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Effets des espèces végétales et du sel de déglacage sur les communautés bactériennes et fongiques dans les biorétentions en climat froid

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Henry Beral, Danielle Dagenais, Jacques Brisson, Margit Kõiv-Vainik. Effets des espèces végétales et du sel de déglacage sur les communautés bactériennes et fongiques dans les biorétentions en climat froid. Novatech 2023, Jul 2023, Lyon, France. hal-04167770

HAL Id: hal-04167770

<https://hal.science/hal-04167770v1>

Submitted on 21 Jul 2023

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Impact of plant species and de-icing salt on microbial and fungal communities in cold climate bioretention

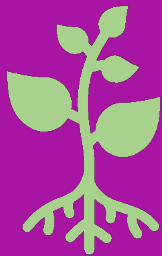
Henry Beral,

Danielle Dagenais, Jacques Brisson, Margit Kõiv-Vainik

Session: B7

06/06/2023 11:00 – 12:00

Bacterial and fungal diversity in bioretention

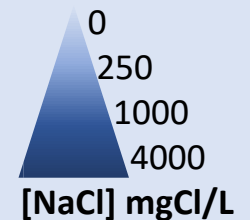
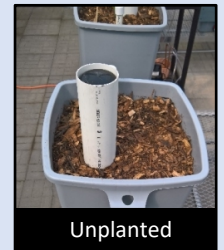
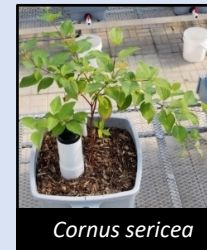
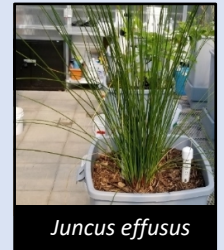
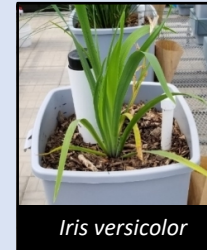


Effect of plant species?



Effect of de-icing salts?

Experimental design



12

Months of acclimatization

9

Months of maturation

4

Salt runoff application

6

Months of monitoring

Sampling : Initial



Nursery pot
(soil + rhizosphere)



Substrate for BR
Savaria Inc.



Inoculum
MykePro landscape



01/06/2018

Initial

12

Months of acclimatization

9

Months of maturation

4

Salt runoff application

6

Months of monitoring

Sampling : Before Salt

5 repetitions of the 5 treatments:

- UC = Unplanted control
- CS = *Cornus sericea*
- IV = *Iris versicolor*
- JE = *Juncus effusus*
- SA = *Sesleria autumnalis*

Randomized complete block design



Soil + rhizosphere from soil cores at 10 cm depth



28/02/2020

Before Salt

Initial

12

Months of acclimatization

9

Months of maturation

4

Salt runoff application

6

Months of monitoring

Sampling : After Salt

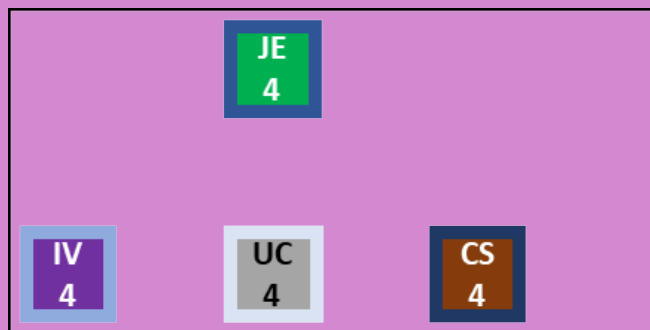
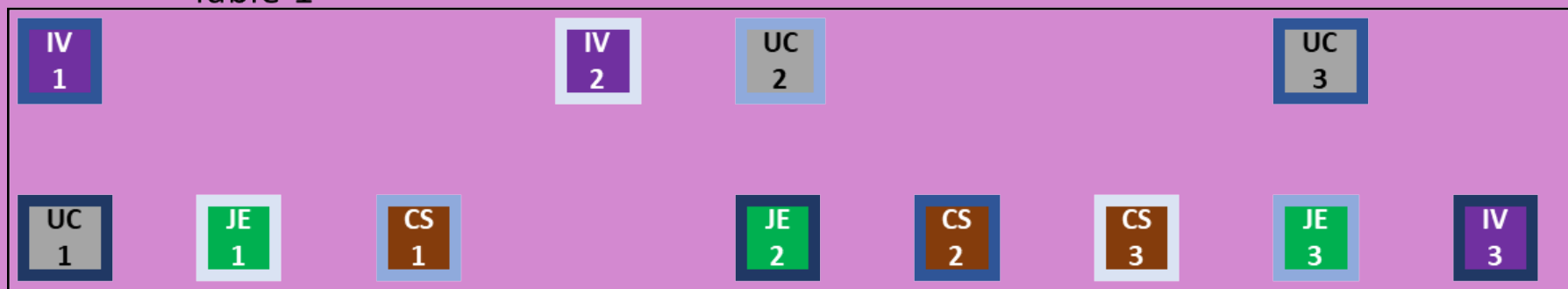


Table 2
Table 1

Each plant treatment received one of the 4 [NaCl]

- 0 mgCl/L
- 250 mgCl/L
- 1000 mgCl/L
- 4000 mgCl/L

(Latin square)



