

Biogeochemical characterization of soils affected by more than 100 years of lead mining activity.

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Introduction

Mining works modifies physicochemical characteristics of soils leading to changes in activity and diversity of in soil living organisms, including microorganisms with consequences on supported ecosystem services^{1,2}. A study was carried out on a metal polluted soil to assess the impact of mining on the activity, abundance and diversity of microorganisms, to evaluate the level of disturbance in the soil health.

Research and Methodology

The selected study area was originally a lead-silver mine. Later, a mineral treatment plant was established in the area in order to recover Zn from the old dumps. In addition spills of olive mill residues were later deposited in the area. Four composite samples from the five distinct sites were collected: tailings, dumps, olive mill residues (OMW), contaminated soil and reference soil. A range of analyses was done on these samples including pH, electrical conductivity, organic matter, multi-elemental contents, enzymatic activities and bacterial diversity (16S rRNA amplicon sequencing).

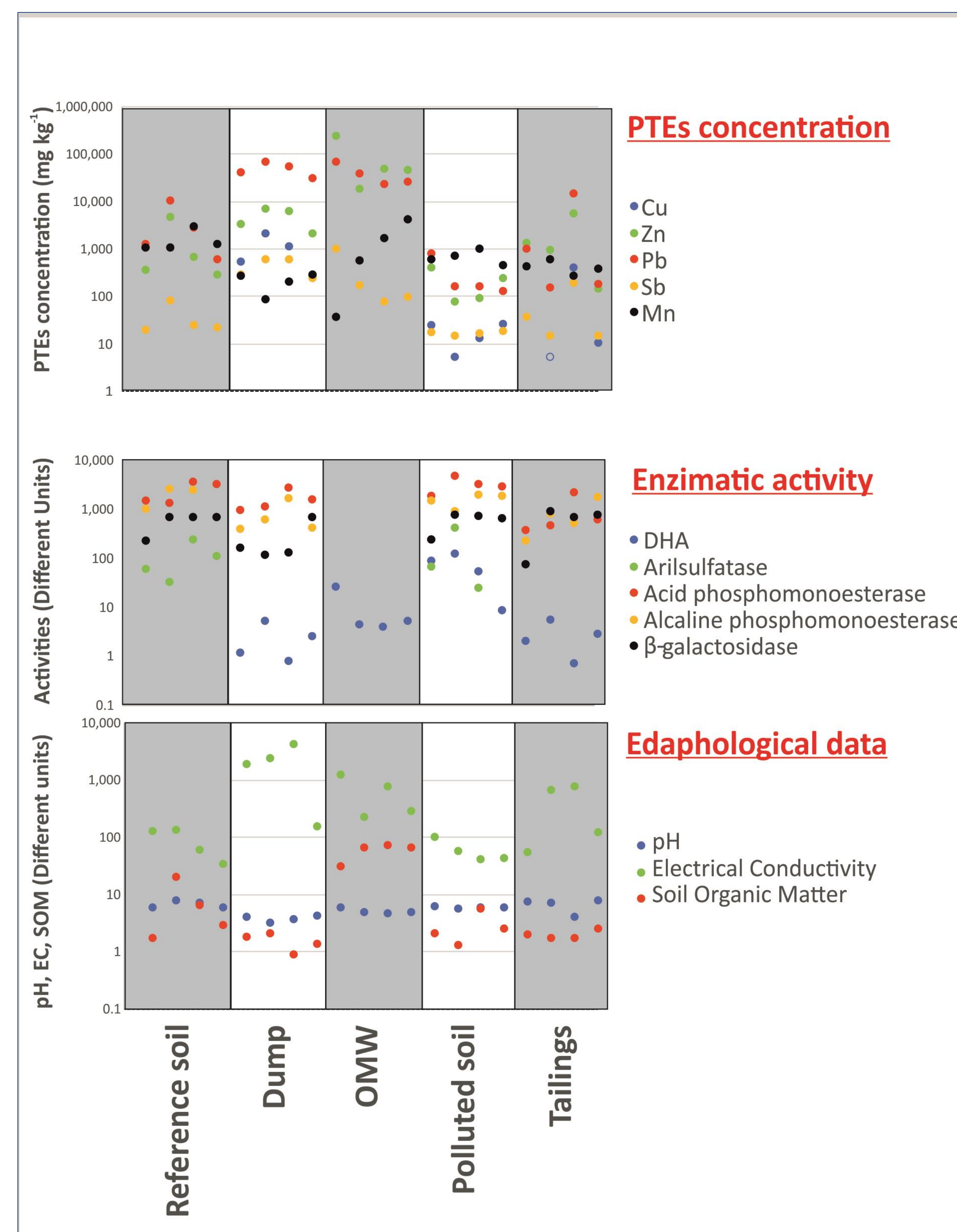


Figure 2. Potential toxic elements concentration, enzymatic activities and edaphological data

