

Aeration and mineral composition of soil mediate microbial CUE

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Supplementary material

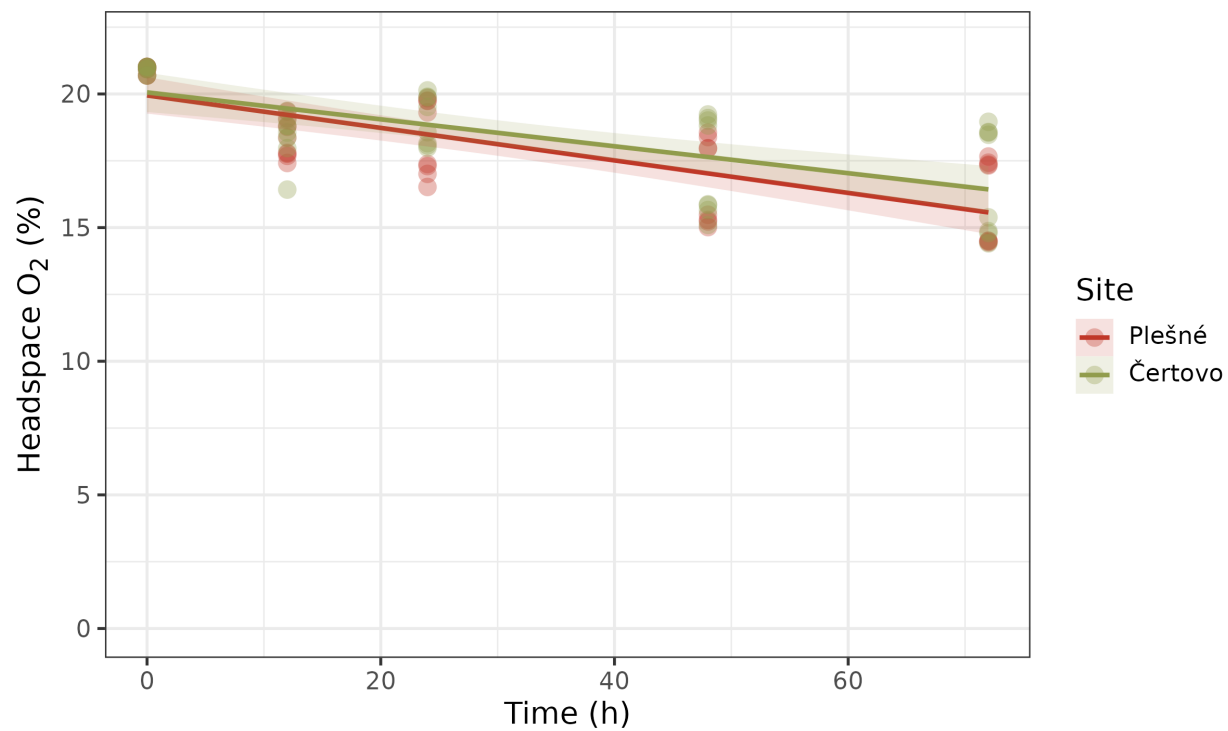


Figure S1. Headspace oxygen values during the incubation of forest soil from PL (Plešné) and CT (Čertovo) sites (oxic incubations only).

