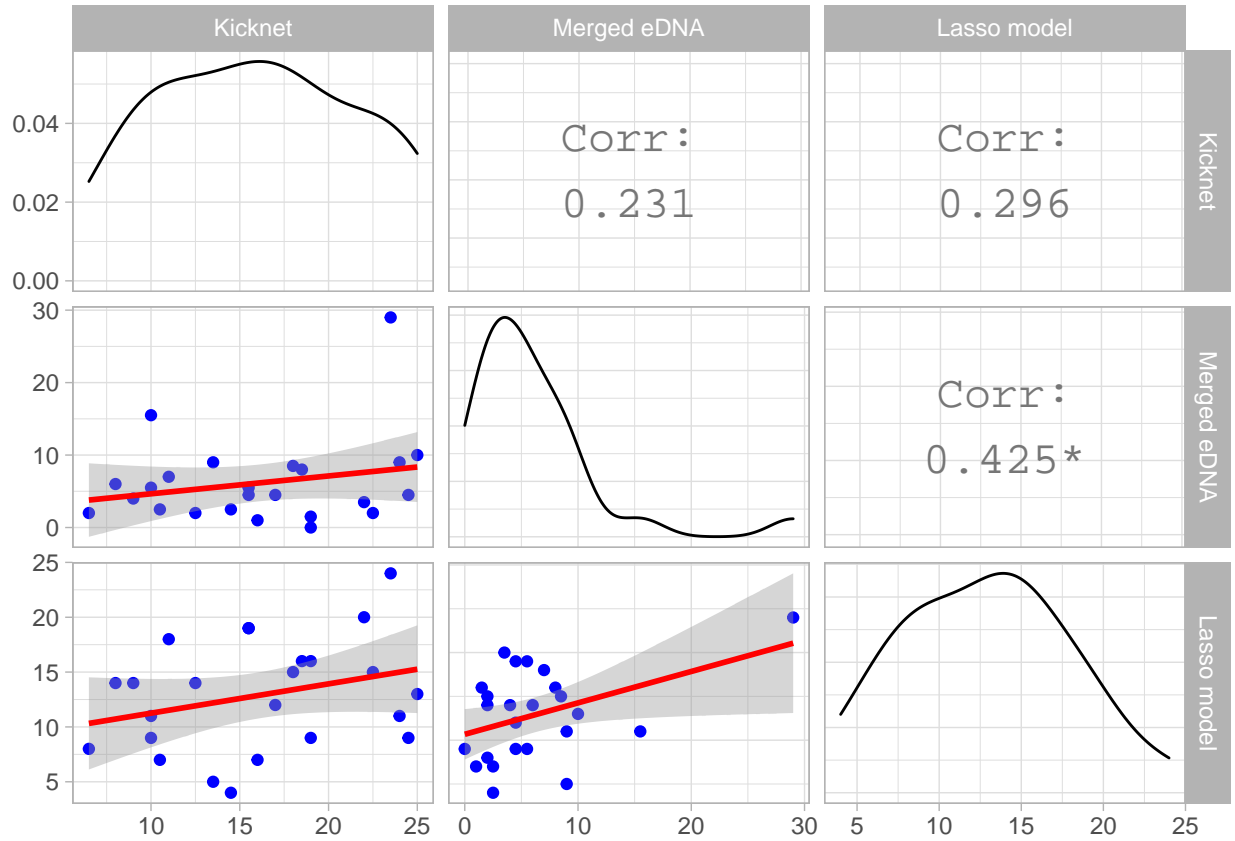
Supplementary Figure 1. Species accumulation curves of the EPT taxa detected using the mlCOI-intF/HCO2198 primers. Locations where EPT taxa were not detected are not shown.



