UNICAMP

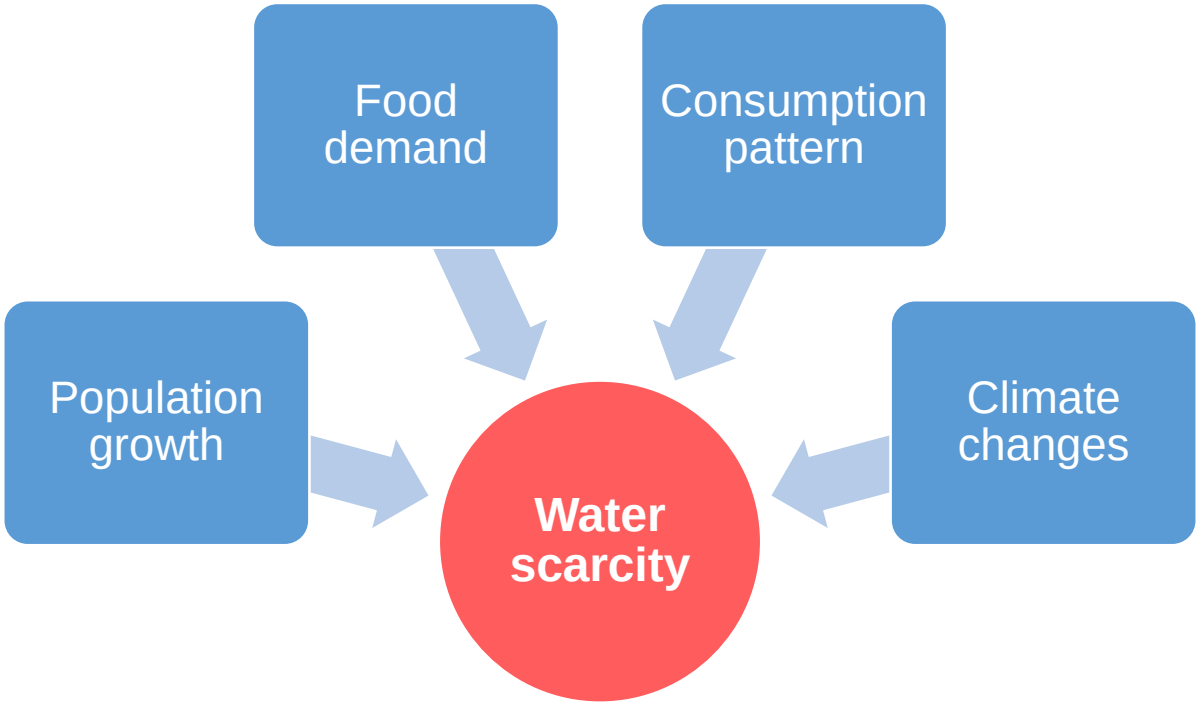
GRUPO DE PESQUISA EM TRATAMENTO DE EFLUENTES E RECUPERAÇÃO DE RECURSOS

Impact of safe wastewater reuse in agriculture on soil properties and crop yield

Lays LEONEL

FAPESP

Background



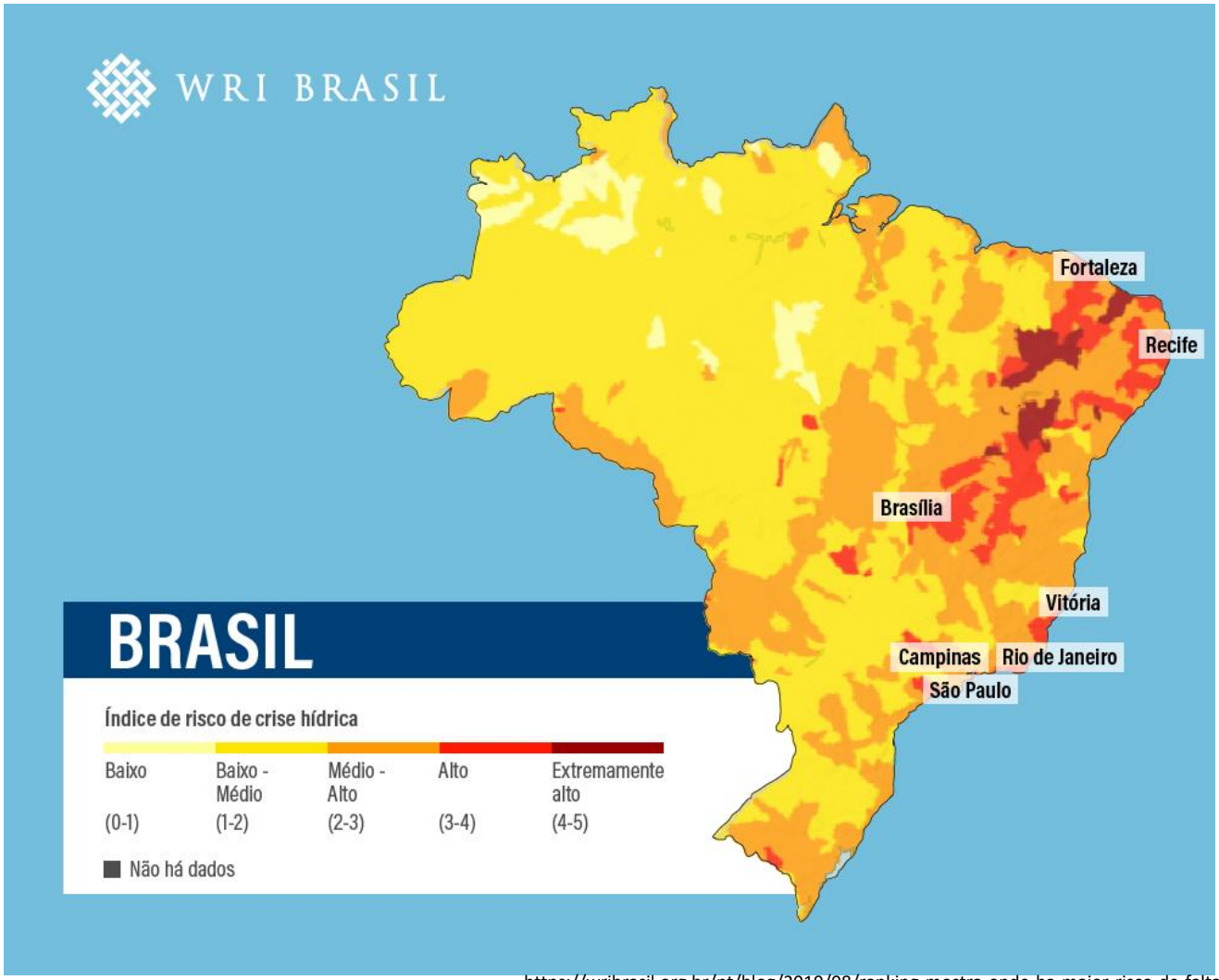
WWAP, 2017; Ricart; Rico, 2019

Background

- UN: water reuse practice fundamental tool to achieve SDG;
- (United Nations, 2016). And the agricultural sector, as the main consumer of the water available portion on Earth (70% of water global uses), plays an important role in the integrated water management plan (WWAP, 2019).
- Agricultural sector is the main water consumer → 70% of water global use
- Wastewater reuse → alternative to supply the agricultural sector demand
- Common practice in arid and semi-arid regions → wastewater treatad or not
- It is not common in Brazil.

WWAP, 2019;

Background



https://wribrasil.org.br/pt/blog/2019/08/ranking-mostra-onde-ha-maior-risco-de-faltar-agua-no-brasil-e-no-mundo

Background

Cantareira system: water source for 7 mi people

Background

Iguaçu Falls

Background

Concerns

- Public health
- Impacts on crop yield
- Soil health

Wastewater reuse in agriculture

Advantages

- Supply the water demand
- Reduce the water ecosystems degradation
- Wastewater as a valuable resource instead of a waste

