

Fig. S1. AD microbial community composition at family-level taxonomic groupings for all sampling dates along the time-series. Replicate samples for each date are averaged, and the relative abundances of all ASVs within a given family are summed.

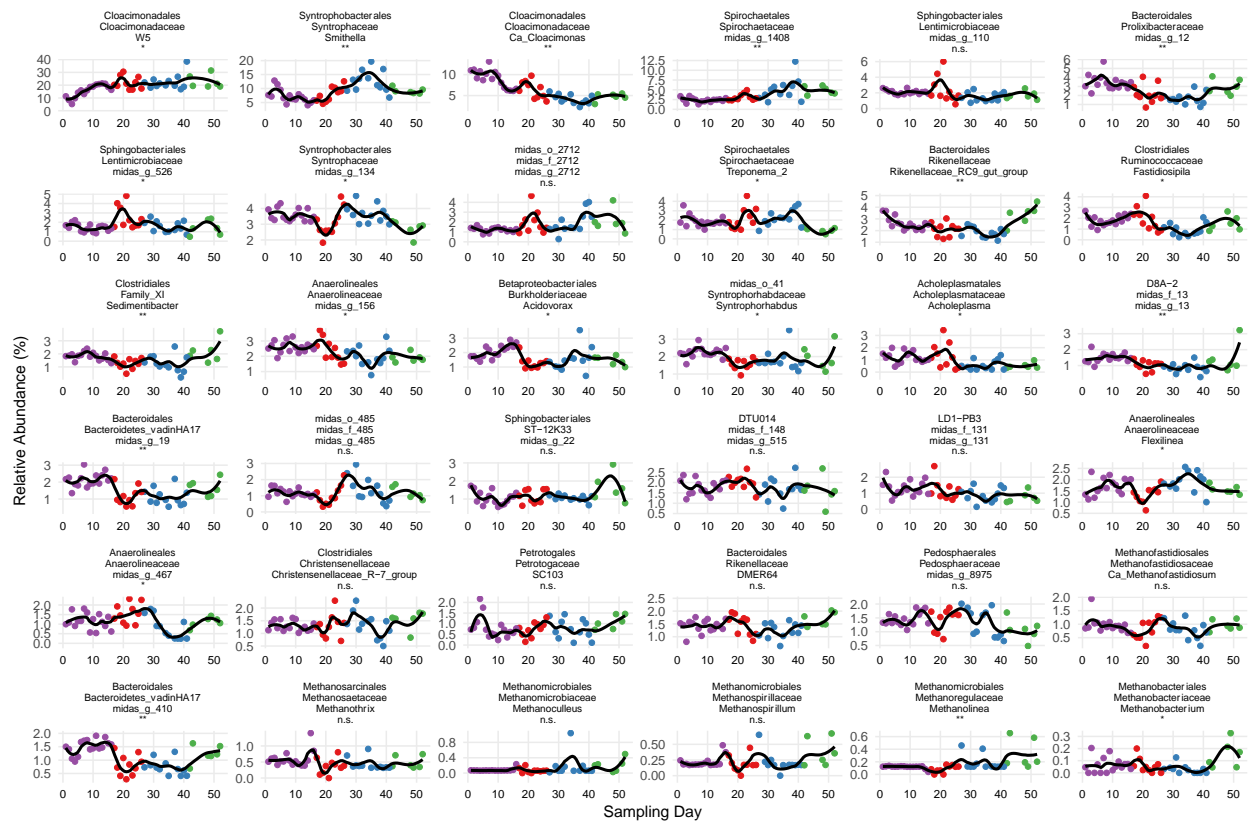


Fig. S2. The relative abundances of genus-level taxa across the time-series. All ASVs within each genus are summed. The y-axis represents sample number (1-52) – date and sample name information can be found in Supplemental Table S1. Points are samples colored by configuration (violet = SOI, red = CEPT, blue = SOII, green = SER). Each graph facet includes the order, family, and genus name, and whether a two-sided ANOVA test determined that the genus had differential abundance between configurations (n.s. = not significant, * = $p < 0.05$, ** = $p < 0.01$, *** = $p < 0.001$).

