

Depth-driven ecology and metabolic specialization of marine Chloroflexi (SAR202 lineages) across the global ocean

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1 BACKGROUND

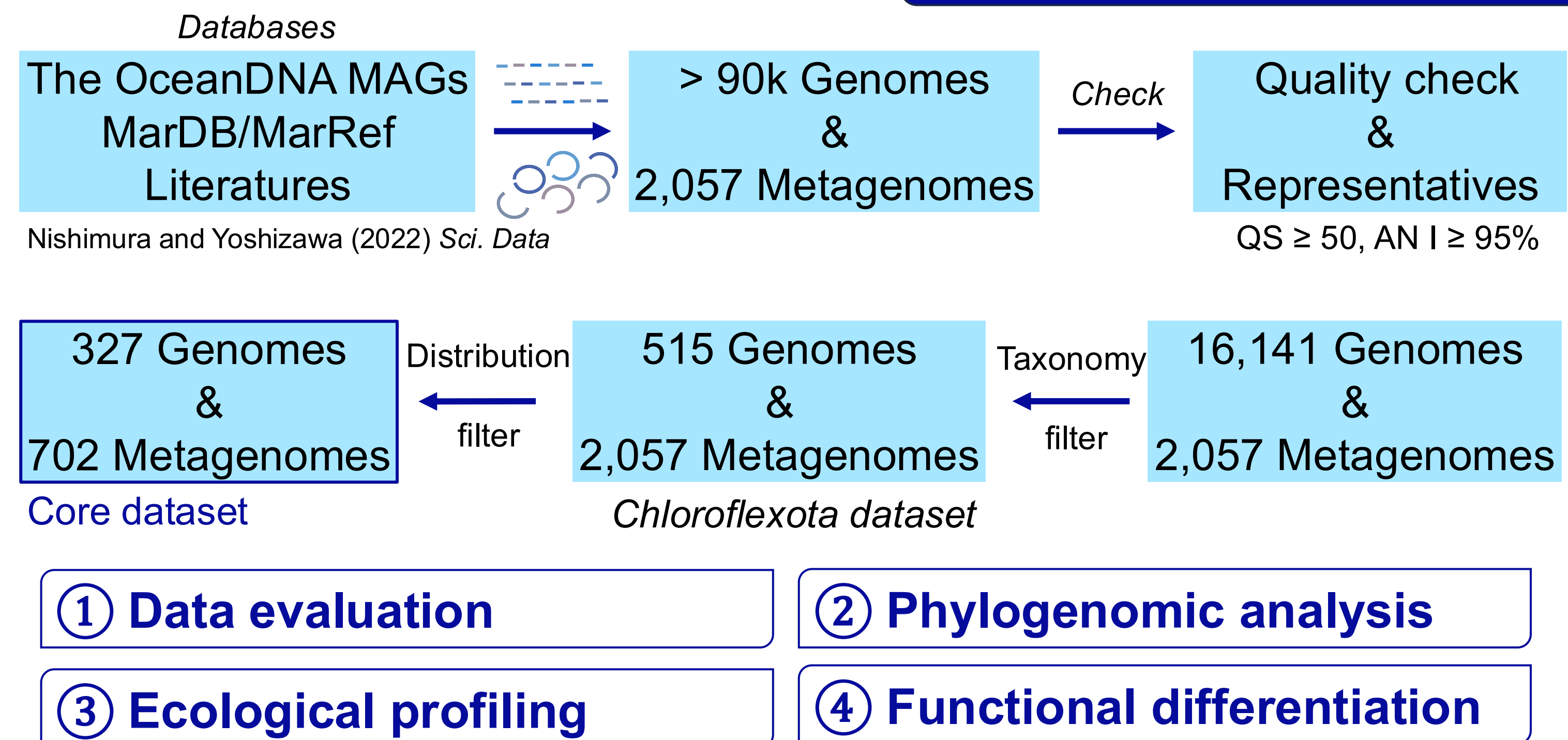
- Marine Chloroflexi (especially SAR202) are abundant but poorly characterized.
- Limited cultured representatives hinder understanding of their ecology.
- We integrated global genomes and metagenomes to investigate ecological differentiation.



