

Microbial diversity and functional potential of sediment microbial fuel cells (SMFCs)

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1. Background

- SMFCs harness microbes' ability to conduct external electron transfer to oxidize reduced compounds in the sediment
- SMFCs generate electricity by assimilating and remediating point-source contaminants, that accumulate in highly reducing anoxic sediments (i.e. Coastal regions, beneath fish pens)
- Question:** How do microbes transfer electrons to the anode of SMFCs and how can we then optimize and tailor the design of SMFCs to remove contaminants (i.e. H₂S, Geosmin, Methyl-Isoborneol)

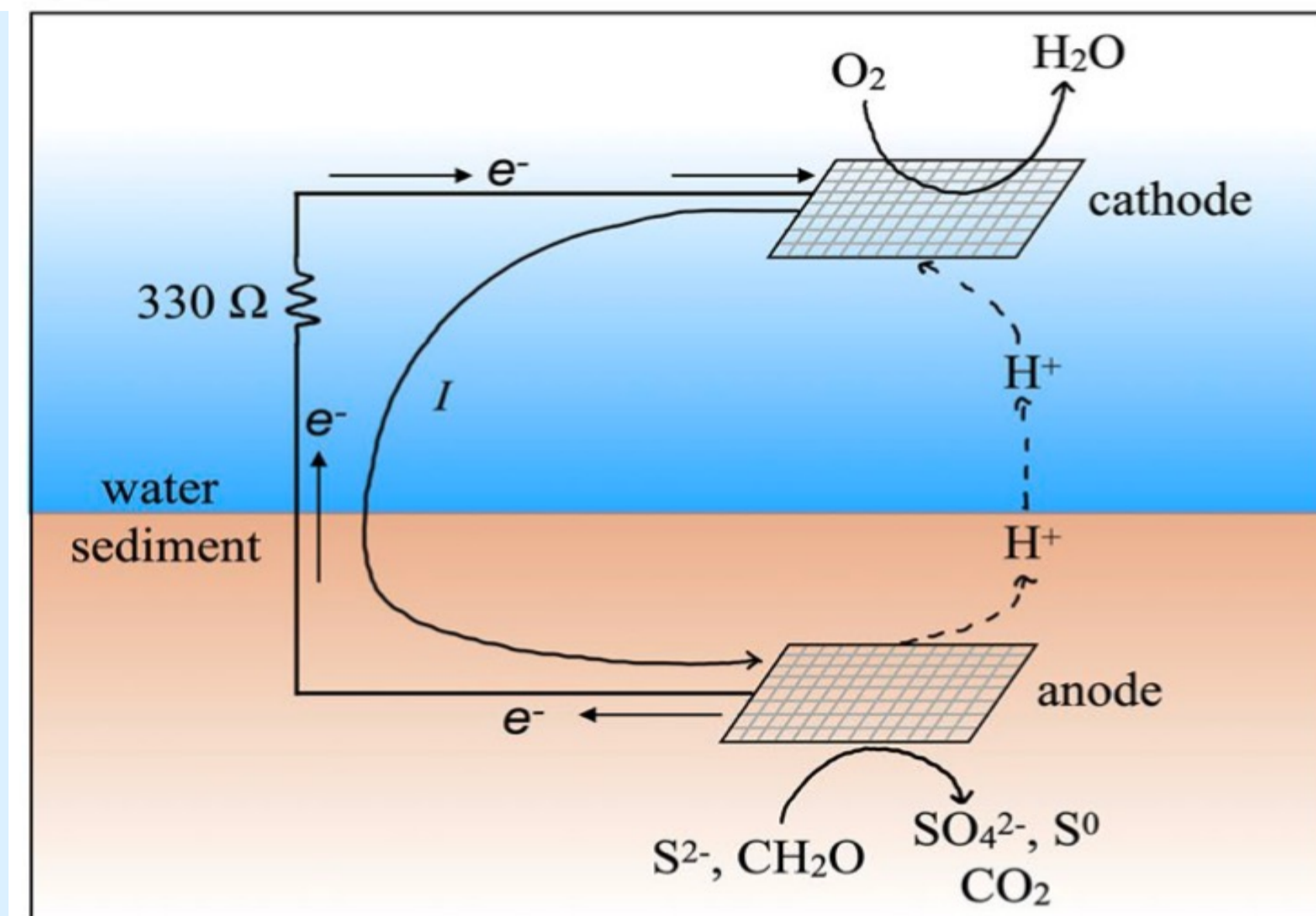
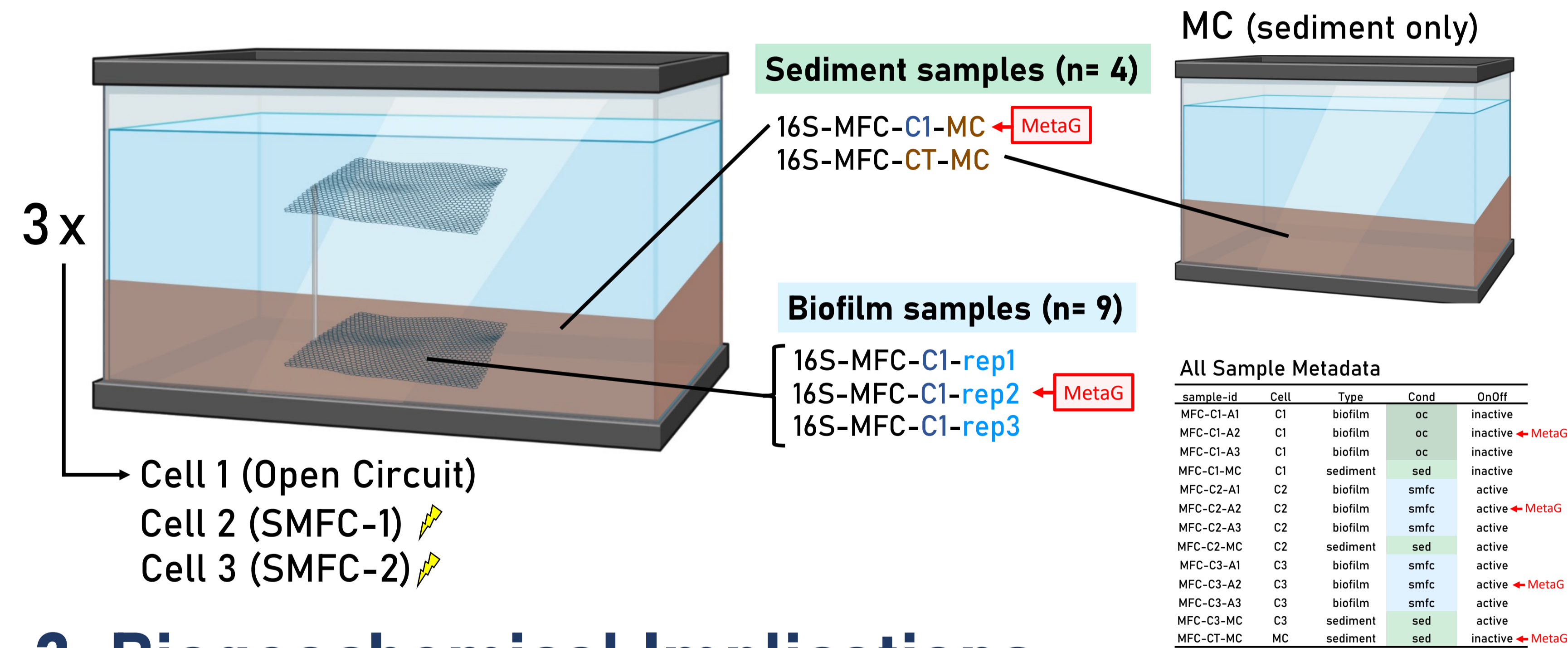


Figure 1. SMFC schematic of anode-cathode redox couplings (Algar et al. 2020).

