

**Supporting Information for
DNA-based Identification of Plants and the Genomic Nature of Plant
Species Differences**

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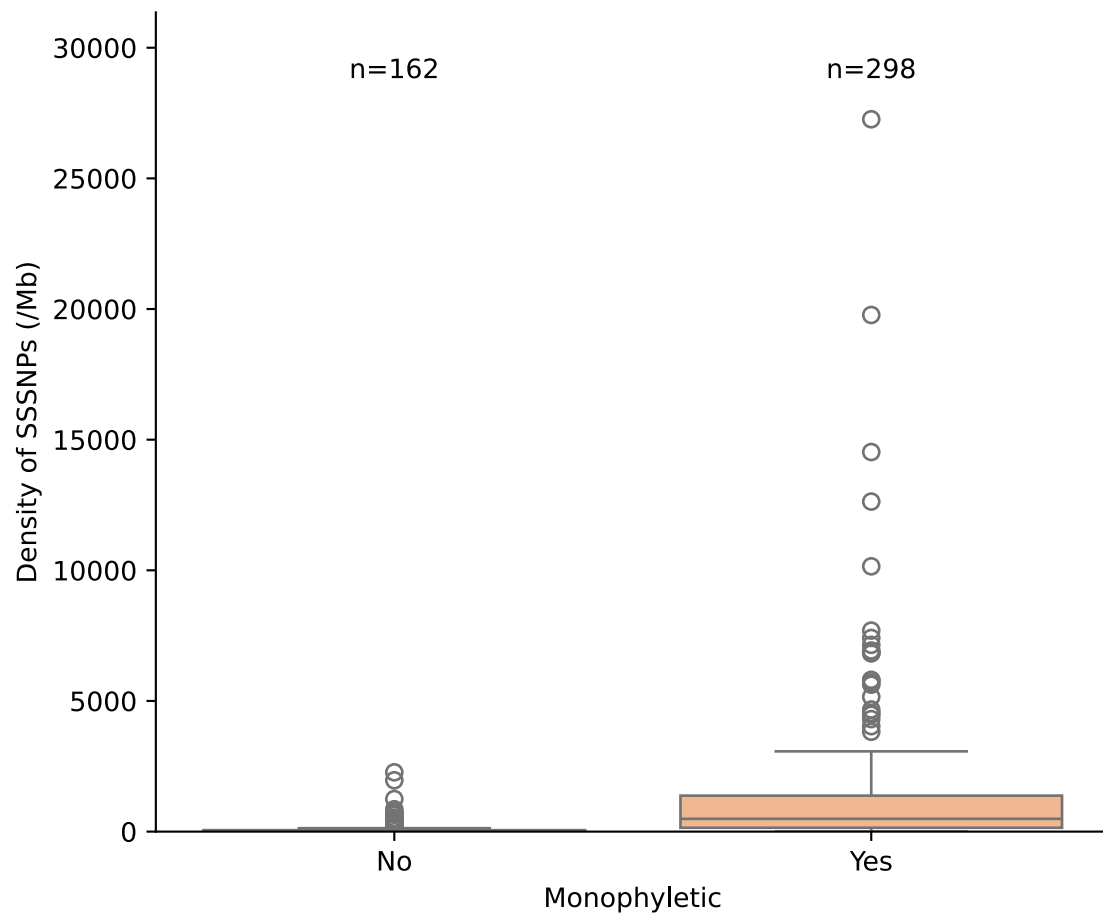


Fig. S1. The density of SSSNPs comparison between monophyletic species and non-monophyletic species (all genera) (p-value <0.001).