Question:

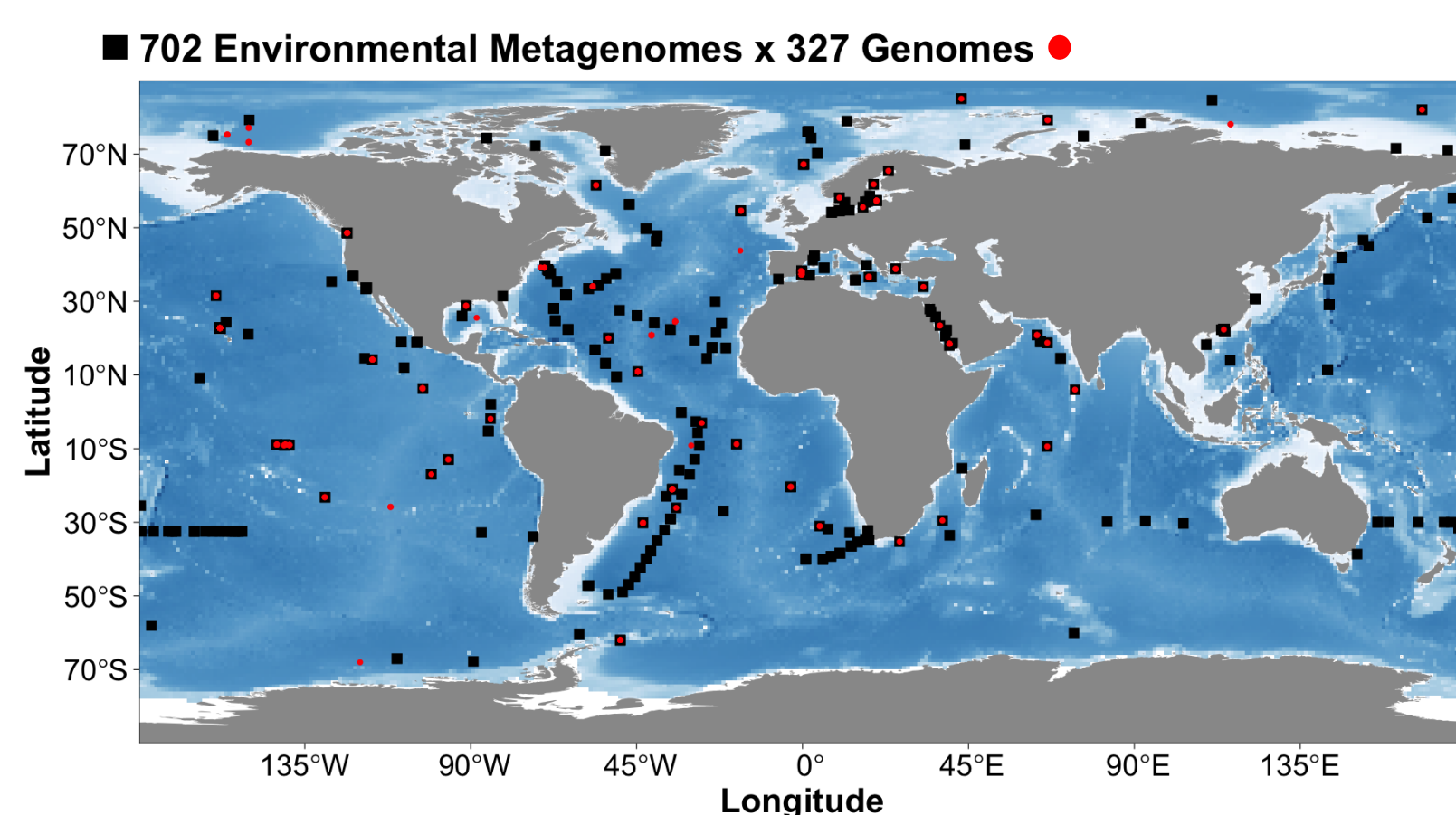
How do marine Chloroflexi differ in their distribution, evolution, and functional adaptation across the global ocean?

