

Co-activity networks reveal the structure of planktonic symbioses in the global ocean

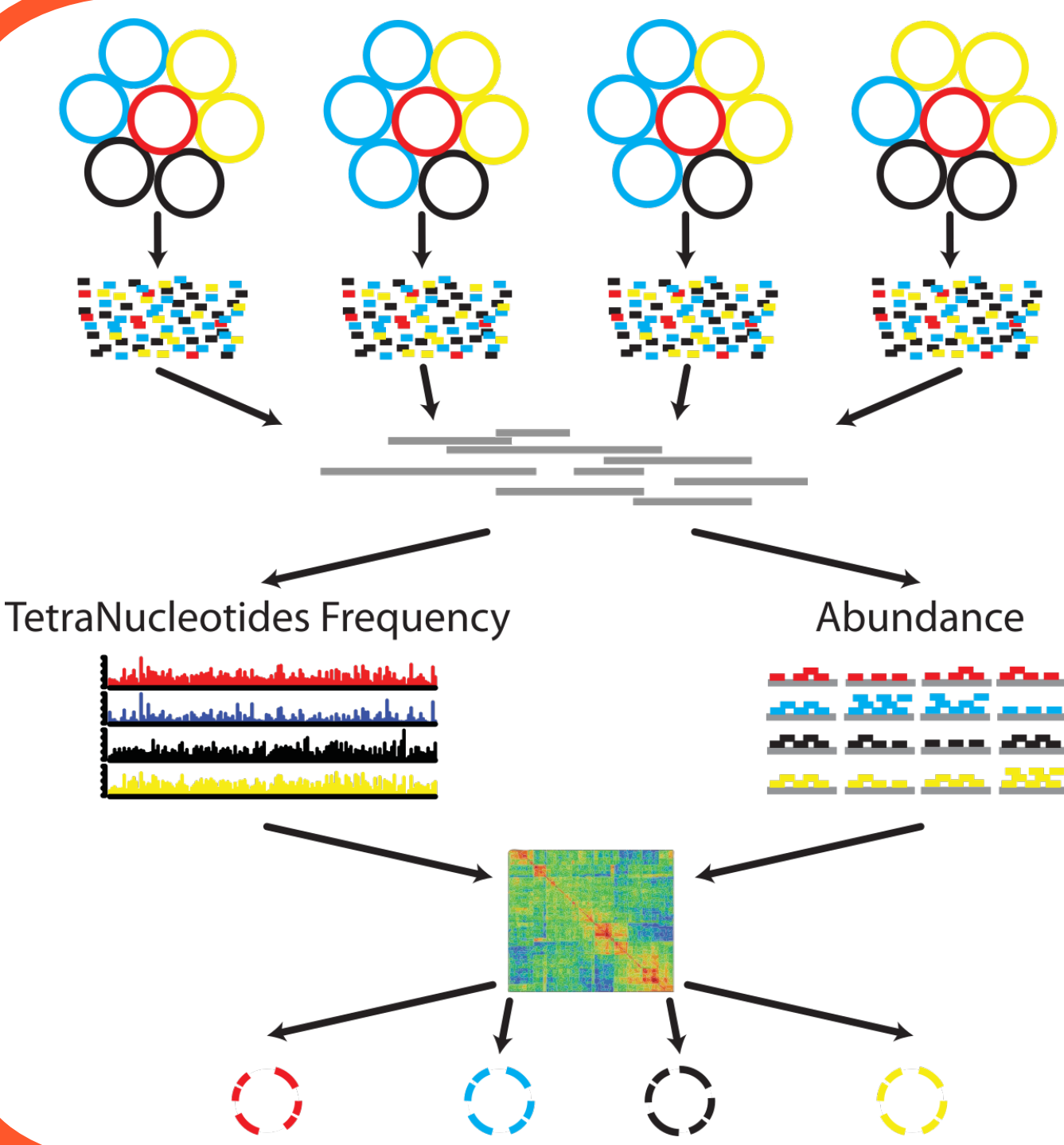


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