Supplementary Information
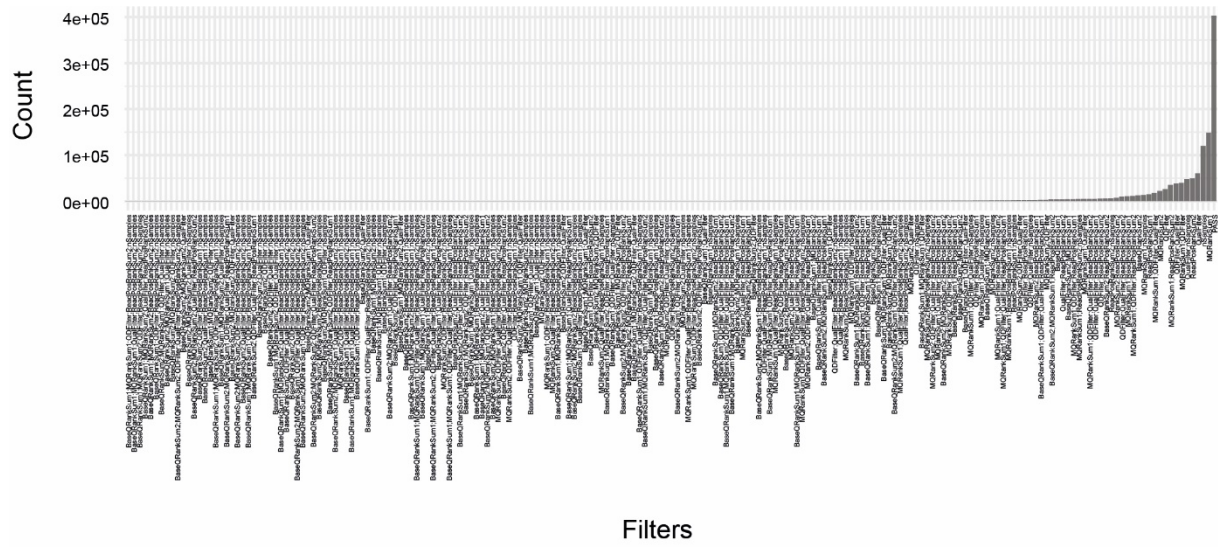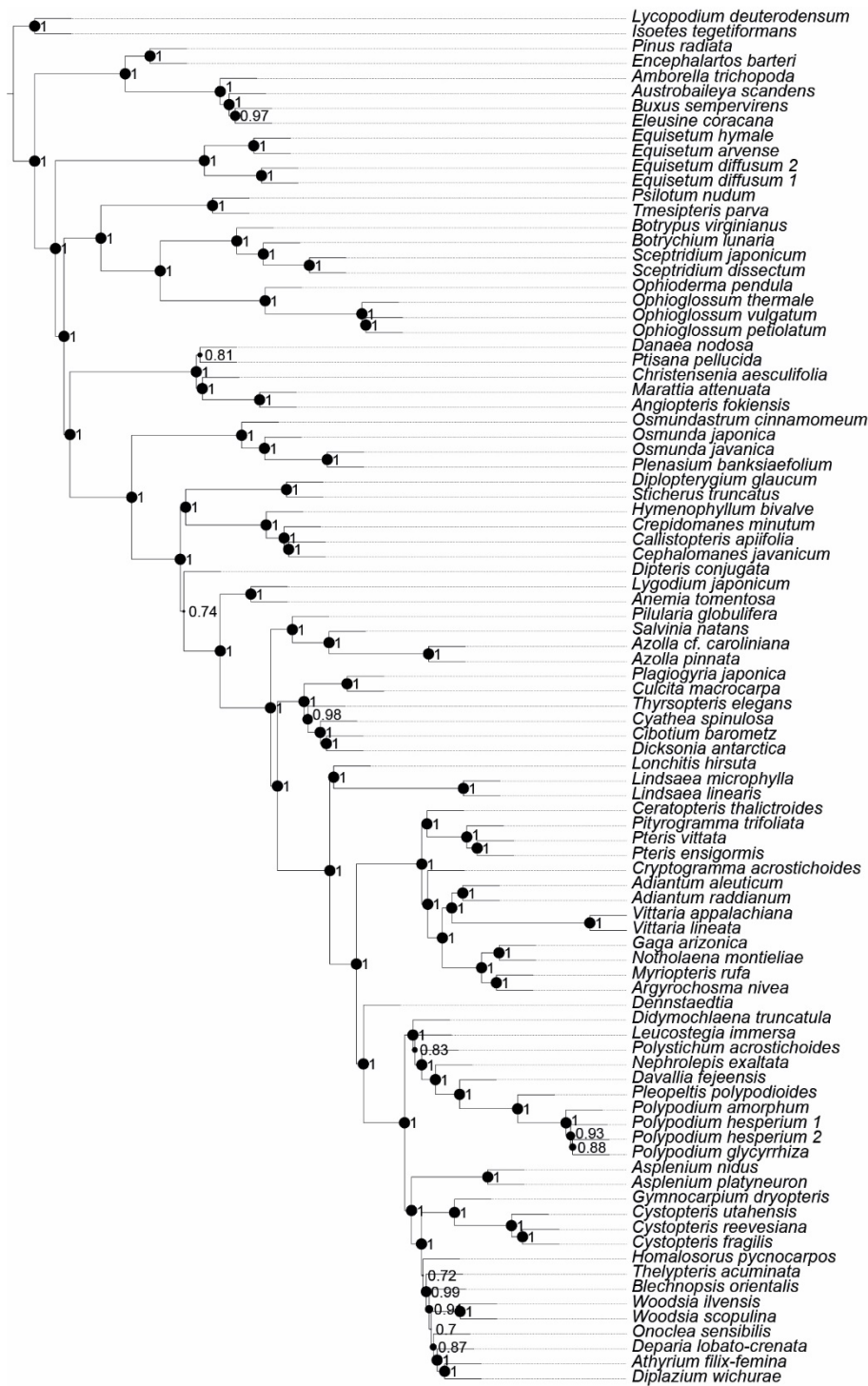
A transcriptome for the early-branching