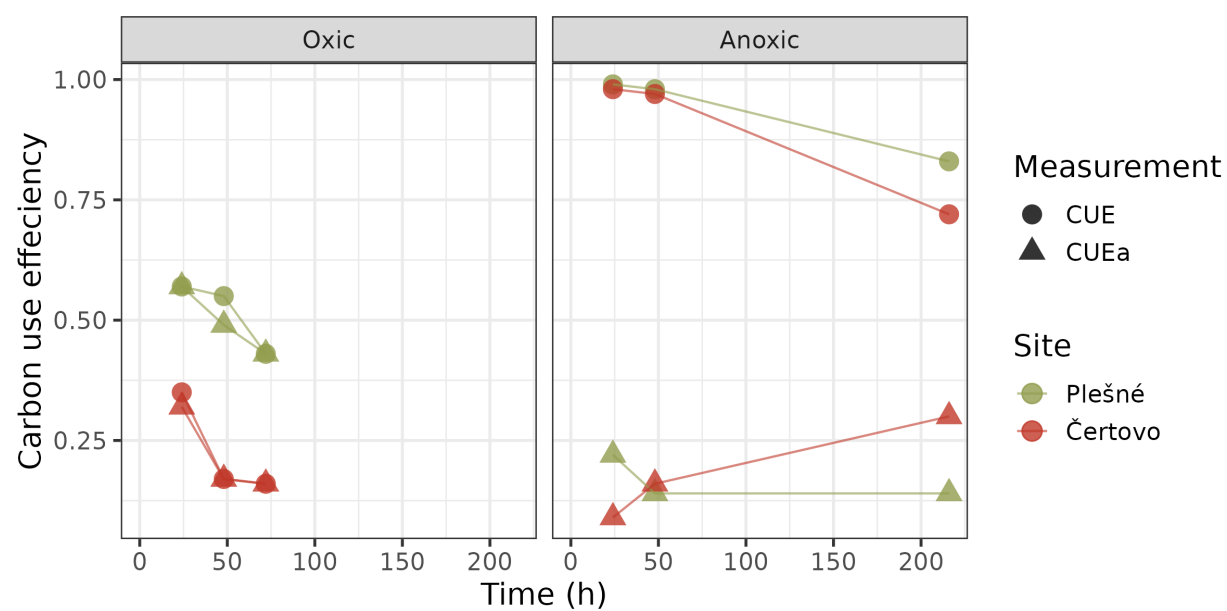


Figure S2. Changes in CUE and CUEa over time in the oxic and anoxic incubations.

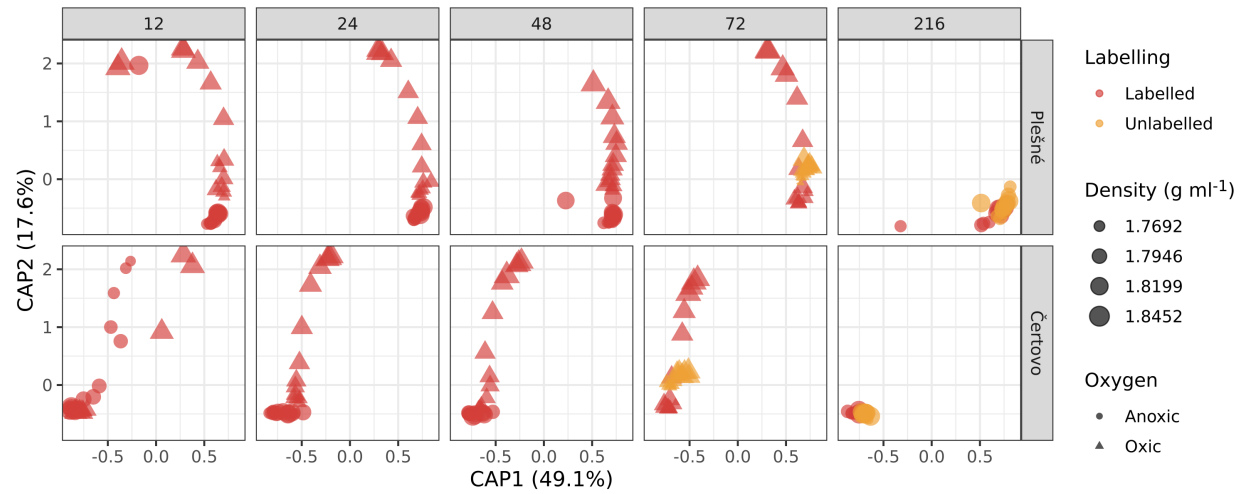


Figure S3. Principal coordinate analyses plots of the bacterial community composition based on Morisita–Horn distances in the different SIP fractions. The plots represent a single model obtained using the constrained model: distance matrix Site * Oxygen * Time * Density.zone. The plot was faceted for visual clarity.

