

1 **Description of Additional Supplementary Files:**

2 File name: Supplementary Data 1

3 Description: Monophyletic Ratio of 151 datasets

4 File name: Supplementary Data 2

5 Description: P-values of Welsh's t-test between the monophyly ratio and growth form
6 or sequencing approach

7 File name: Supplementary Data 3

8 Description: 27 genera representing 20 plant families with sequence data and
9 metadata available

10 File name: Supplementary Data 4

11 Description: Statistics and basic attributes of each species (27 genera)

12 File name: Supplementary Data 5

13 Description: Number of SSSNPs in comparison between original and randomised
14 labels

15 File name: Supplementary Data 6

16 Description: Number of species told apart by full dataset and whether to keep the
17 dataset in down-sampling. NO means the dataset is excluded from the analysis, YES
18 means included in this analysis. (23 genera)

19 File name: Supplementary Data 7

20 Description: The number of species discriminated in rank order of the number of
21 SNPs randomly selected

22 File name: Supplementary Data 8

23 Description: Six individual datasets analysed to assess the performance of individual
24 loci for species discrimination

25 File name: Supplementary Data 9

26 Description: Single gene diagnosability for *Geonoma*

27 File name: Supplementary Data 10

28 Description: Correlation between nucleotide diversity and density of SSSNPs, and

29 nucleotide diversity and number of species that are monophyletic

30 File name: Supplementary Data 11

31 Description: Dataset source and contacting information for the owners

32 File name: Supplementary Data 12

33 Description: Comparisons between the resolution of nuclear data verses

34 plastome/ITS/other barcodes from a selection of papers.

35 File name: Supplementary Data 13

36 Description: A list of datasets used in the meta-analysis. The full data can be

37 downloaded at Zenodo DOI: [10.5281/zenodo.17603347](https://doi.org/10.5281/zenodo.17603347)

38