

Metabolic Network Analysis and Metatranscriptomics of a Cosmopolitan and Streamlined Freshwater Lineage

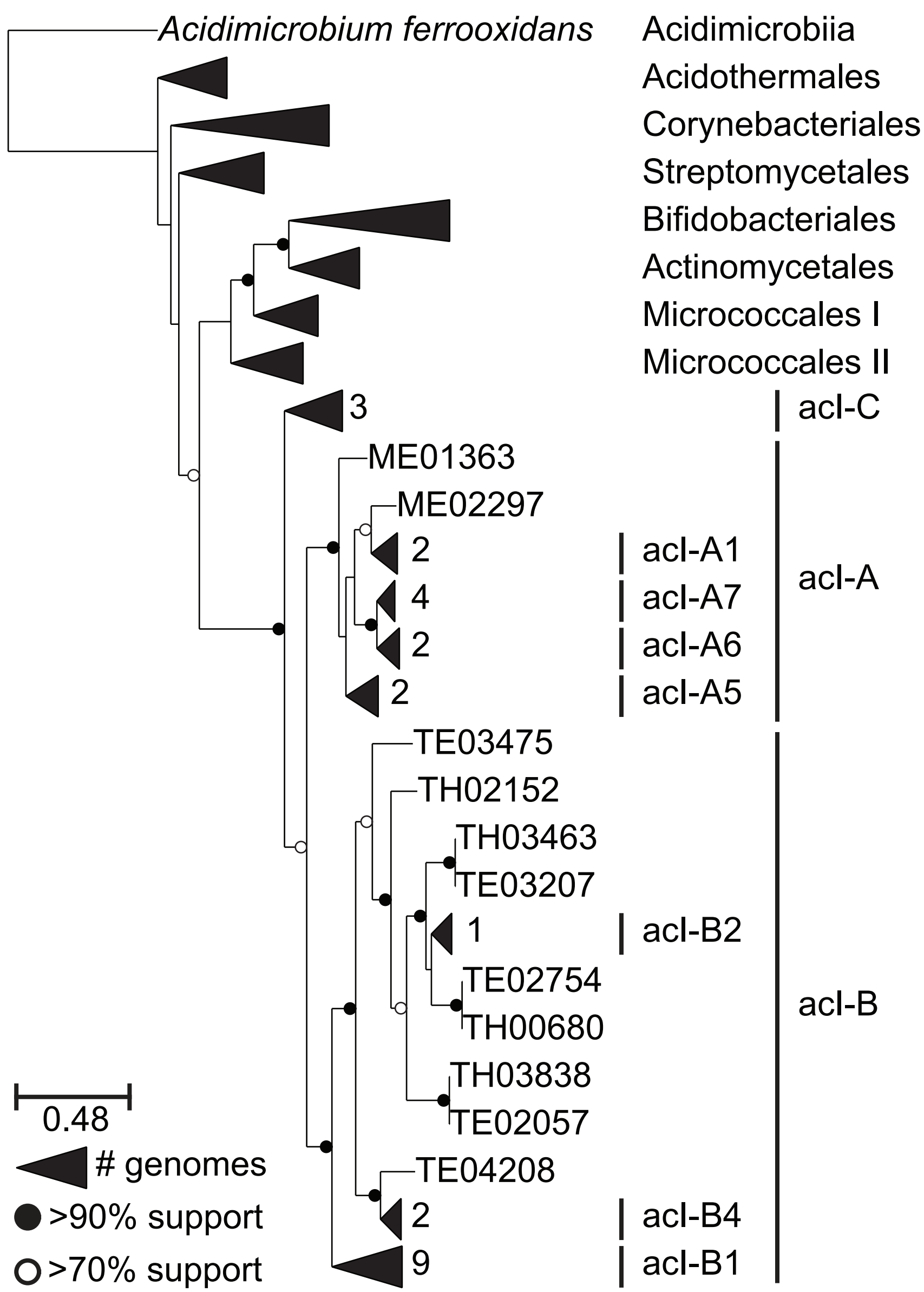
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INTRODUCTION