IBEKWE; GONZALEZ-RUBIO; SUAREZ, 2018, BECERRA-CASTRO et al., 2015; BIXIO et al., 2006; TOZE, 2006

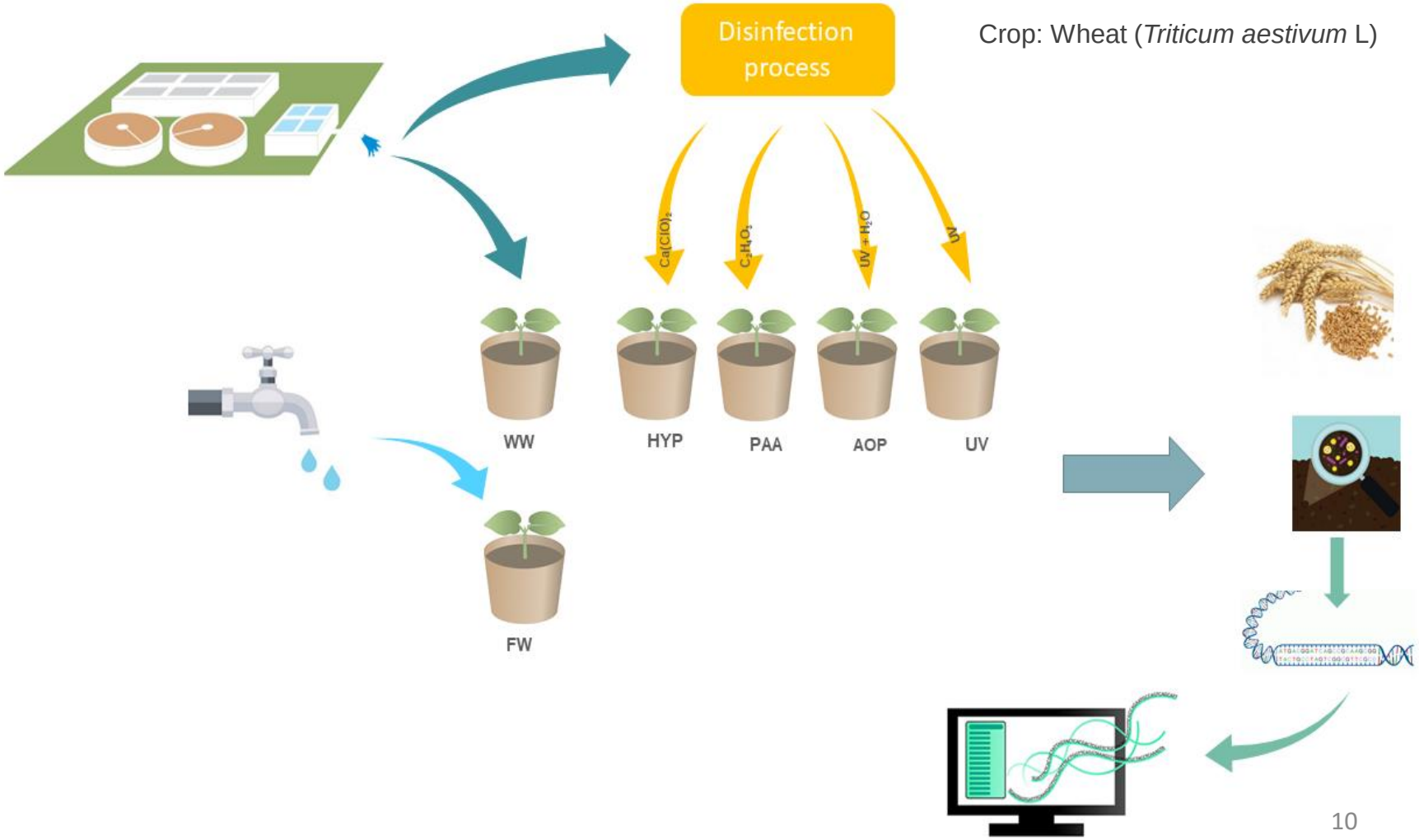
Background

- Big challenge: a disinfectant effective in inactivating pathogen resistant form and not generating harmful by-products for the soil and for the crop production

Aim

The aim of the research was to evaluate the impact caused by agricultural reuse of treated and disinfected wastewater on the soil physicochemical properties, on soil microbiota diversity and on the crop yield in a short term.

Method



Crop: Wheat (*Triticum aestivum* L)

Method

- Pot assay
- Greenhouse
- Wheat (*Triticum aestivum* L)
- 6 treatments: WW, FW, HYP, PAA, UV, AOP
- Irrigation: twice a day

Method

Effluent

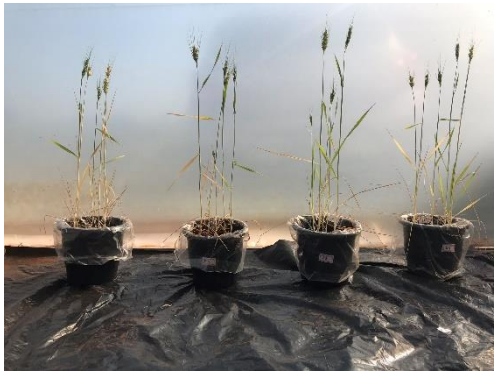
- Effluent collection and reservoir supplied once a week.

Parameters	WW	HYP	PAA	AOP	UV
COD (mg/L)	62.5	85.2	150.5	95.0	72.5
TOC (mg/L)	14.8	18.1	45.7	15.7	19.2
N (mg/L)	58.0	68.0	56.0	54.0	49.0
P (mg/L)	4.4	4.3	4.9	5.6	4.2
EC (dS/m)	0.75	0.78	0.74	0.74	0.75
pH	8.0	7.8	7.1	8.1	8.0
Turbidity	8.1	7.9	8.0	10.0	9.5

