

Supplementary

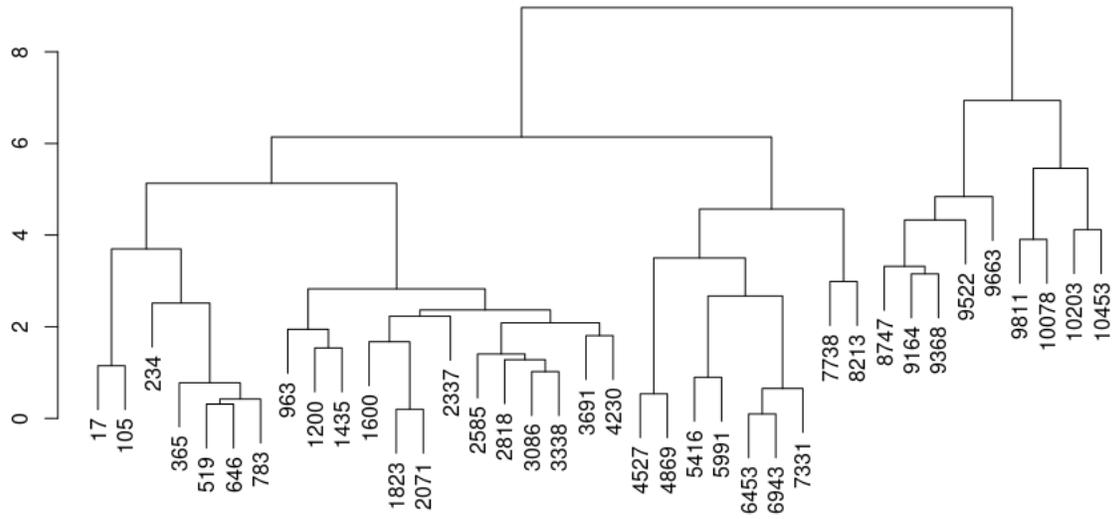


Figure S1. CONISS clustering based on proportions of PCR replicates. Sample ages are displayed on the labels of leaves.

