

Ilaria Mania^{1,3*}, Roberta Gorra¹, Nicola Colombo², Michele Freppaz¹, Maria Martin¹, Alexandre Anesio³

¹Department of Agricultural, Forest and Food Science, University of Turin - ² Department of Earth Sciences, University of Turin - ³School of Geographical Sciences, University of Bristol

*ilaria.mania@unito.it

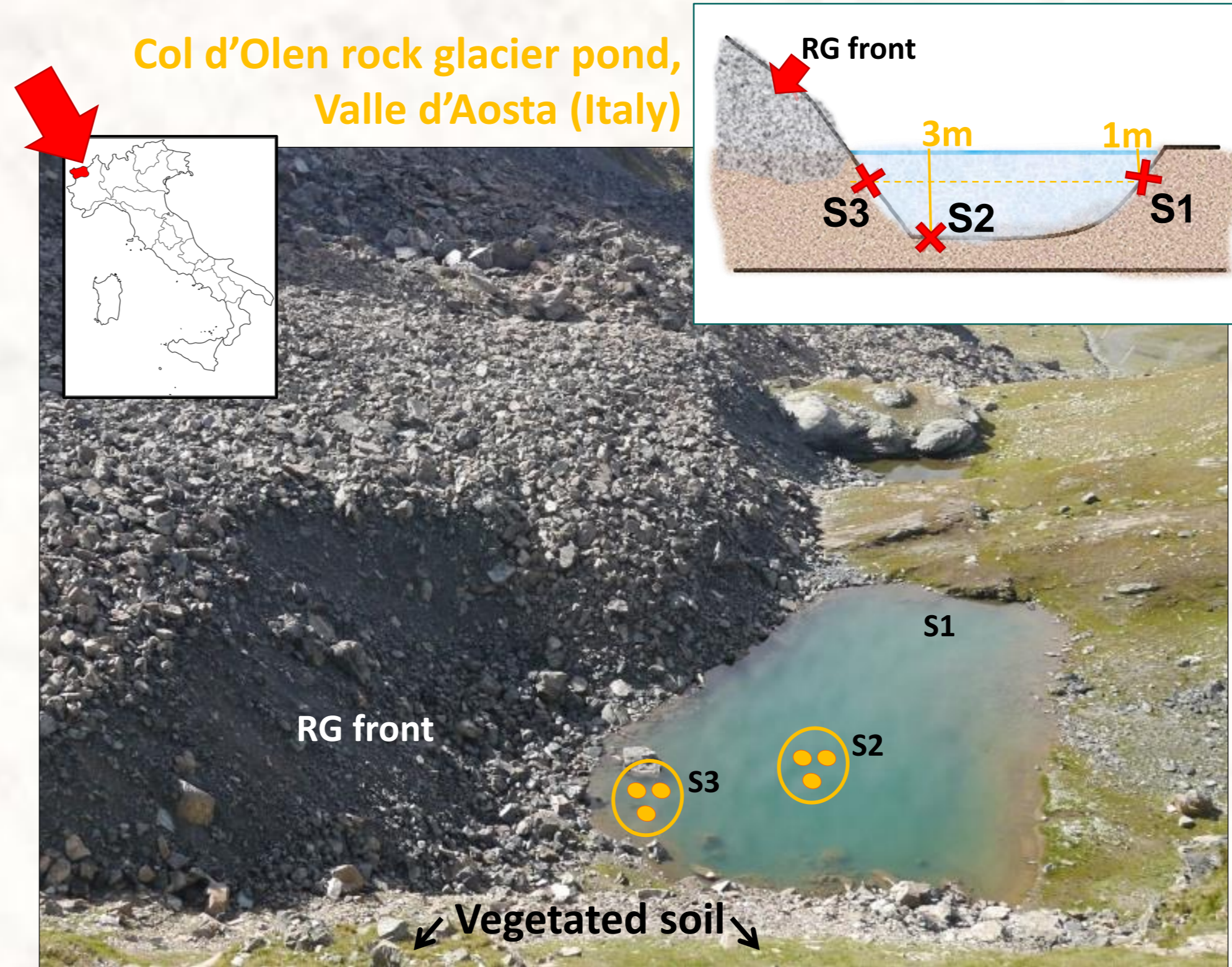
Background

Rock glaciers (RGs) are geomorphological features widespread in high-elevation alpine environments, consisting of **slow-flowing mixtures of rocks and ice**, and are considered indicators of ice-rich permafrost presence. Due to their capability to influence waters passing through and originating from them, RGs have the **potential to influence** connected alpine water bodies, both in terms of **water geochemistry**^[1] and, as pointed out mainly in the last years, overall **ecosystem ecology**^{[2][3]}.

Objectives

- Describe **prokariotic communities** inhabiting the sediments of an alpine RG-associated pond with serpentinitic mineralogy
- Investigate the **potential influence of RG** inputs on prokariotic community and sediments geochemistry, by analyzing lacustrine sediments along a distance gradient from the RG front

Methods



Sampling:

- 3 sampling points
 - distance gradient from RG front
 - Top 10 cm of lacustrine sediment
 - 2 water depths (1m, 3m)
- 2 sampling times
 - September 2015, July 2016

Analysis:

- 16S rRNA abundance (qPCR)
- 16S rRNA diversity (Illumina MiSeq)
 - Archaea } DNA
 - Bacteria } DNA
- Sediments geochemistry
 - DOC, TDN, NO₃⁻, NH₄⁺ } KCl extracts
 - pH, major anions and cations } Pore H₂O

Fig. 1a: Alpha diversity estimated by Chao1 and Shannon indexes. 2015 and 2016 data were pooled. Different letters indicate significant differences (Kruskal-Wallis + Dunn's test).

