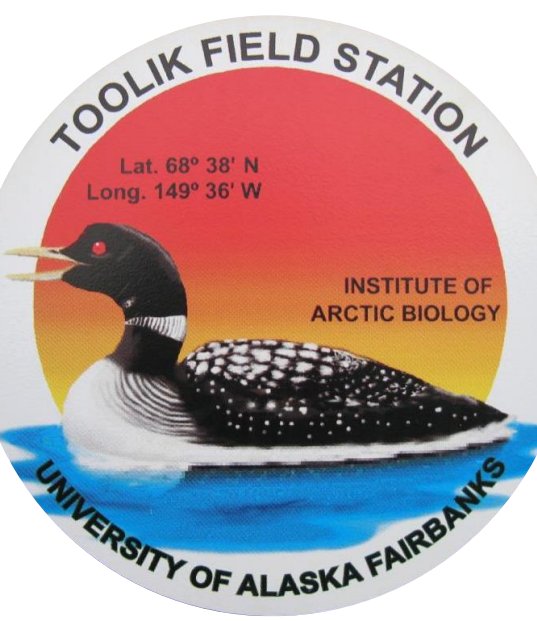
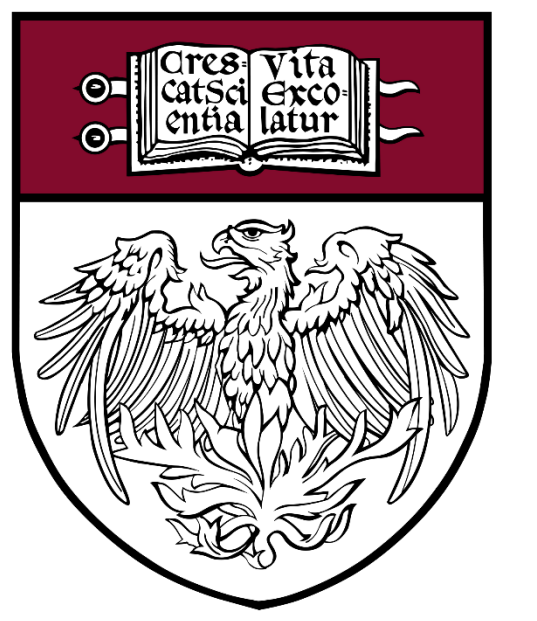


Novel Metaproteomic Approaches Reveal Systematic Variations in Microbial Biogeochemical Pathways with Arctic Vegetation Types