2. Experimental Design

(Algar et al. 2020)



3. Biogeochemical Implications

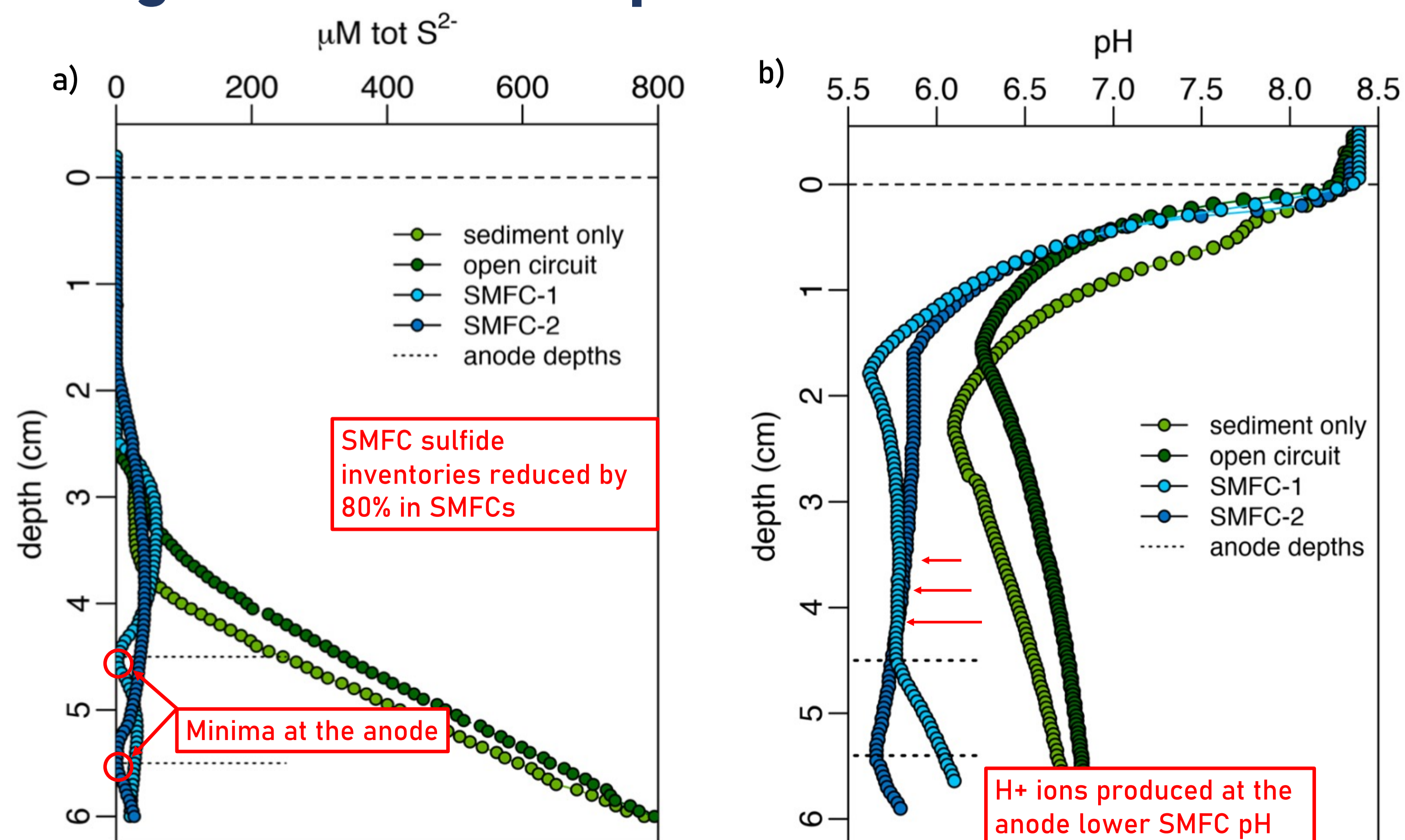


Figure 2. Microsensor profiles of (a) porewater sulfide (tot-S²⁻ = H₂S + HS⁻ + S²⁻), and (b) porewater pH, for all conditions and microcosm tanks on day 96 (Algar et al. 2020).