Initial

Before Salt

25/08/2020

After Salt

12

9

4

6

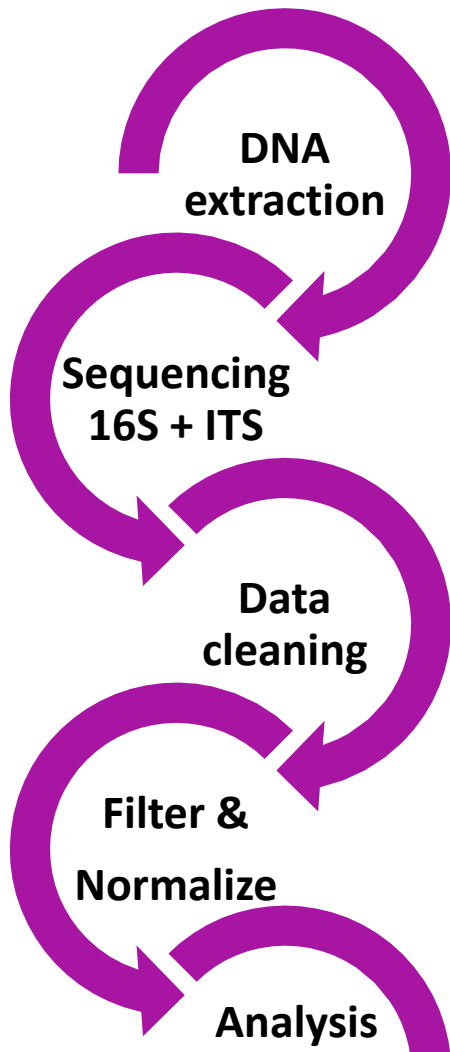
Months of acclimatization

Months of maturation

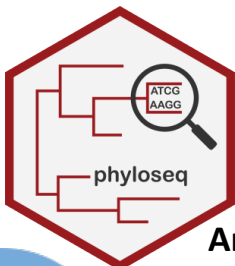
Salt runoff application

Months of monitoring

Analysis



- Filter & trim
- Inference
- Merge
- Chimeras
- Assign taxonomy

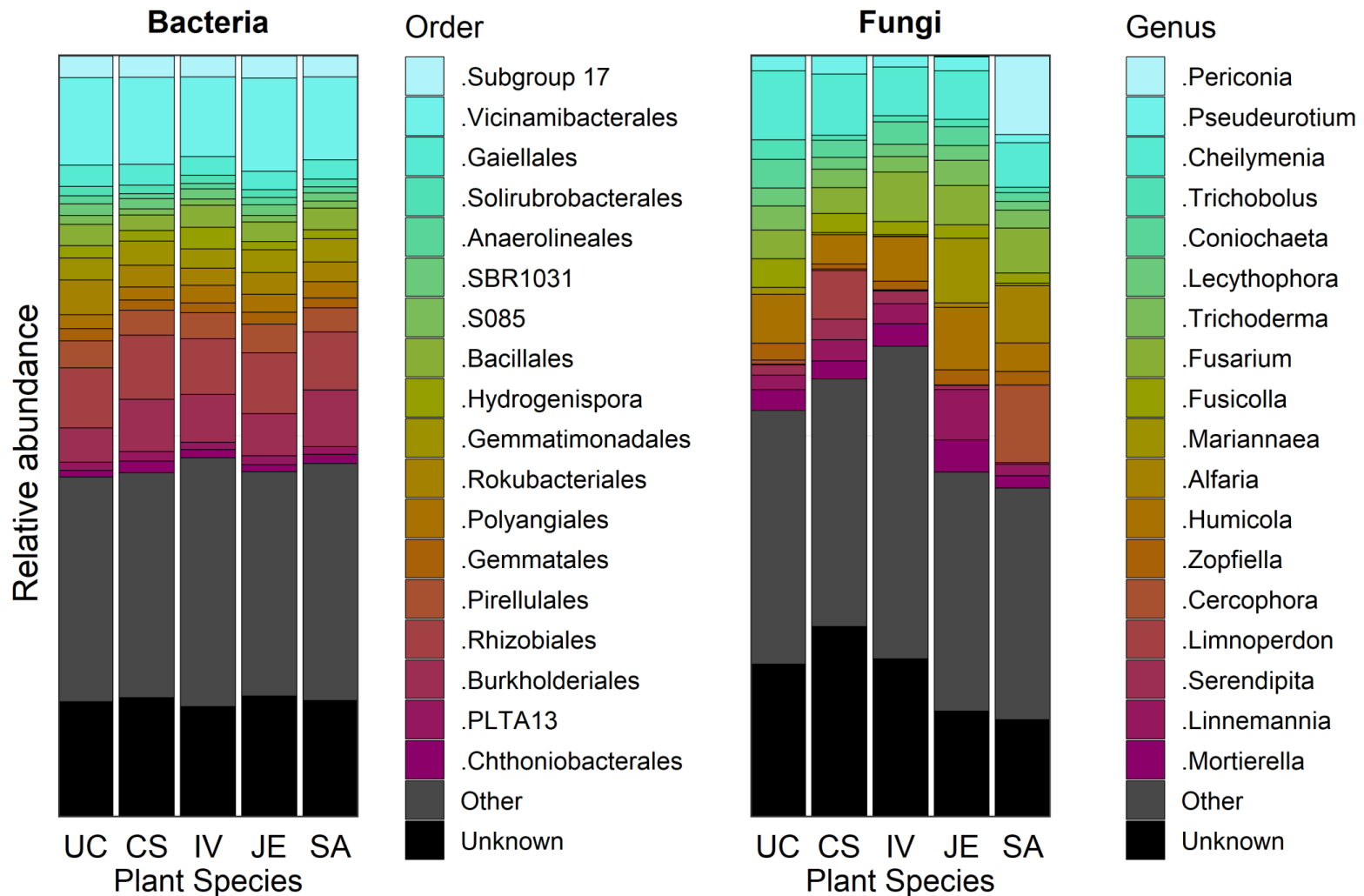


- Artefacts
- Prevalence
- Rarefaction
- VST

Results

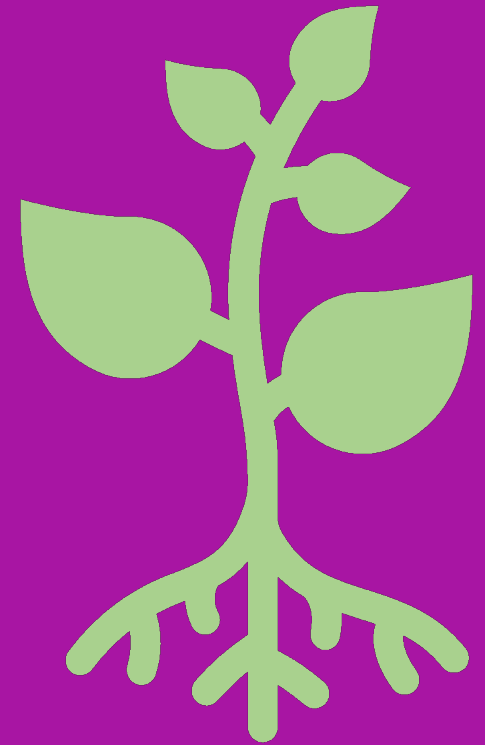
General portrait

Before salt: Bacterial and fungal top 20

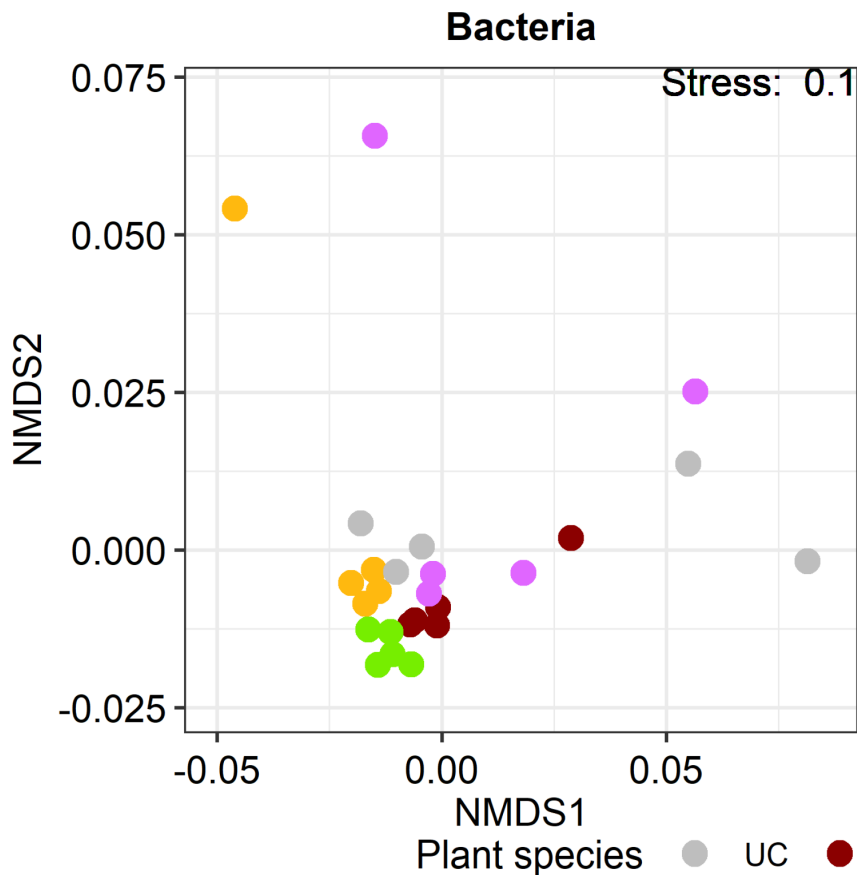


Results

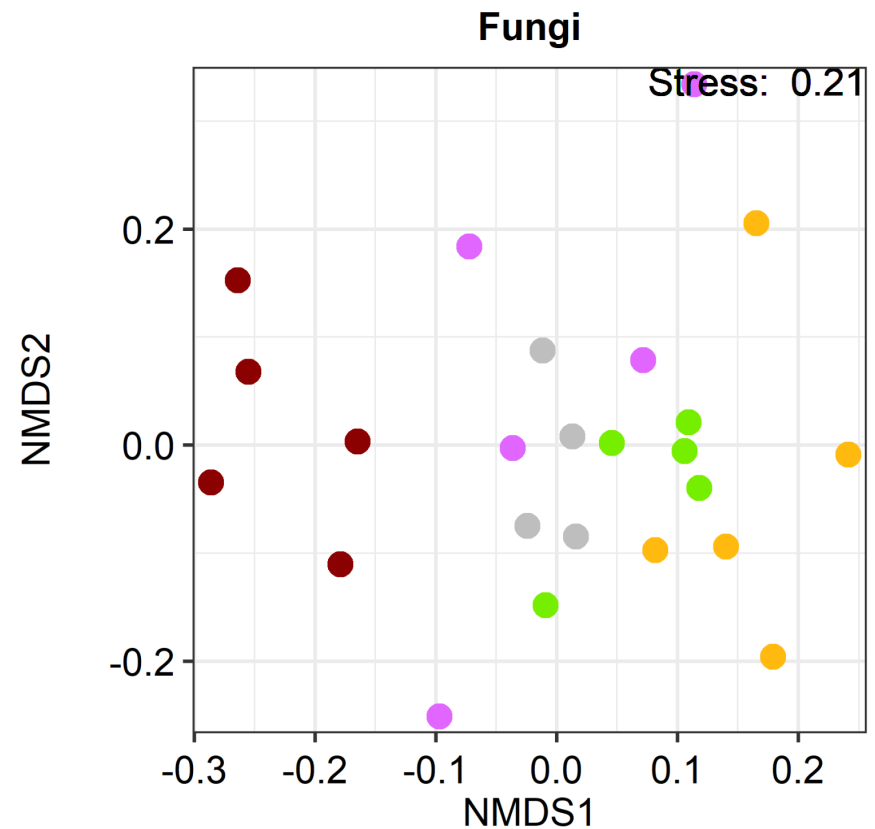
Effect of Plants



Before salt: β diversity (nMDS)



