SUPPORTING INFORMATION

Summary

In this Supporting Information, we report additional methods details with respect to the trait data, the climate data, and the analysis. In addition, to more fully explain the method, we include several additional figures. We show the top-five lineages, including the population of lineages from which they were selected, for five important traits (Figure S1 on five separate pages); the bivariate distribution of three selected clades with respect to SLA and leaf N, components of the leaf economic spectrum (Figure S2), the geographic distribution of the clades where this proved useful for interpretation (Figure S3); the procedure for selecting the top six nodes in the leaf N trait, to illustrate the internal behavior of our new comparative method, especially the relative contribution of components of extremeness and the sample size weighting to the results (Figure S4). Finally, we provide references for data used in analyses.

SUPPORTING METHODS

TRAITS DATABASE

We compiled a database for five plant functional traits. Each of these traits is the result of a separate research initiative in which data were gathered directly from researchers leading those efforts and/or the literature; in most, but not all cases, these data have been published elsewhere. Detailed methods for data collection and assembly for each trait are available in the original publications; further data were added for some traits from the primary literature (for references see description of individual traits and Supporting References below). For our compilation, all data were brought to common units for a given trait and thoroughly error checked. Anomalies were discussed with original data set collectors. To map species traits to phylogenies, species geometric means were taken for all traits except maximum height, for which maximum values were used.

Most data sets reside within the TRY Initiative on Plant Traits (Kattge et al. 2011), which is an ongoing effort to collate, error-check, and make available these types of data. Because of data sharing agreements, we are unable to make the raw trait data matrix available here, but the vast majority of data are available via TRY. Upon request, we can provide the taxonomic and trait error corrections that we used for this analysis.

Leaf economics traits (Specific leaf area and Leaf nitrogen content) We used data from previously published sources with the largest contribution being the data from Wright et al. (2004, available in the supplement of that paper). To include more recent data, we added many other recent papers (see Supporting References).

Leaf size is assembled from LEDA (Kleyer et al. 2008), with the addition of published data including many recent references (see Supporting References). Aside from the data from LEDA, these data are curated by Ian Wright. Leaf size of compound leaves is far more commonly interpreted (and reported) as leaflets rather than entire leaves. When including leaflet data for compound-leaved species our dataset included 36,003 observations for “leaf” size (from 8751 species; this equals number of species with leaflets plus with entire leaves for simple leaves) versus 9233 observations (5731 species) when using entire-leaf data (both totals include all simple-leaved species). In

this paper, we report analyses with compound leaves represented as leaflets. We analyzed both datasets, and results were quantitatively similar.

Seed mass is based on the data curated at Kew (Royal Botanic Gardens Kew Seed Information Database (SID), April 2011). We included additional data (see Supporting References). The seed mass data are freely available from Kew Botanic Garden (Royal Botanic Gardens Kew Seed Information Database (SID)), within the papers listed above and from TRY.

Maximum height: the majority of the plant height data were compiled in 2006, under a range of data sharing agreements, most of which require us not to pass on or reproduce the data. The data that can be made available have been submitted to the TRY database. We provide a list of references and sources for the height data in the Supporting References.

