

# Microplastics in soil induce a new microbial habitat, with consequences for bulk soil microbiomes

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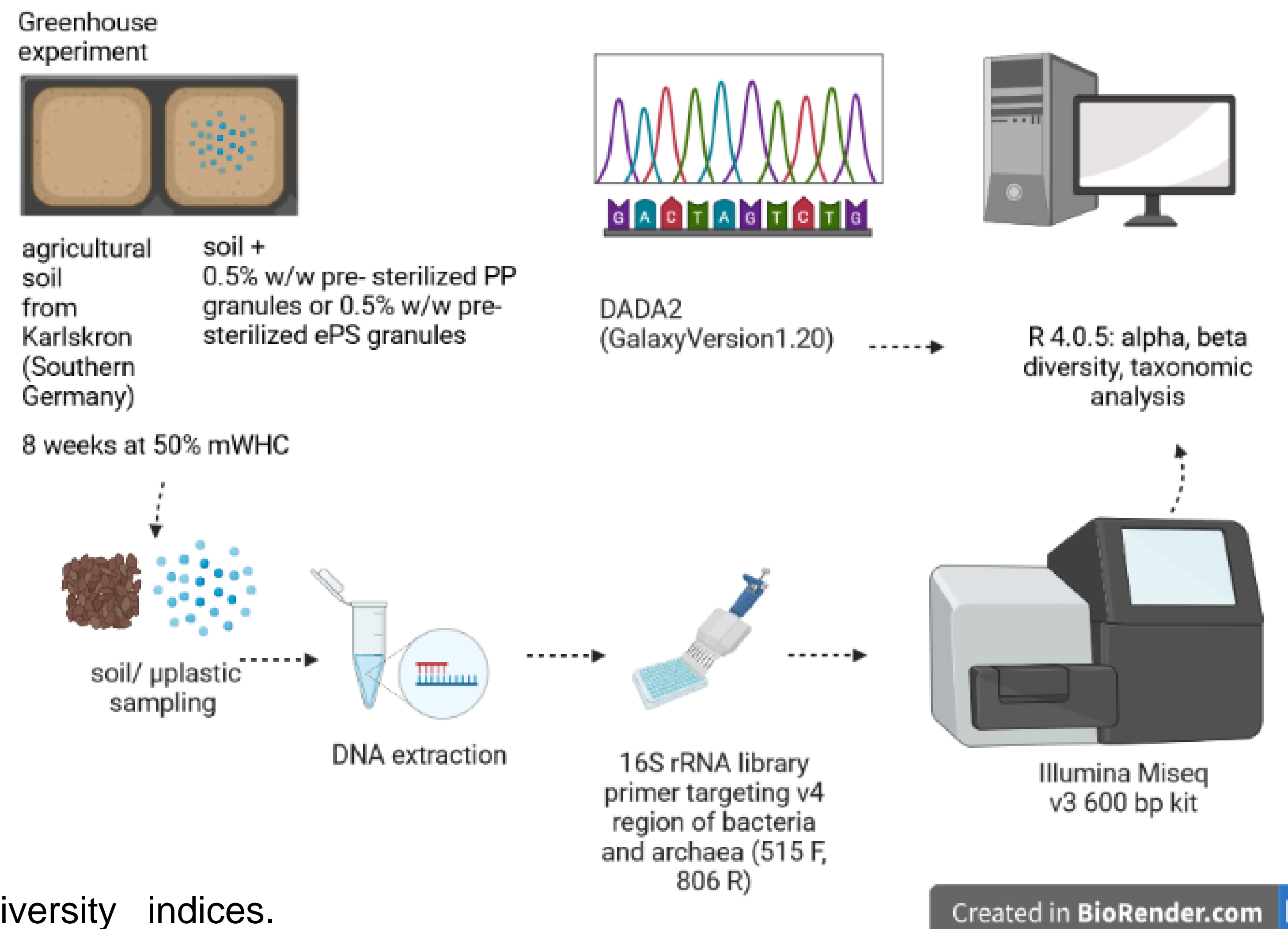
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## Background

