

1 Supplemental material

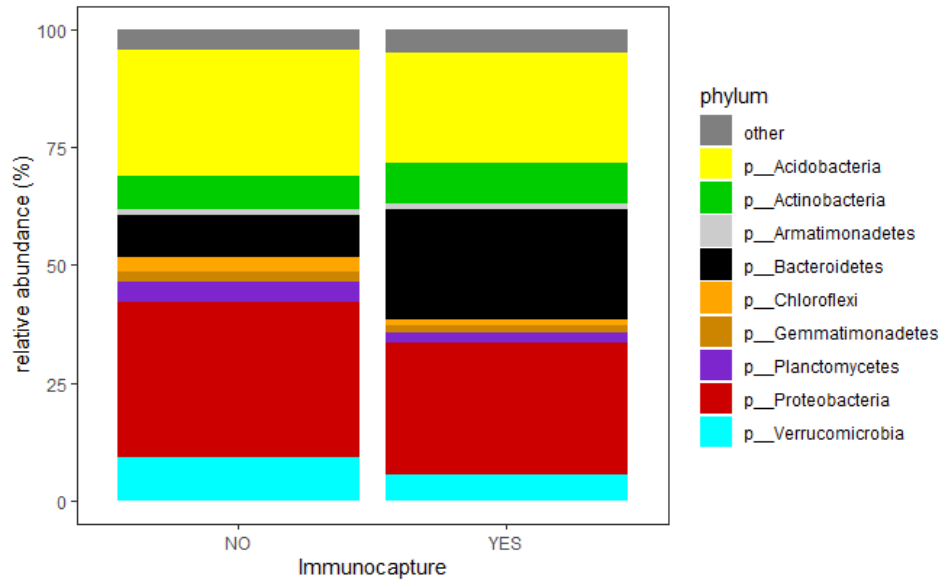


Figure S1. Phylum-level relative abundance of reads in immunocaptured and total 16S communities. Only samples for which paired total-immunocaptured data were available are included (n=75 pairs). ANCOM was used to determine which phyla differ between immunocaptured and total communities, using a threshold of 0.8 and a p-value cutoff of 0.05.

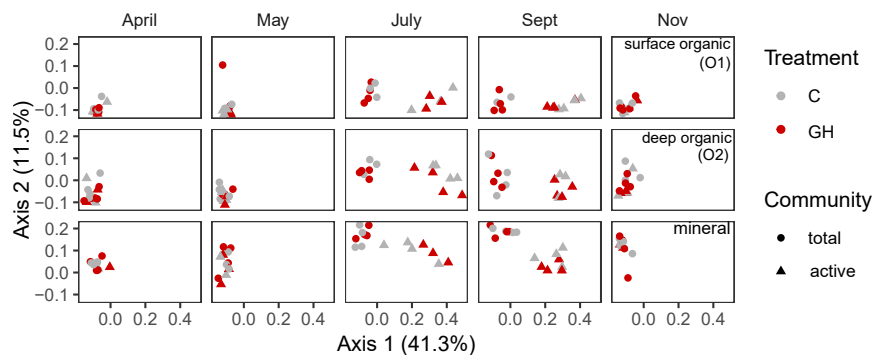


Figure S2. Unifrac-based principal coordinates analysis plot of bacterial communities. A single ordination was generated for all samples, but samples are separated out into different panels according to time of sampling and soil horizon. Symbol colour denotes whether the sample was derived from a greenhouse or control plot, and symbol shape denotes whether the sample came from a BrdU (“actively growing”) or the total community.