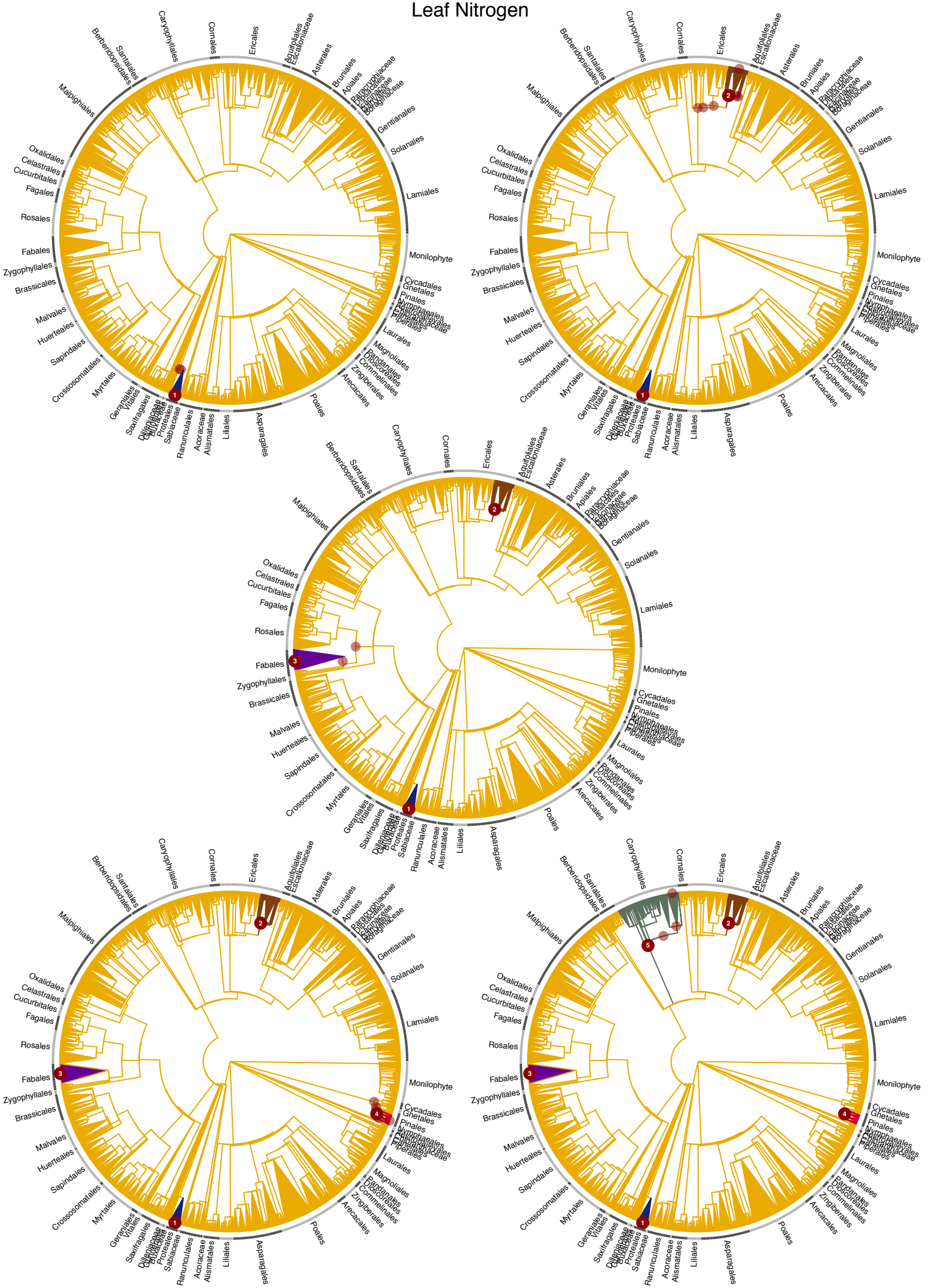
CLIMATE AND GEOGRAPHY

To determine the geographic and climatic niches species occupy, binomials were queried against the global biodiversity information facility (GBIF: http://www.gbif.org/) and georeference points were extracted. Cleaning scripts in R were applied to filter reliable locations. We used the following criteria to filter the GBIF records:

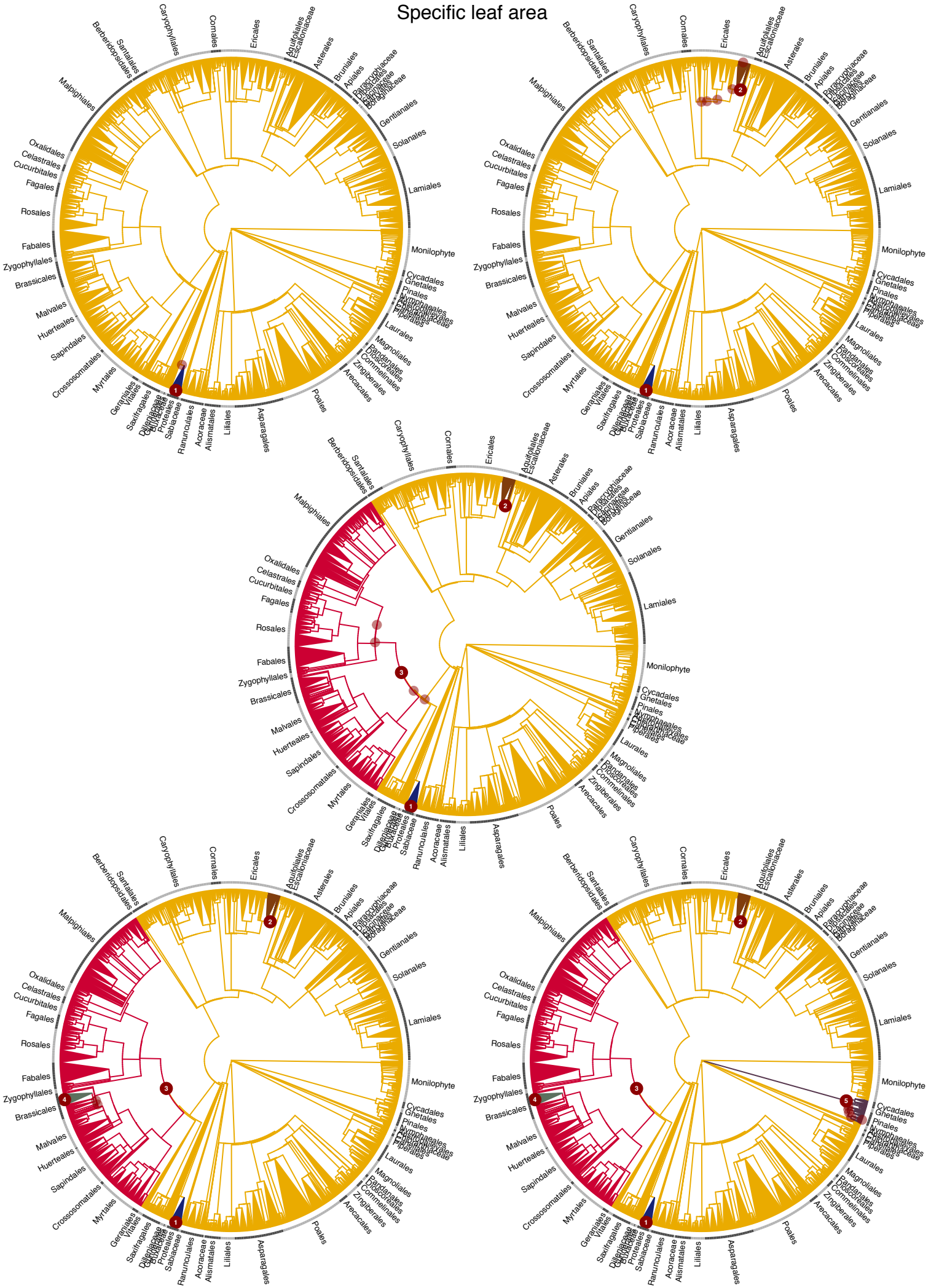
1. The scientific names were in a reasonable format of a Latin binomial or trinomial (e.g., only letters).
2. The record had to have numeric latitude and longitude in decimal degrees where the latitude was between -90 and 90 and the longitude was between -180 and 180, and neither coordinate was exactly equal to zero.
3. The record's latitude was not equal to longitude, as this would most likely be indicative of a data entry error.
4. The record was not a duplicate record according to the GBIF "occurrence_id" field.
5. The record was not located within 50 km of the GBIF headquarters in Copenhagen, Denmark (55.68°N, 12.59°E), to minimize the chance that a record was given a coordinate that corresponded to where the data were housed but not where the plant was actually collected.
6. The record contained a valid entry in the GBIF field "country_interpreted". This country information was independently checked against a global country shape file. The spatial coordinate of the record had to match the record in the "country_interpreted" field or at the minimum match the continent with which "country_interpreted" field was associated. These comparisons provided a benchmark of reasonable geospatial accuracy that the record had to possess and it ensured the record was from a terrestrial location.

