# Microbial diversity in the SOCLIM study region

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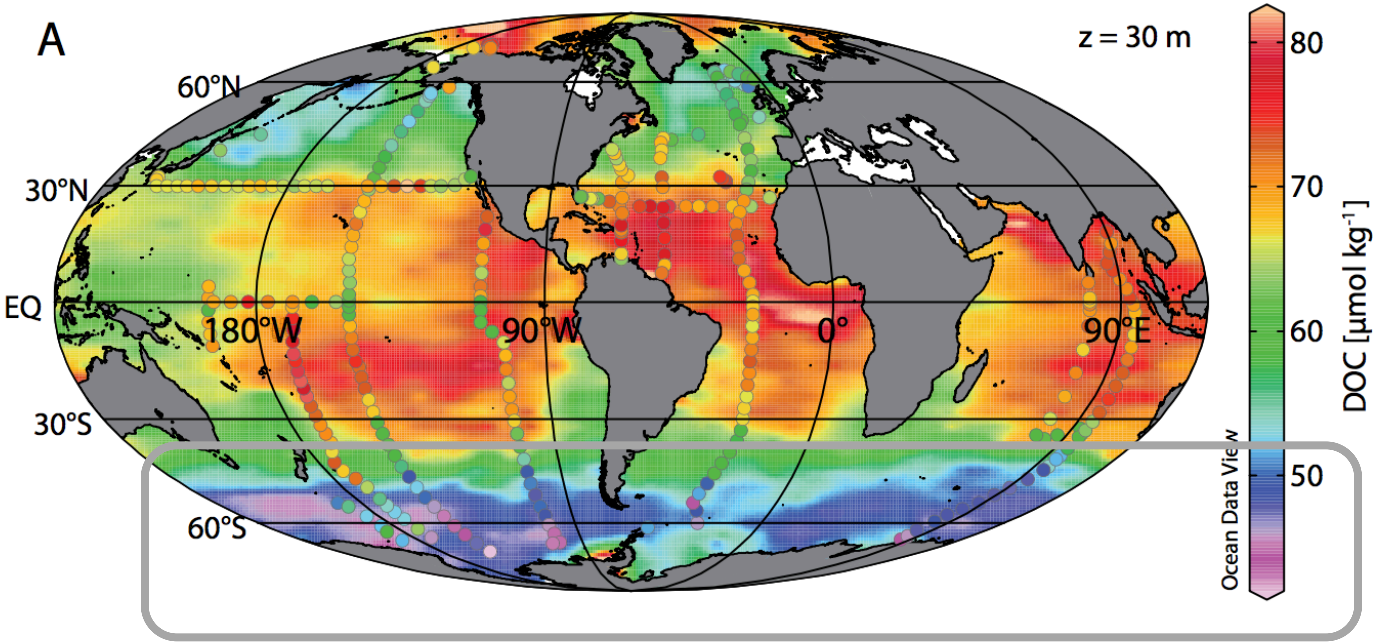
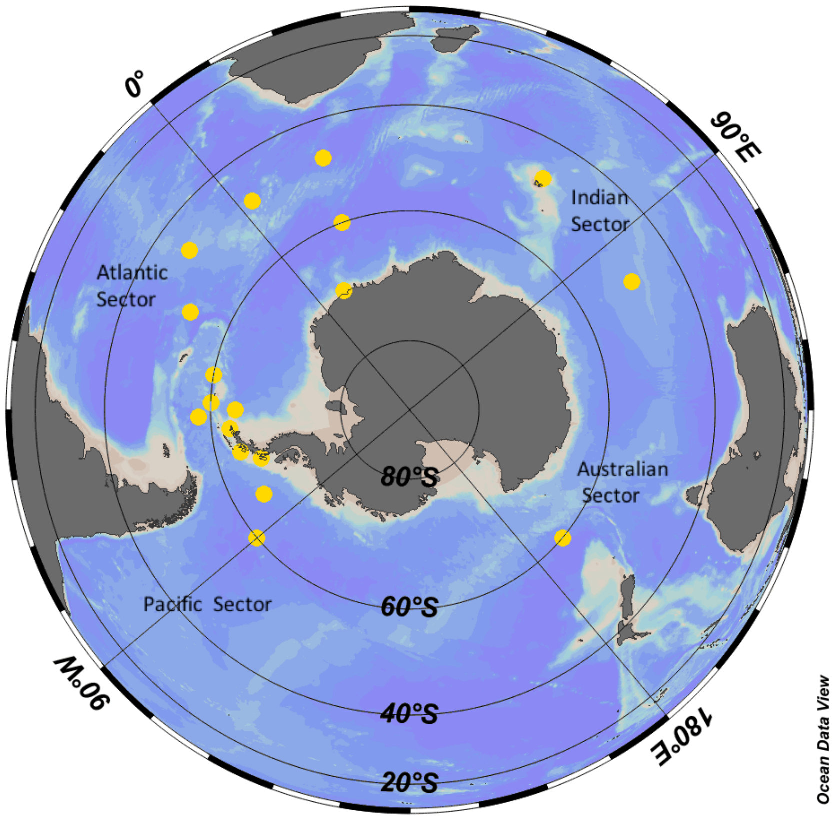
PhD thesis
Establishing links between the variability of microbial respiration, diversity and organic matter characteristics