Microplastic (MP) pollution poses a threat to agricultural soils and may induce a significant loss of the soil quality and services provided by these ecosystems. Studies in marine environments suggest that this impact is mediated by shifts in the microbiome. However, studies on the mode of action of MP materials on the soil microbiome are rare, particularly when comparing the effects of different MP materials. In this study, we characterized the microbiota colonizing two different MP materials, granules made of polypropylene (PP) and expanded polystyrene (ePS), introduced into arable soil and incubated for 8 weeks, using a molecular barcoding approach. We further assessed the consequences on the microbiome of bulk soil. **We hypothesized that (i) soil bacteria could colonize MP particles introduced into soil, that (ii) the bacterial community colonizing the MP particles will differ from the soil bacterial community, that (iii) the soil bacterial community will be influenced by the addition of MP.**

## Results and Discussion

## Materials and Methods



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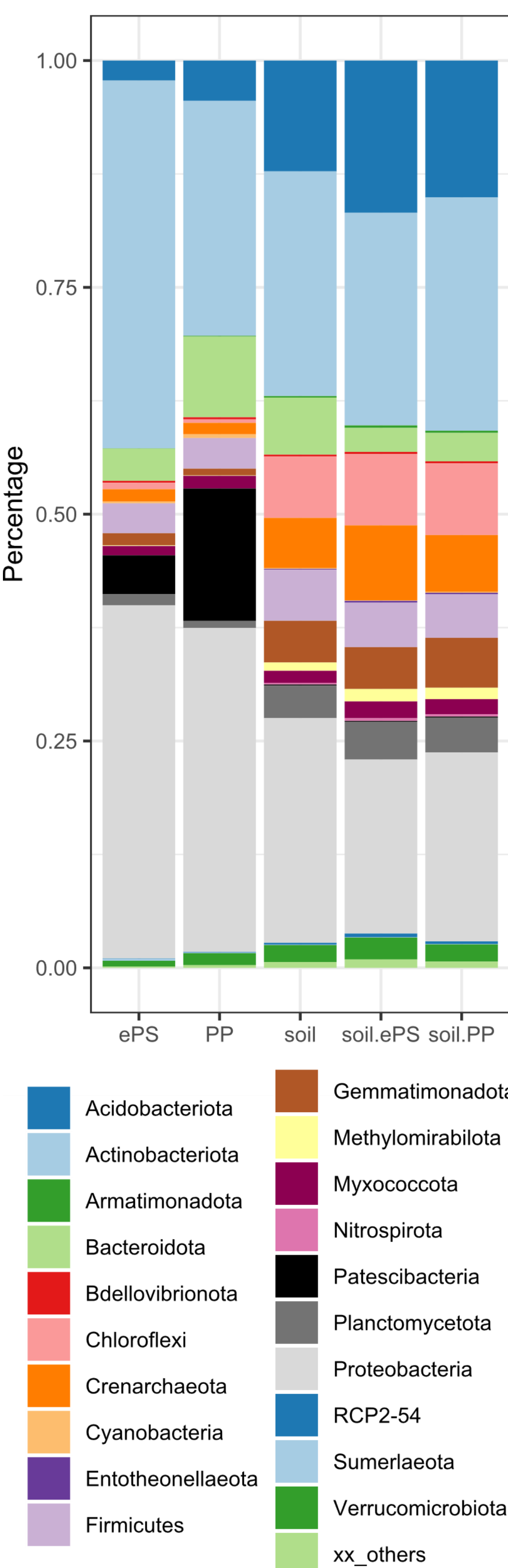
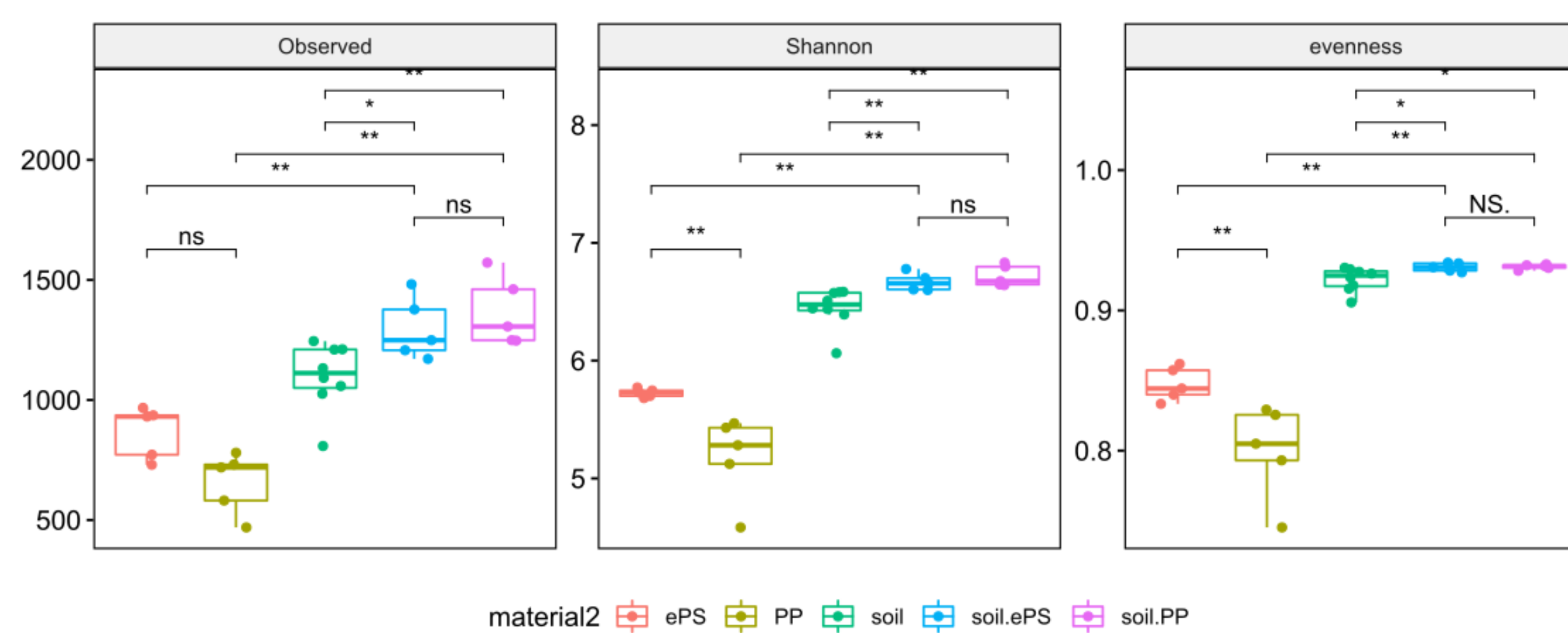