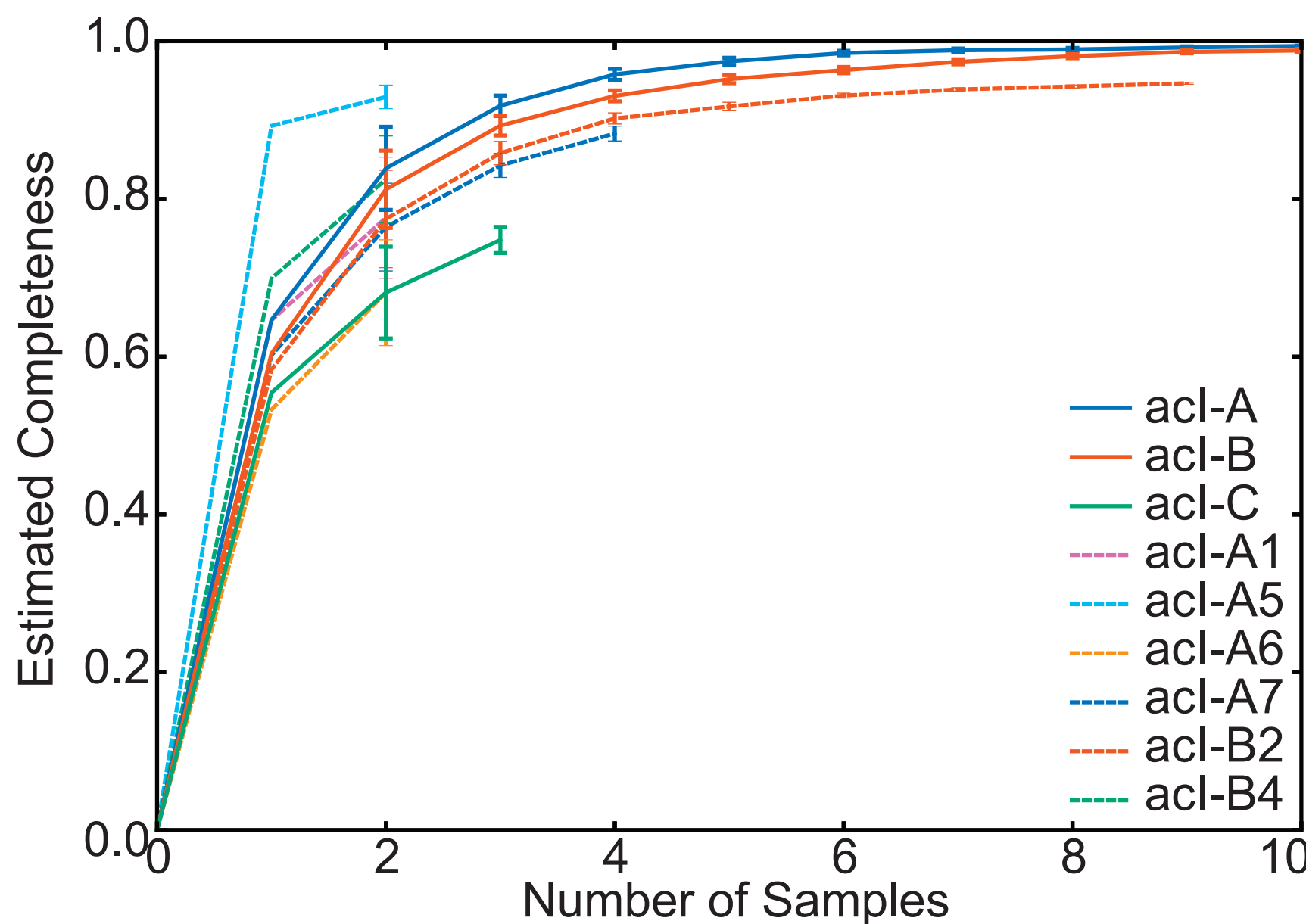
- Uncultured actinobacteria of the *acl* lineage are a dominant phylum in freshwater ecosystems
- Reference genome collection enables metabolic reconstruction of freshwater lineages
- A computational pipeline linking metabolic network reconstruction and metatranscriptomics provides insight into *acl* ecophysiology

PHYLOGENY



- *acI* form a monophyletic group within the class Actinobacteria
- 36 genomes across three previously defined clades (*acI*-A, -B, and -C)

GENOME COMPLETENESS



Estimated completeness of clade- and subclade-level population genomes based on single-copy marker genes.