fern *Botrychium lunaria* enables fine-grained resolution of population structure
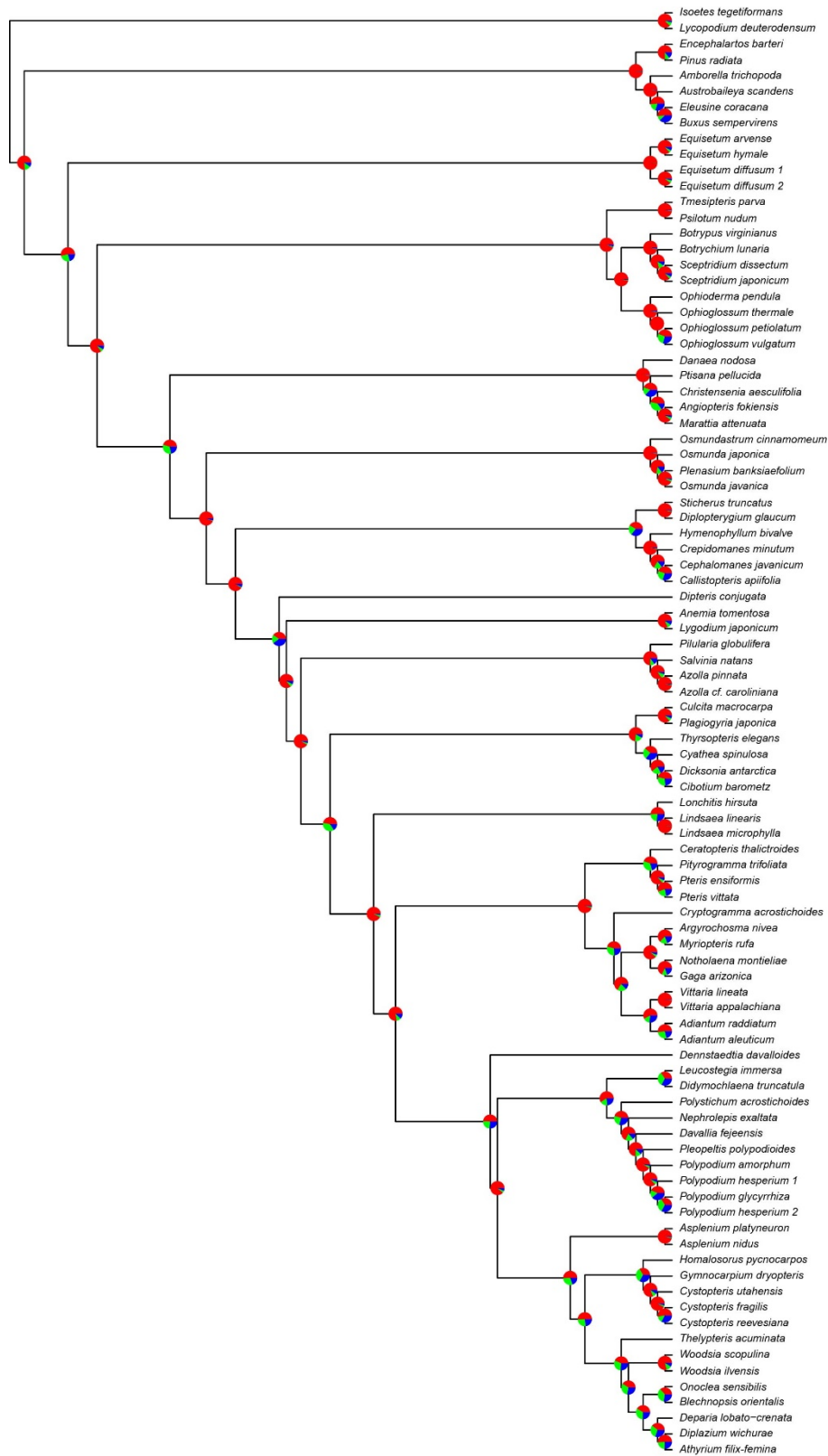
Supplementary Figures