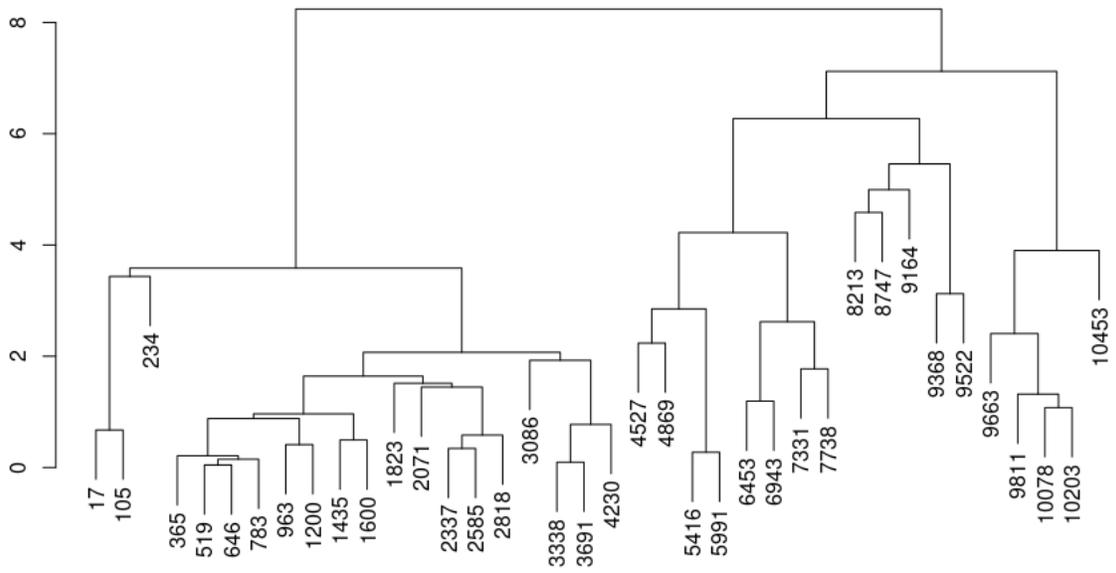
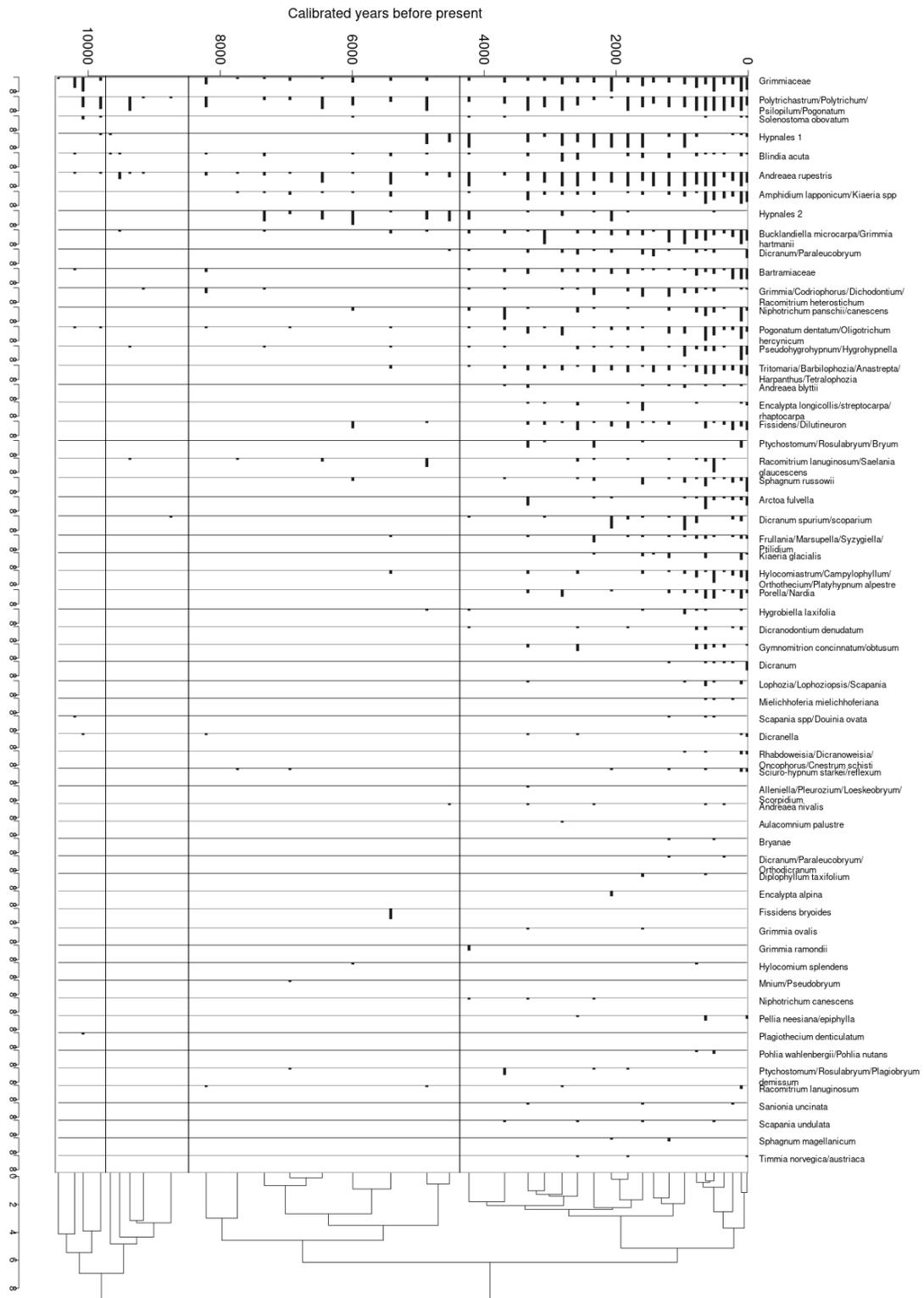
