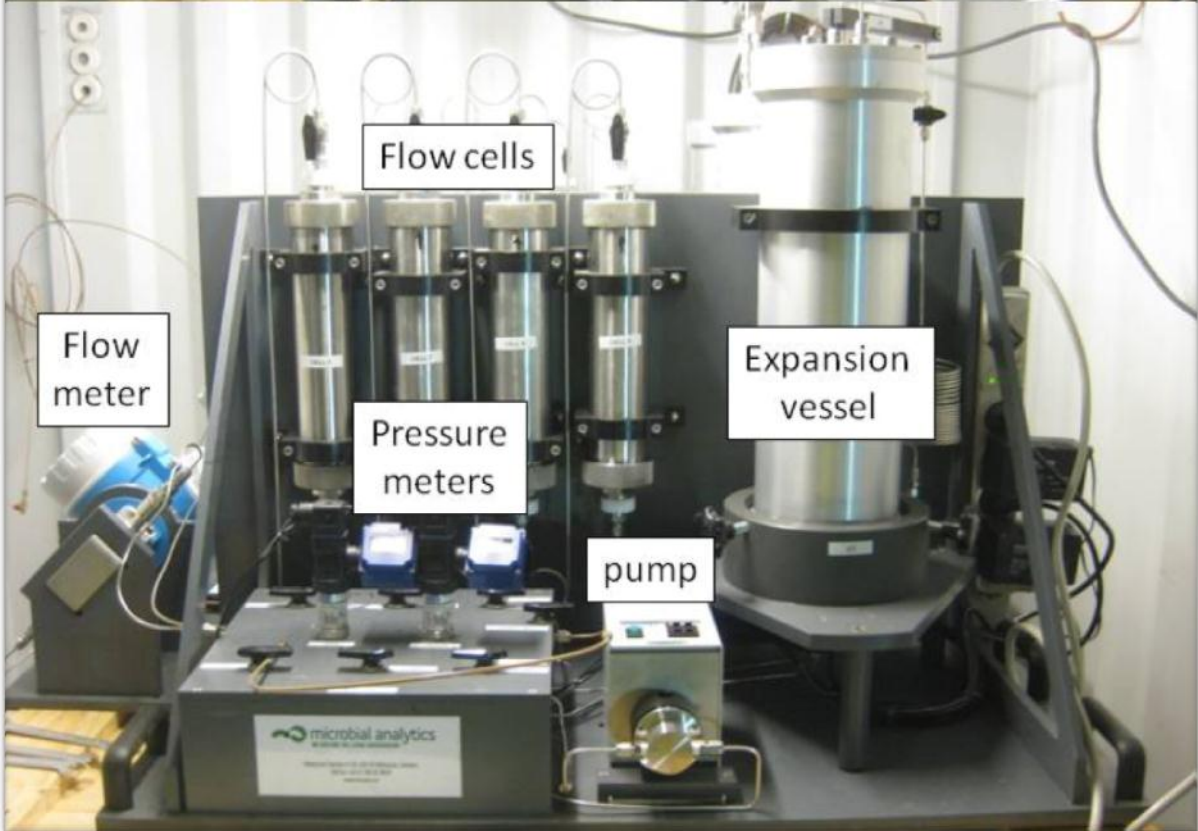
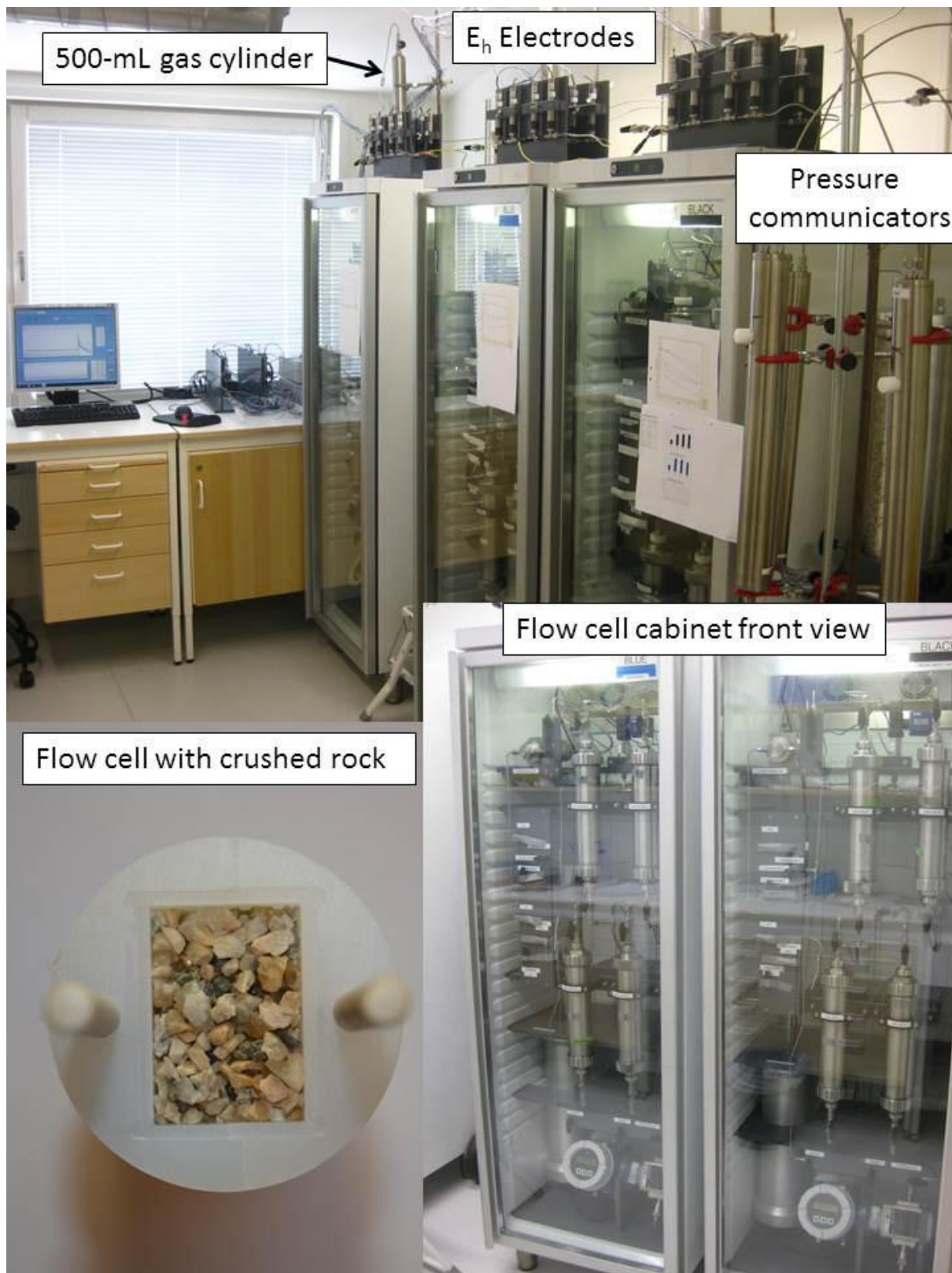