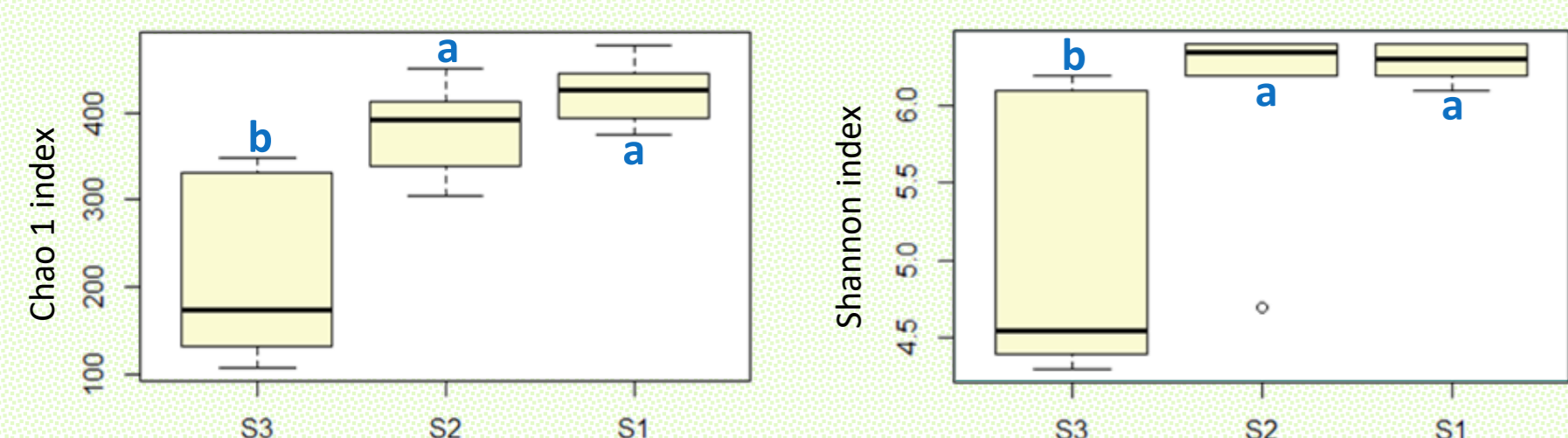
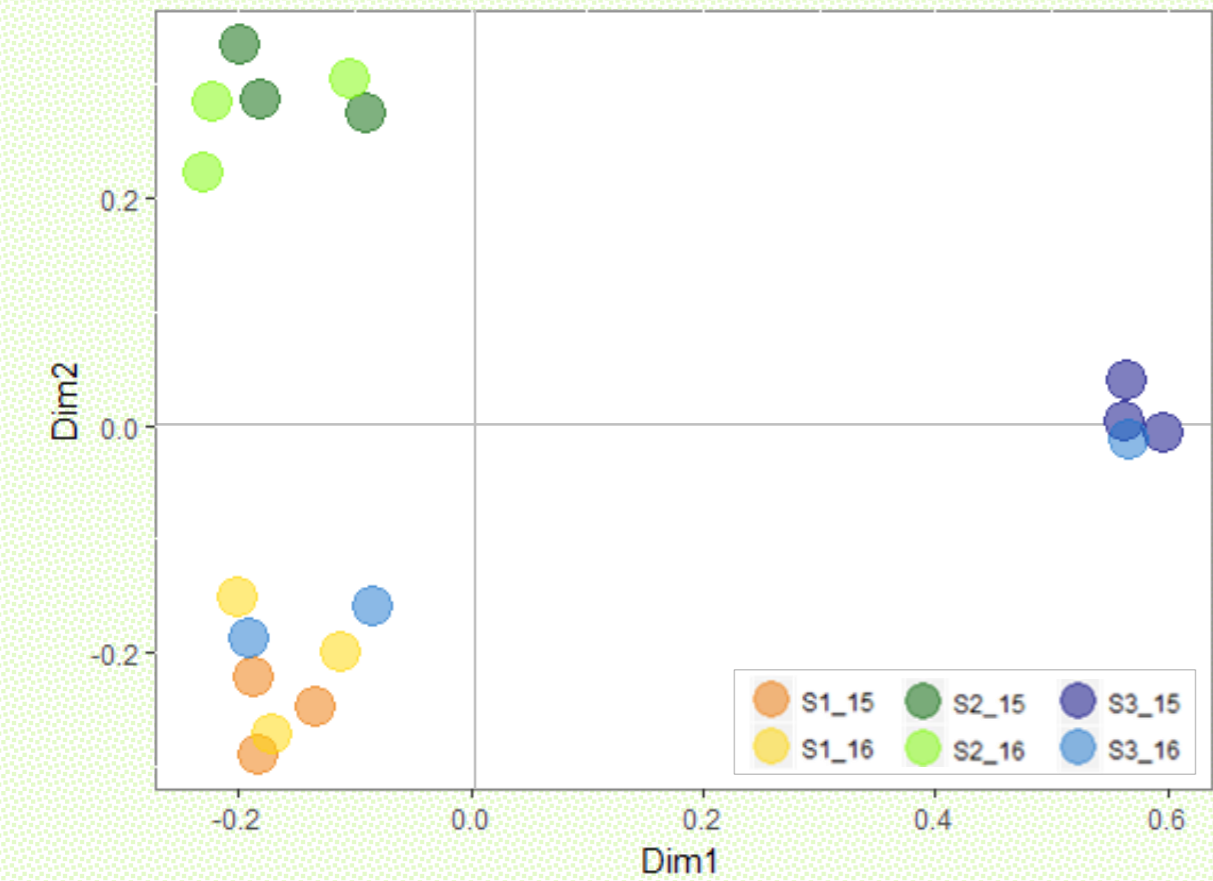


