



Supplementary Figure 3. Relative abundance of top 50 abundant genera in the top 4 cm sediment layer of Cock Soda lake identified by amplicon sequencing of 16S rRNA genes and transcripts. Two different sediment layers were sampled (“0-2 cm” or “2-4 cm”) for parallel DNA and RNA extraction to target 16S rRNA genes (“DNA”) or 16S rRNA gene transcripts (“cDNA”), respectively. Each column in the heat map represents the average of three or four biological replicates. The minimum relative abundance of an OTU shown is 0.01% (white).

In each layer, DNA and RNA profiles varied substantially between one another. The most abundant transcripts in the top 2 cm layer were assigned to the genera *Nodosilinea* (filamentous benthic cyanobacterium) and an unknown genus within the ML635J-40 aquatic group (*Bacteroidetes*). In the 2-4 cm layer of sediments, the most abundant transcripts originated from members of the *Nitiliruptoraceae* and *Nitrincola*. Overall, the relative abundance of transcripts with phylogenetic affinity to sulfidogenic genera was higher in the top layer with the exception of *Dethiobacter*, from which transcripts were more abundant in the second layer. The relative abundance of transcripts from SOB was higher in the second layer compared to the top layer.