

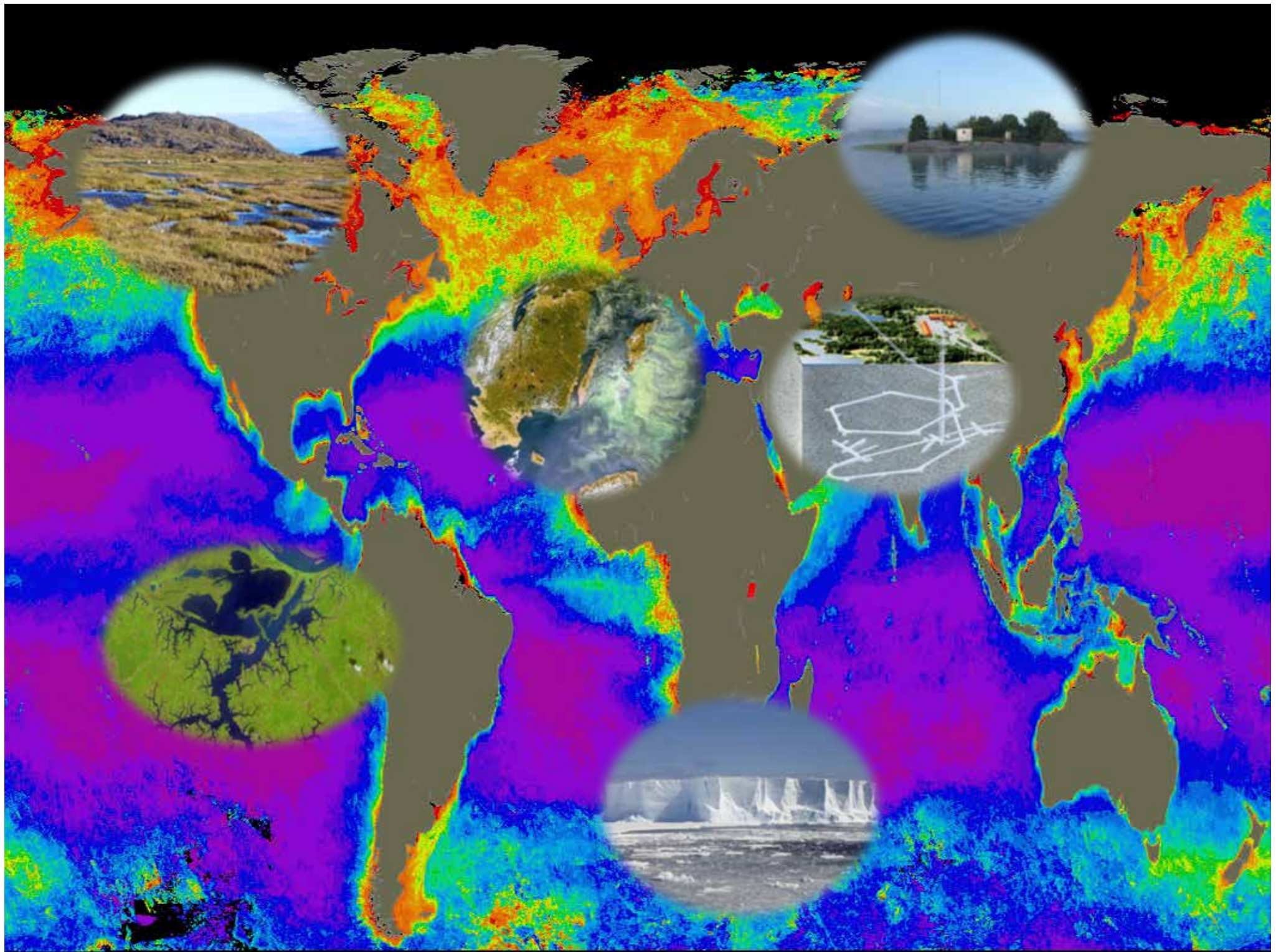
MICROBIAL PROCESSES AND DIVERSITY IN THE AQUATIC LANDSCAPE

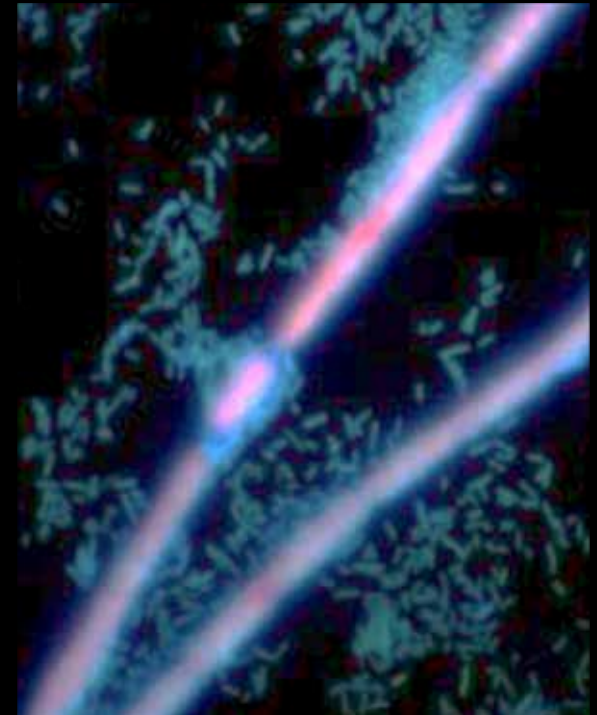
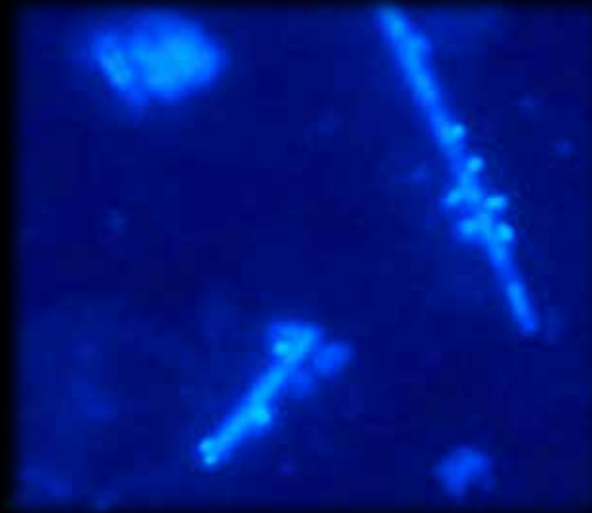
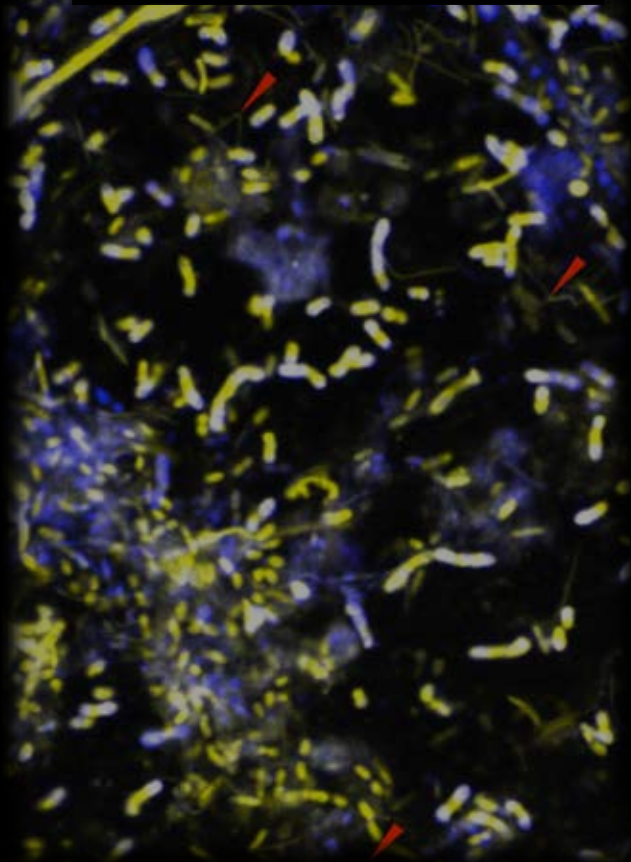
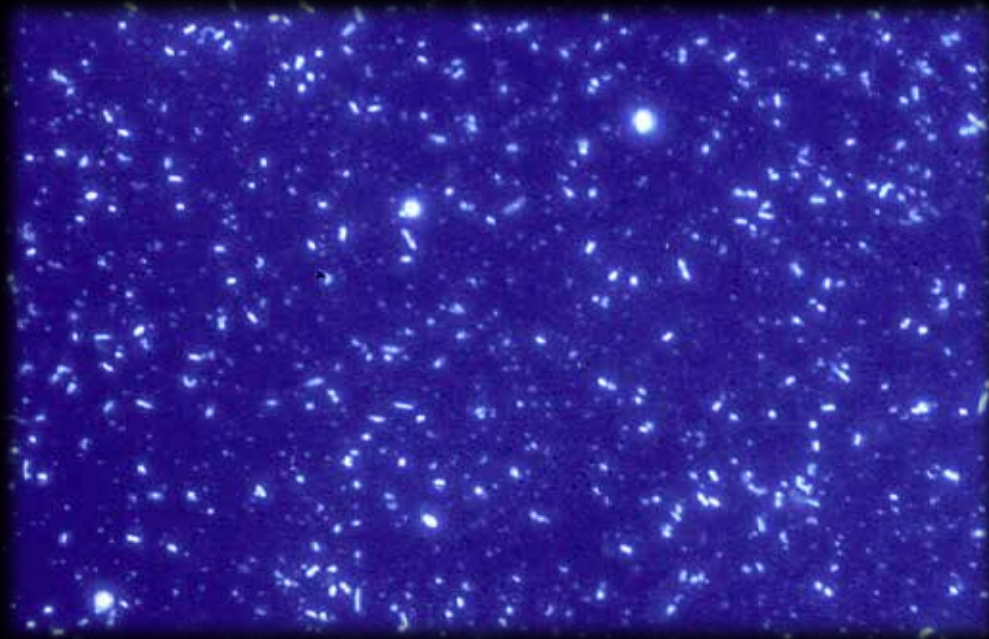
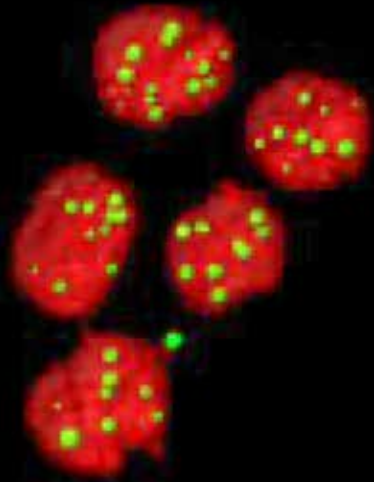