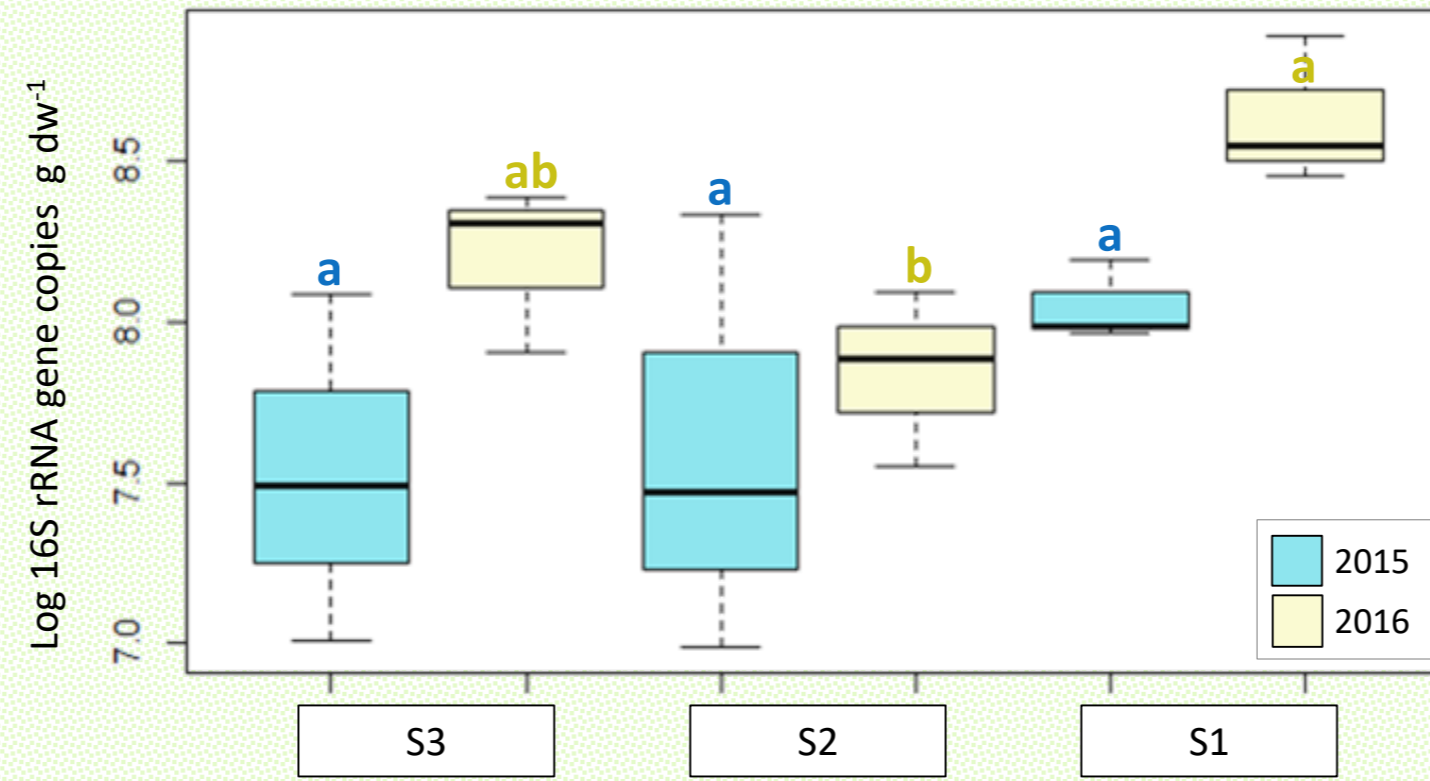
Fig. 2a: PCoA ordination based on Bray-Curtis distance matrix



- Lower richness and evenness in S3
- Clear separation among sampling points in terms of beta diversity (excluding S3-2016)