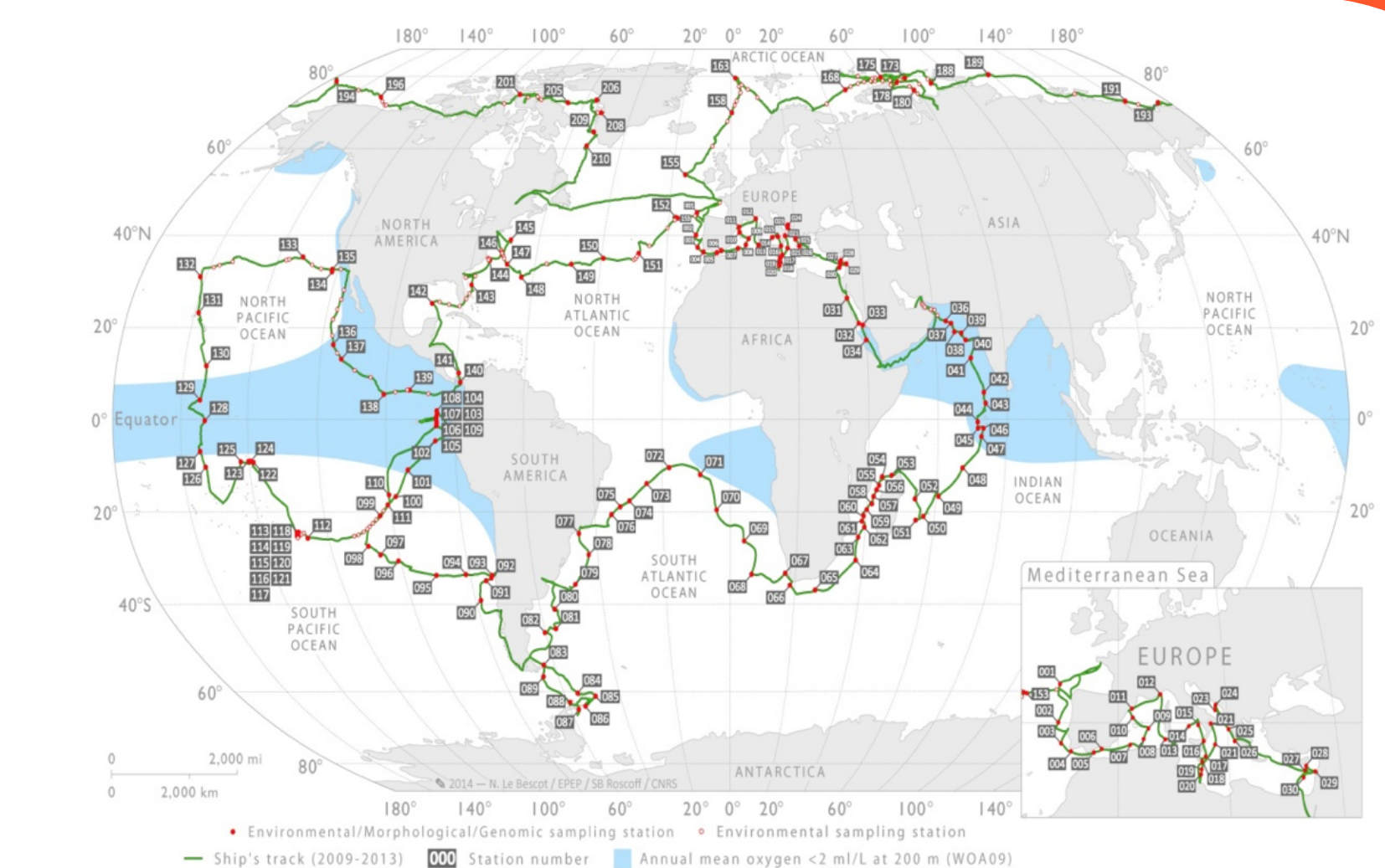


Metagenome Assembled Genomes improve our knowledge of the ocean



Less than 10% of microbial species are cultivable!