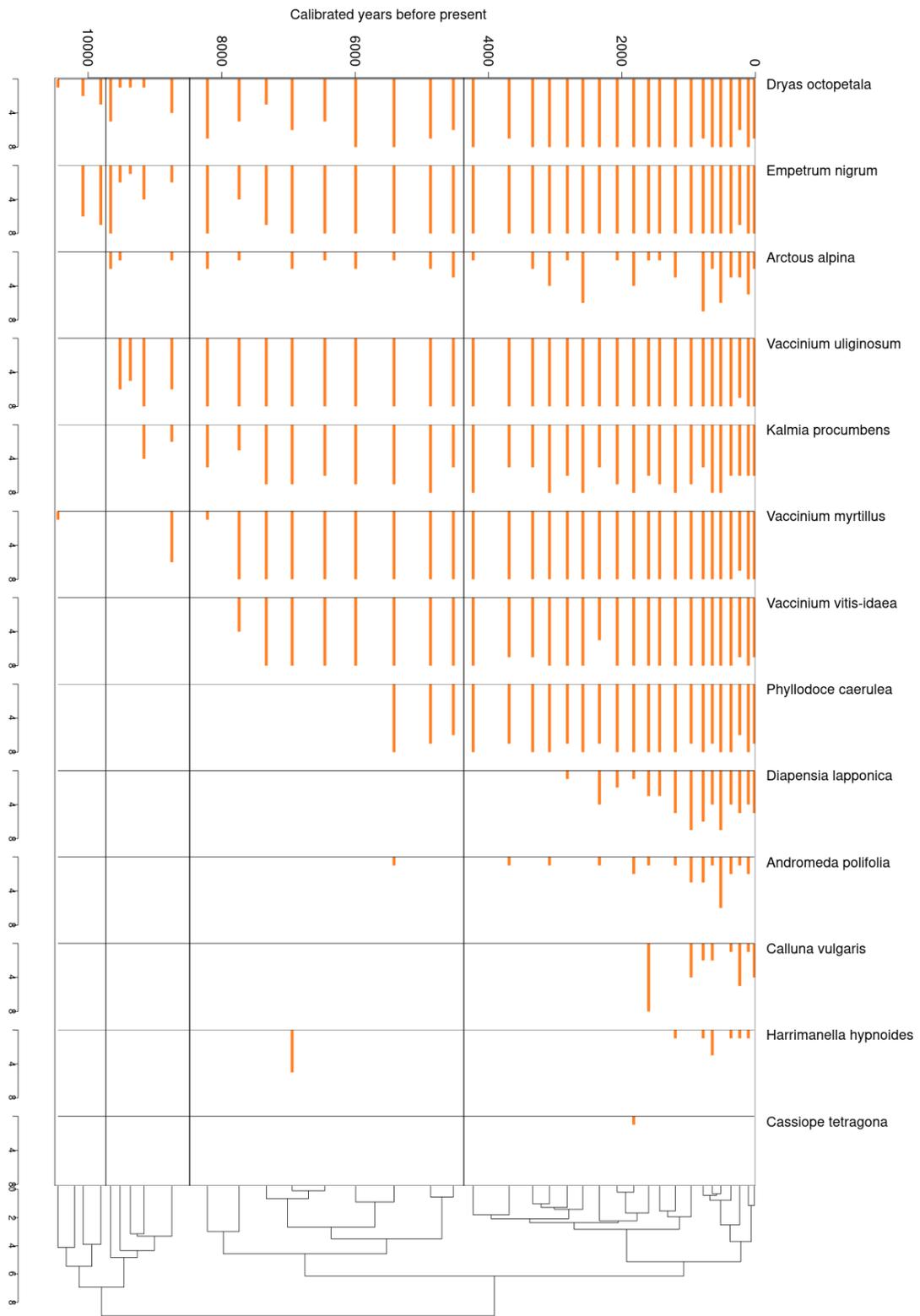