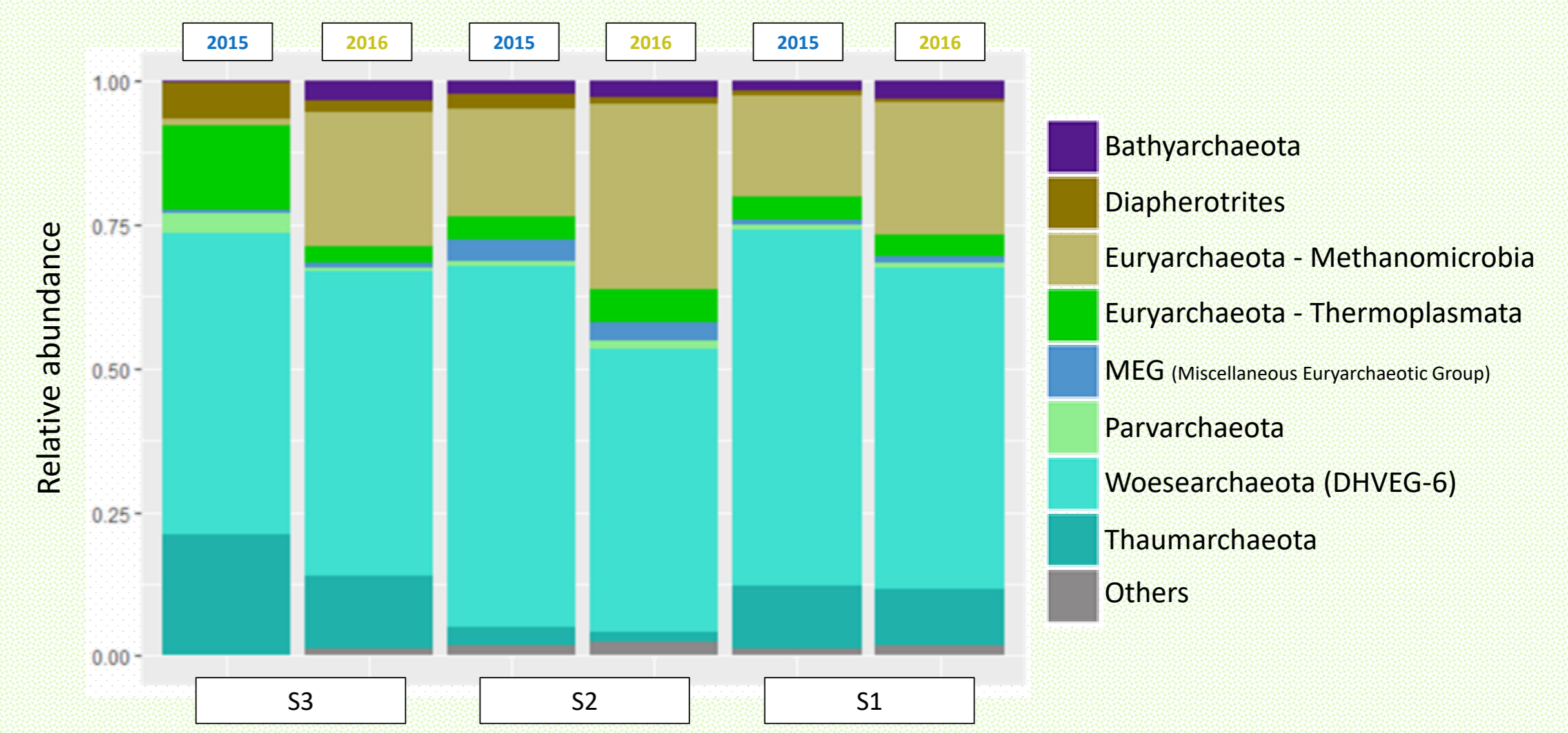
Results - Archaea

Fig. 3a: 16S rRNA genes abundance estimated by qPCR. Different letters indicate significant differences in sampling points within the same year (Kruskal-Wallis + Dunn's test)



- No horizontal differences in 2015
- 2016 abundances follow depth profile

Fig. 4a: Community composition in terms of main archaeal phyla



- Dominant group: Woesearchaeota
- < Thaumarchaeota in centre
- S3 (2015): <Methanomicrobia, >Thermoplasmata

Fig. 1b: Alpha diversity estimated by Chao1 and Shannon indexes. 2015 and 2016 data were pooled. Different letters indicate significant differences (Kruskal-Wallis + Dunn's test)