# Background

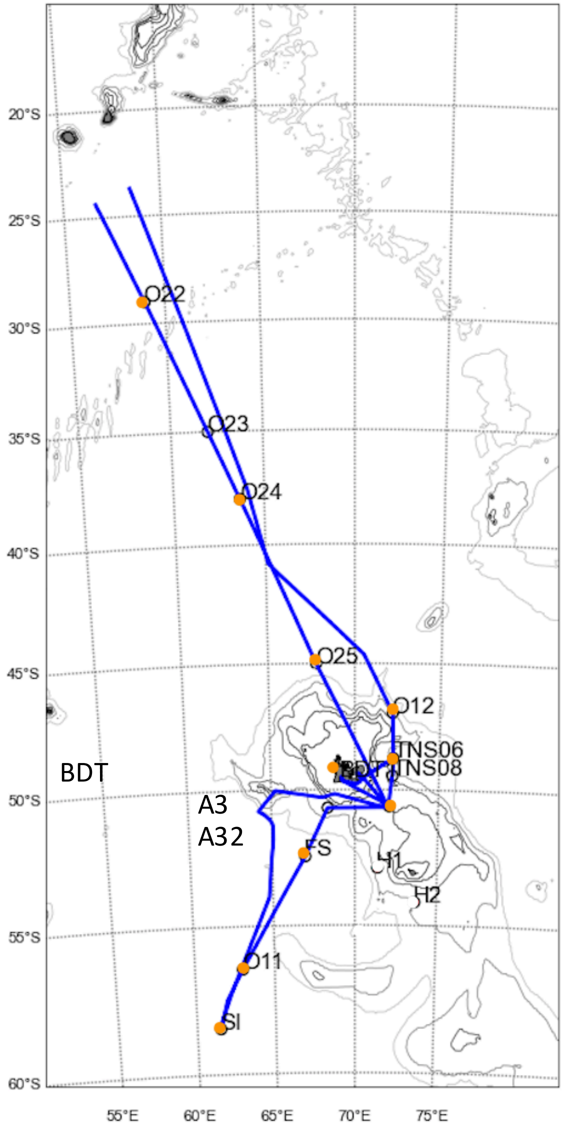
Distributions of DOC in surface waters



Hansell et al., 2009



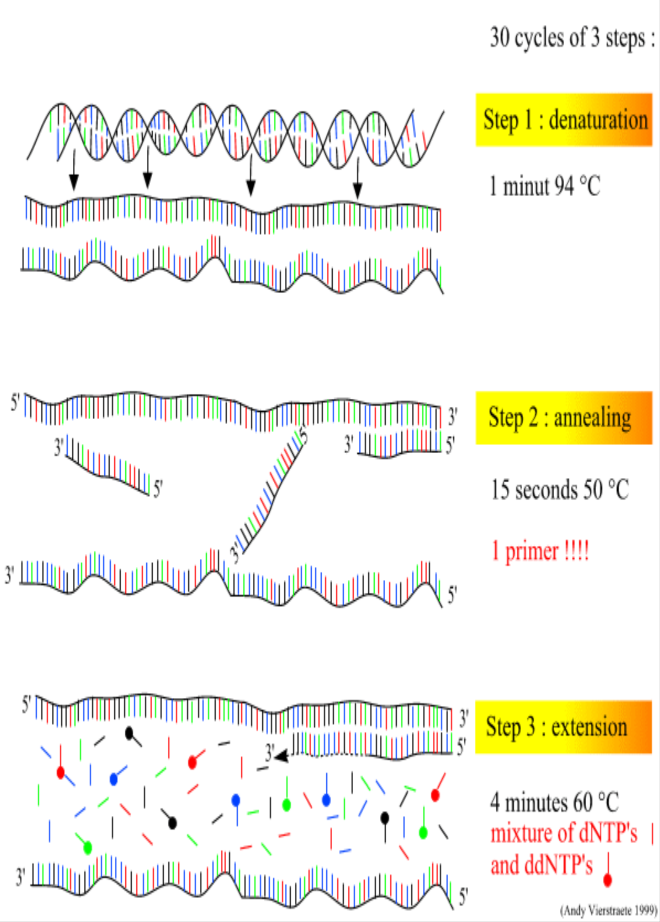
# SOCLIM sampling sites (Oct. 2016)