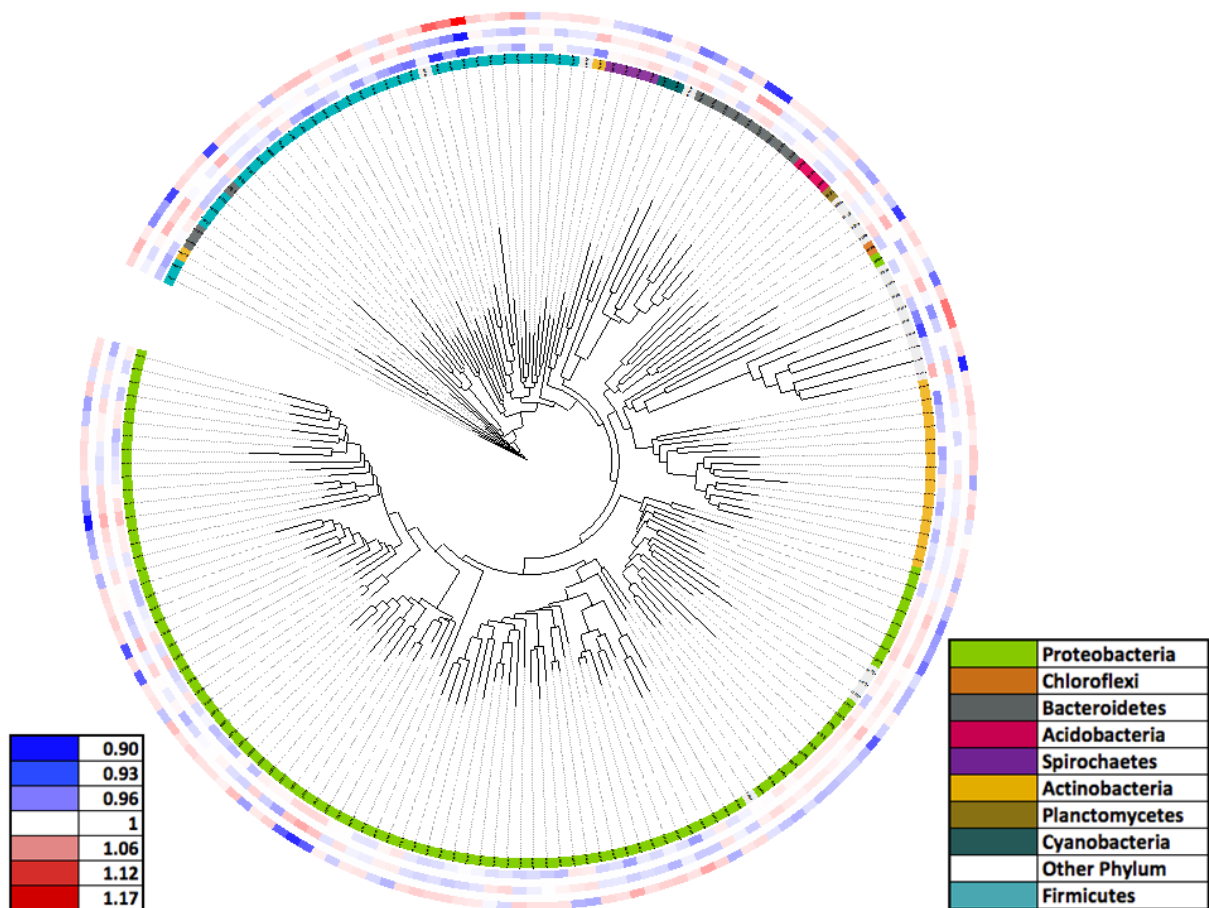
Supplementary Figure 1. The packer system: The yellow sections are expandable polyurethane packers, while the green rings are Teflon-coated stainless steel casings. The grey components are made of PEEK, as are the 1/8" (outer diameter) sampling tubes. Groundwater sampling and circulation are mediated via two small holes opposite each other in the grey portion in the middle of the packer assembly (the dark spot in the top drawing). The depicted section is 100 mm long.



