

**Supplementary Figures: Large, old pools of carbon and microbial communities are present deep
in soils under a temperate planted forest**

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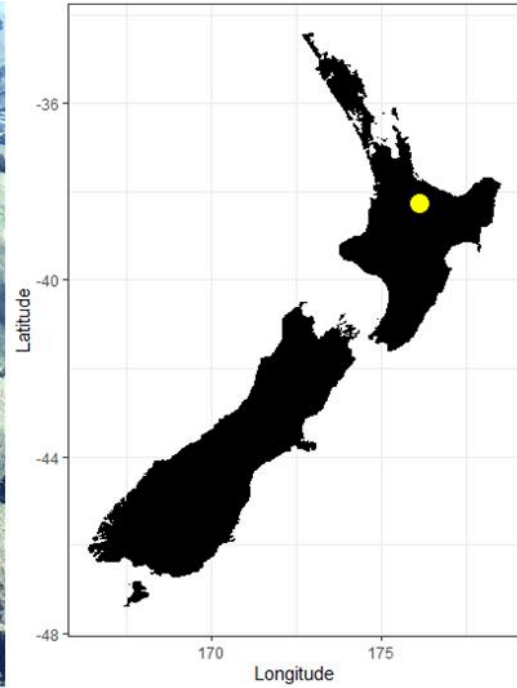


Figure A.1. (Left) An aerial image of Puruki Experimental Forest taken in 1981 which shows the coverage of the 35-hectare *P. radiata* forest area and surrounding land use types (Brownlie and Kelliher, 1989). (Right) The location of Puruki Experimental Forest in the Central North Island of New Zealand.

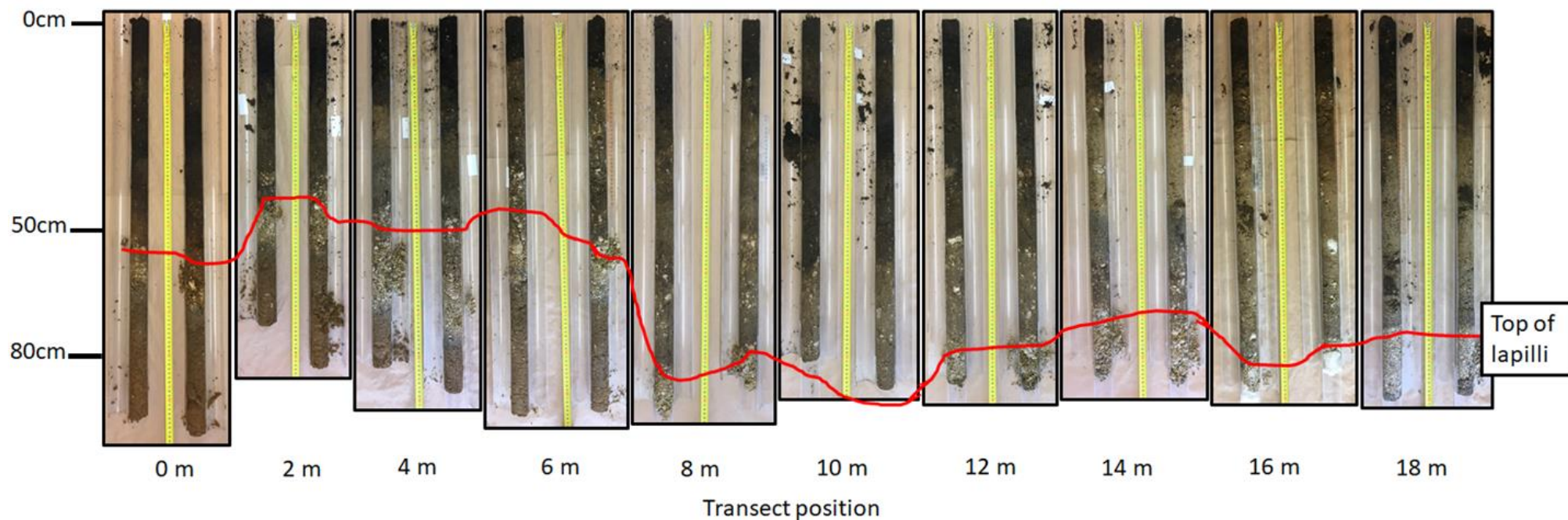


Figure A.2. The 1 metre deep soil cores taken from each transect sampling position across Puruki Forest. Two paired soil cores were extracted from each transect position for soil chemistry/DNA analysis and bulk density analysis. A visual inspection of paired soil cores was undertaken after sampling to check for considerable differences in soil colour and texture by depth. The top of the Taupo pumice lapilli layer in each soil core can be seen in the image.