2 WORKFLOW



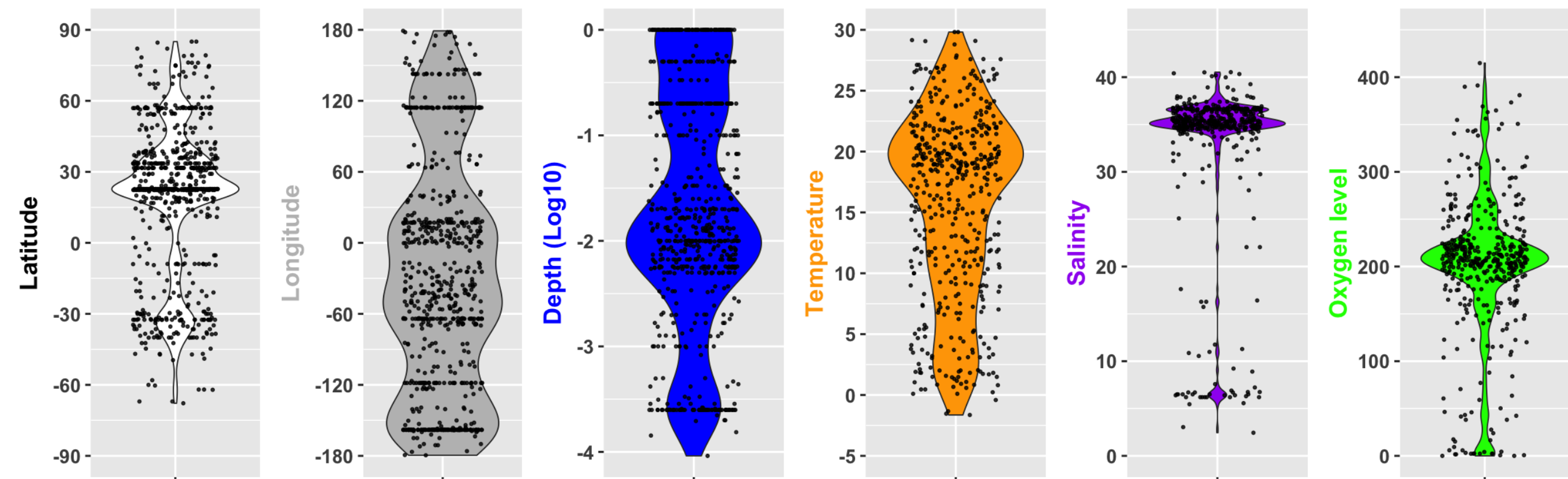
3 RESULTS

① Evaluation of the Global Framework Dataset



Comprehensiveness:

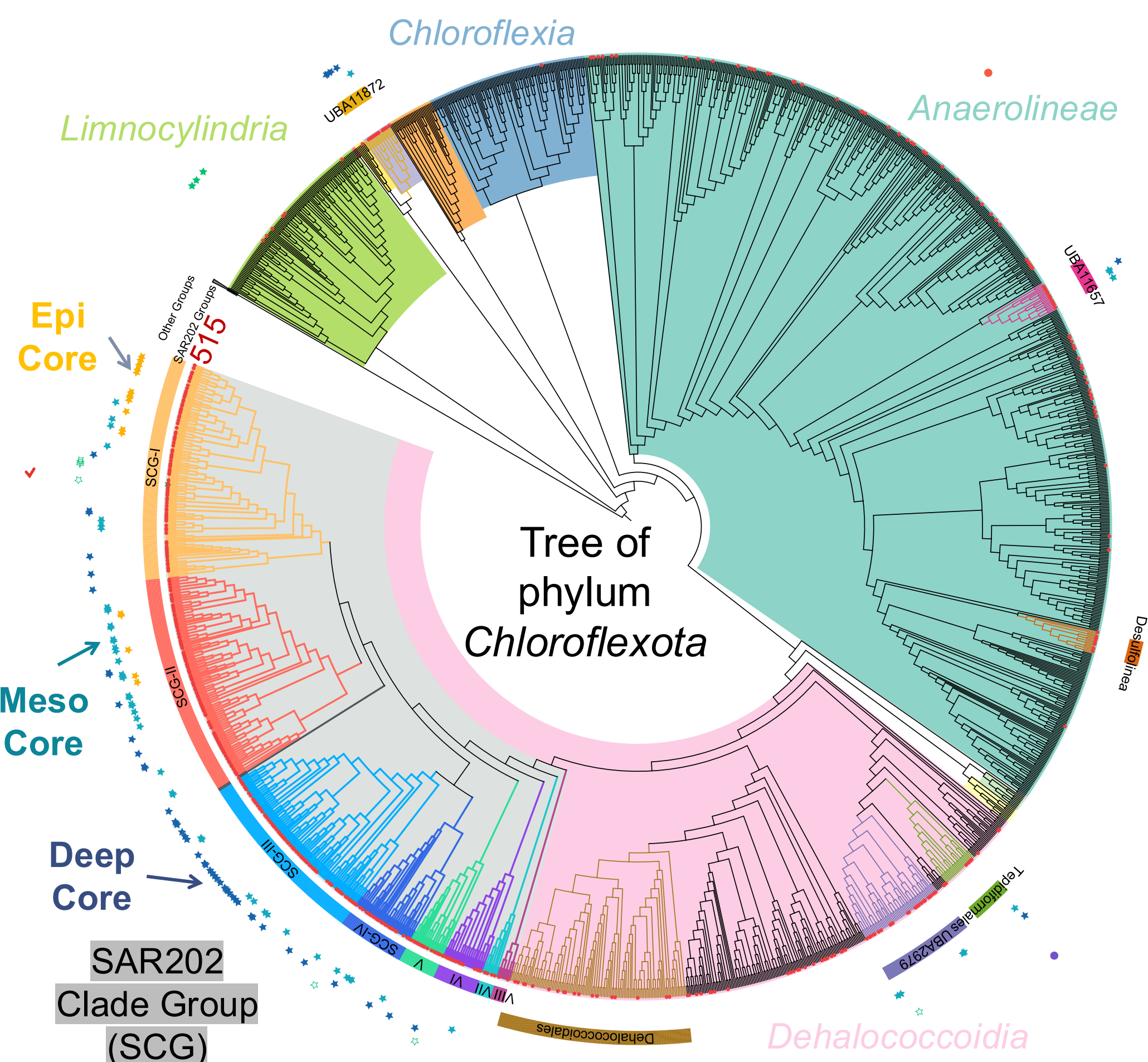
- Range (67°S – 85°N)
- Depth ~ -10,899 m
- Diverse Salinity/Oxygen levels
- Sources Biofilm/Sediment trap