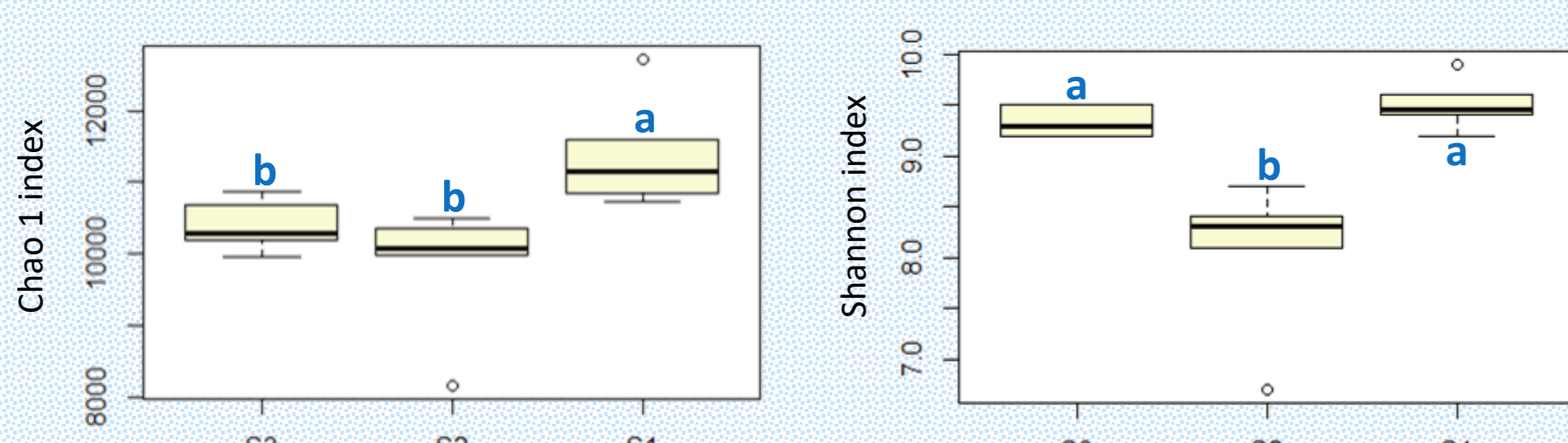
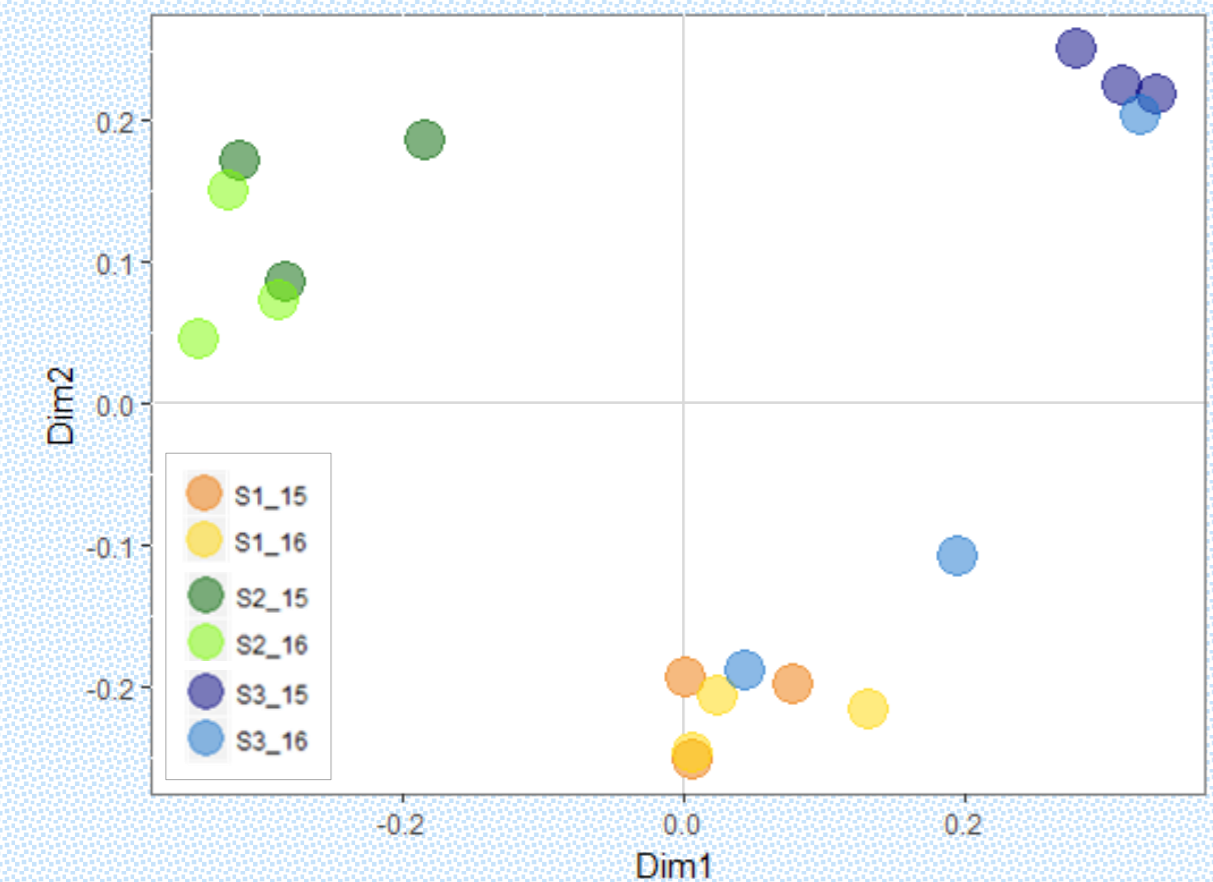


