

Thanks for stopping by my poster!

- This is my project website:
<https://www.ufz.de/spp-rhizosphere/index.php?en=46041>
- For more experimental details, hover over the images (does not work in browser).
- If you have any questions or suggestions, email me at minh.ganther@ufz.de.



SPATIAL SAMPLING APPROACH TO UNRAVEL THE IMPACT OF SOIL TEXTURE AND ROOT GENOTYPE ON MAIZE ROOT GENE EXPRESSION PROFILES

Minh Ganther¹, Marie-Lara Bouffaud¹, Lucie Gebauer¹, Francois Buscot¹, Doris Vetterlein¹, Anna Heintz-Buschart^{1,2}, Mika Tapio Tarkka¹

¹Helmholtz-Centre for Environmental Research, Halle, Germany

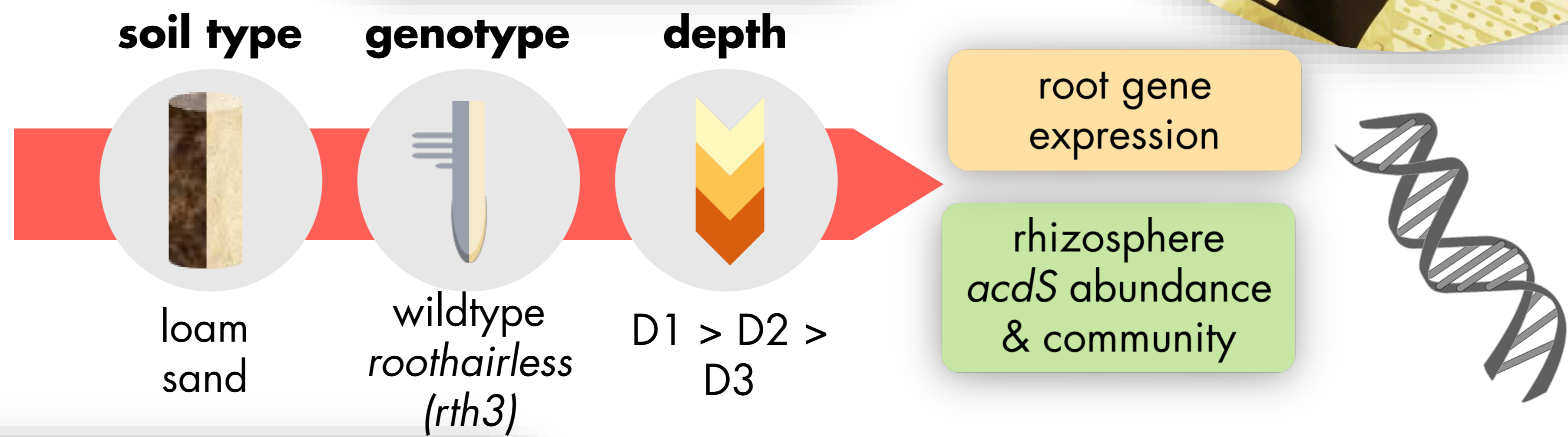
²German Centre for Integrative Biodiversity Research (iDiv), Halle-Jena-Leipzig, Germany



INTRODUCTION

Rhizosphere interactions are shaped by soil and plant properties¹. *acdS* bacteria decrease plant ethylene levels and thereby contribute profoundly to plant health². We investigated in a soil column experiment how soil types, root genotype, and depth gradients shape gene expression patterns of maize roots and rhizosphere *acdS* bacterial communities.