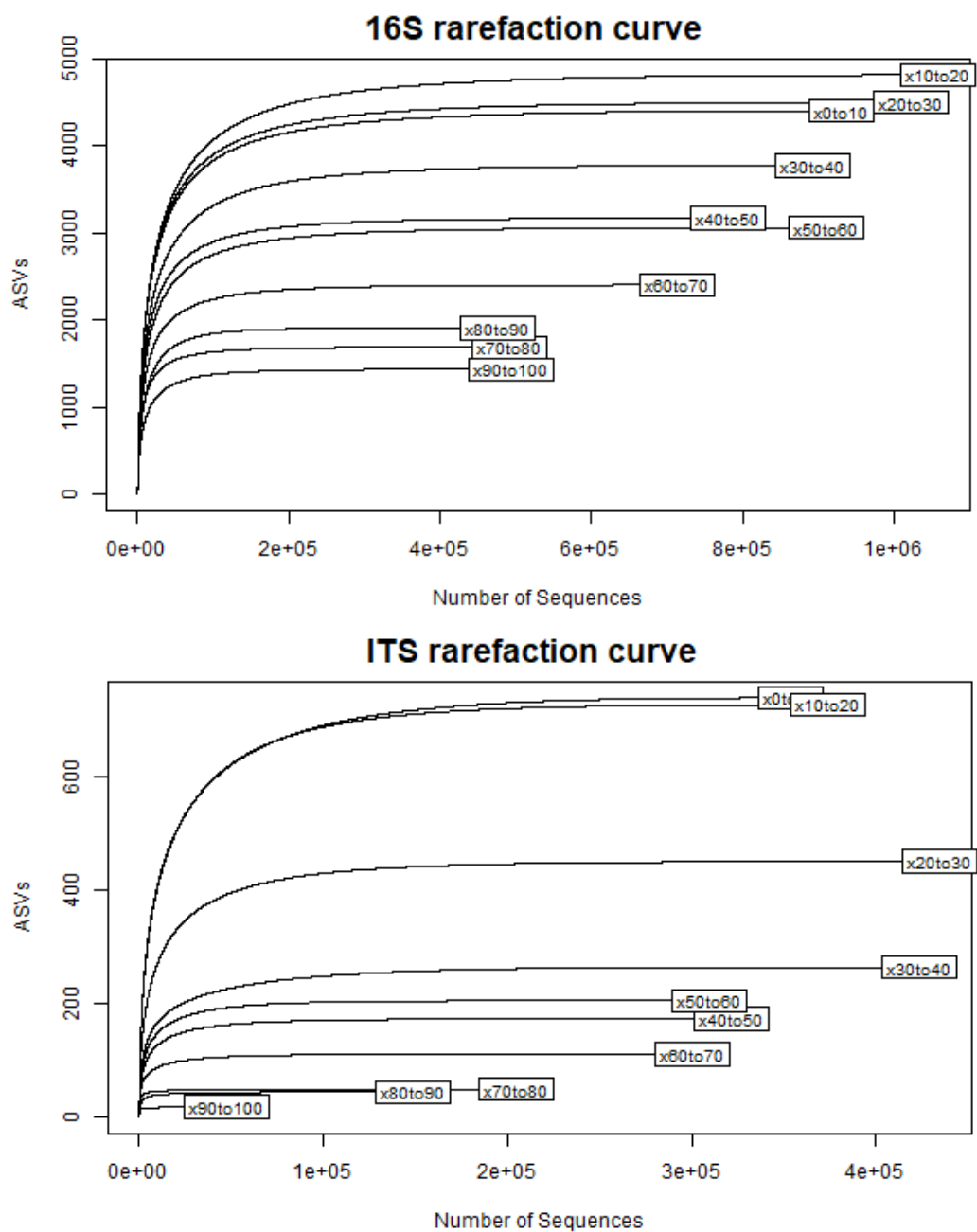


Figure A.3. Rarefaction curves showing the 16S (a) and ITS (b) ASV richness for each depth increment.