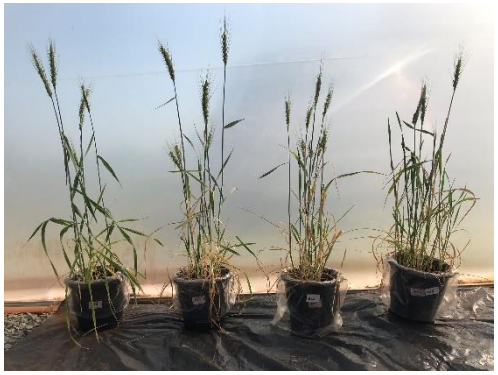
Results – Crop yield

46 days after planting

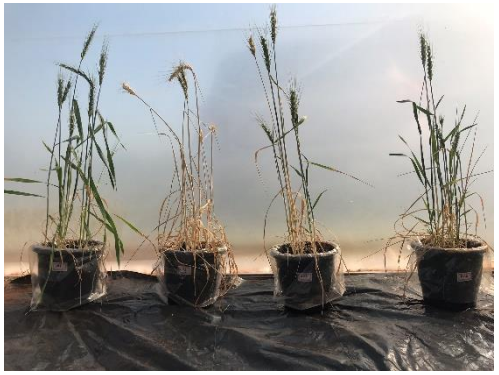
Results



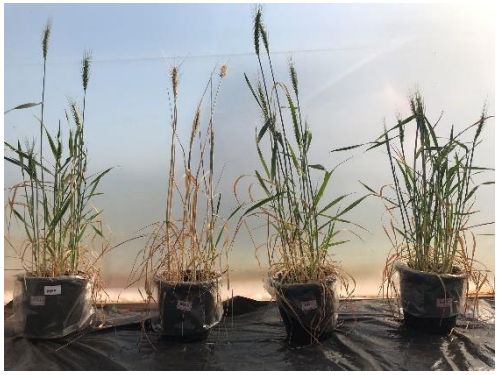
FW



WW

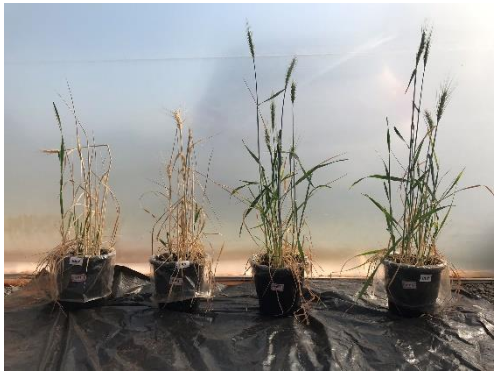


UV



PAA

AOP



HYP

88 days after planting

Results

The end of the crop cycle

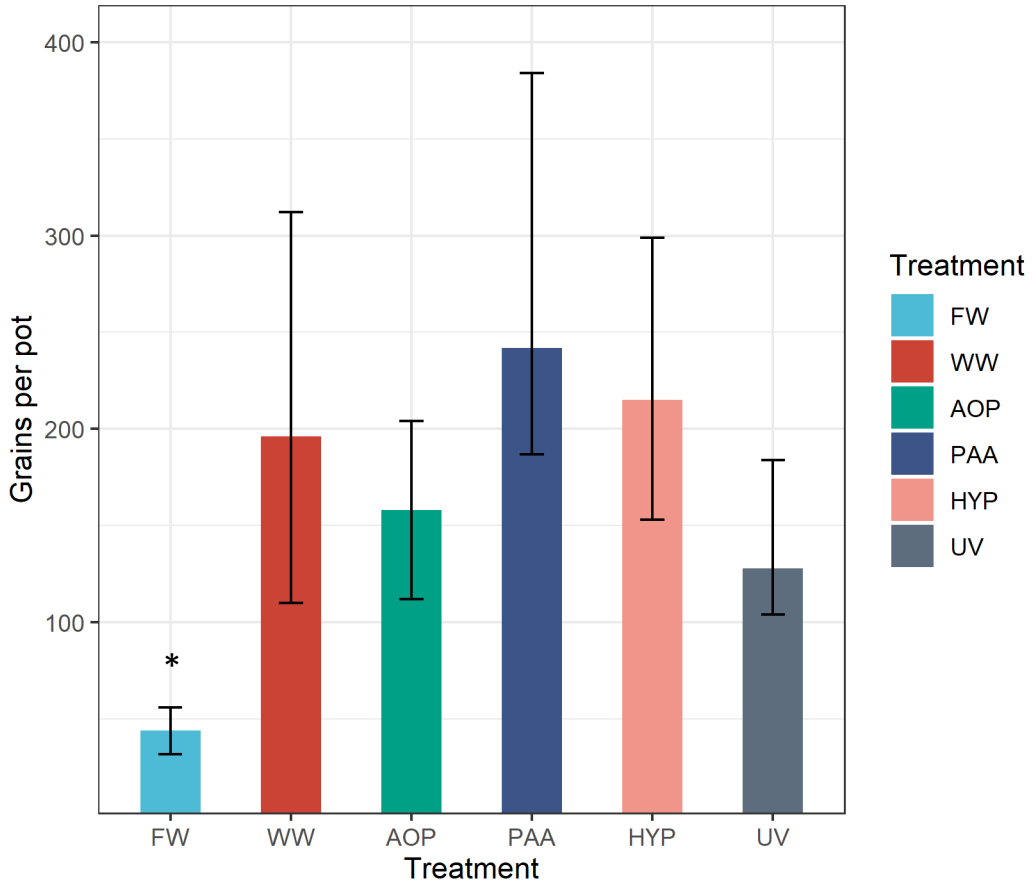
Results

FW

WW

130 days after planting
The end of crop cycle

Results



*p-value < 0.05

ANOVA followed by Tukey's test

Results – Soil Physicochemical data

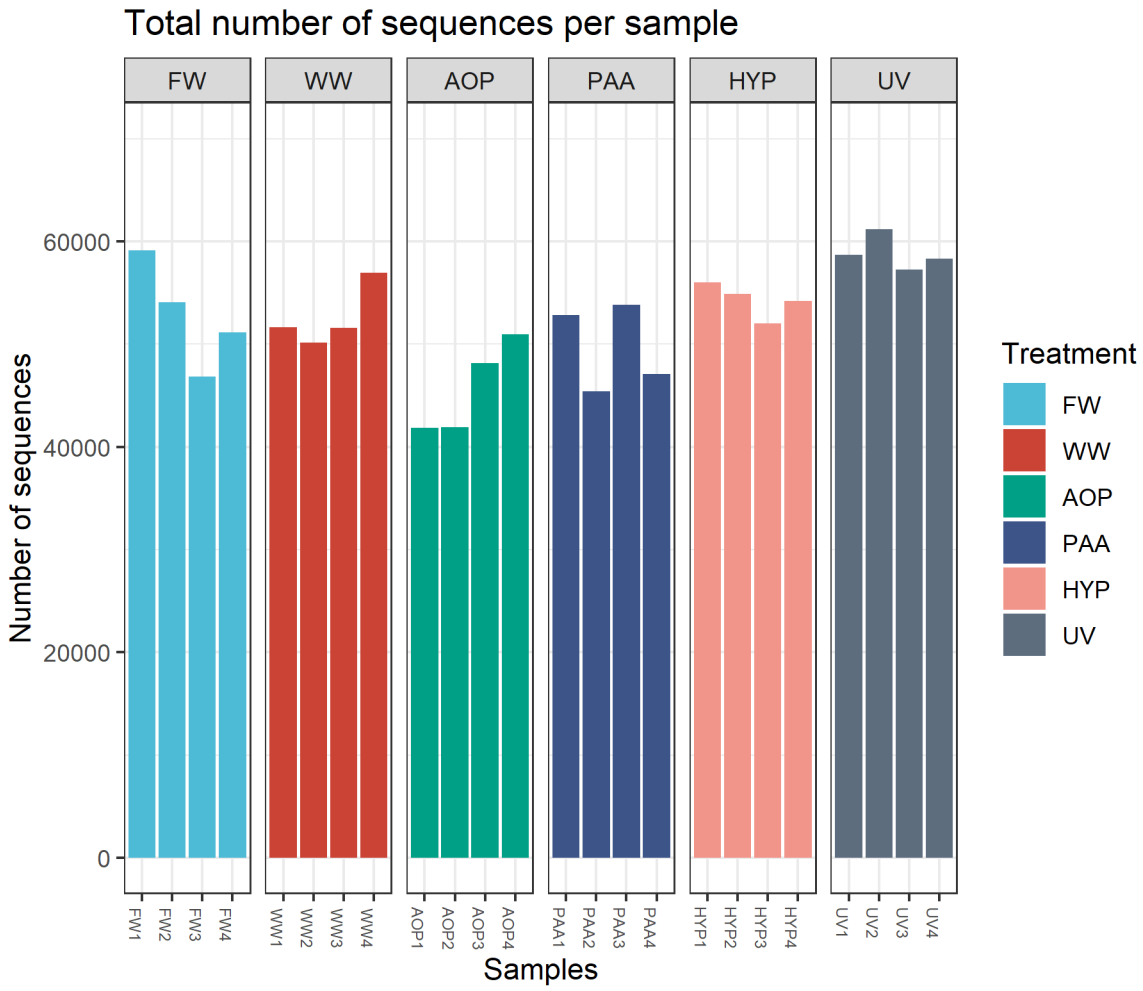
Parameters	FW	WW	HYP	PAA	AOP	UV
Organic matter (g/dm3)	38.0	39.0	38.2	40.8	39.5	38.8
CEC (mmolc/dm3)	107.4	120.1	116.1	104.4	115.0	116.0
P (mg/dm3)	26.0*	30.0	36.8	33.5	40.8	32.5
EC (dS/m)	0.42*	1.15	1.32	1.10	1.37	0.87
pH	6.2*	6.5	6.6	6.8	6.7	6.7

*p-value < 0.05

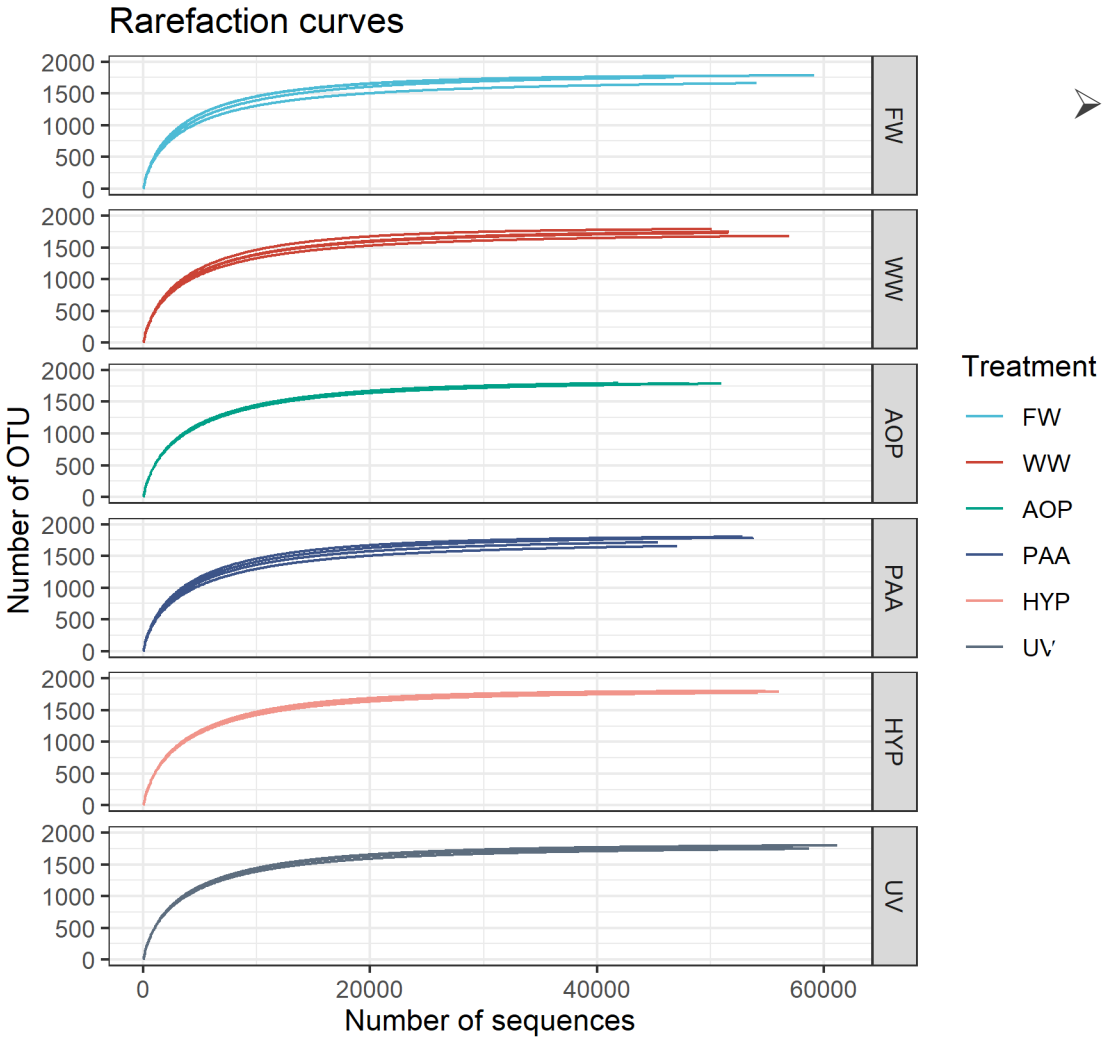
ANOVA followed by Tukey's test

Results – Microbial diversity

- Paired end - MiSeq 2x150bp Illumina platform (V4 Region)
- Total of sequences: 1,759,806
- Post process on FROGS: 1,284,215
- Post filtering: 1,257,112.
- Average number of sequences per sample 52,333.