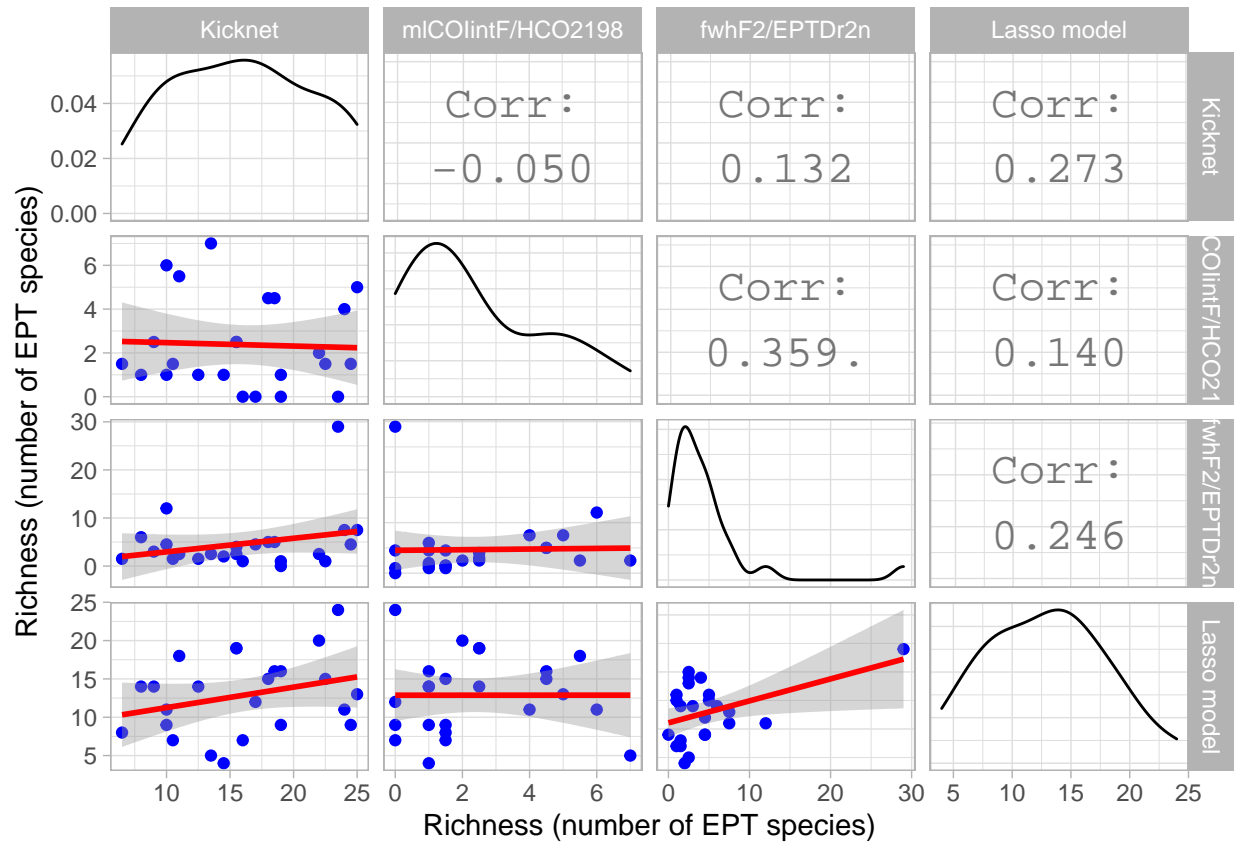
Supplementary Figure 2. Species accumulation curves of the EPT taxa detected using the fwHf2/EPTDr2n primers. Locations where EPT taxa were not detected are not shown.



Supplementary Figure 3. Species accumulation curves of the EPT taxa detected using the kicknet method.



Supplementary Figure 4. Relationships between the EPT richness estimates provided by the Kicknet, eDNA (mlCOIintF/HCO2198 and fwH2/EPTDr2n primers merged), and the predictive model. The upper triangle provides the correlation values between each method (star indicates p-value < 0.05). Lower triangle shows the scatterplots with linear regressions (red lines). The diagonal shows the density estimate for each variable.



Supplementary Figure 5. Relationships between the EPT richness estimates provided by the four investigated methods. The diagonal panels show the density estimate of EPT richness for each method. For each combination of methods, panels located in the lower triangle show the scatterplot of the EPT richness estimated by each method (x- and y-axis) with linear regression (red lines). Panels located in the upper triangle provides the Spearman correlation values between each method.