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Introduction

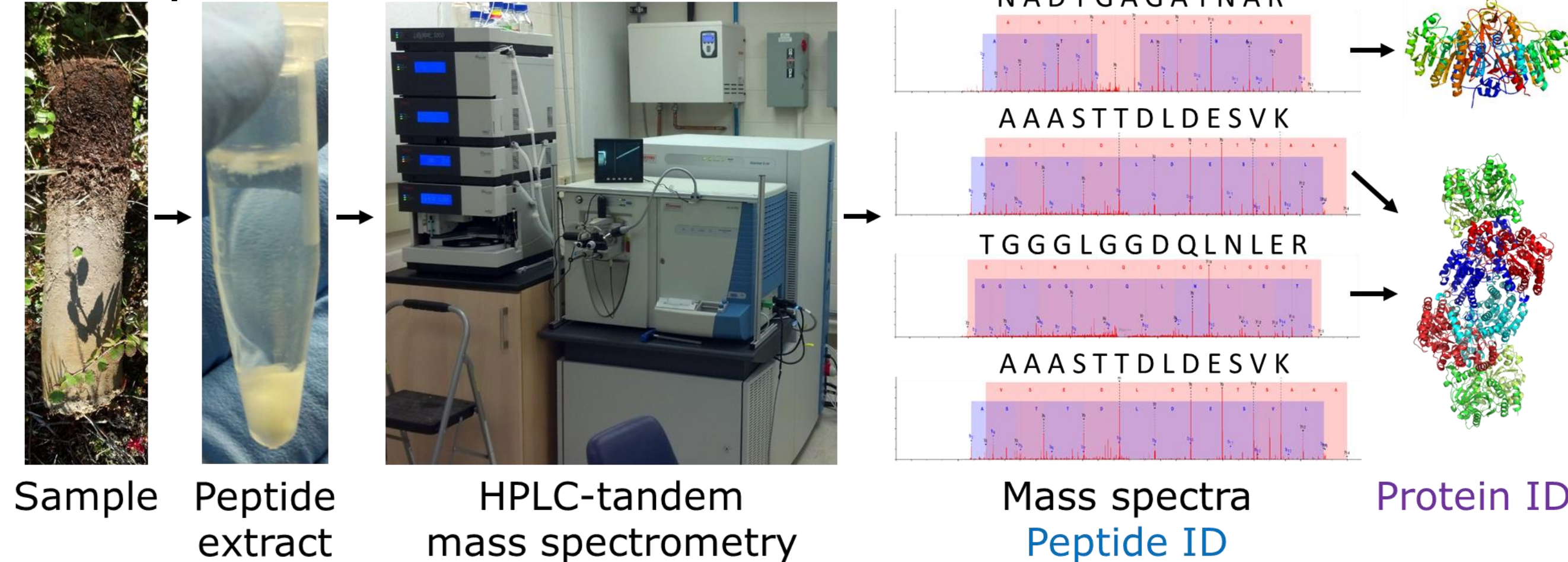


- How will Arctic warming affect soil C storage?
 - Greater plant growth increases C storage, but trivial in global budget
 - Replacement of nonvascular by vascular plants
 - Accelerated microbial decomposition of massive soil C pool
 - Loss of up to 9 yr worth of current anthropogenic emissions by 2100
 - How does floral turnover interact with microbial activity?
- How can microbial processing of organic molecules be measured in situ?
 - Do certain microbial groups perform specific heterotrophic functions?
 - Metagenomes suggest functions are widely distributed among taxa
 - Genomic potential may not correlate well with enzymatic activity
- Characterization of proteomes as a more direct proxy for activity
 - Our recent computational advances enable soil metaproteomics
 - *Postnovo* boosts accuracy of de novo peptide sequencing by 10-fold
 - *ProteinExpress* greatly increases the amount of protein information