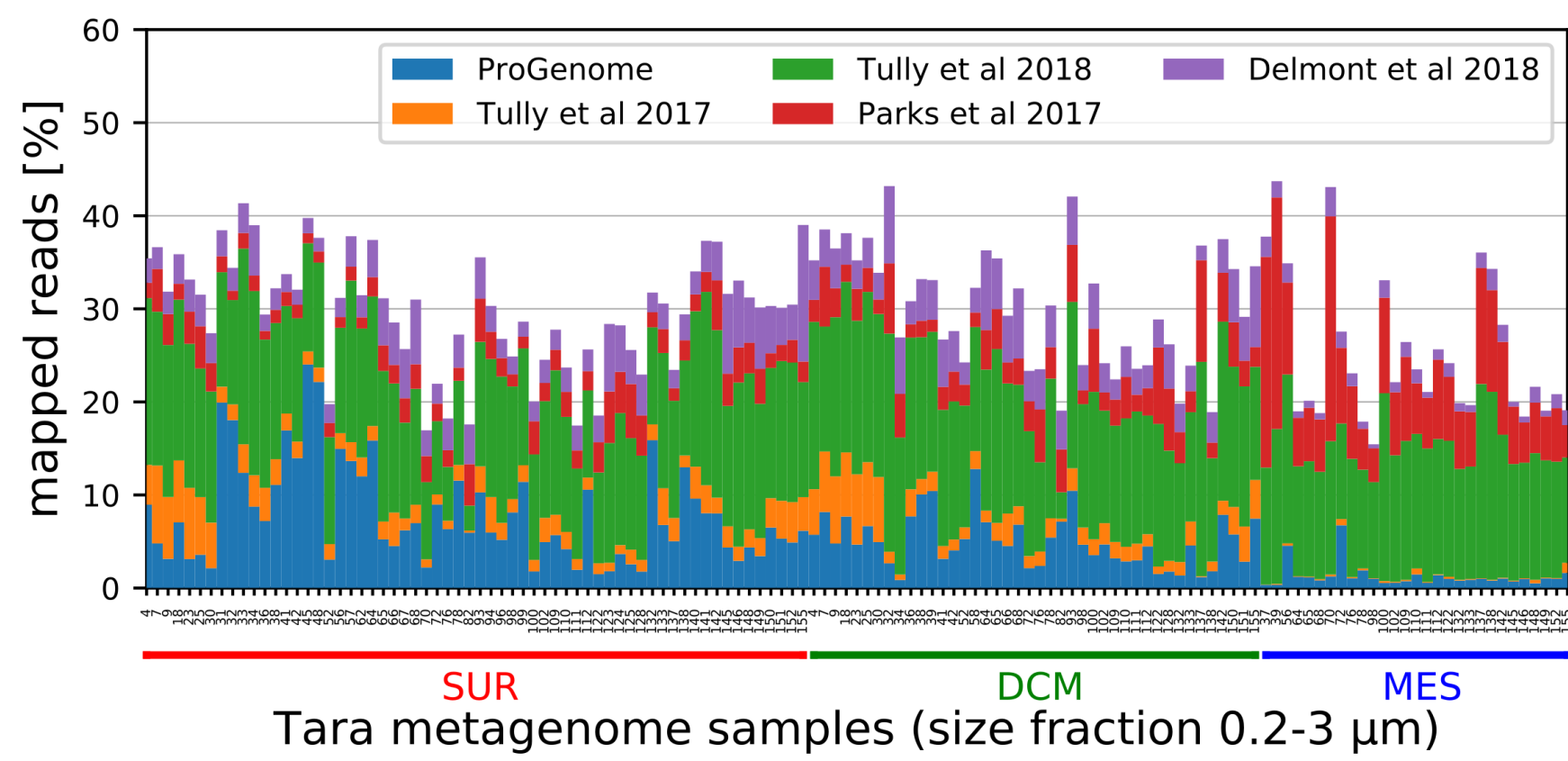
Most of our knowledge of the microbial world comes from lab-cultivated species, which are the exception rather than the norm. While large planet-scale expeditions sequence DNA directly from the environment (TARA expeditions, right figure), recent advances allow to reconstruct environmental genomes from such metagenomes (MAGs, left figure). Thousands of marine MAGs have been recovered in a few years, but not much is known about the structure of the complex communities they form in the ocean...



Can we use MAGs to predict, characterize and explain the communities of non-cultivable marine microorganisms?

Database of 5319 published MAGs

Authors	Total nb.	dRep95 nb.	HQ nb.	dRep95 HQ nb.
Parks et al 2017	1765	538	673	272
Tully et al 2017	290	41	24	11
Tully et al 2018	2307	644	378	223
Delmont et al 2018	957	324	197	141
ProGenomes 2017	566	545	526	525
Total	5885	2092	1798	1172