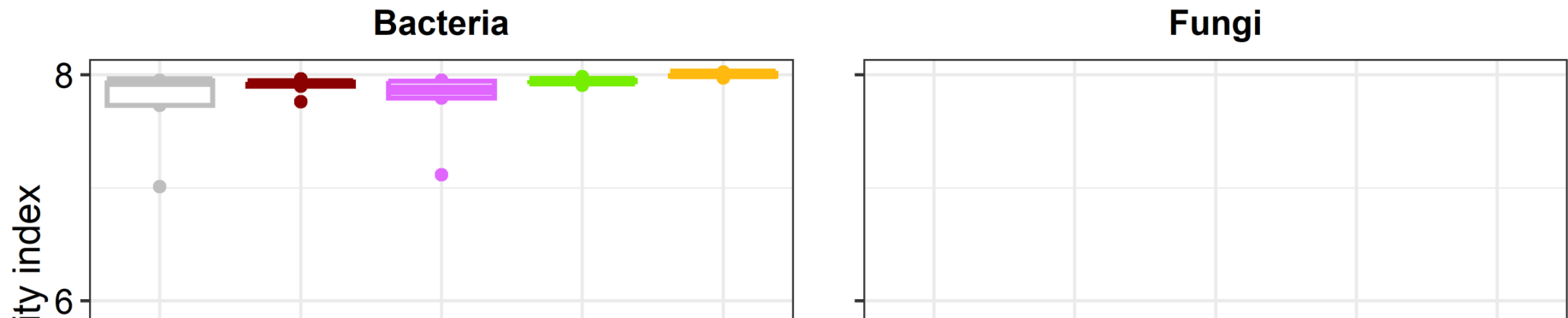
JE \neq CS \neq IV = SA \approx UC



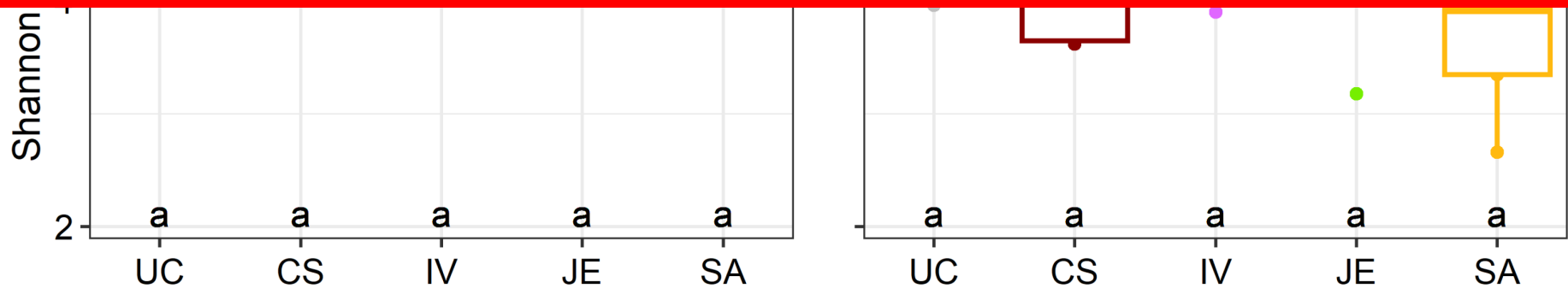
All species \neq

Plant species changed bacterial and fungal communities

Before salt: α diversity (Shannon index)



If the \neq in β div. were not explained by a change in α div.
Then, the β div. \neq must be explained by the ASVs identity present



Plant species didn't change alpha bacterial and fungal diversity (richness/uniformity)



Before salt: Differential abundance 16S

Cornus

- + Propionibacteriales, Chloroplast
- Nitrososphaerales

Iris

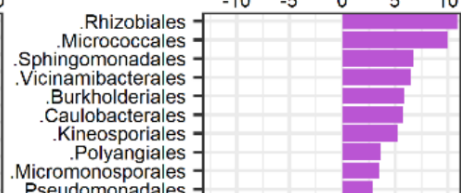
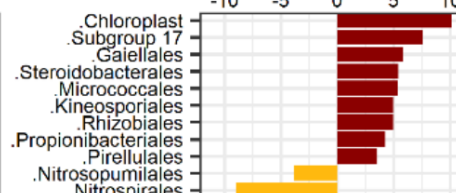
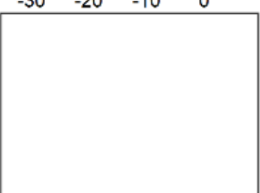
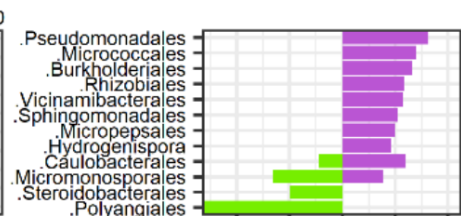
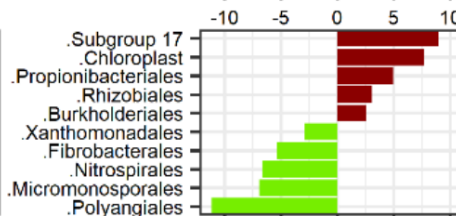
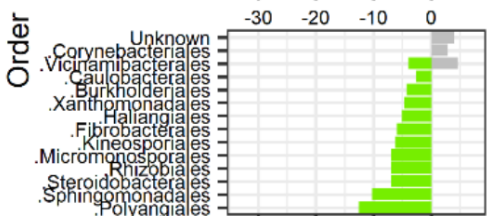
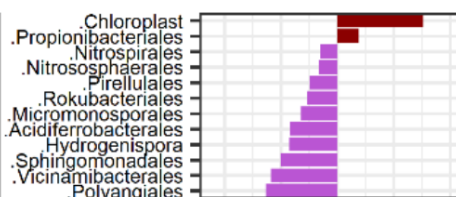
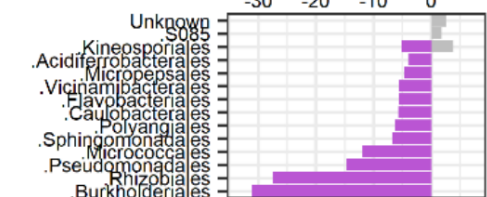
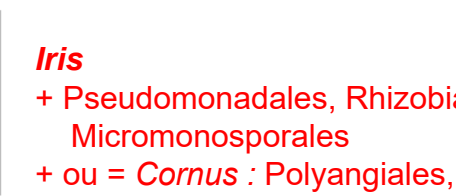
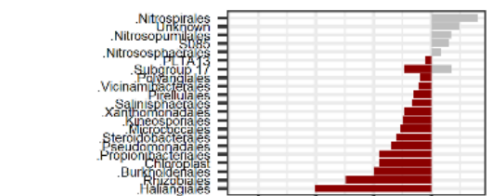
- + Pseudomonadales, Rhizobiales, Micrococcales, Burkholderiales, Caulobacterales, Micromonosporales
- + ou = *Cornus* : Polyangiales, Vicinamibacteriales, sphingomonadales,

unplanted = *Sesleria*

- + unknow
- Burkholderiales, Rhizobiales, Polyangiales
- ≠ or - Vicinamibacteriales and Kineosporiales