# Diversity of total prokaryotic community and active prokaryotic community

Extraction
- DNA
- RNA → Reverse transcription → cDNA

## Amplification of 16S rDNA/rRNA



Sequencing
by Illumina MiSeq

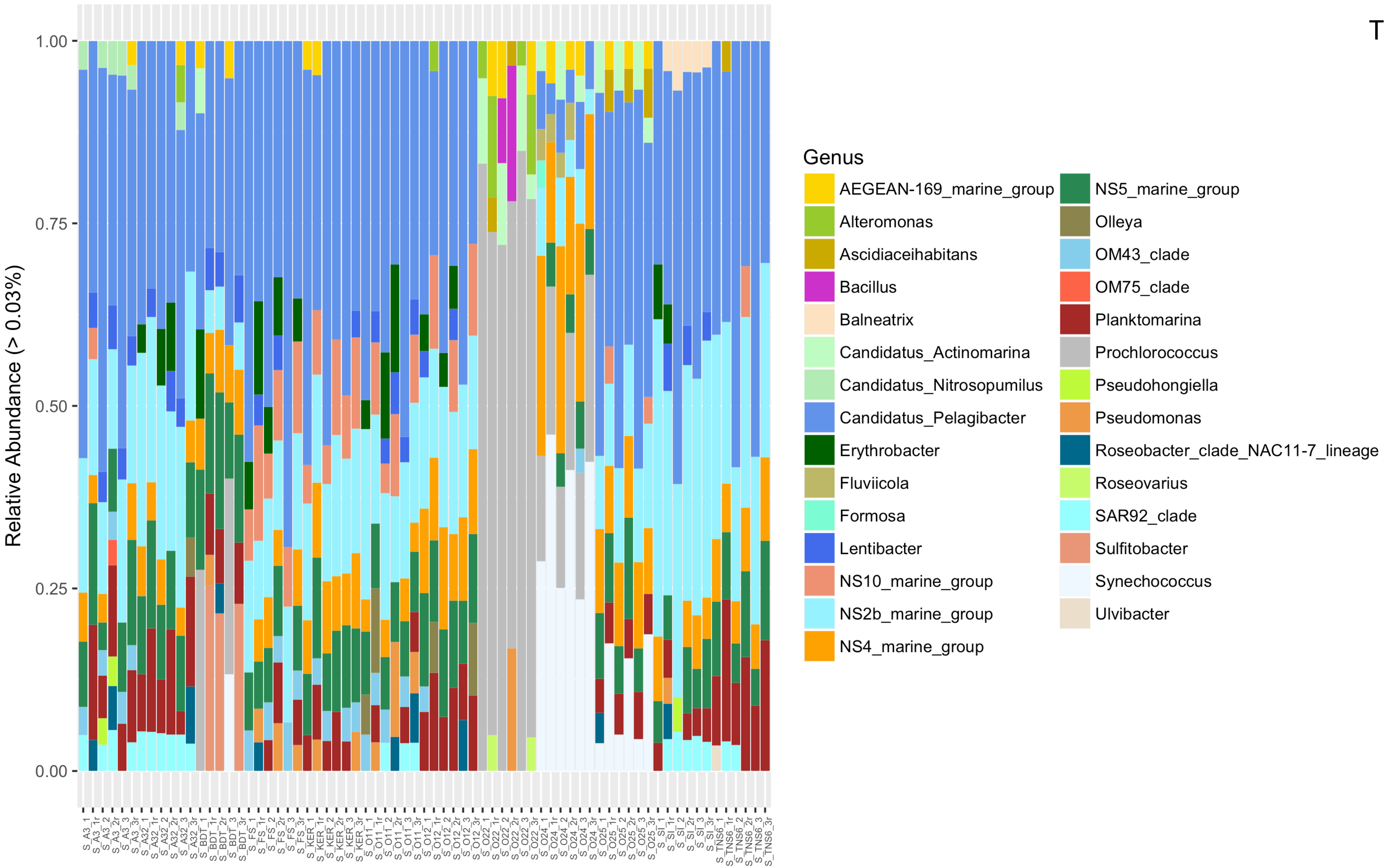
→

Data processing
DADA2 pipeline

## Seq. no. of OTUs (on Genus level): 972,057 in total

| Total prok. | OTUs (no.) | Active prok. | OTUs (no.) |
|---|---|---|---|
| S_O22_1 | 9553 | S_O22_1r | 8286 |
| S_O22_2 | 8843 | S_O22_2r | 10810 |
| S_O22_3 | 8550 | S_O22_3r | 8933 |
| S_O24_1 | 9882 | S_O24_1r | 13359 |
| S_O24_2 | 9998 | S_O24_2r | 16017 |
| S_O24_3 | 8500 | S_O24_3r | 9721 |
| S_O25_1 | 11222 | S_O25_1r | 9495 |
| S_BDT_1 | 8078 | S_O25_2r | 11828 |
| S_BDT_2 | 5358 | S_BDT_2r | 15864 |
| S_BDT_3 | 8574 | S_BDT_3r | 14436 |
| S_A3_1 | 11812 | S_A3_1r | 13119 |
| S_A3_2 | 10045 | S_A3_2r | 8989 |
| S_A3_3 | 9741 | S_A3_3r | 11082 |
| S_KER_1 | 14023 | S_KER_1r | 11420 |
| S_KER_2 | 14430 | S_KER_2r | 26531 |
| S_KER_3 | 22822 | S_KER_3r | 11449 |
| S_FS_1 | 10480 | S_FS_1r | 17295 |
| S_O25_2 | 9675 | S_FS_2r | 12198 |
| S_O25_3 | 9442 | S_O25_3r | 10274 |
| S_TNS6_1 | 12591 | S_TNS6_1r | 16817 |
| S_TNS6_2 | 10390 | S_TNS6_2r | 19729 |
| S_TNS6_3 | 9161 | S_TNS6_3r | 17077 |
| S_SI_1 | 15465 | S_BDT_1r | 17524 |
| S_SI_2 | 10999 | S_SI_2r | 18754 |
| S_SI_3 | 15522 | S_SI_3r | 15061 |
| S_A32_1 | 14479 | S_A32_1r | 20121 |
| S_A32_2 | 22056 | S_A32_2r | 16094 |
| S_A32_3 | 11357 | S_A32_3r | 11330 |
| S_O12_1 | 15200 | S_O12_1r | 17711 |
| S_O12_2 | 13832 | S_O12_2r | 22495 |
| S_O12_3 | 11361 | S_O12_3r | 19817 |
| S_FS_2 | 23957 | S_FS_3r | 16517 |
| S_FS_3 | 10015 | S_O11_1r | 18176 |
| S_O11_1 | 12939 | S_O11_2r | 18943 |
| S_O11_2 | 10741 | S_O11_3r | 13893 |
| S_O11_3 | 11614 | S_SI_1r | 18185 |