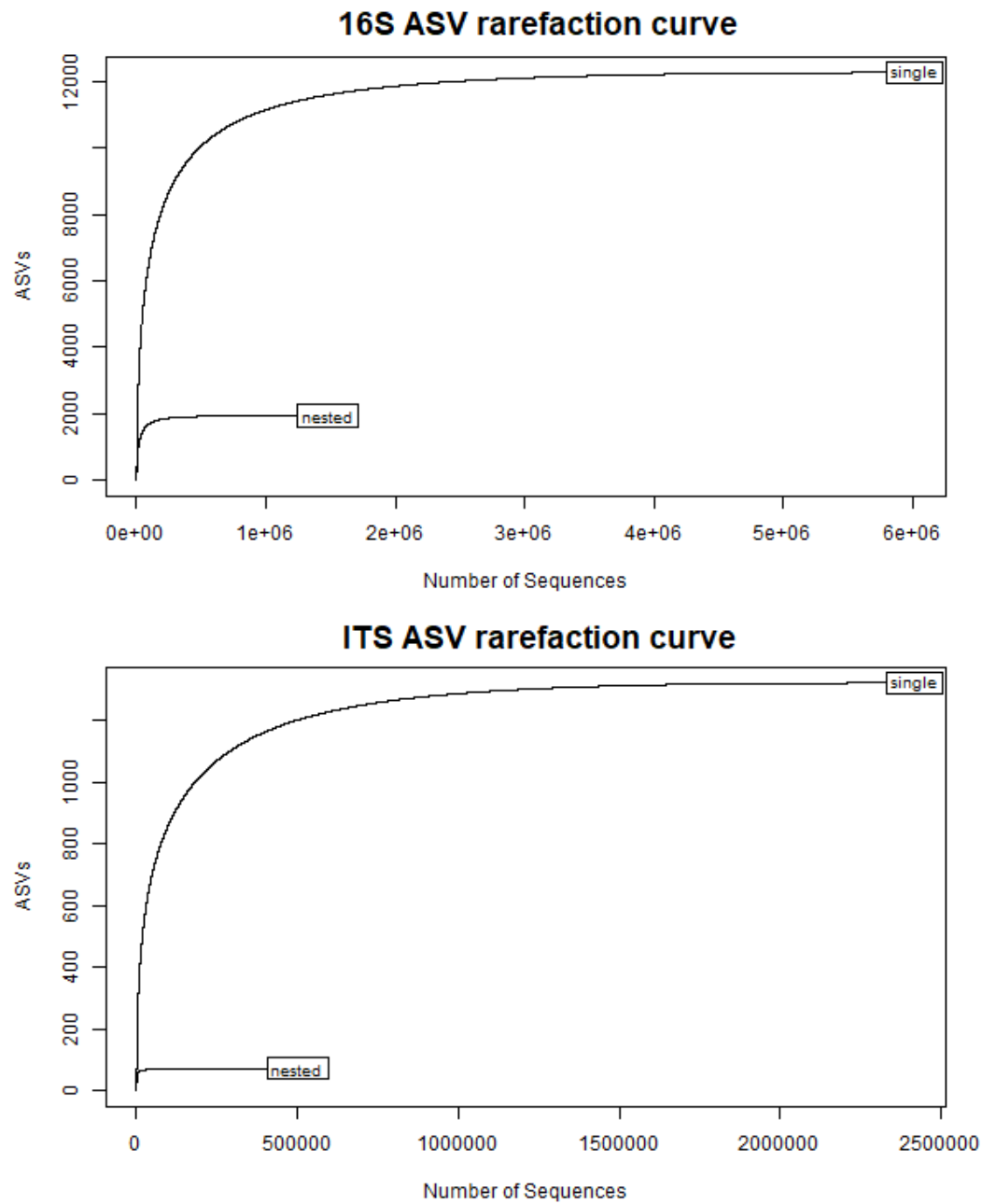


Figure A.4. Rarefaction curves showing the 16S (a) and ITS (b) ASV richness between DNA samples amplified using nested vs single PCR.

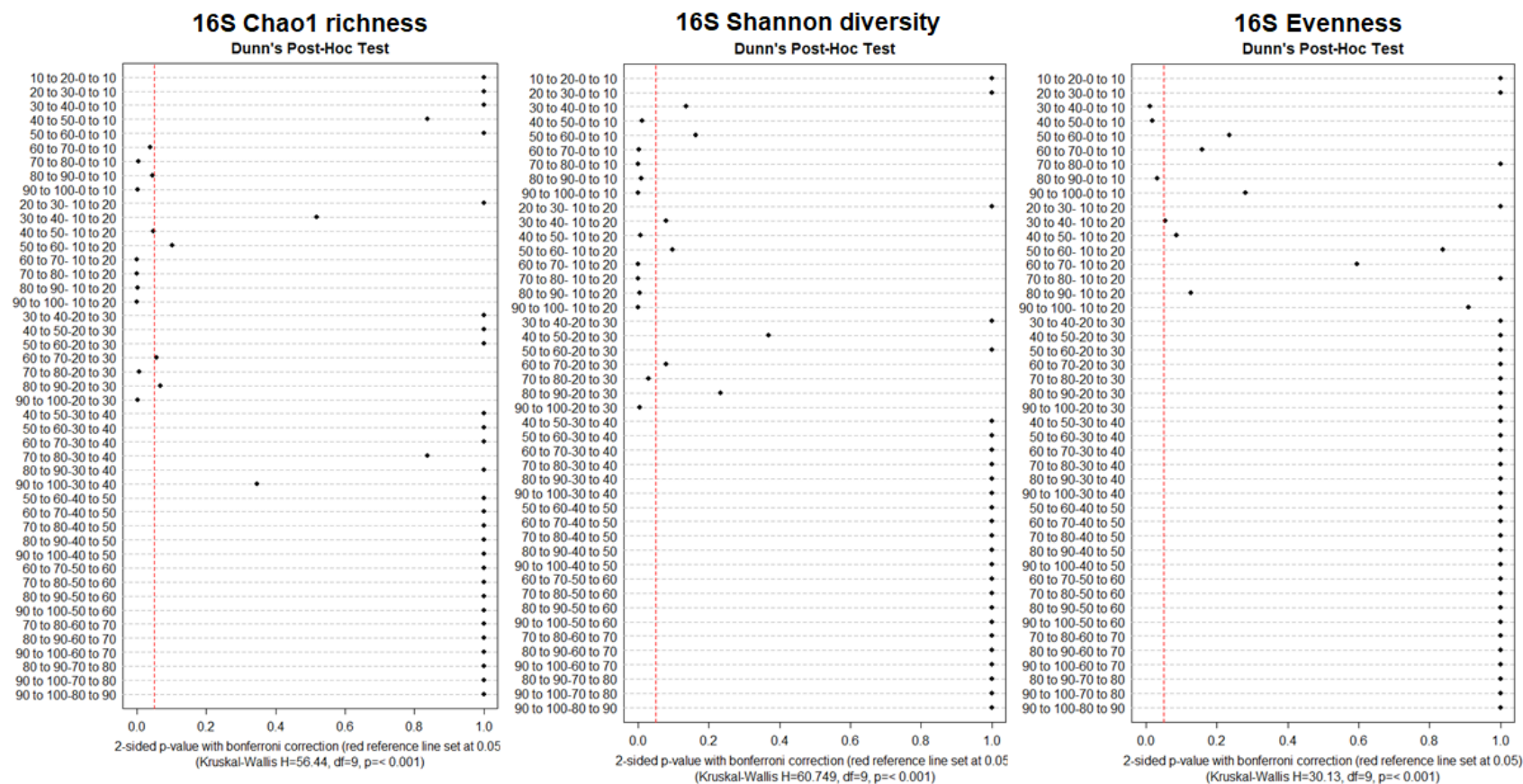


Figure A.5. The results of Dunn's tests (with Bonferroni adjustment) performed to identify significant pairwise differences in 16S alpha diversity values between depth increments. The red line on the dot chart indicates a p-value 0.05 threshold, meaning all pairs with p-values below the red line are significantly different.