Figure 1. Bar plot showing the relative abundance of top 20 phyla on MP materials and in MP-treated and untreated bulk soil.

Figure 2. Box plots of different alpha diversity indices. Statistical analysis was performed using Kruskal-Wallis and Wilcoxon Rank-Sum test with Benjamini-Hochberg correction for multiple comparisons, respectively.



- MP particles in soil were colonized by bacteria
- Clear differences between the bacterial community structure on the MP particles and in bulk soil
- Alpha diversity: lower in control soil compared to MP-treated soils
- Beta diversity: different bacterial community structure on the two MP materials and differences in bacterial diversity between bulk soil and MP
- Bulk soil: Actinobacteriota (25%), Proteobacteria (22%), and Acidobacteriota (14%) most abundant
- MP: Proteobacteria (37%), Actinobacteriota (33%) and Patescibacteria (9%) most abundant
- Several candidates on MP, which might be able to degrade it like *TM7a*, *Phenylobacterium*, *Nocardia*, *Arthrobacter* and *Streptomyces*
- Enriched on PP compared to ePS: Acidobacteriota, Bacteroidota, Myxococcota, Planctomycota and Verrucomicrobiota
- Consequences of the applied MP materials detected for the bulk soil, e.g. Crenarchaeota, Acidobacteriota, Chloroflexi, Myxococcota, Gemmatimonadota, Planctomycota and Verrucomicrobiota enriched in MP treated soil samples
- Most genera enriched on MP, e.g., *Bacteroides*, *Nocardia*, *Rhizobacter* and *TM7a* lower abundant in the MP treated bulk soil samples compared to control soil
- MP induces a new microbial habitat in soil