STEFAN BERTILSSON

FUnctional Microbial Ecology group

Department of Aquatic Sciences and Assessment, SLU



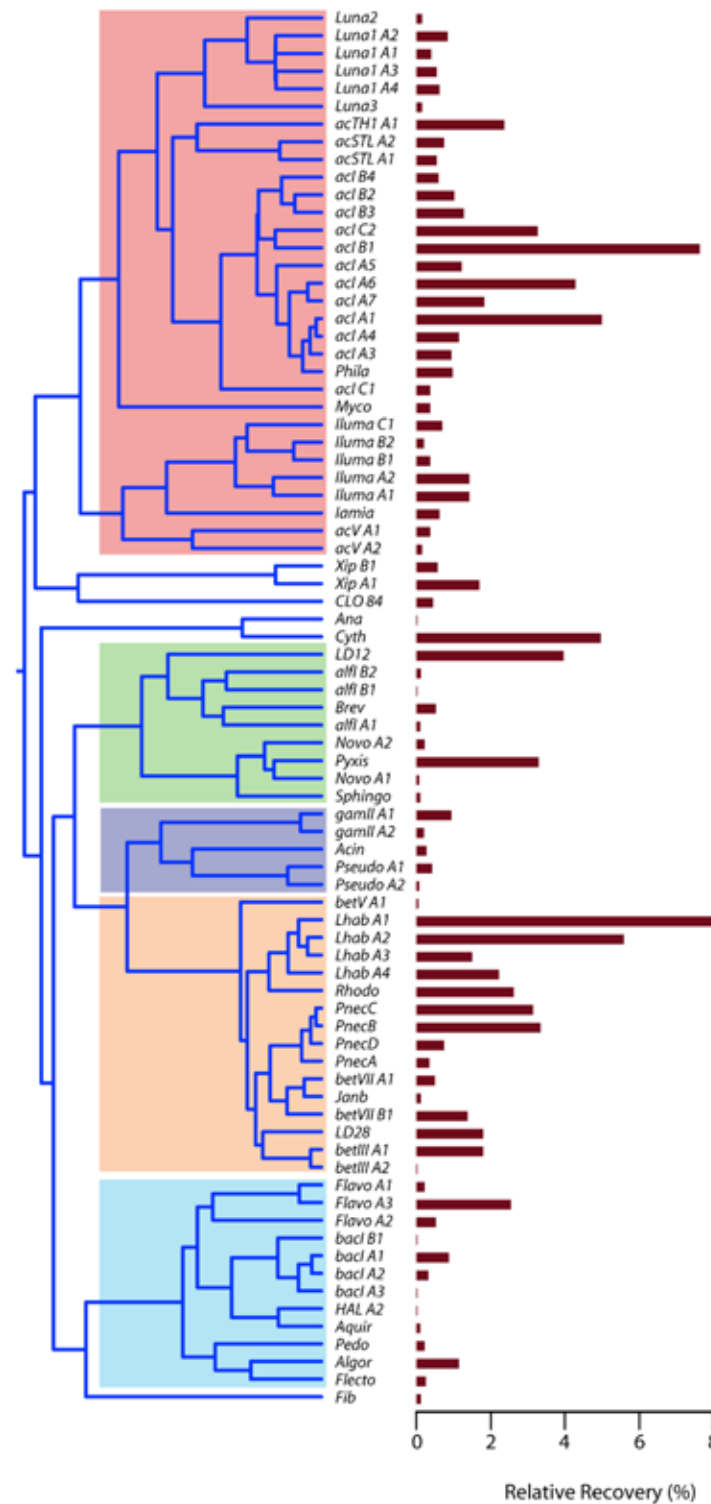




16S rRNA MARKERS TO CHARACTERIZE LAKE BACTERIA

- PHYLOGENETICALLY DISTINCT
- WIDESPREAD (GLOBALLY)
- MOST ARE EXCLUSIVE TO FRESHWATERS

BACTERIAL FRESHWATER "TRIBES"