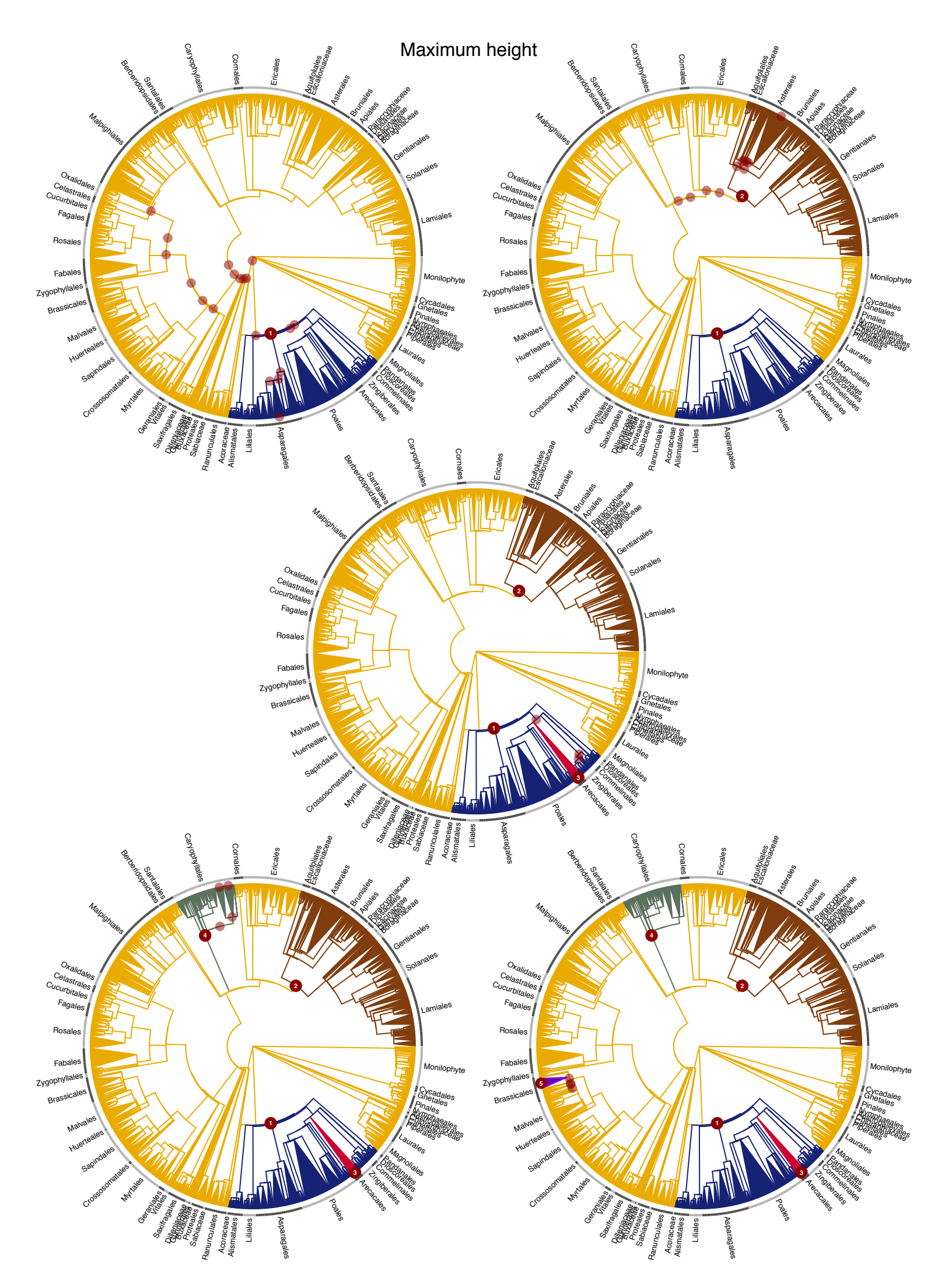
SUPPORTING FIGURES

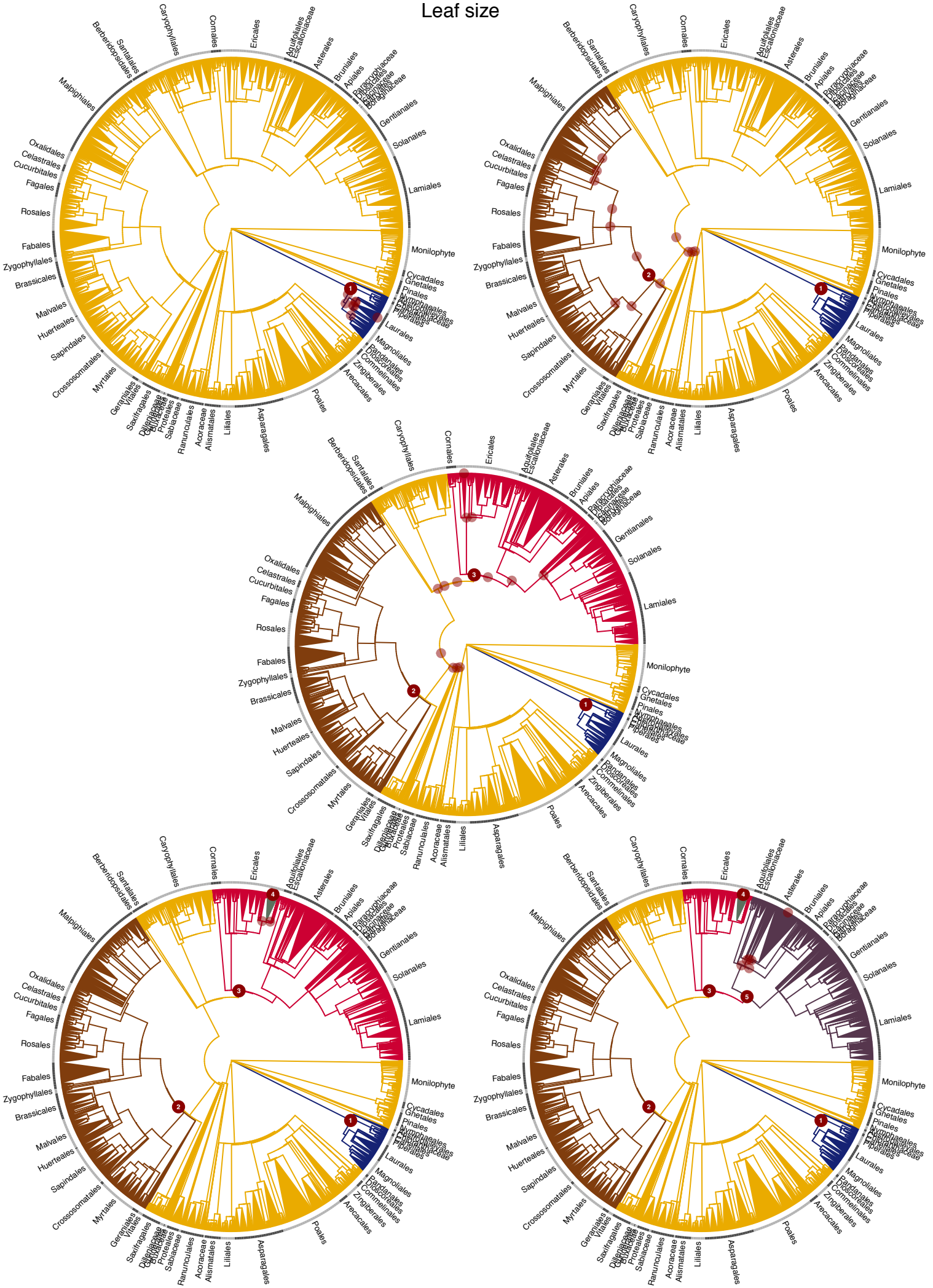
Leaf Nitrogen



Specific leaf area




Maximum height
Caryophyllales
Cornales
Ericales
Aquifoliales
Escalloniaceae
Asterales
Bruniales
Apiales
Paracryphiaceae
Escalloniaceae
Pittosporaceae
Boraginaceae
Gentianales
Solanales
Lamiales
Monilophyte
Cycadales
Gnetales
Pinales
Nymphaeales
Chloranthales
Piperales
Laurales
Magnoliales
Piperales
Dioscoreales
Commelinales
Zingiberales
Arecacales
Poales
Asparagales
Liliales
Alismatales
Acoraceae
Ranunculales
Sabiaceae
Proteales
Dilleniaceae
Saxifragales
Vitales
Geraniales
Myrtales
Crossosomatales
Sapindales
Huerteales
Malvales
Brassicales
Zygophyllales
Fabales
Rosales
Fagales
Cucurbitales
Celastrales
Oxalidales
Malpighiales
Berberidopsidales
Santalales


