

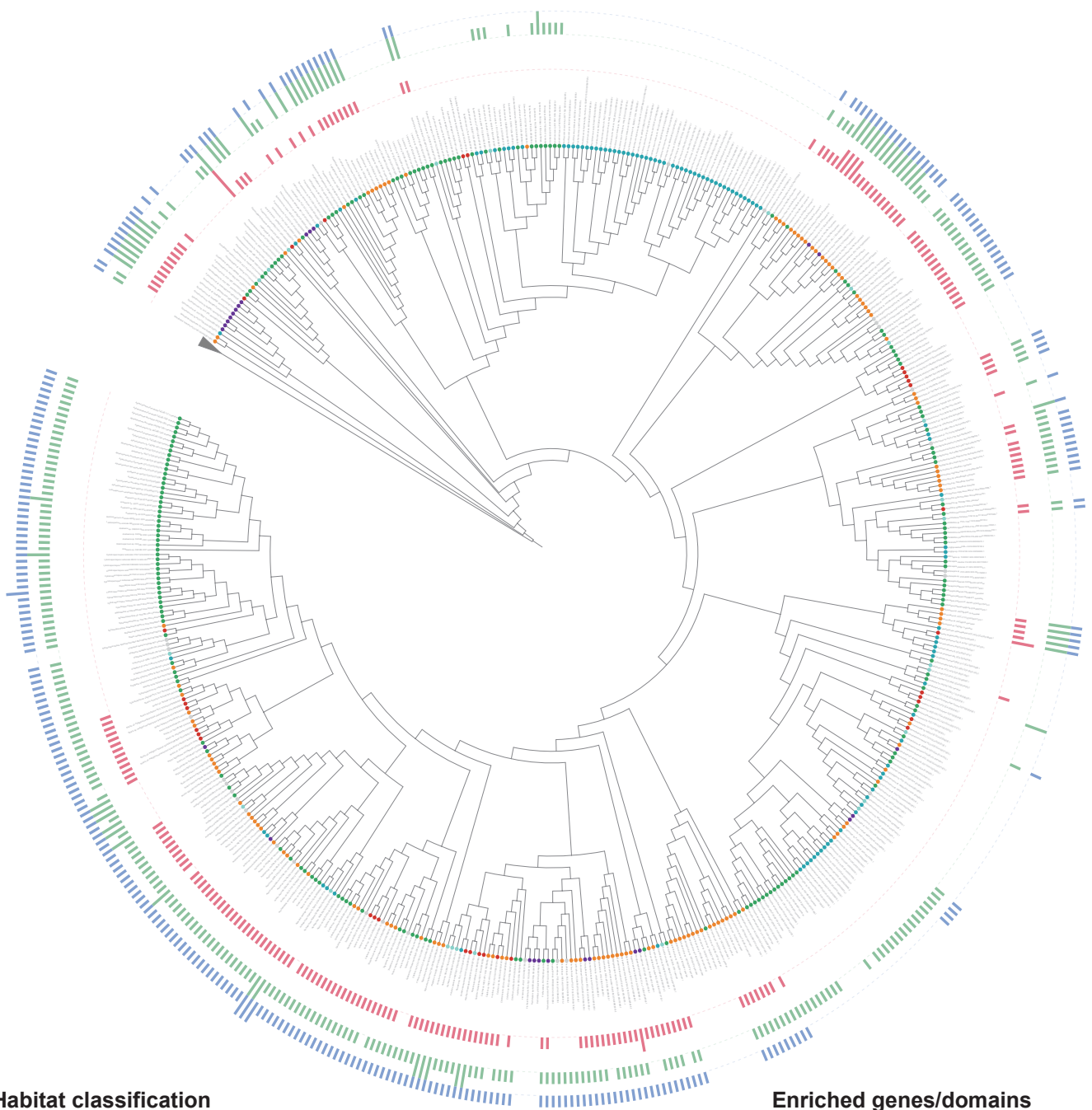
Habitat classification

- 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

- | *treZ*
- | *treY*
- | sucrose synthase

Fig S10. Phylogenetic distribution of terrestrial-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.



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

- | *opuC*
- | *opuBD*
- | *opuA*

Fig S10. (Continued). Phylogenetic distribution of terrestrial-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.