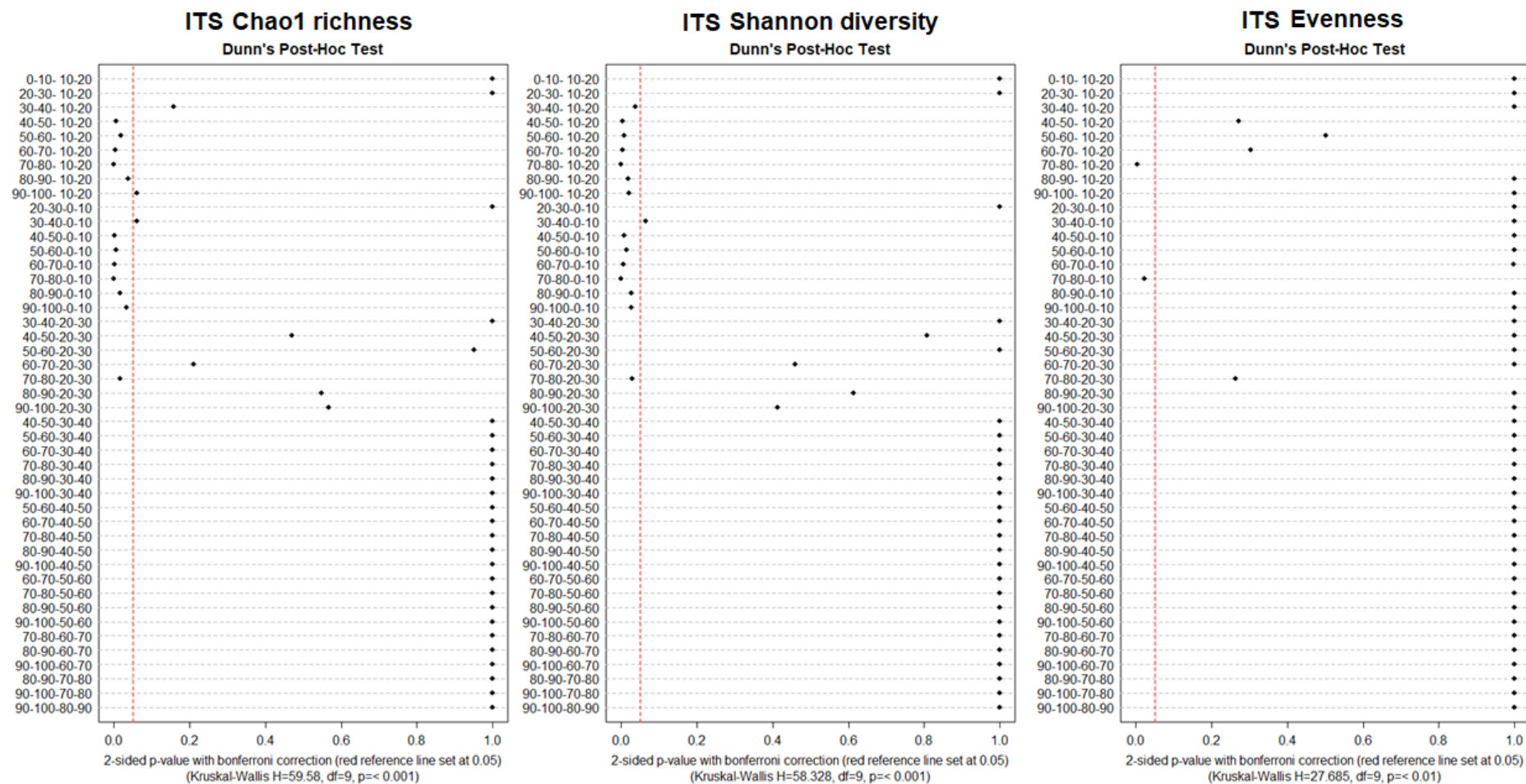


Figure A.6. The results of Dunn's tests (with Bonferroni adjustment) performed to identify significant pairwise differences in ITS alpha diversity values between depth increments. The red line on the dot chart indicates a p-value 0.05 threshold, meaning all pairs with p-values below the red line are significantly different.