# Relative abundance of total prokaryotes (%) and active prokaryotes (%) on Genus level



Taxonomic rank

Kingdom

Phylum

Class

Order

Family

Genus

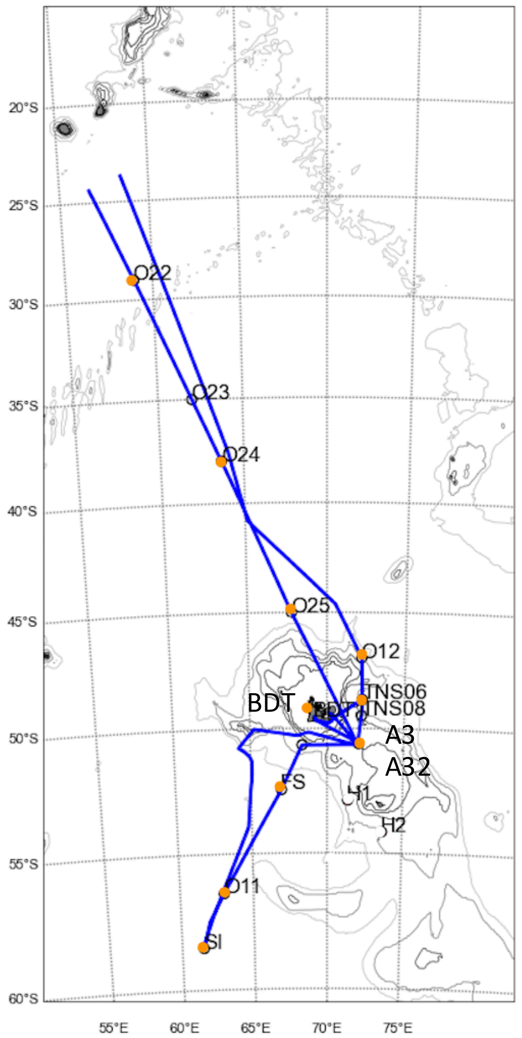
Species