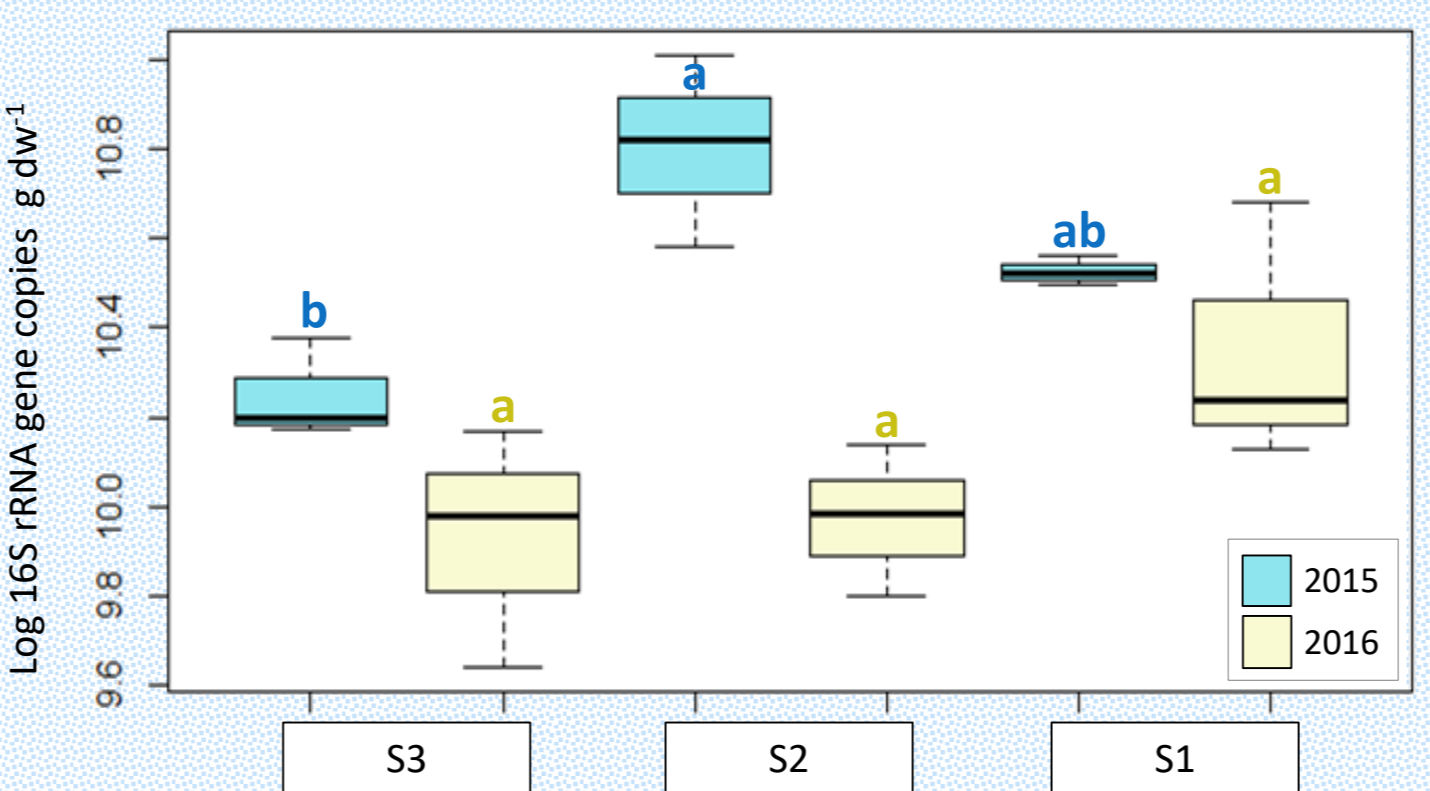
Fig. 2b: PCoA ordination based on Bray-Curtis distance matrix



- Lower richness in S2 and S3
- Lower evenness in S2
- Clear separation among sampling points in terms of beta diversity (excluding S3-2016)

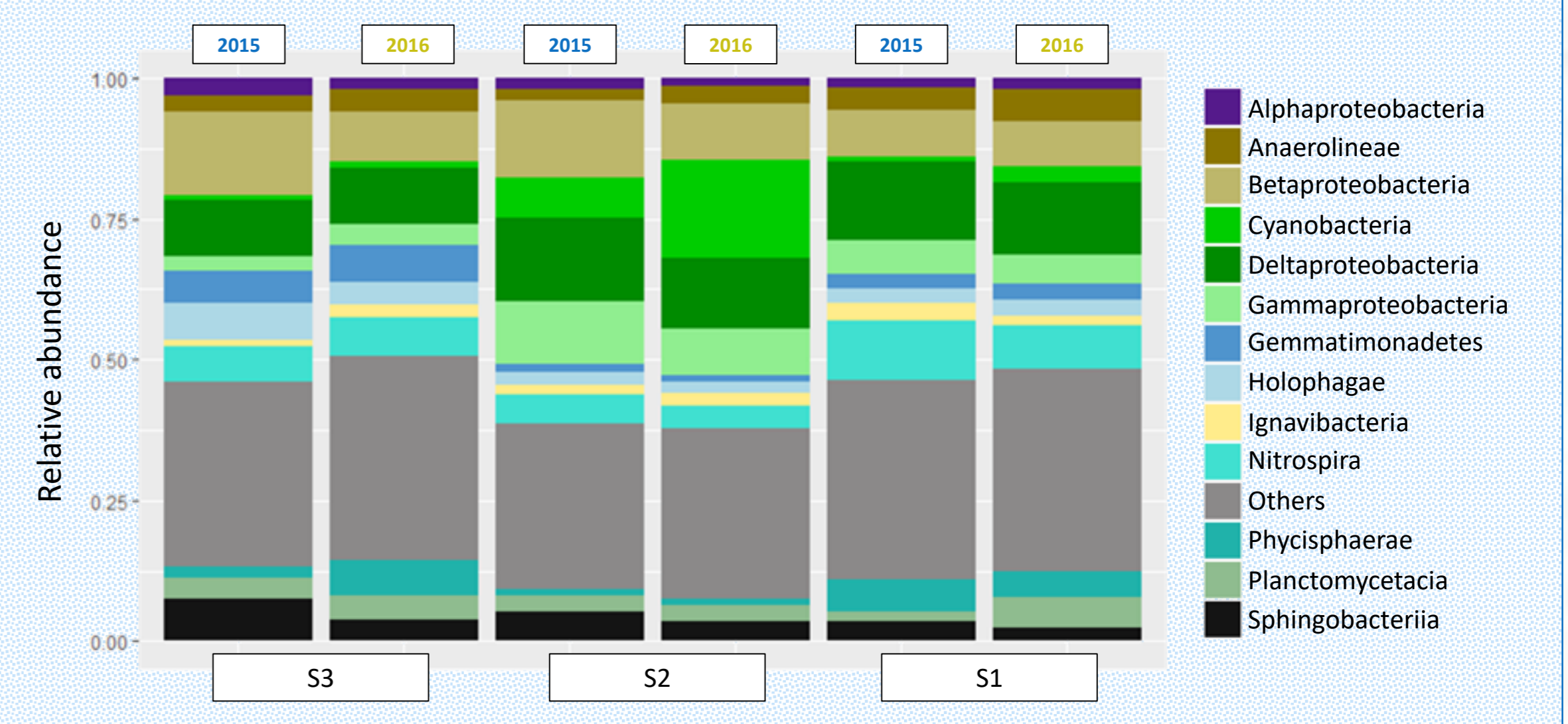
Results - Bacteria

Fig. 3b: 16S rRNA genes abundance estimated by qPCR. Different letters indicate significant differences in sampling points within the same year (Kruskal-Wallis + Dunn's test)