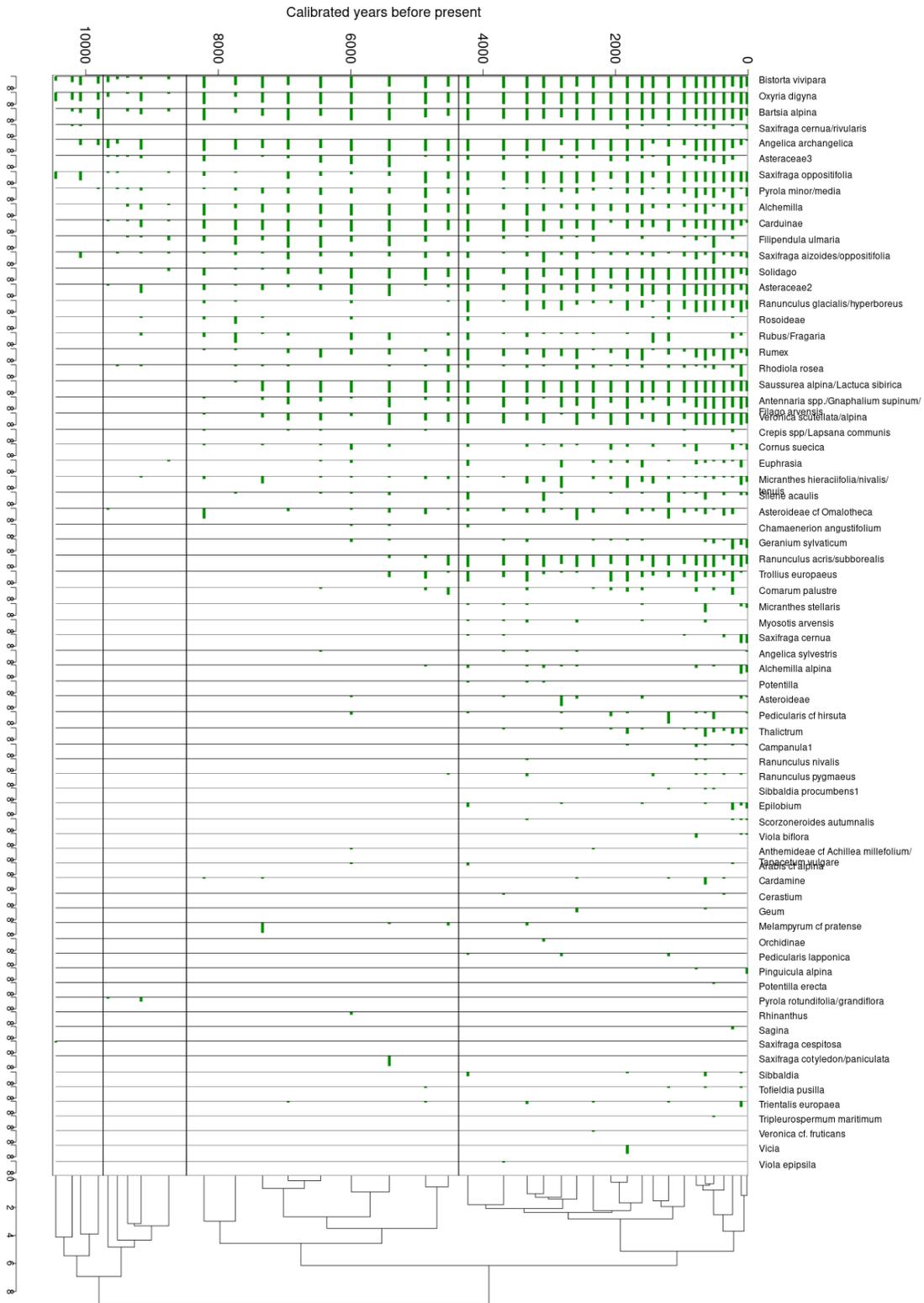
Figure S2. CONISS clustering based on proportions of total filtered reads. Sample ages are displayed on the labels of leaves.