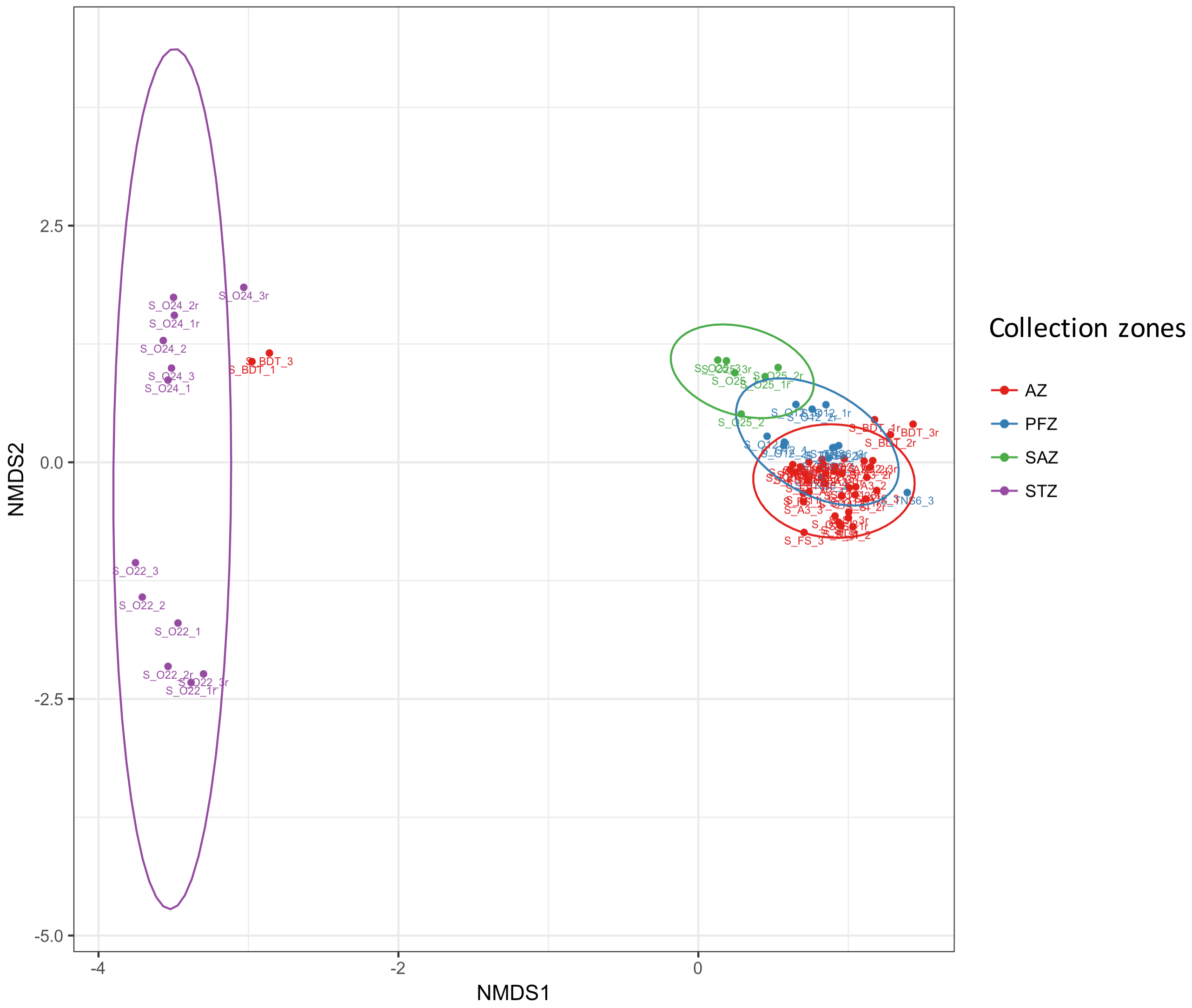
# Questions

1. Can we identify the prokaryotic pattern?

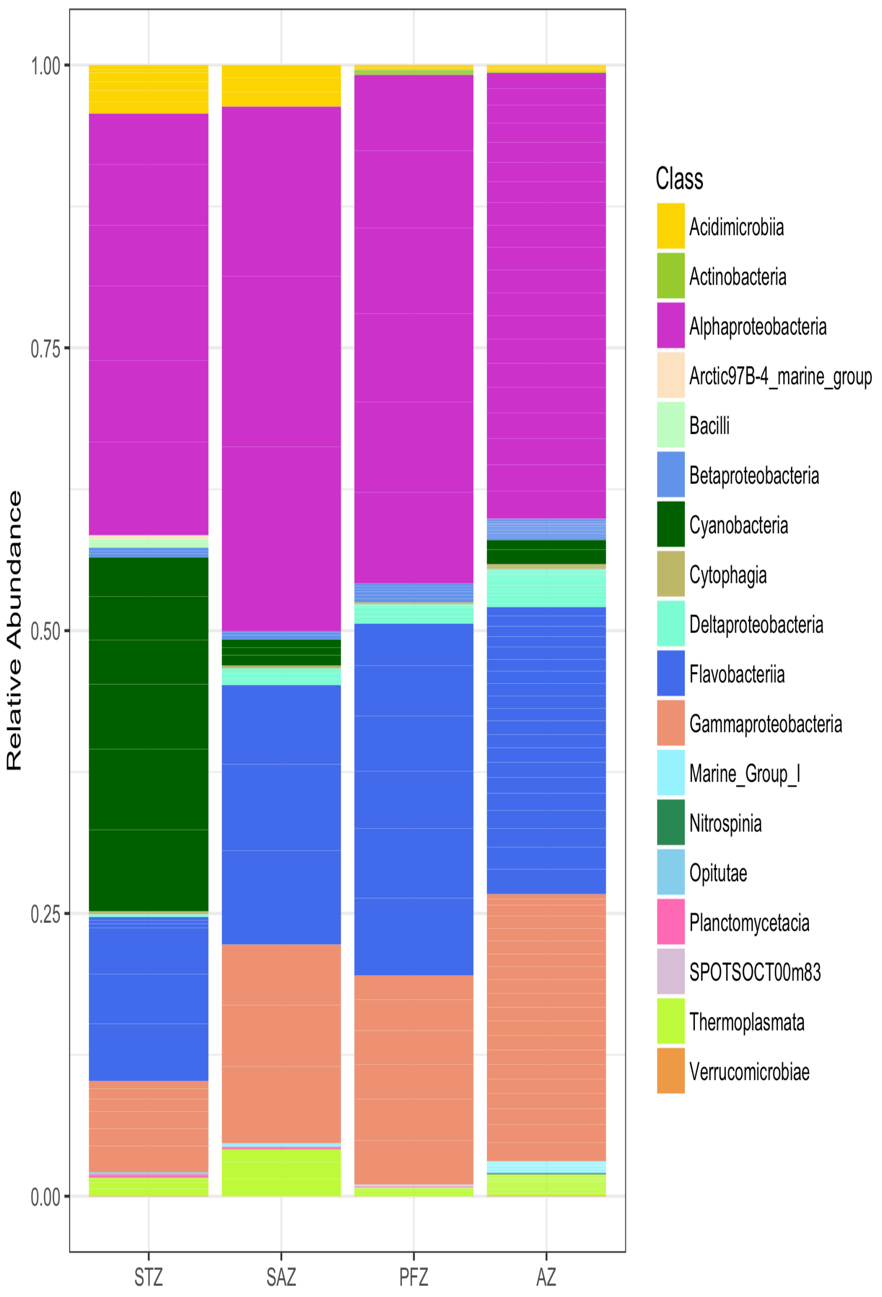
2. Can we explain the prokaryotic community composition across the transect ?