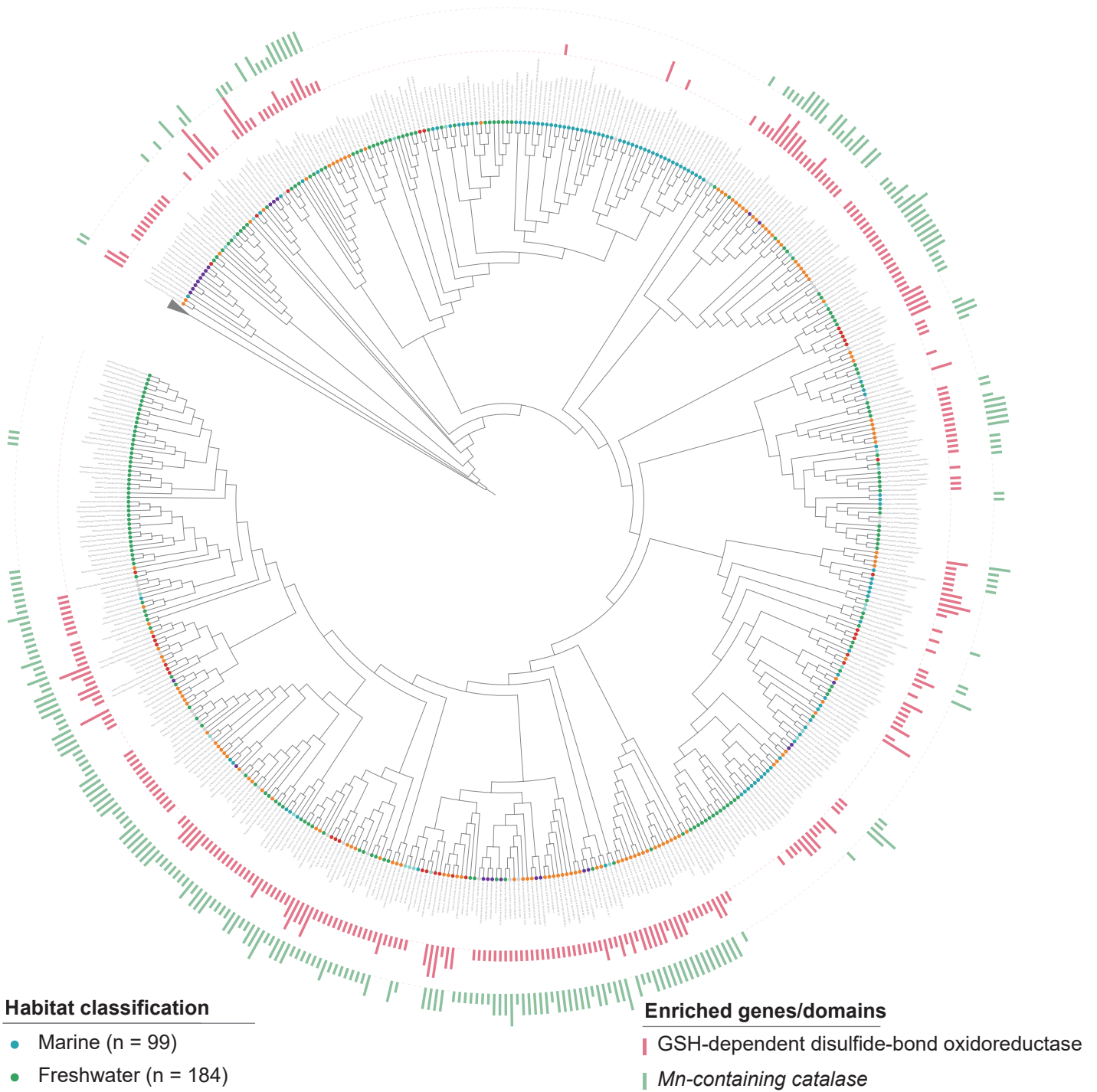


Fig S10. (Continued). Phylogenetic distribution of terrestrial-enriched gene/domains. The phylogenetic tree is a subtree of genomic tree in Fig.1 that low-quality genomes were pruned. Grey triangle on the tree denotes outgroups. Colored circles represent ecosystems where strains derived from. Colored bars denote copy numbers of enriched genes or domains.