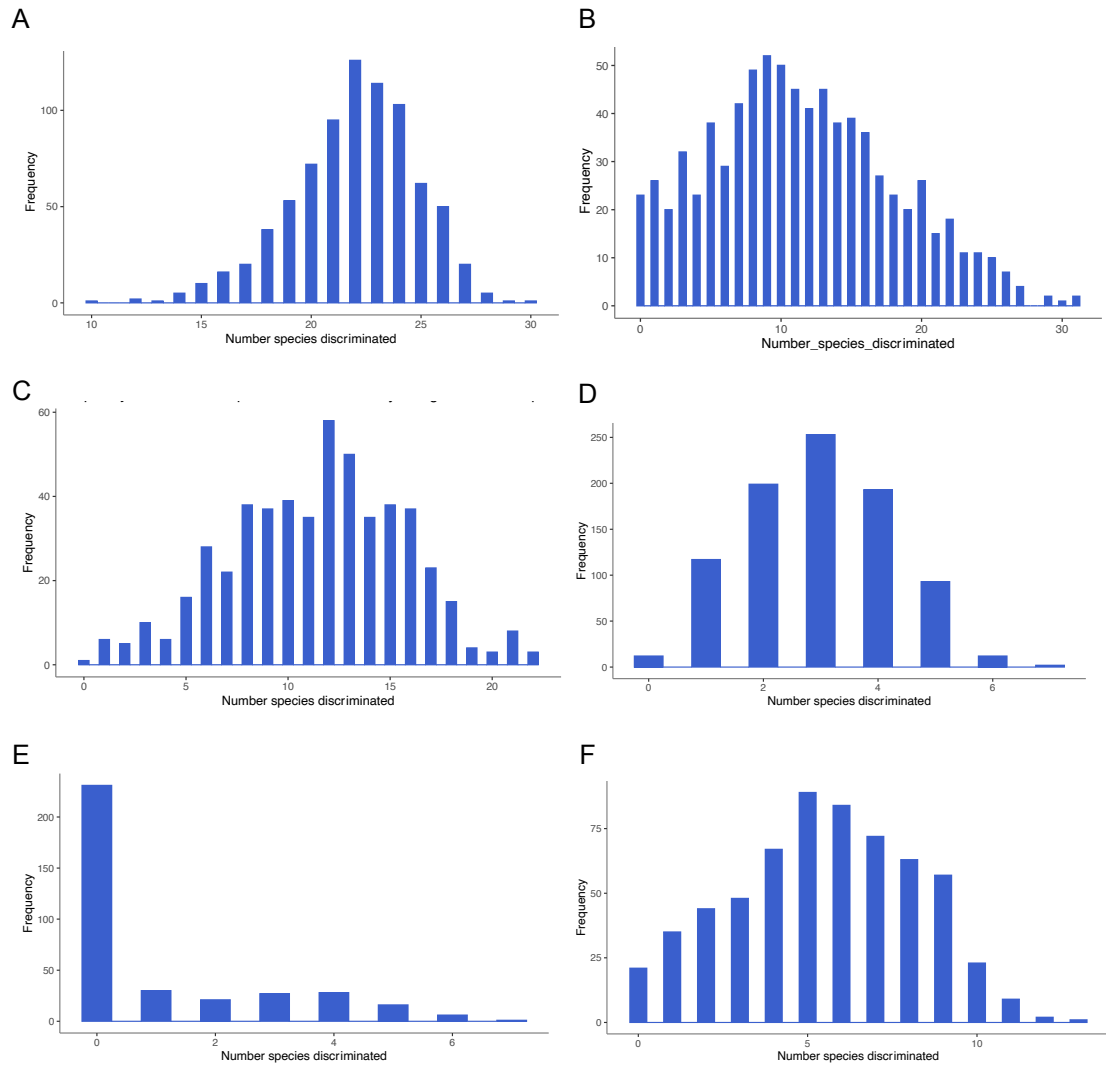


Fig. S2. Frequency distribution of the number of species discriminated by individual loci. The x-axis is ordered from the genes with the lowest discriminatory power to those with the greatest discriminatory power. A. *Geonoma*, B. *Inga*, C. *Artocarpus*, D. *Tsuga*, E. *Polemonium*, and F. *Capurodendron*.