Actinobacteria

Verrucomicrobia

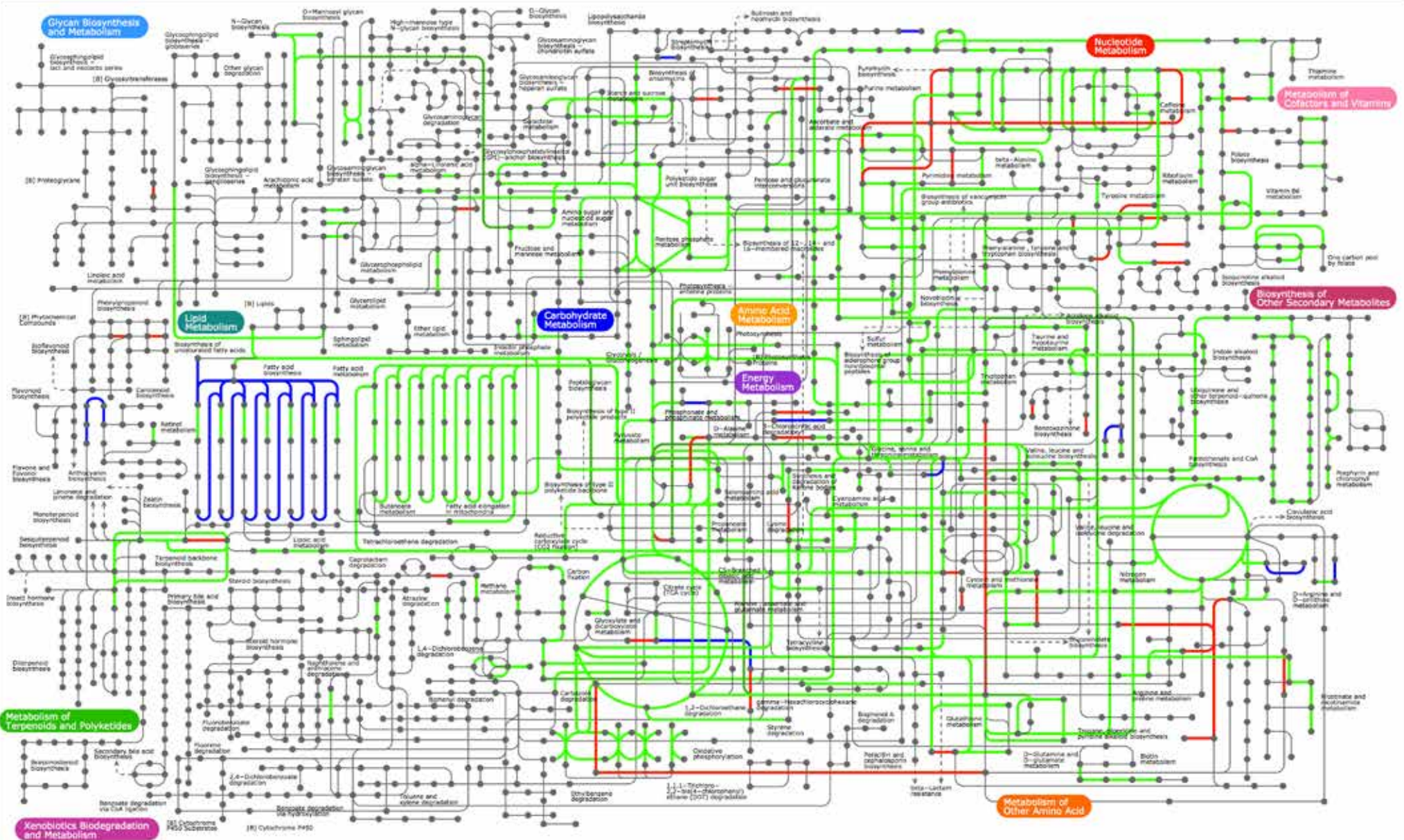
α-Proteobacteria

γ-Proteobacteria

β-Proteobacteria

Bacteroidetes

Metabolic function of the uncultured



Recovering genomes from metagenomes

Going beyond a marker gene

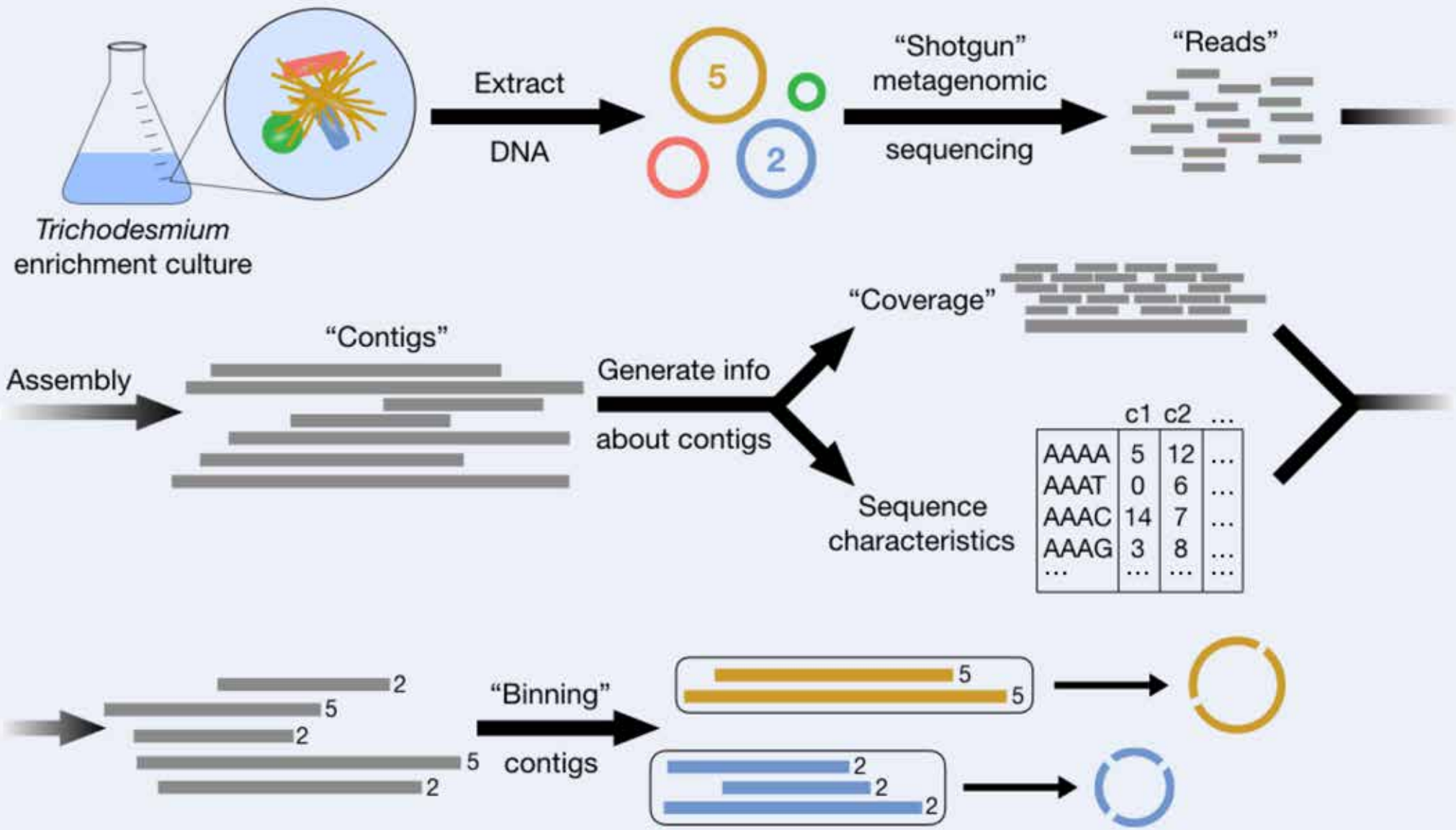
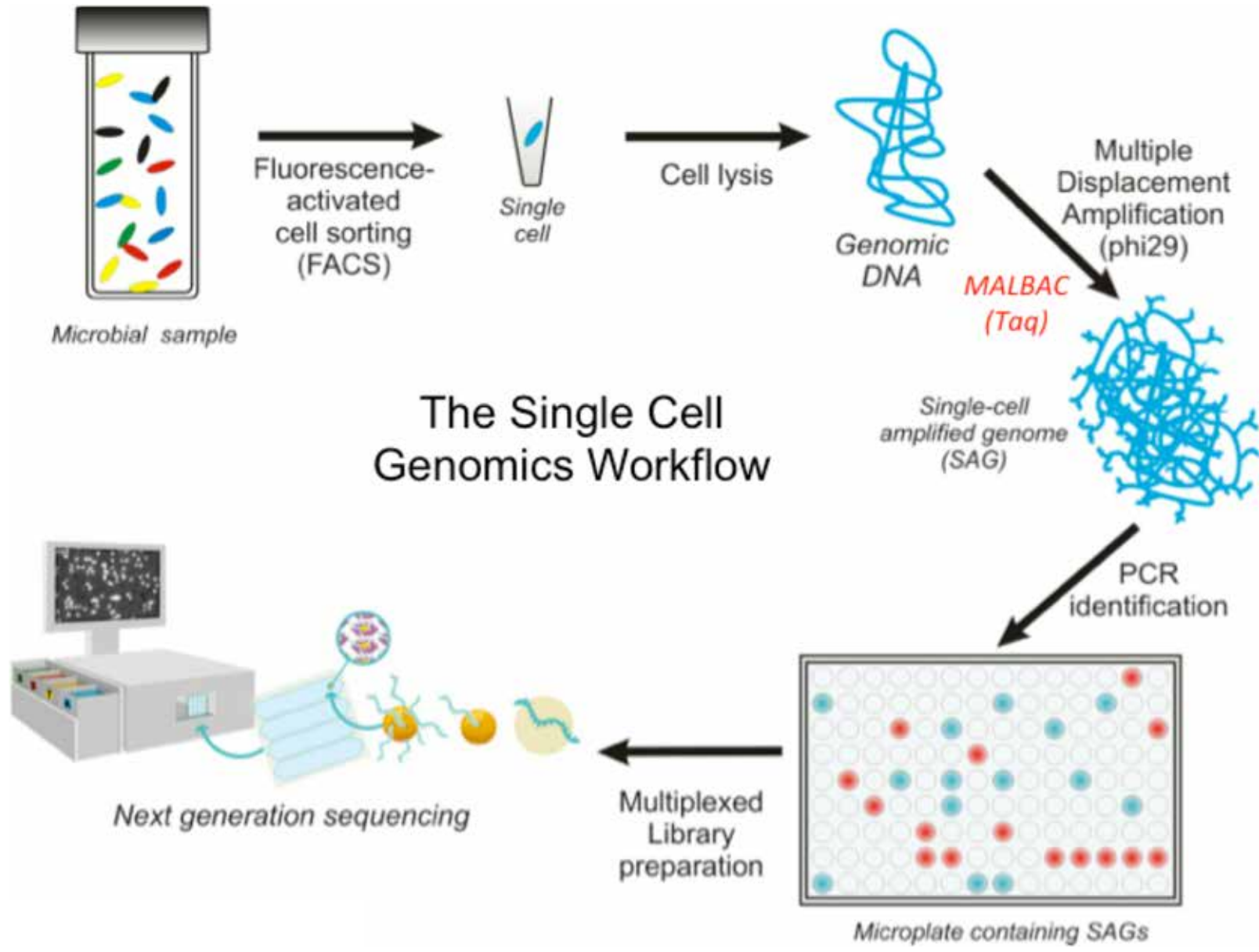
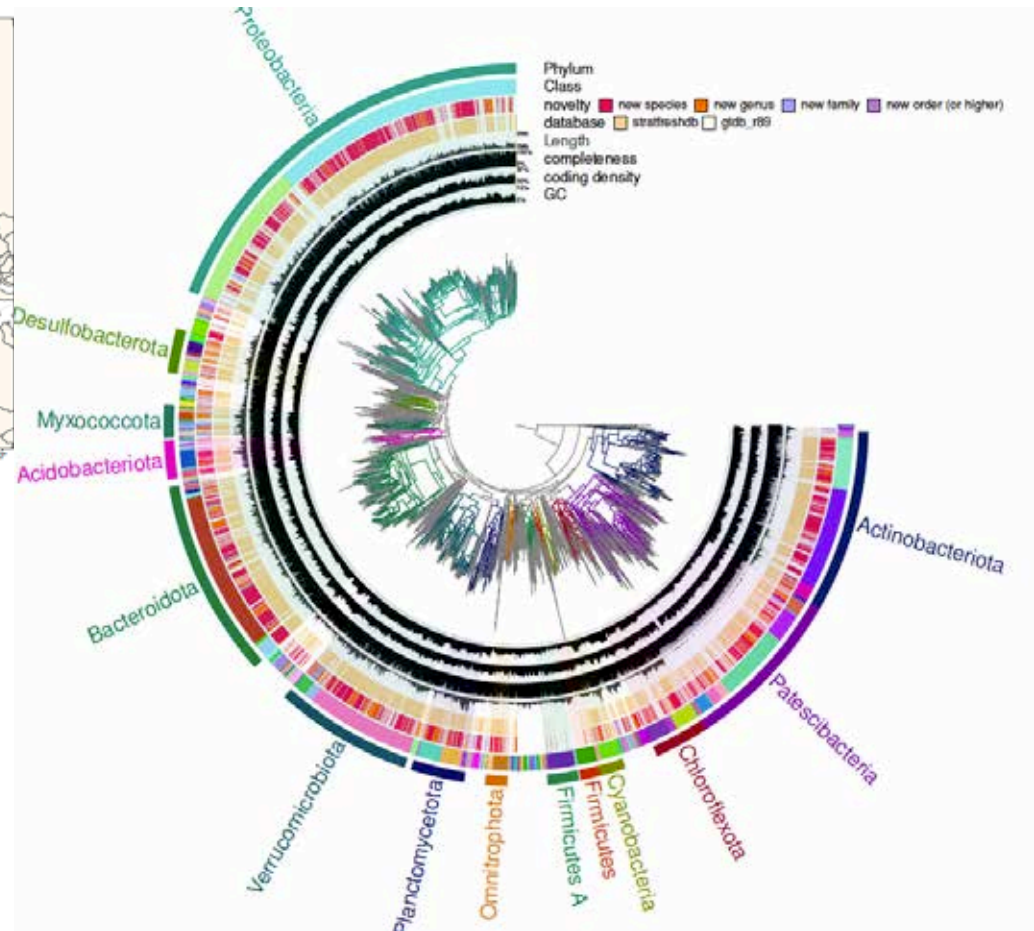
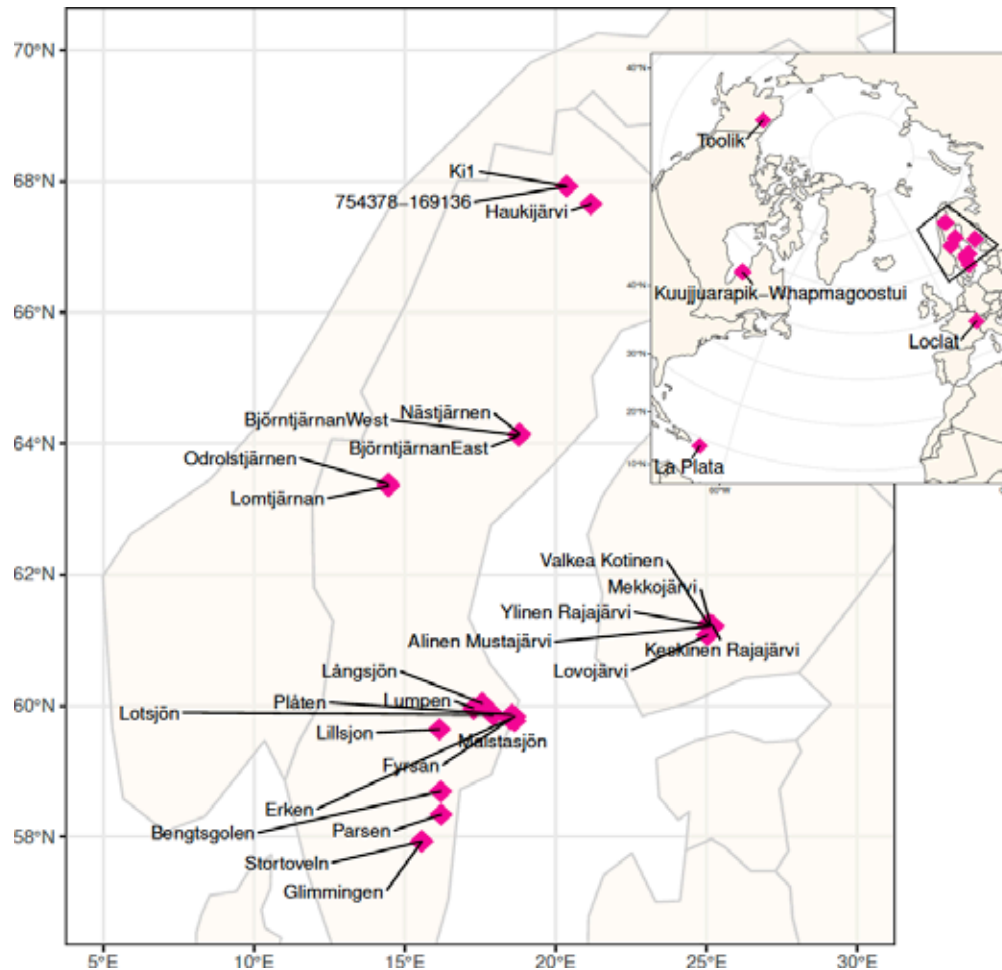