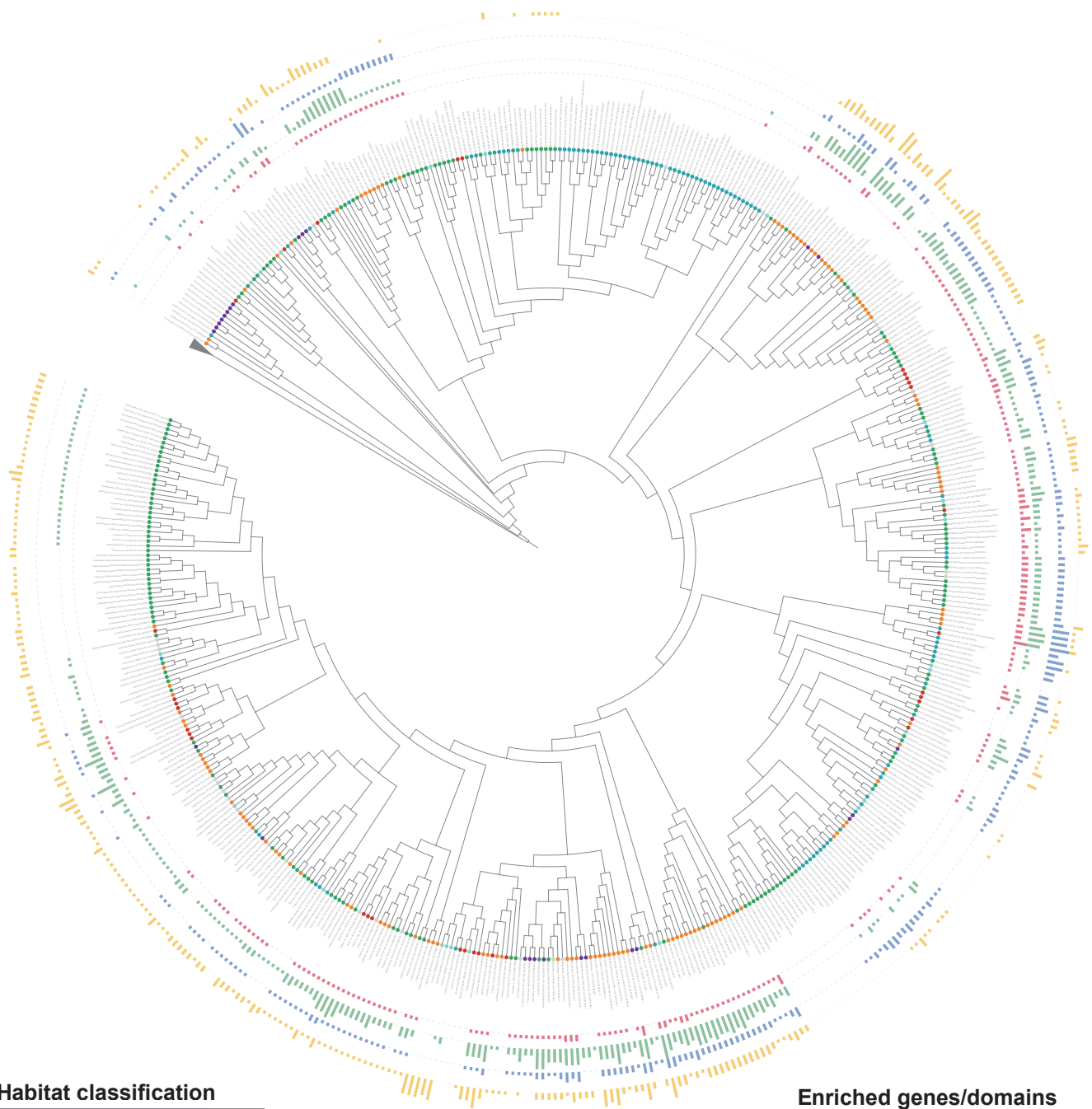
Habitat classification

- 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

| *uvdE*

Fig S10. (Continued). Phylogenetic distribution of terrestrial-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.



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

- *cheA*
- *cheW*
- *cheB*
- *cheR*

Fig S10. (Continued). Phylogenetic distribution of terrestrial-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.