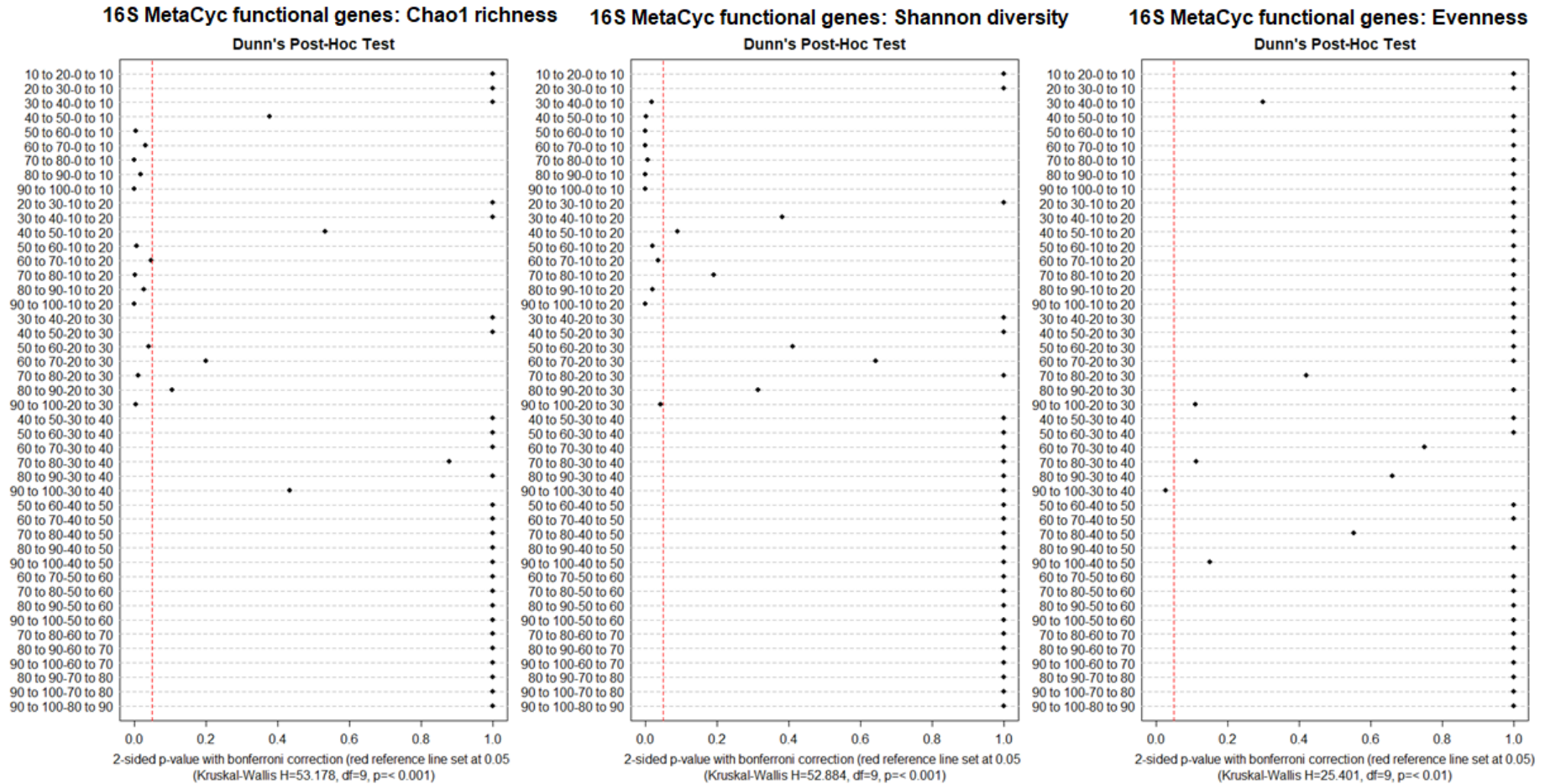


Figure A.7. The results of Dunn's tests (with Bonferroni adjustment) performed to identify significant pairwise differences in 16S functional genes (predicted MetaCyc pathway abundances) between depth increments. The red line on the dot chart indicates a p-value 0.05 threshold, meaning all pairs with p-values below the red line are significantly different.