EXP. DESIGN



root genes

RESULTS

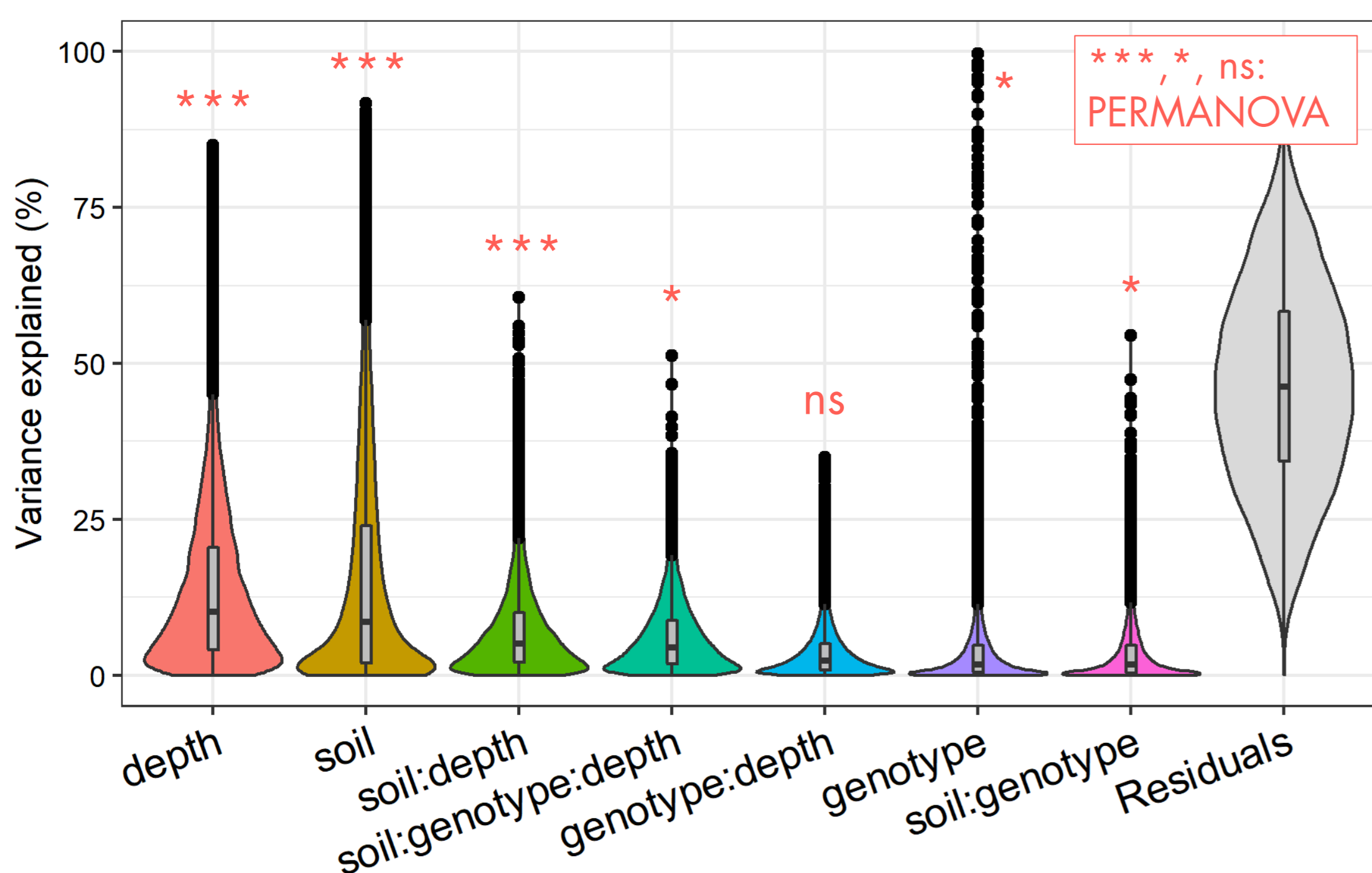
acdS bacteria

DRIVERS

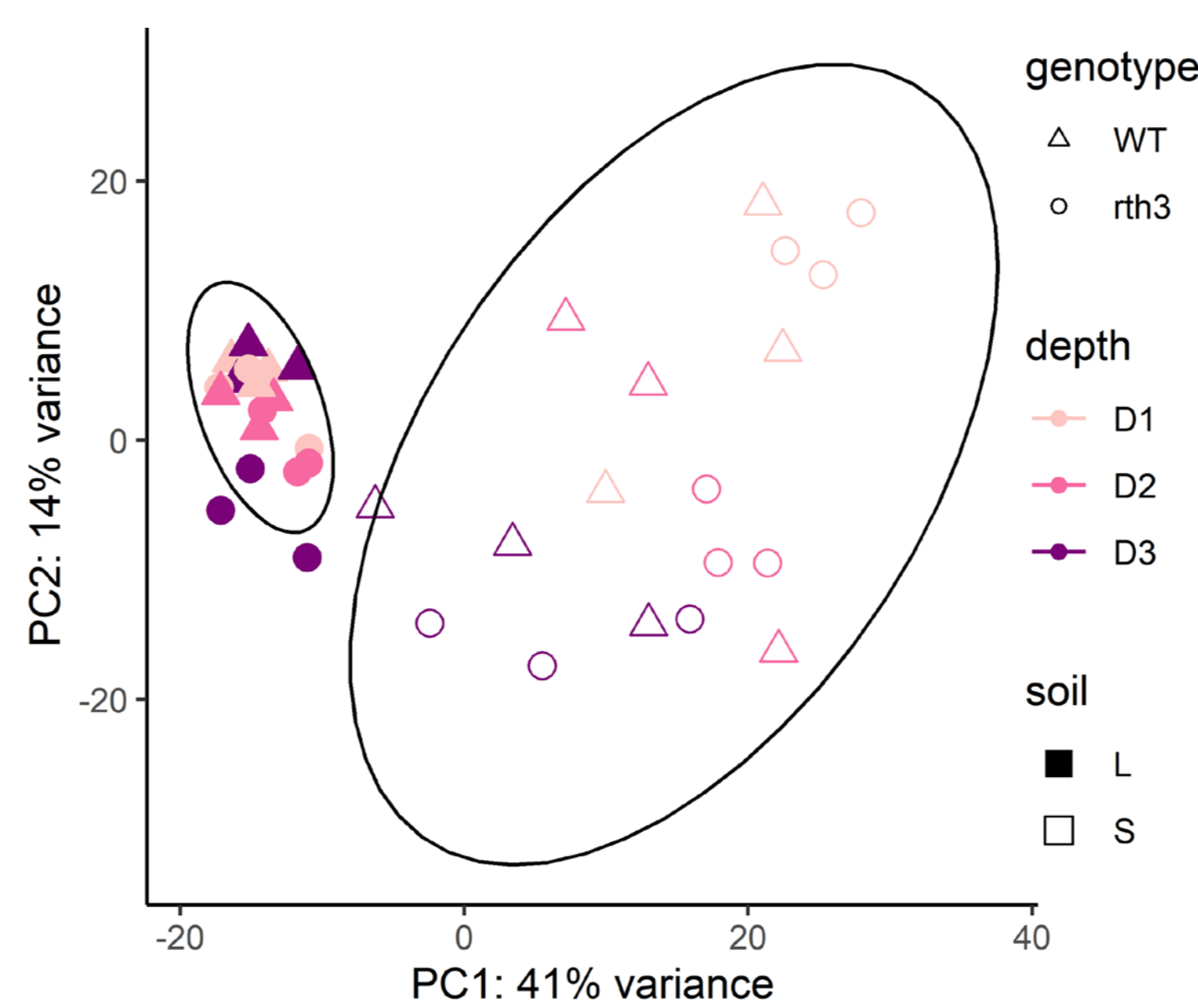
Root expression patterns are mainly explained by soil and depth, but genotype effect is surprisingly minor.

acdS bacteria community composition is also driven by soil and depth.