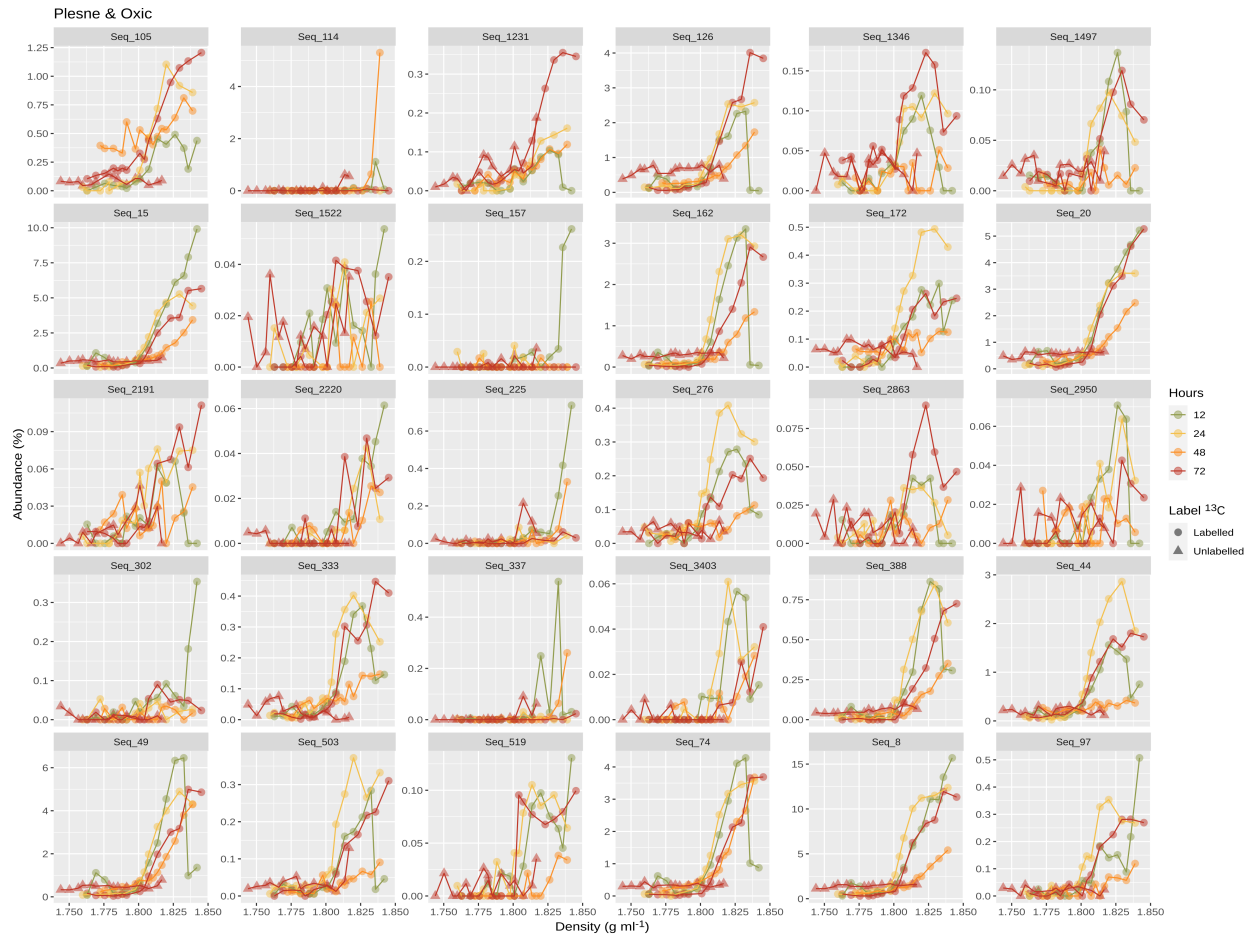


Figure S4. Relative abundances of 30 ASVs with the highest fold change (\log_2) between 'heavy' and 'light' density gradient zones detected using DESeq2. Plešné Lake soil incubated under oxic conditions.