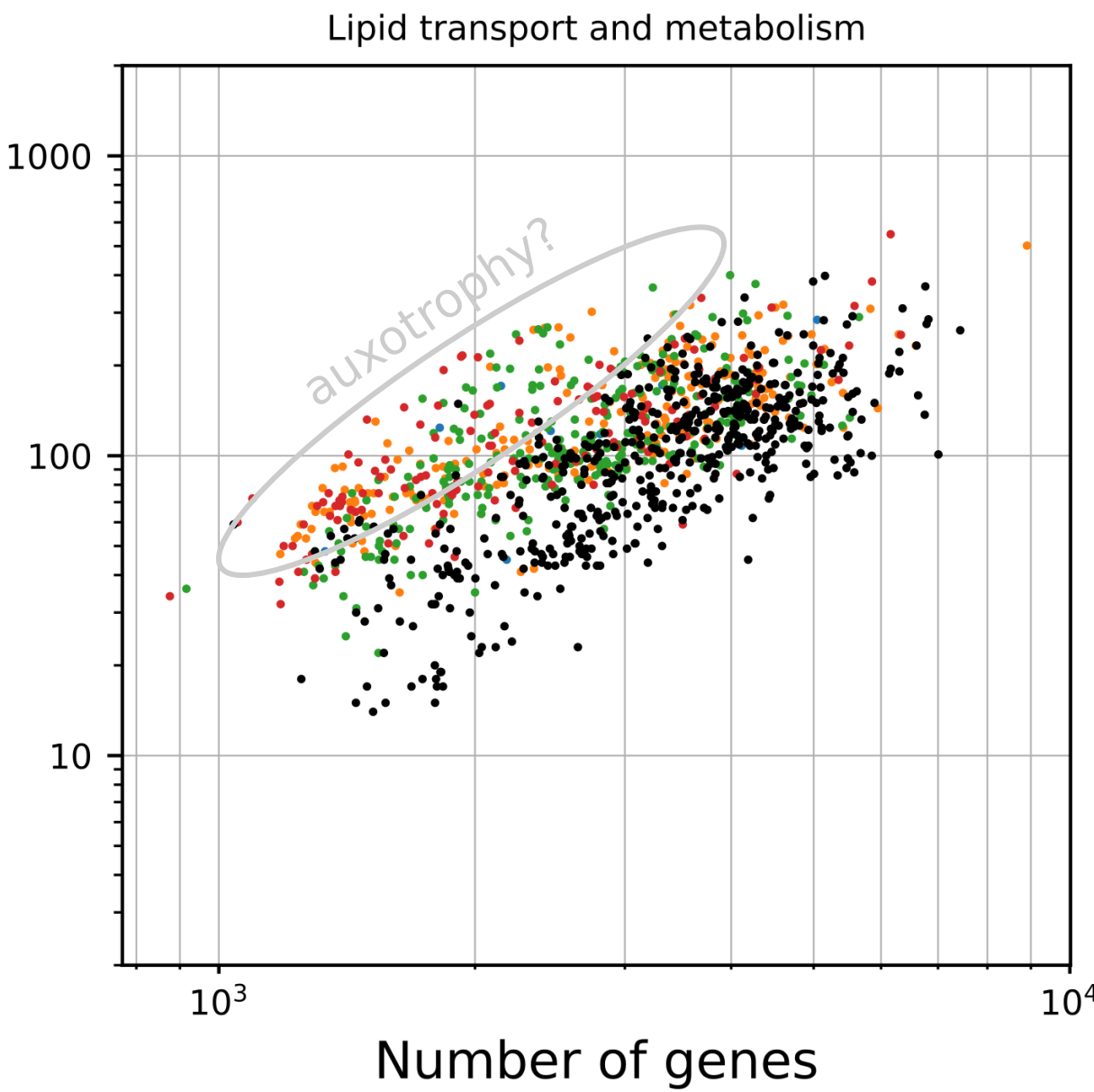