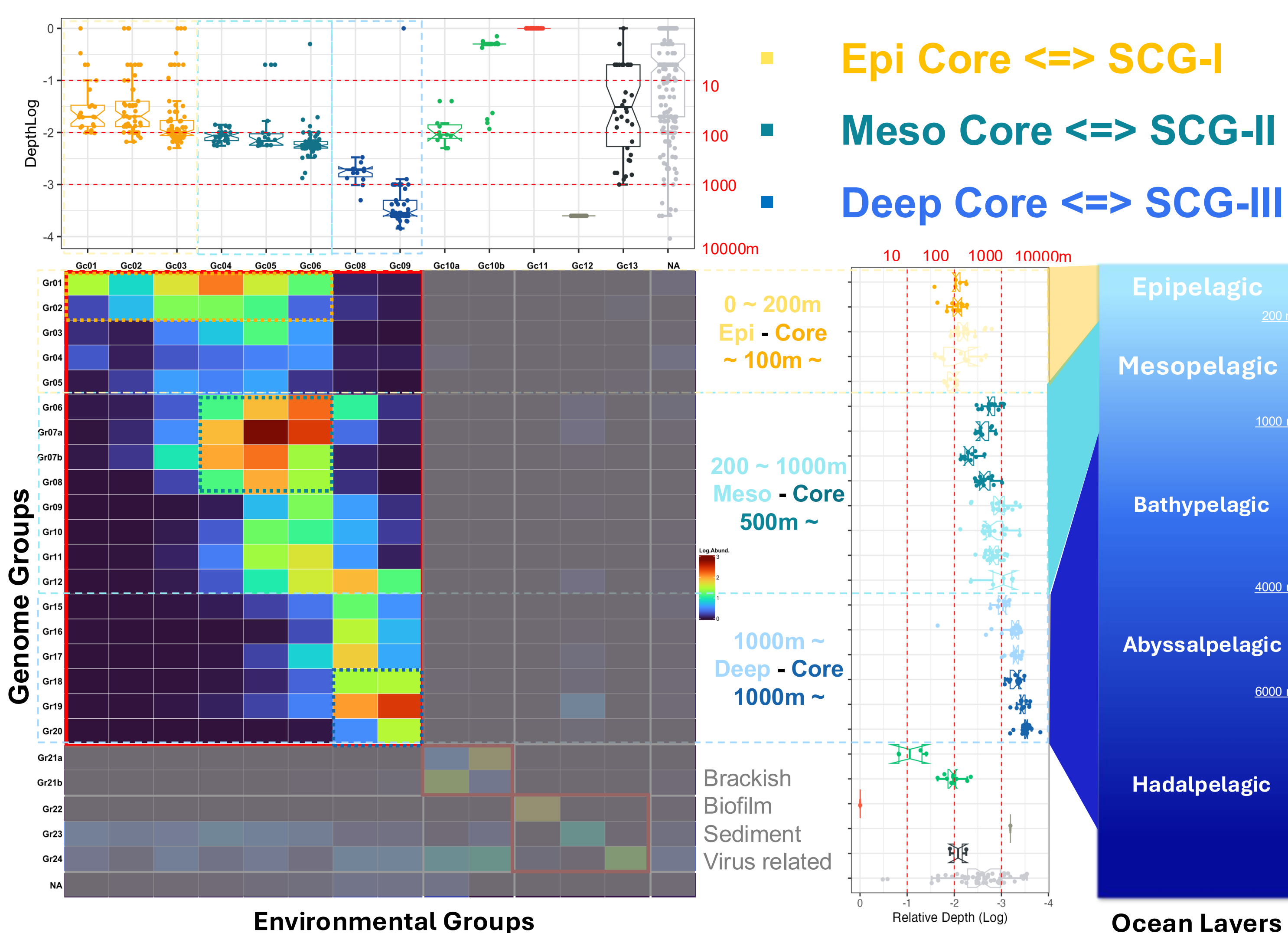
② Global phylogeny of marine Chloroflexi

p__Chloroflexota (n=1,902):

- 515 genomes
- 1,387 references
- 327 Core dataset
- Dehalococcoidia 88%, SAR202 81%
- SAR202 resolved into 8 subclades (SCG I – VIII)