Illustration: The Trichodesmium consortium



GENOMIC LAKE MICROBIOME INVENTORY

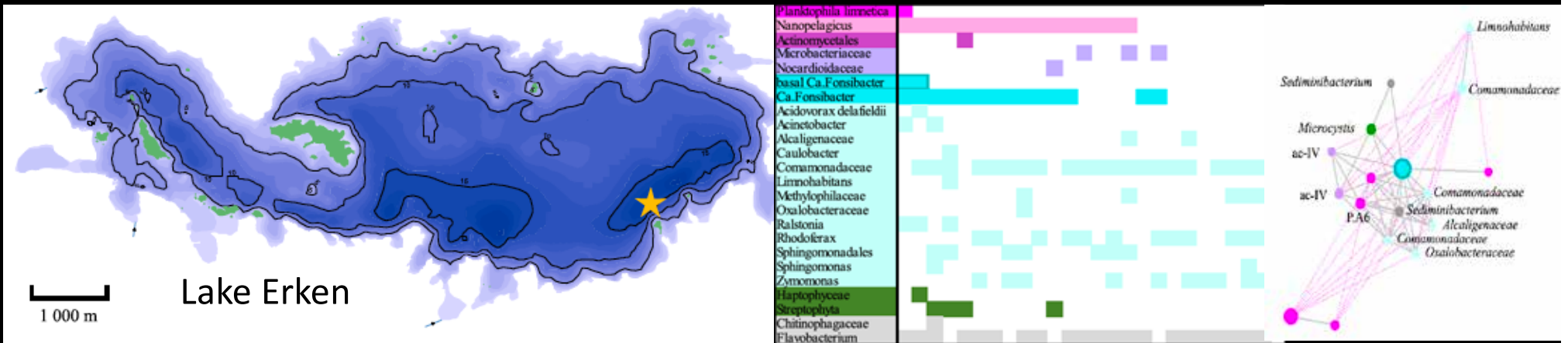


267 SHOTGUN METAGENOMES/ 3TBP AND COMPLEMENTARY SAGs
 12.665 RECONSTRUCTED GENOMES GROUPING INTO 3640 MOTUs

UNCOVERING SEASONALITY AND FUNCTIONAL BACTERIAL CONSORTIA

Polymicrobial enrichments

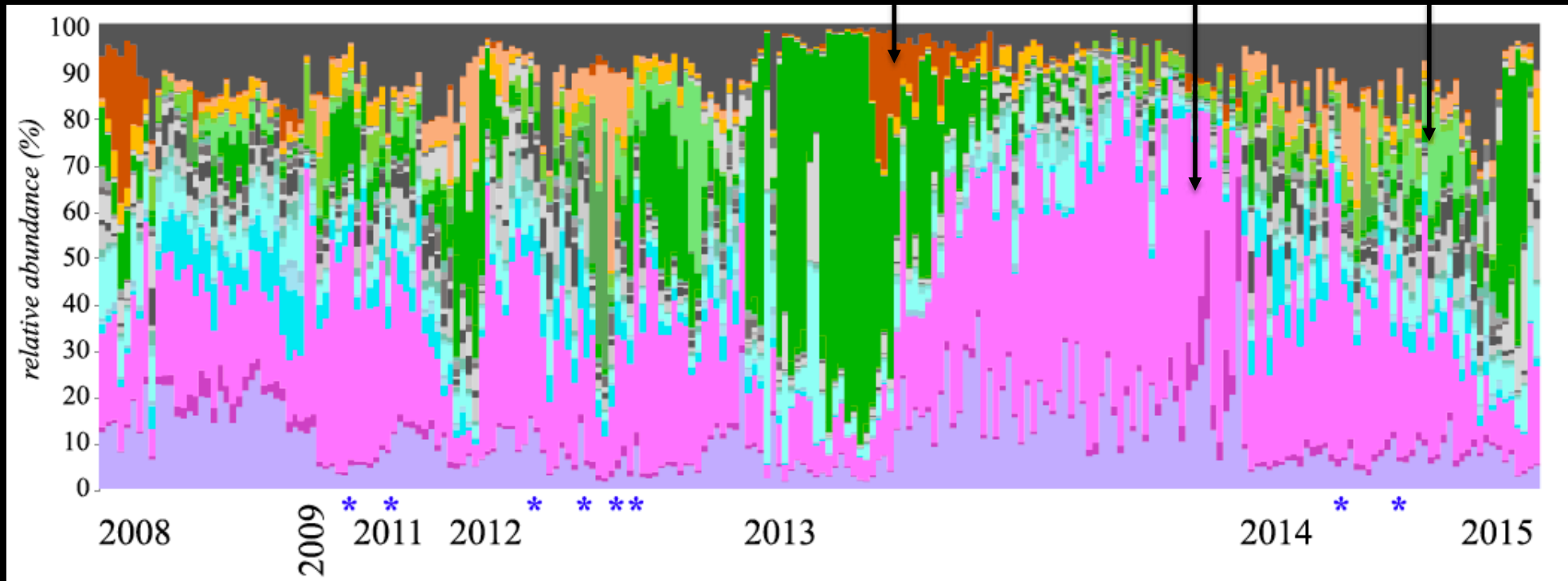
Consortia



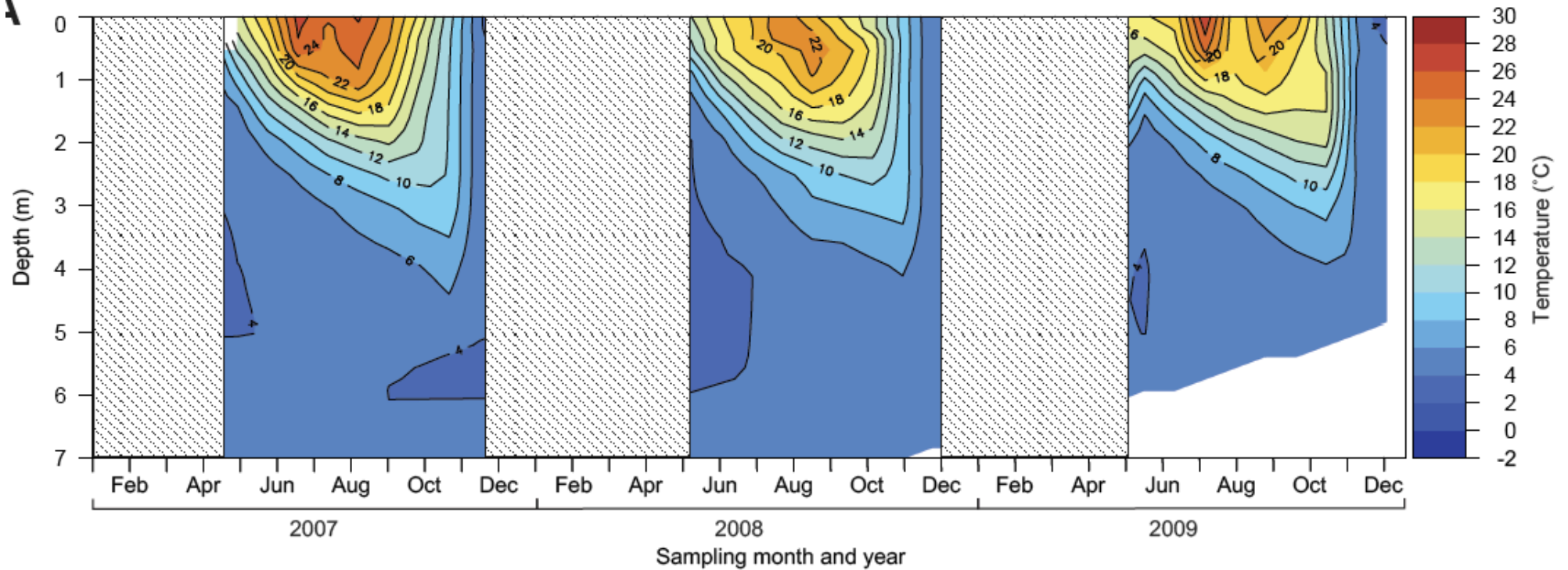
Verrucomicrobiaceae

Actinobacteria ac1

Microcystis

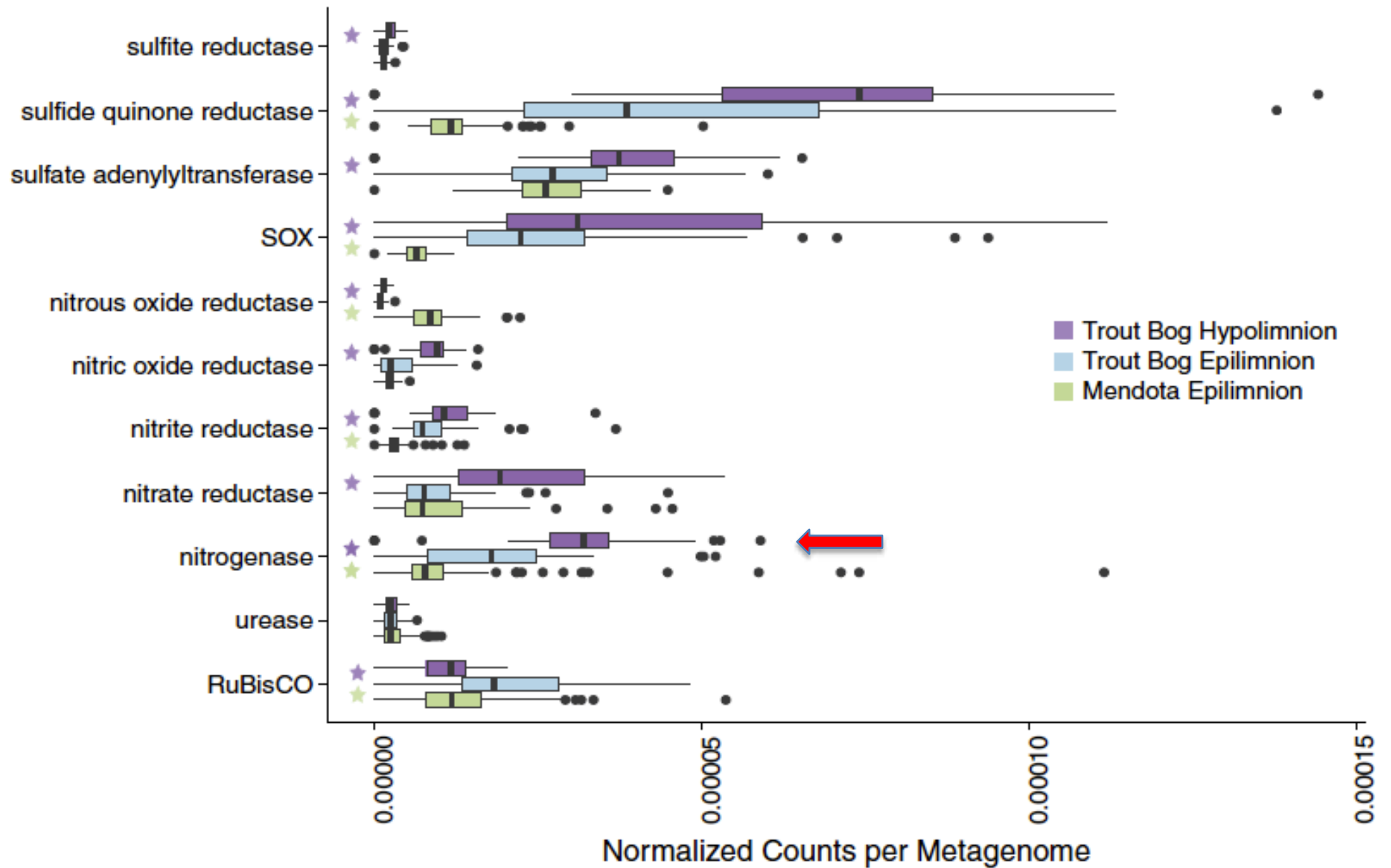


Metagenome time series

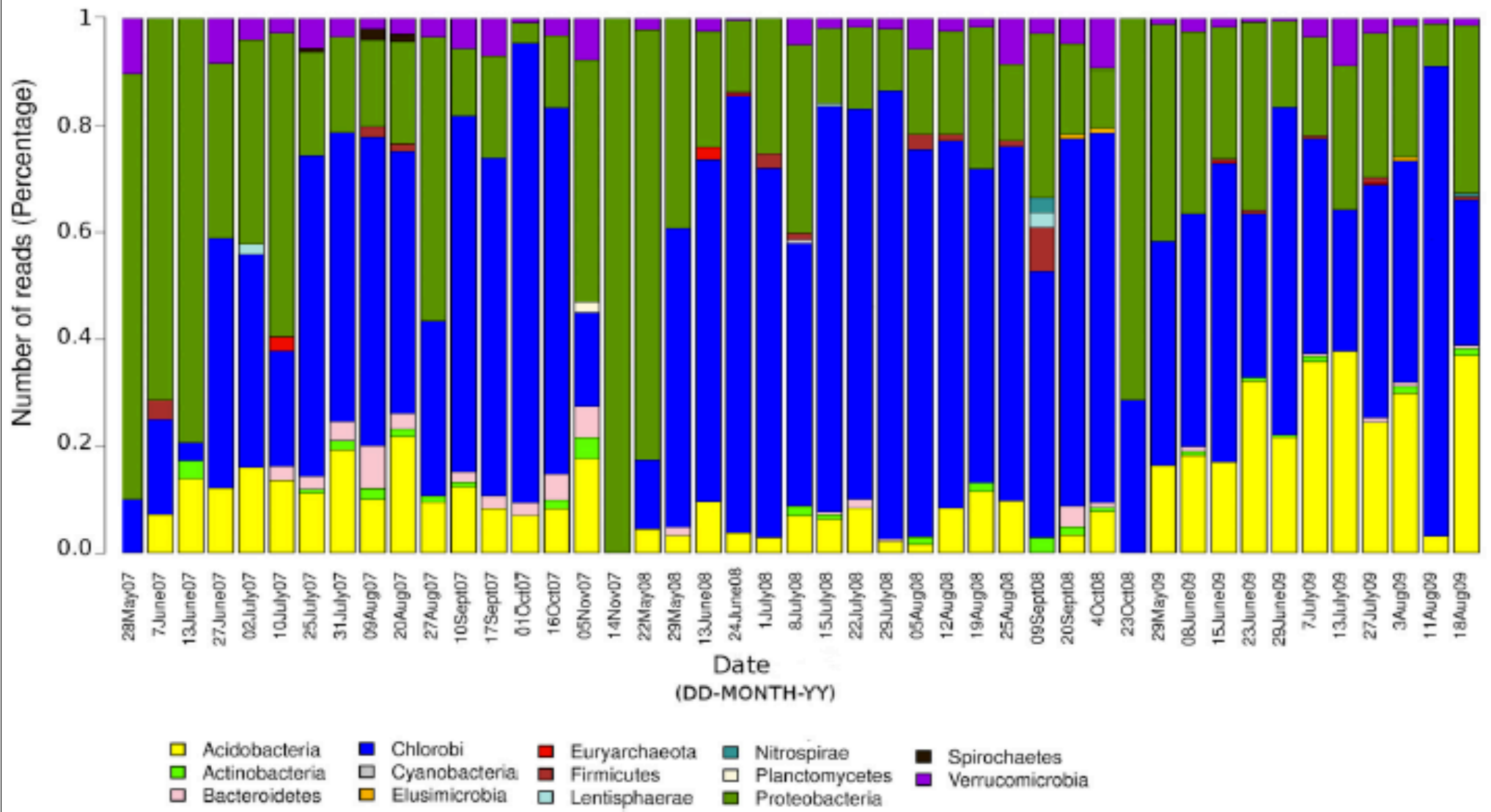


3-YEAR SAMPLING OF TROUT BOG LAKE

COMMUNITY-LEVEL DIFFERENCES IN METABOLIC TRAITS



SEASONAL DYNAMICS OF DIAZOTROPHS IN HYPOLIMNETIC WATERS



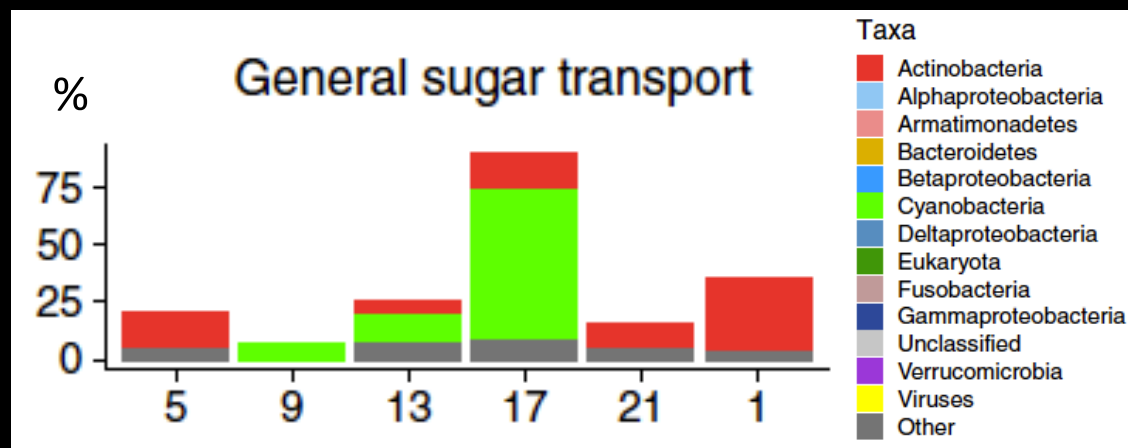
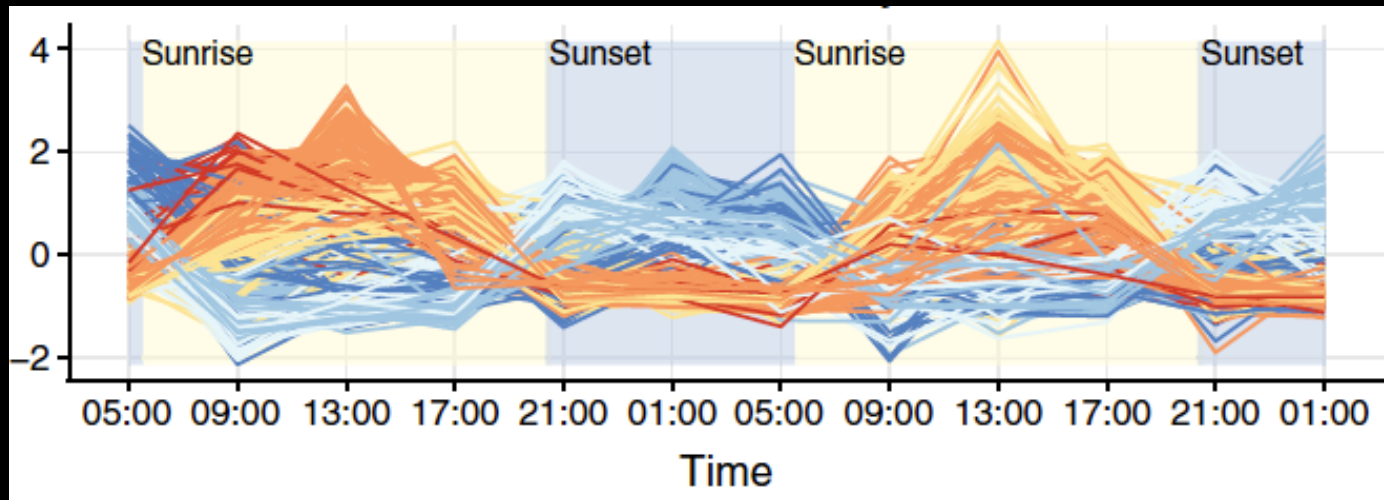