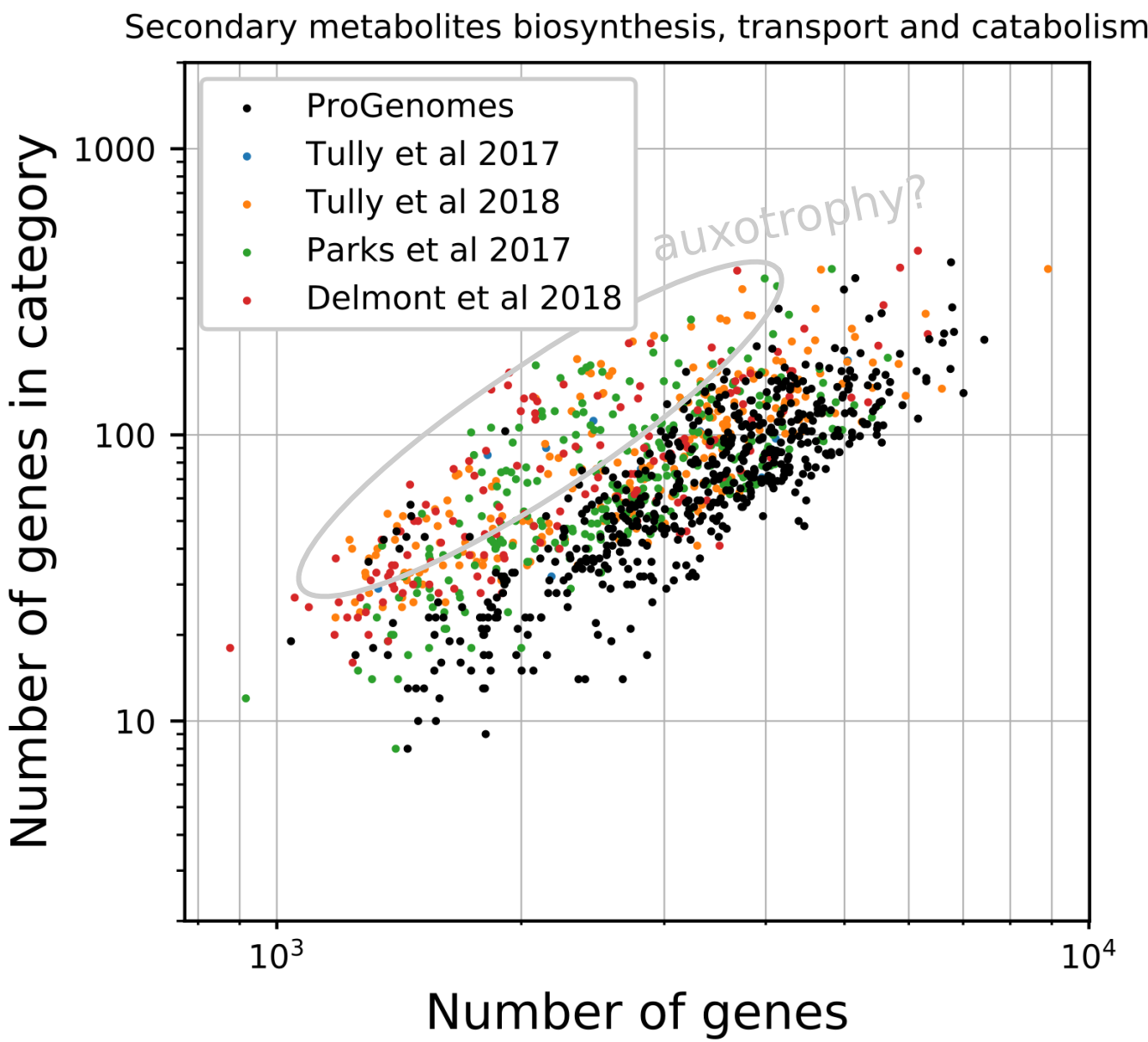