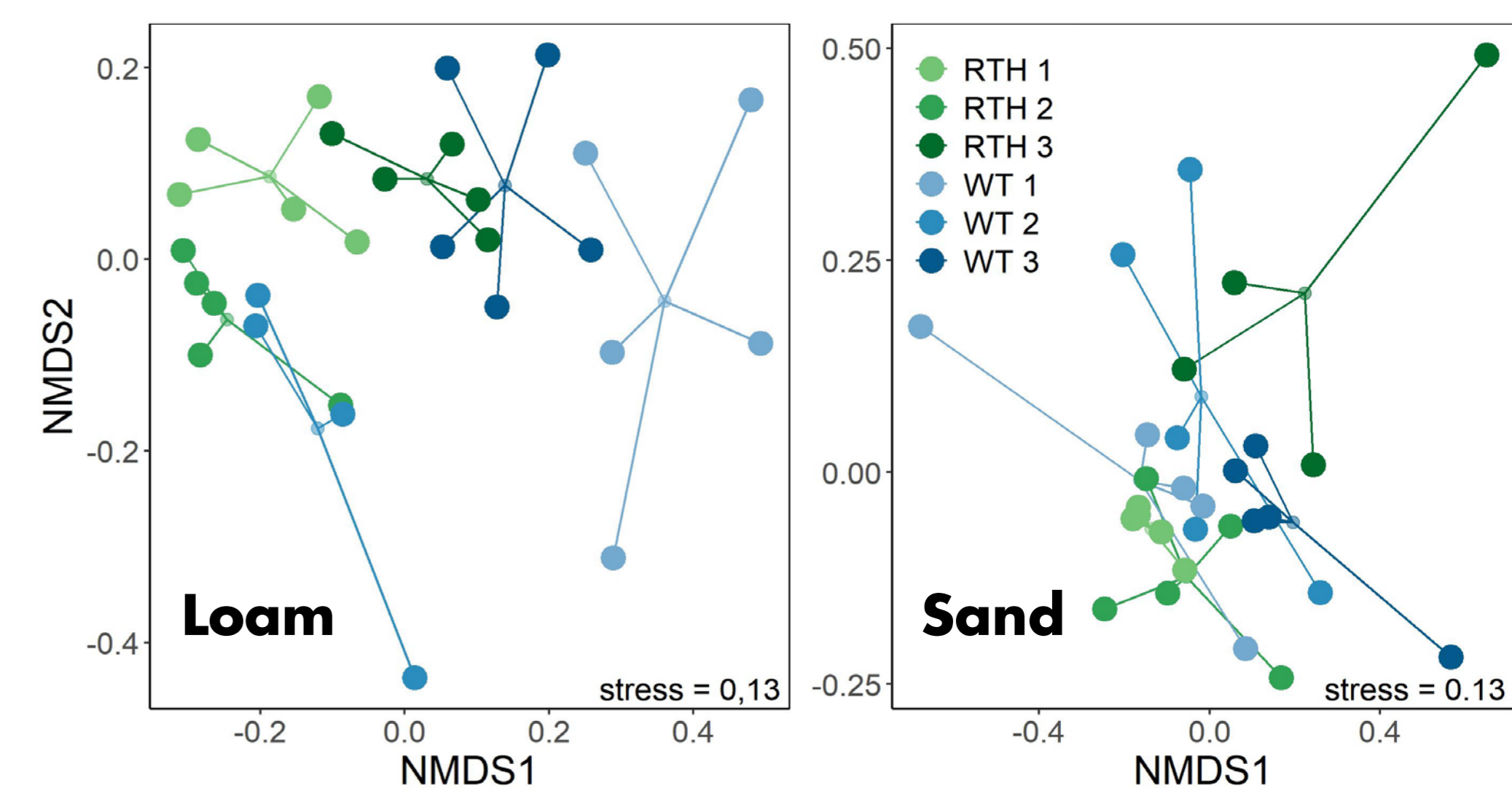
VariancePartitioning / PERMANOVA



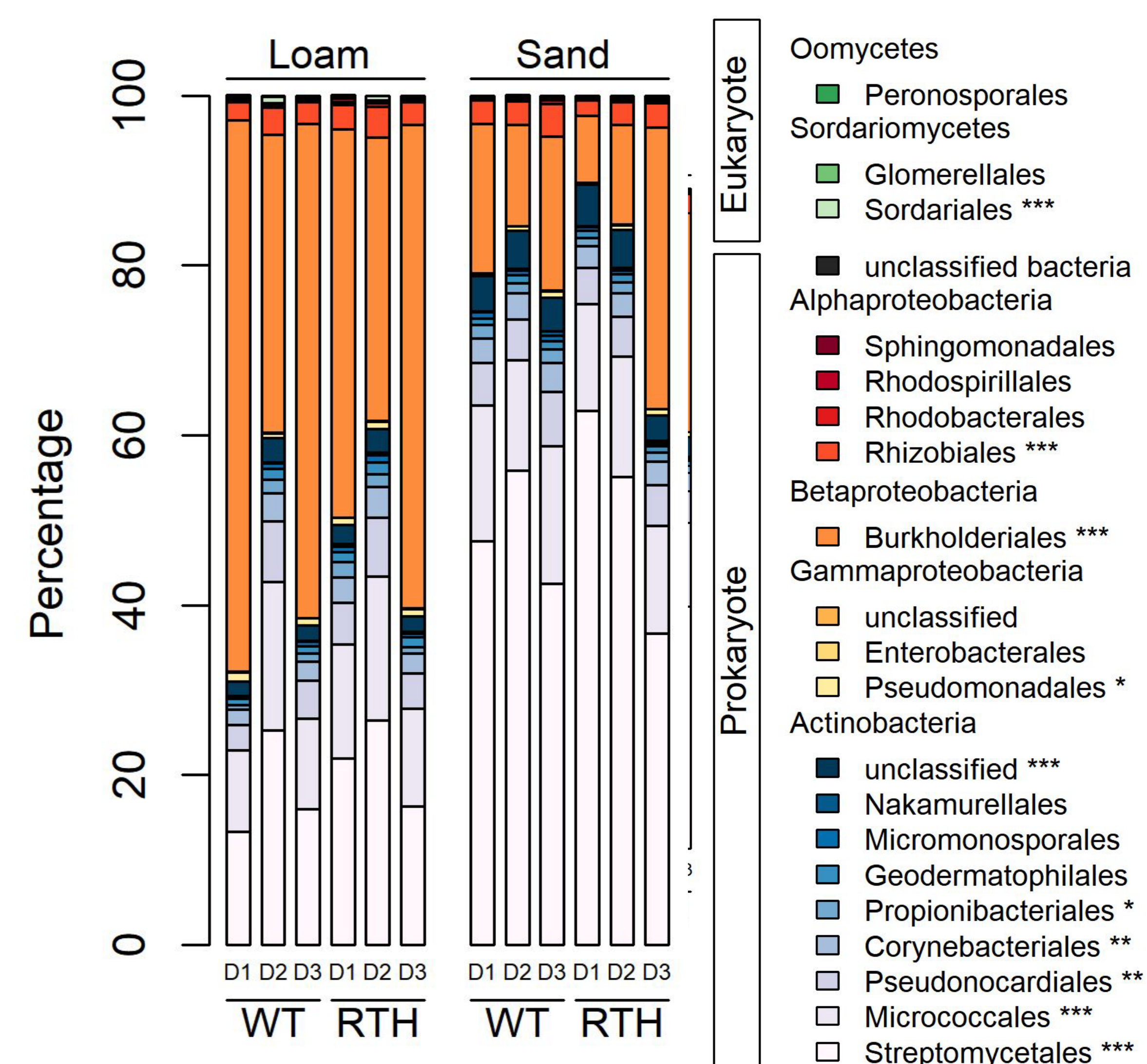
PCA



NMDS of acdS genes in the rhizosphere



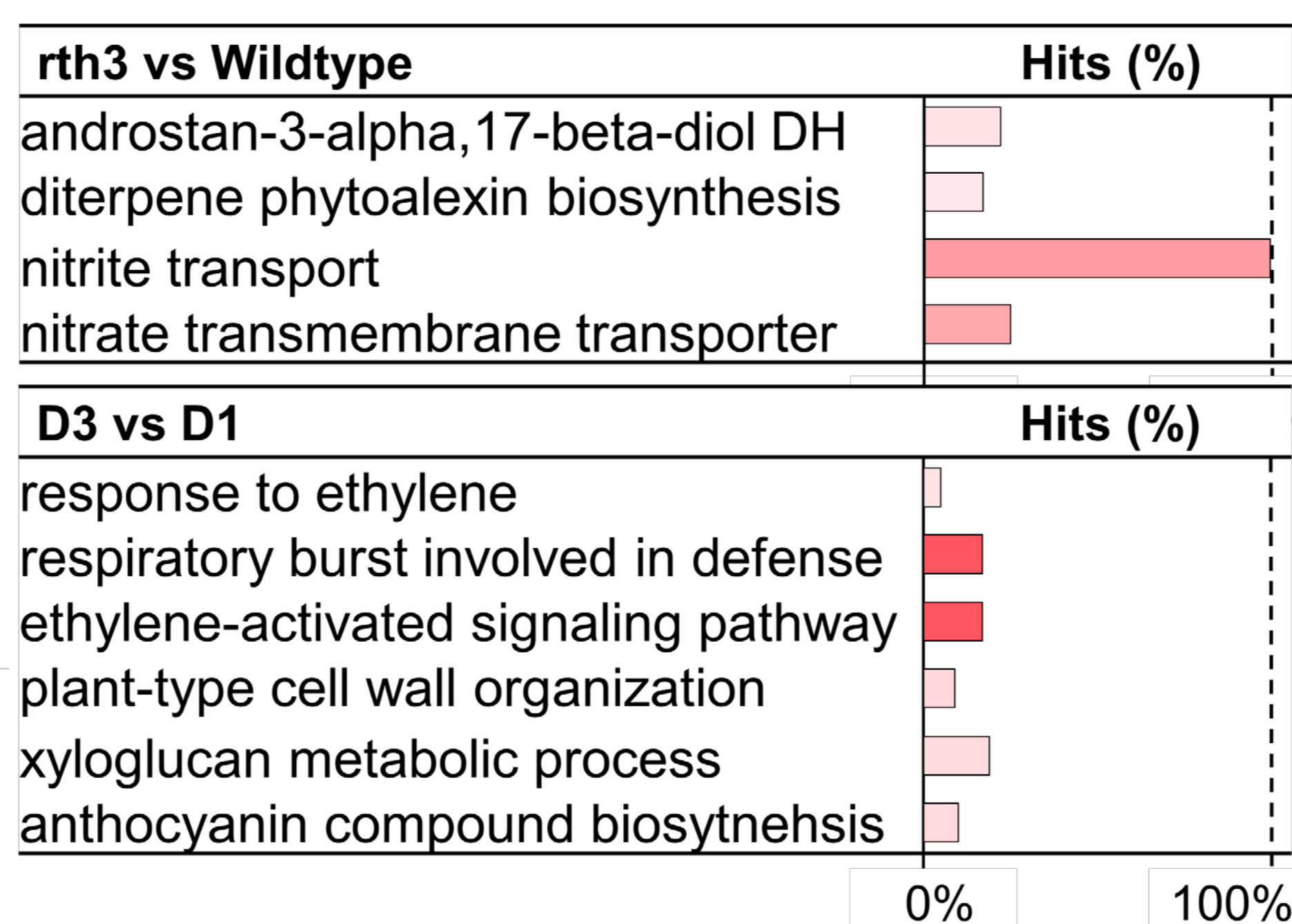
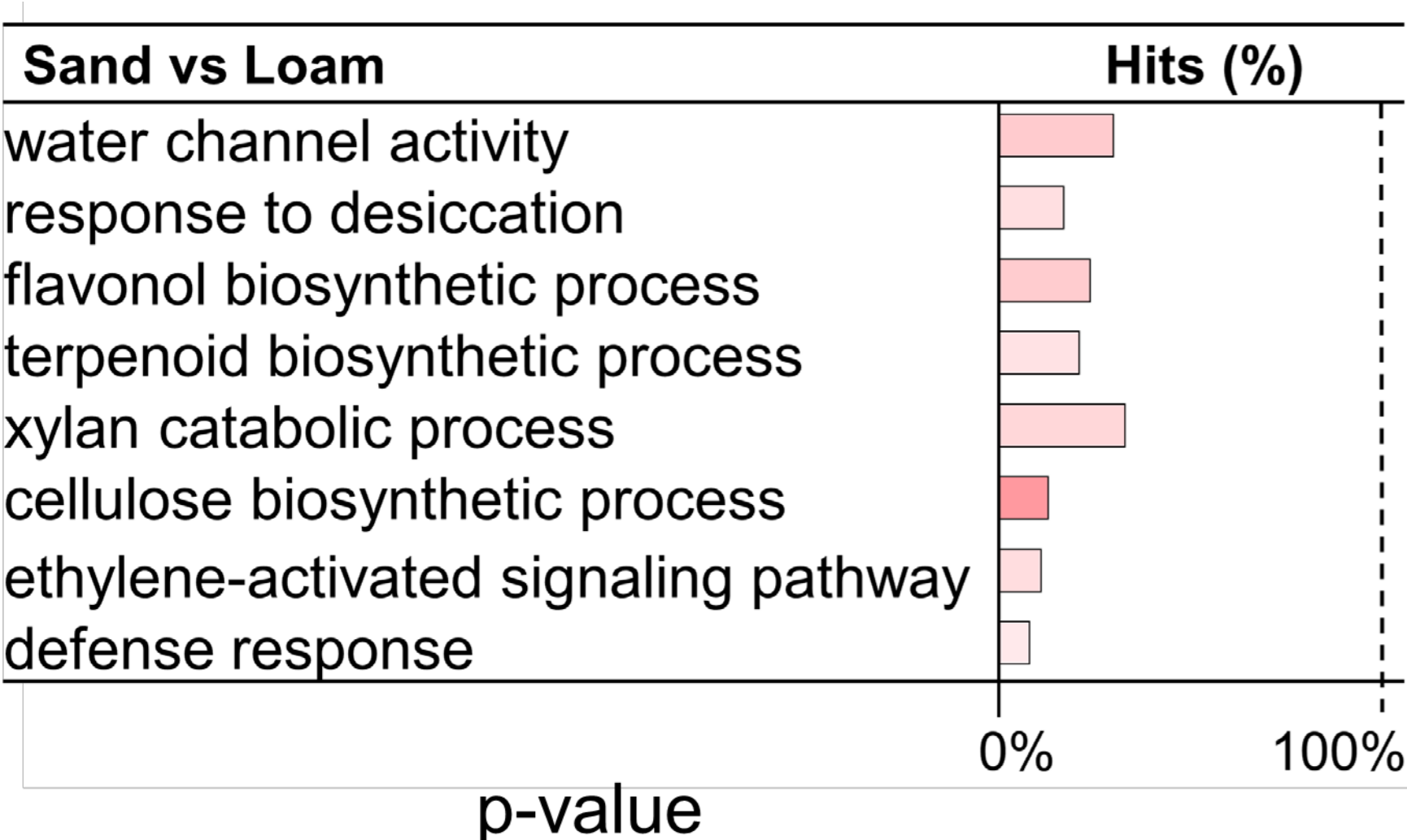
Relative abundance of acdS genes at the order level



FUNCTIONS

Differentially expressed genes comprise various interesting functions and pathways:

GO term analysis (genes with padj <0.05, >2-fold differential expression)



CONCLUSION

References

- 1 Berg G, Smalla K (2009) FEMS Microbiol Ecol 68: 1-13.
- 2 Glick BR (2014) Microbiol Res 169: 30-39.

Gefördert durch



- Soil and Depth are main drivers for both root gene expression and *acdS* bacteria community composition
- Differentially expressed genes relate to multiple functional categories such as: growth, water/nutrient uptake, secondary metabolism, stress, and phytohormone signaling.
- In Loam, *acdS* relative abundance is shifted towards proteobacteria, whereas in Sand, actinobacteria are more abundant.