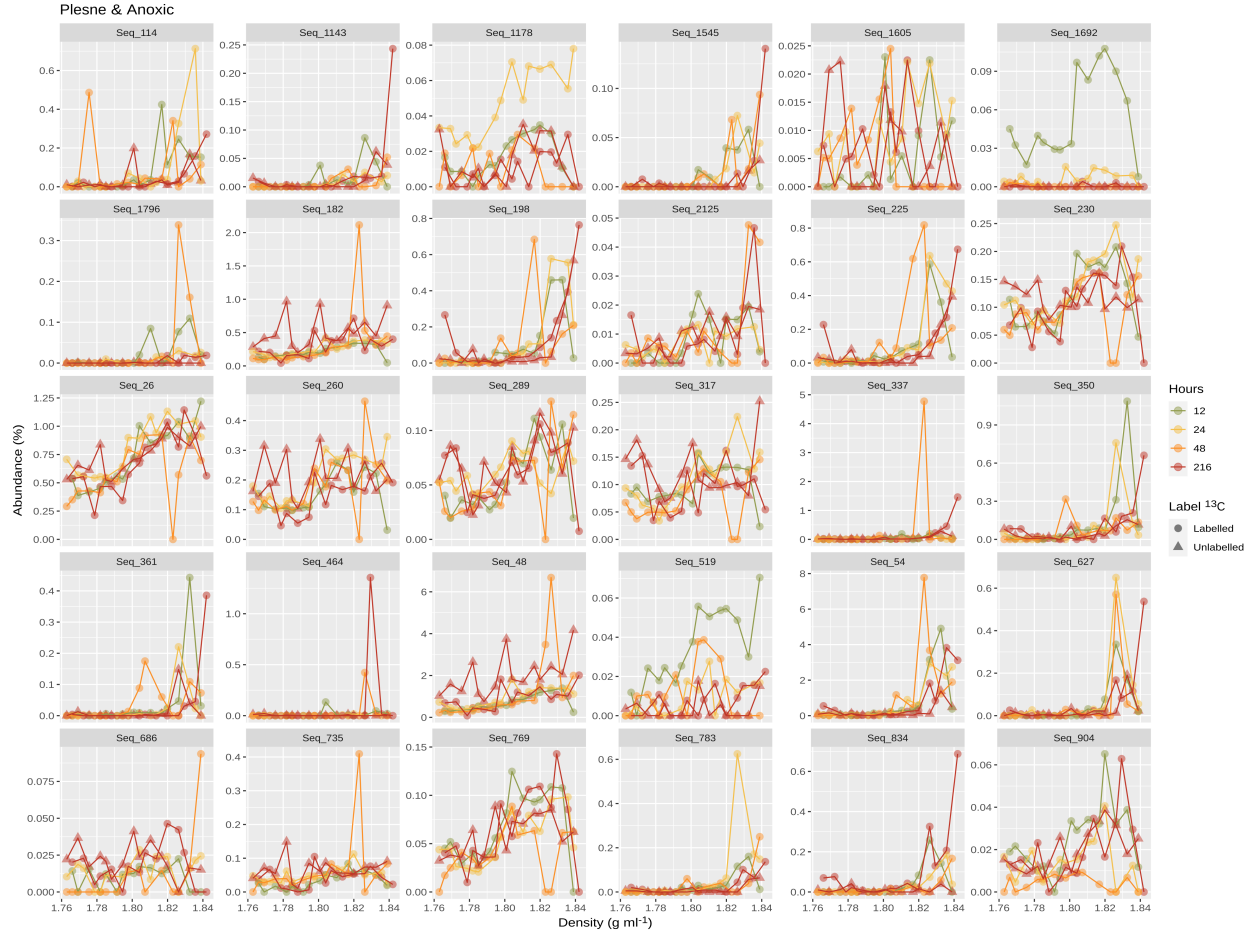


Figure S5. Relative abundances of 30 ASVs with the highest fold change (log₂) between 'heavy' and 'light' density gradient zones detected using DESeq2. Plešné Lake soil incubated under anaerobic conditions.