# Prokaryotic community composition markedly changed across the transect

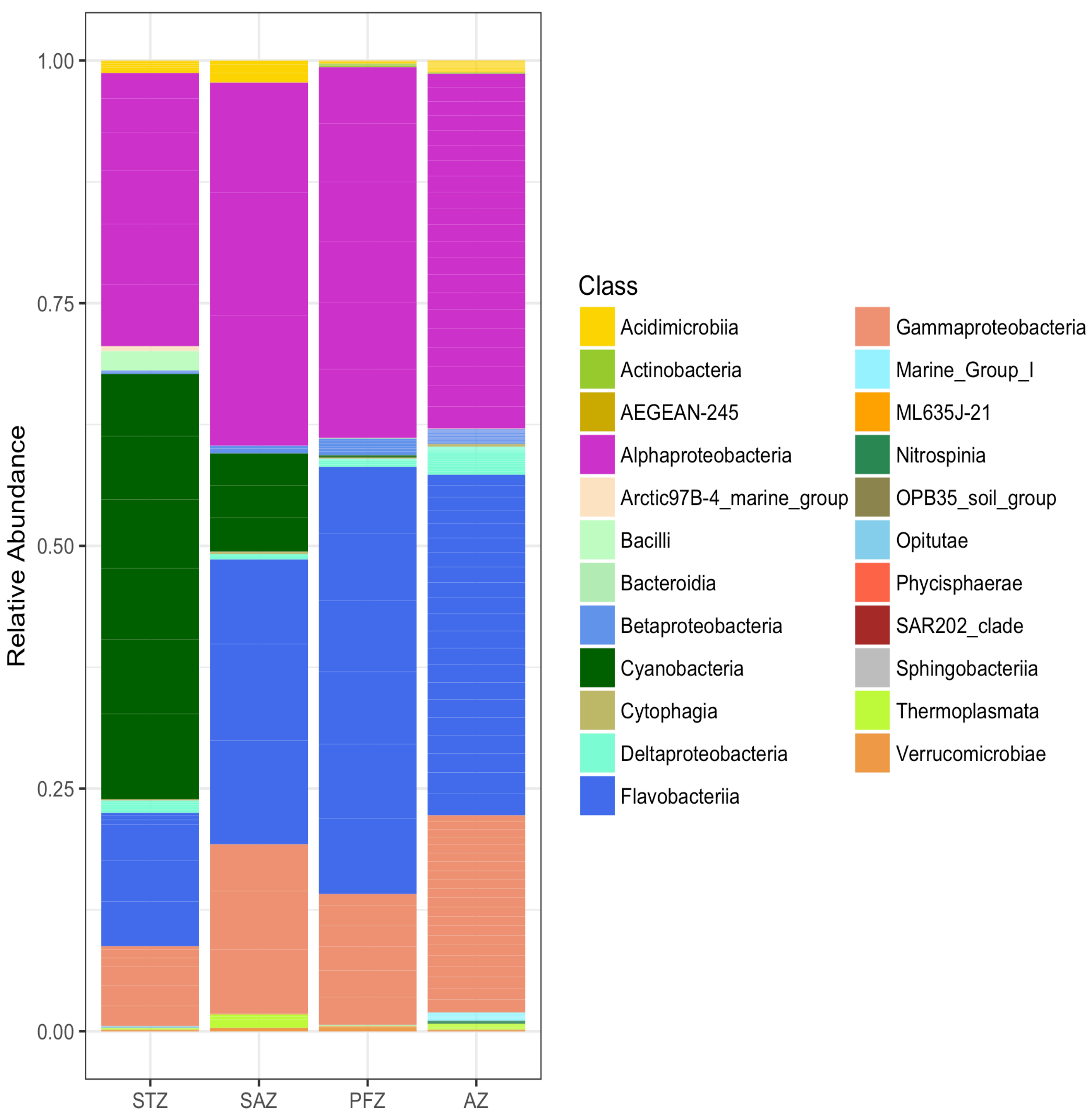




Relative abundance of total prokaryotes (%) on Class level



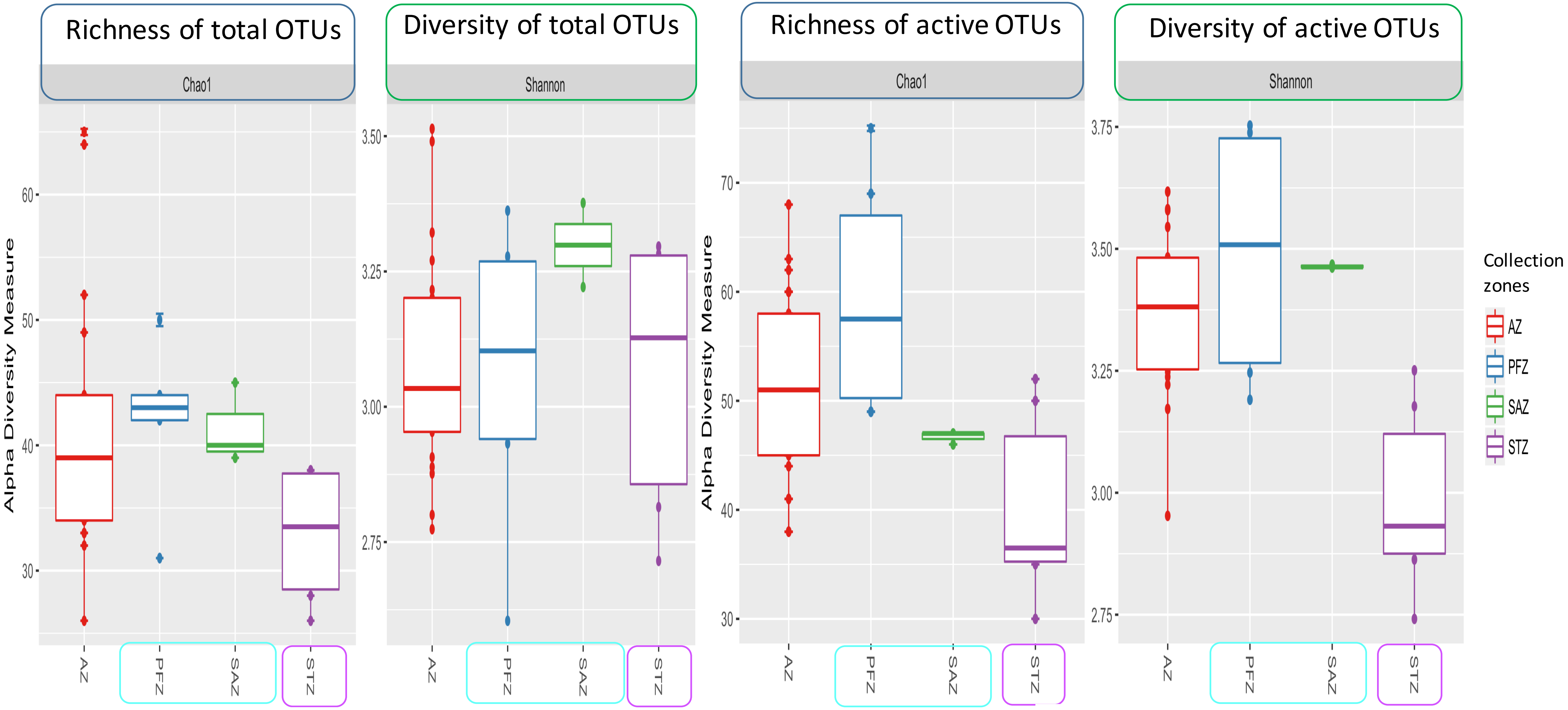
Relative abundance of active prokaryotes (%) on Class level



