

Continent-wide assessment of the strain-level diversity of *Bradyrhizobium*, a dominant soil bacterial genus

Introduction

-*Bradyrhizobium* is an ecologically important soil bacterial genus that includes many nitrogen-fixing taxa

-*Bradyrhizobium* is one of the most dominant soil bacterial genera on Earth^{1,2,3}

-One possible explanation for its dominance is a high degree of strain-level variation that is adaptive to different conditions

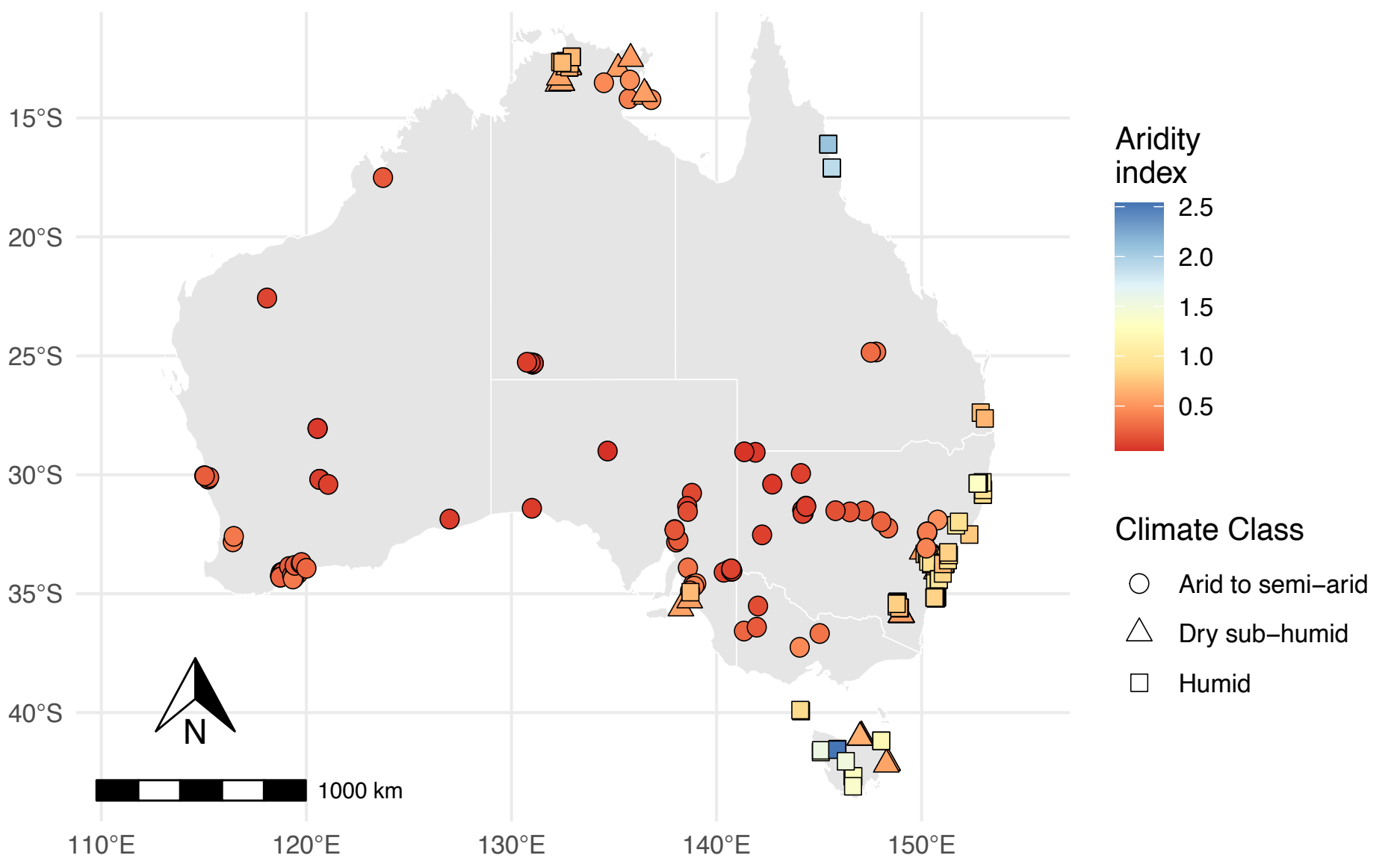
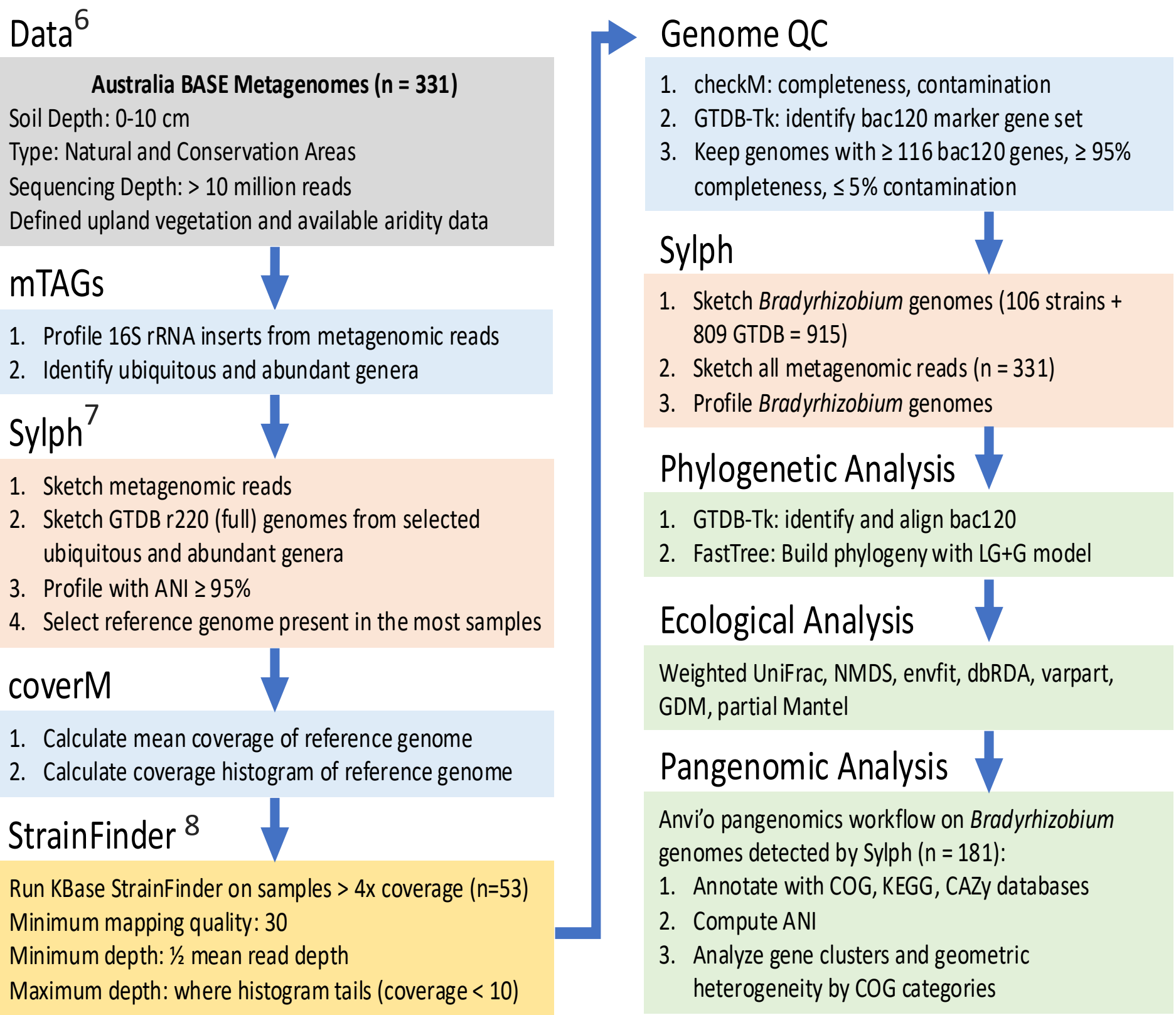
-We developed a pipeline using shotgun metagenomics, reference databases⁴, and targeted genome assembly to perform genome-resolved strain-level analyses on complex soils⁵

Hypotheses:

- H1: No single strain is dominant across a wide range of soils; different strains are found in different environments**
- H2: Both geographic distance and environmental differences are associated with *Bradyrhizobium* strain-level community composition**
- H3: The detected strains have a diverse pangenome, with many differences in gene content, and only a small number of shared genes**