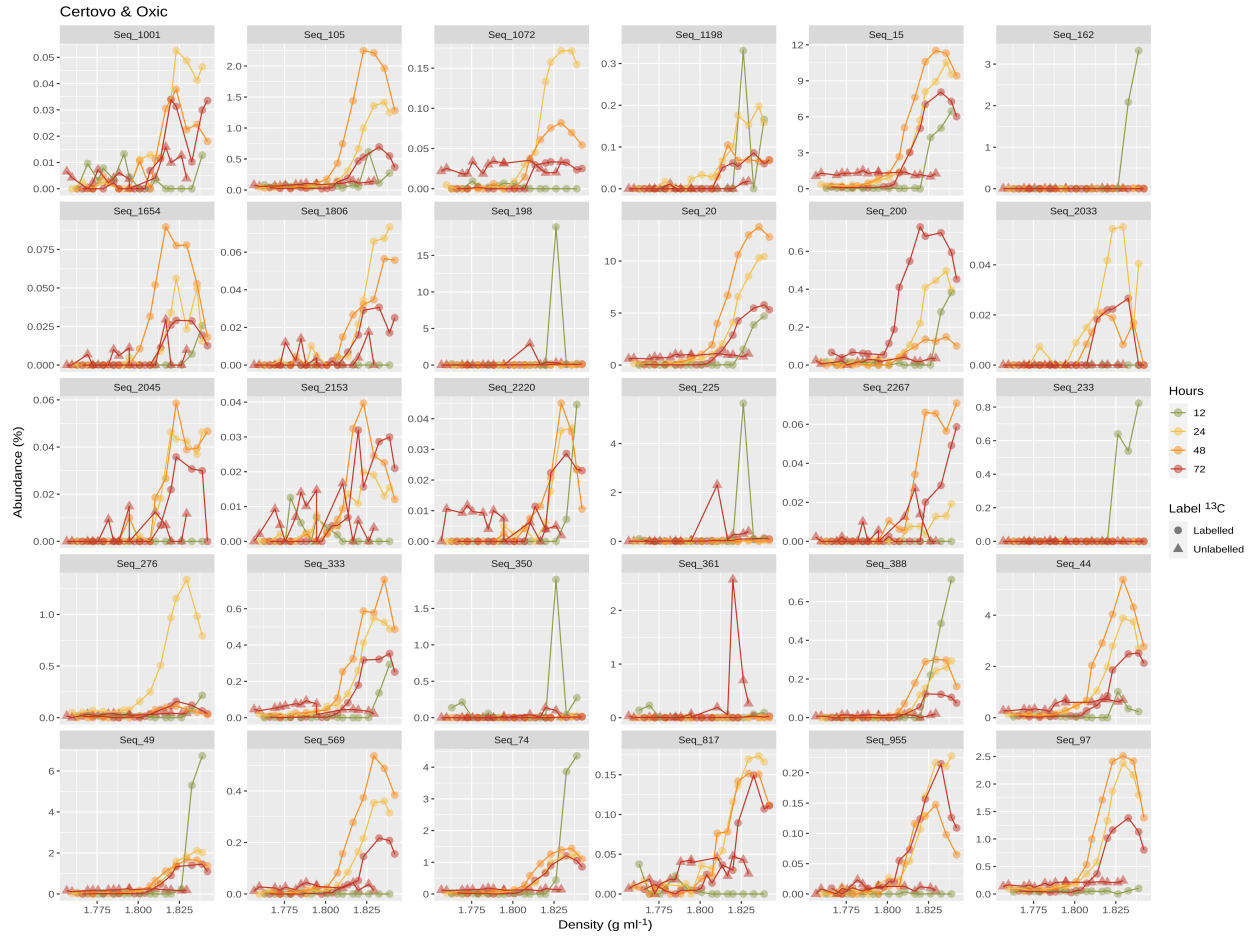


Figure S6. Relative abundances of 30 ASVs with the highest fold change (log₂) between 'heavy' and 'light' density gradient zones detected using DESeq2. Čertovo Lake soil incubated under oxic conditions.

