Figure S1 — Environmental variables across the transect fit with a loess smoother.

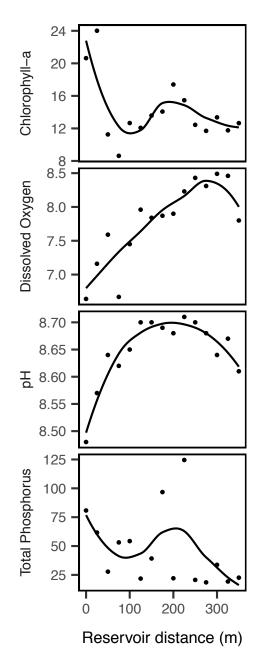


Figure S2 – Sensitivity of terrestrial-derived OTU fate to threshold of OTU incidence cutoff (minimum fraction of sites detected). We present cutoff of 0.75 in the main text, but qualitative conclusions remain consistent across thresholds, with some taxa declining and others maintained along the gradient.

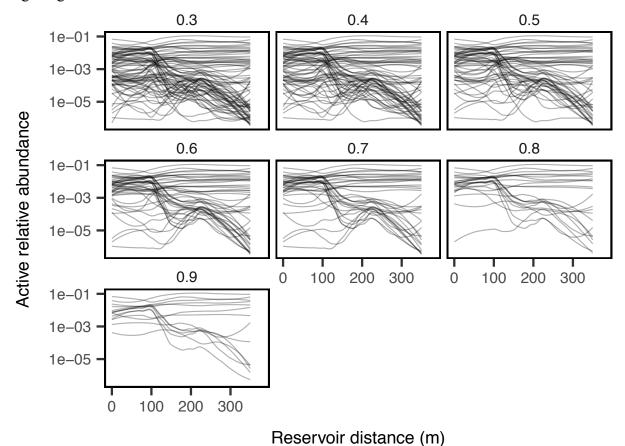


Figure S3 – Partitioning β -diversity into nestedness and turnover components in the aquatic samples relative to the terrestrial soil samples. Partitioning was done on the Sørensen dissimilarity index, a presence-absence analogue of the Bray-Curtis dissimilarity used in the main figures. Note that the main text converted the dissimilarity values to similarity, but here, the partitions of Sørensen index remain partitions of a dissimilarity metric and therefore represent community differences due to nestedness and turnover components.

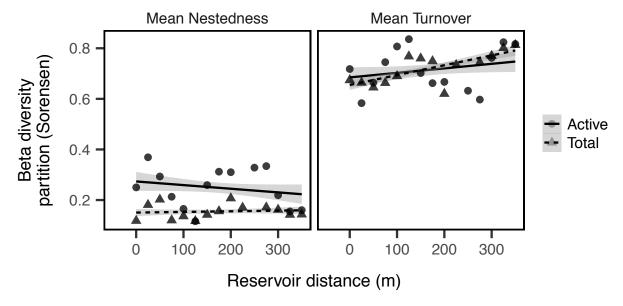
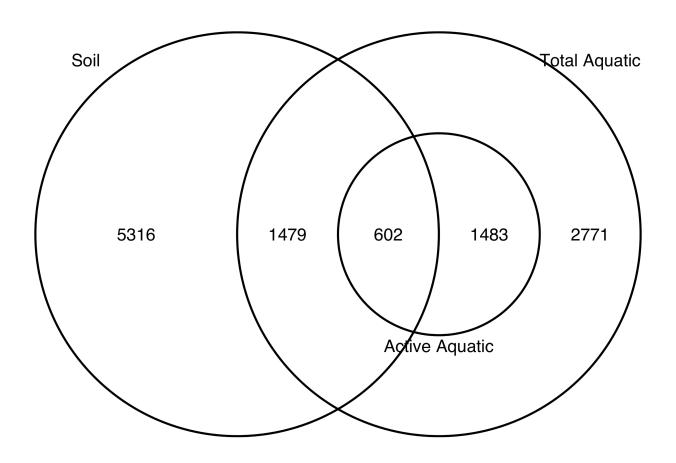


Figure S4 – Overlap of OTUs between the different subsets of the meta-ecosystem. Of the 7397 OTUs detected in the soil samples, 28% (n = 2081) were detected in the aquatic samples, and only 8% (n = 602) were detected in an active state. Of the 6335 OTUs detected in the total aquatic community, 32% (n = 2081) were also detected in soils, and 67% were not detected in soils. Of the 2085 OTUs in the active aquatic community, 29% were detected in soils, while 71% were not.



REFERENCES

- Baselga, A. 2010. Partitioning the turnover and nestedness components of beta diversity. Global Ecology and Biogeography 19:134–143.
- Baselga, A., and C. D. L. Orme. 2012. betapart: an R package for the study of beta diversity.

 Methods in Ecology and Evolution 3:808–812.
- Caporaso, J. G., C. L. Lauber, W. A. Walters, D. Berg-Lyons, J. Huntley, N. Fierer, S. M. Owens, J. Betley, L. Fraser, M. Bauer, N. Gormley, J. A. Gilbert, G. Smith, and R. Knight. 2012. Ultra-high-throughput microbial community analysis on the Illumina HiSeq and MiSeq platforms. The ISME Journal 6:1621–1624.
- Cole, J. R., Q. Wang, E. Cardenas, J. Fish, B. Chai, R. J. Farris, A. S. Kulam-Syed-Mohideen, D.
 M. McGarrell, T. Marsh, G. M. Garrity, and J. M. Tiedje. 2009. The Ribosomal Database
 Project: Improved alignments and new tools for rRNA analysis. Nucleic Acids Research
 37:141–145.
- Quast, C., E. Pruesse, P. Yilmaz, J. Gerken, T. Schweer, P. Yarza, J. Peplies, and F. O. Glöckner. 2013. The SILVA ribosomal RNA gene database project: improved data processing and web-based tools. Nucleic Acids Research 41:590–596.
- Rognes, T., T. Flouri, B. Nichols, C. Quince, and F. Mahé. 2016. VSEARCH: a versatile open source tool for metagenomics. PeerJ 4:e2584–e2584.
- Schloss, P. D., S. L. Westcott, T. Ryabin, J. R. Hall, M. Hartmann, E. B. Hollister, R. A.
 Lesniewski, B. B. Oakley, D. H. Parks, C. J. Robinson, J. W. Sahl, B. Stres, G. G.
 Thallinger, D. J. Van Horn, and C. F. Weber. 2009. Introducing mothur: Open-source, platform-independent, community-supported software for describing and comparing microbial communities. Applied and Environmental Microbiology 75:7537–7541.

Wetzel, R. G., and G. E. Likens. 2000. Limnological analyses. 3rd ed. Springer, New York, NY.