METABOLISM FUELING NITROGEN FIXATION?

MAGs:

- ANOXYGENIC PHOTOSYNTHESIS (CHLOROBI)
- C1 METABOLISM (GAMMAPROTEOBACTERIA)

Fernandez-Vidal et al. 2020,
Frontiers in Microbiology

Resolving diurnal shifts in lake microbial communities with metatranscriptomes



Time of day

Linz et al 2019, Limnol. Oceanogr.



Photo K.W. Anthony, Univ Alaska Fairbanks

Phosphorus availability as a constraint for under-ice methane oxidation?

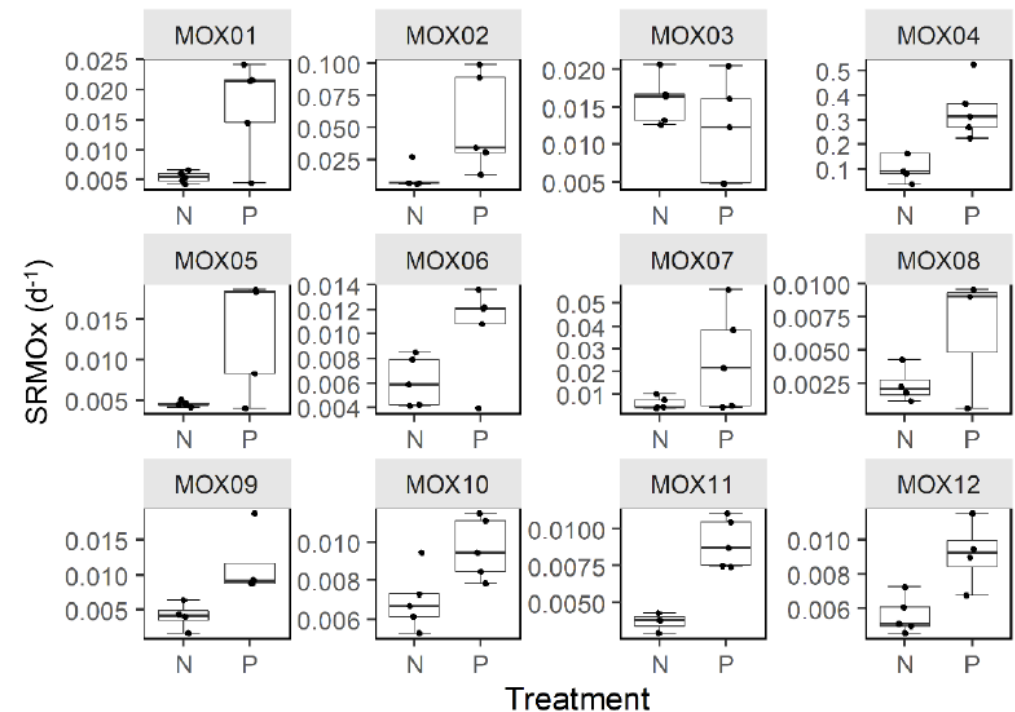
Field observation: Under-ice methane oxidation only detected in high-P lakes
(Denfeld et al 2016, J Geophys Res Biogeosciences) +

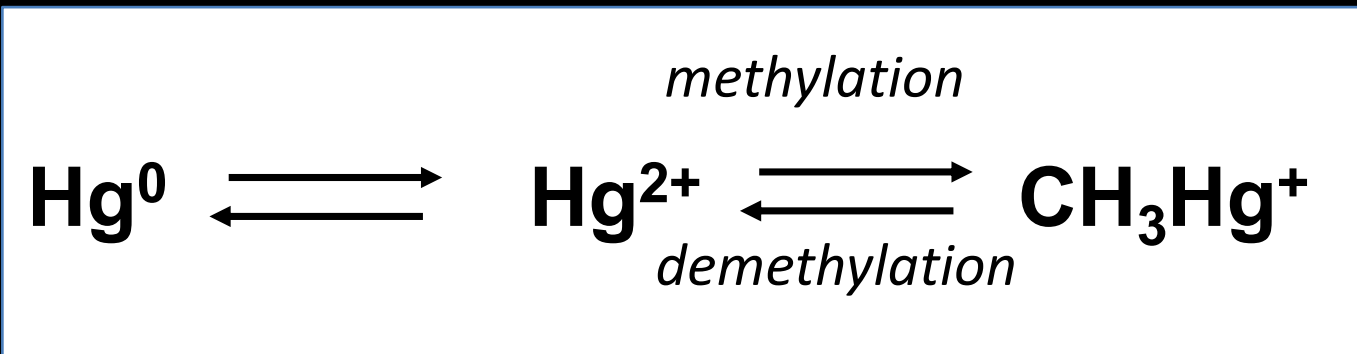
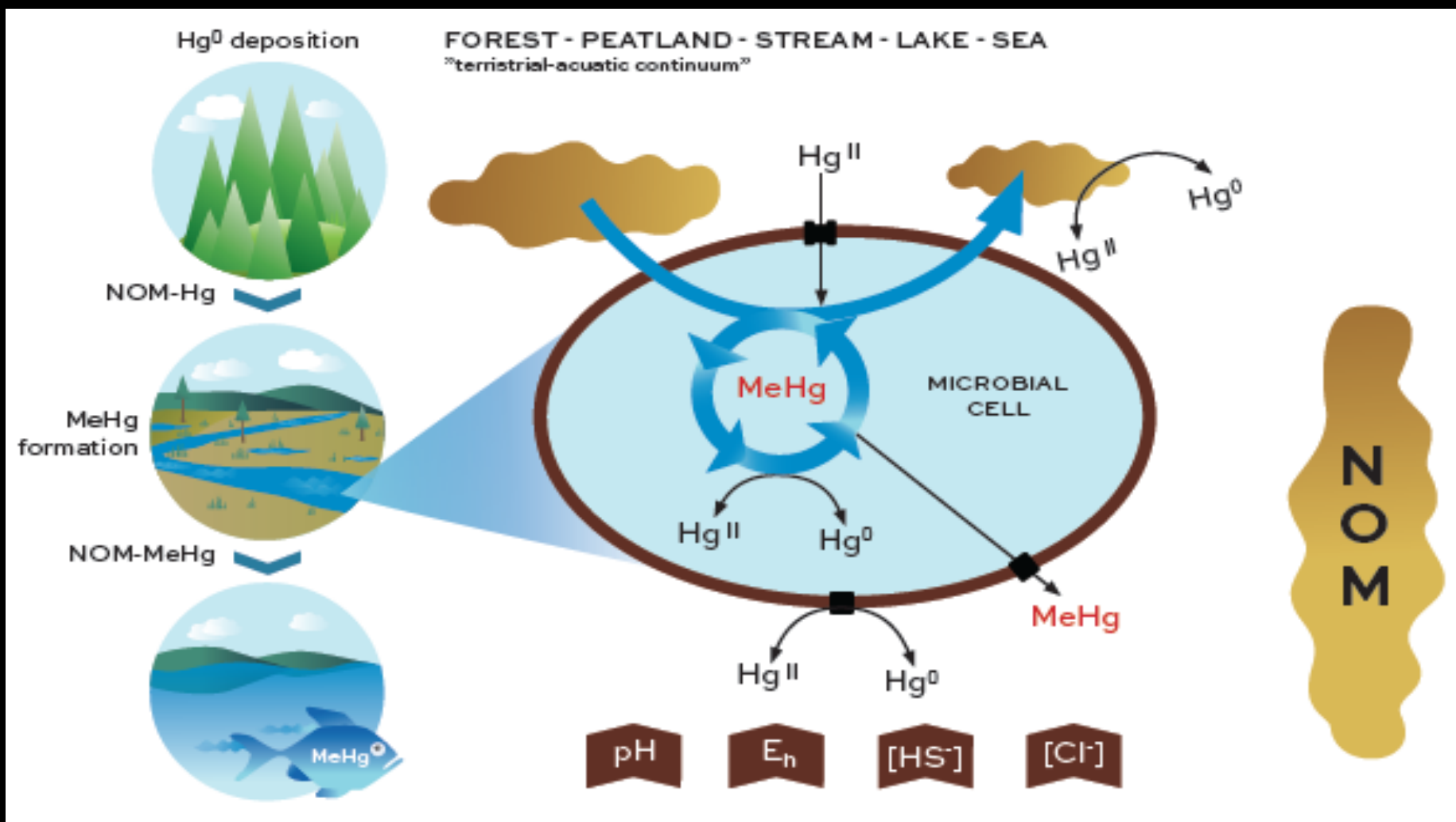
Follow up with P-amendment experiments to demonstrate causality (Samakuchi et al 2021, submitted)