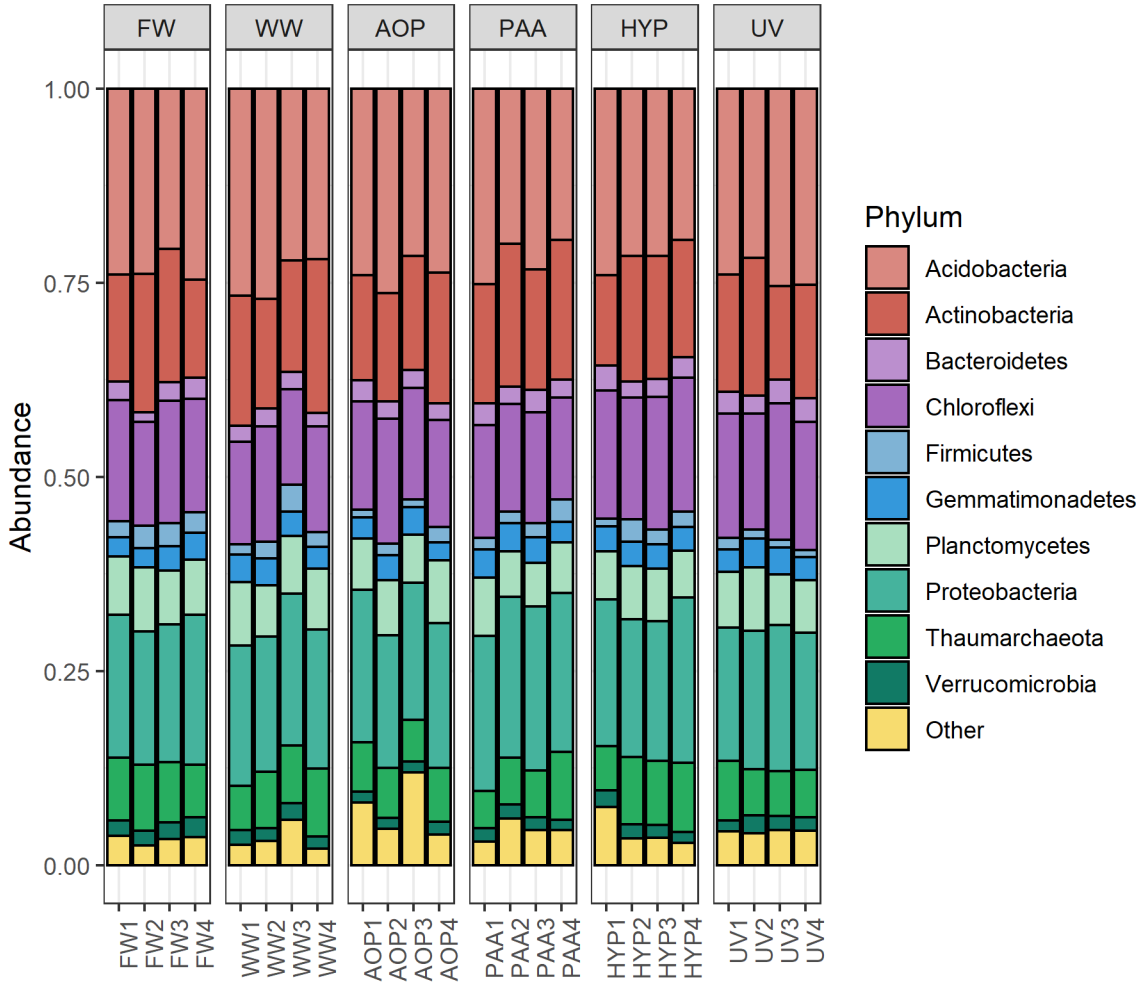
Results



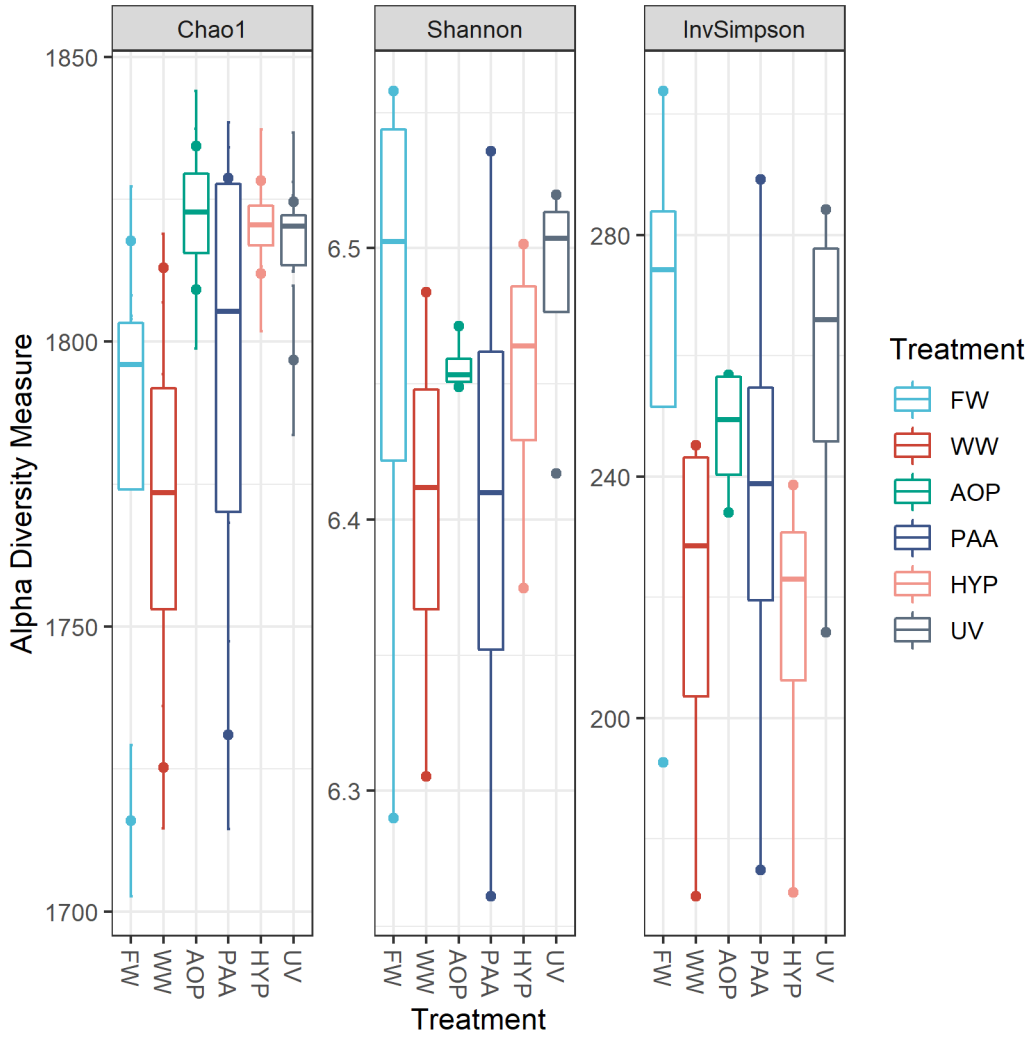
➢1859 OTU total (97% similarity)

Results

- 26 phyla:
  - 24 Bacteria:
    - Acidobacteria: 23%
    - Proteobacteria: 19%
    - Actinobacteria: 15%
    - Chloroflexi: 15%
  - 2 Archaea:
    - Thaumarchaeota: 7%



Results

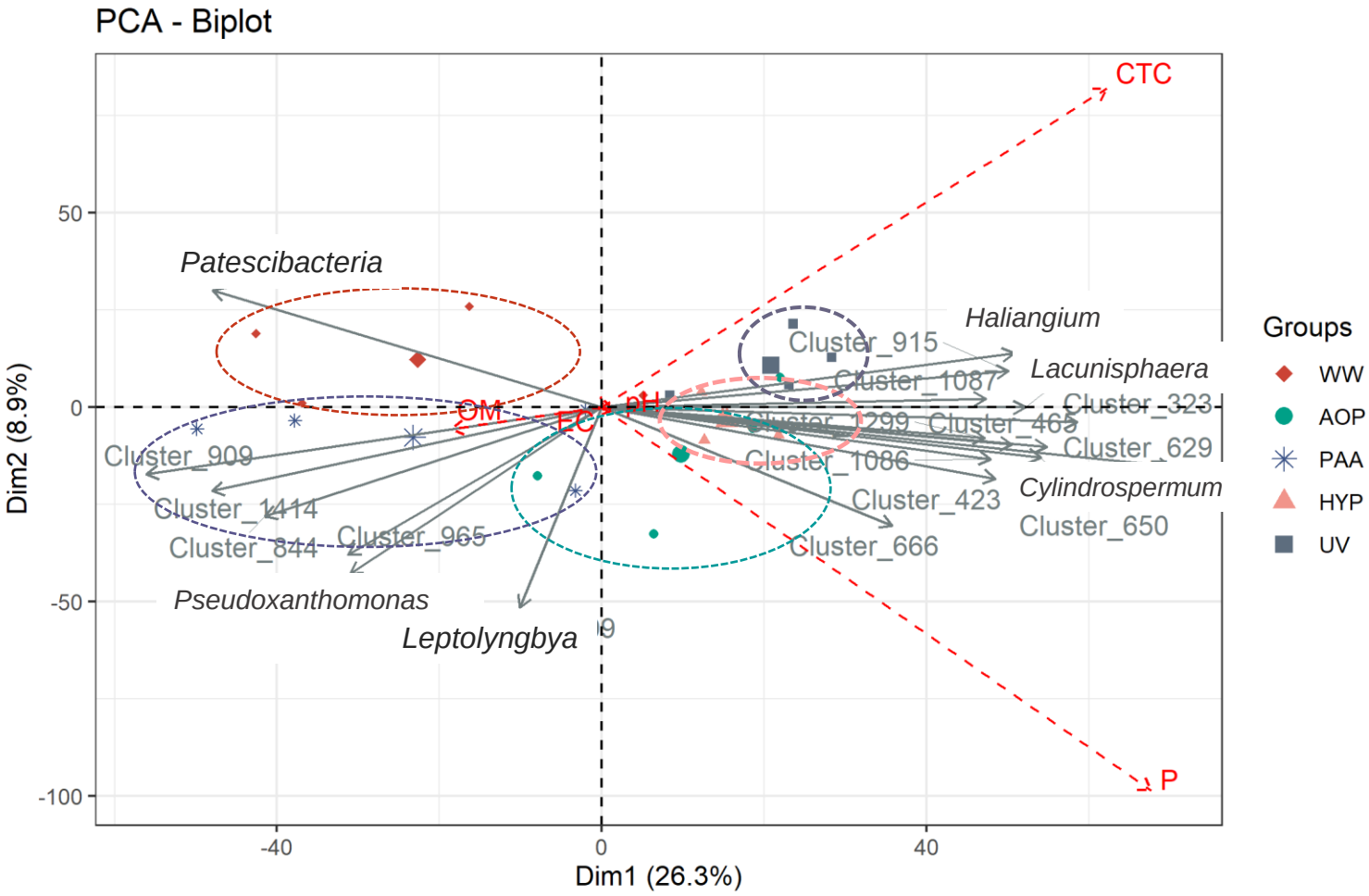

Chao1
Shannon
InvSimpson
Alpha Diversity Measure
1850
1800
1750
1700
6.5
6.4
6.3
280
240
200
FW
WW
AOP
PAA
HYP
UV
Treatment
Treatment
FW
WW
AOP
PAA
HYP
UV

Results

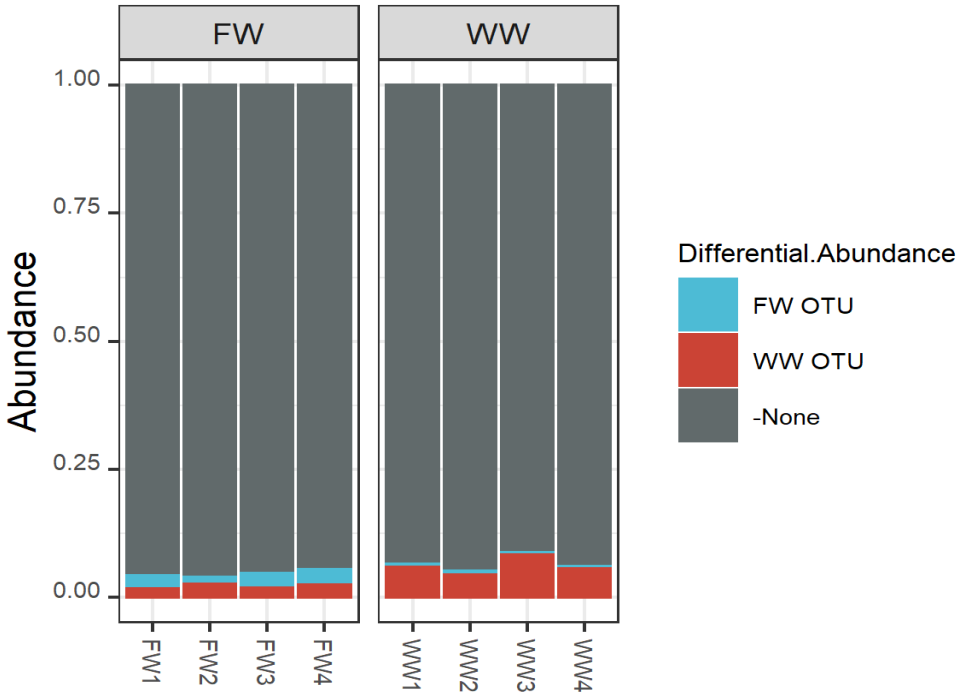
- β-Diversity: Based in Bray-Curtis distance