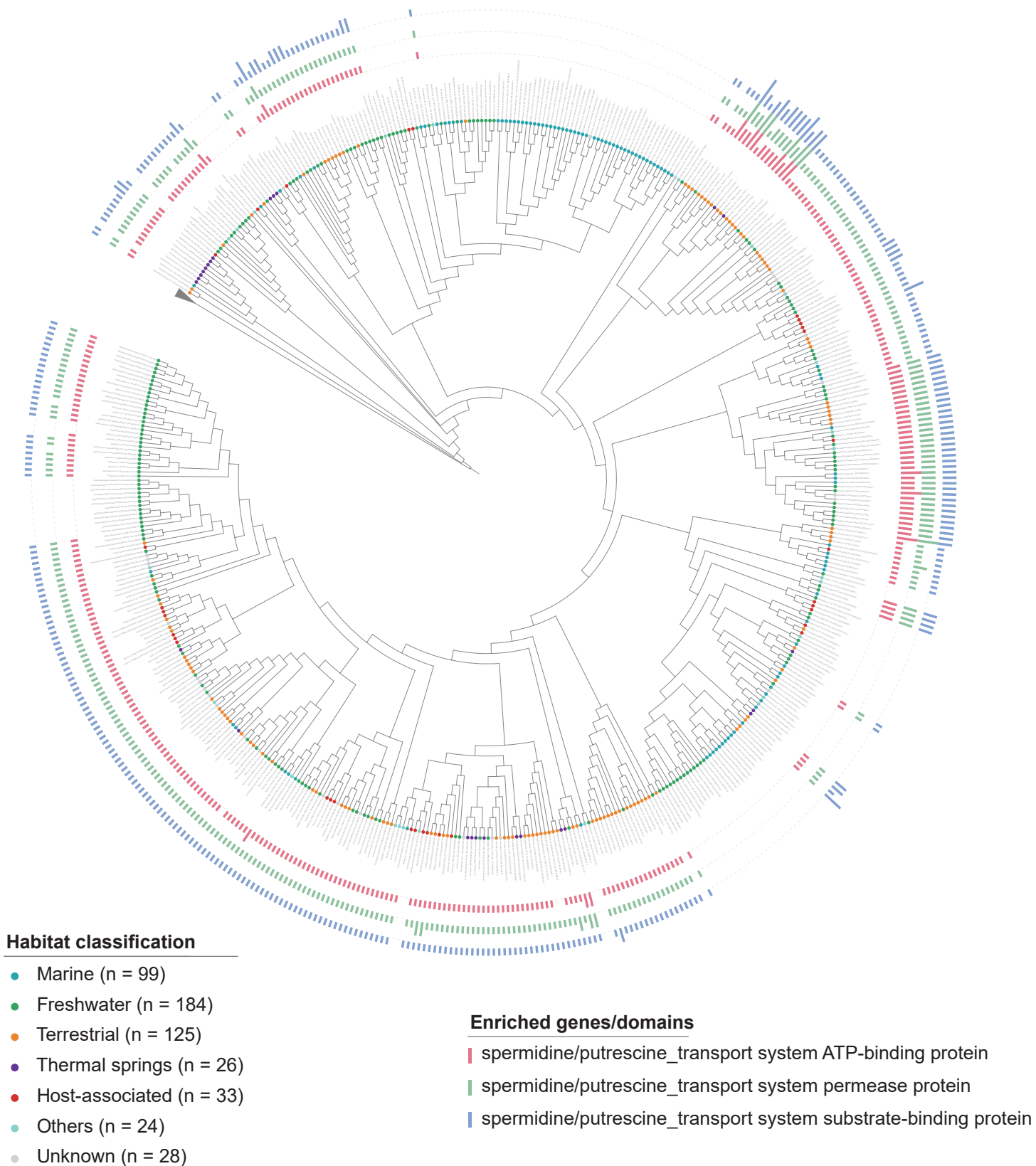


Fig S10. (Continued). Phylogenetic distribution of terrestrial-enriched gene/domains. The phylogenetic tree is a subtree of genomic tree in Fig.1 that low-quality genomes were pruned. Grey triangle on the tree denotes outgroups. Colored circles represent ecosystems where strains derived from. Colored bars denote copy numbers of enriched genes or domains.