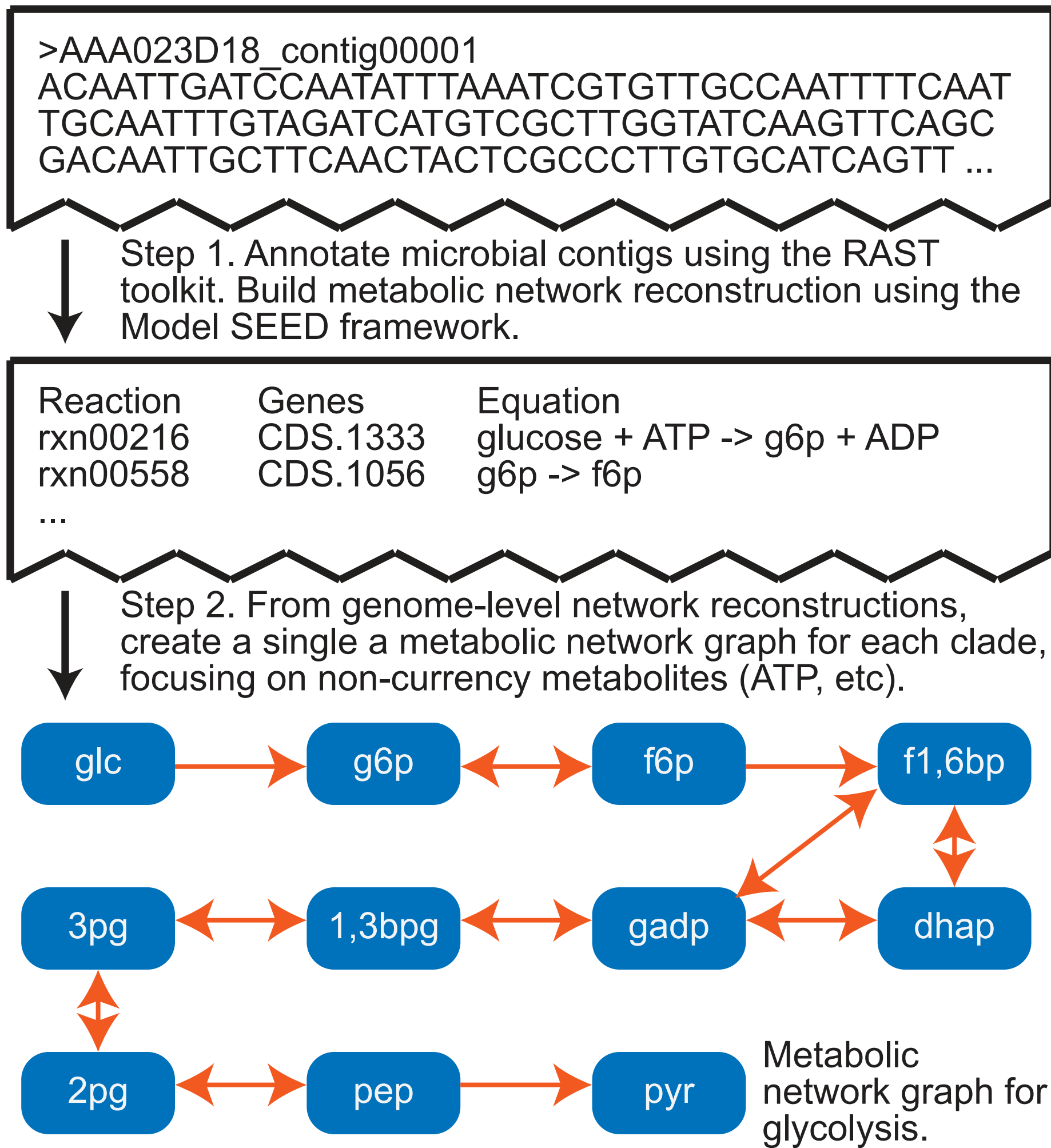
AVAILABILITY



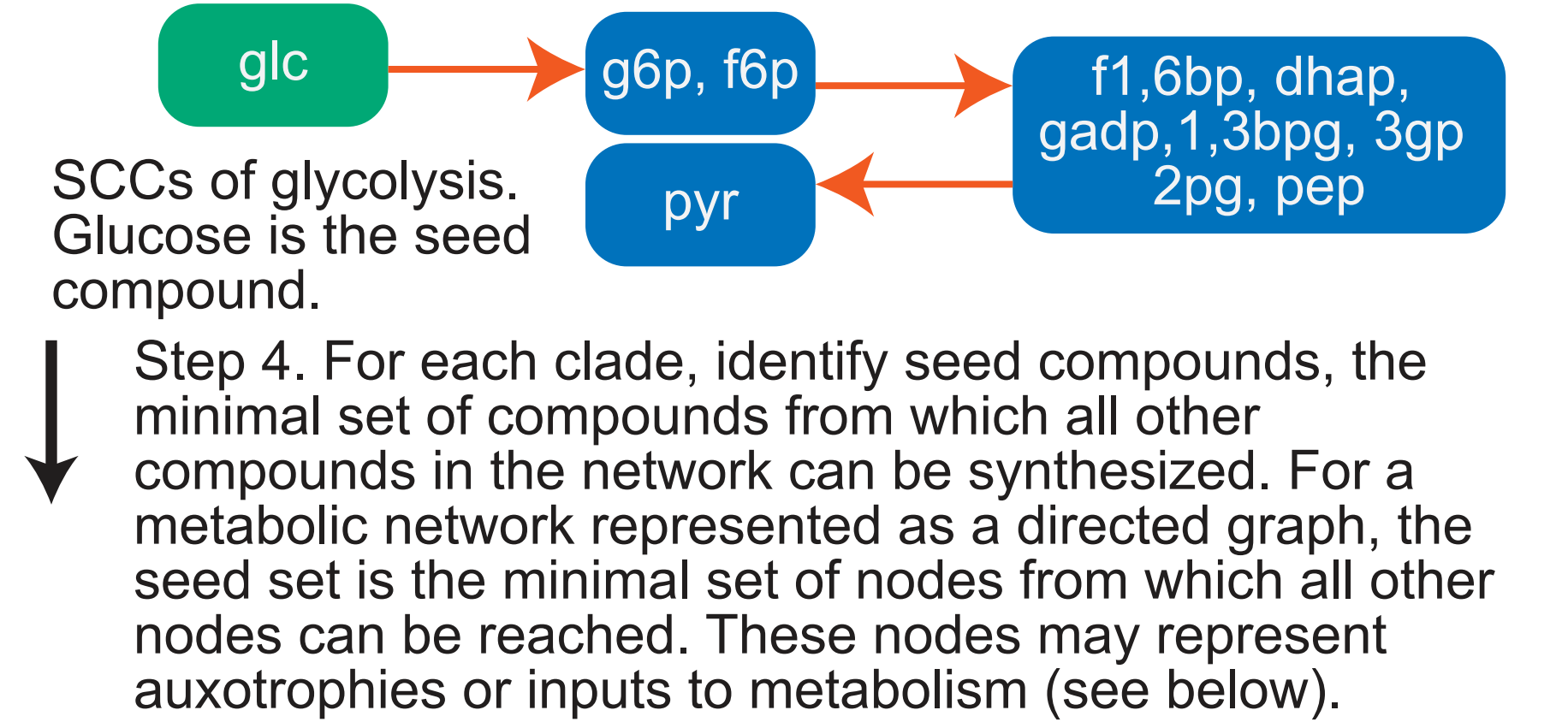
joshamilton

Code, example Jupyter notebooks, this poster, and more available on GitHub.

METABOLIC NETWORK RECONSTRUCTION



↓ Step 3. Decompose the metabolic graph into its strongly connected components (SCCs), groups of compounds which are interconvertible. These graphs typically exhibit a “bow-tie” structure, with a single component containing many metabolites.