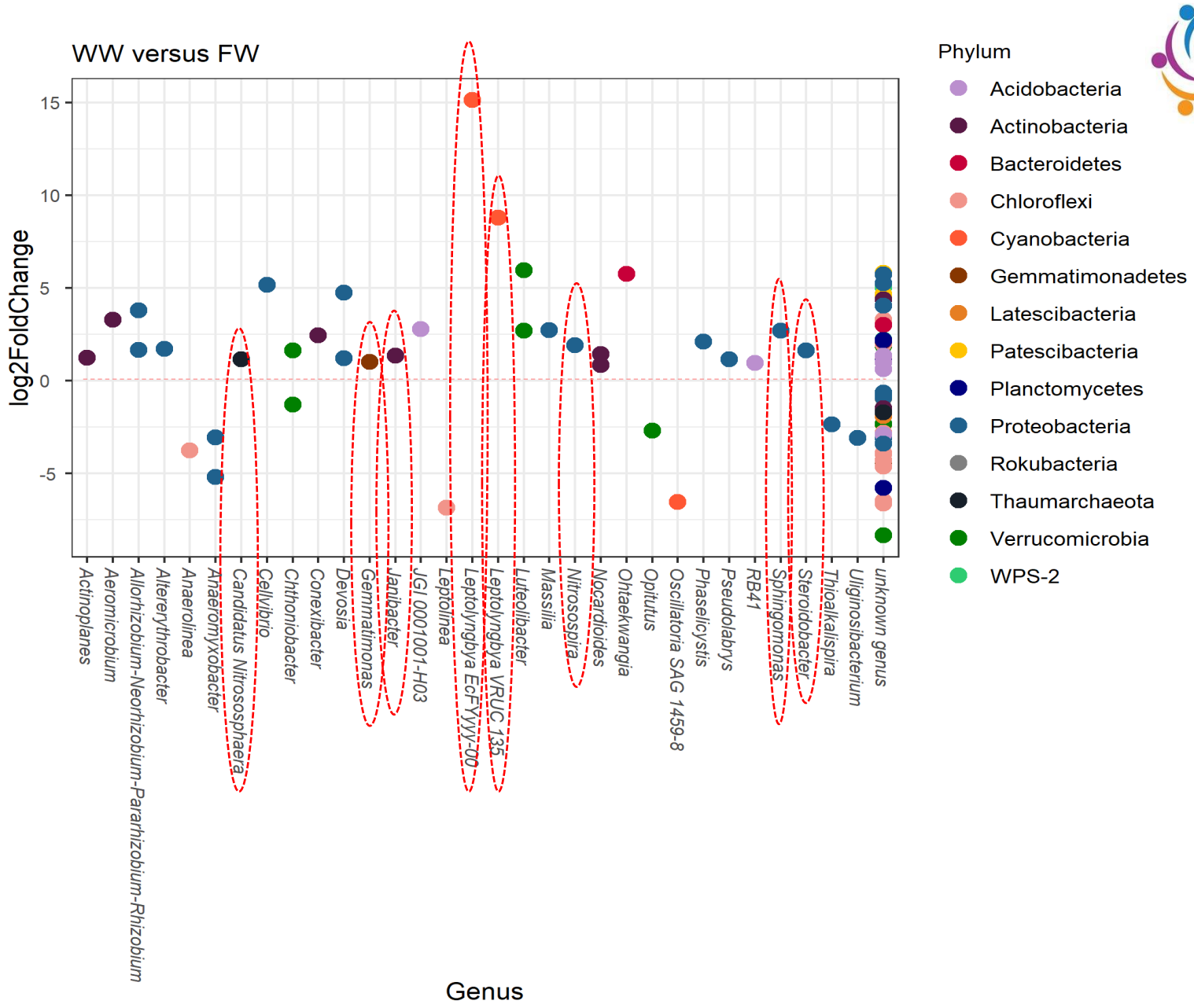
PERMANOVA	R^2	Pr
Water type	0.092	0.0067
Treatment	0.371	0.0001