4. Diversity Metrics

- 16S rRNA: diversity and communal shifts - *QIIME2*
- Metagenomic: functional potential - *Anvi'o*

Alpha Diversity

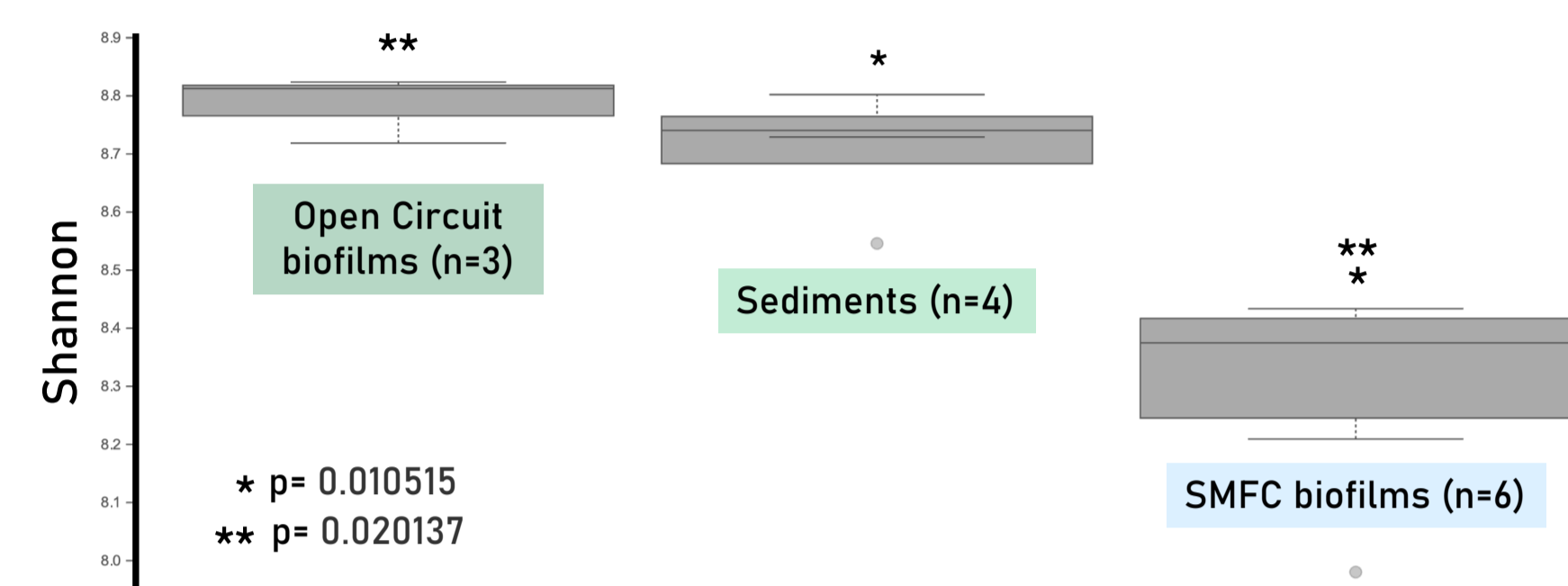


Figure 3. Shannon diversity of microbial communities sampled from Open Circuit biofilms, Sediments, and SMFC biofilms.