Supplementary Figure 2. Top image: three circulation set-ups. Bottom image: four flow cells with a micropump, flow meter, pressure meters, and expansion vessel installed in a container 320 m underground in the ONKALO research tunnel.



Supplementary Figure 3. Three flow cell cabinets installed in the laboratory, showing the flow cells from the circulation set-ups depicted in Supplementary Figure 2. Micropumps, pressure meters, flow meters, and expansion vessels similar to those shown in Supplementary Figure 2 were permanently installed in these cabinets. A flow cell insert with rock grains is shown in the lower left image. The microelectrodes were installed on top of the cabinets as shown in the top image.



Supplementary Figure 4. A circular phylogenetic tree comparing the microarray hybridization results for DNA extracted from biomass attached to rock grains from flow cells treated with methane (CH_4) and hydrogen and methane ($\text{H}_2:\text{CH}_4$). DNA was obtained from pooled $\text{CH}_4 \times 4$, $\text{CH}_4 \times 40$, and $\text{H}_2:\text{CH}_4 \times 4$ extractions, respectively. In total, 4694 OTUs were present in at least one of the samples. Each of the three samples had an abundance score for each OTU. OTUs for which the difference between the maximum and minimum abundance scores exceeded 300 were selected, bringing the total to 1193 OTUs, in which 182 families were represented. A representative 16S rRNA gene from each of the 182 families was aligned and used to infer a phylogenetic tree. The tree, taxonomy labels, and abundance data were rendered using Interactive Tree of Life Software (iTOL; <http://itol.embl.de>). The rings around the tree, from innermost to outermost, are $\text{CH}_4 \times 40$, $\text{CH}_4 \times 4$, and $\text{H}_2:\text{CH}_4 \times 4$. The tree shows each sample's abundance score for an OTU divided by the average abundance score for that OTU for all three samples. Blue indicates that the OTU was less abundant in that sample, and red indicates that the OTU was more abundant. The color saturation indicates the degree of difference from the mean abundance score of the three samples, dark blue indicating a ratio of 0.90, white = 1.0, and dark red = 1.17.

A full-resolution image of the circular tree can be found in a separate file named Supplementary Figure 5.pdf. The individual OTU numbers can be zoomed in on and viewed in that file.