Key organisms: *Methylobacter tundripaludum*, *Methylovulum psychrotolerans*

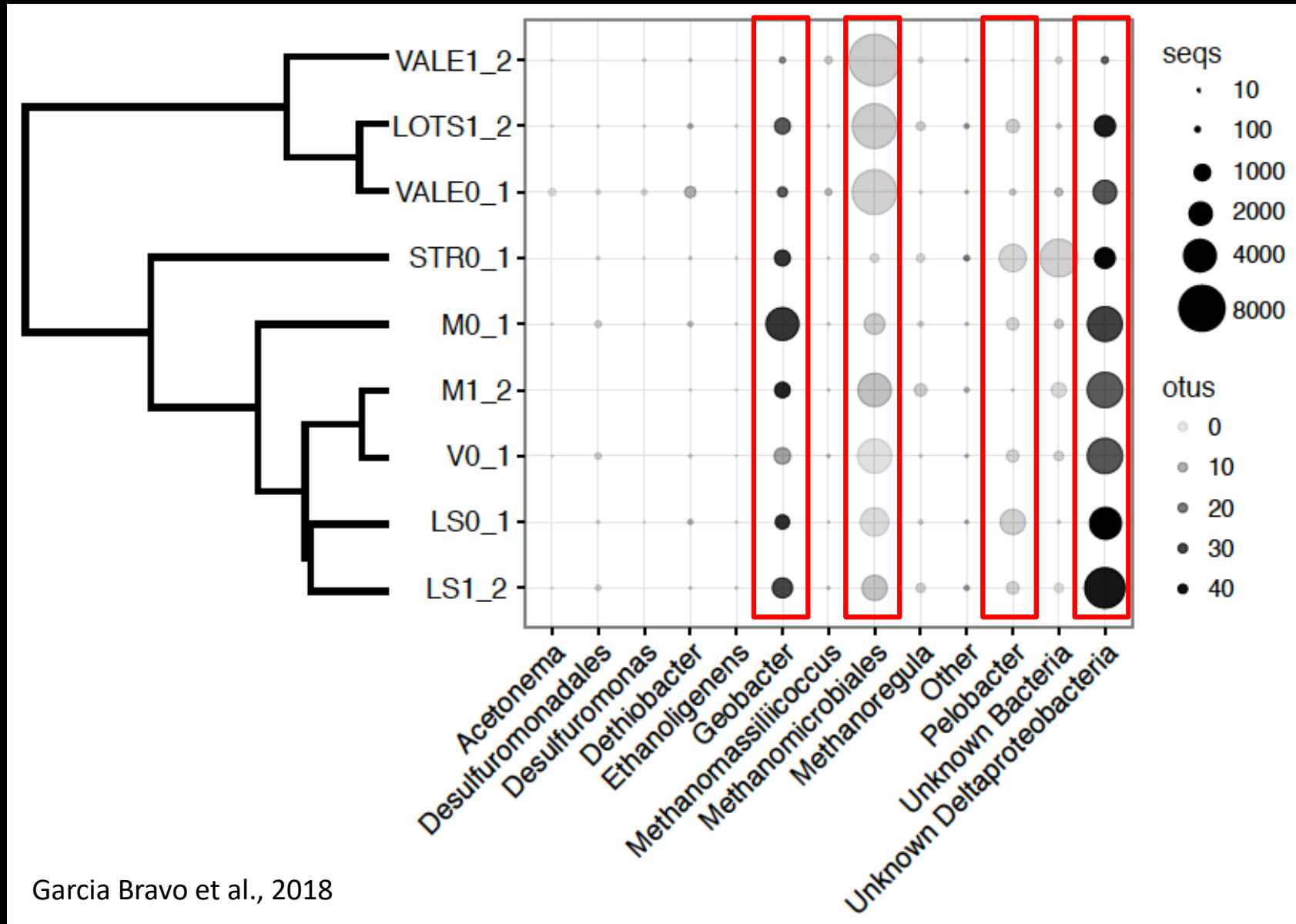


Lake ID	Lakes	DO (mg/L)	CH ₄ (μM)	TP (μg/L)
MOX01*	Lumpen	6.7	0.08	14.9 +
MOX02*	Björklinge-Långsjön	11.8	1.14	9.9
MOX03*	Erken	13.4	0.12	24.6 +
MOX04*	Malstasjön	3.8	0.07	74.3 +
MOX05*	Fysjön	8.6	0.07	10.5
MOX06*	Plåten	3	0.04	14.7
MOX07*	Lötsjön	8	0.06	24.9
MOX08	Glimmingen	11.3	0.11	5.3
MOX09	Stortoveln	10.6	0.24	5.3
MOX10	Bengtsgolen	0	0.14	34.7
MOX11	Lillsjön	5.9	0.16	15.9
MOX12	Parsen	4.2	0.1	15.8

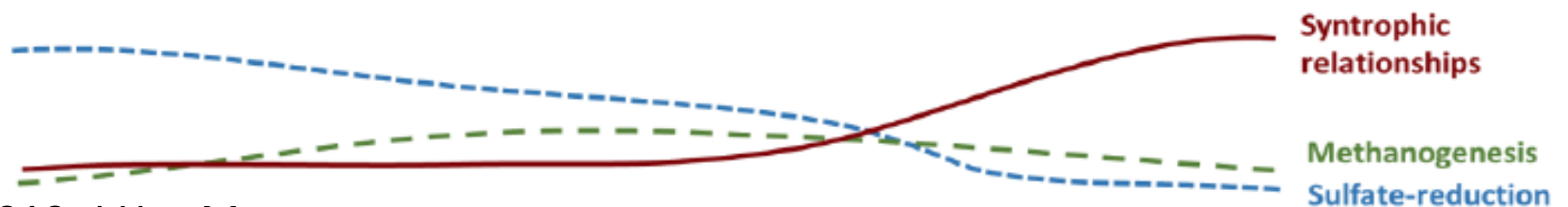
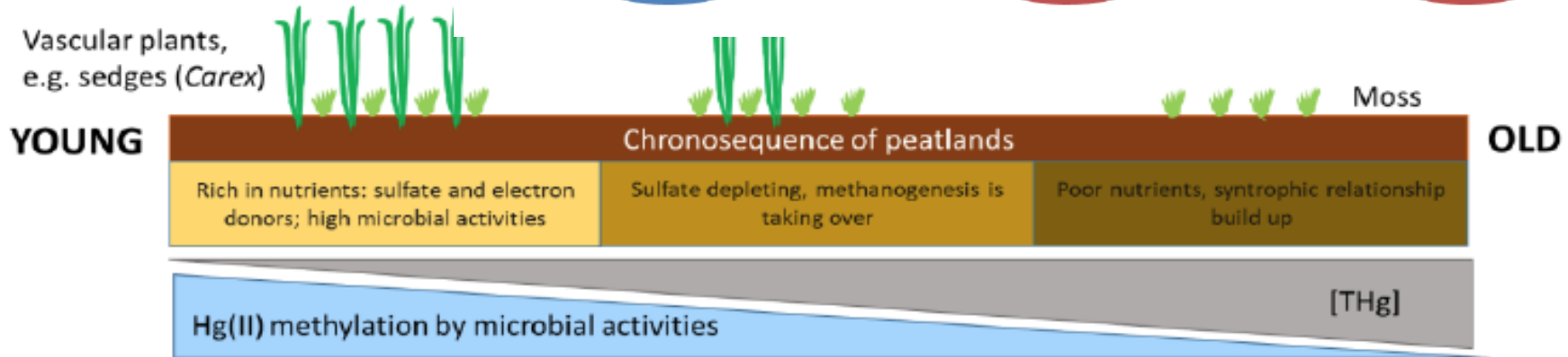
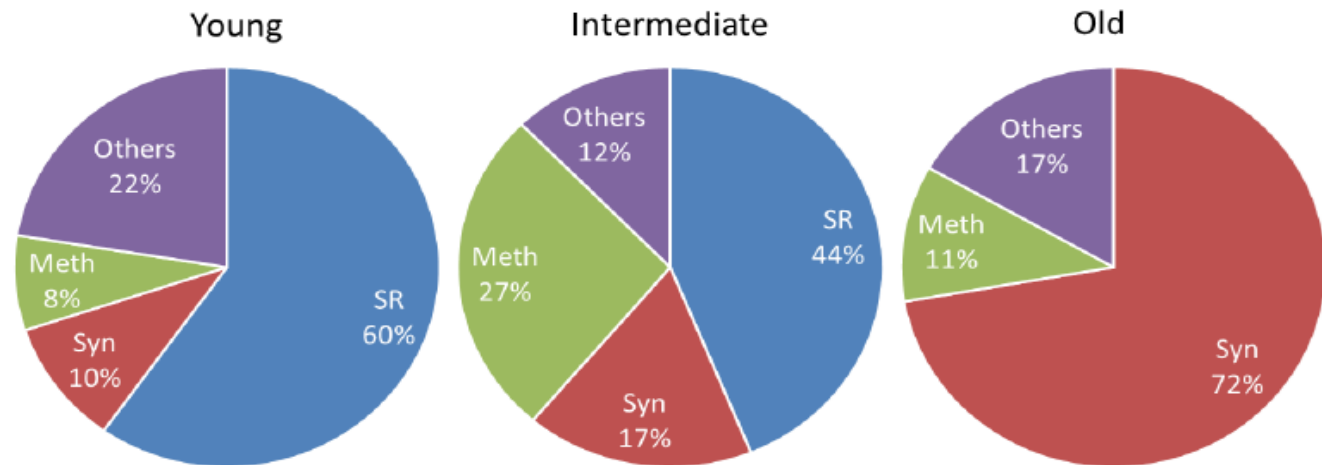
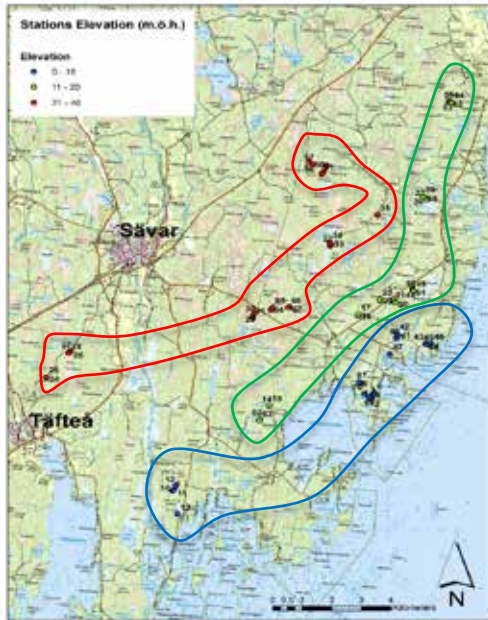