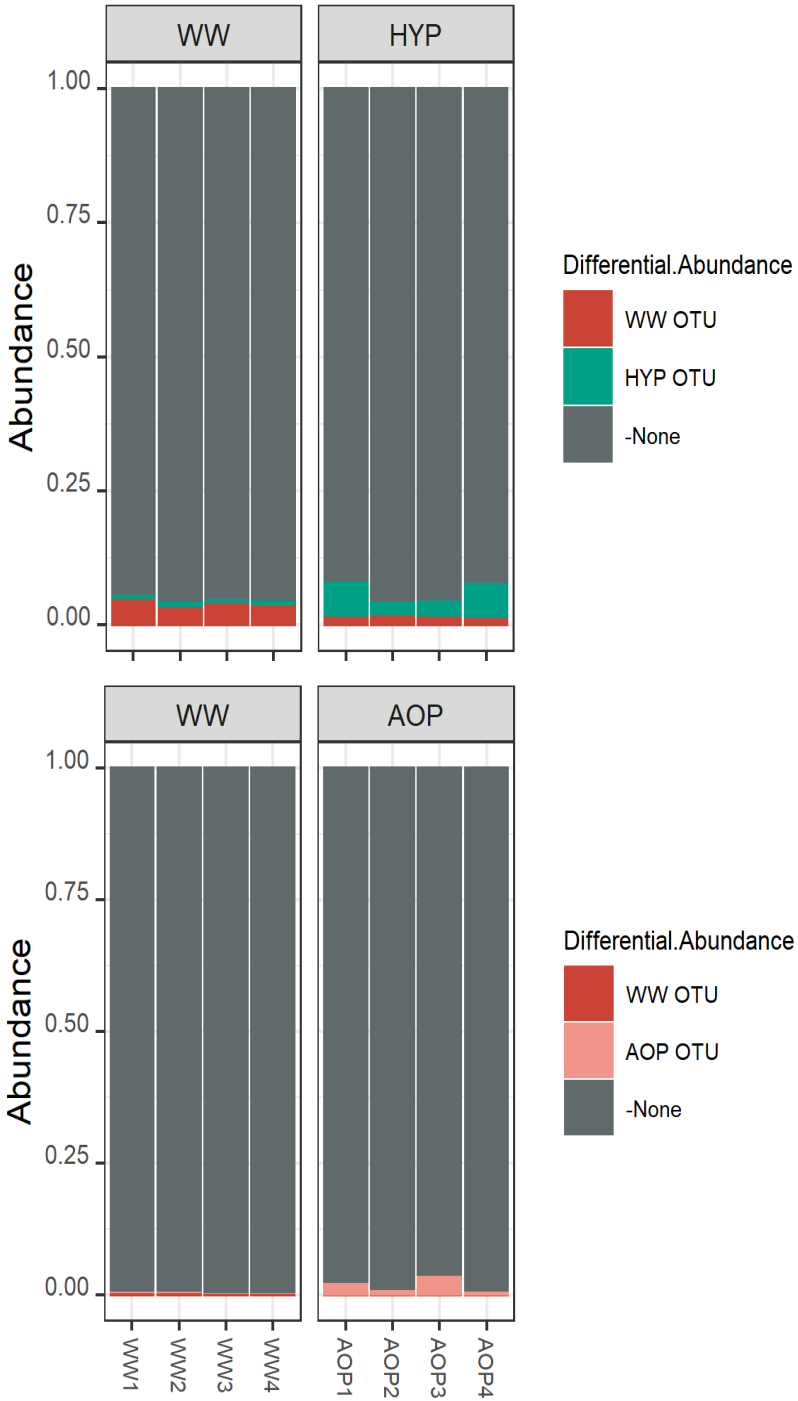
Results

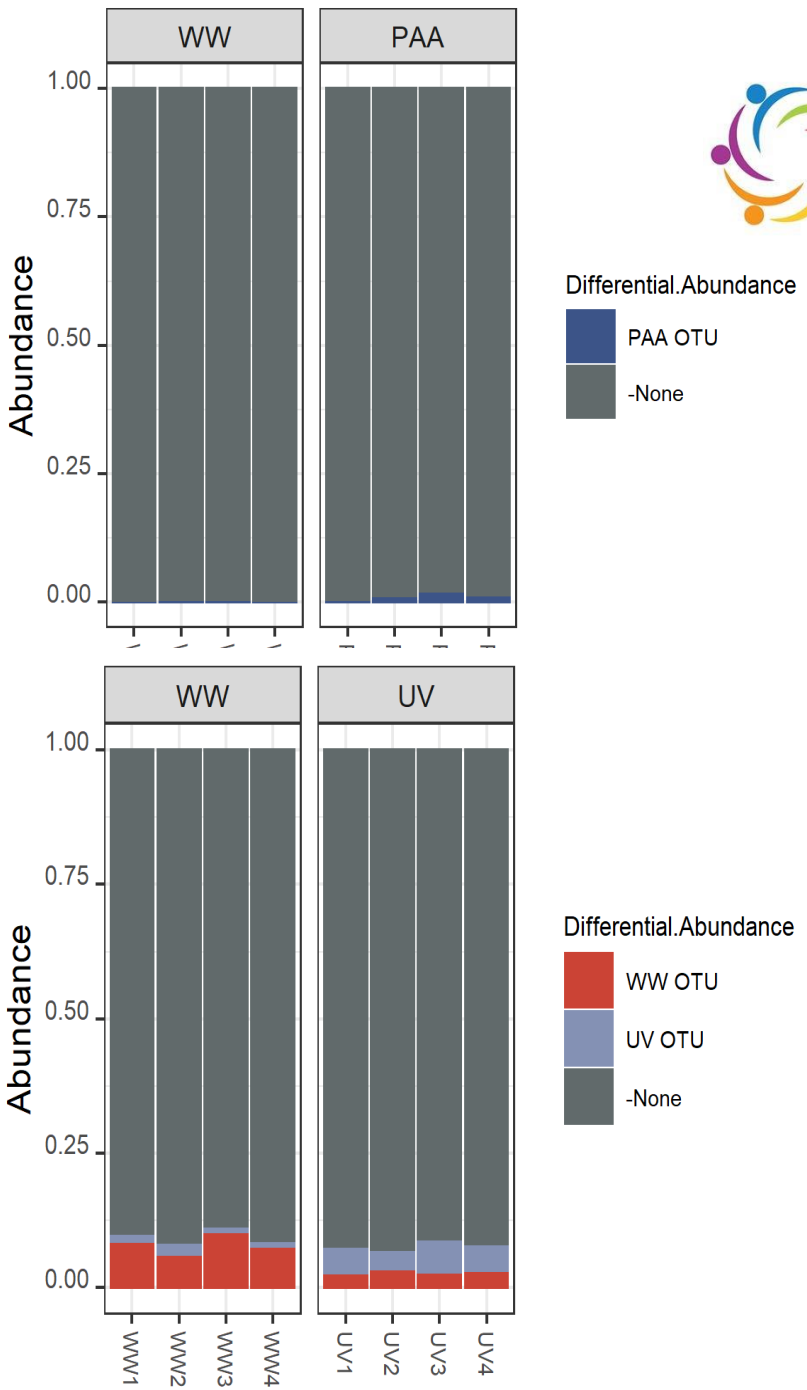

PCA - Biplot
CTC
P
OM
EC
pH
Patescibacteria
Haliangium
Lacunisphaera
Cylindrospermum
Pseudoxanthomonas
Leptolyngbya
Cluster_915
Cluster_1087
Cluster_323
Cluster_1299
Cluster_465
Cluster_629
Cluster_1086
Cluster_423
Cluster_650
Cluster_666
Cluster_909
Cluster_1414
Cluster_844
Cluster_965
Groups
WW
AOP
PAA
HYP
UV
Dim2 (8.9%)
Dim1 (26.3%)
50
0
-50
-100
-40
0
40

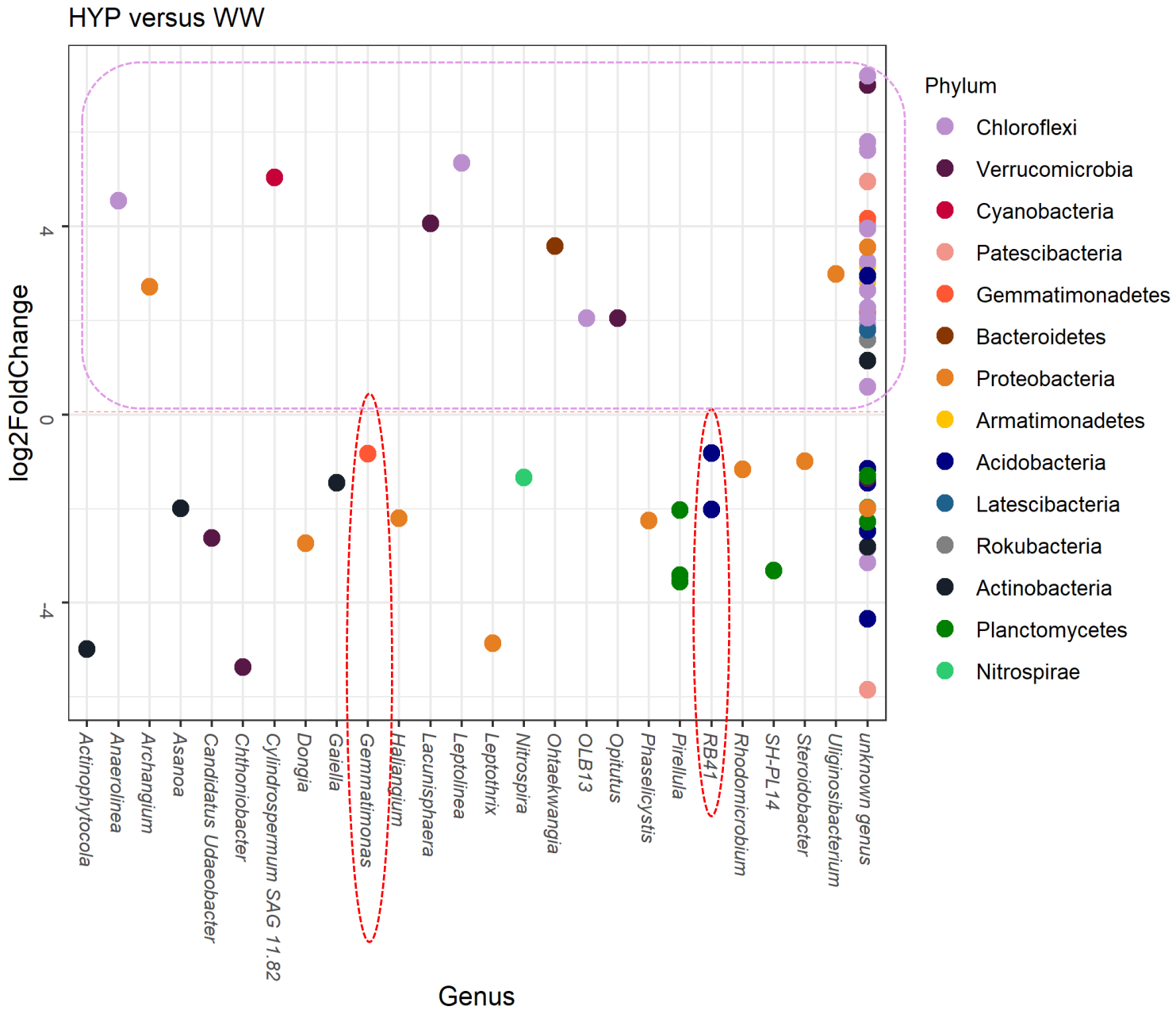
Results

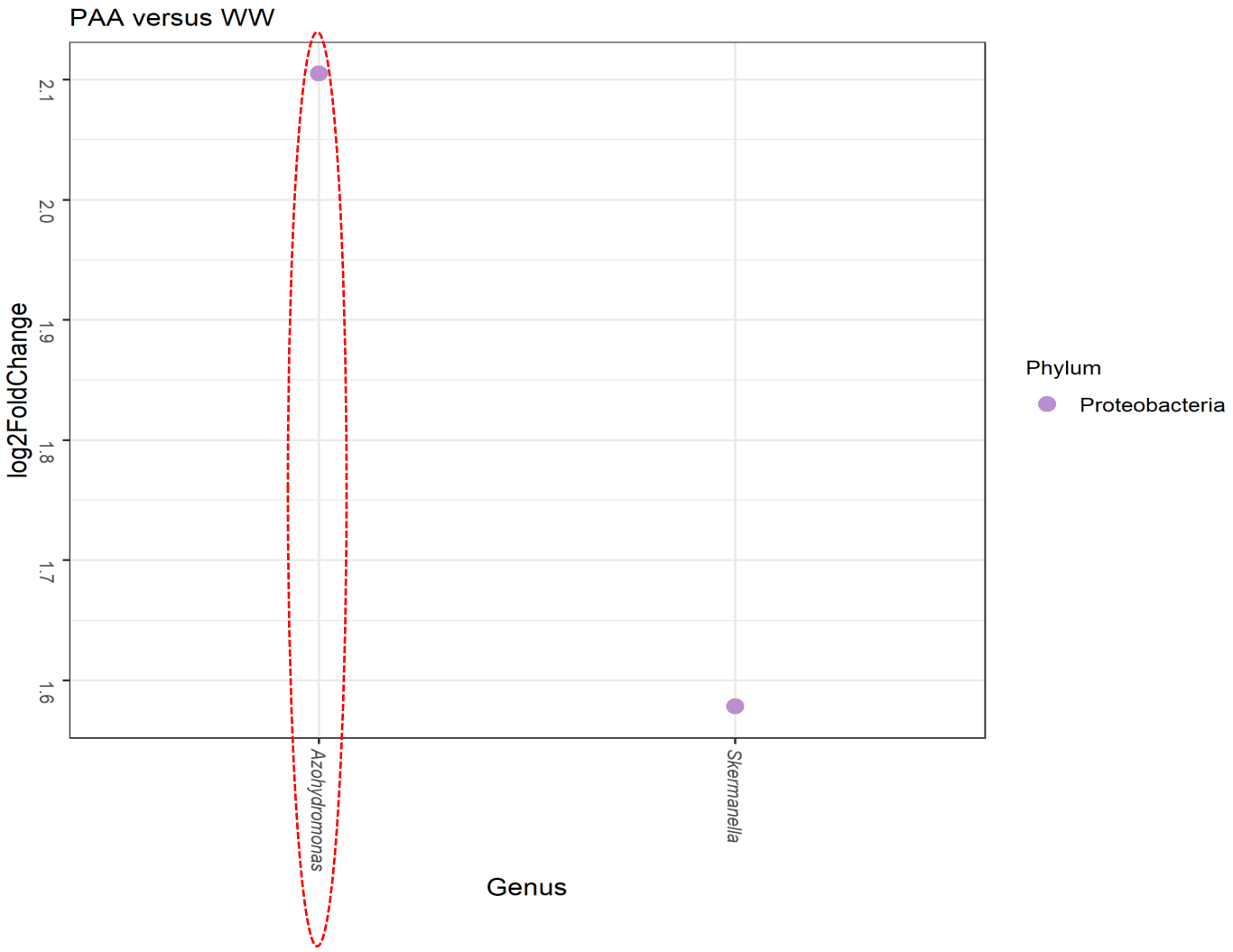

FW
WW
1.00
0.75
0.50
0.25
0.00
Abundance
FW1
FW2
FW3
FW4
WW1
WW2
WW3
WW4
Differential.Abundance
FW OTU
WW OTU
-None

