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Alteration in the bacterial community composition in creosote polluted soils

Objective

- Polyaromatic hydrocarbons (PAHs):
 - Originate from the combustion of fossil fuels & pyrolysis of organic matter
 - >70% deposited in soil
 - Chronic exposure linked to cardiovascular & immune disorders
- We studied the effect of PAH contamination in microbial community in four different pristine soil types

2. Most abundant bacterial phylotypes

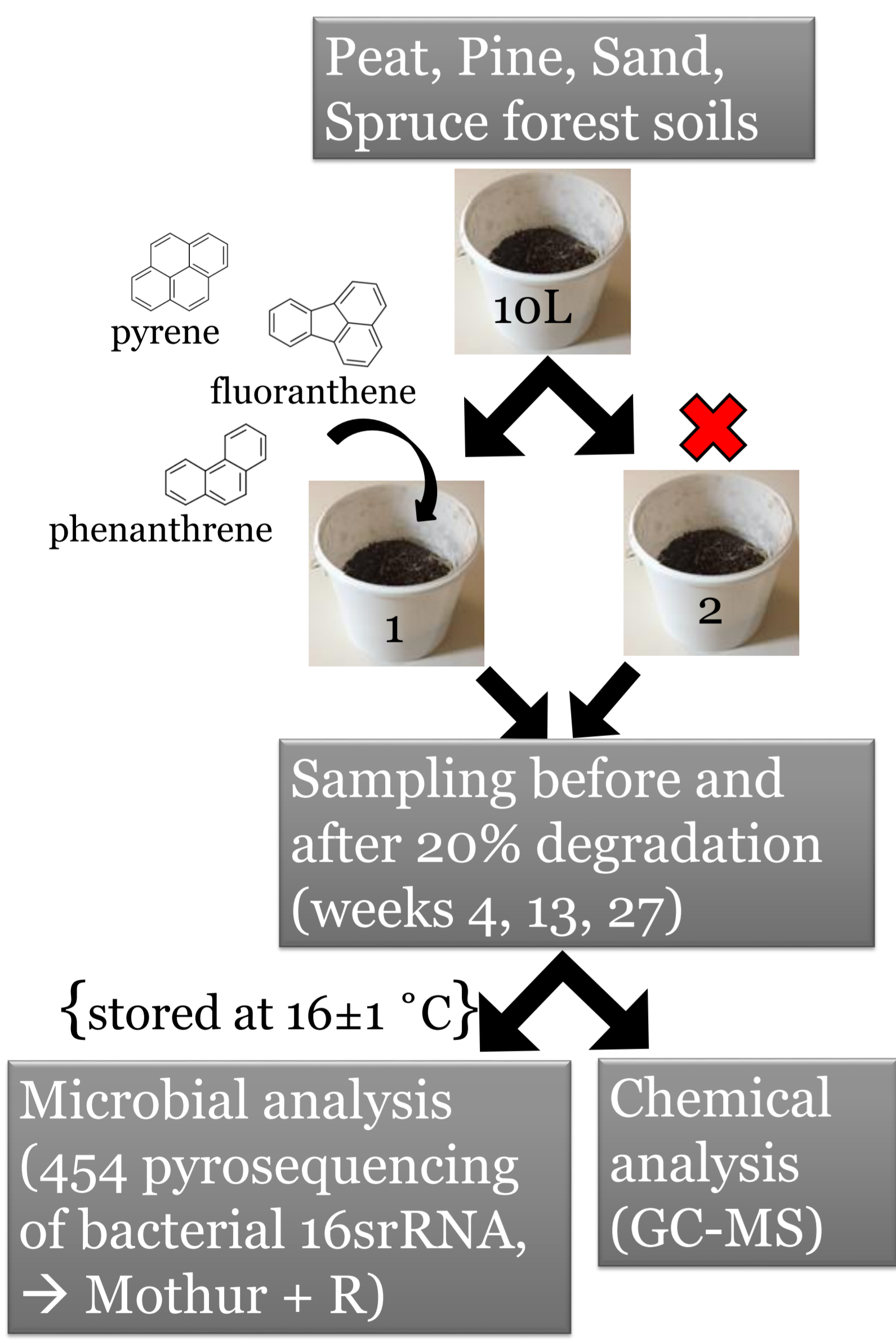
Phylogenetic Group	No creosote		Creosote added	
	Mean	SD	Mean	SD
Acidobacteria	39.04	12.40	23.33	12.75
Actinobacteria	6.01	4.65	9.90	7.41
Bacteroidetes	3.38	4.14	3.37	2.91
Firmicutes	0.71	0.59	2.57	4.63
Proteobacteria	39.97	13.19	41.80	14.70
unclassified	2.32	2.09	9.91	9.04
Verrucomicrobia	6.88	4.28	5.09	3.50