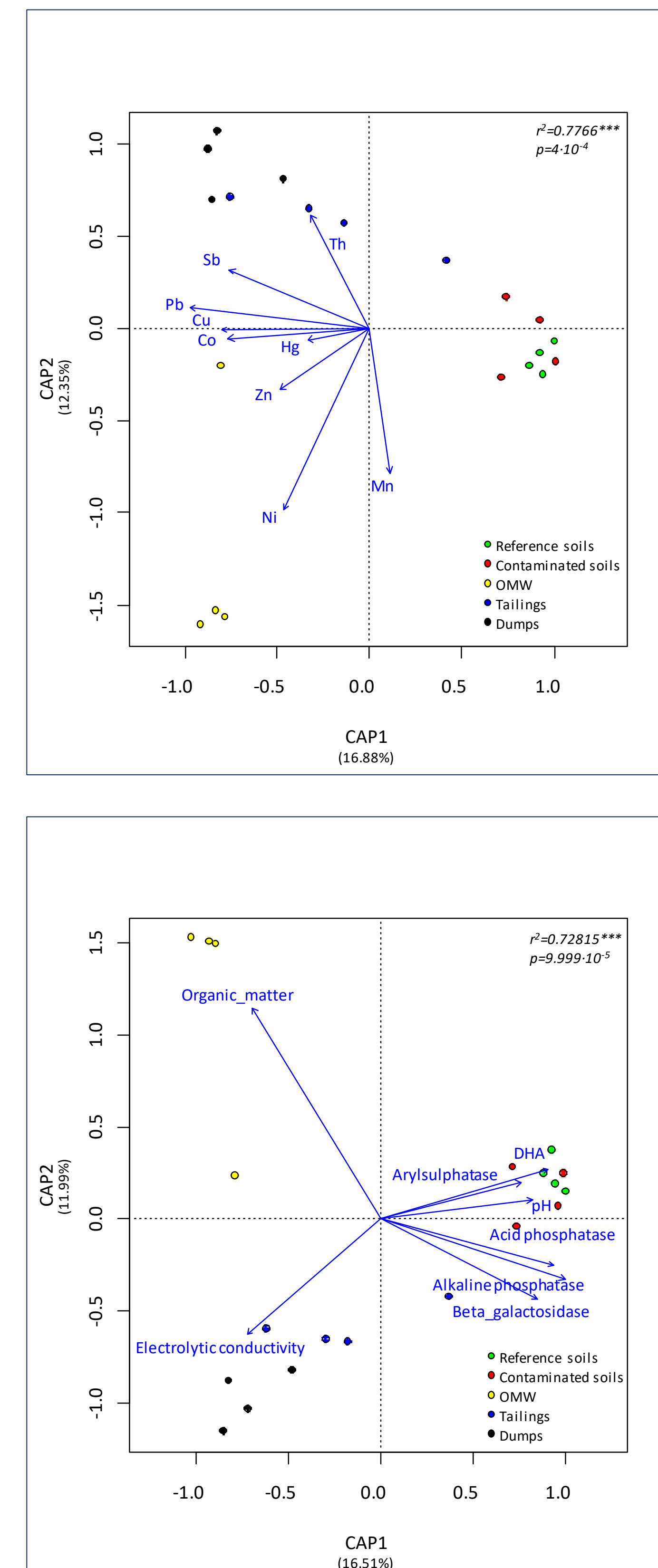


Figure 3. β-diversity analyses of bacterial communities and explanatory factors