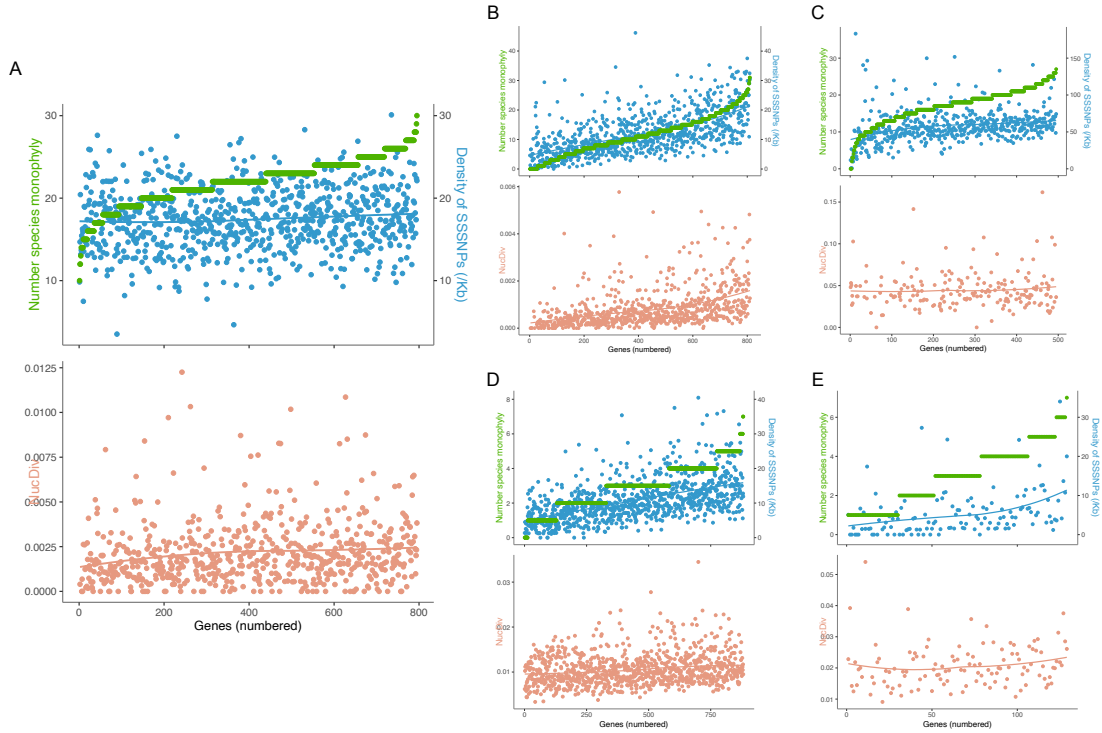


Fig. S3. The genetic features of individual genes for five genera – A. *Geonoma*, B. *Inga*, C. *Artocarpus*, D. *Tsuga*, and E. *Polemonium*. The x-axis is ordered by individual loci from the worst to the best-performing genes in terms of the number of species they discriminate. The green dots represent the number of species resolved as monophyletic by each locus; the blue dots represent the density of SSSNPs (per kilobases) for each locus, and the peach dots represent the nucleotide diversity of a given locus across the whole genus.