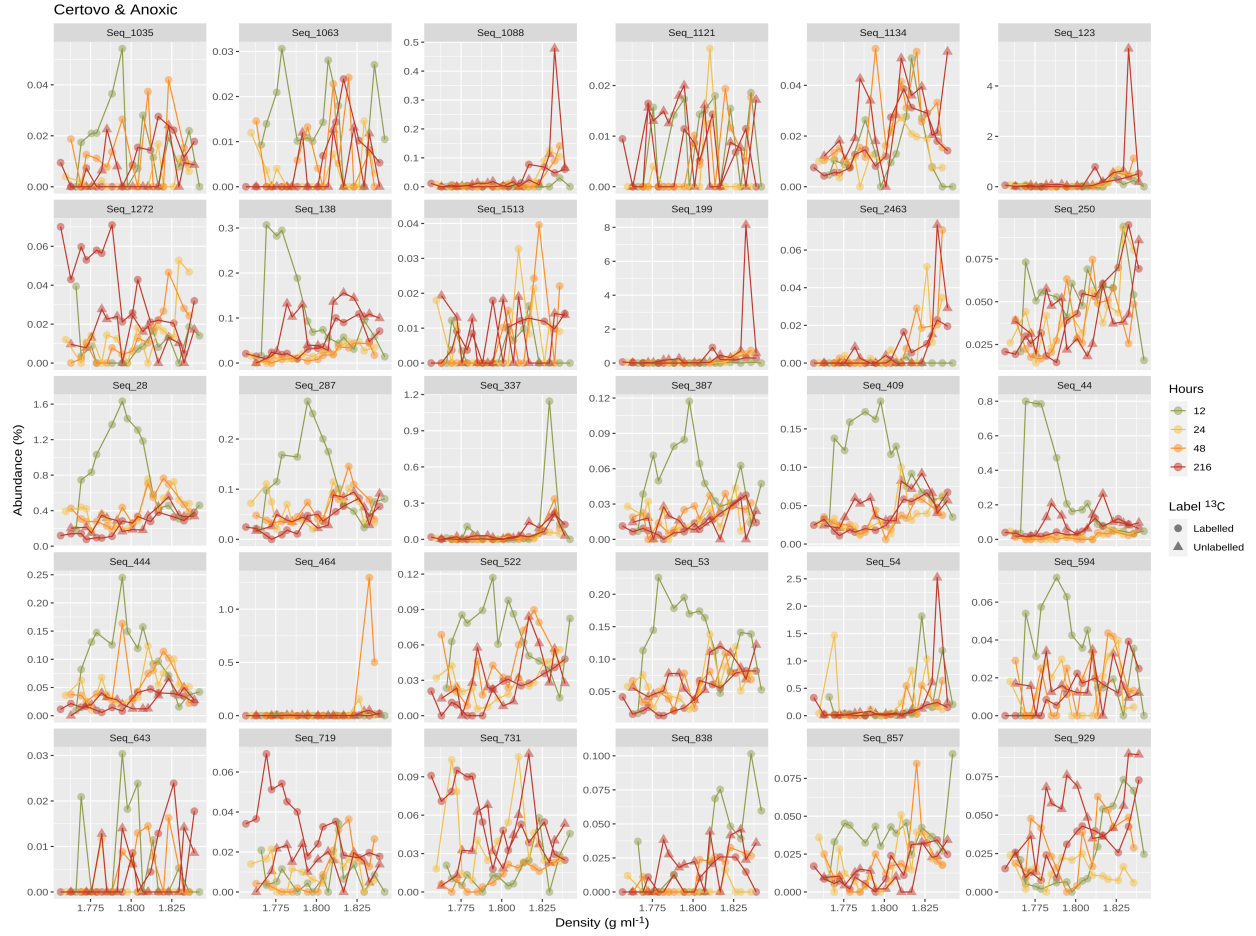


Figure S7. Relative abundances of 30 ASVs with the highest fold change (\log_2) between 'heavy' and 'light' density gradient zones detected using DESeq2. Čertovo Lake soil incubated under anoxic conditions.