Sampling at Toolik Field Station, Arctic Alaska

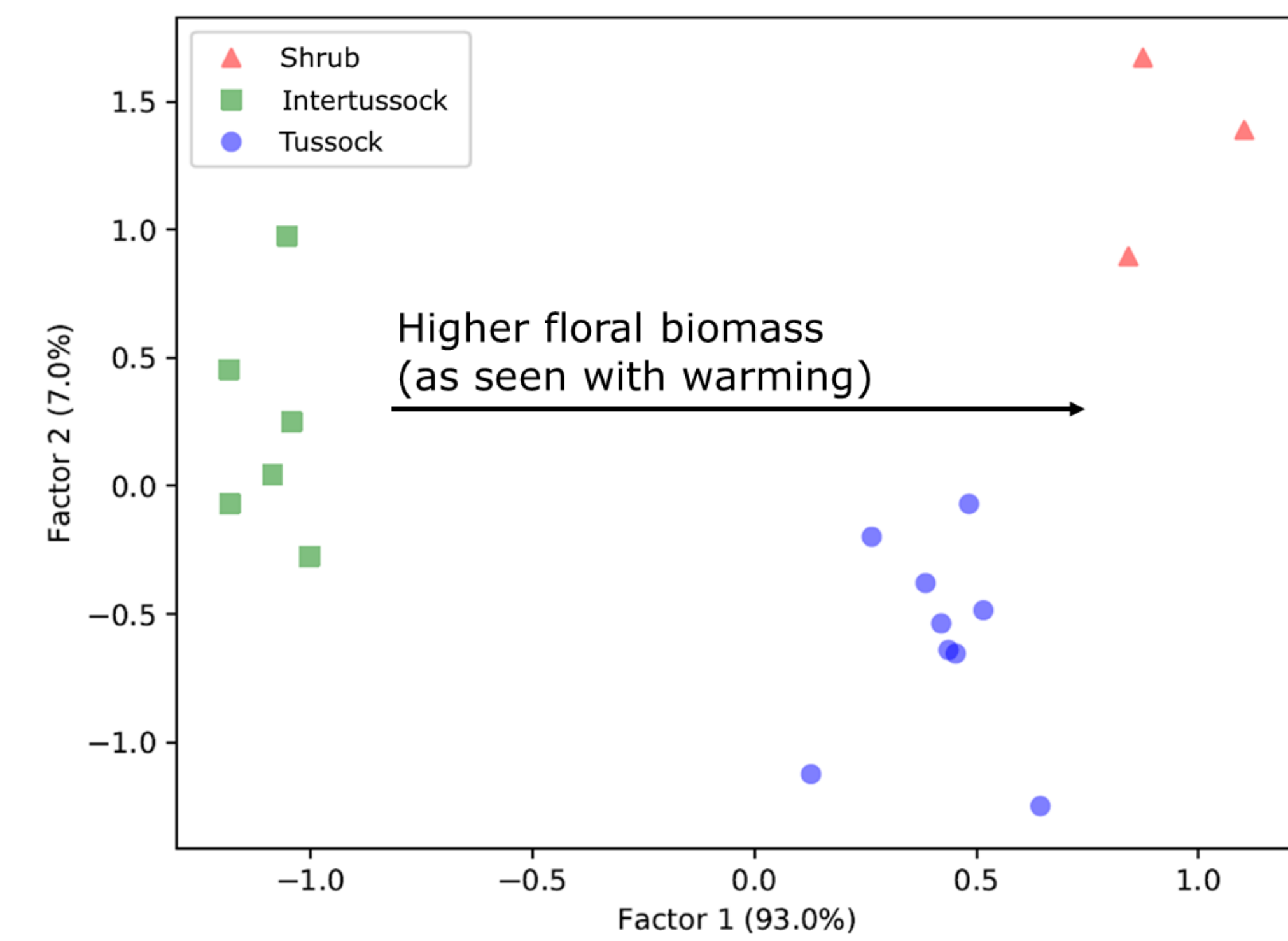