Juncus

- + Polyangiales & Micromonosporales
- or = *Cornus* : Steroidobacteriales



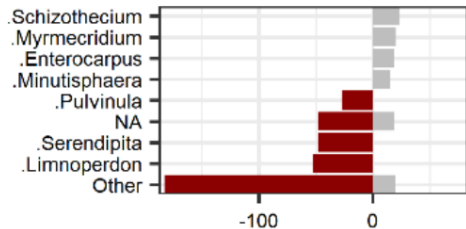
Log2 Fold Change

Before salt: Differential abundance ITS



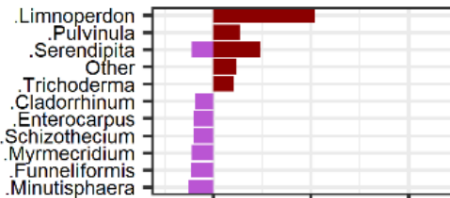
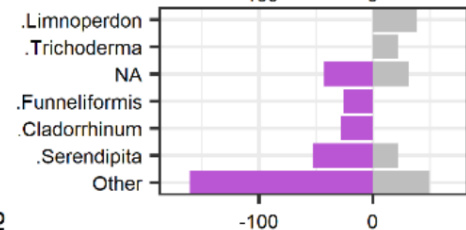
Juncus

- *Aspergillus*, *Mariannaea*



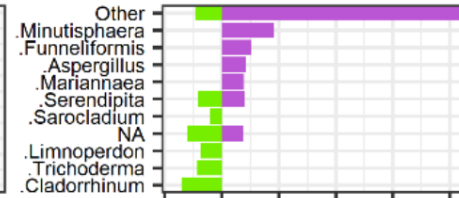
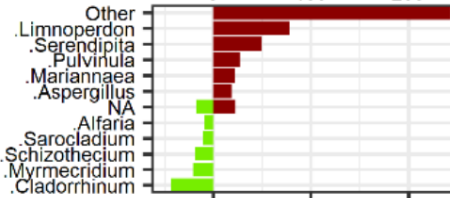
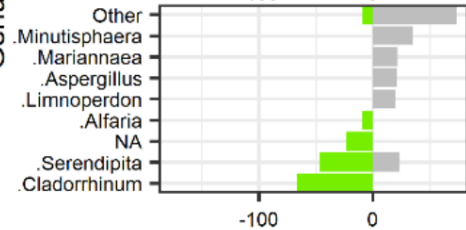
Cornus

+ *Limnoperdon*, *Serendipita*, *Pulvinula*
- *Schizothecium*



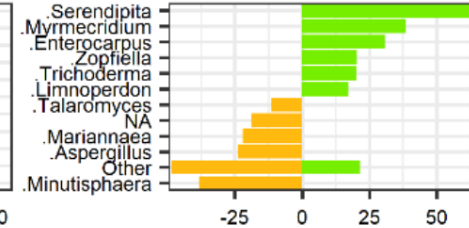
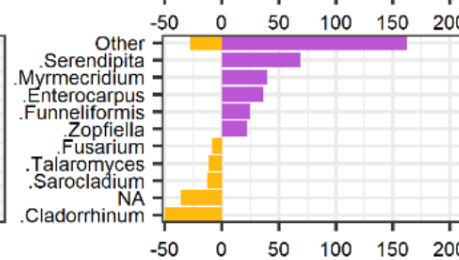
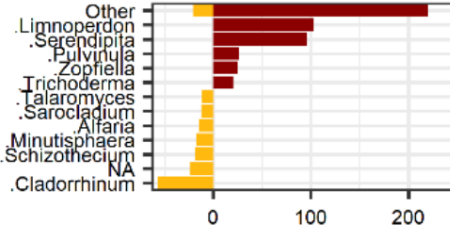
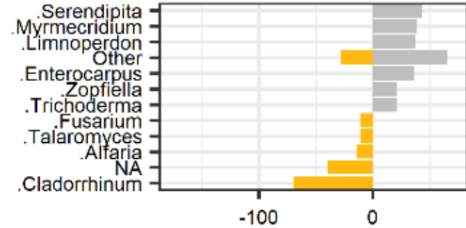
Sesleria

+ NA, *Talaromyces*
- *Serendipita*, *Zopfiella*



Iris

+ ou = *Cornus*
Funneliformis



Log2 Fold Change

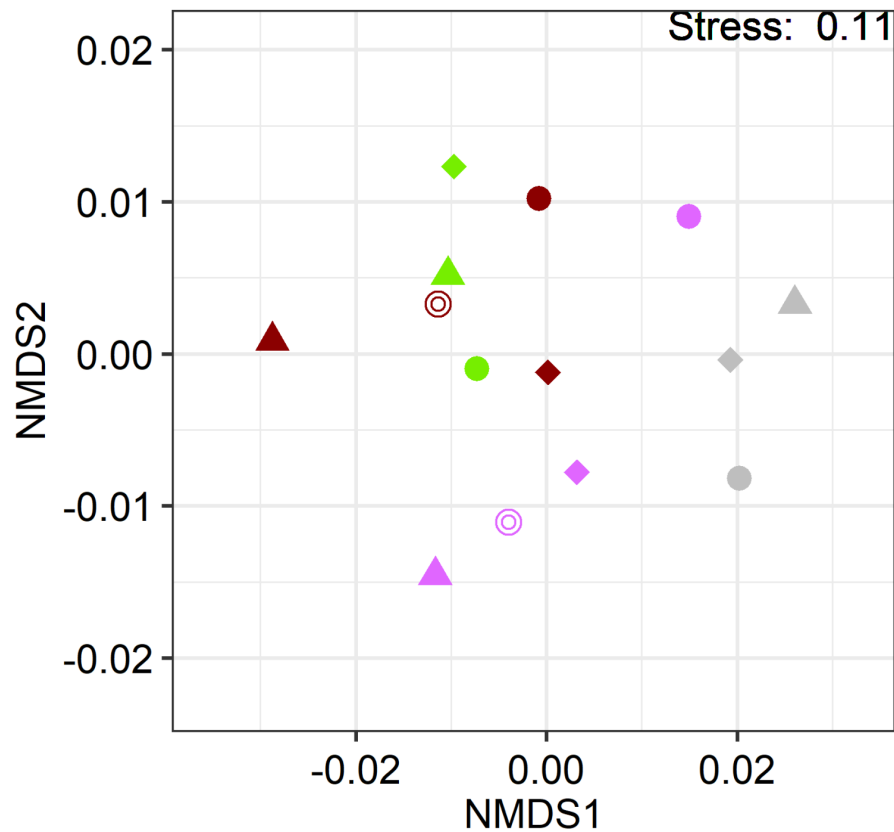
Results

Effect of NaCl

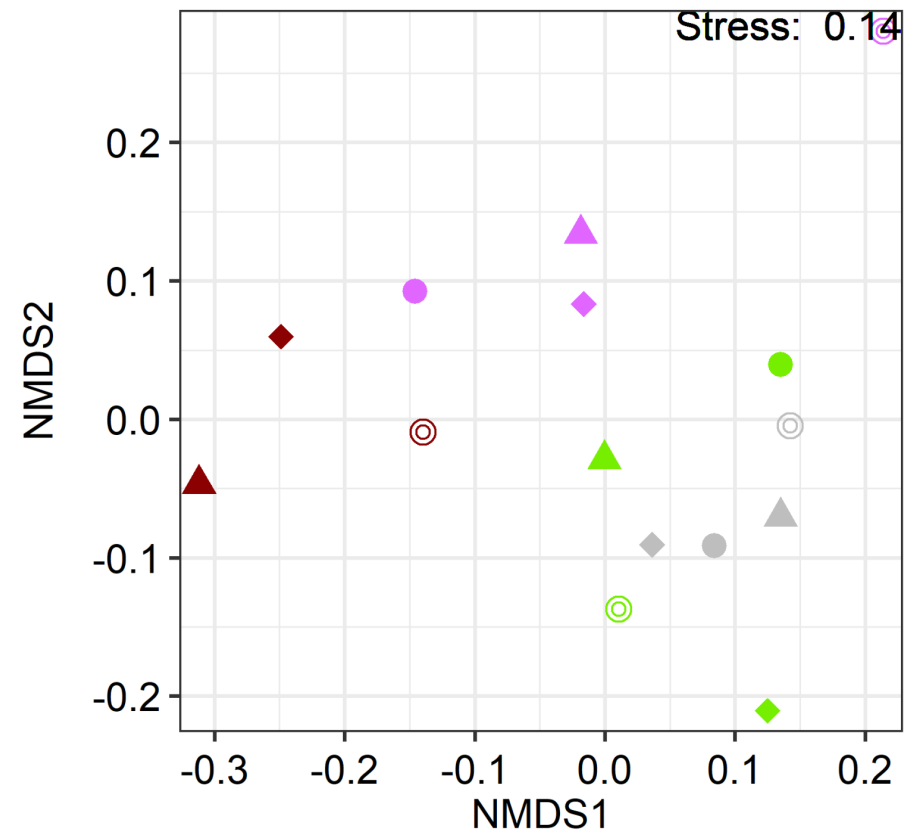


After Salt: β diversity (nMDS)