Beta Diversity

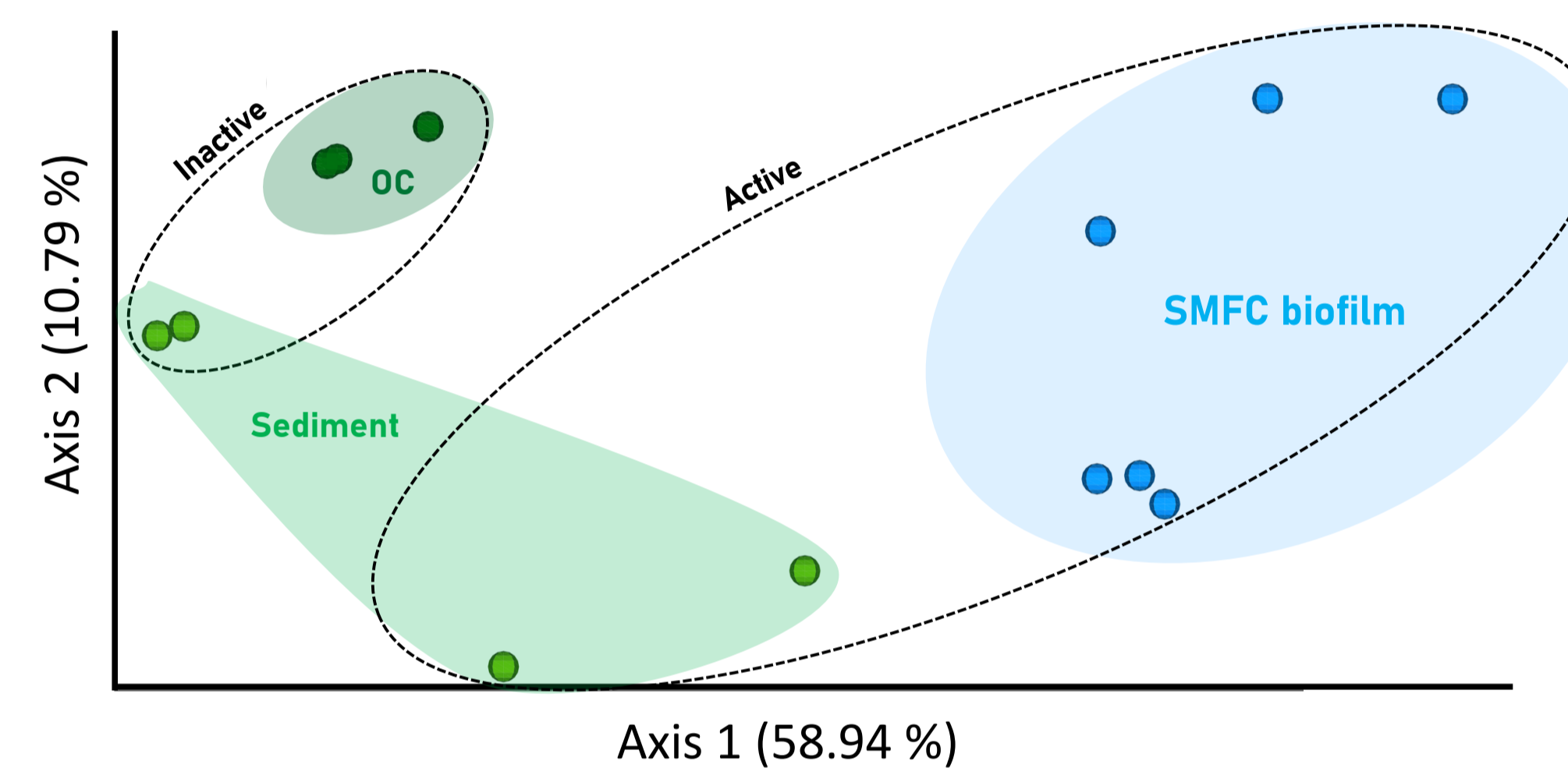


Figure 4. PCoA ordination of Bray-Curtis distances between all samples. Microbial communities from Open Circuit biofilms (OC) are dark green, SMFC biofilms are blue, and Sediment samples are light green. Dotted lines encircle samples based on the activity of the fuel cell (Active or Inactive).