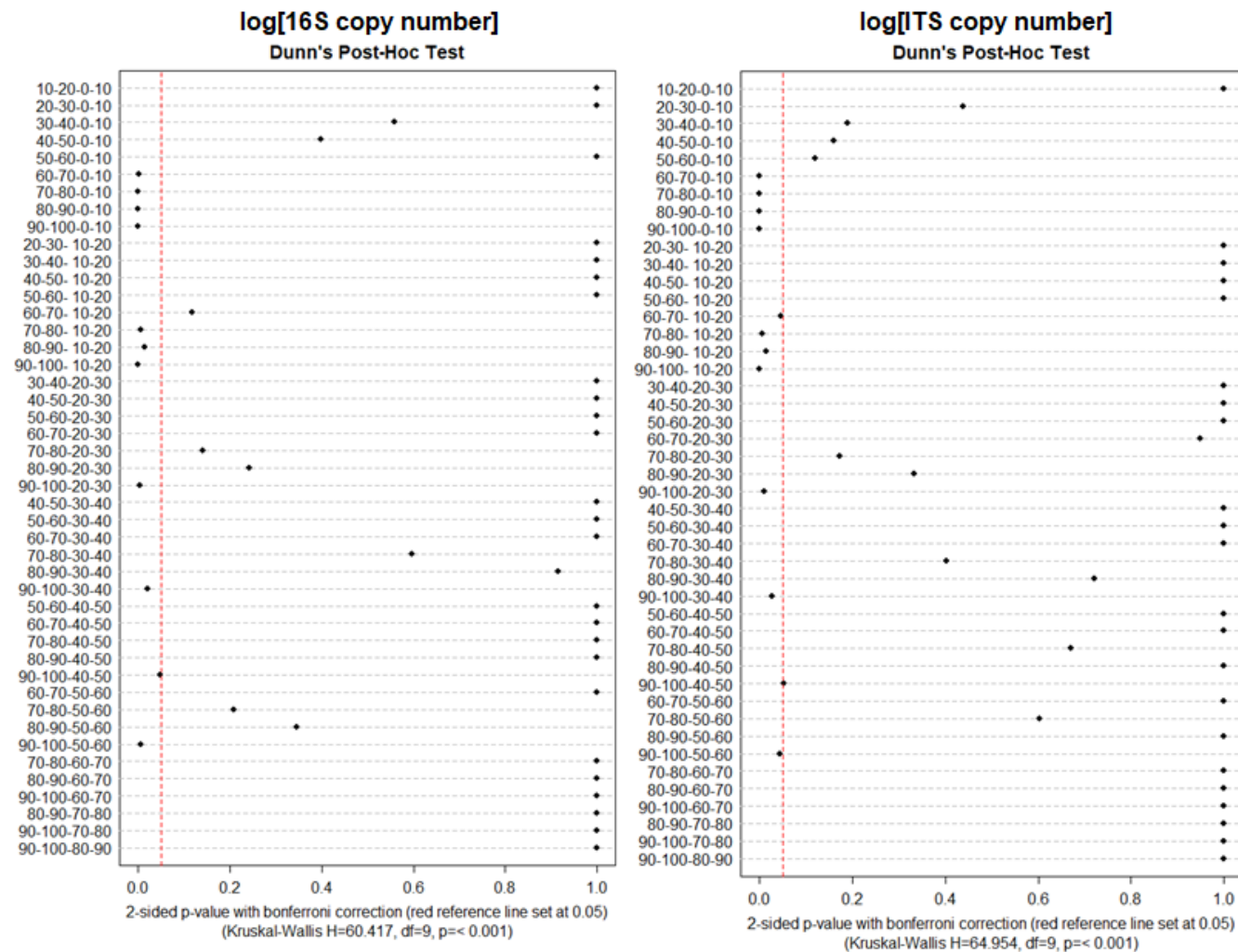


Figure A.8. The results of Dunn's tests (with Bonferroni adjustment) performed to identify significant pairwise differences in 16S and ITS copy numbers between depth increments. The red line on the dot chart indicates a p-value 0.05 threshold, meaning all pairs with p-values below the red line are significantly different.