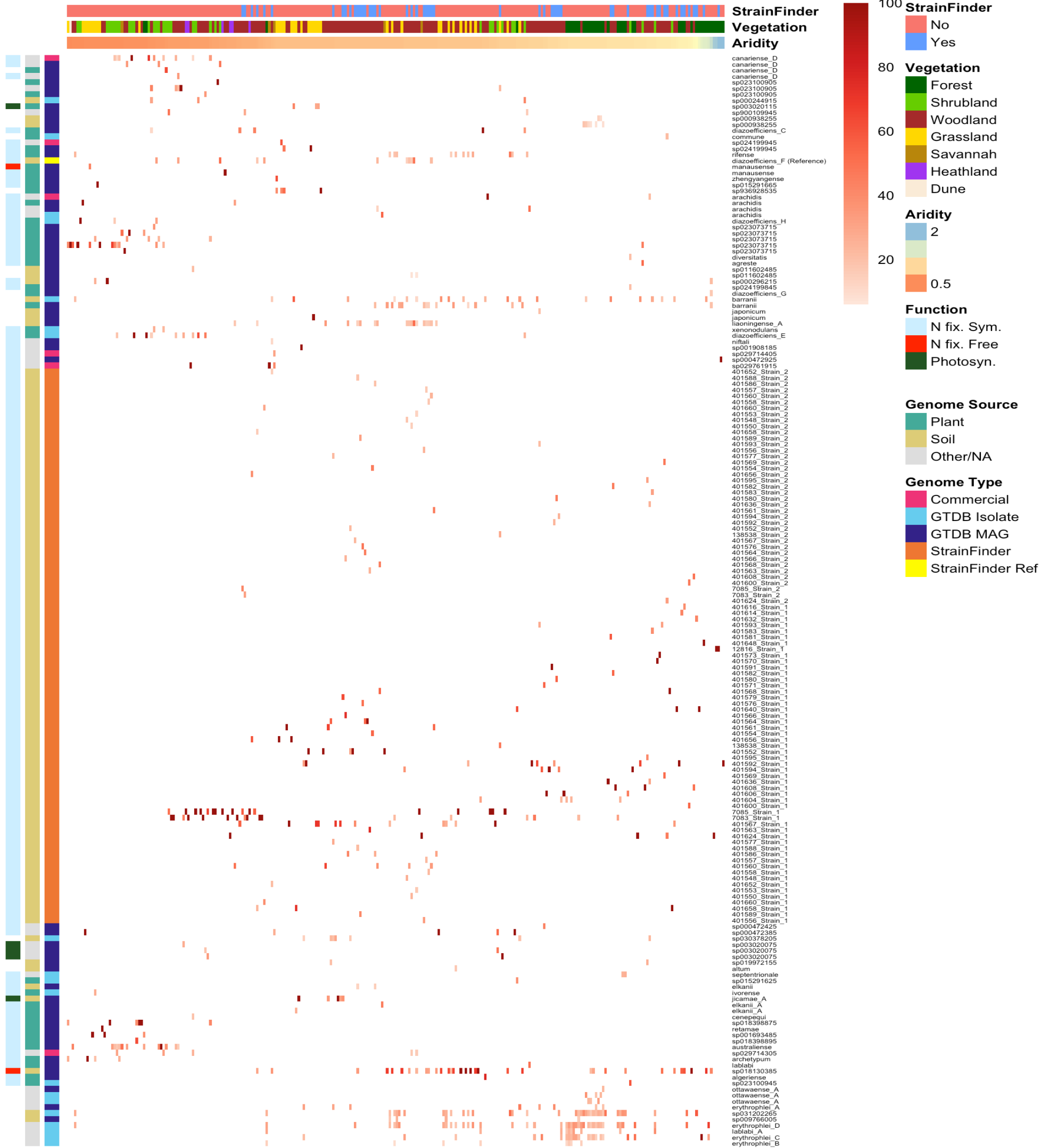
Methods

Analysis Pipeline

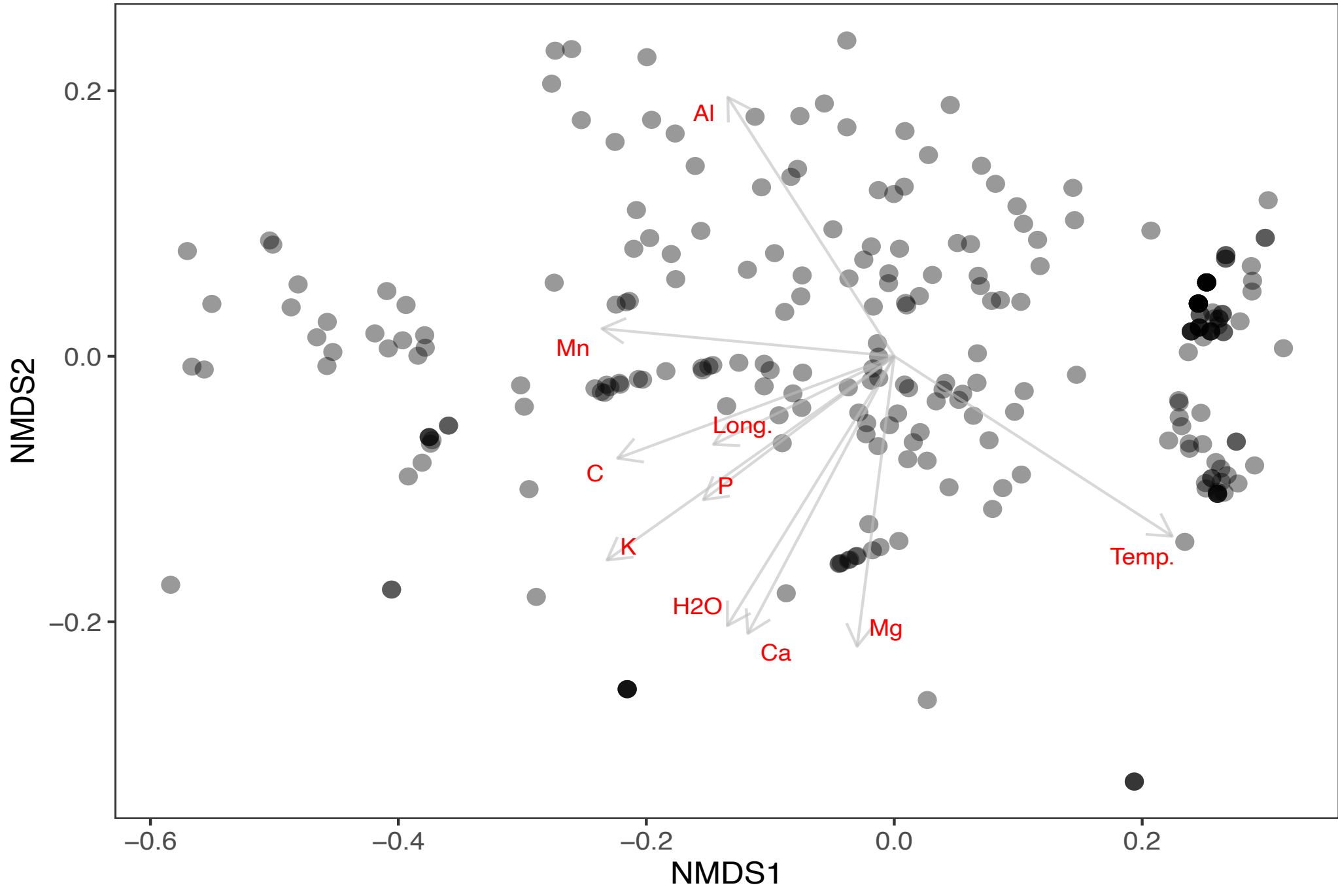