Bacteria



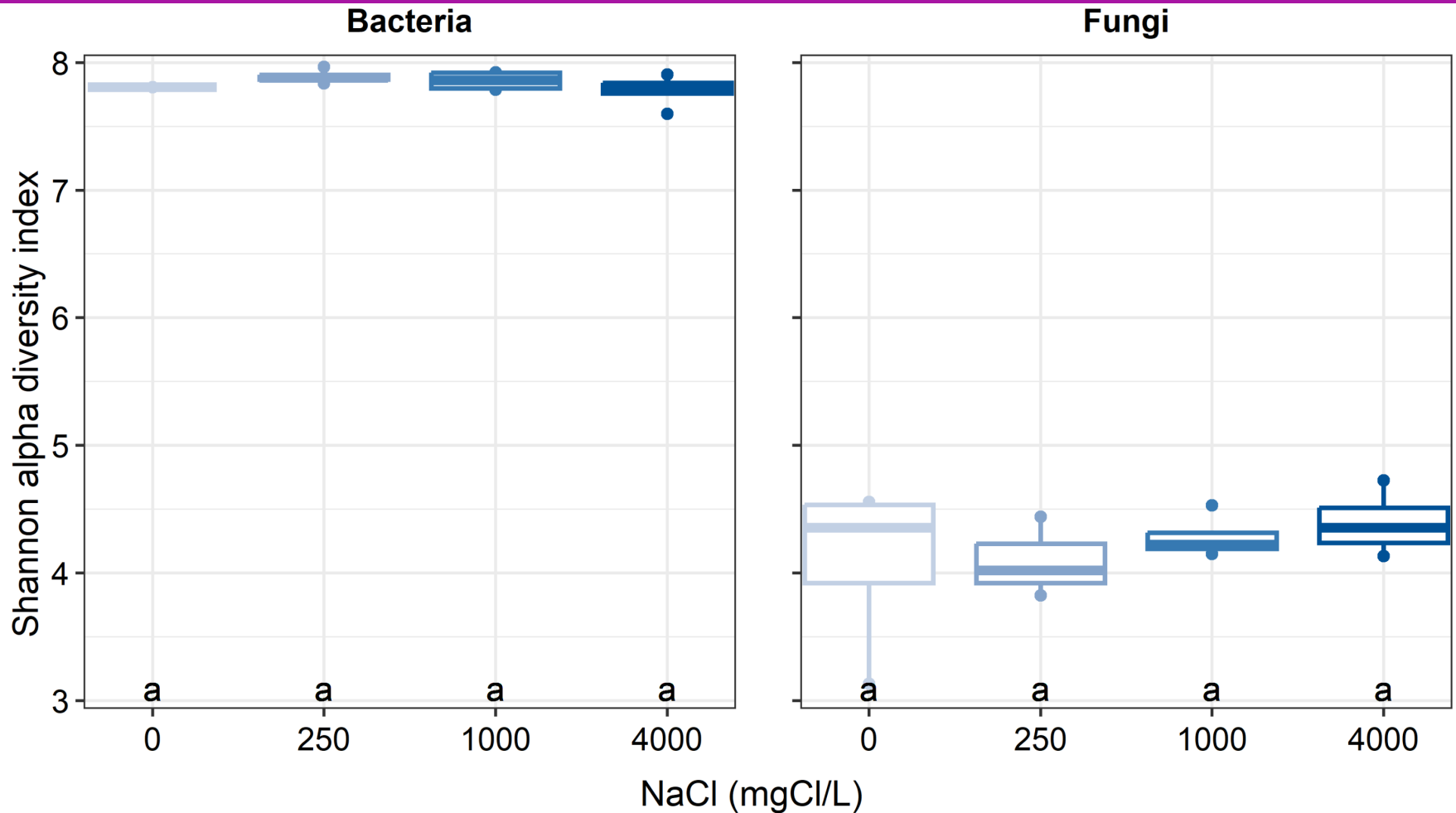
Fungi



Plant species ● UC ● CS ● IV ● JE NaCl (mgCl/L) ⊙ 0 ● 250 ◆ 1000 ▲ 4000

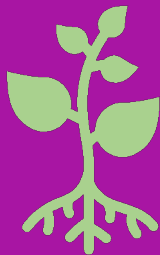
No significant effect of NaCl on communities

After Salt: α diversity



No significant \neq in α div. between the tested NaCl concentrations

Bacterial and fungal diversity in bioretention



Plant species selected
some specific taxa.

Impact on BR performance?



No effect of de-icing salts

Tolerated or recovered?

thank you for your
attention

Any questions?

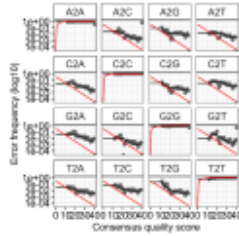
Henry.beral@umontreal.ca

Analysis



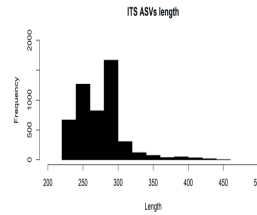
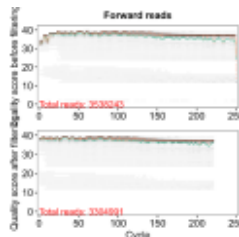
DNA
extraction

16S + ITS
sequencing



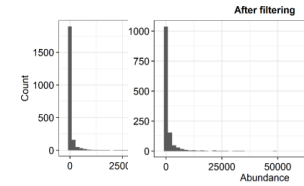
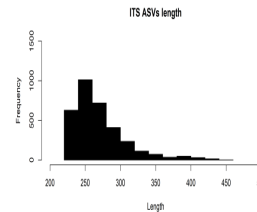
Inference

Filter &
trim



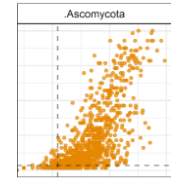
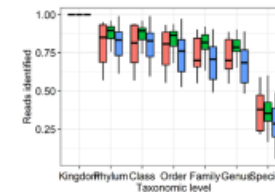
Merge
paired
reads