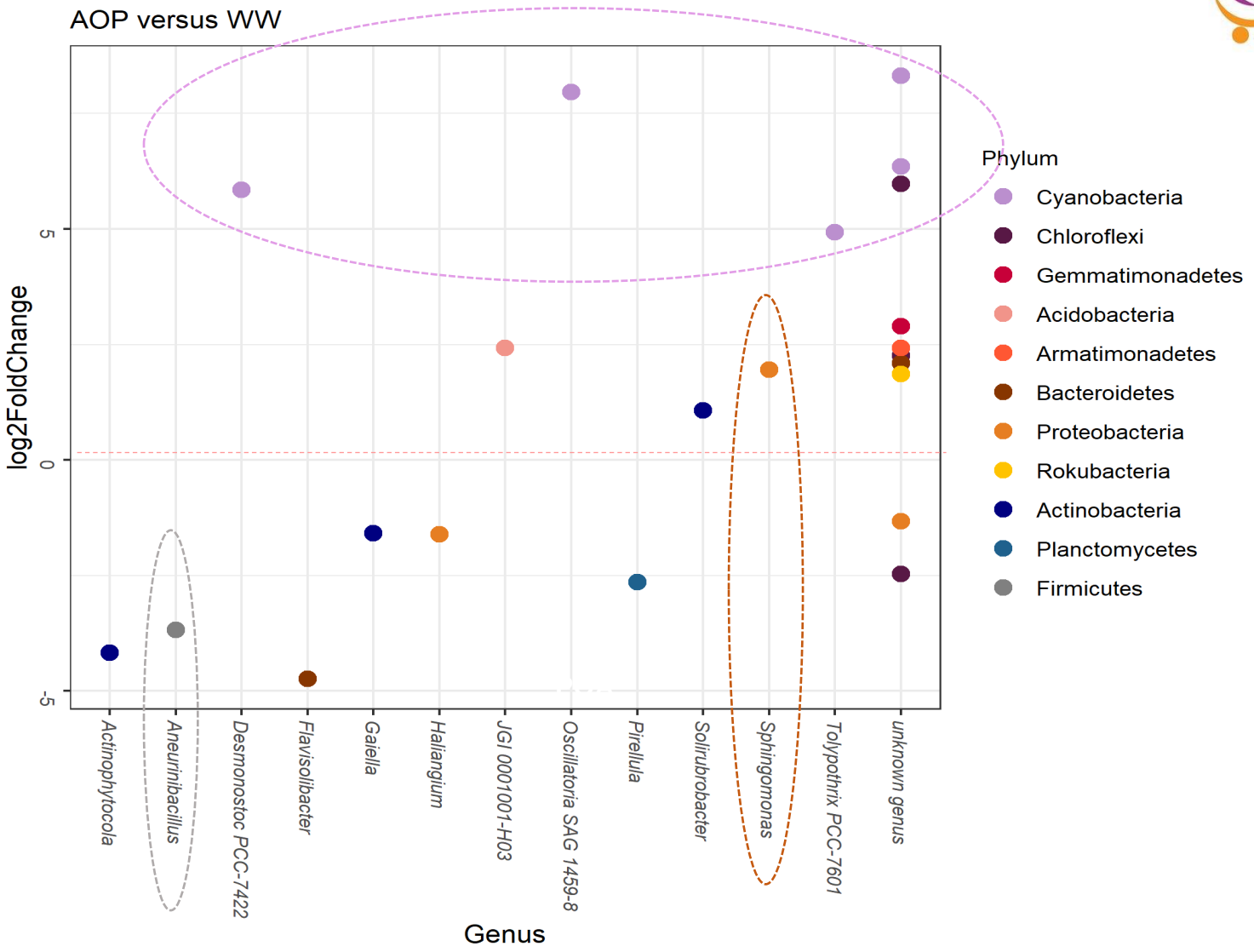

WW versus FW
log2FoldChange
15
10
5
0
-5
Actinoplanes
Aeromicrobium
Allorhizobium-Neorhizobium-Pararhizobium-Rhizobium
Altererythrobacter
Anaerolinea
Anaeromyxobacter
Candidatus Nitrososphaera
Cellvibrio
Chthoniobacter
Conexibacter
Devosia
Gemmatimonas
Janibacter
JGI 0001001-H03
Leptolinea
Leptolyngbya EcFYyyy-00
Leptolyngbya VRUC 135
Luteolibacter
Massilia
Nitrosospira
Nocardioides
Ohtaekwangia
Opitutus
Oscillatoria SAG 1459-8
Phaselicystis
Pseudolabrys
RB41
Sphingomonas
Steroidobacter
Thioalkalispira
Uliginosibacterium
unknown genus
Genus
Phylum
Acidobacteria
Actinobacteria
Bacteroidetes
Chloroflexi
Cyanobacteria
Gemmatimonadetes
Latescibacteria
Patescibacteria
Planctomycetes
Proteobacteria
Rokubacteria
Thaumarchaeota
Verrucomicrobia
WPS-2

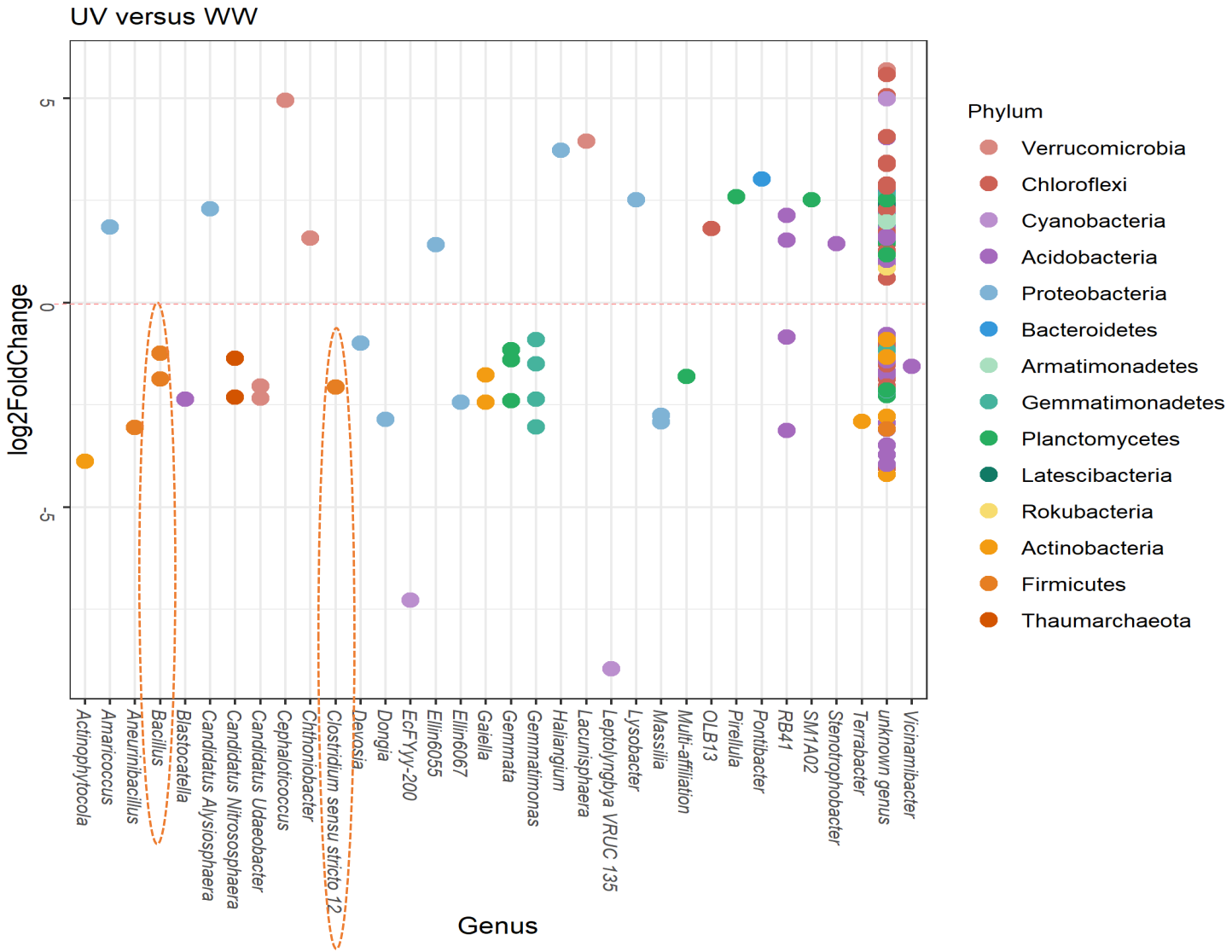

WW
HYP
Abundance
1.00
0.75
0.50
0.25
0.00
Differential.Abundance
WW OTU
HYP OTU
-None
WW
AOP
Abundance
1.00
0.75
0.50
0.25
0.00
Differential.Abundance
WW OTU
AOP OTU
-None
WW1
WW2
WW3
WW4
AOP1
AOP2
AOP3
AOP4


WW
PAA
Abundance
1.00
0.75
0.50
0.25
0.00
Differential.Abundance
PAA OTU
-None
WW
UV
Abundance
1.00
0.75
0.50
0.25
0.00
Differential.Abundance
WW OTU
UV OTU
-None
WW1
WW2
WW3
WW4
UV1
UV2
UV3
UV4