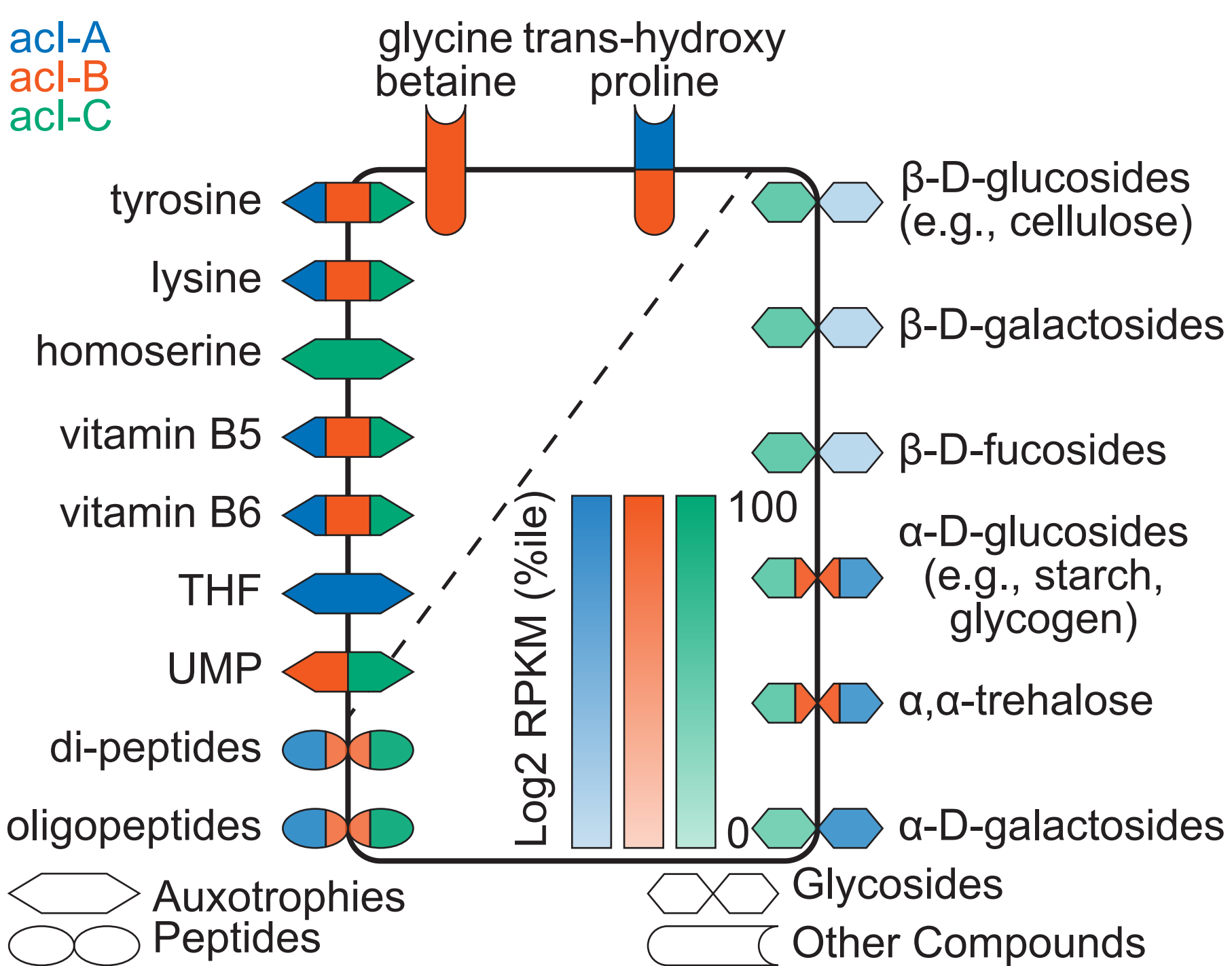
Metabolic network reconstruction for *acl-A*, showing its SCCs. Seed compounds are in green. The largest SCC (red circle) contains 60% of the metabolites.