Bryophytes

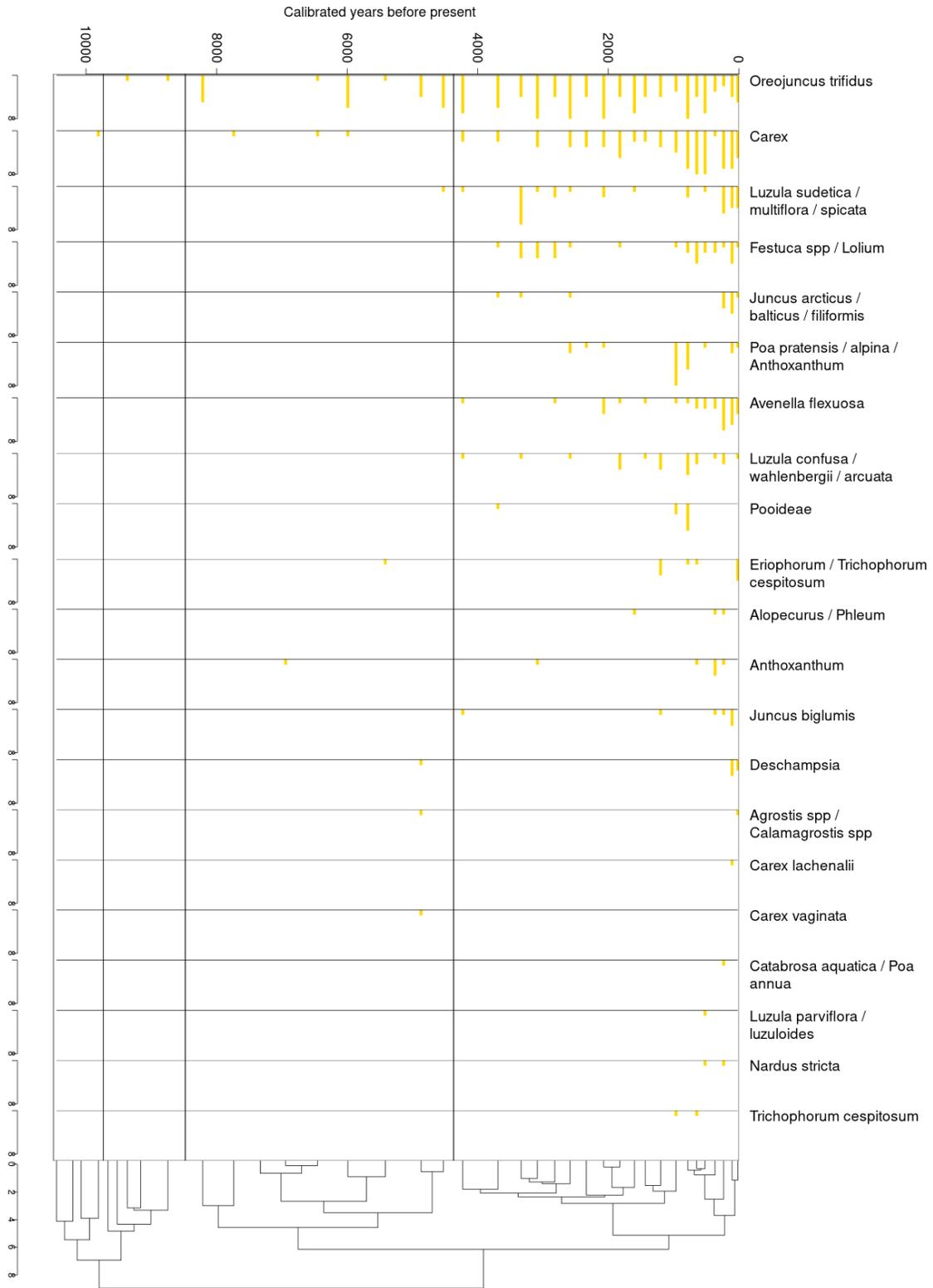




Forbs



Graminoids



Trees

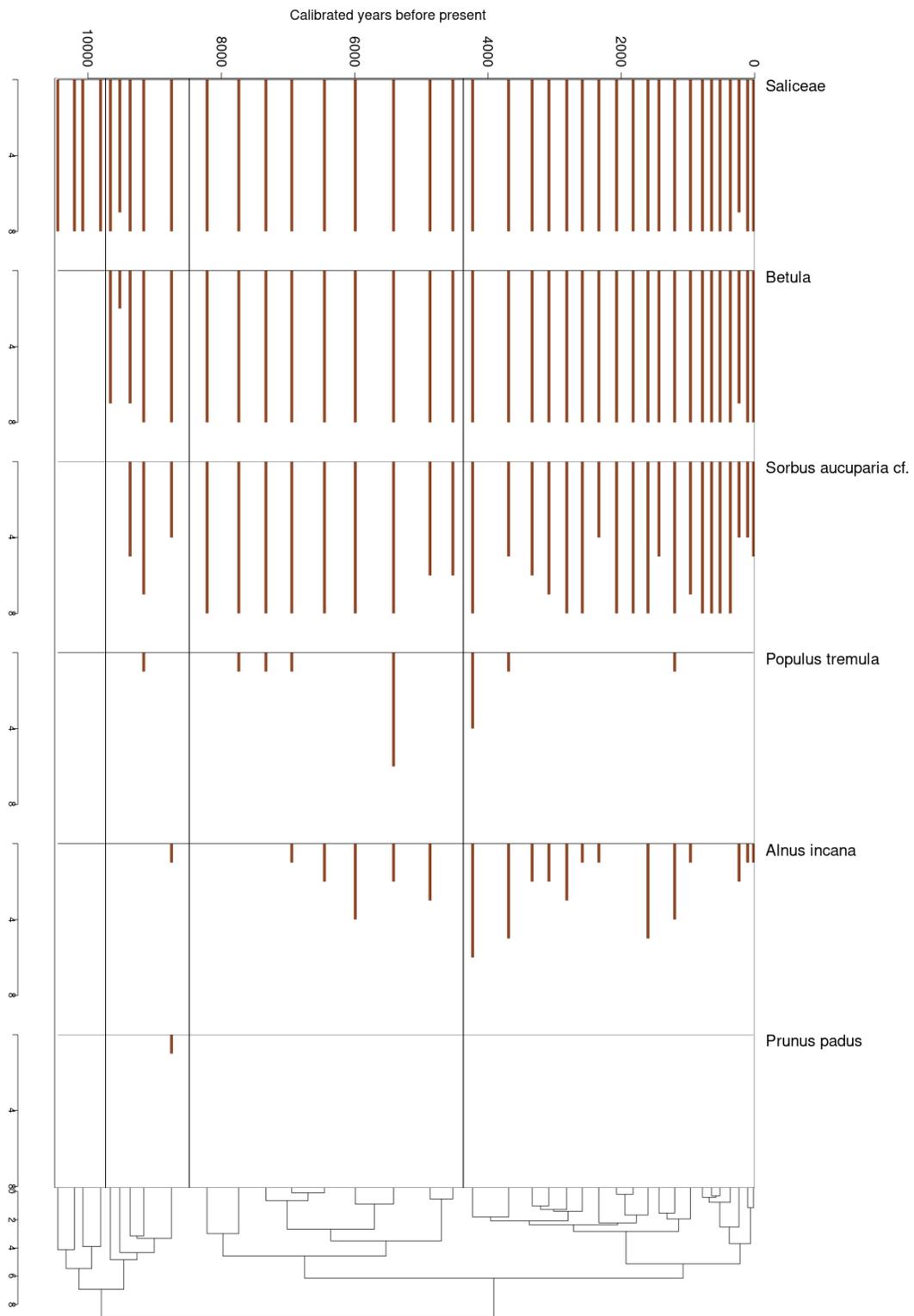


Figure S3. Number of PCR replicates each species appears in separated by functional group. CONISS boundaries are indicated by vertical