



**Figure S1:** Phylogenetic tree of environmental isolates from Neusiedler See and reference strains, based on multi-locus sequence analysis. Red (Phenotypic antibiotic resistance testing (ABR) and whole genome sequencing (WGS)) and yellow bars (phenotypic antibiotic resistance testing only) indicate the selected isolates analysed in this study. Figure modified after Pretzer et al 2017.

**Reference cited:**  
Pretzer, C., Druzhinina, I. S., Amaro, C., Benediktsdóttir, E., Hedenström, I., Hervio-Heath, D., et al. (2017). High genetic diversity of *Vibrio cholerae* in the European lake Neusiedler see is associated with intensive recombination in the reed habitat and the long-distance transfer of strains. Environ. Microbiol. 19, 328 -344. doi: 10.1111/1462-2920.13612