



Figure S5. Phylogenetic tree of the operational taxonomic units with high loadings in the Principle Component Analysis. Full length 16S rRNA sequences (>1000 bp) were used to calculate a core tree based on related environmental and reference sequences, using maximum-likelihood analysis (PhyML). Short sequences from this study (300 bp), were added without changing the global tree topology using the ARB parsimony tool. Numbers indicate the link to Figure S6.