lines and clustering is present at the bottom of the figure.

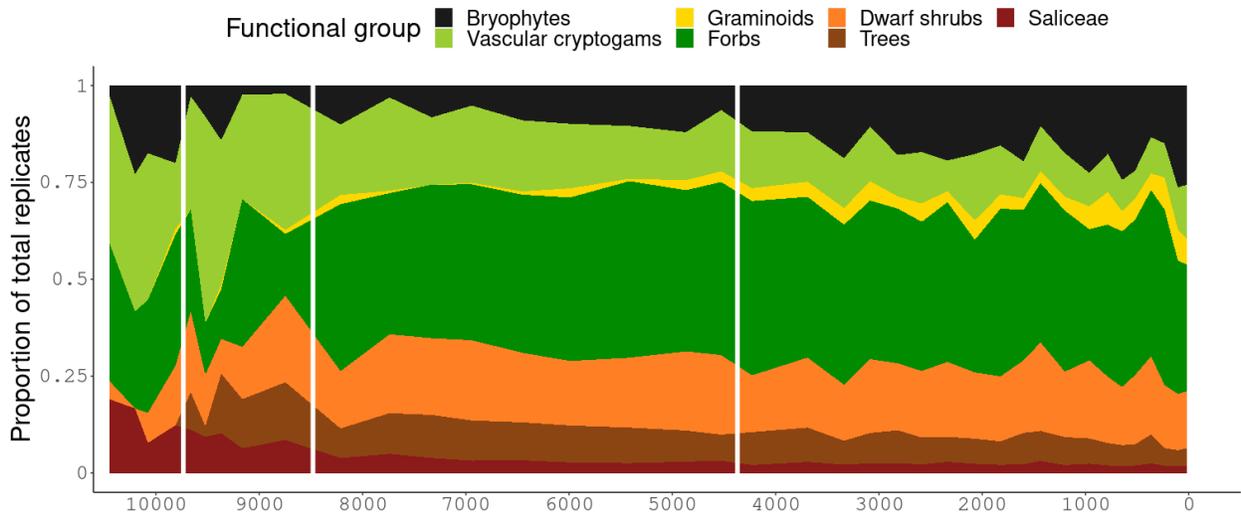
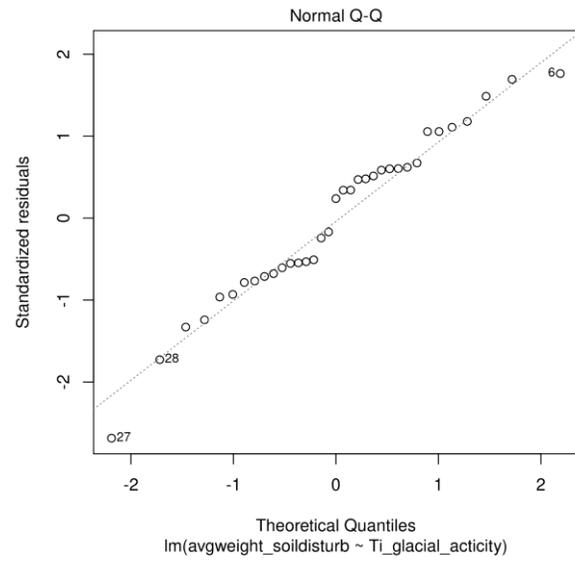
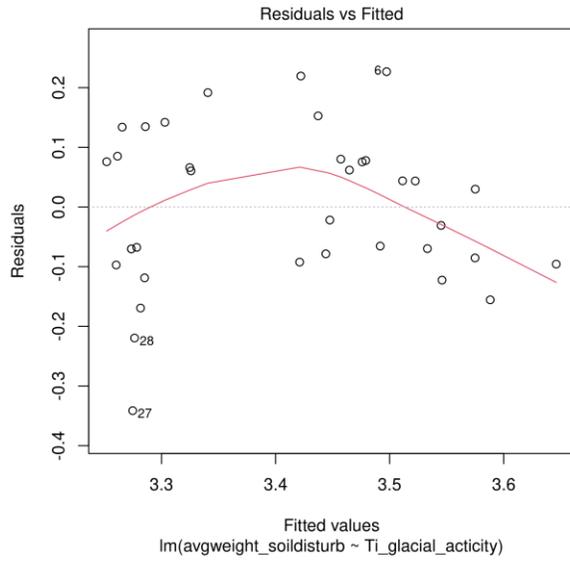
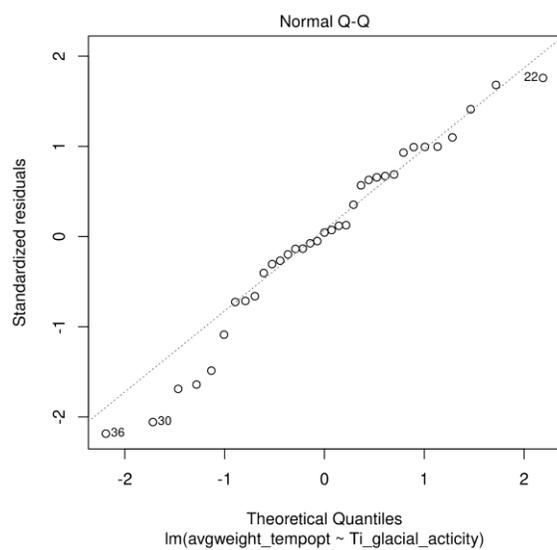
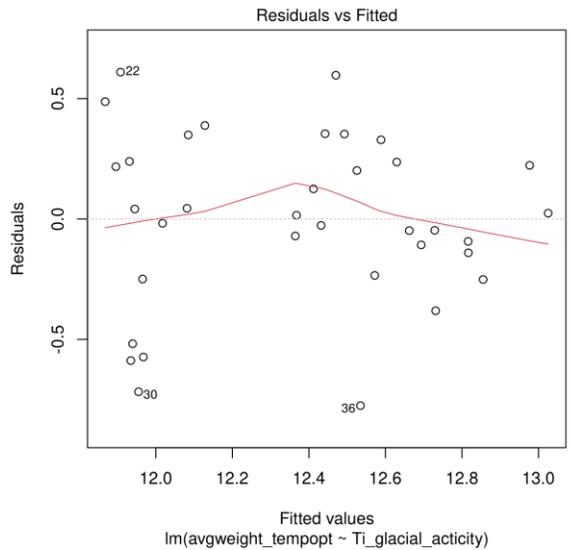