Remove
chimeras



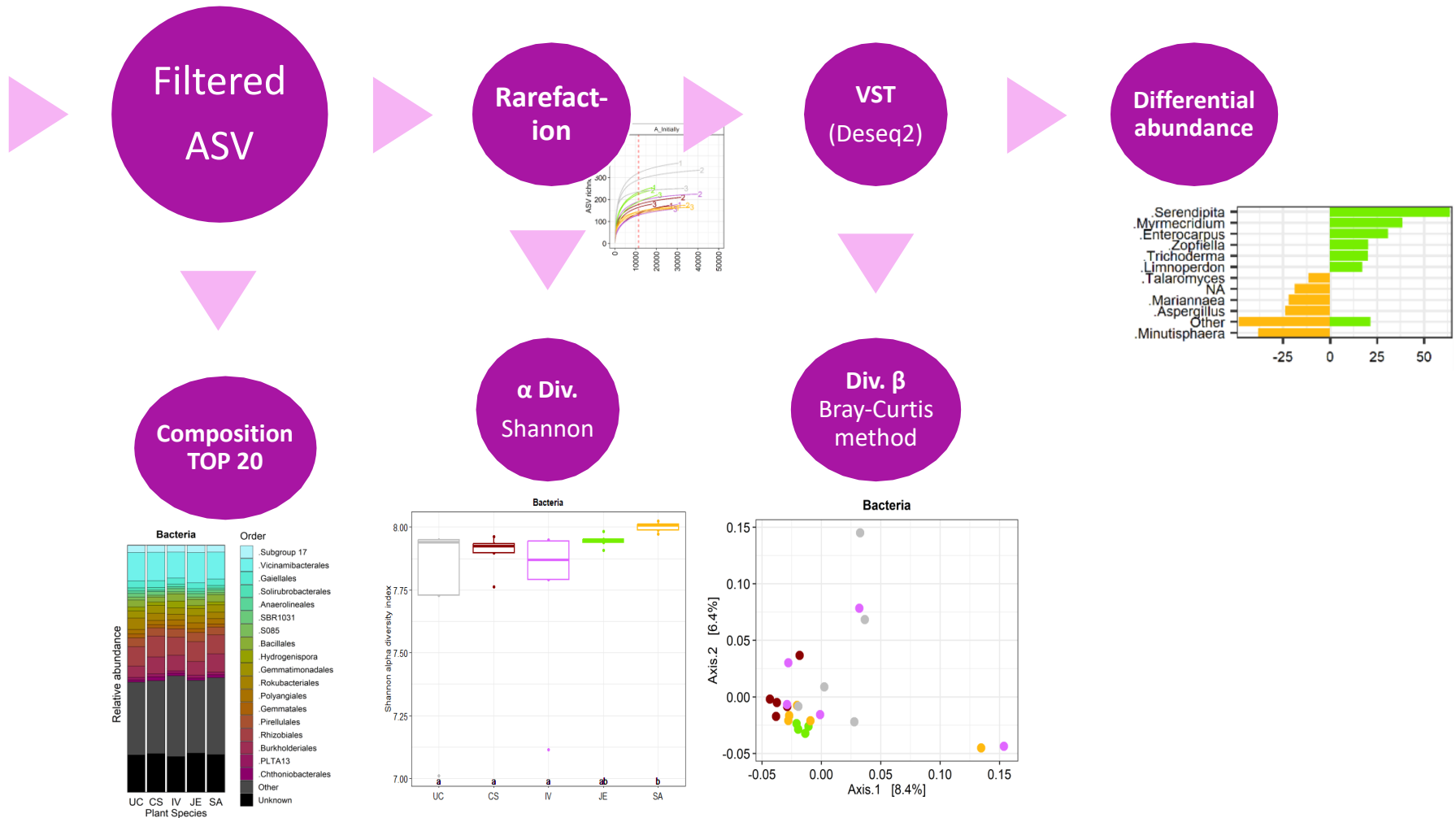
Filter
artefacts

Assign
taxonomy
Silva &
UNITE

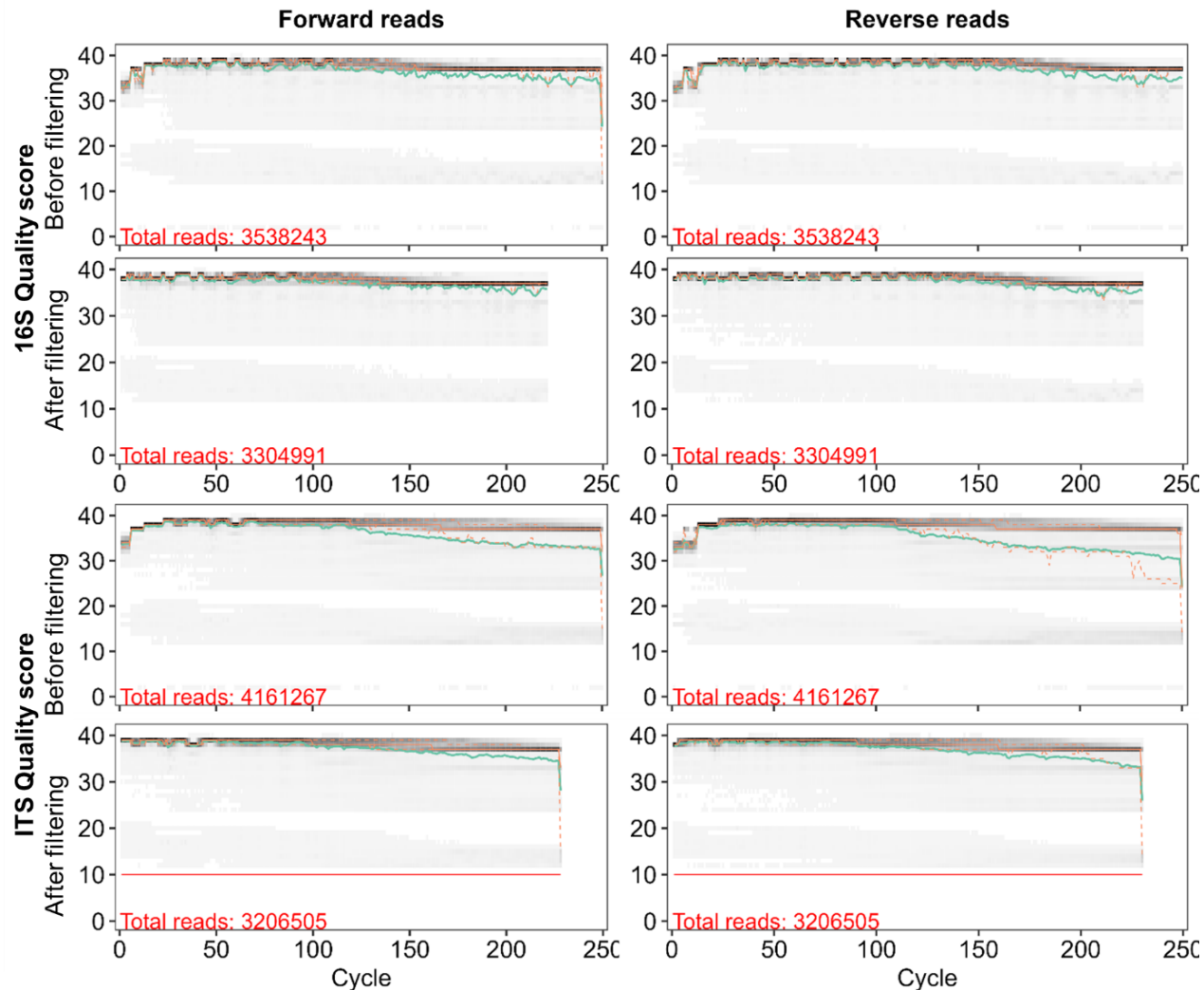


Filter
weakly
represented