Results

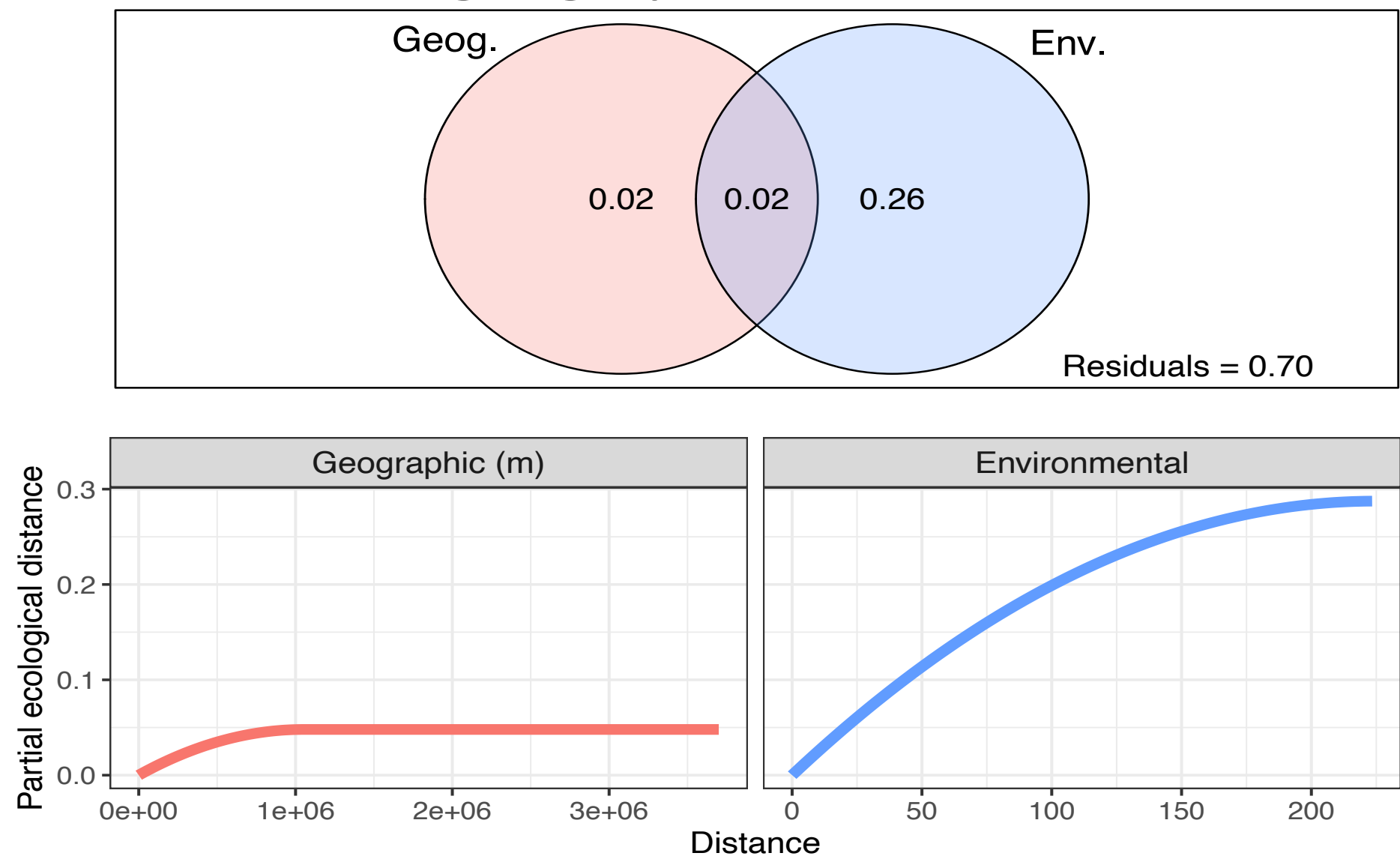
181/915 strains detected in 268/331 samples. Most ubiquitous strain detected in 41 soils. Most strains (98%) detected in < 10% of samples.