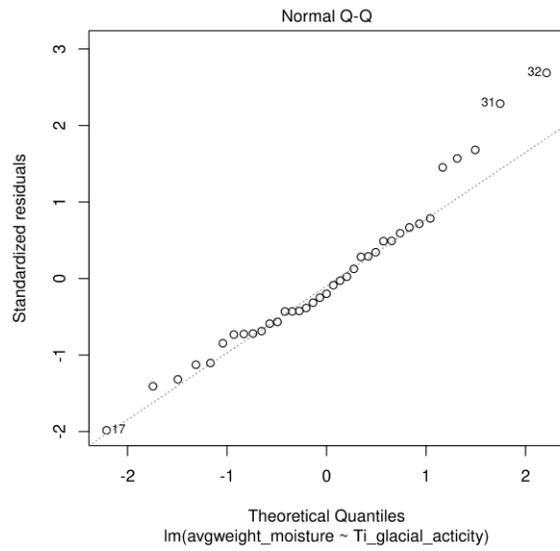
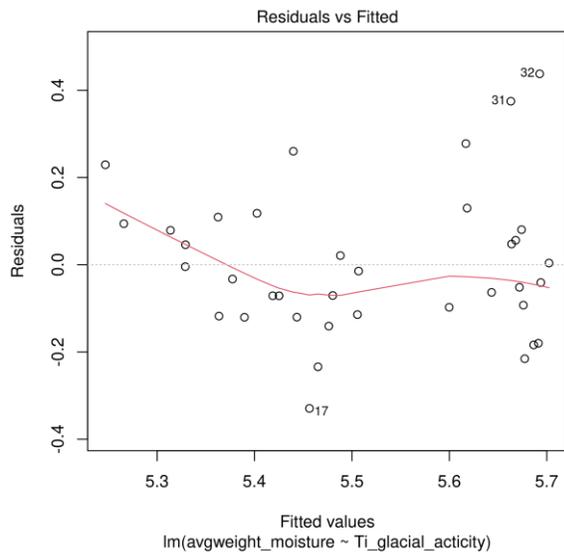
Figure S4. Proportion of PCR replicates based on functional groups. Vegetation zone boundaries based on CONISS analyses are demarcated with vertical white bars.