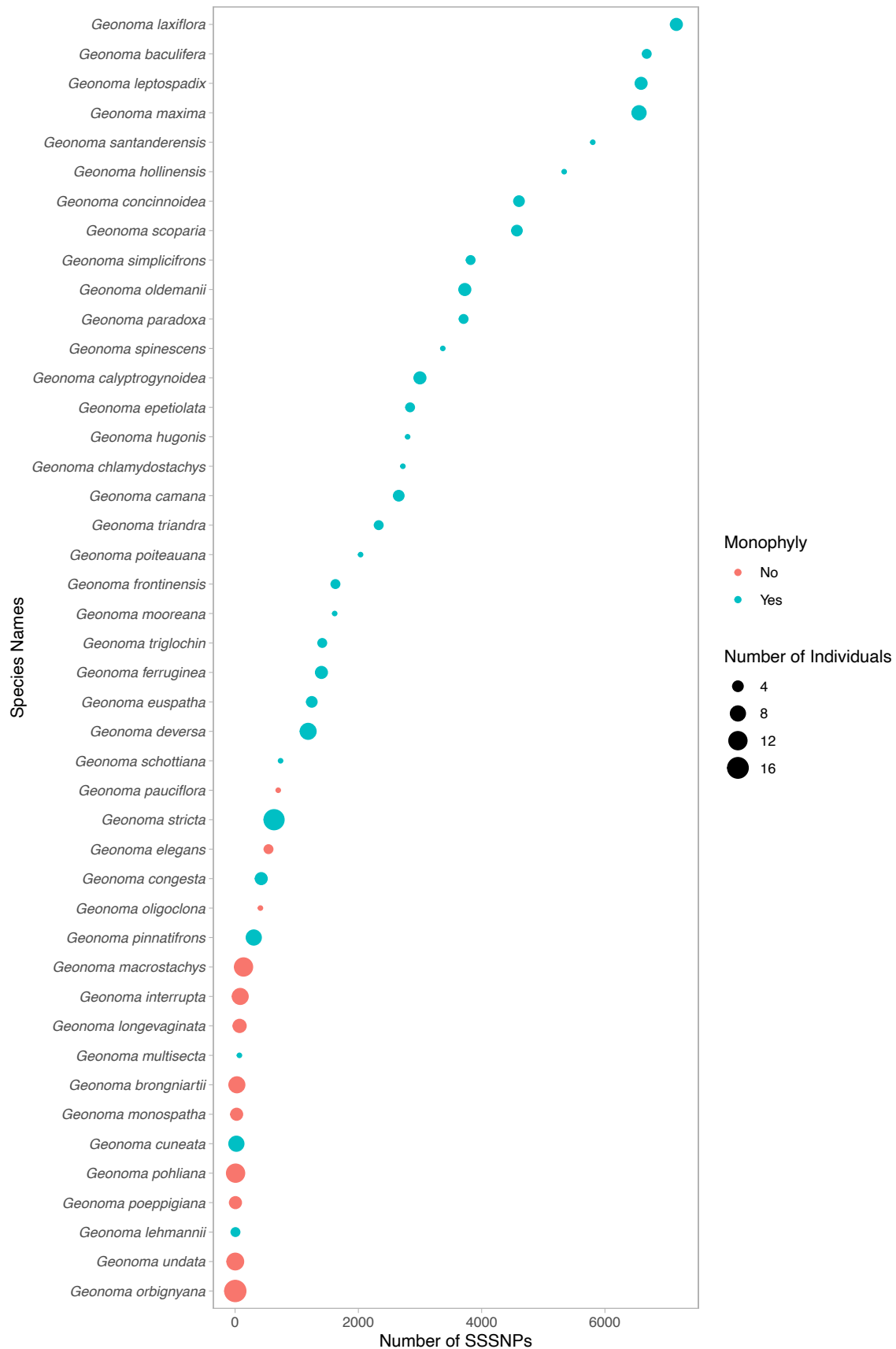


Fig. S4. The distribution of species-specific SNPs for all multi-sampled plant species of genus *Geonoma* (Figures for all other genera can be found in the supplementary folder Fig.S4. Number_of_SSSNPs_vs_Monophyly_correlation_for_all_genus which can be found at Zenodo DOI: 10.5281/zenodo.17603347). The blue dots represent a species being monophyletic, and the peach dots represent non-monophyletic; the size of the dots represents the number of individuals sampled in each species.

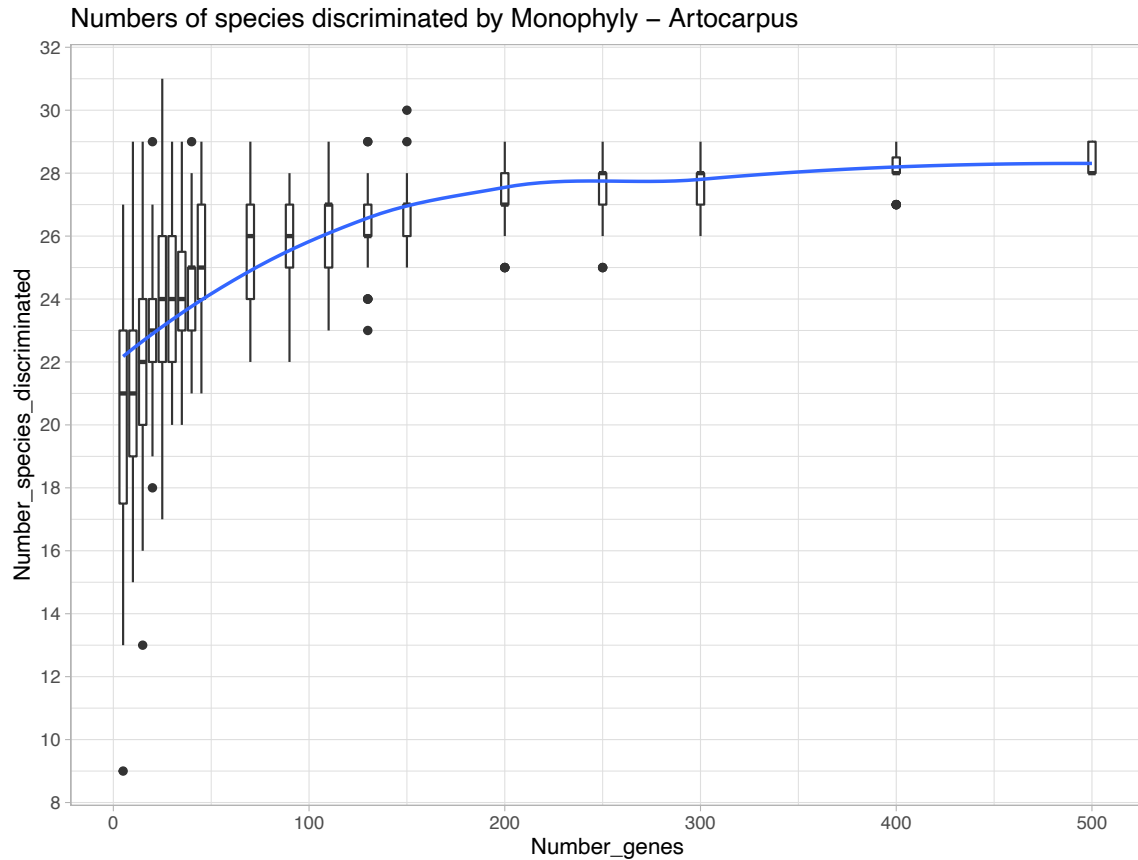


Fig. S5. The subsampling curve of the individual genera by SNPs of genus *Autocarpus*. The name of each individual dataset is on the top of each plot. Figures for all other genera could be found in the supplementary folder Fig.S5. Downsampling – boxplot which can be found at Zenodo DOI: 10.5281/zenodo.17603347.

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