Supplementary Figure S1: SNP filtering outcome. The number of filter flagged loci per individual (or combination of quality criteria). PASS identifies the number of SNPs passing all filtering criteria.

Supplementary Figure S2: Species tree estimated out of 525 orthologous genes including 90 taxa using Astral. The branch support is indicated by the bootstrap values at the nodes. Larger node sizes correspond to higher bootstrap values.

Supplementary Figure S3: Astral species tree on which the branches quartet support values were depicted by pie charts. Inside each pie chart, the red, the green and the blue slices correspond to the normalized quartet scores for the main topology, the first and the second alternative, respectively.

Supplementary Tables

(see separate files)

Supplementary Table S1: Information about the transcriptomes used in the phylogenomic analyses. The identifiers refer to those originally published by Leebens-Mack et al. (2019), Qi et al. (2018) and Shen et al. (2017) and used in this study.

Supplementary Table S2: Raw and trimmed read distribution for the *Botrychium lunaria* transcriptomes. Percentage of retained reads after trimming, pseudo-aligned reads by Kallisto and reads aligned by Bowtie.

Supplementary Table S3: Information regarding the CRY2cA sequence dataset used for the phylogenetic inference of Botrychium species. The individual identifiers refer to those used by Daupin et al. (2018) and in this study.

Supplementary Table S4: **Orthogroups table given by OrthoFinder.**

Supplementary Table S5: Filtered orthogroups table.

Supplementary Files

[Available from Zenodo: https://doi.org/10.5281/zenodo.3959727]

File S1: Alignment of Botrychium CRY2cA sequences used to infer the genus-level phylogeny.

File S2: Peptide sequences used to infer the orthogroups named according species names or identifiers (see Table S1).

File S3: Alignments of the orthogroup sequences subset used to infer the phylogenomy.

File S4: Output files from modeltest-ng named by orthogroup names.

File S5: Output files from raxml-ng named by orthogroup names.