>60% of DNA can still not be mapped!

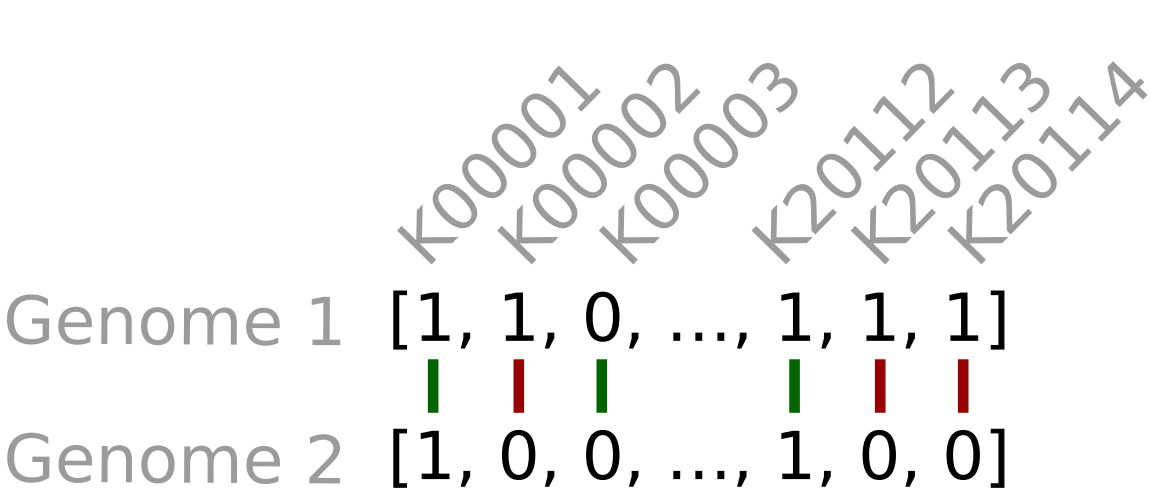
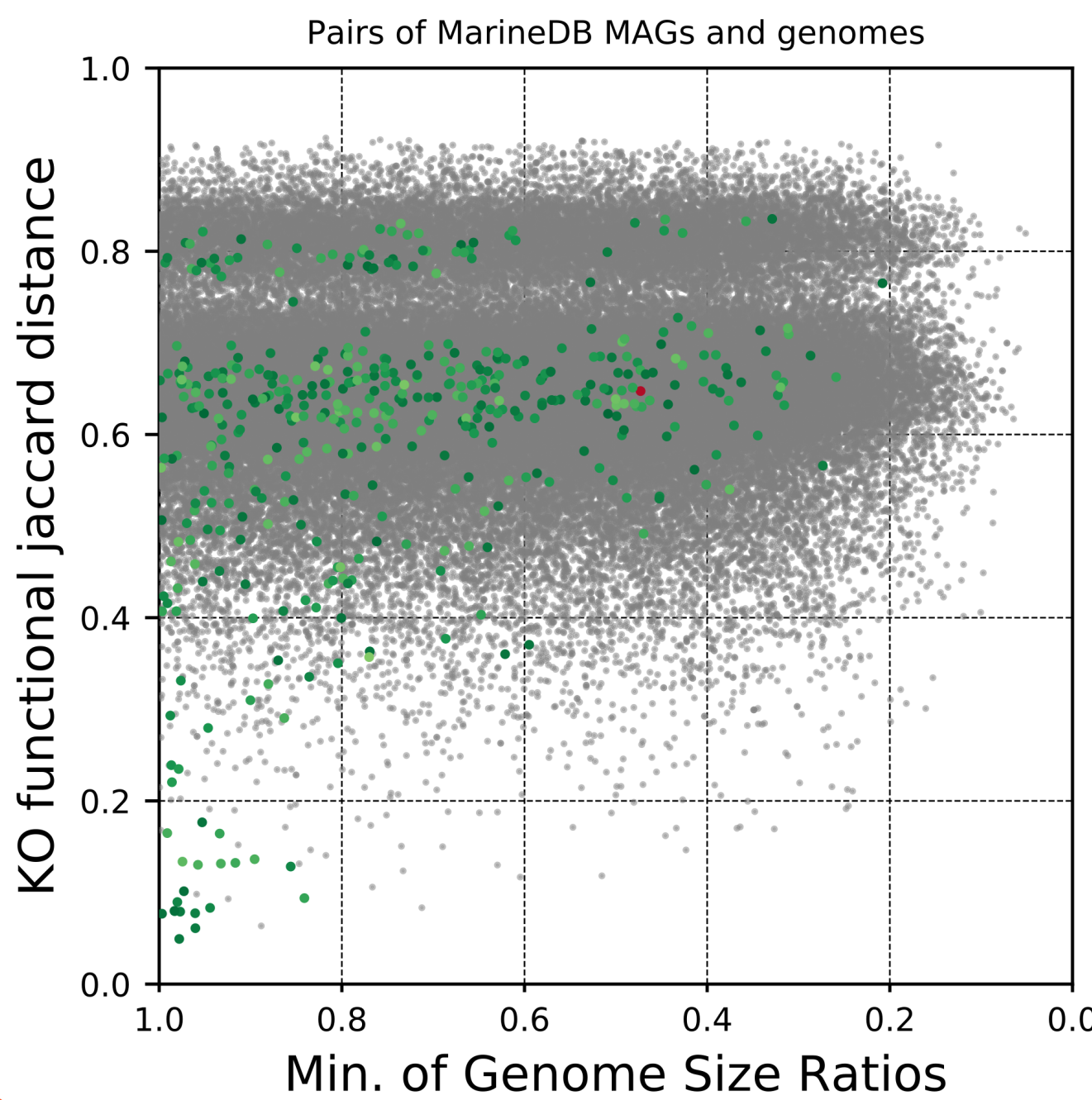
Functional scaling laws $n_c \propto n_{tot}^{\alpha_c}$

Do MAGs follow the same genomic scaling laws than lab-cultivated genomes?

The gene content of prokaryotic genomes is known to obey scaling laws. But these laws have been historically identified on lab-cultivated genomes. Do marine uncultivable organisms still follow these laws?



Is auxotrophy widespread in marine communities?