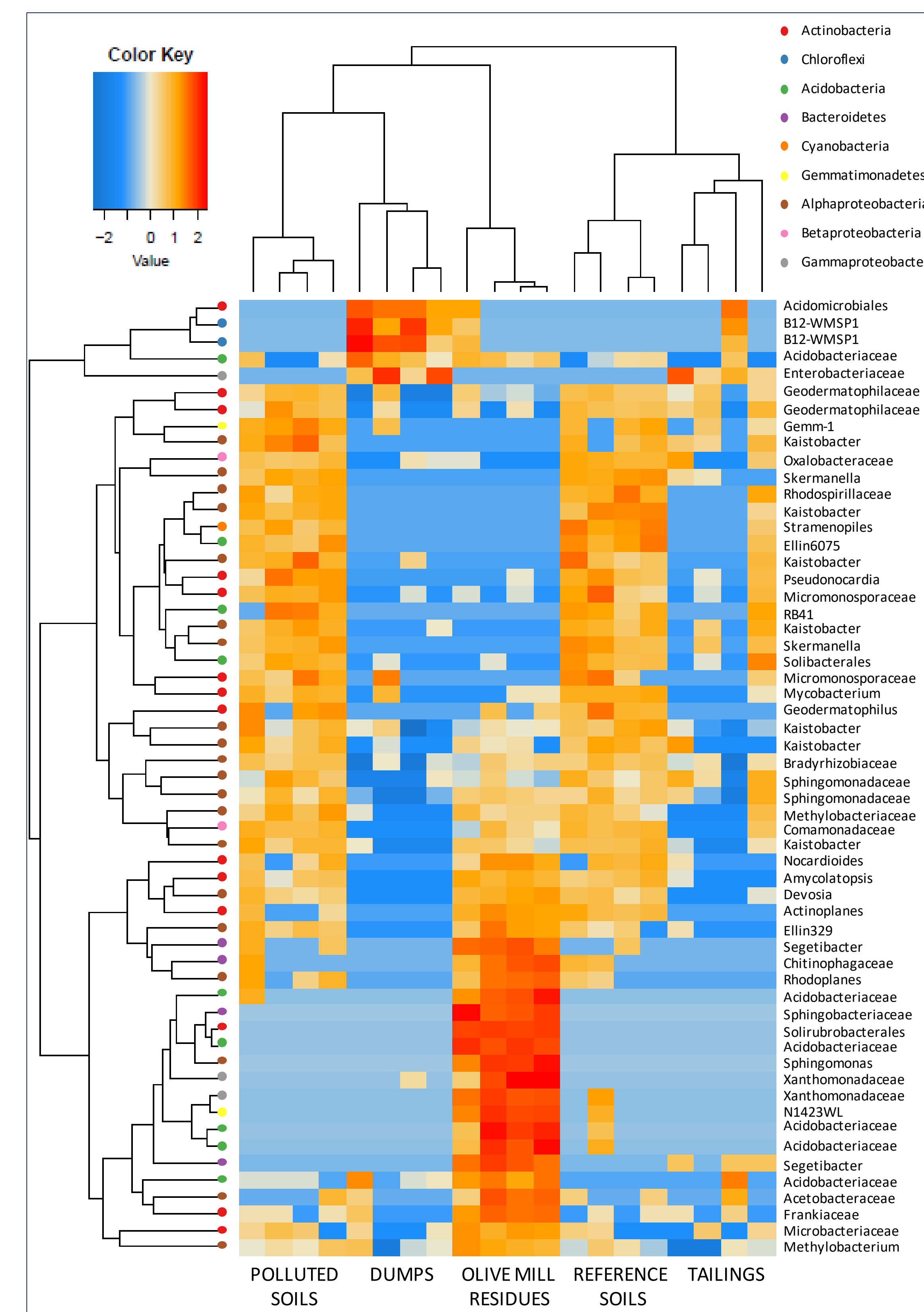


Figure 4. Heatmap of the OTUs significantly differing in their relative abundance between selected sites