- No significant horizontal differences in 2016
- In 2015 higher bacterial 16S abundance in central than shallower sediments

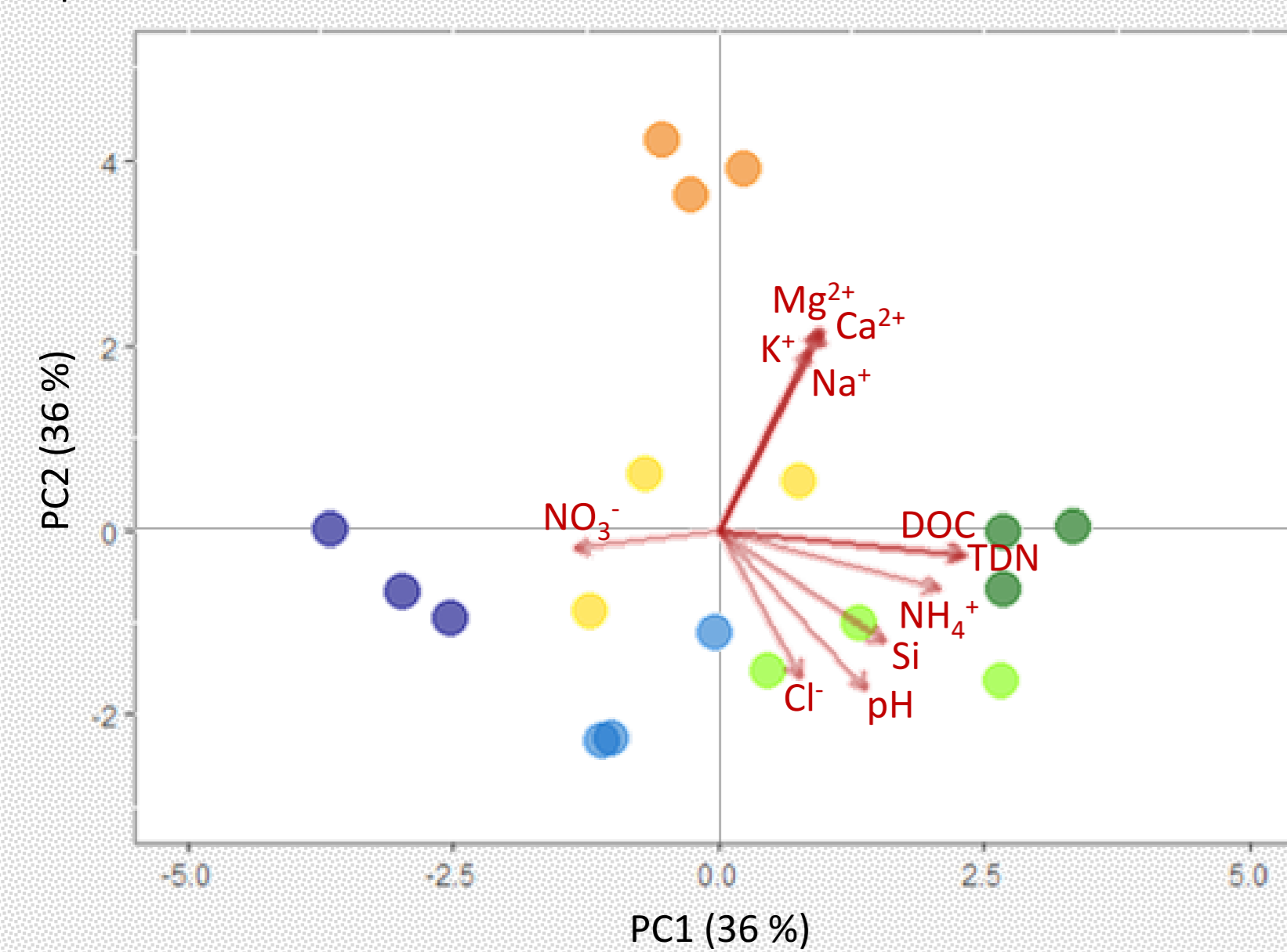
Fig. 4b: Community composition in terms of main bacterial classes



- In centre: > Cyanobacteria, Gammaproteobacteria
- In S1, S3: > Nitrospira, Phycisphaerae
- closer to RG: > Gemmatimonadetes, Holopagae, Sphingobacteriia

Results - Geochemistry

Fig. 5: PCA based on sediments and pore water geochemical properties. The range of values measured for each parameter is reported in the table beside.