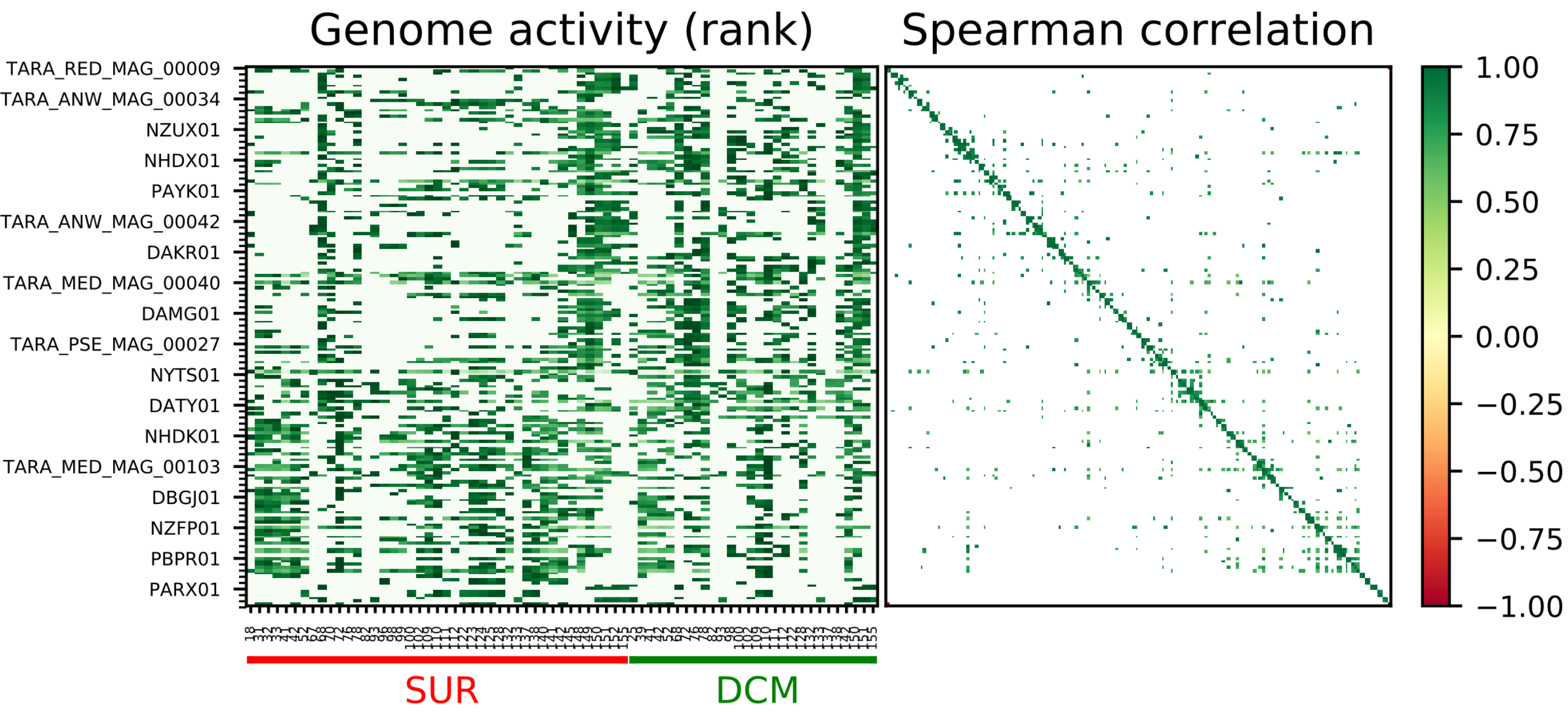


Most pairs of co-active MAGs do not share the same functions.