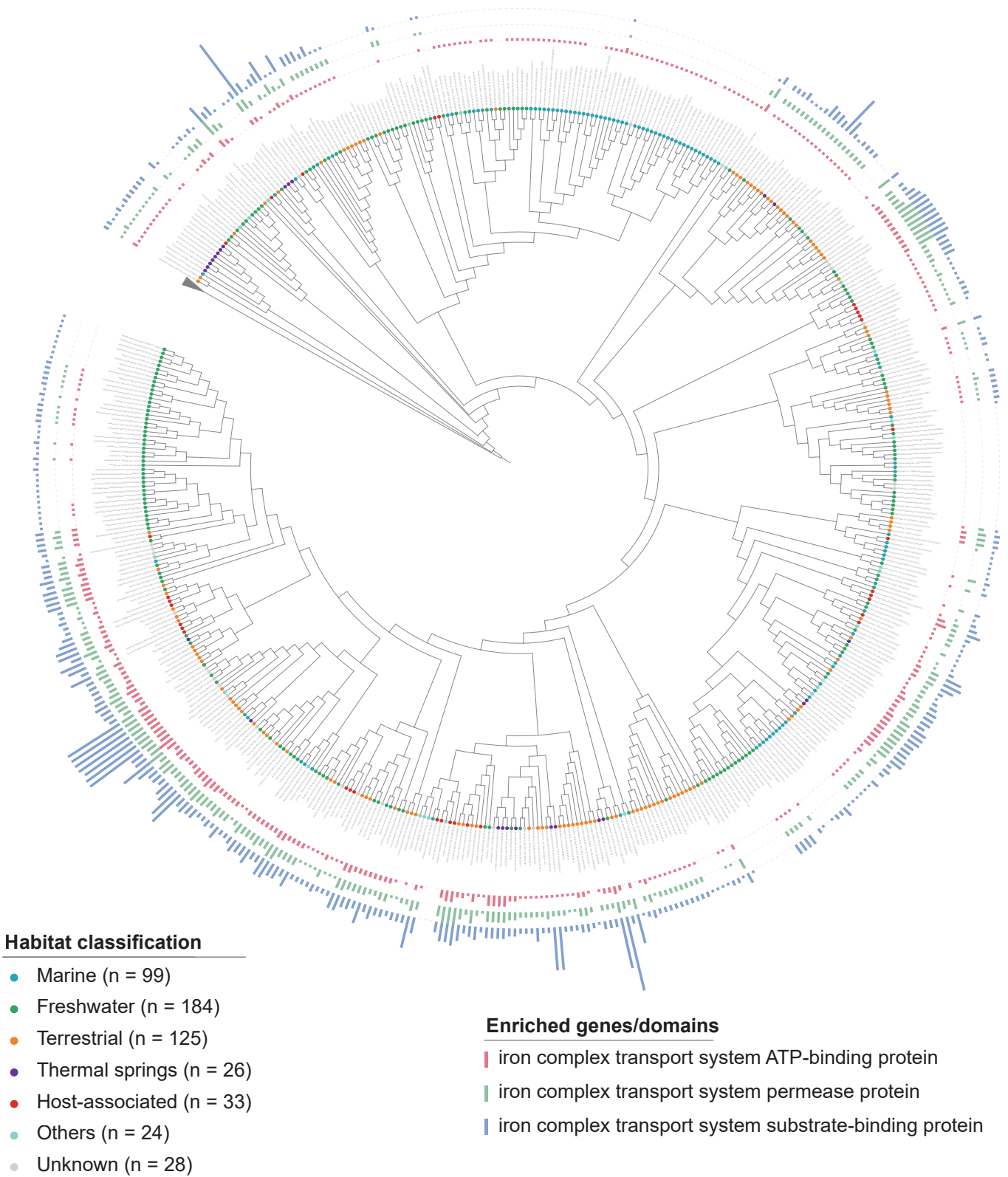


Fig S10. (Continued). Phylogenetic distribution of terrestrial-enriched gene/domains. The phylogenetic tree is a subtree of genomic tree in Fig.1 that low-quality genomes were pruned. Grey triangle on the tree denotes outgroups. Colored circles represent ecosystems where strains derived from. Colored bars denote copy numbers of enriched genes or domains.