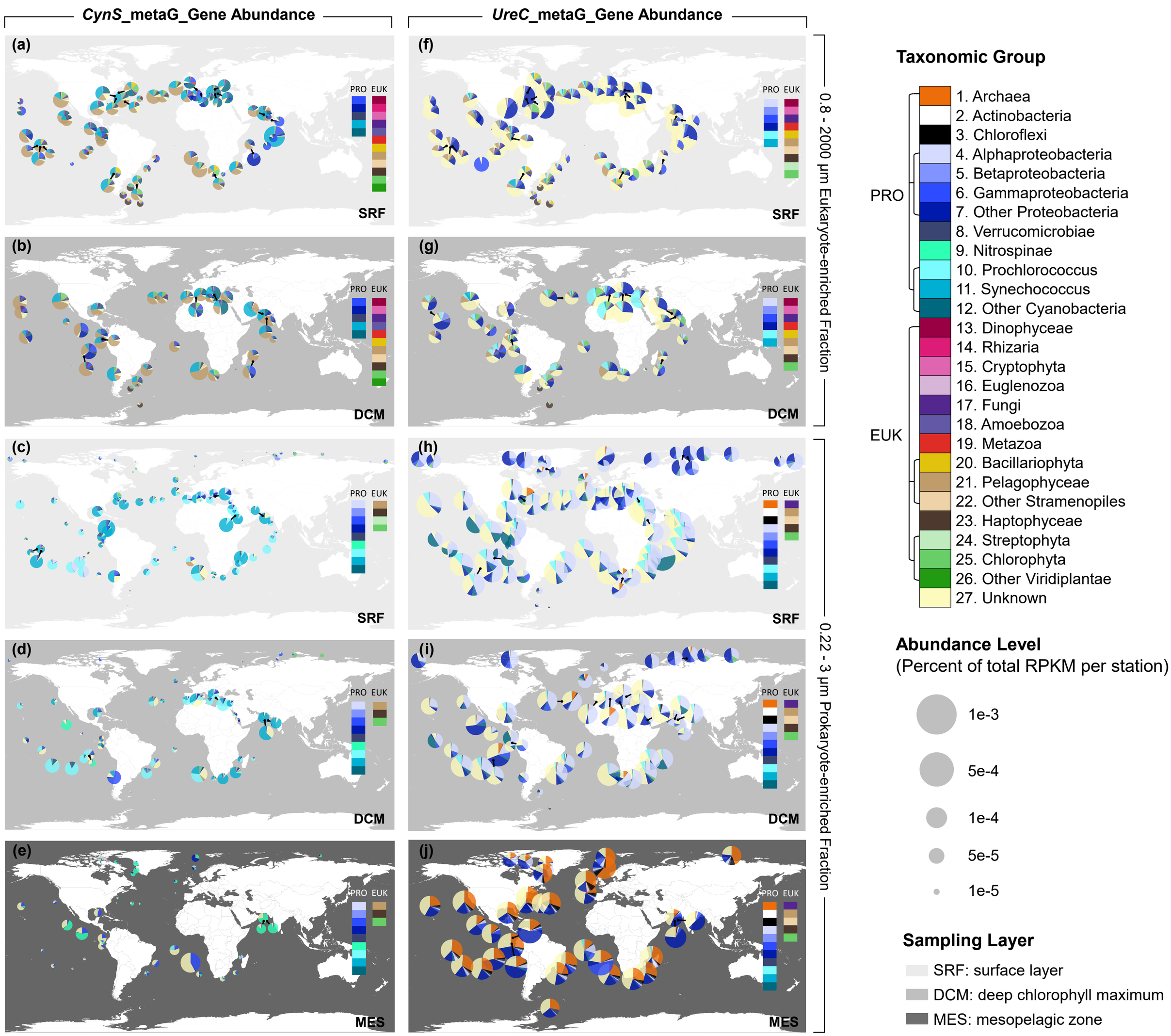
CynS_metaG_Gene Abundance
UreC_metaG_Gene Abundance
(a)
(b)
(c)
(d)
(e)
(f)
(g)
(h)
(i)
(j)
PRO EUK
SRF
DCM
MES
0.8 - 2000 µm Eukaryote-enriched Fraction
0.22 - 3 µm Prokaryote-enriched Fraction
Taxonomic Group
PRO
EUK
1. Archaea
2. Actinobacteria
3. Chloroflexi
4. Alphaproteobacteria
5. Betaproteobacteria
6. Gammaproteobacteria
7. Other Proteobacteria
8. Verrucomicrobiae
9. Nitrospinae
10. Prochlorococcus
11. Synechococcus
12. Other Cyanobacteria
13. Dinophyceae
14. Rhizaria
15. Cryptophyta
16. Euglenozoa
17. Fungi
18. Amoebozoa
19. Metazoa
20. Bacillariophyta
21. Pelagophyceae
22. Other Stramenopiles
23. Haptophyceae
24. Streptophyta
25. Chlorophyta
26. Other Viridiplantae
27. Unknown
Abundance Level
(Percent of total RPKM per station)
1e-3
5e-4
1e-4
5e-5
1e-5
Sampling Layer
SRF: surface layer
DCM: deep chlorophyll maximum
MES: mesopelagic zone