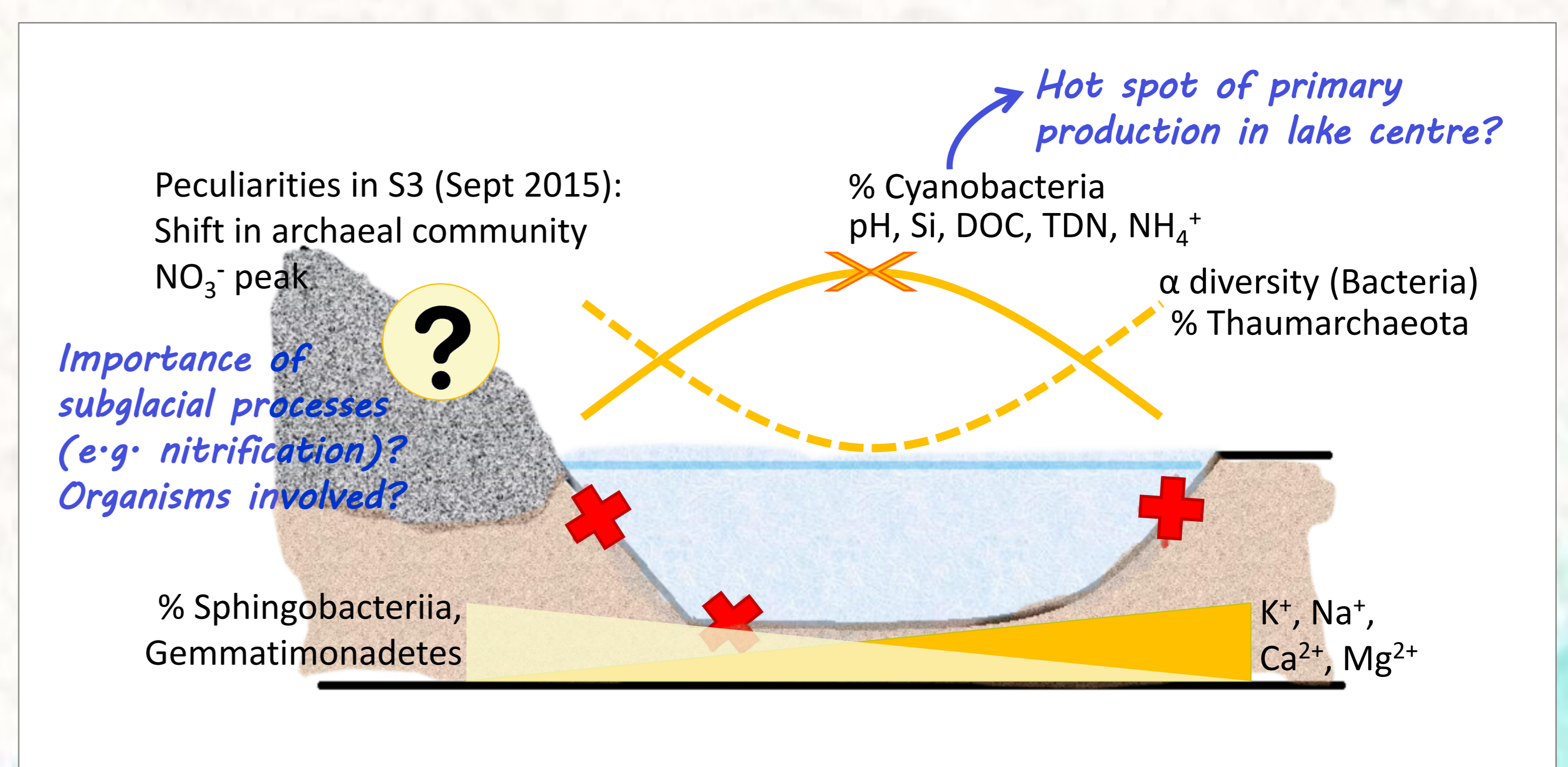


Parameter	(min - max)
DOC (µg C/g dw)	83 - 252
TDN (µg N/g dw)	10 - 61
NH ₄ ⁺ (µg N/g dw)	1 - 38
NO ₃ ⁻ (µg N/g dw)	0.1 - 1.1
Ca ²⁺ (mg/L)	3 - 51
Mg ²⁺ (mg/L)	1 - 22
Na ⁺ (mg/L)	0.4 - 1.7
K ⁺ (mg/L)	1 - 4.6
Si (mg/L)	0.25 - 3.9
pH	5.7 - 8.5

- Separation among sampling points (but main differences in chemical properties are found in samples 2015)
- Central sample: higher DOC, TDN, pH, Si and Cl
- S1: higher concentration of Ca²⁺, Mg²⁺, Na⁺ and K⁺
- S3: in 2015 reported a peak in NO₃⁻ concentration

Conclusions ... and future directions

Our results suggest that a **complex net of environmental factors**, such as **water depth**, in addition to the environmental **gradient derived from icemelt waters**, can have a significant impact on the distribution of the prokariotic community and geochemistry along the sediments of the Col d'Olen Rock Glacier Pond.



References

- [1] Williams M, Knauf M, Cory R, Caine N & Liu F (2007) - Nitrate content and potential microbial signature of rock glacier outflow, Colorado Front Range. *Earth Surface Processes and Landforms* 32: 1032-1047
- [2] Ilyanushuk BP, Ilyanushuk EA, Psenner R, Tessadri R, Koenig KA (2014) - Rock glacier outflows may adversely affect lakes: lessons from the past and present of two neighboring water bodies in a crystalline-rock watershed. *Environmental Science & Technology* 48: 6192-6200
- [3] Fegel TS, Baron JS, Fountain AG, Johnson GF, Hall EK (2016) - The differing biogeochemical and microbial signatures of glaciers and rock glaciers. *Journal of Geophysical Research: Biogeosciences* 121: 919-932