5. Community Composition

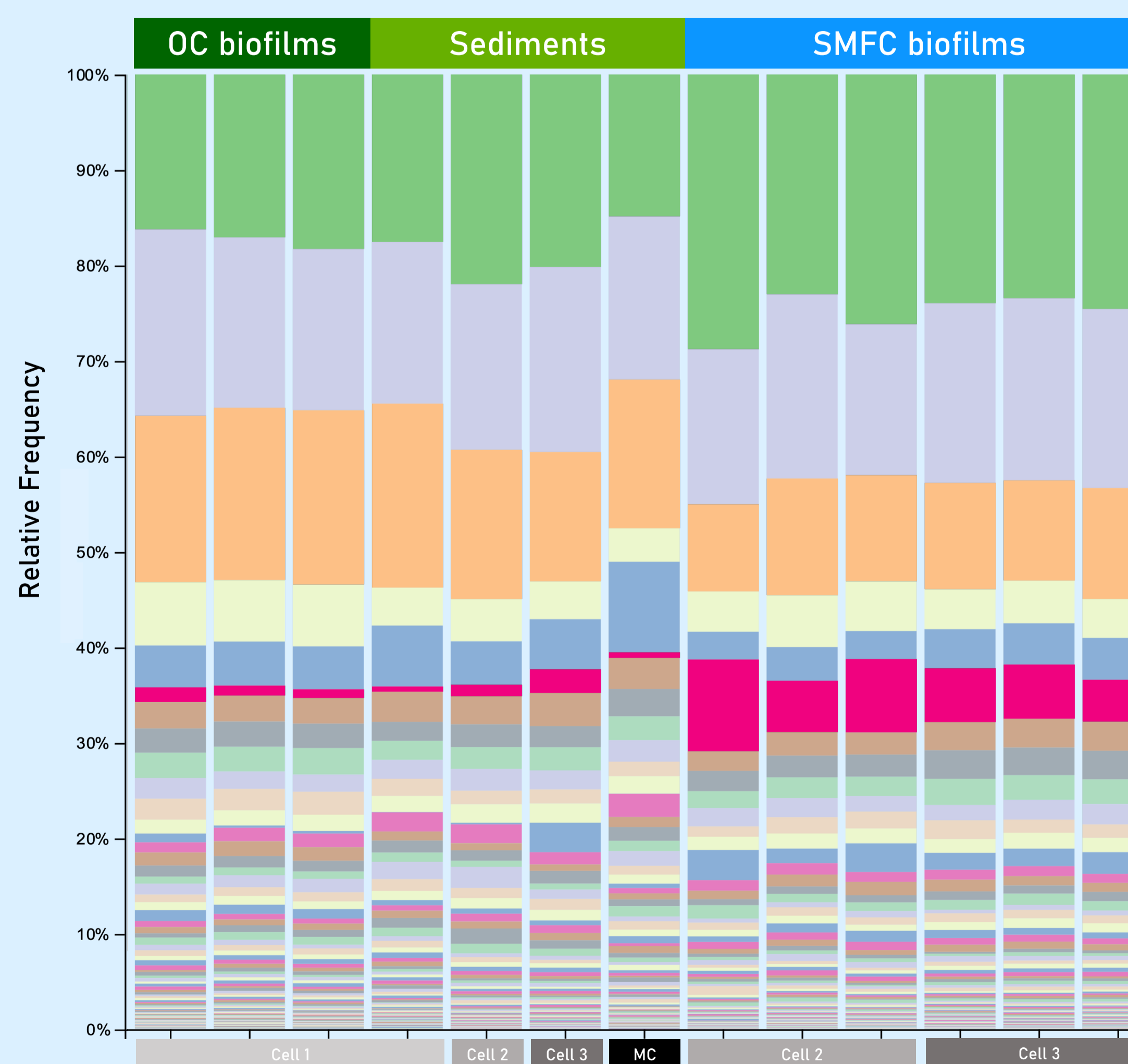


Figure 5. Taxa barplot of the relative frequency (%) of 1360 identified taxa colonizing Open Circuit biofilms (OC), SMFC biofilms (SMFC), and background sediments.