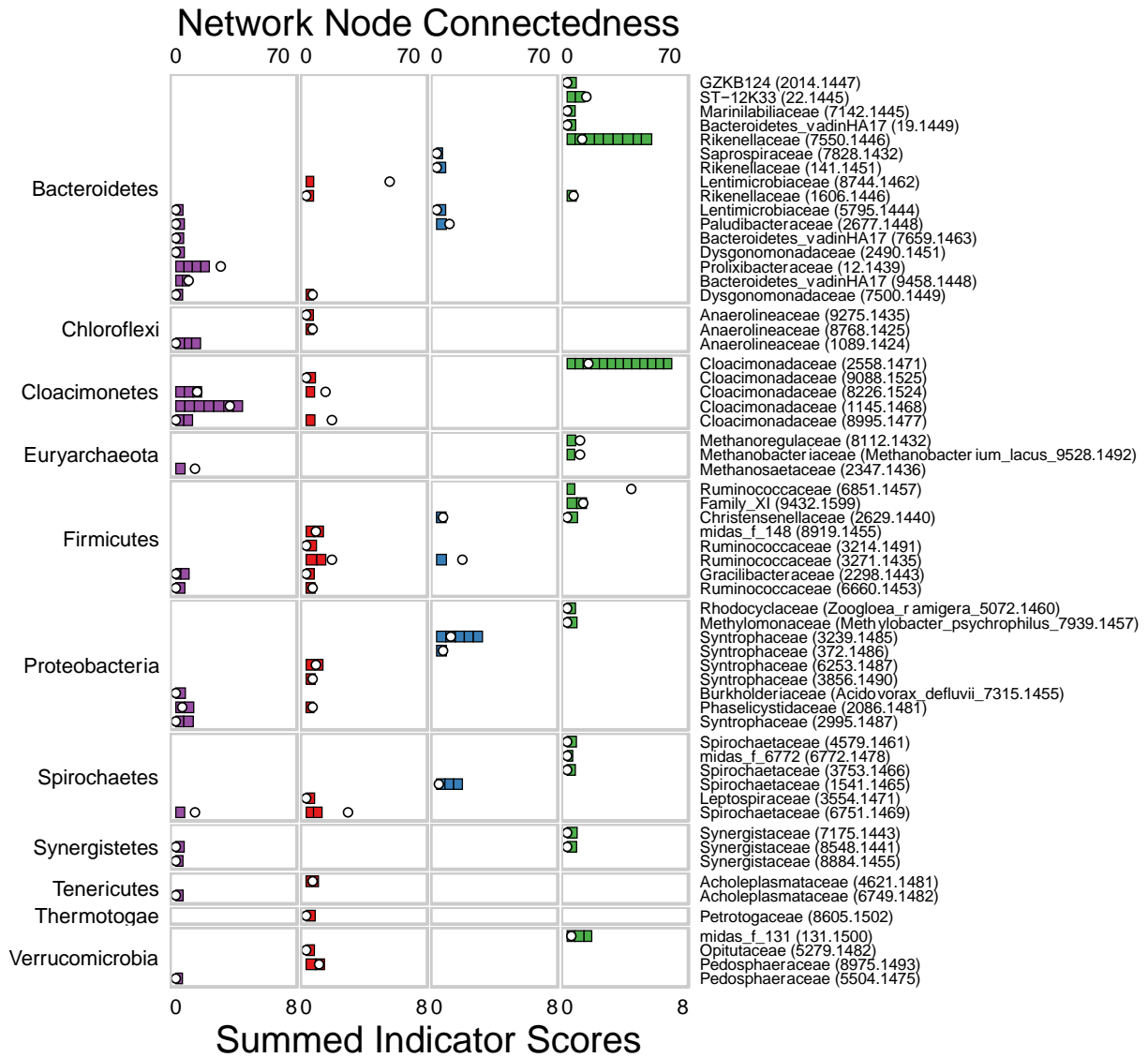


Fig. S3. Indicator ASVs are shown as individual boxes, faceted by the configuration that they are indicators for (left to right: violet = SOI, red = CEPT, blue = SOII, green = SER). Each ASV box is in a row which indicates its family-level taxonomy (and MIDAS ID) on the right axis and its phylum-level taxonomy on the left axis. The bottom x-axis shows the summed and individual multi-pattern-level analysis score for indicator ASVs and the top x-axis shows the summed network connectedness of indicator ASVs from each family (see Methods and Figure 4).

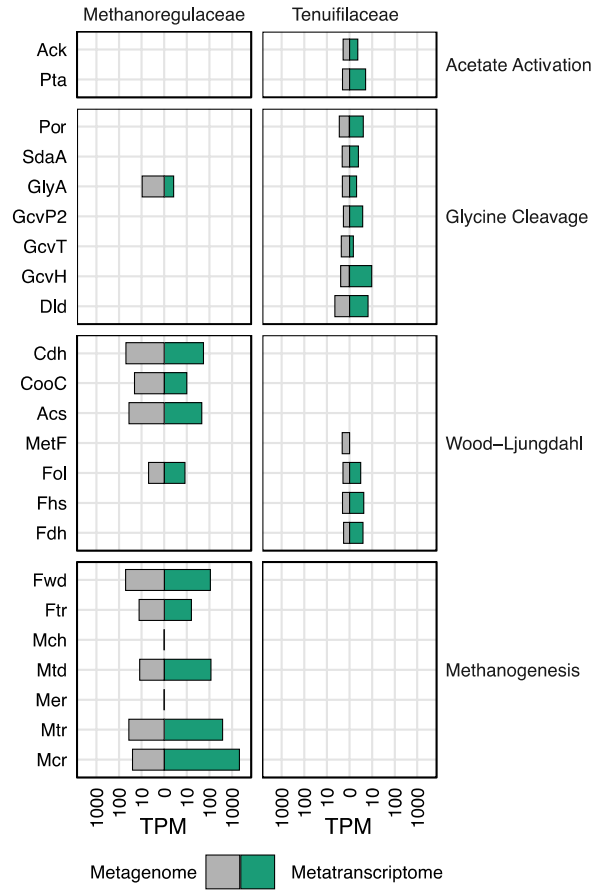


Fig. S5. TPM values from metagenomic and metatranscriptomic read mapping to select genes in the Subnetwork 1 MAGs from Methanoregulaceae (3300036947_39) and Tenuifilaceae (3300028576_27). TPM values and other genomic features are available in Table S11.