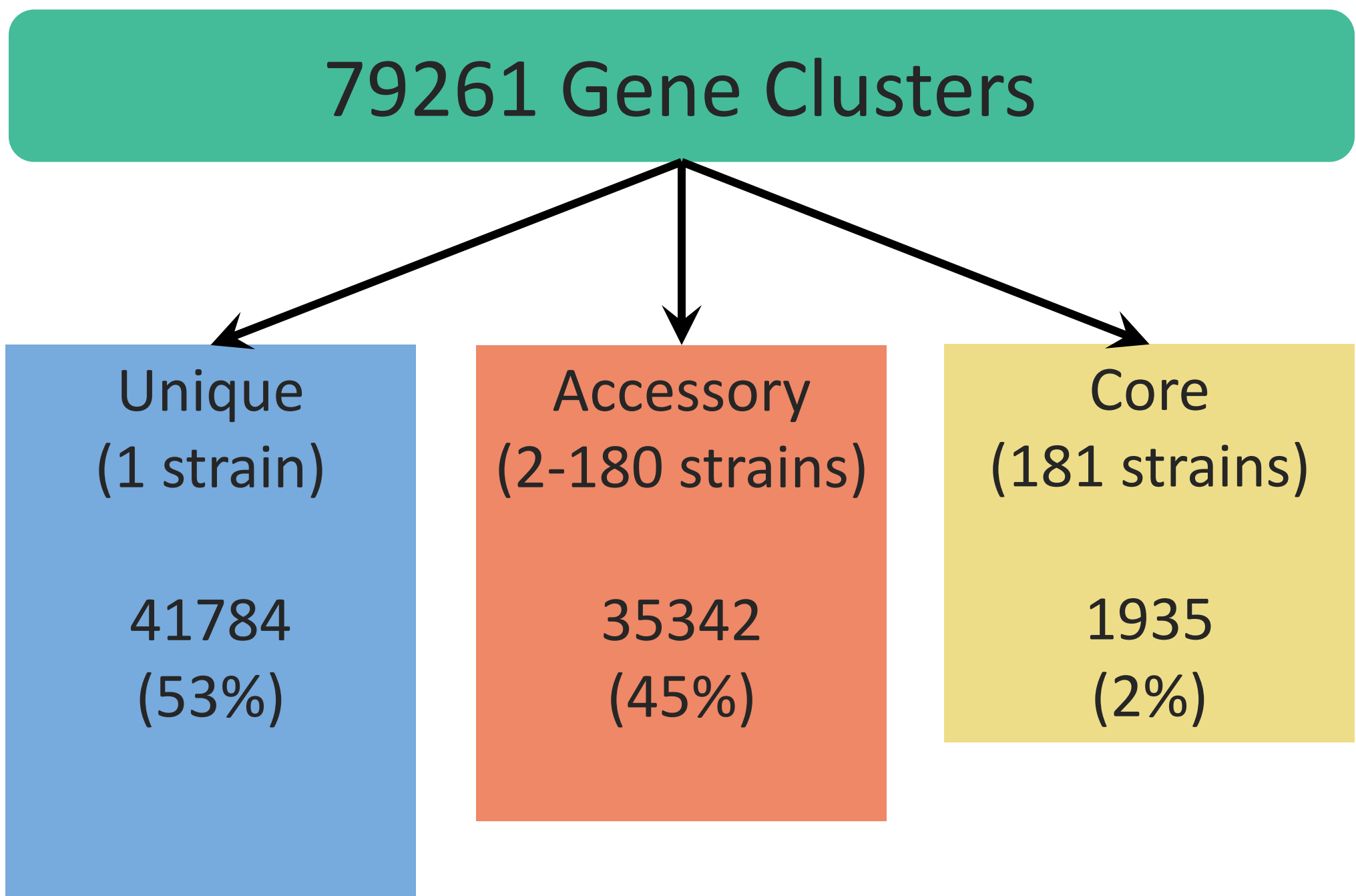
Bradyrhizobium composition was significantly associated with climate and soil variables



Bradyrhizobium composition was more strongly associated with environmental dissimilarity than geographic distance



The 181 detected strains have a large and diverse pangenome characterized by many unique genes and few core genes shared by all strains.



Conclusions

- We developed a general framework and methodology for strain-level analyses in soil and tested it on a dominant and ecologically relevant soil bacterial genus
- H1: *Bradyrhizobium* strains were detected in > 80 % of soils, but most individual strains had restricted distributions
- H2: *Bradyrhizobium* composition is structured more by environmental variables than by geographic distance
- H3: The Australian *Bradyrhizobium* pangenome is large and diverse

References

1. Delgado-Baquerizo et al. 2018. Science 359:320–325; 2. Oliverio et al. 2020. mBio 11:e01718-20; 3. Labouyrie et al. 2023. Nat Commun 14:3311; 4. Parks et al. 2022. Nucleic Acids Research 50:D785–D794; 5. Crits-Christoph et al. 2020. The ISME Journal 14:1834–1846; 6. Bissett et al. 2016. GigaSci 5:21; 7. Smillie et al. 2018. Cell Host & Microbe 23:229-240.e5; 8. Shaw J, Yu YW. 2024. Nat Biotechnol 1–12.

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