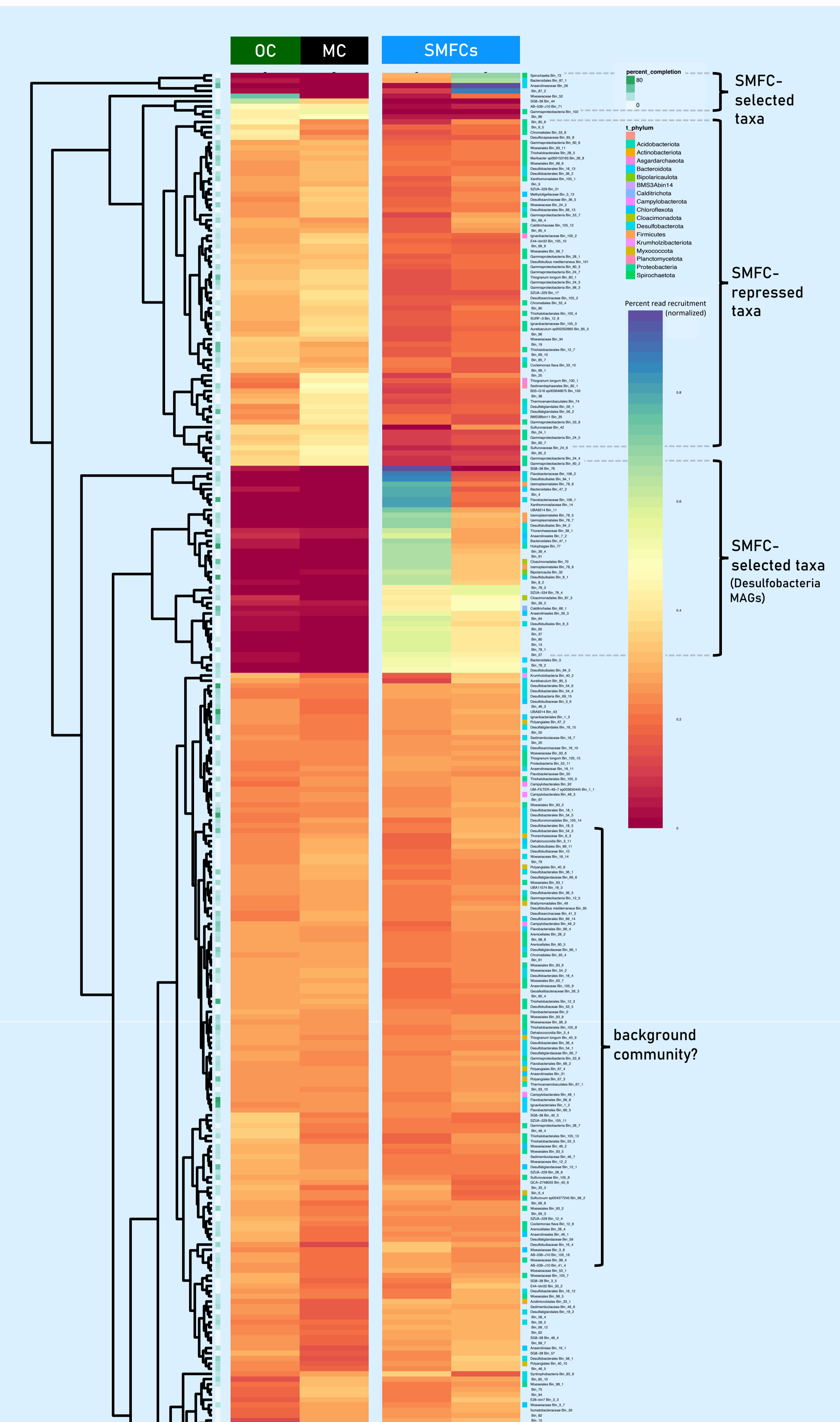


Figure 6. Heatmap of MAGs (bin) percent read recruitment normalized to each of the 4 microcosm tanks sampled: Open Circuit (OC), Microbial Control (MC), and two SMFCs.

6. Findings and What's Next?

- Distinct SMFC microbial communities:
 - Less diverse (selective pressure)
 - PCoA clustering
 - Deltaproteobacteria (sulfur oxidizers) and Archaeal SMFC-associated communal shifts
- Metabolic reconstruction and functional annotation of each microcosm