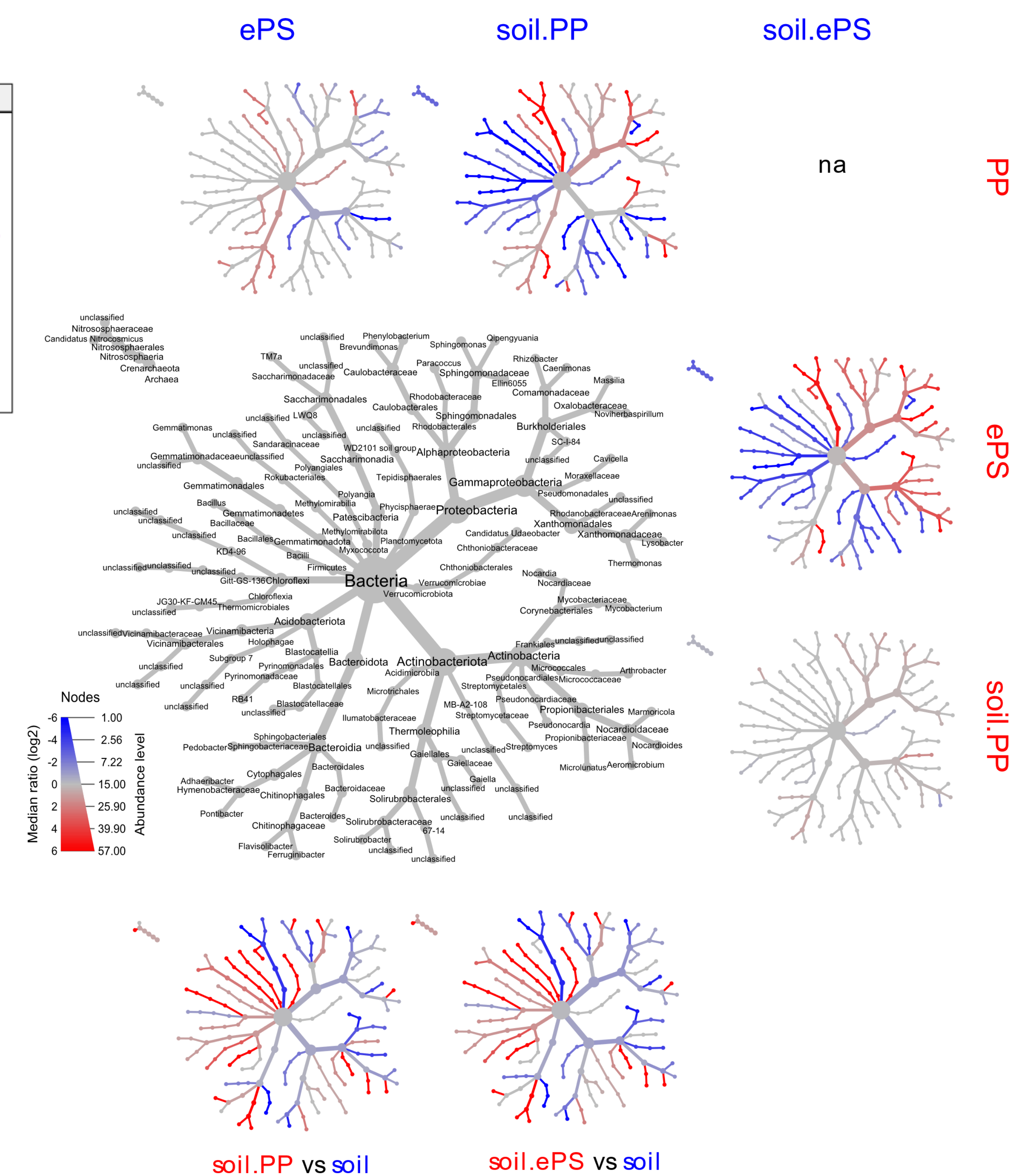


Figure 3. Heat tree including genera  $\geq 1\%$  of all reads in at least one sample. The labelled tree in the middle shows the taxonomic information (domain to genus) and is the key for the unlabelled smaller trees. Smaller trees represent a comparison between MP and soil in the columns and rows. Coloured taxa are more abundant (based on  $\log_2$ -transformed ratio of median proportions) in the samples indicated in the respective column or row. Only significant changes ( $p < 0.05$ ) are coloured according to the legend. Statistical analysis was performed using Wilcoxon Rank-Sum test with Benjamini-Hochberg correction for multiple comparisons.