Taxonomic rank

Kingdom
Phylum
Class
Order
Family
Genus
Species

# Comparison between total prokaryotic community and active prokaryotic community



Richness of total OTUs

Diversity of total OTUs

Richness of active OTUs

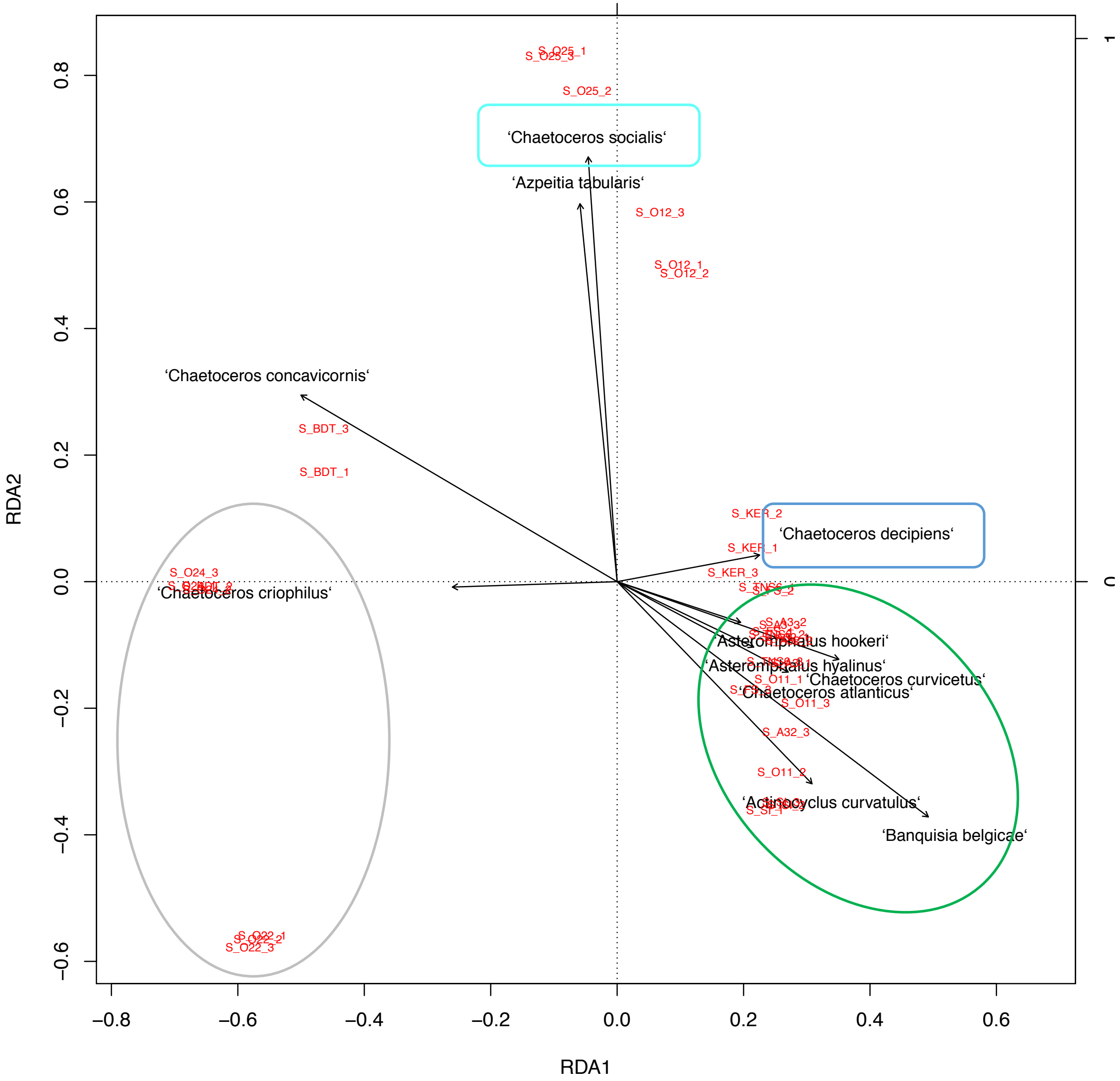
Diversity of active OTUs

# Questions

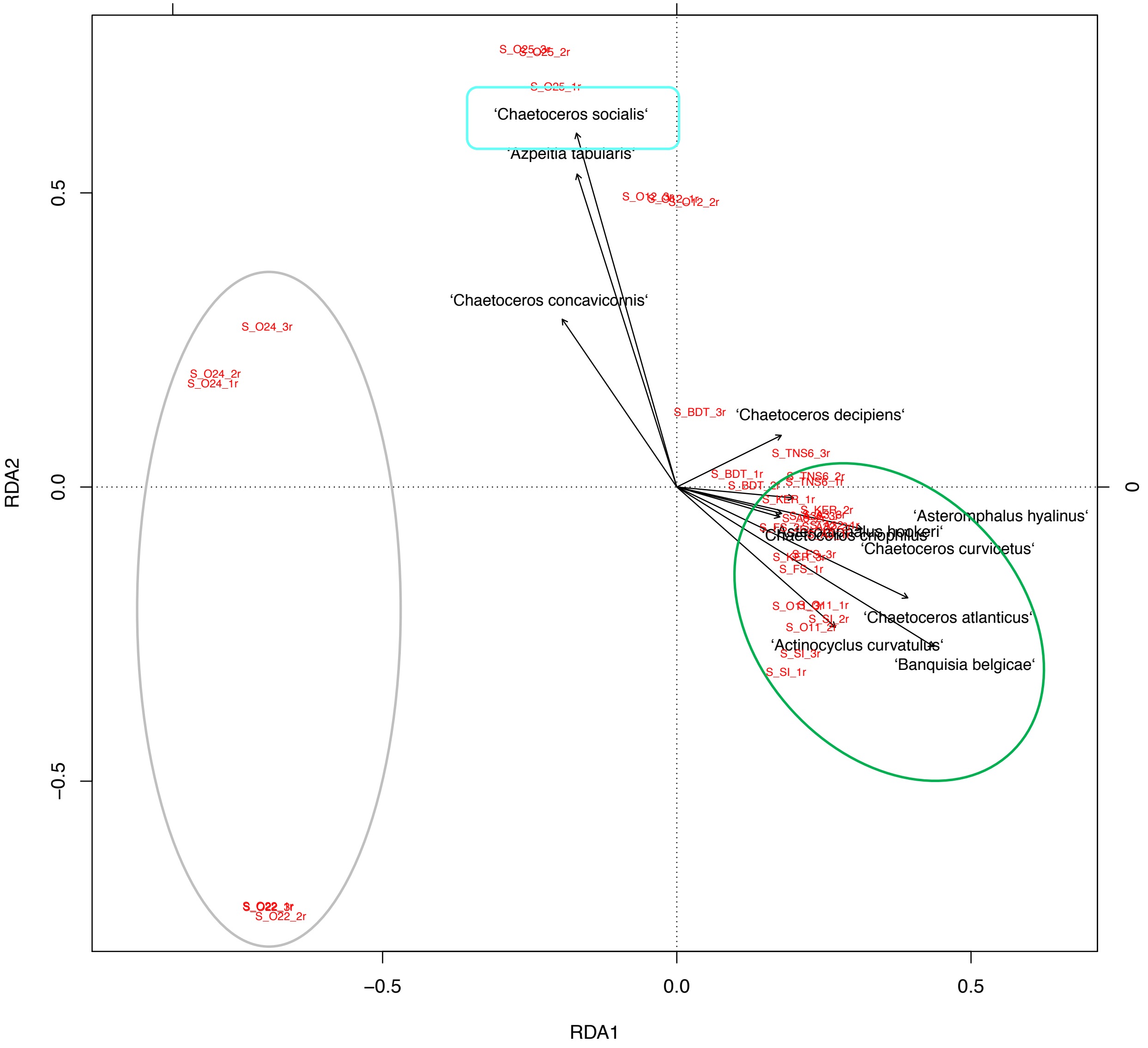
1. Can we identify the prokaryotic pattern?

2. Can we explain the prokaryotic community composition across the transect ?

# Correlations between (active) prokaryotic communities and phytoplankton species



prokaryotic communities and phytoplankton species



active prokaryotic communities and phytoplankton species

# Summary

- Prokaryotic community composition markedly changed across the transect .
- The diversity of dominant groups in total and active community composition are similar, with different relative abundance.
- Phytoplankton species has the potential effect on shifting the prokaryotic community composition.

# Ongoing work

- Reanalyze the connection between the prokaryotic communities and pigments data

- Changes in prokaryotic community composition along time series samples fixed by $HgCl_2$ and glutaraldehyde by remote automated sampler (RAS)

# Thanks for your attention