Taxonomic affiliation of hgcA genes in lakes with high methylation (k_m)

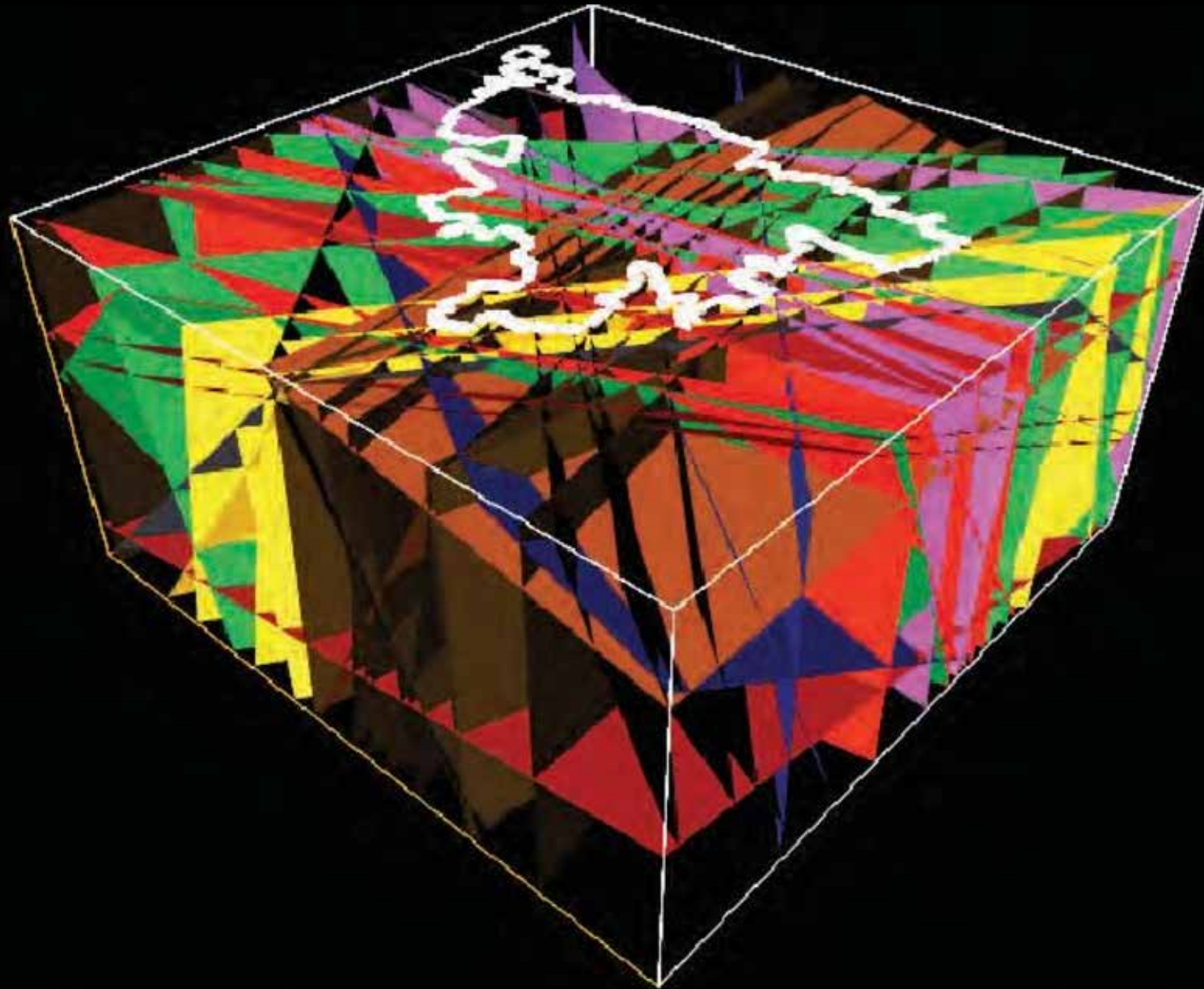


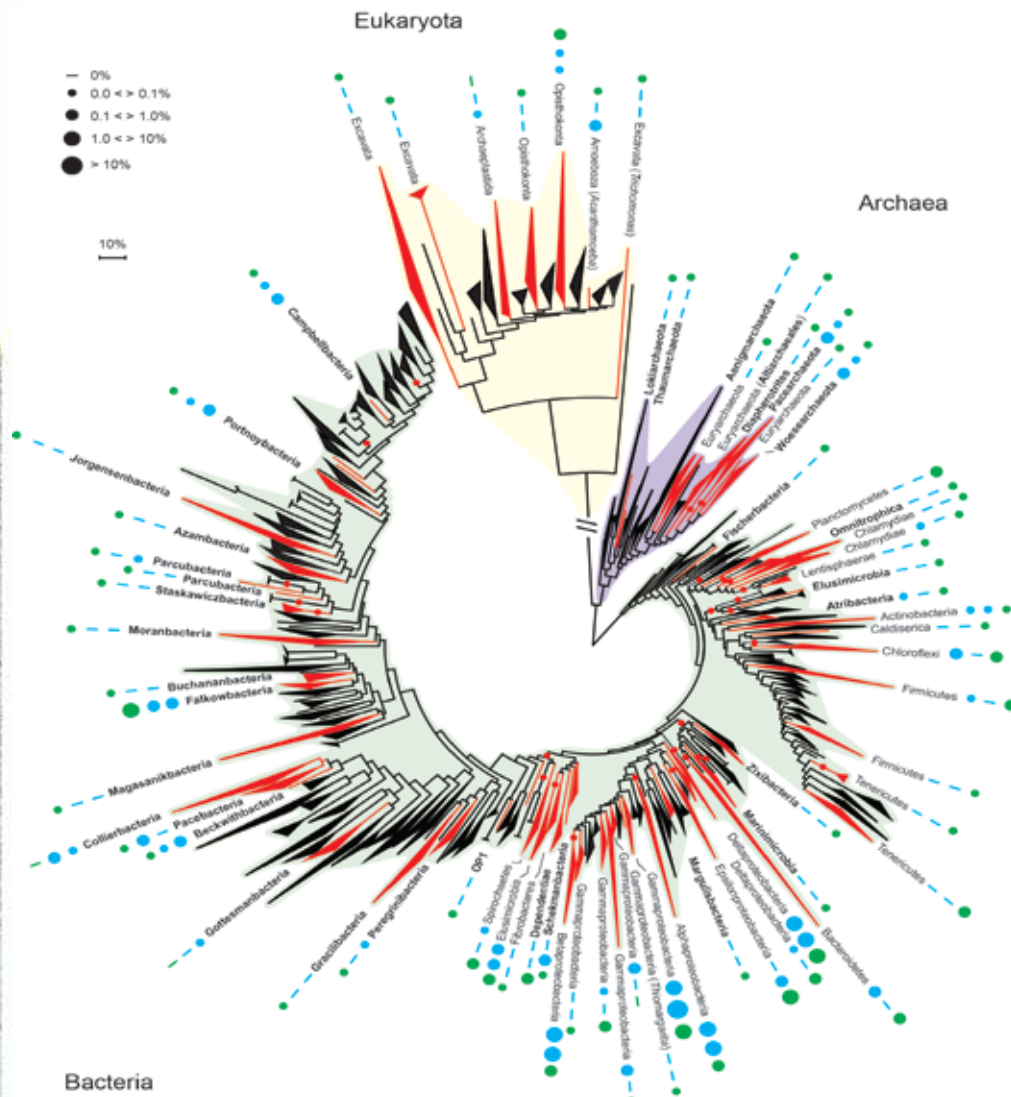
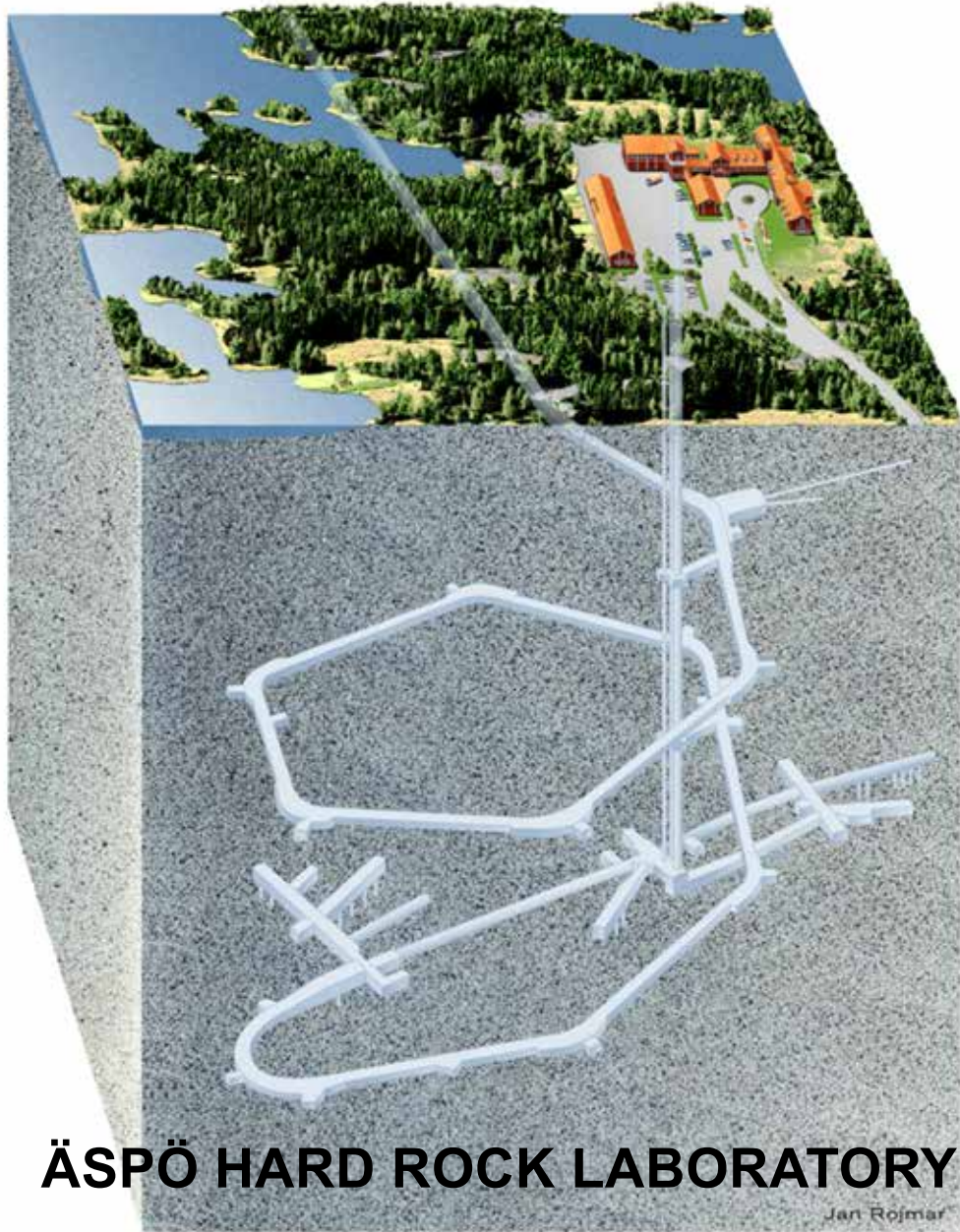
Variable metabolic processes fuel MeHg production along the otogeny of peatlands