Leaf size
Caryophyllales
Cornales
Ericales
Aquifoliales
Escalloniaceae
Asterales
Bruniales
Apiales
Paracryphiaceae
Escalloniaceae
Pittosporaceae
Boraginaceae
Gentianales
Solanales
Lamiales
Monilophyte
Cycadales
Gnetales
Pinales
Nymphaeales
Chloranthales
Piperales
Laurales
Magnoliales
Piperales
Chloranthaceae
Canellales
Dioscoreales
Commelinales
Zingiberales
Arecacales
Poales
Asparagales
Liliales
Alismatales
Acoraceae
Ranunculales
Sabiaceae
Proteales
Dilleniaceae
Saxifragales
Vitales
Geraniales
Myrtales
Crossosomatales
Sapindales
Huerteales
Malvales
Brassicales
Zygophyllales
Fabales
Rosales
Fagales
Cucurbitales
Celastrales
Oxalidales
Malpighiales
Berberidopsidales
Santalales

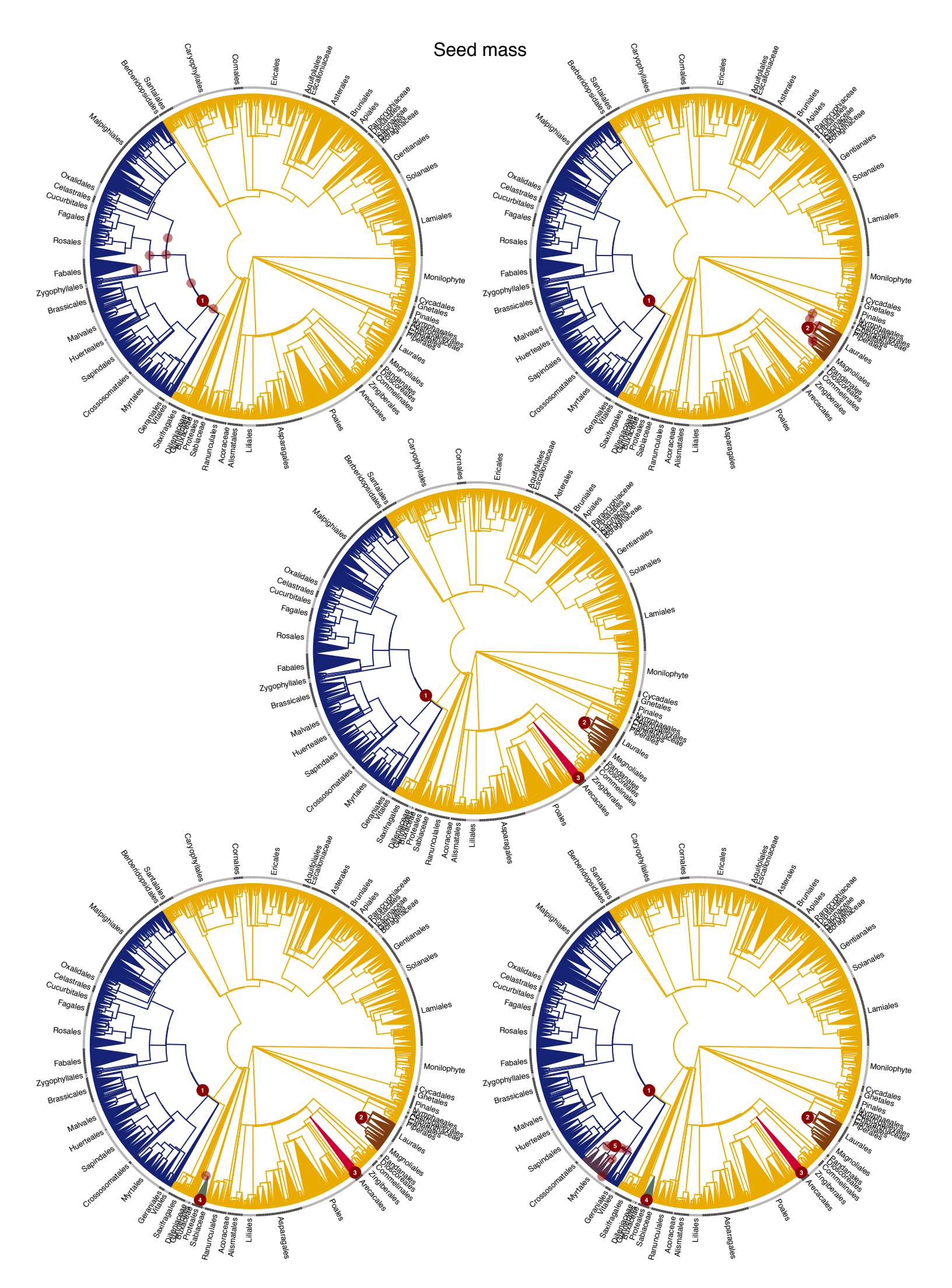

Seed mass
Caryophyllales
Cornales
Ericales
Aquifoliales
Escalloniaceae
Asterales
Bruniales
Apiales
Paracryphiaceae
Escalloniaceae
Pittosporaceae
Boraginaceae
Gentianales
Solanales
Lamiales
Monilophyte
Cycadales
Gnetales
Pinales
Nymphaeales
Chloranthales
Piperales
Laurales
Magnoliales
Pandanales
Dioscoreales
Commelinales
Zingiberales
Arecacales
Poales
Asparagales
Liliales
Alismatales
Acoraceae
Ranunculales
Sabiaceae
Proteales
Dilleniaceae