Metaproteomic Workflow

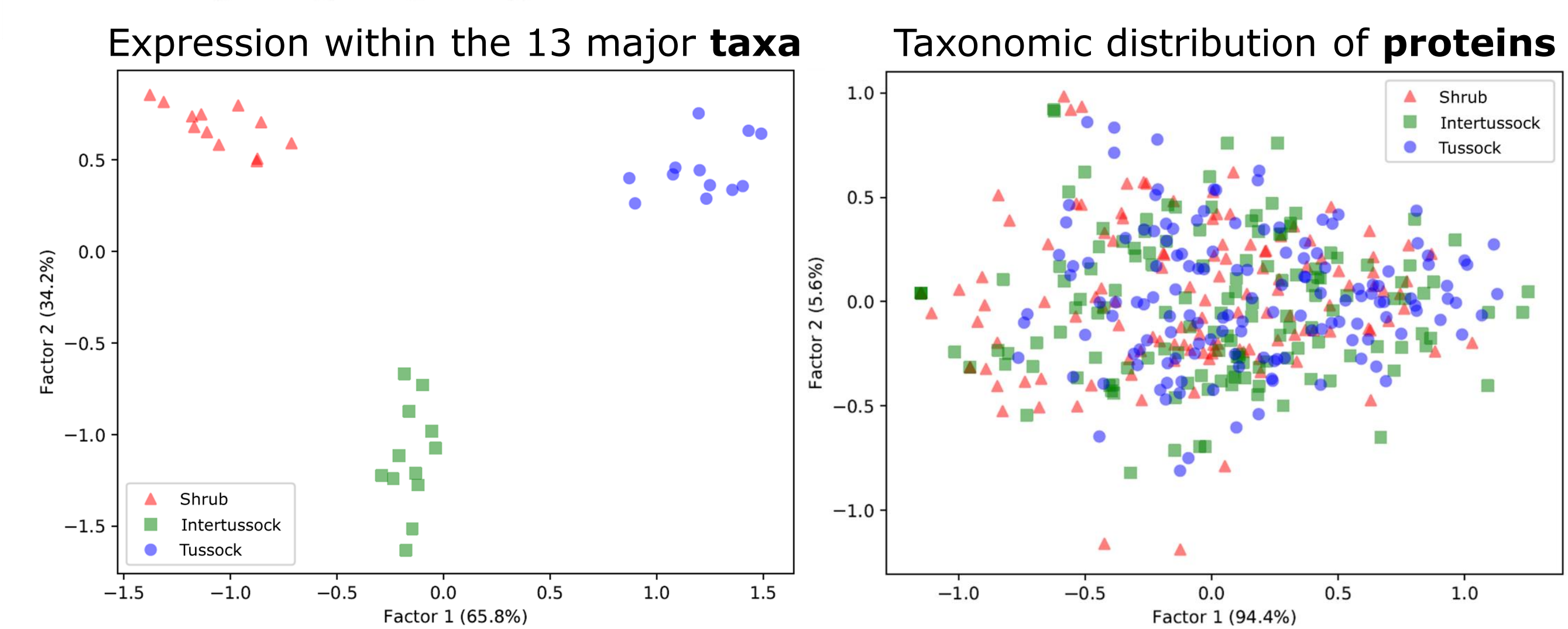
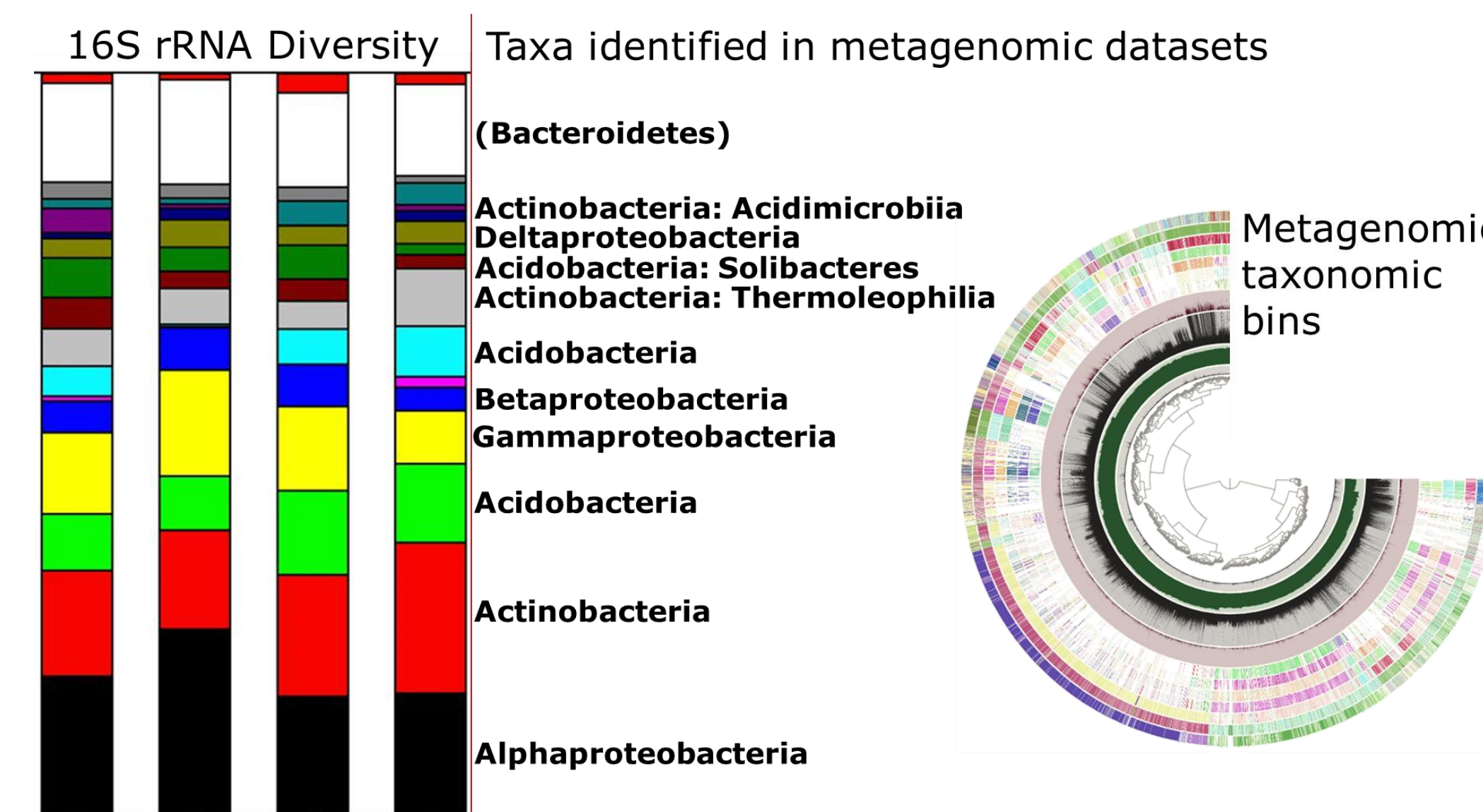