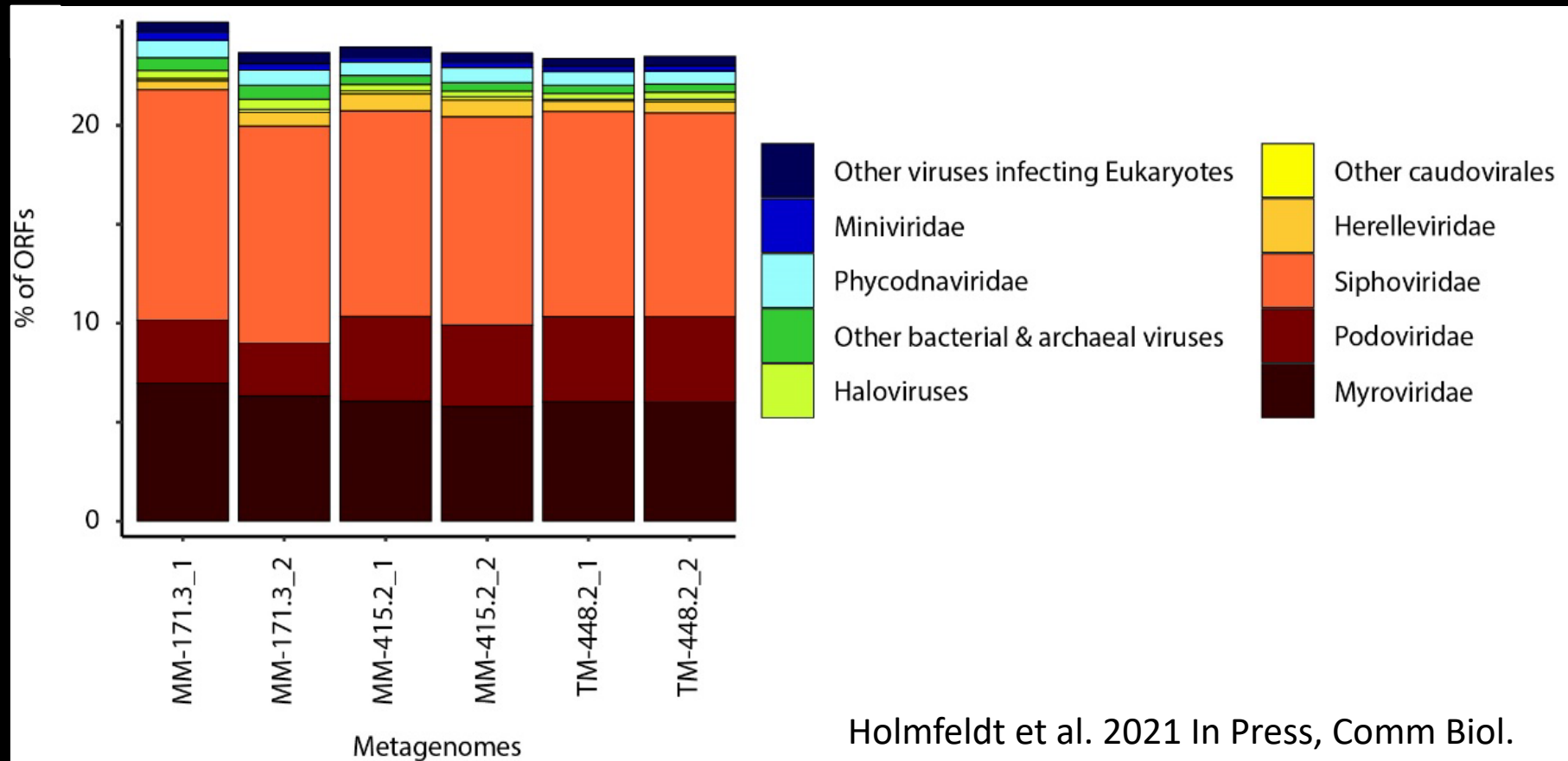
Hu et al, 2019, J Haz Mat.

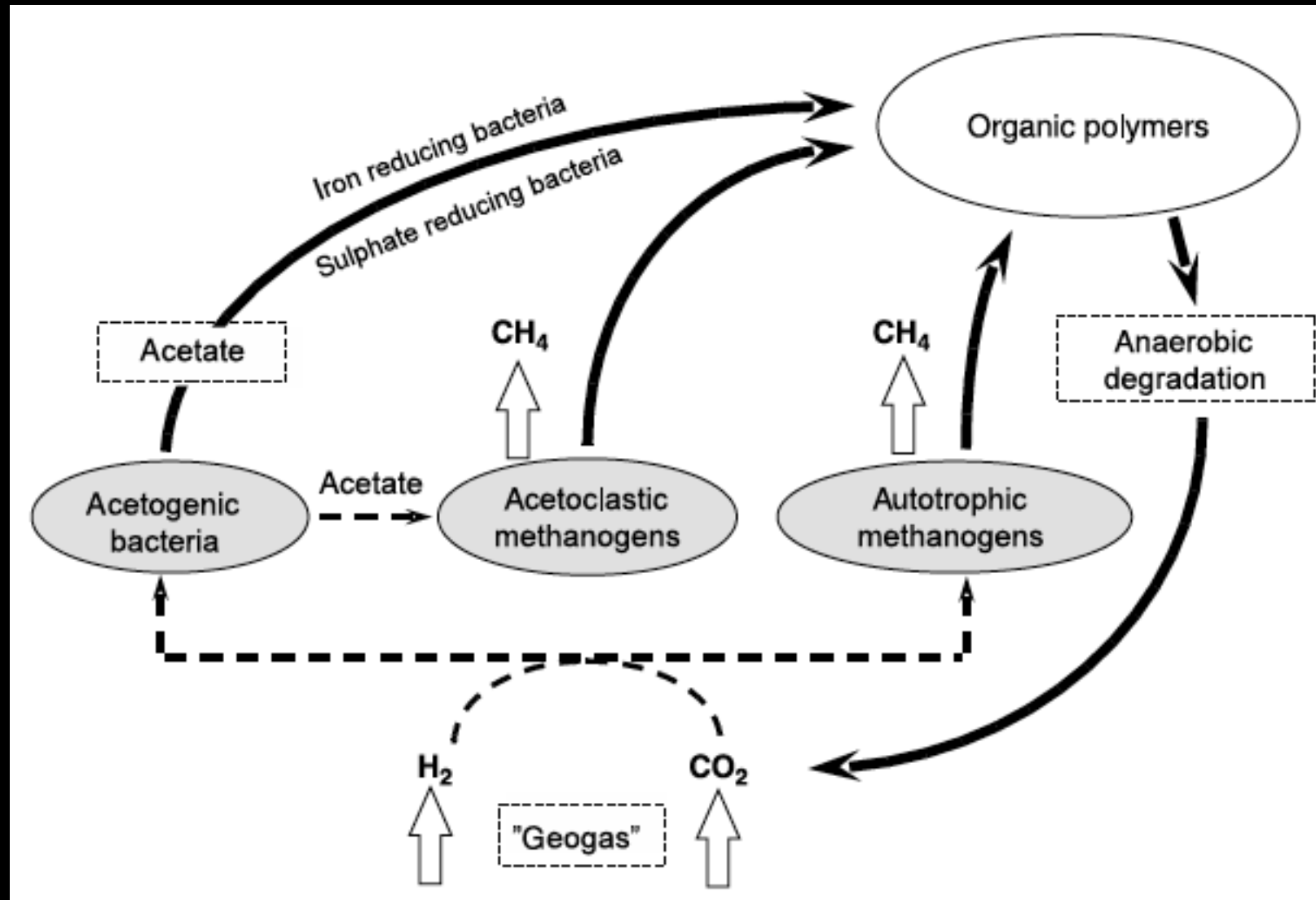
Fractures and isolation of aquifers in the deep terrestrial subsurface





Viruses in the deep? Yes!

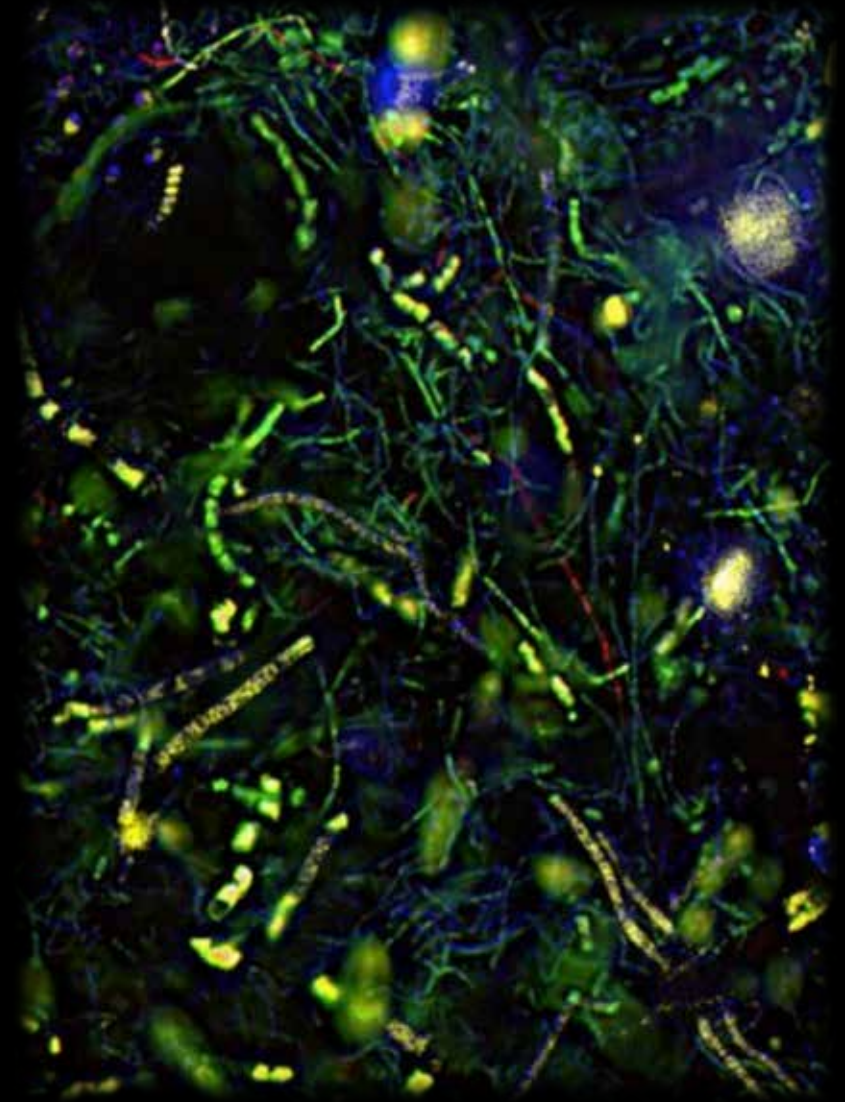




Conceptual model of the hydrogen-driven deep biosphere from Pedersen, 2010

AQUATIC MICROBIAL COMMUNITIES
ARE TAXONOMICALLY AND
FUNCTIONALLY DIVERSE, VARIABLE
AND DYNAMIC.

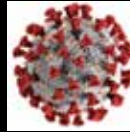
LARGE SCALE SEQUENCING
APPROACHS CAN ADVANCE OUR
UNDERSTANDING OF THEIR
DIVERSITY AND FUNCTIONAL TRAITS



FUME: FUncional Microbial Ecology



Environmental
virus profiling



Forskningrådet
Formas



Vetenskapsrådet

*Knut och Alice
Wallenbergs
Stiftelse*



UPPSALA
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