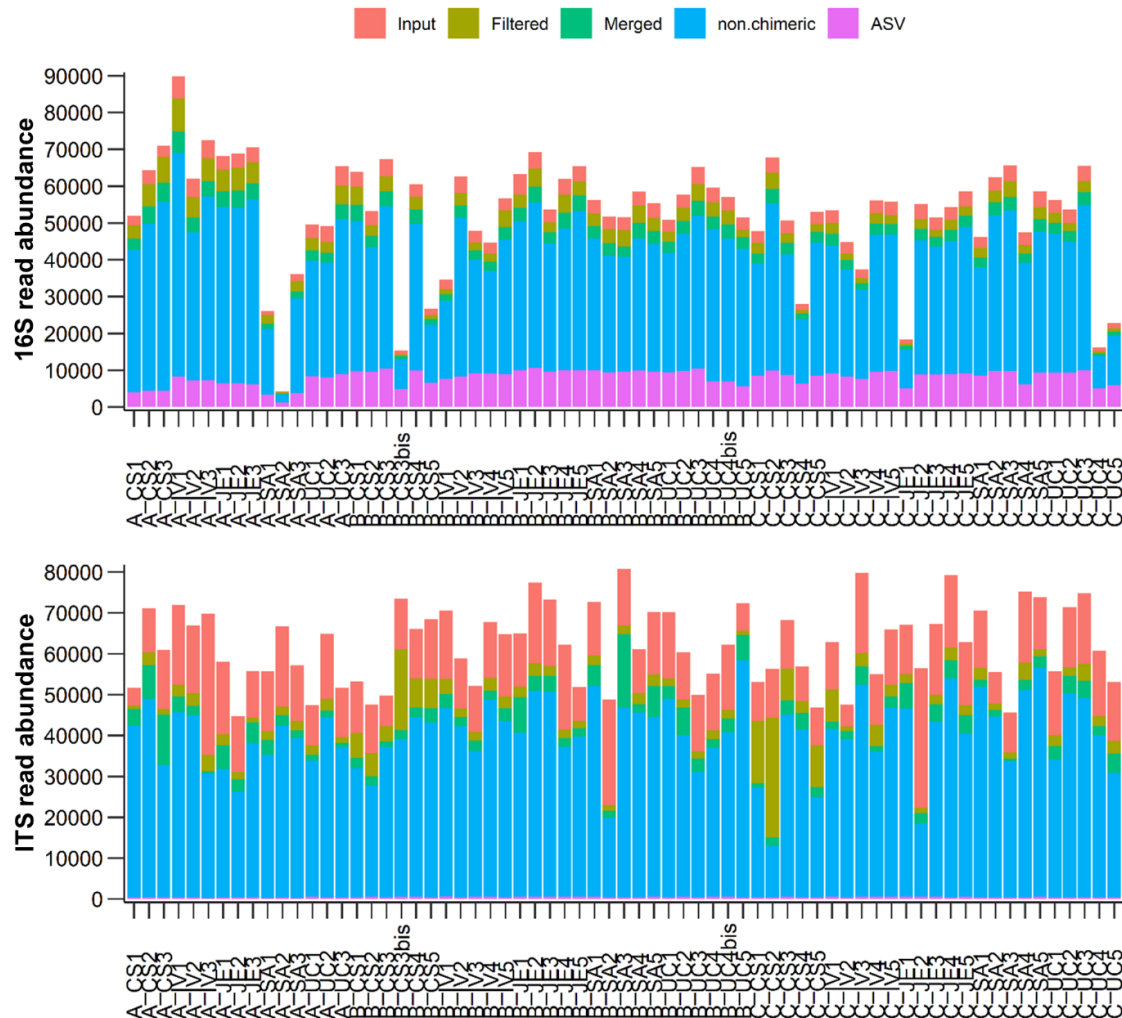
Analysis



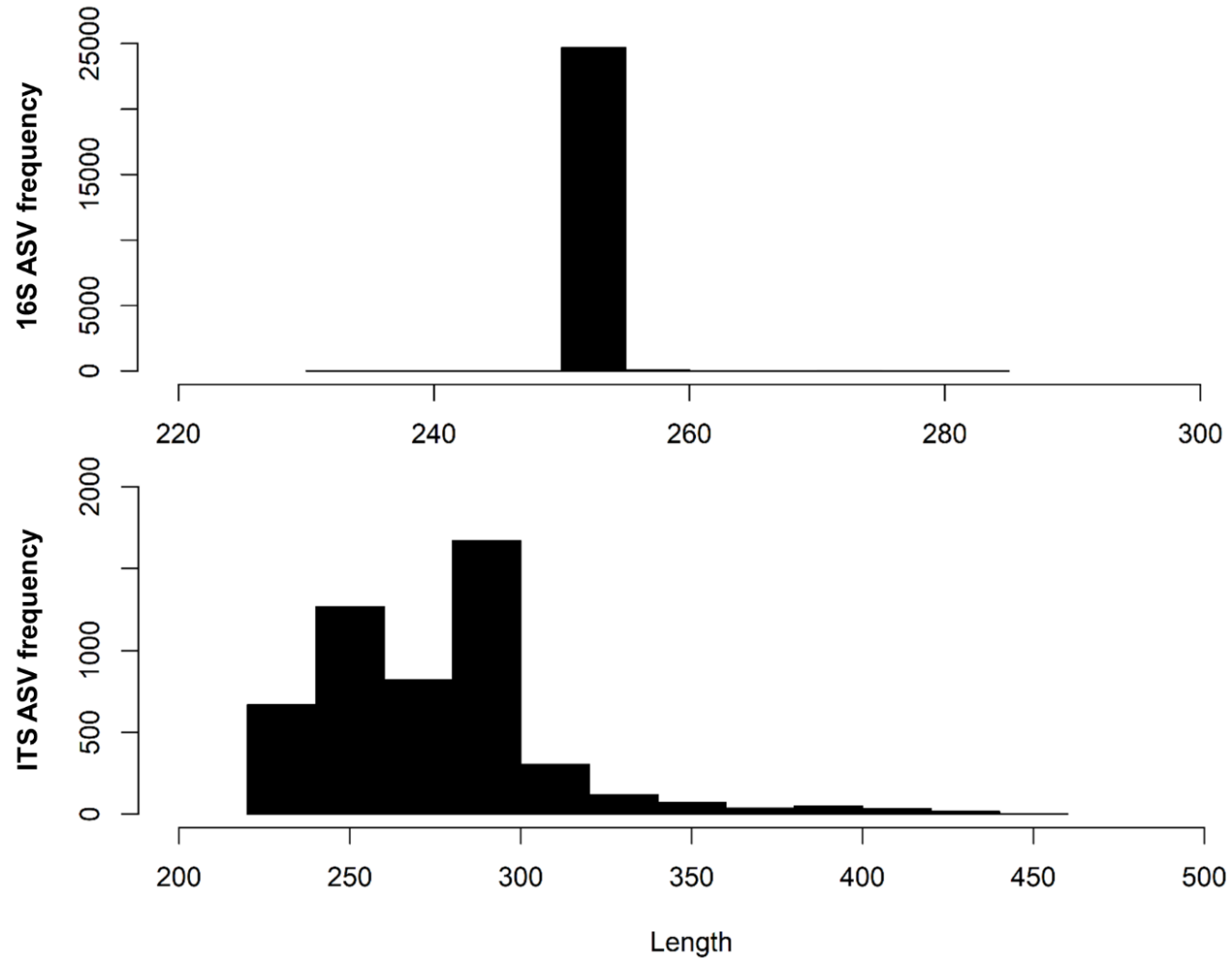
16S and ITS quality profile of the 67 aggregated samples before or after filtering.