Results: Differences between Floras

- Relative abundances of proteins were compared between samples
- Proteins were identified from pooled meta-genomes/transcriptomes
- Proteins were classified by Functional Group (glycolysis, cellulases, ...)
- Sample Functional Group profiles naturally cluster by floral type (LDA)
- First factor accounts for 93% of discrimination between floras
- Clear separation of low and high biomass floras

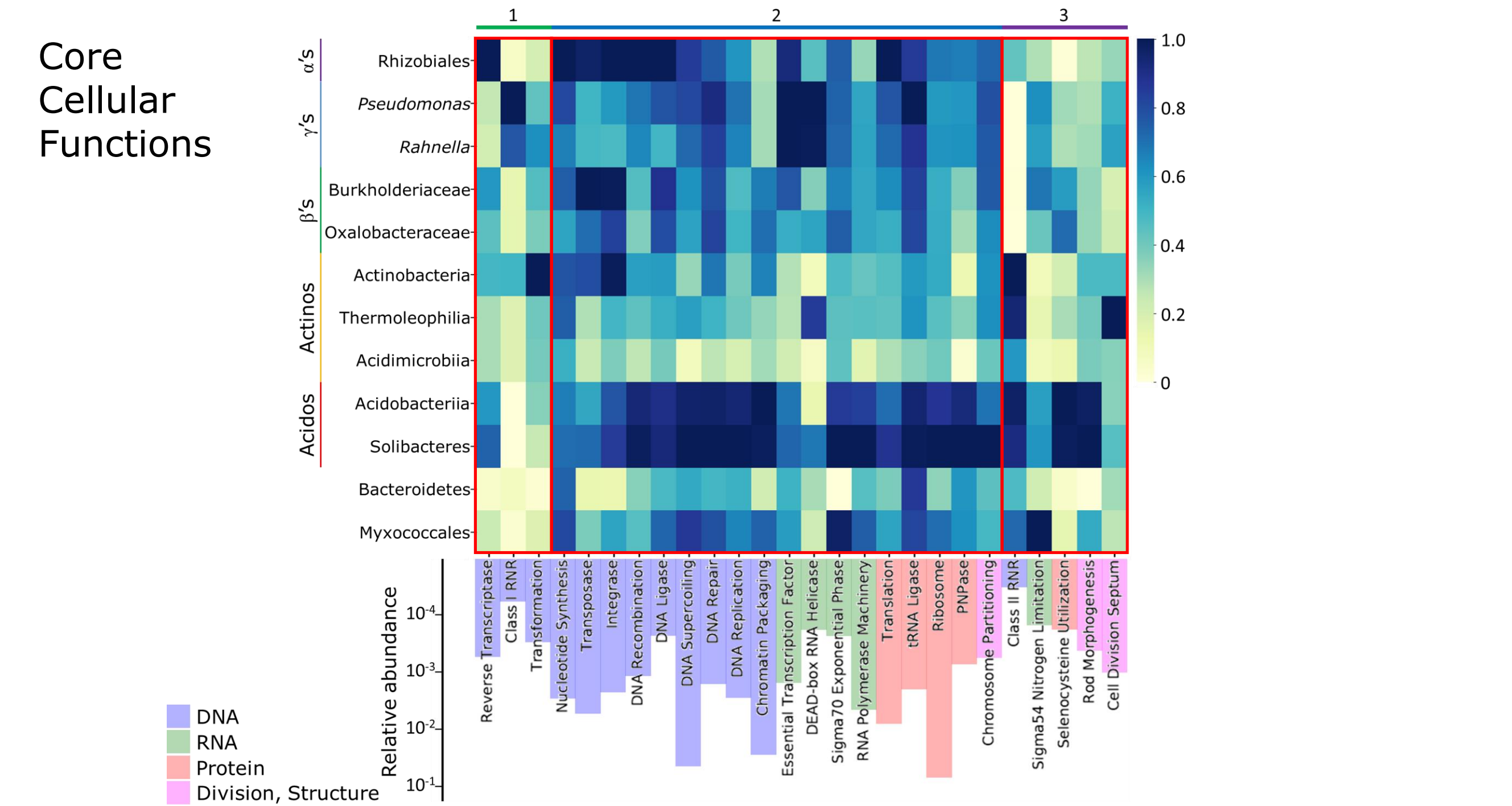


- Certain functions are more strongly expressed in more vegetated soils
- Statistically significant pairwise differences (*t*-test, *P* = 0.01)
 - Sugar transporters (ribose, xylose/arabinose, sugar alcohols)
 - Succinoglycan (extracellular polysaccharide) biosynthesis
- Core cellular functions such as the ribosome load strongly on Factor 1
 - Indicates greater microbial activity in more vegetated soils
- How do protein expression profiles differ between taxa?
 - Metagenomic sequence bins corresponding to 16S taxa were identified
 - Protein expression by a taxon was measured by a novel metric, Φ
 - Relative abundance * similarity between protein and bin sequences
- Taxa express similar suites of functions in different floras, with certain functions strongly changing in relative level within but not between taxa