Saxifragales
Vitales
Geraniales
Myrtales
Crossosomatales
Sapindales
Huerteales
Malvales
Brassicales
Zygophyllales
Fabales
Rosales
Fagales
Cucurbitales
Celastrales
Oxalidales
Malpighiales
Berberidopsidales
Santalales

Fig. S1. Locations of the top five lineages for each of the five traits (leaf N, SLA, maximum height, leaf size, and seed mass), including uncertainty in their position. Numbered circles indicate the clade that subtends the most distinct trait distribution; regions of the tree included are colored differently. Smaller, semi-transparent circles indicate nearby lineages that have similar support; these had Kolmogorov-Smirnov Index values that were in the top 5% of those observed that are connected to the focal lineage by an unbroken chain of clades also in this set. Each terminal group in the tree represents a family, with the width of the end of the triangle proportional to the square root of the number of species.

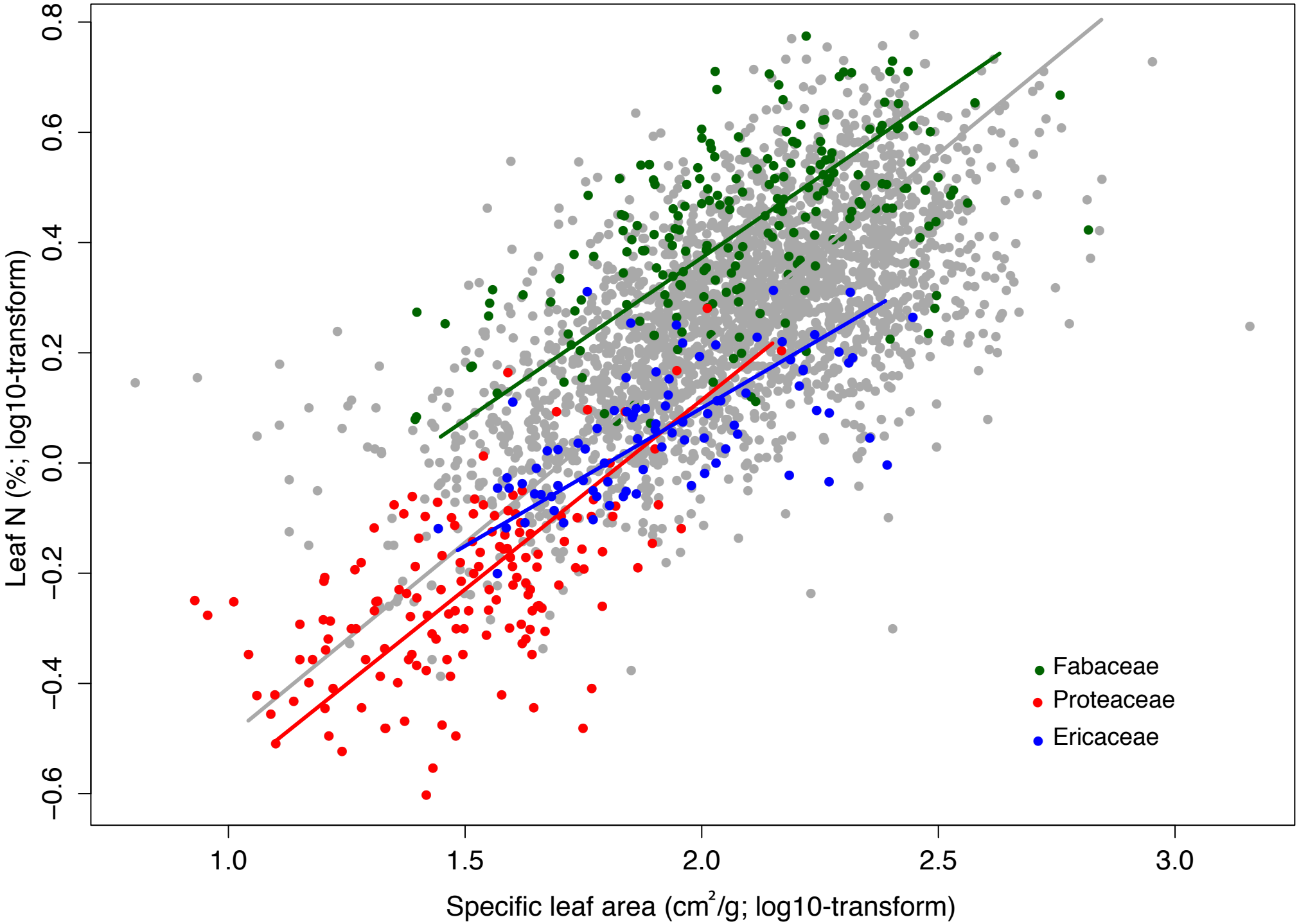

Leaf N (%; log10-transform)
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
1.0
1.5
2.0
2.5
3.0
Specific leaf area (cm²/g; log10-transform)
Fabaceae
Proteaceae
Ericaceae

