

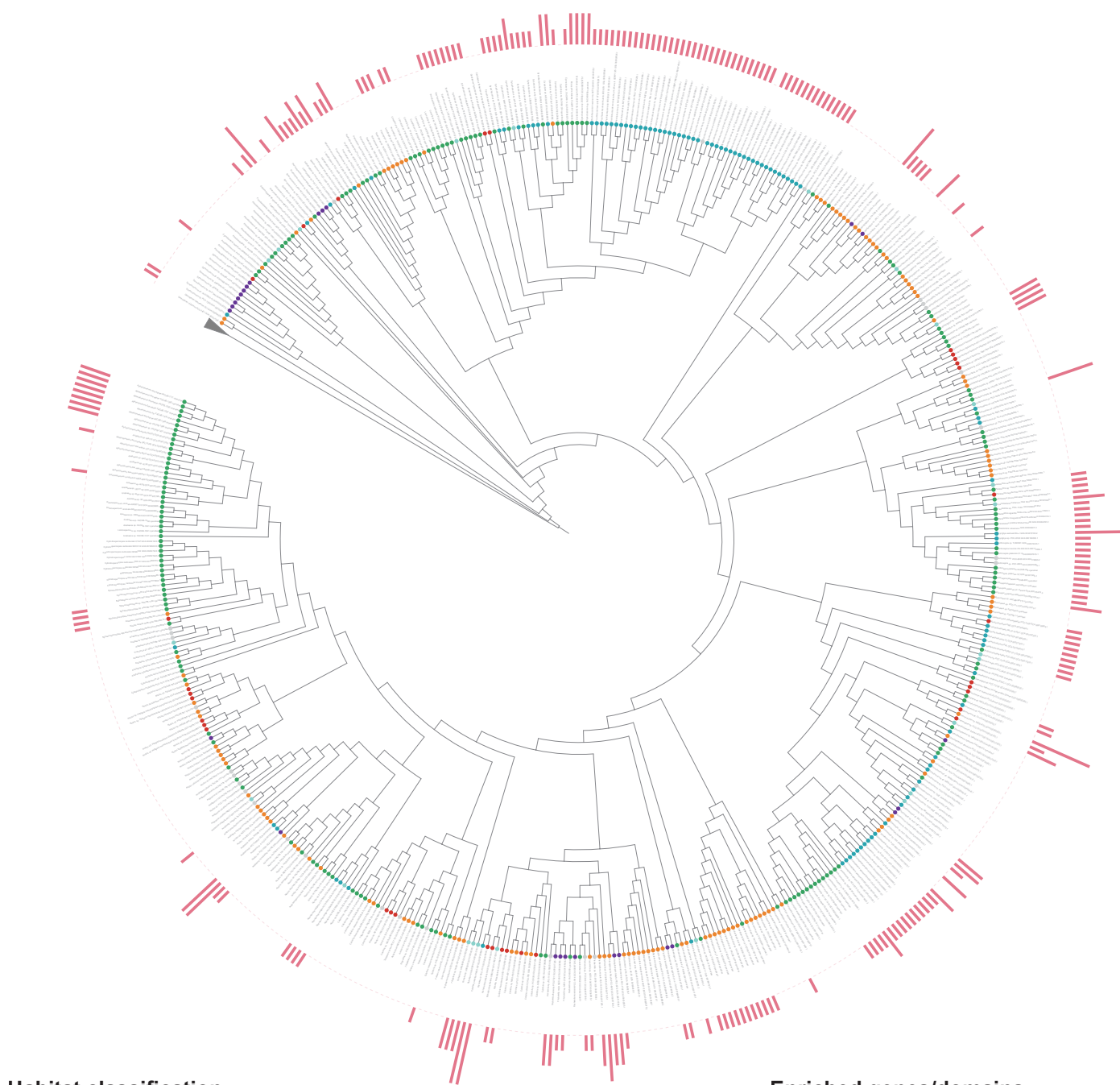
**Habitat classification**

- Marine (n = 99)
- Freshwater (n = 184)
- Terrestrial (n = 125)
- Thermal springs (n = 26)
- Host-associated (n = 33)
- Others (n = 24)
- Unknown (n = 28)

**Enriched genes/domains**

- mannosyl-3-phosphoglycerate phosphatase
- glucosylglycerol 3-phosphatase
- glucosyl-3-phosphoglycerate synthase

Fig S8. Phylogenetic distribution of marine-enriched gene/domains. The phylogenetic tree is a subtree of genomic tree in Fig.1 that low-quality genomes were pruned. Grey triangle on the tree denotes outgroups. Colored circles represent ecosystems where strains derived from. Colored bars denote copy numbers of enriched genes or domains.