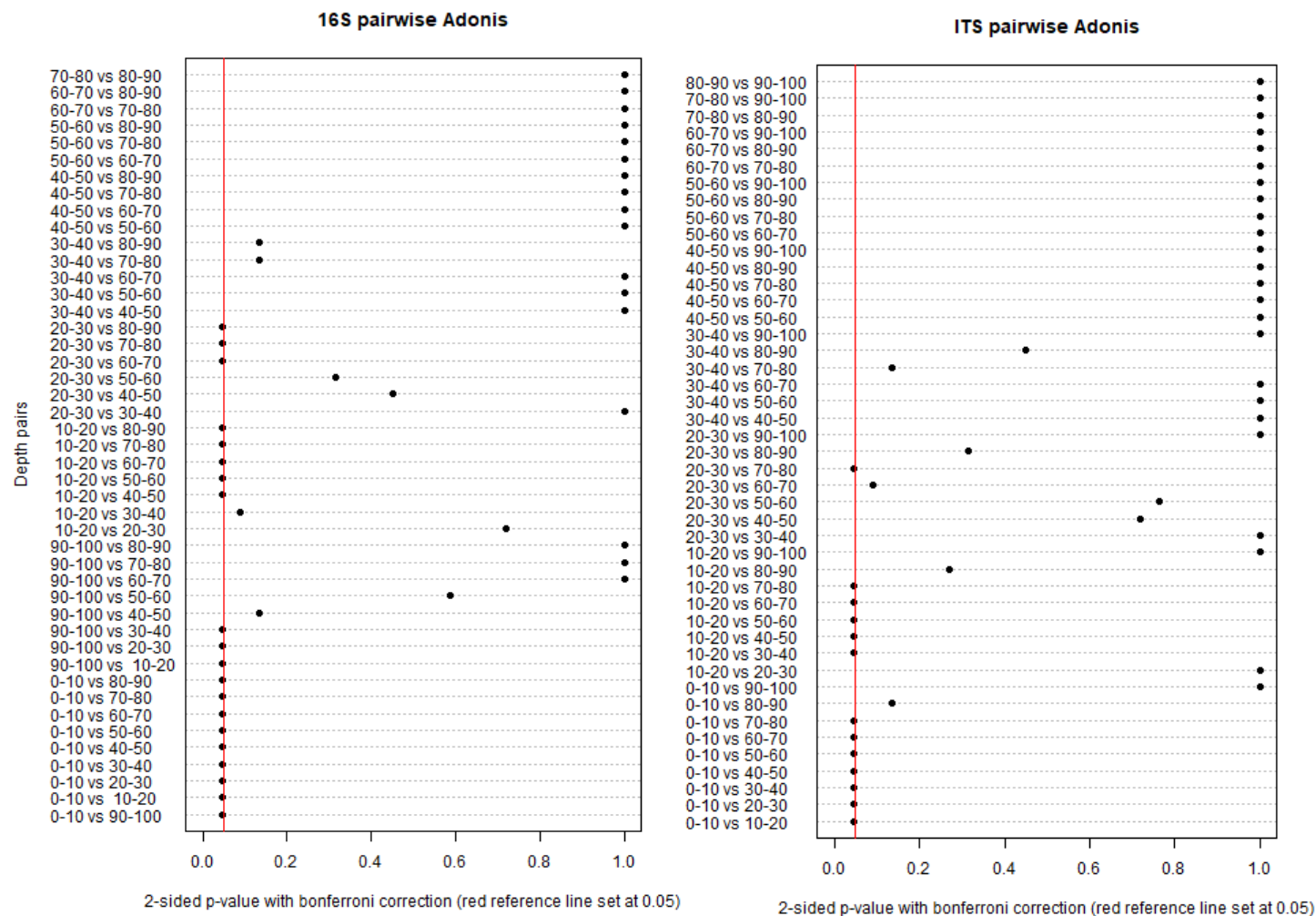


Figure A.9. The results of Dunn’s tests (with Bonferroni adjustment) performed to identify significant pairwise differences in Bray Curtis community dissimilarity between depth increments. The red line on the dot chart indicates a p-value 0.05 threshold, meaning all pairs with p-values below the red line are significantly different.

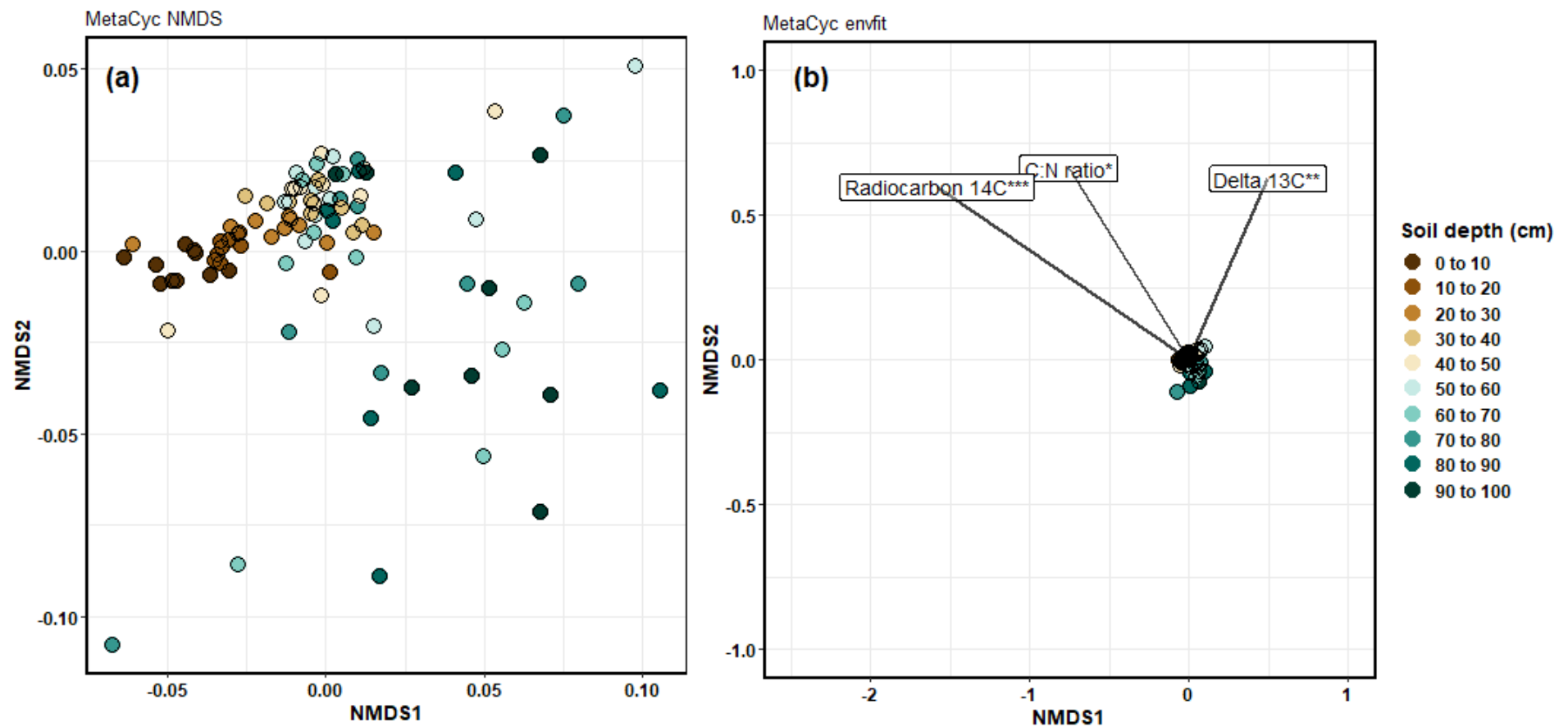
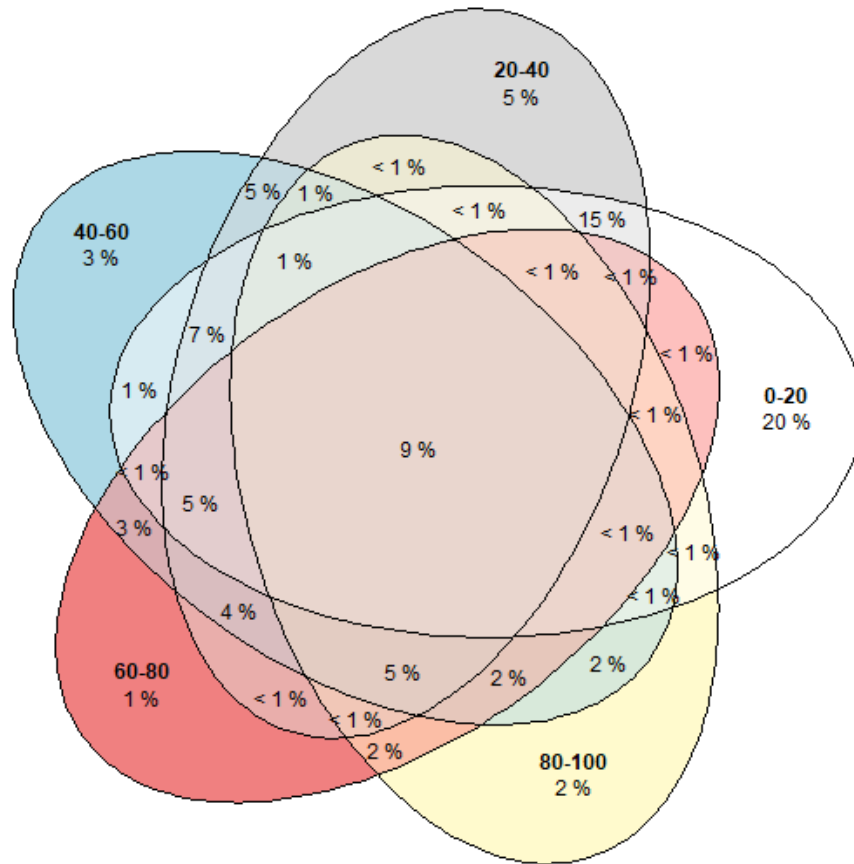