Fig. S2. SLA and leaf N (leaf economic spectrum; LES) for all plants in the dataset with members of Proteaceae, Ericaceae, and Fabaceae highlighted. Standard major axis line fitting finds significant deviations in slope and intercept for all three clades, with the largest magnitude departure from the global LES being the shift in elevation for Fabaceae species.

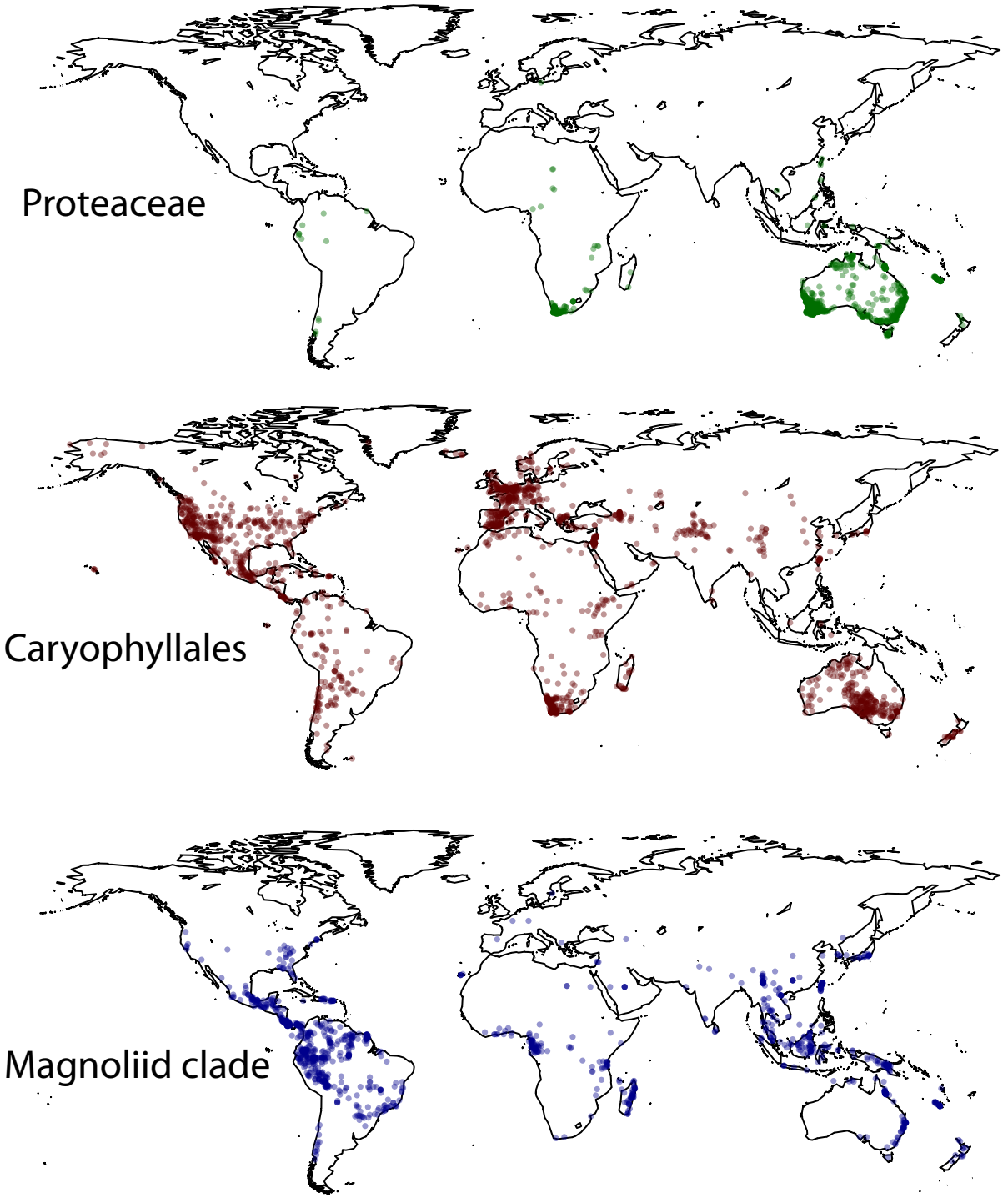

Proteaceae
Caryophyllales
Magnoliid clade

Fig. S3. Geographic medians for three clades indicated by the trait analysis to be particularly distinct: Proteaceae, Caryophyllales, and Magnoliidae. Note that because these are medians of both latitude and longitude, there are not necessarily populations at the exact point for each species. Original data from GBIF. Proteaceae is confined to the southern hemisphere and the tropics. Caryophyllales is speciose in arid parts of the world. The Magnoliidae clade is speciose in tropical forests throughout the world.