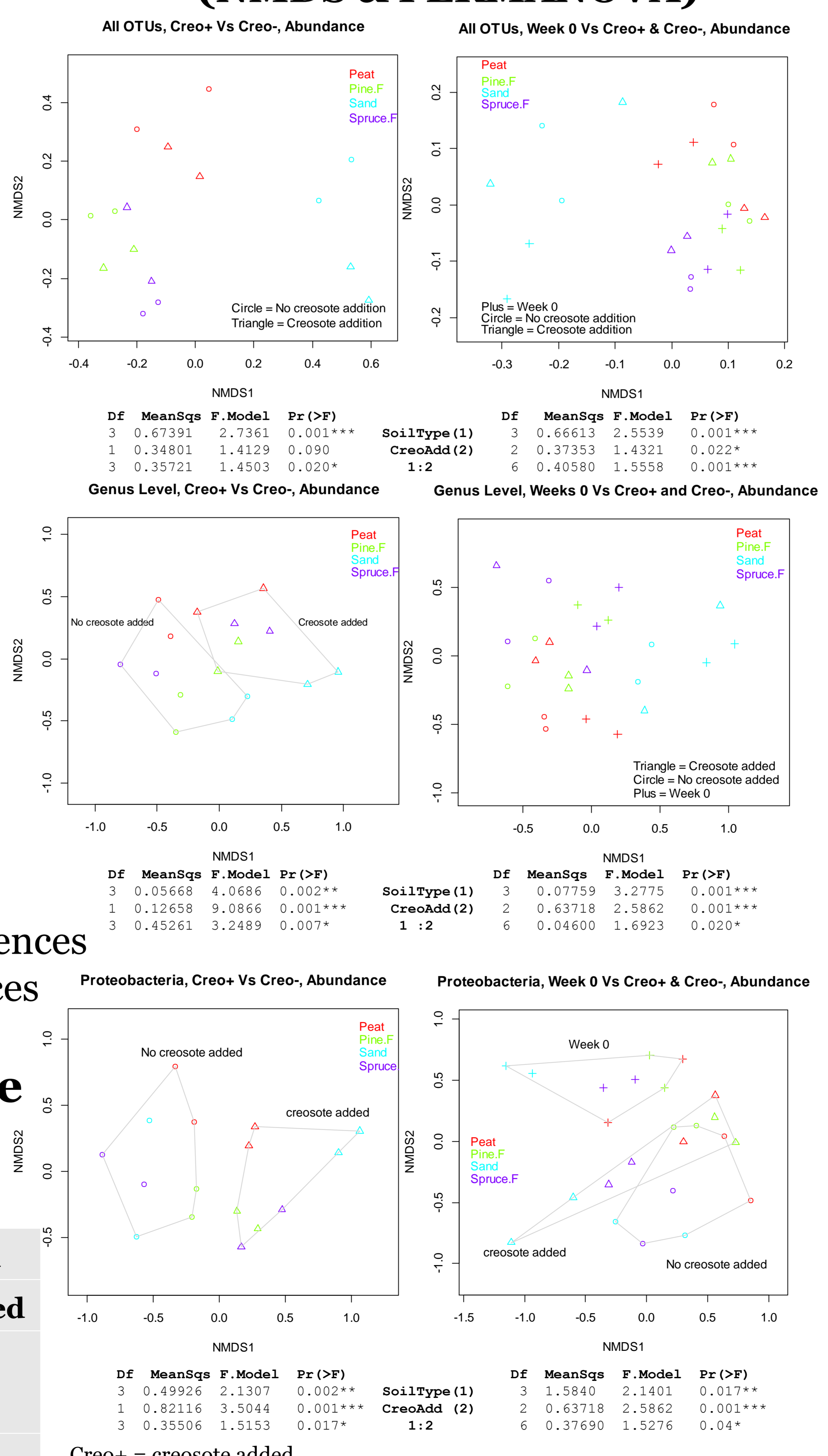
4. Indicator species analysis (INDVAL)

OTU	Creo+	Phylum	Class	Genus	ind. val	p-value
Otu0021	Yes	Proteobacteria	Betaproteobacteria	Burkholderia	0.56	0.029
Otu0024	No	Acidobacteria	Acidobacteria_Gp3	unclassified	0.6	0.037
Otu0037	No	Acidobacteria	Acidobacteria_Gp2	unclassified	0.62	0.023
Otu0048	Yes	Proteobacteria	Alphaproteobacteria	unclassified	0.58	0.029
Otu0081	Yes	Proteobacteria	Betaproteobacteria	unclassified	0.5	0.046
Otu0139	No	Bacteroidetes	Sphingobacteriia	Mucilaginibacter	0.59	0.012
Otu0208	No	Bacteroidetes	Sphingobacteriia	unclassified	0.33	0.04
Otu0399	No	Bacteroidetes	Sphingobacteriia	unclassified	0.38	0.032

Study design



3. Shift in bacterial community (NMDS & PERMANOVA)



Results

- No creosote added: 3802 sequences
- Creosote added : 4653 sequences
- 3626 OTUs

1. Difference in sequence number (Student's t-test & Mann-Whitney test)

Higher abundance of phylotypes in creosote added	no creosote added
Proteobacteria (W=10, p<0.05)	Bacteroidetes (W=59, p<0.05)
Betaproteobacteria (df= 8.3, p<0.05)	Sphingobacteriia (df=7.59, p<0.05)

Conclusion

- ✓ Shift in bacterial community due to creosote pollution observed at the genus level
- ✓ Relative abundance of Proteobacteria and specifically Betaproteobacteria increased in polluted soil
- ✓ Abundance of Bacteroidetes and sphingobacteriia decreased in polluted soil
- ✓ Abundance of Mycobacterium, a known degrader of 4-ring PAHs unaltered

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