16S and ITS reads passed through each stage of the pipeline for each sample

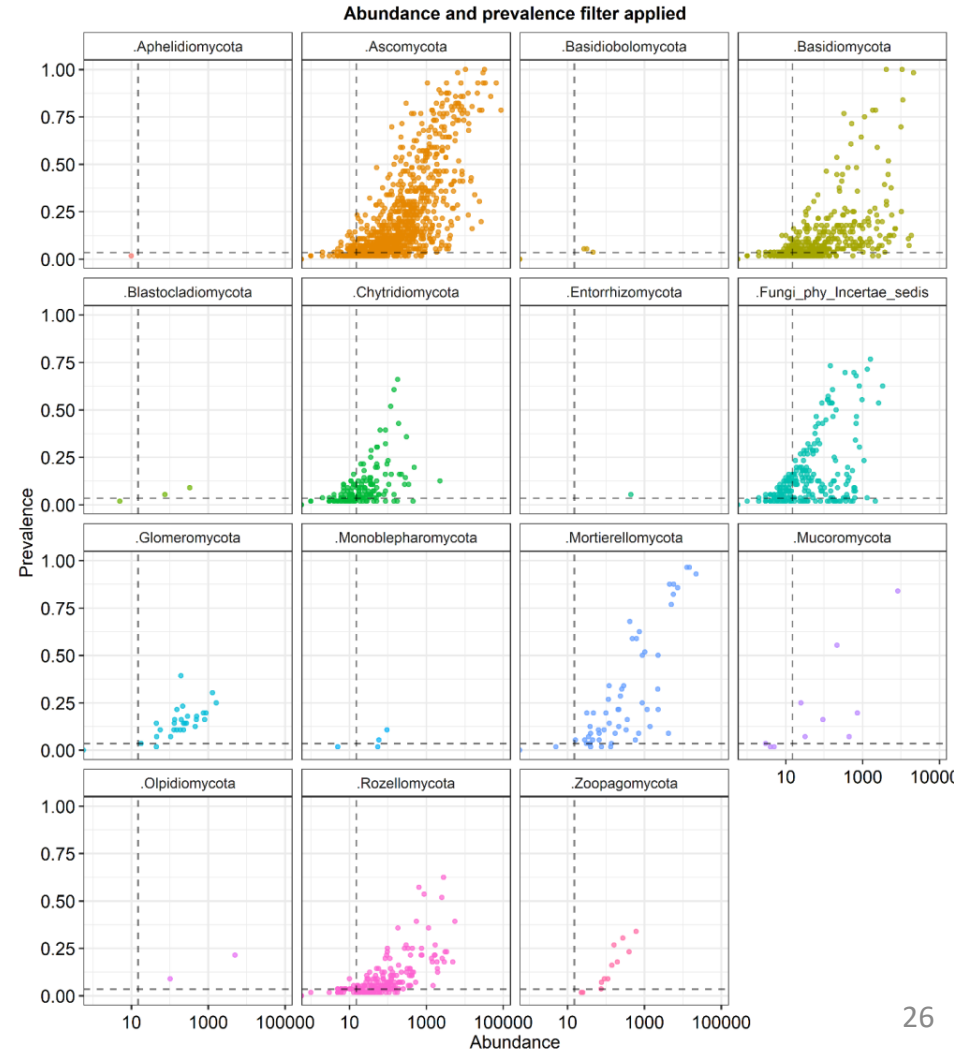
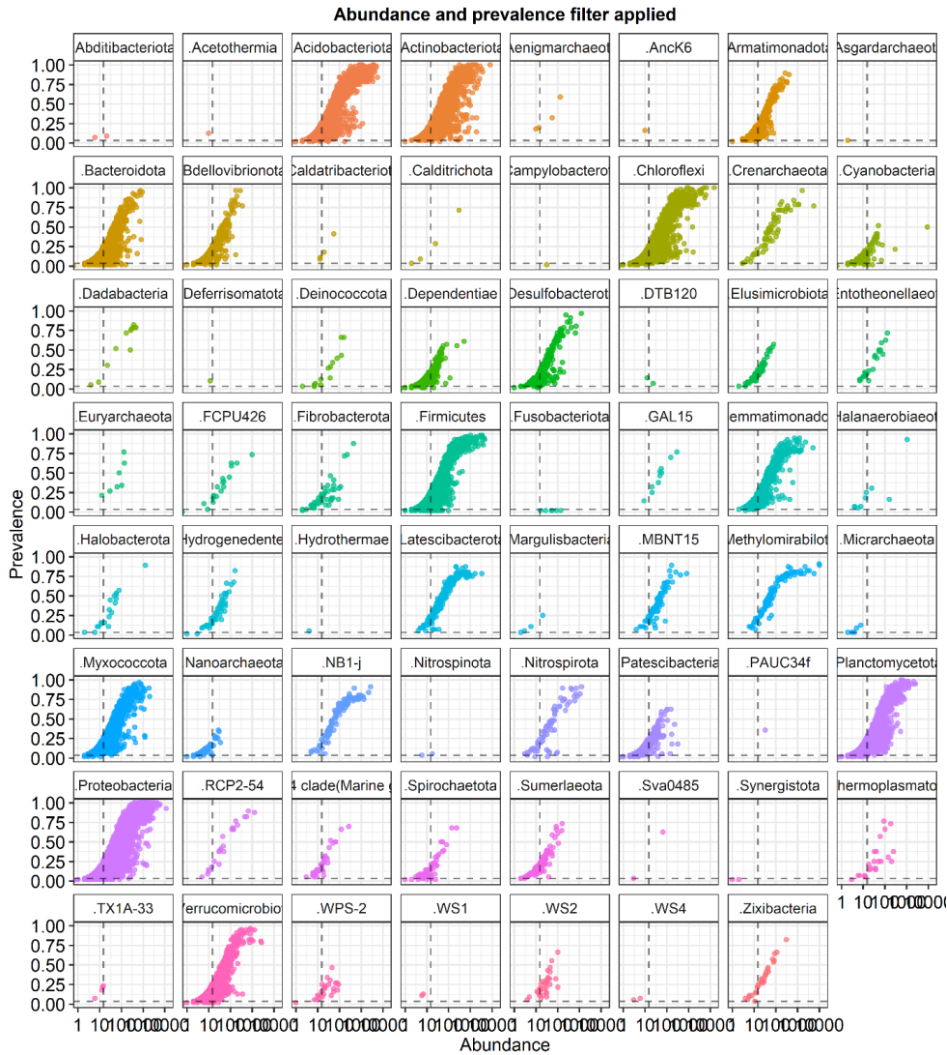


16S and ITS ASVs length frequency.

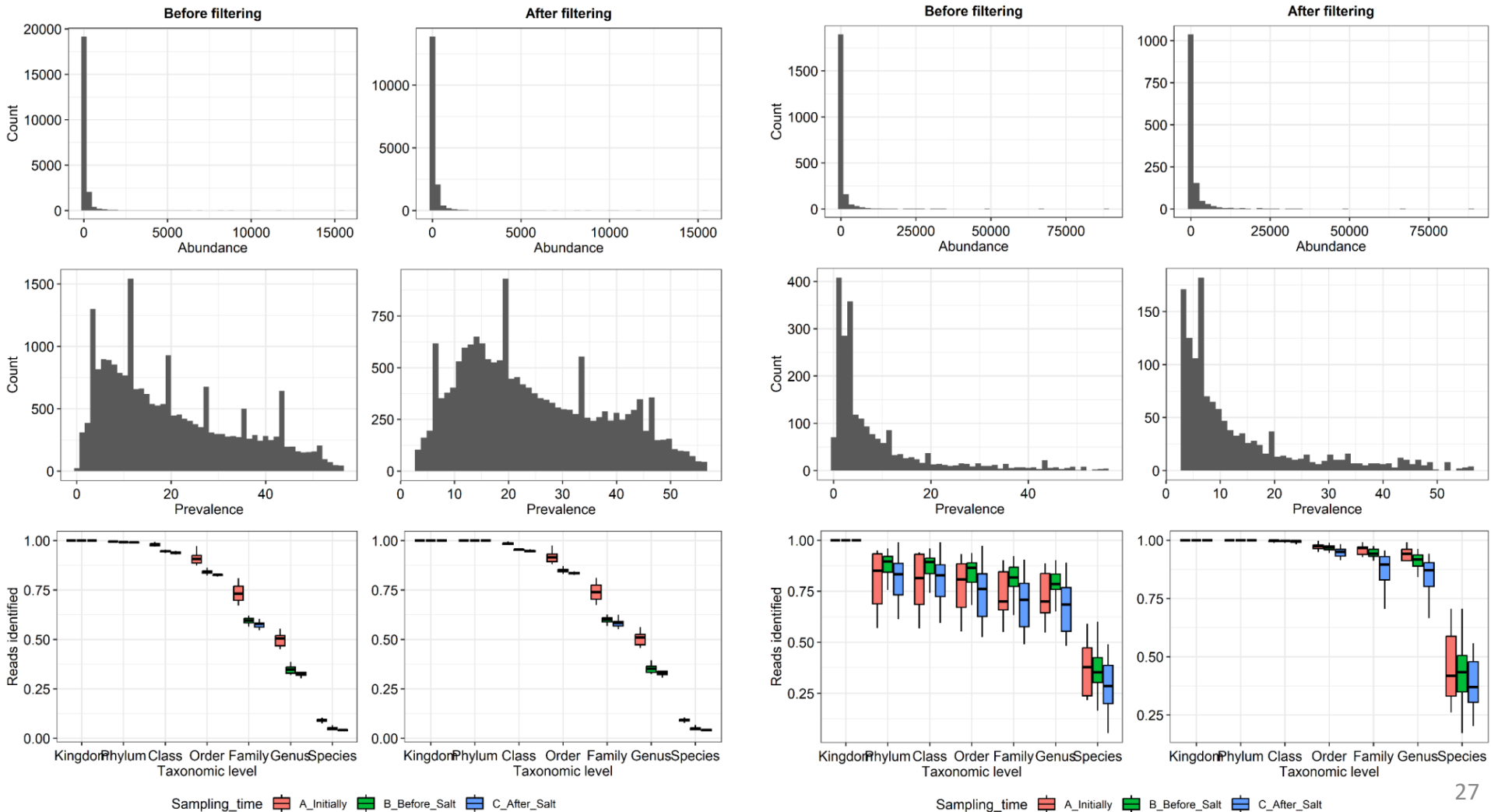


16S and ITS ASVs prevalence by abundance in each phylum (colors).

The dotted lines represent the filters threshold



16S and ITS ASVs ASVs number and proportion of reads assigned by taxonomic level before or after filtering.



16S and ITS rarefaction curves