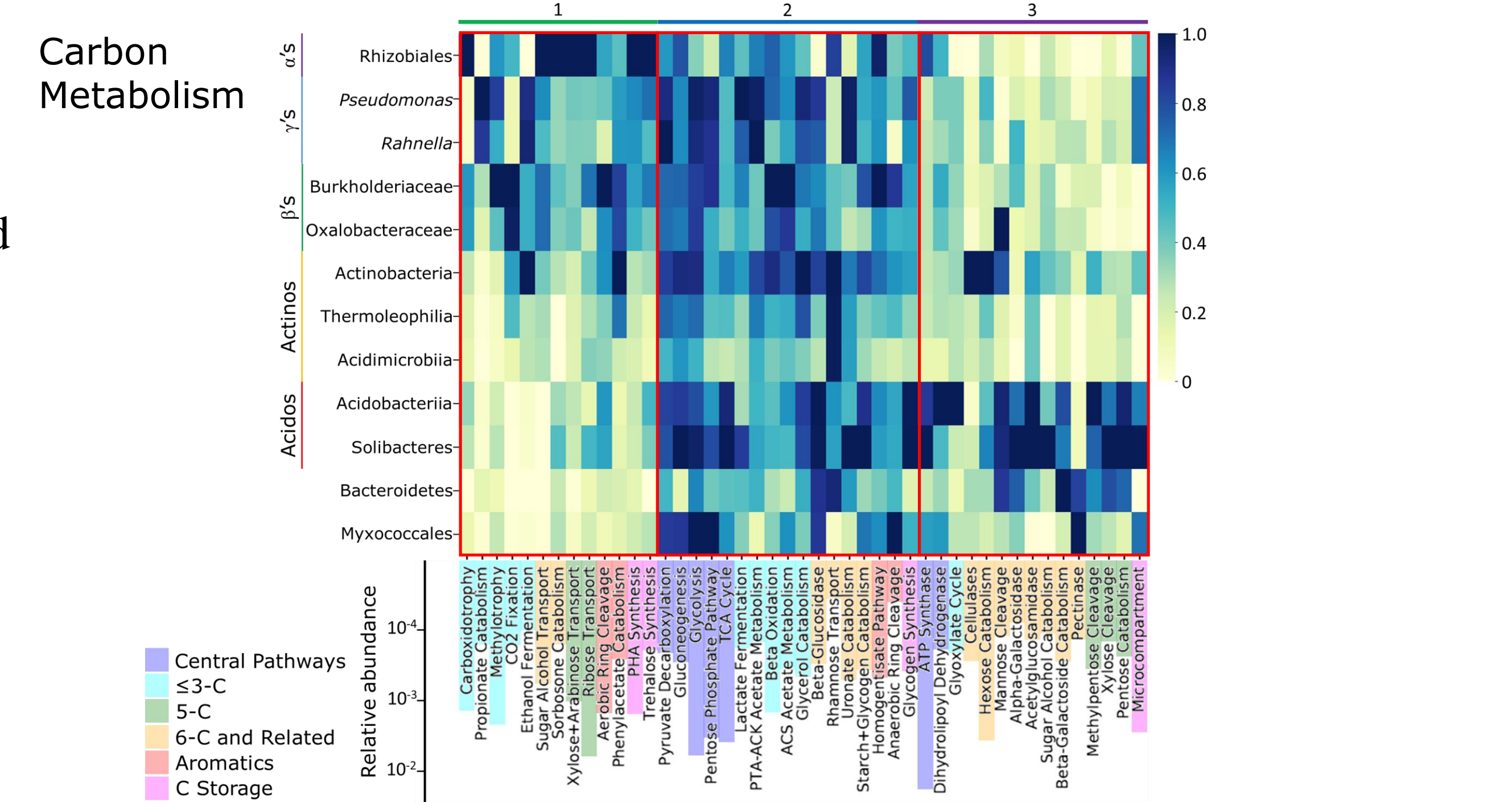


Results: Taxonomic Niche Partitioning

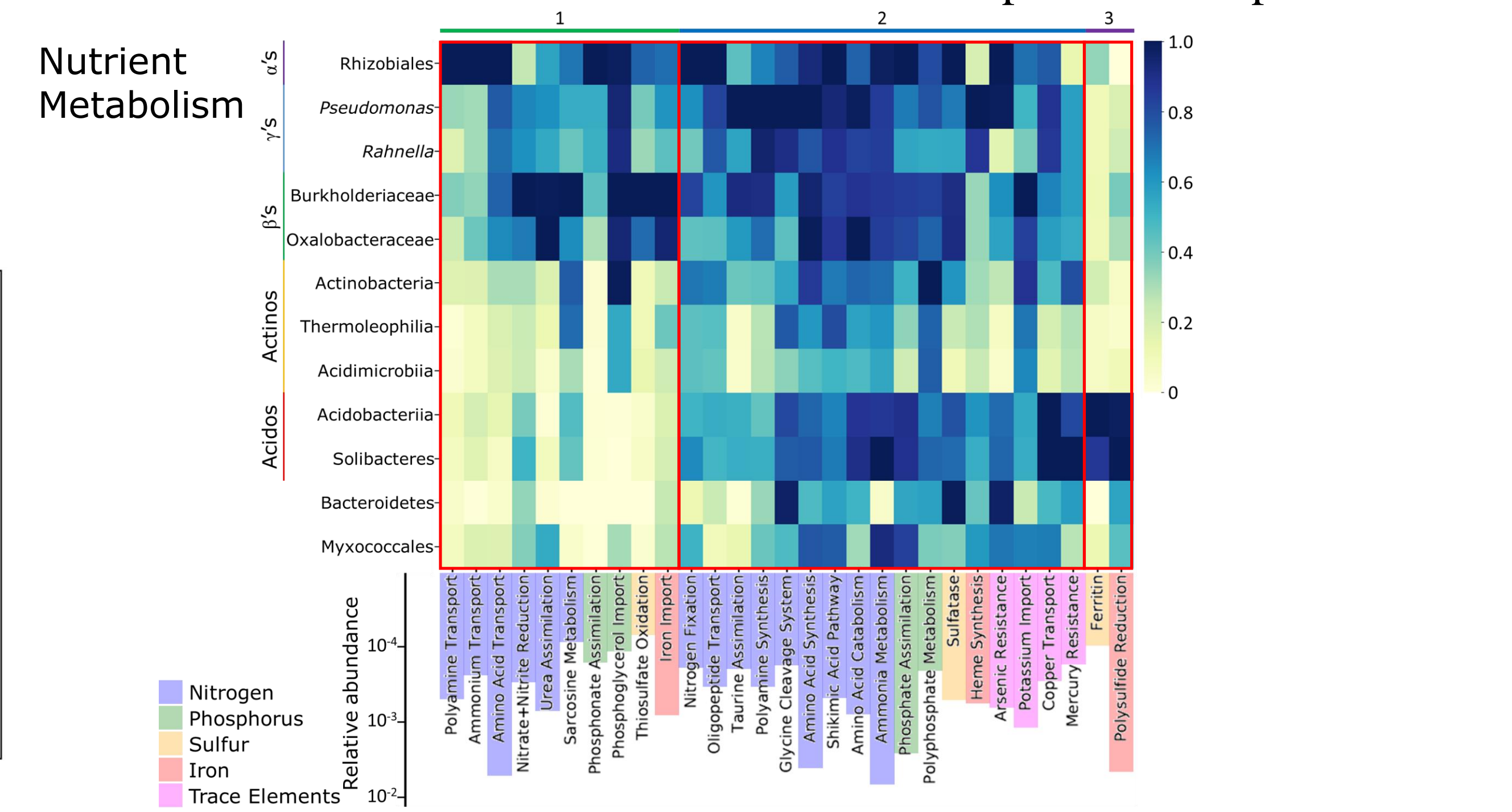
- Acidobacteria are the most active group, as measured by Φ
- Three natural *k*-means clusters of protein expression profiles (red boxes)
 1. High Proteobacteria; low non-Proteobacteria
 2. Moderate to high Proteobacteria; high non-Proteobacteria
 3. Low Proteobacteria; high non-Proteobacteria