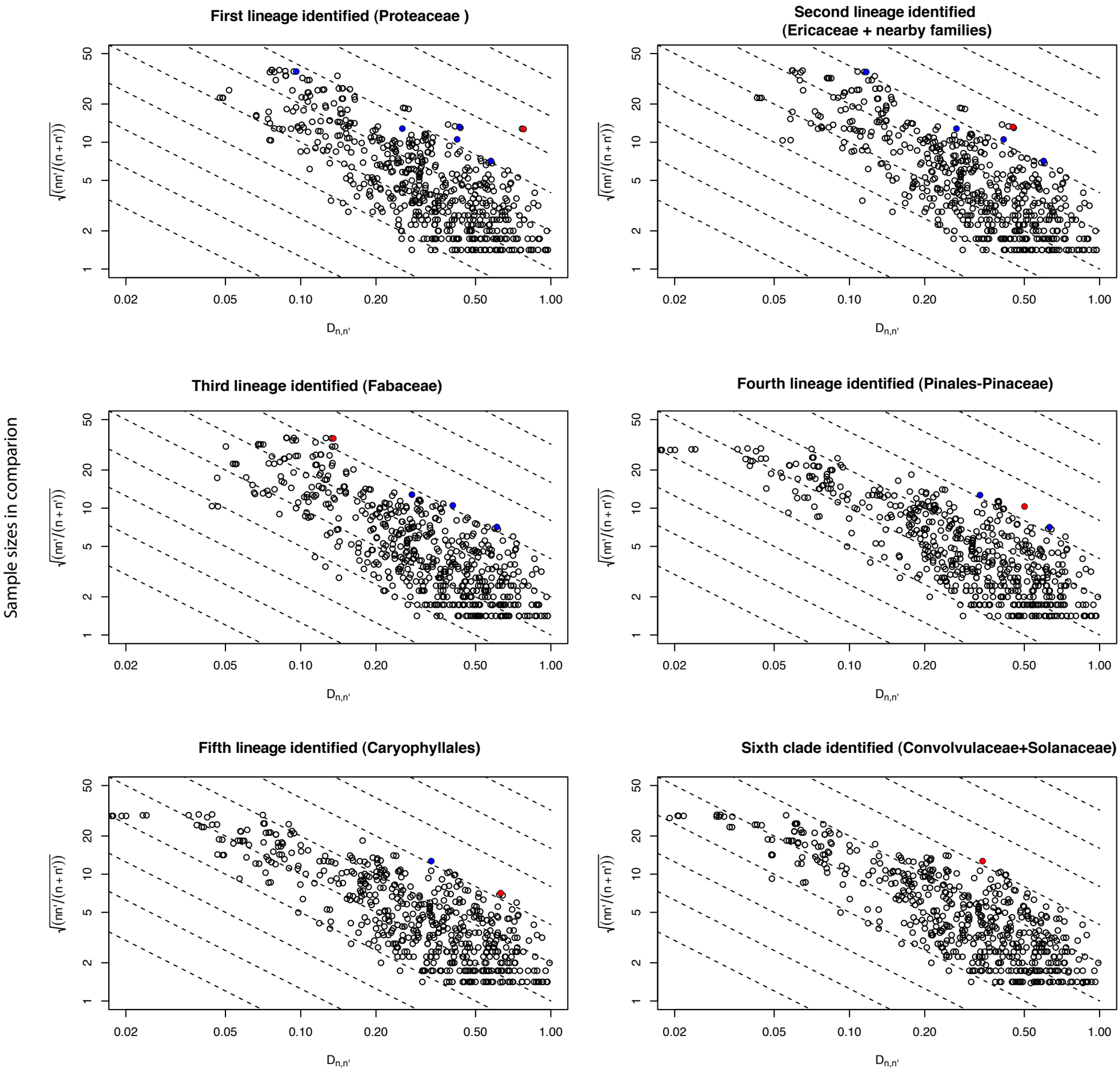

First lineage identified (Proteaceae)
Second lineage identified
(Ericaceae + nearby families)
Third lineage identified (Fabaceae)
Fourth lineage identified (Pinales-Pinaceae)
Fifth lineage identified (Caryophyllales)
Sixth clade identified (Convolvulaceae+Solanaceae)
Sample sizes in comparion
Greater difference in CDFs ->
$\sqrt{(nn'/(n+n'))}$
$D_{n,n'}$
1
2
5
10
20
50
0.02
0.05
0.10
0.20
0.50
1.00

Fig. S4. Statistical behavior of the KS test in a phylogenetic context, illustrated with the data used to identify the first 6 lineages for the leaf N trait. The lines are isoclines along which the test statistic (Eq 2) is unchanging. At each step, the method chooses the point (=lineage) that lies on the isocline that is furthest from the origin (indicated in red). This is also the point that has the most statistical evidence (lowest *P*-value) for splitting the distributions. The lineages that are eventually selected by the algorithm are shown in blue. Because of the nested nature of phylogenies and the sequential nature of the Alfaro et al. (2009) algorithm, the statistics and the rankings change after each lineage is identified. Note that the extreme set of points in panel A are Proteaceae and nearby clades.

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