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**Enriched genes/domains**

| *yrbG*

Fig S8. (Continued). Phylogenetic distribution of marine-enriched gene/domains. The phylogenetic tree is a subtree of genomic tree in Fig.1 that low-quality genomes were pruned. Grey triangle on the tree denotes outgroups. Colored circles represent ecosystems where strains derived from. Colored bars denote copy numbers of enriched genes or domains.

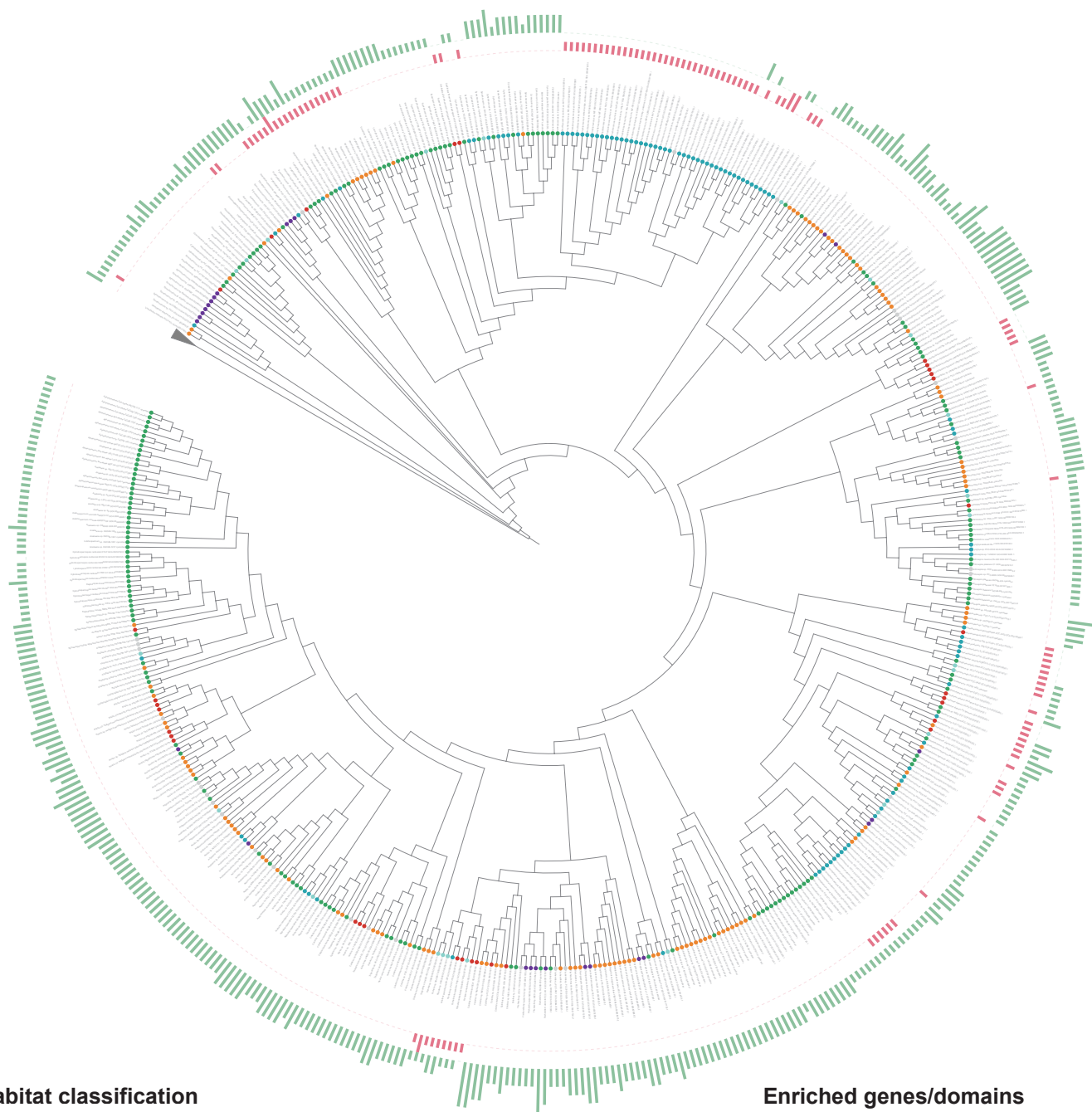
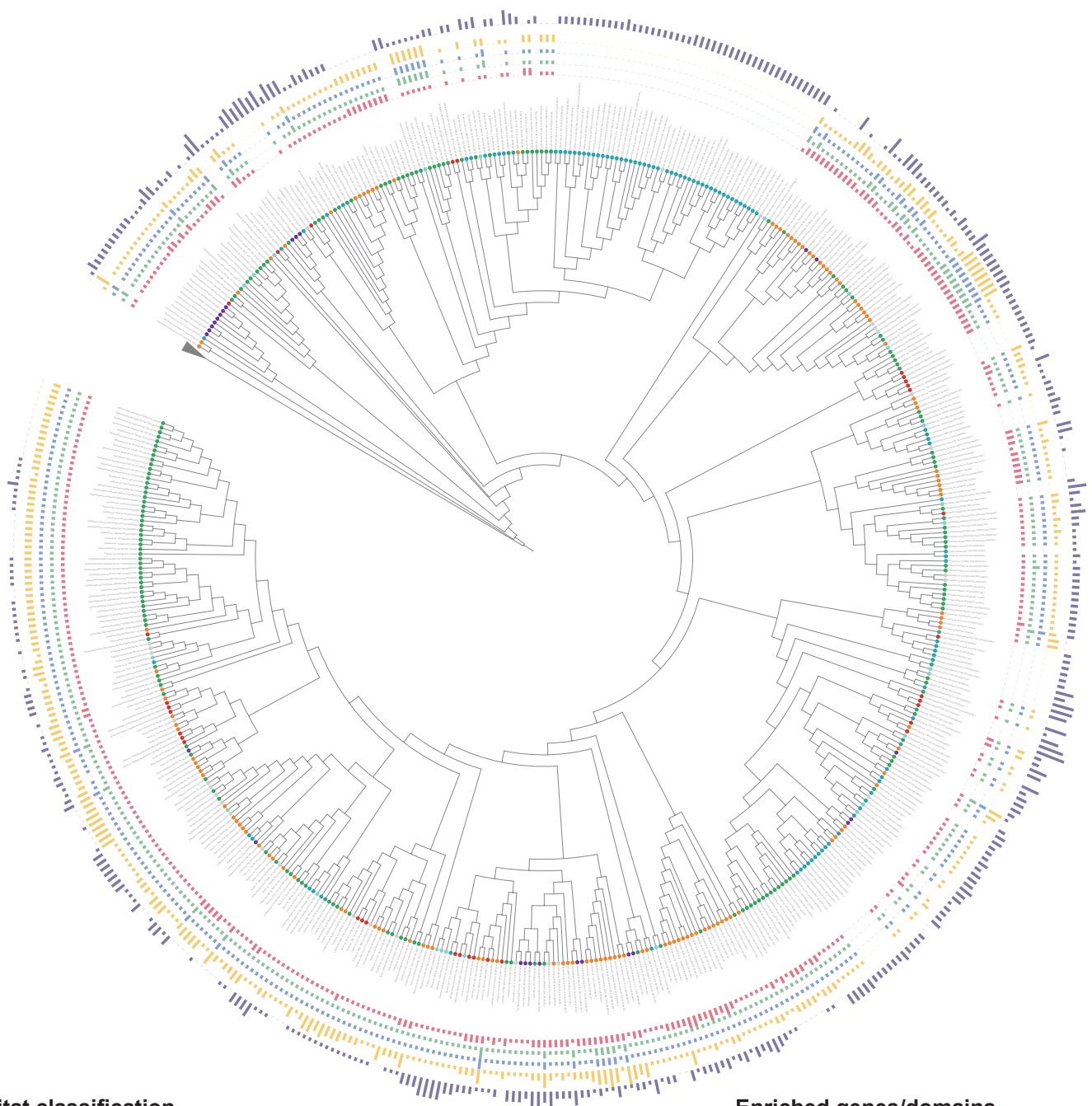