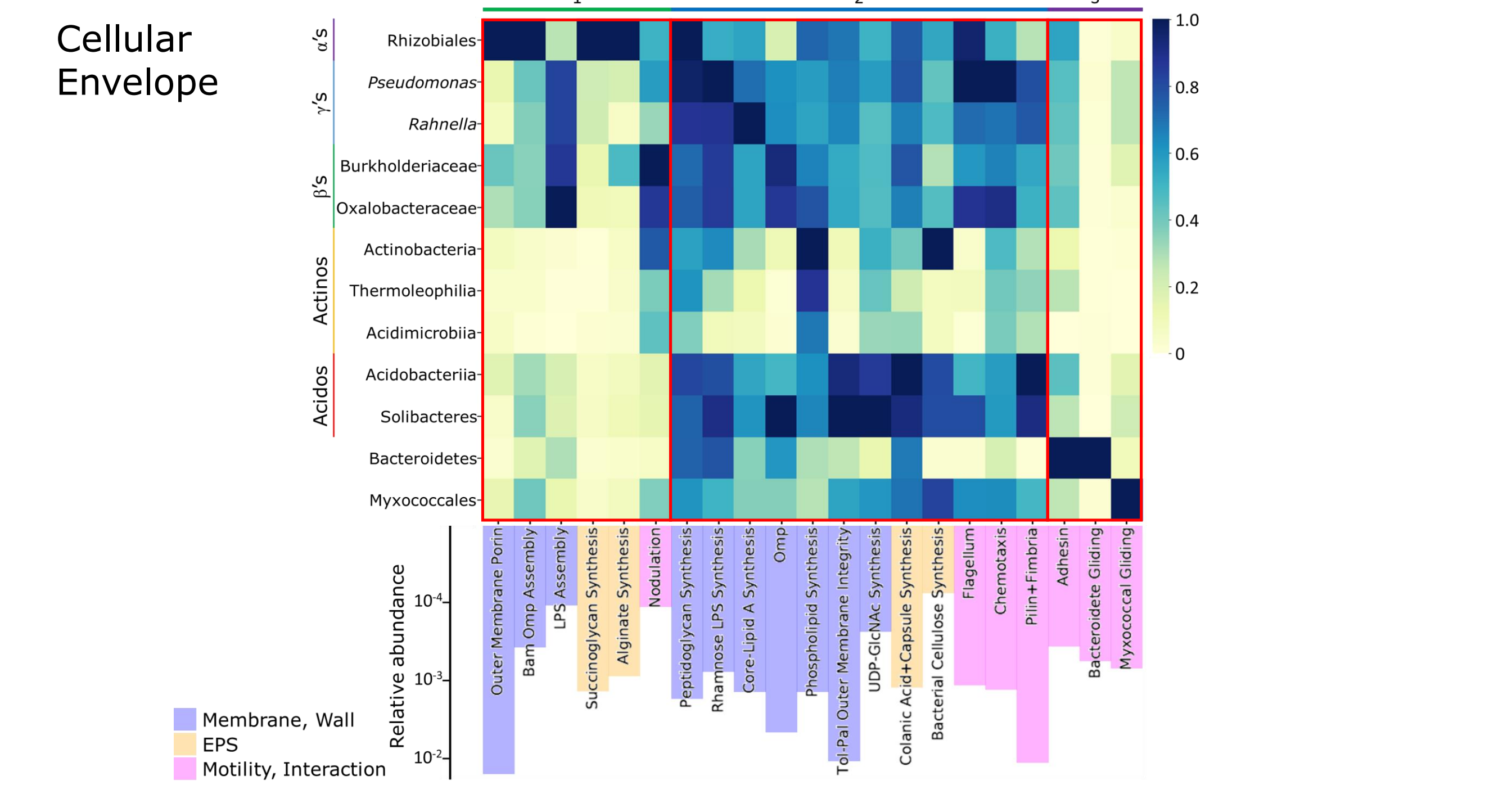
- Proteobacteria consume small, soluble molecules, e.g., simple sugars, CO
- Rhizobiales dominate expression of sugar transporters (root exudates)
- Rhizobiales-associated functions increase most with floral biomass
- Non-Proteobacteria degrade polymers (cellulose, hemicelluloses, lignin)
- Acidobacteria specialize in hemicelluloses; Actinobacteria in cellulose