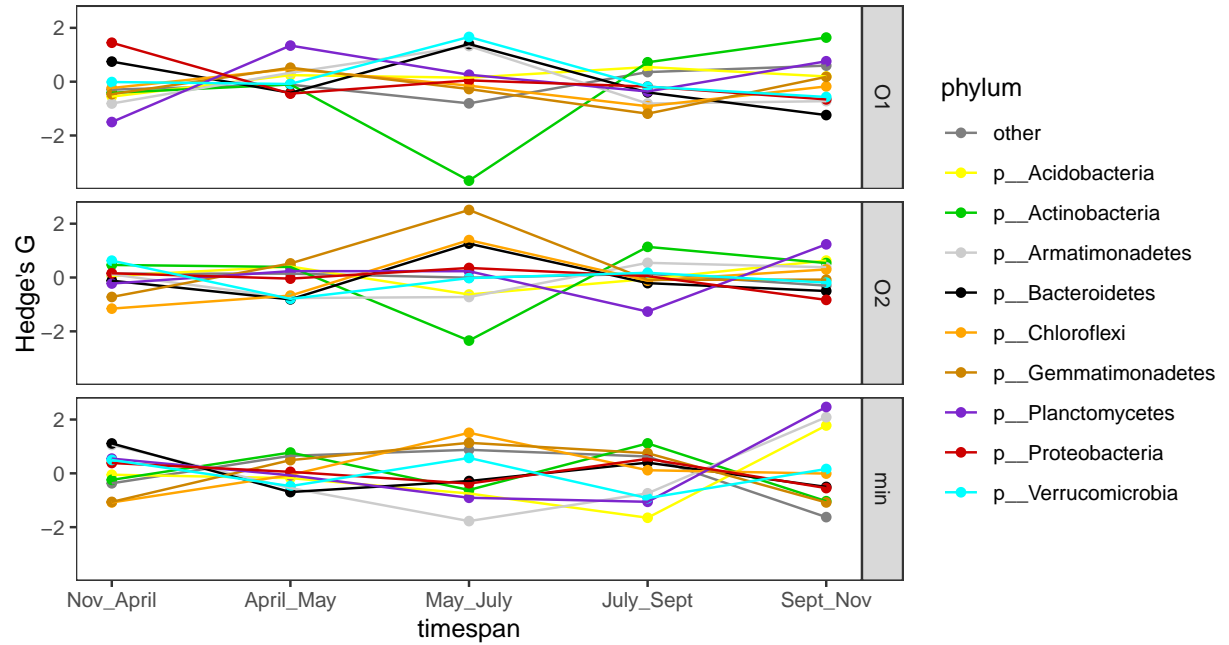


Figure S3. Change in relative abundance of dominant phyla between timepoints. Data are presented with one line per phylum, separated by soil horizon sampled. Only the total communities are shown. The metric depicted is Cohen's D, calculated as the difference in mean abundance between the two timepoints, divided by the pooled standard deviation of relative abundance weighted by the sample size. Thus the value is an uncertainty-standardized measure of change in relative abundance for the phylum. Rates are not corrected for the time between successive samplings.

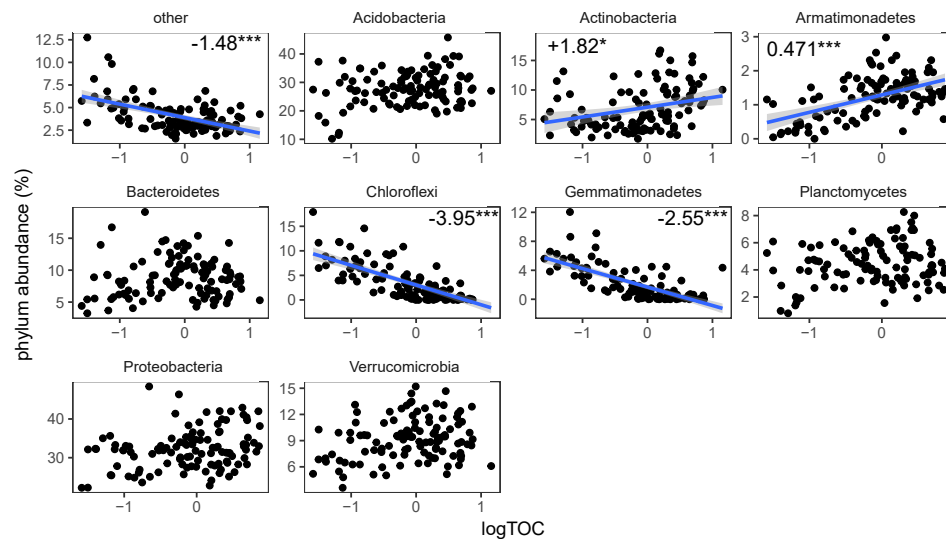


Figure S4. Relationship between the concentration of total organic carbon (here shown as the log) and relative abundance of dominant phyla in the total communities. Plot was included as a random effect in a linear mixed model to account for sampling horizons within plots and plots multiple times across timepoints. Only regressions where the Benjamini-Hochberg-corrected p-value for the slope being different from zero is less than 0.05 are shown

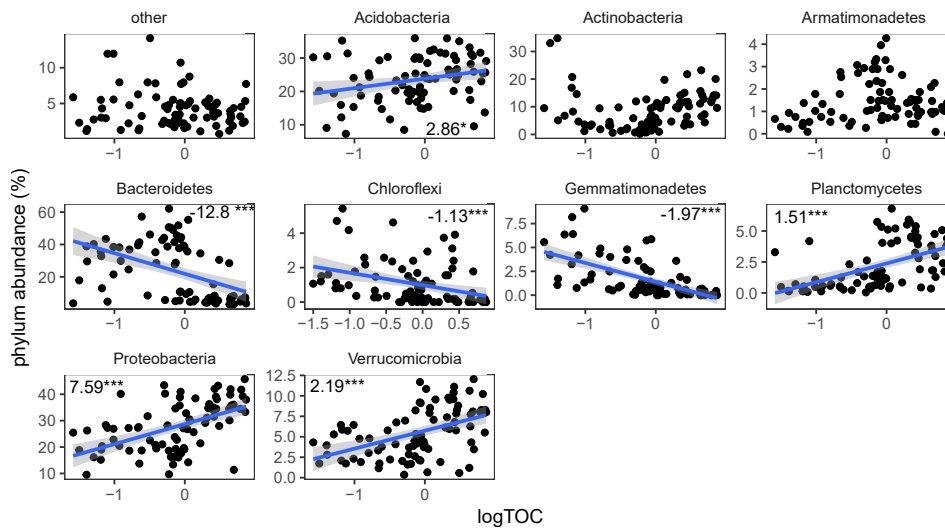


Figure S5. Relationship between the concentration of total organic carbon (here shown as the log) and relative abundance of dominant phyla in the actively-growing communities. Plot was included as a random effect in a linear mixed model to account for sampling horizons within plots and plots multiple times across timepoints. Only regressions where the Benjamini-Hochberg-corrected p-value for the slope being different from zero is less than 0.05 are shown