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**Enriched genes/domains**

- | *cysA*
- | *cysU*
- | *cysW*
- | *cysP*
- | *sulP*

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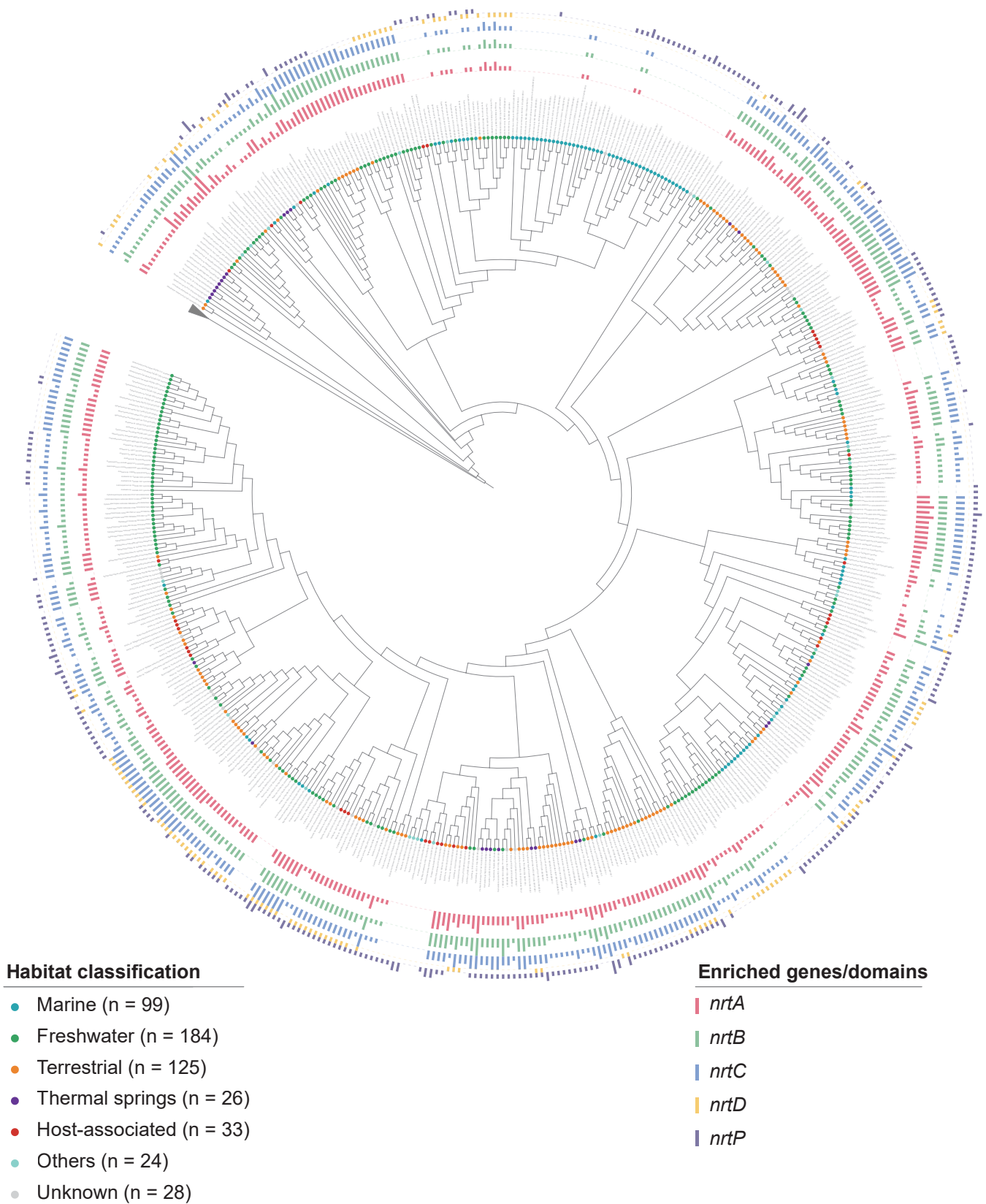


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