S5. Linear Regression diagnostic plots

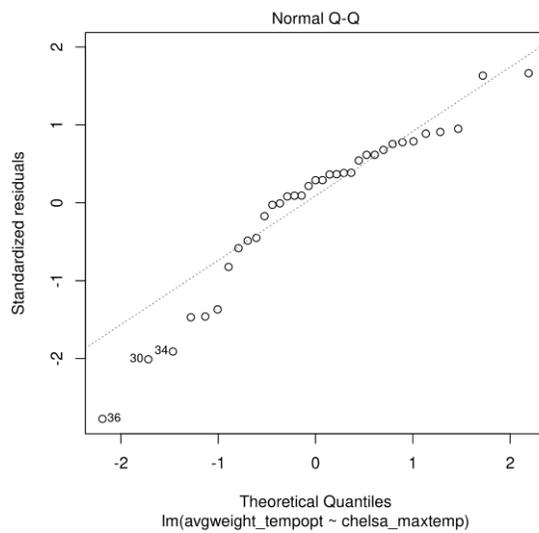
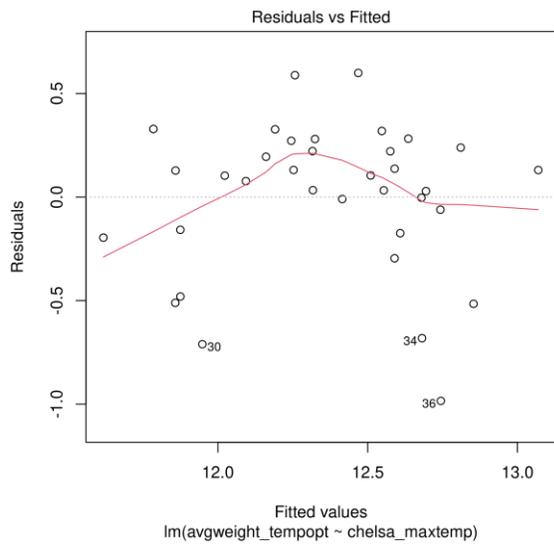


Diagnostic plots of the linear model fit between **soil disturbance trait value** and **glacial activity**.

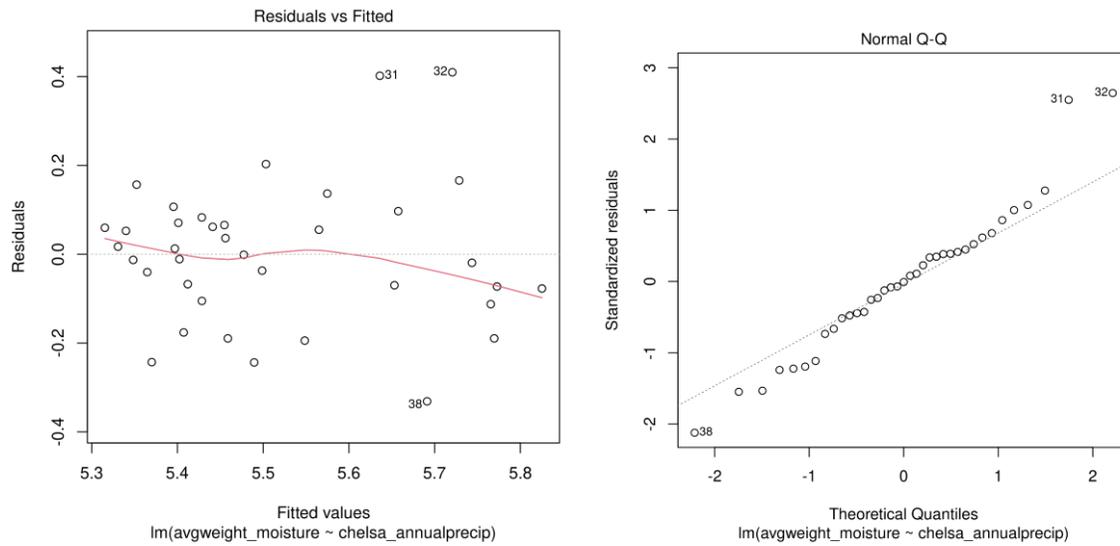




Daignostic plots of the linear model fit between **moisture trait value** and **glacial activity**



Diagnostic plots of the linear model fit between **temperature optimum trait value** and **CHELSA-TraCE21k mean temperature of warmest quarter (bio10)**.



Diagnostic plots of the linear model fit between **moisture trait value** and **CHELSA-TraCE21k annual precipitation (bio12)**.

Figure S5. Diagnostic plots for linear regressions.