- Proteobacteria dominate N uptake functions (mostly N_{org})
- Intracellular N cycling is less skewed and more similar to overall activity
- Corroboration that Proteobacteria inhabit N-depleted rhizosphere

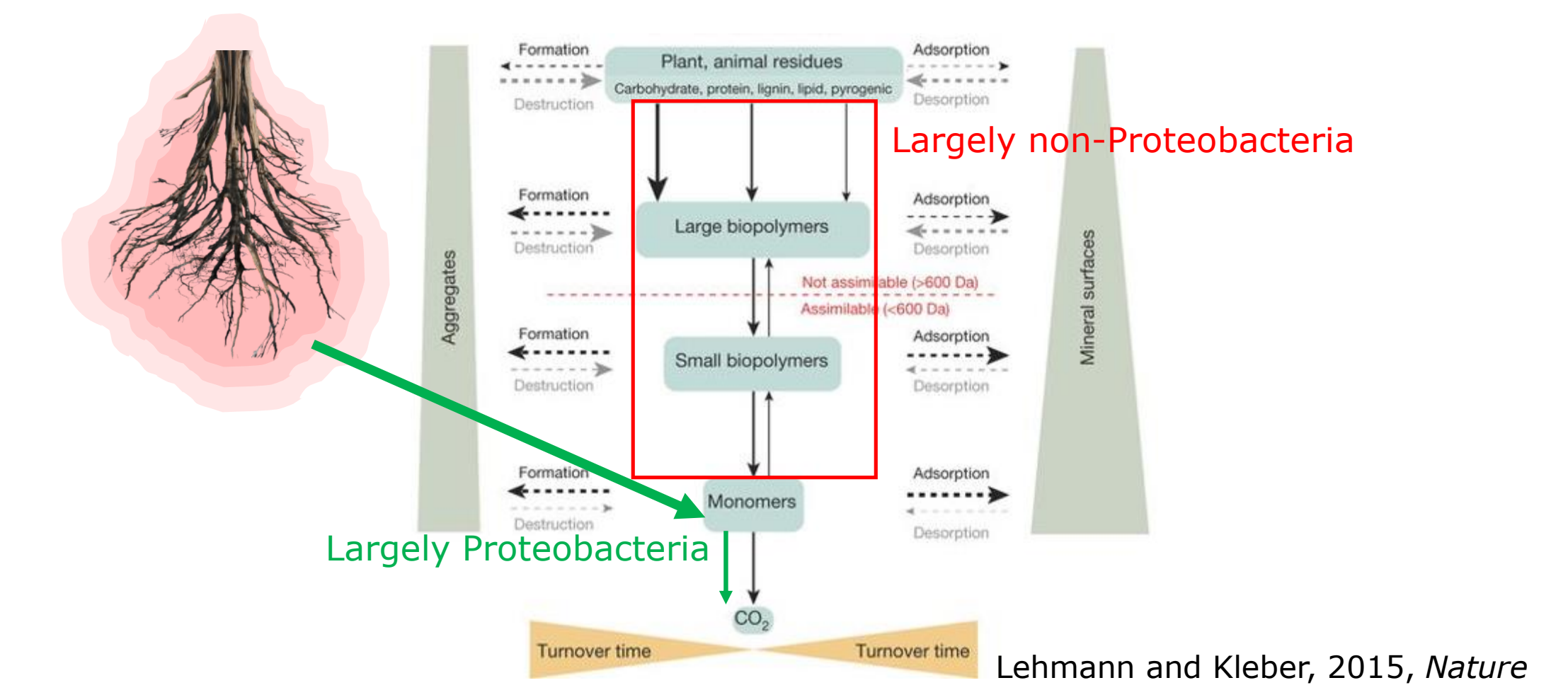


- The utility of Φ is supported by values for certain functions
- Negligible values for outer membrane functions in G+ vs. G- groups



Discussion

- Integrate microbial niche partitioning into current model of decomposition



- A model of Arctic soil biogeochemistry and microbial ecology
- Root-associated taxa/functions likely increase in a greening Arctic