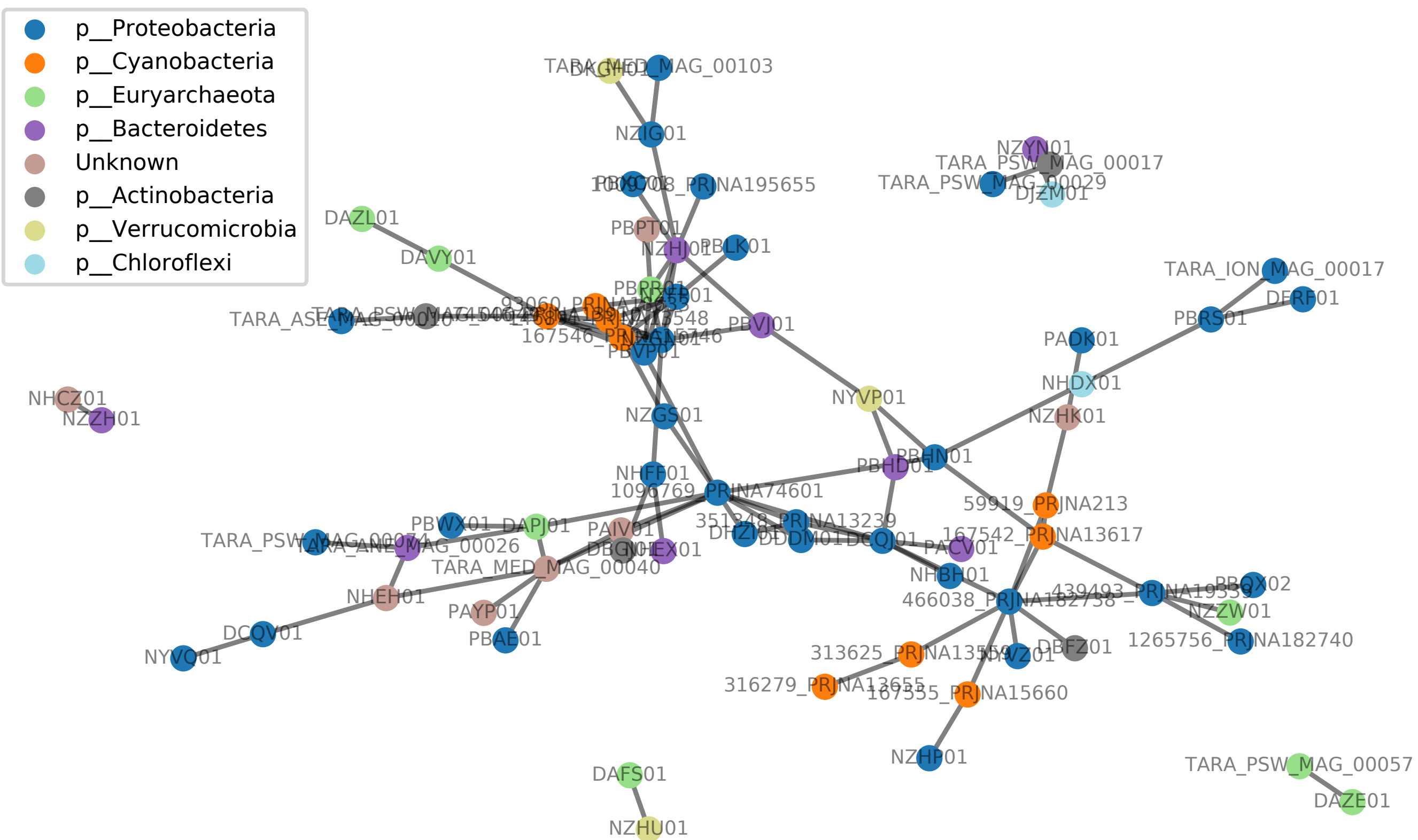
Co-activity networks of MAGs

Co-expressed genomes represent putative interacting organisms.

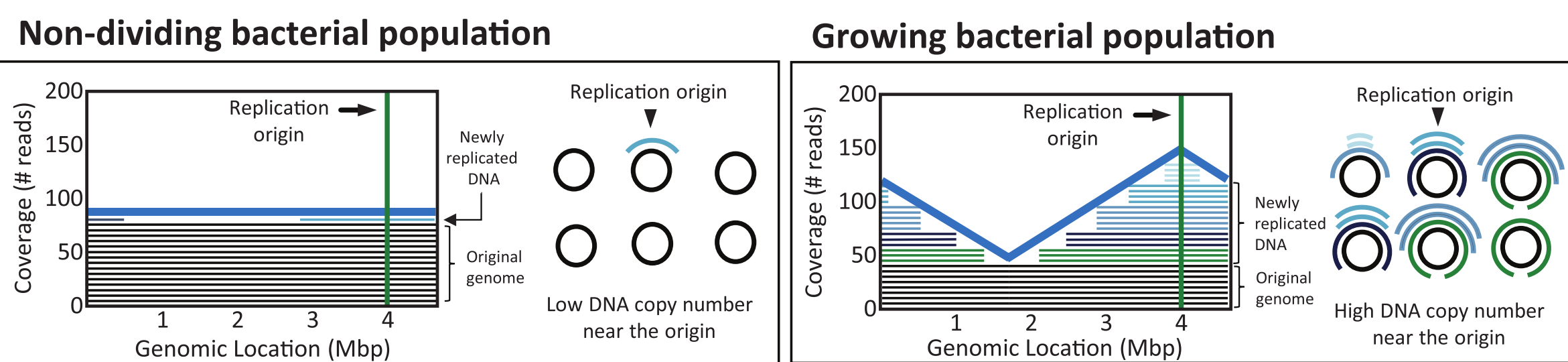
We use 124 metatranscriptomic samples (euphotic zone) recovered during Tara expeditions to compute the whole-genome expression of MAGs. By correlating this activity signal across samples, we can infer putative communities of microorganisms.



176 MAGs with at least 1 significant correlation.



Cross-phyla co-activity is widespread in the euphotic zone.



Co-growth as another signal? (in progress)



(Metabat) Kang, D. D., Froula, J., Egan, R. & Wang, Z. PeerJ 3, (2015)
(Growth) Korem, T. et al. Science 349, 1101-1106 (2015)

MAGs origins
Parks, D. H. et al. Nature Microbiology 2, 1533 (2017)
Tully, B. J., Sachdeva, R., Graham, E. D. & Heidelberg, J. F. PeerJ 5, e3558 (2017)
Tully, B. J., Graham, E. D. & Heidelberg, J. F. Scientific Data 5, 170203 (2018)
Delmont, T. O. et al. Nature Microbiology 3, 804-813 (2018)