

**Additional File 7**. PhyloFlash analysis results. Heatmap of taxonomic assignments (rows) for small-subunit rRNA reads in the six individual metagenomes (columns). The plot was generated using with the comparison script provided with phyloFlash. Color intensities represent the percentage of reads mapping to a given taxon, separated by prokaryotes (blue) and eukaryotes (red). Samples are clustered by their similarity in terms of taxonomic content and taxa are clustered by their co-occurrence across samples. Clustering are based on the euclidean distance and on the Ward's minimum variance method. (PDF 39 kb)