Figure A.10. (A) NMDS ordination plot calculated using Bray Curtis dissimilarity scores showing the differences in 16S functional genes (MetaCyc pathways obtained from PICRUST analysis) between different soil depth increments. (B) Envfit plot showing soil parameters as fitted vectors which significantly correlated ($p < 0.05$) to differences in the composition of 16S functional genes when tested using Mantel tests.

16S shared vs unique ASVs



ITS shared vs unique ASVs

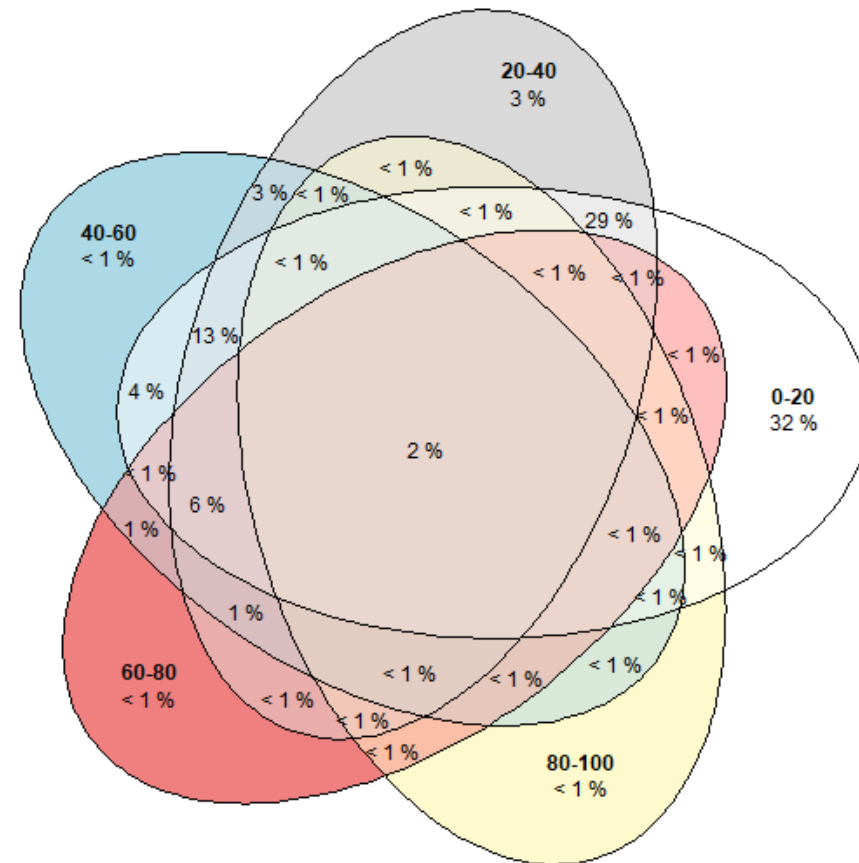


Figure A.11. The proportion (%) of shared vs unique ASVs by depth increments 0 to 20cm, 20 to 40cm, 40 to 60cm, 60 to 80cm, and 80 to 100cm.

References

Brownlie, R.K., Kelliher, F.M., 1989. Puruki Forest climate. FRI Bulletin - New Zealand Forest Service, Forest Research Institute 147.