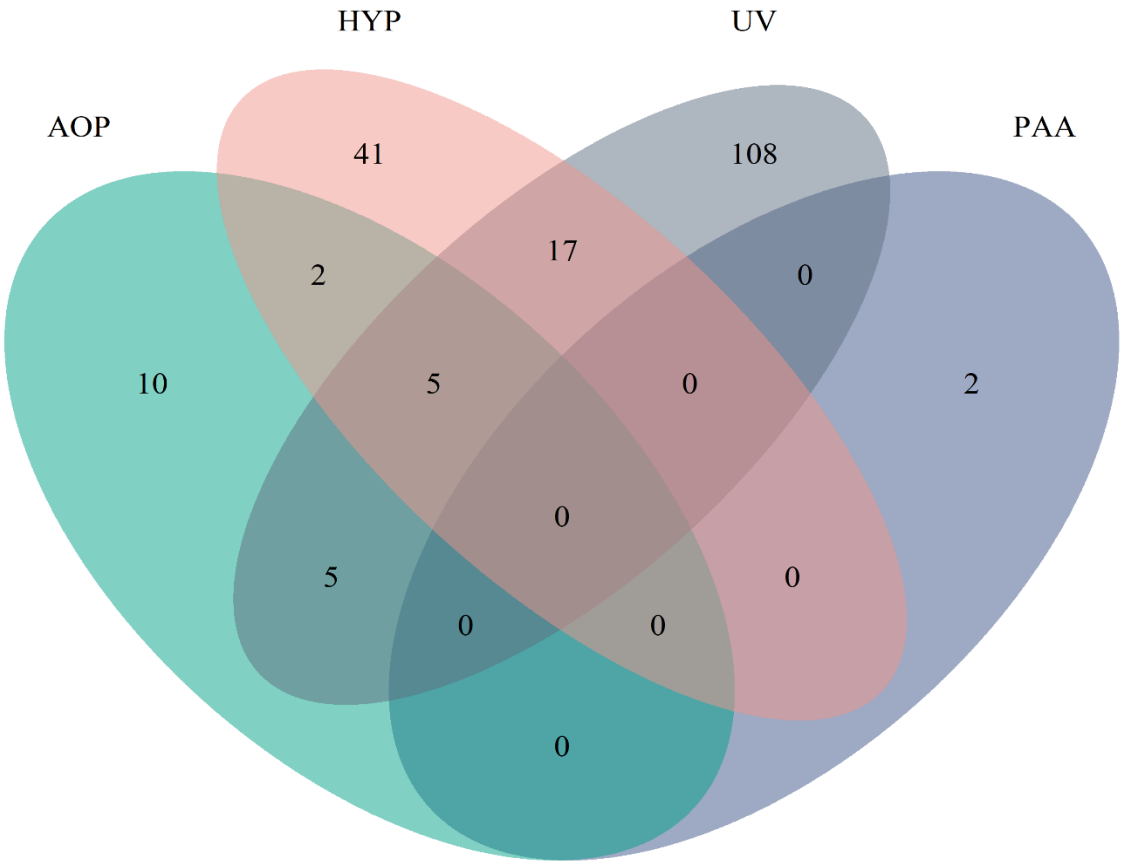

HYP versus WW
log2FoldChange
4
0
-4
Genus
Actinophytocola
Anaerolinea
Archangium
Asanoa
Candidatus Udaeobacter
Chthoniobacter
Cylindrospermum SAG 11.82
Dongia
Gaiella
Gemmatimonas
Haliangium
Lacunisphaera
Leptolinea
Leptothrix
Nitrospira
Ohtaekwangia
OLB13
Opitutus
Phaselicystis
Pirellula
RB41
Rhodomicrobium
SH-PL14
Steroidobacter
Uliginosibacterium
unknown genus
Phylum
Chloroflexi
Verrucomicrobia
Cyanobacteria
Patescibacteria
Gemmatimonadetes
Bacteroidetes
Proteobacteria
Armatimonadetes
Acidobacteria
Latescibacteria
Rokubacteria
Actinobacteria
Planctomycetes
Nitrospirae

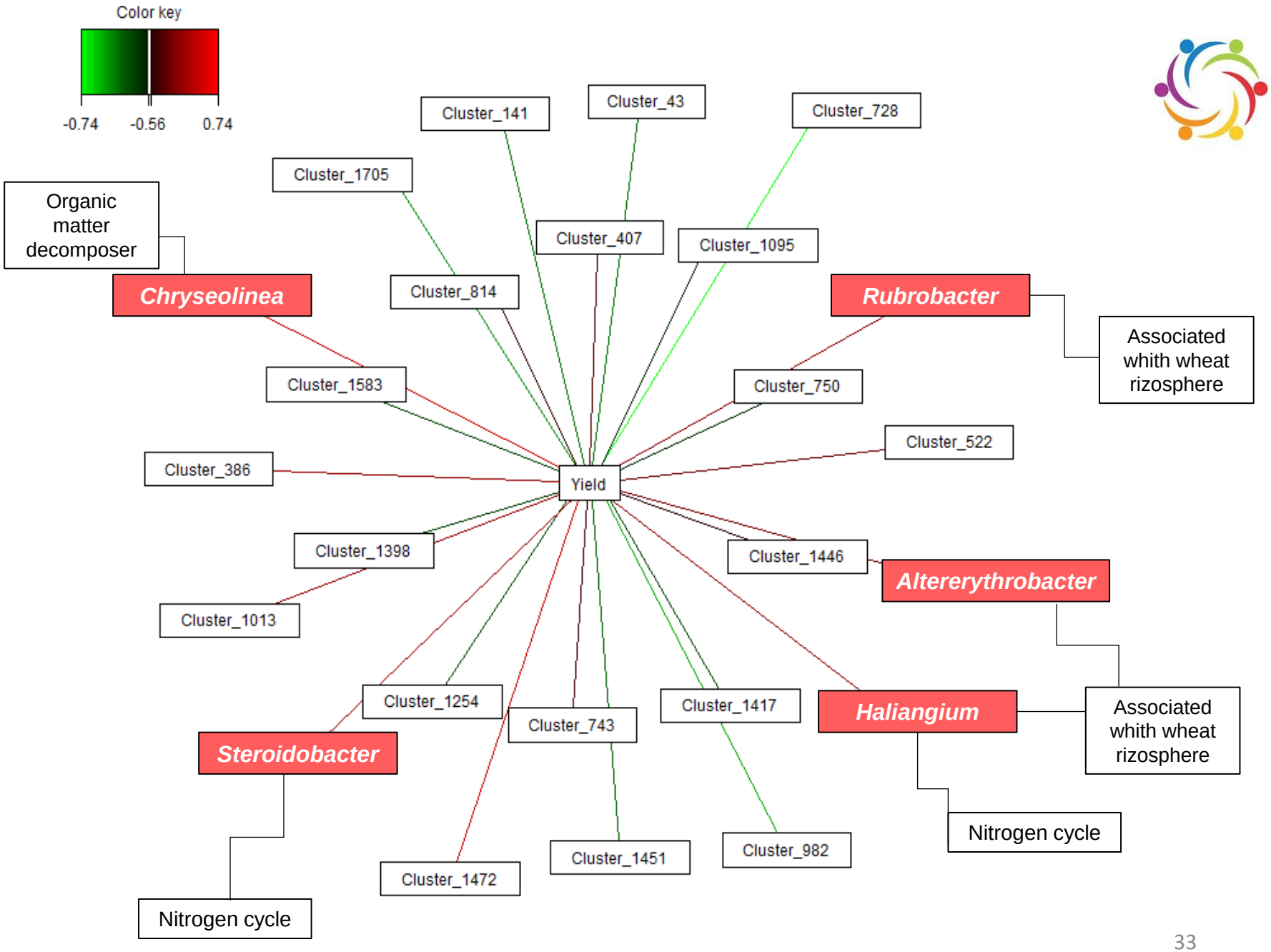

PAA versus WW
log2FoldChange
2.1
2.0
1.9
1.8
1.7
1.6
Azohydromonas
Skermanella
Genus
Phylum
Proteobacteria


AOP versus WW
log2FoldChange
5
0
-5
Genus
Actinophytocola
Aneurinibacillus
Desmonostoc PCC-7422
Flavisolibacter
Gaiella
Haliangium
JGI 0001001-H03
Oscillatoria SAG 1459-8
Pirellula
Solirubrobacter
Sphingomonas
Tolypothrix PCC-7601
unknown genus
Phylum
Cyanobacteria
Chloroflexi
Gemmatimonadetes
Acidobacteria
Armatimonadetes
Bacteroidetes
Proteobacteria
Rokubacteria
Actinobacteria
Planctomycetes
Firmicutes


UV versus WW
log2FoldChange
5
0
-5
Genus
Actinophytocola
Amaricoccus
Aneurinibacillus
Bacillus
Blastocatella
Candidatus Alysiosphaera
Candidatus Nitrososphaera
Candidatus Udaeobacter
Cephaloticoccus
Chthoniobacter
Clostridium sensu stricto 12
Devosia
Dongia
EcFYyy-200
Elin6055
Elin6067
Gaiella
Gemmata
Gemmatimonas
Haliangium
Lacunisphaera
Leptolyngbya VRUC 135
Lysobacter
Massilia
Multi-affiliation
OLB13
Pirellula
Pontibacter
RB41
SM1A02
Stenotrophobacter
Terrabacter
unknown genus
Vicinamibacter
Phylum
Verrucomicrobia
Chloroflexi
Cyanobacteria
Acidobacteria
Proteobacteria
Bacteroidetes
Armatimonadetes
Gemmatimonadetes
Planctomycetes
Latescibacteria
Rokubacteria
Actinobacteria
Firmicutes
Thaumarchaeota

Results




Color key
-0.74
-0.56
0.74
Cluster_141
Cluster_43
Cluster_728
Cluster_1705
Organic matter decomposer
Cluster_407
Cluster_1095
Chryseolinea
Cluster_814
Rubrobacter
Associated whith wheat rizosphere
Cluster_1583
Cluster_750
Cluster_522
Cluster_386
Yield
Cluster_1398
Cluster_1446
Altererythrobacter
Cluster_1013
Cluster_1254
Cluster_1417
Haliangium
Associated whith wheat rizosphere
Cluster_743
Steroidobacter
Nitrogen cycle
Cluster_1472
Cluster_1451
Cluster_982
Nitrogen cycle

Conclusion

- In a short term: do not disinfectant impact on crop yield and soil physicochemical characteristics
- Disinfection treatments do not influence the microbial richness and alpha diversity
- Disinfection influence only the subdominant taxa.
- Among the differentially abundant OTUs, the disinfection played an important role in shaping soil bacteria community structure through eliminating sensitive and enriching resistant microorganism.

Merci beaucoup!

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http://www.fec.unicamp.br/~saneamentorural/