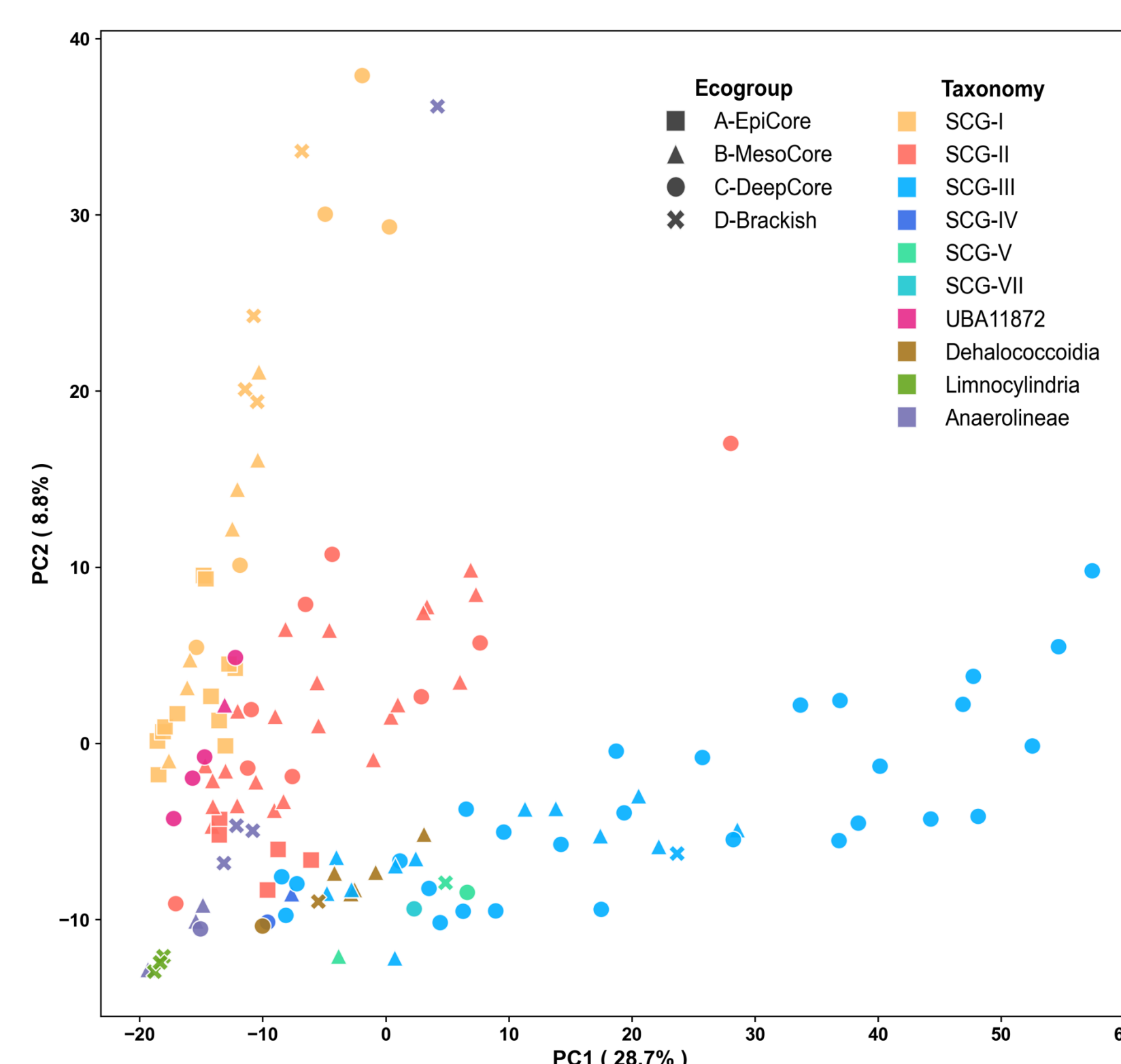
③ Distribution patterns reveal ecological differentiation



Ocean depth is the primary driver of SAR202 ecological differentiation.

④ Functional differentiation across depth-associated groups

KO function profile PCA



Enriched KO functions

EpiCore: photolyases (phrB), proteorhodopsins, oxidative stress responses, ...

MesoCore: transitional zone

DeepCore: DNA repair, stress tolerance, CAZyme expansion, complex DOM utilization, ...

Data not shown

4 CONCLUSIONS

- ✓ SAR202 dominated marine Chloroflexi and was resolved into eight distinct subclades.
- ✓ Ocean depth is the primary driver of SAR202 ecological differentiation.
- ✓ Distinct functional repertoires underpin adaptation across depth zones.
- ✓ Highlighting the ecological significance of SAR202 in marine biogeochemical cycling.

Acknowledgements

- ❖ Partial travel support: The Oceanographic Society of Japan
- ❖ Research support: JSPS KAKENHI (JP25K18284)

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