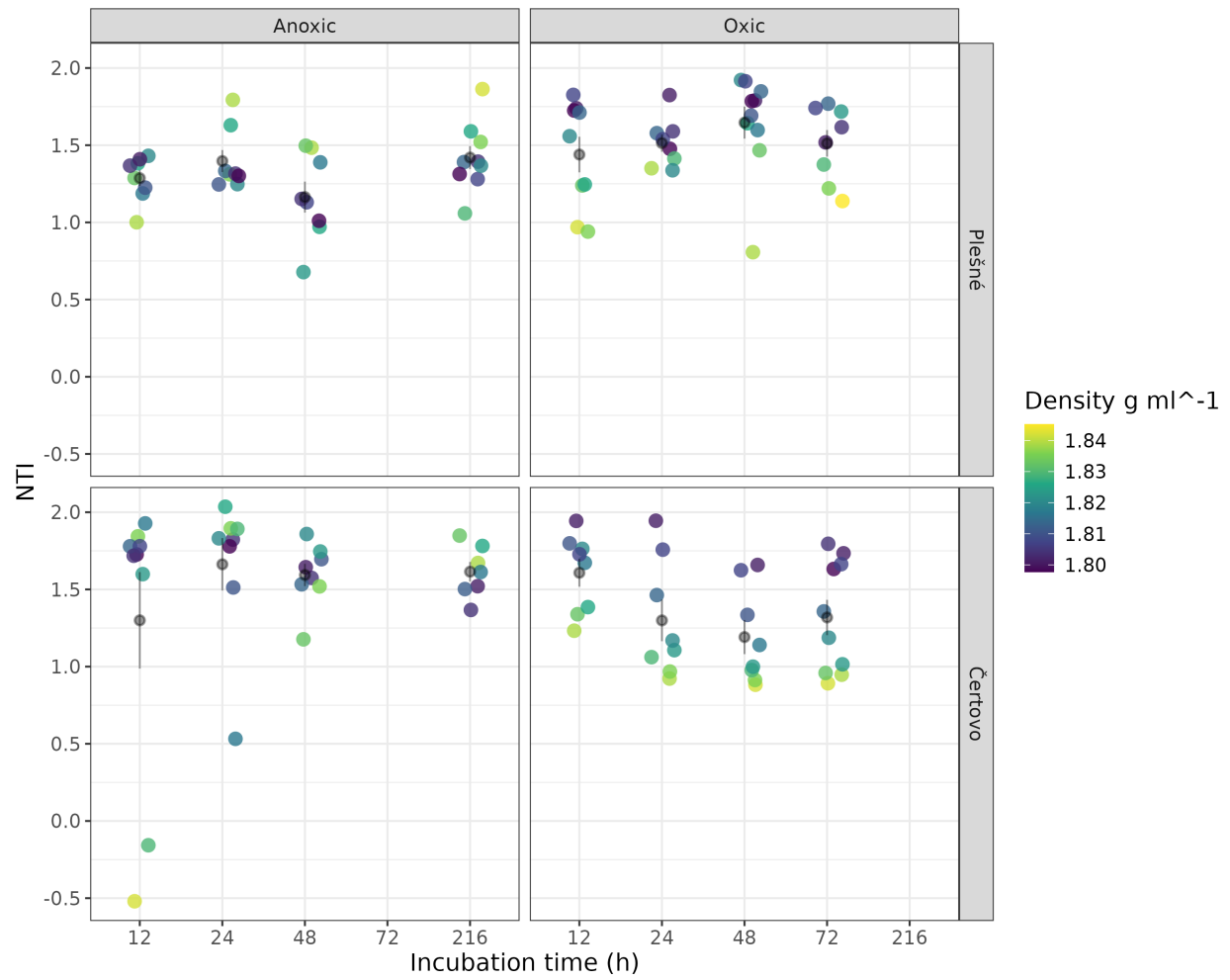


Figure S8. Nearest taxon index (NTI) values for phylogenetic trees comprised of labelled ASVs from the ‘heavy’ fractions of each labelled gradient. Positive values indicate higher phylogenetic clustering than expected by chance.