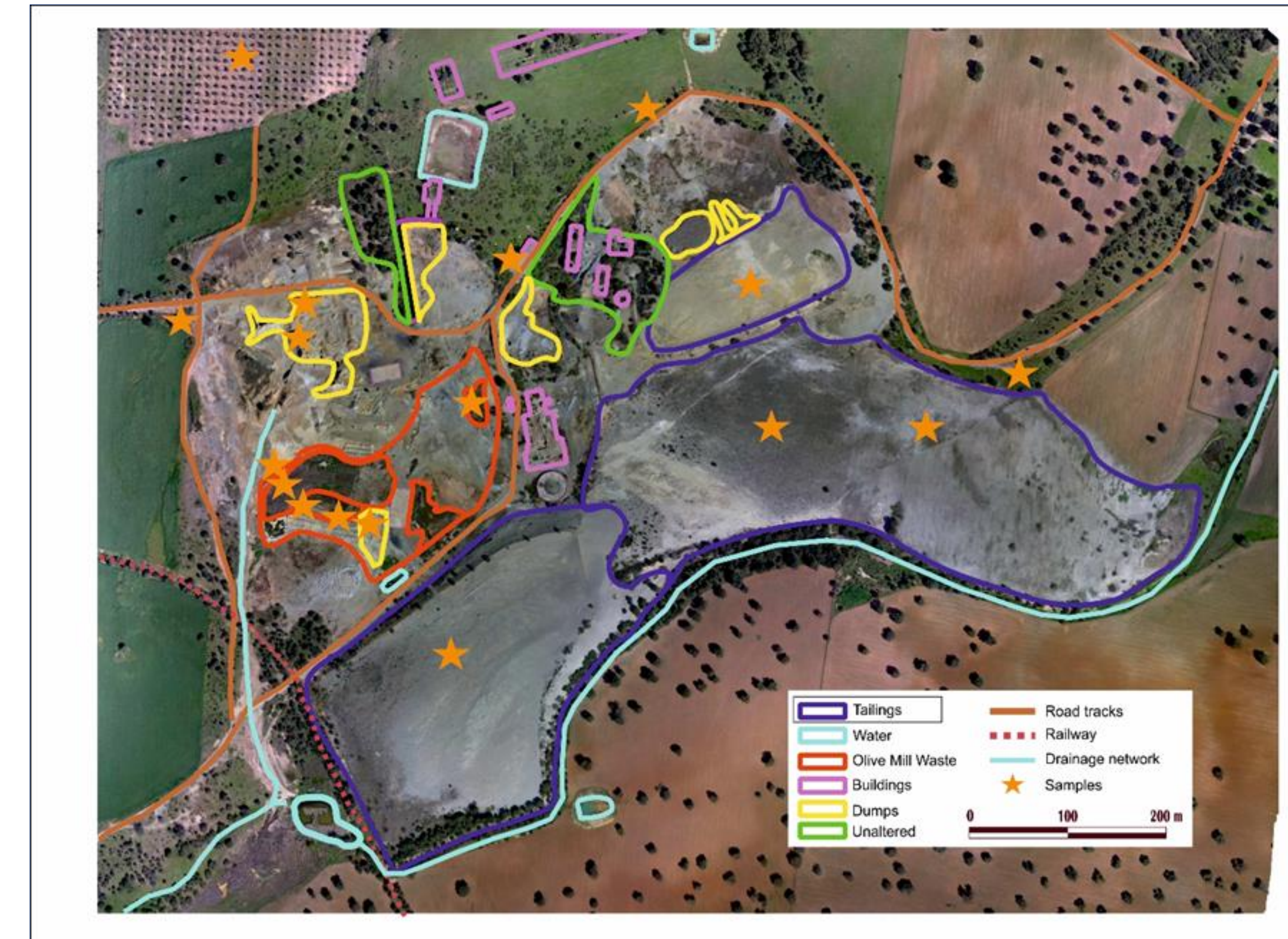


Figure 1. Geographical area and sampling sites

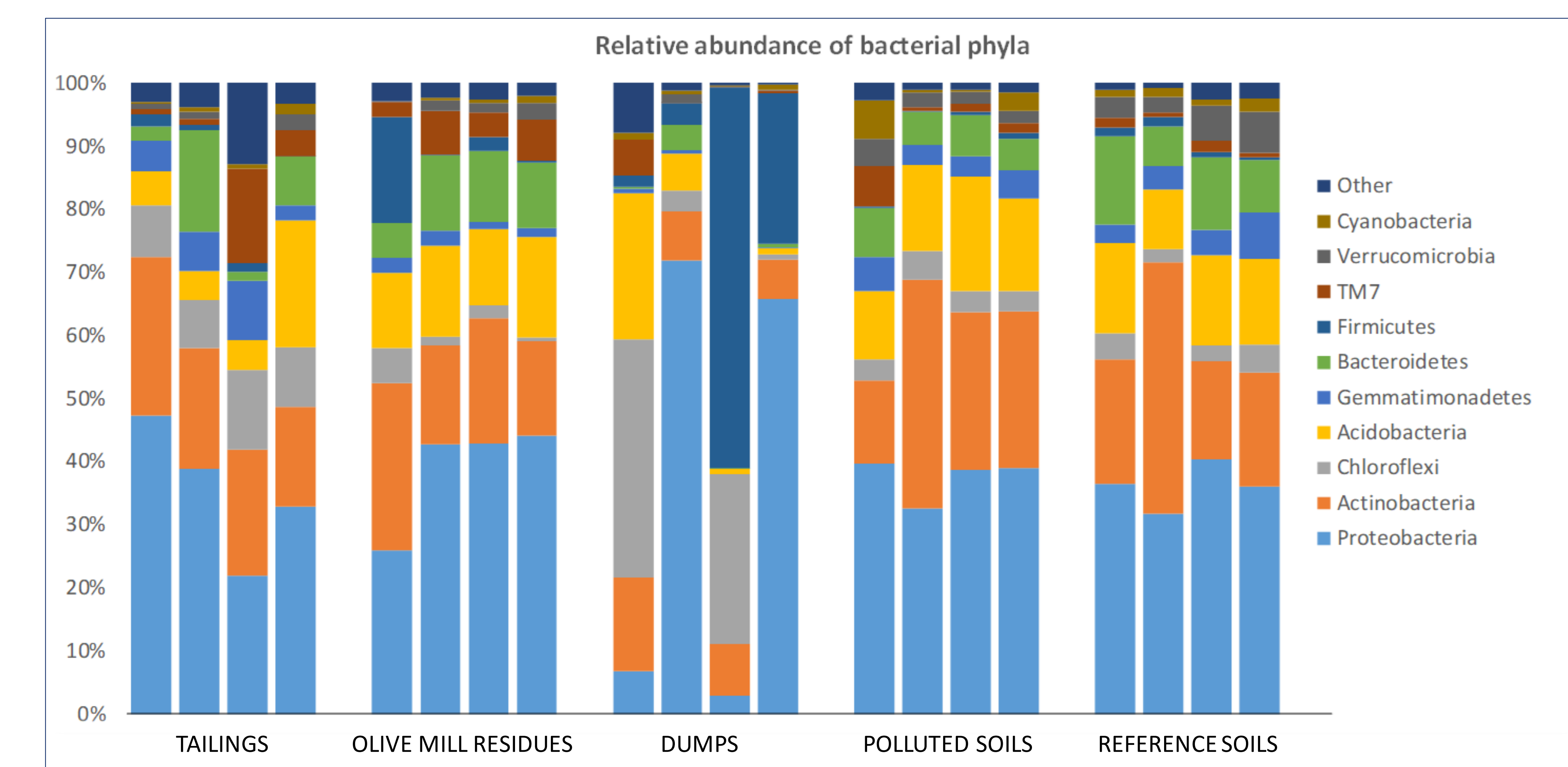


Figure 5. Relative abundance of most abundant bacterial phyla

Acknowledgements

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References

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Conclusions

Results showed that heavy metals were the main driving force in tailings, dump and OMW sites, while enzymatic activities were positively correlated with reference and contaminated soils. The most abundant phyla were Proteobacteria, Actinobacteria, Chloroflexi, Acidobacteria, Gemmatimonadetes, Bacteroidetes, Firmicutes, Verrucomicrobia and Cyanobacteria. A total of 57 OTUs were responsible of differences observed in the composition of soil bacterial communities.