Figure S2 Biplot showing the first two axes of a principal coordinate analysis of the *Nitrospira* communities (OTUs) in nine saline-alkaline lakes grouped by hierarchical clustering of a Bray-Curtis dissimilarity matrix using the Ward agglomeration method. The axes cumulatively explain 79.94% of the observed variation. *Nitrospira* OTUs were retrieved from the 16S rRNA gene amplicon dataset using a sequence identity threshold of 97%. Lake identifiers and grouping of lakes are the same as in main text Fig. 1.