NETWORK ANALYSIS AND METATRANSCRIPTOMICS

NETWORK CURATION AND READ MAPPING

- Curated list of seed compounds
- Re-annotated peptidases, glycoside hydrolases, and transporters
- Metatranscriptomes collected from Lake Mendota (Madison, WI) and mapped to reference *acI* genomes
- Gene expression calculated for orthologous gene clusters, as identified by OrthoMCL

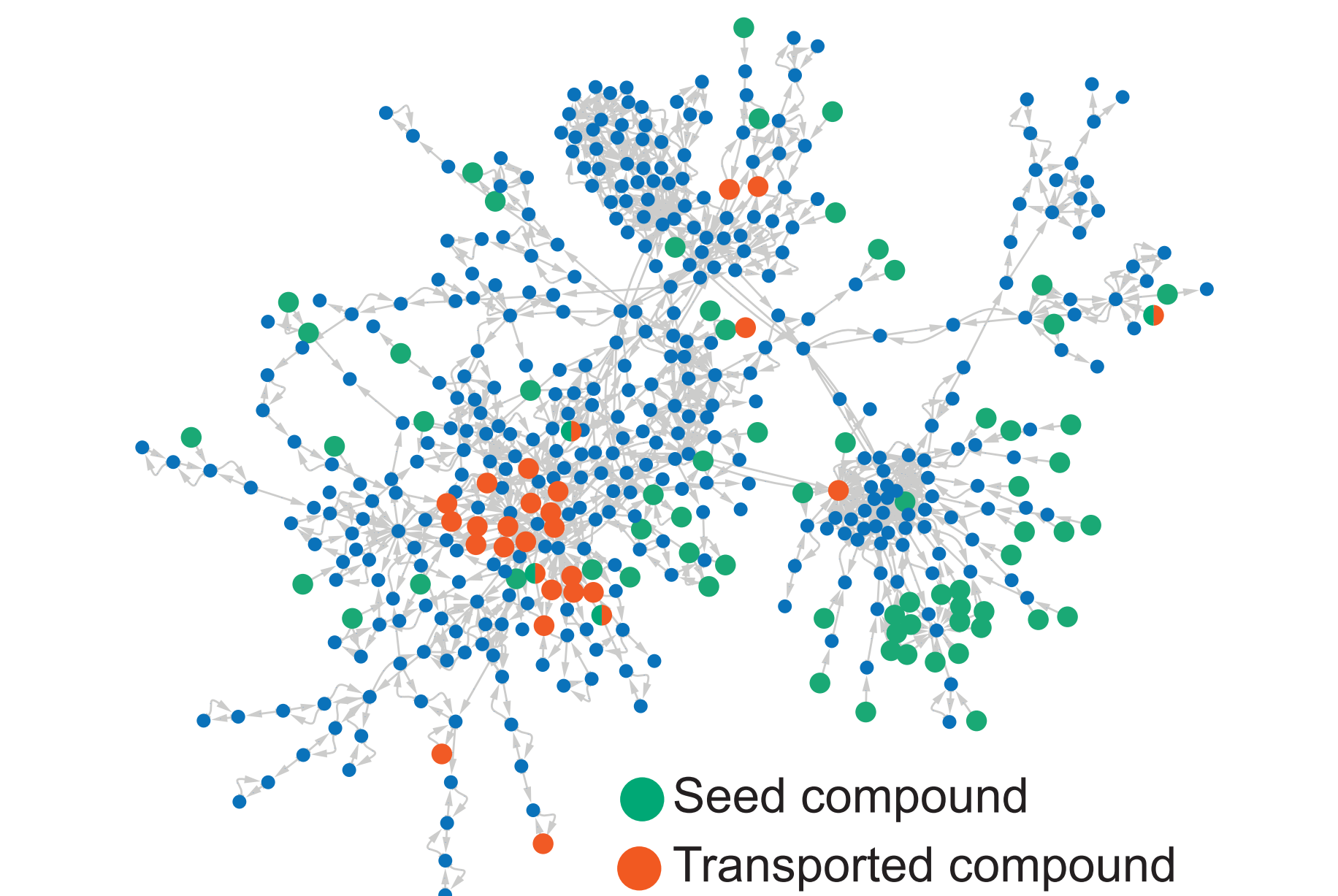
CURATED SET OF SEED COMPOUNDS



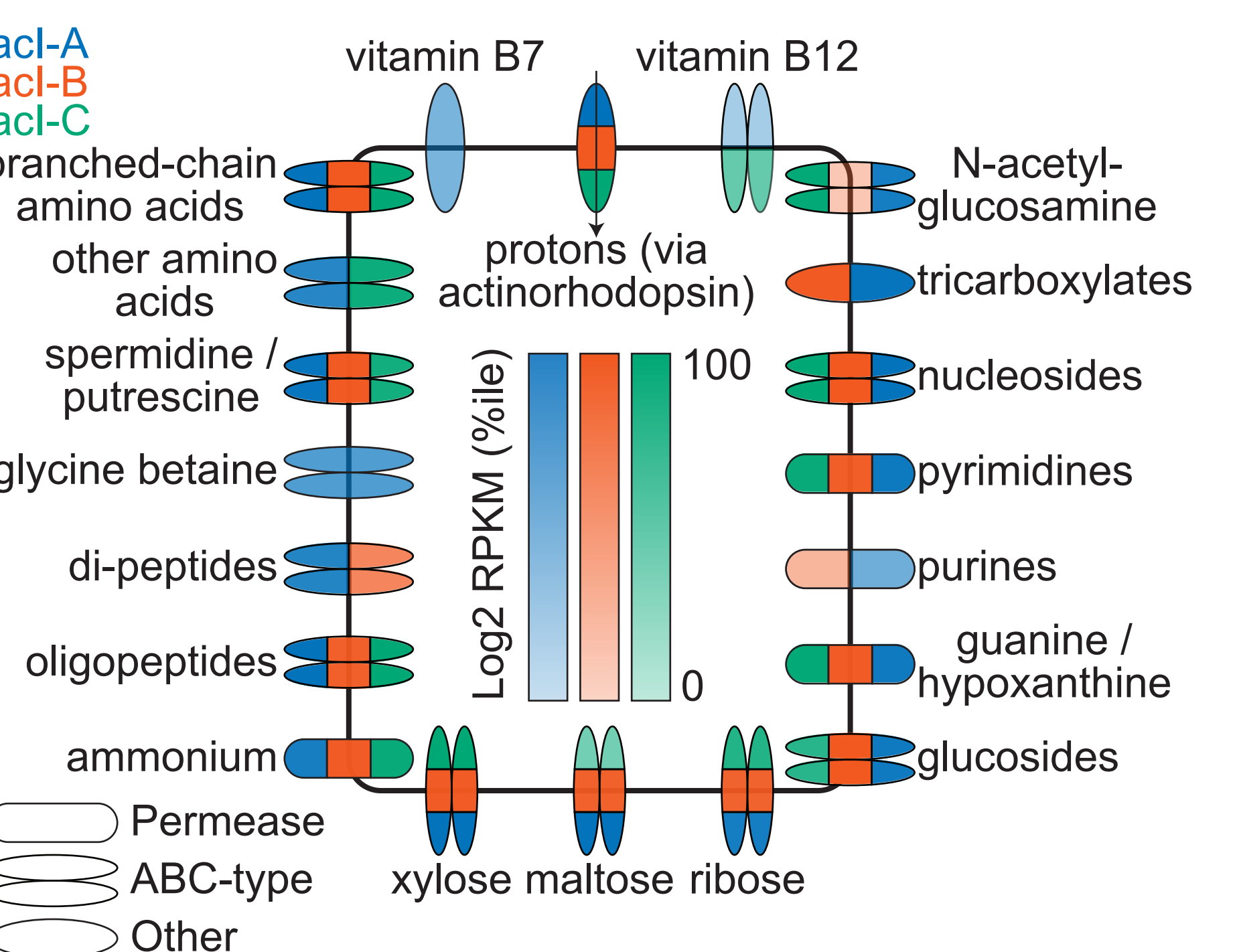
CONCLUSIONS

- Members of the *acl* lineage consume substrates near the center of their metabolic network, rather than the periphery
- Auxotrophies for vitamins and amino acids are consistent with *acl* from other lakes
- Broad substrate specificity may explain the ubiquity of the *acl* lineage

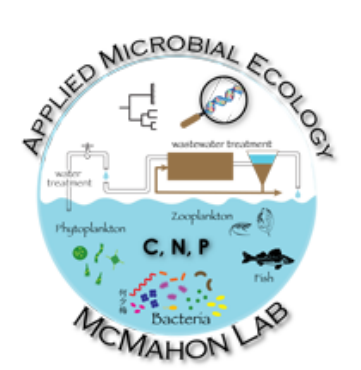
METABOLIC NETWORK OF CLADE ACI-C



EXPRESSED TRANSPORT PROTEINS



ACKNOWLEDGEMENTS



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