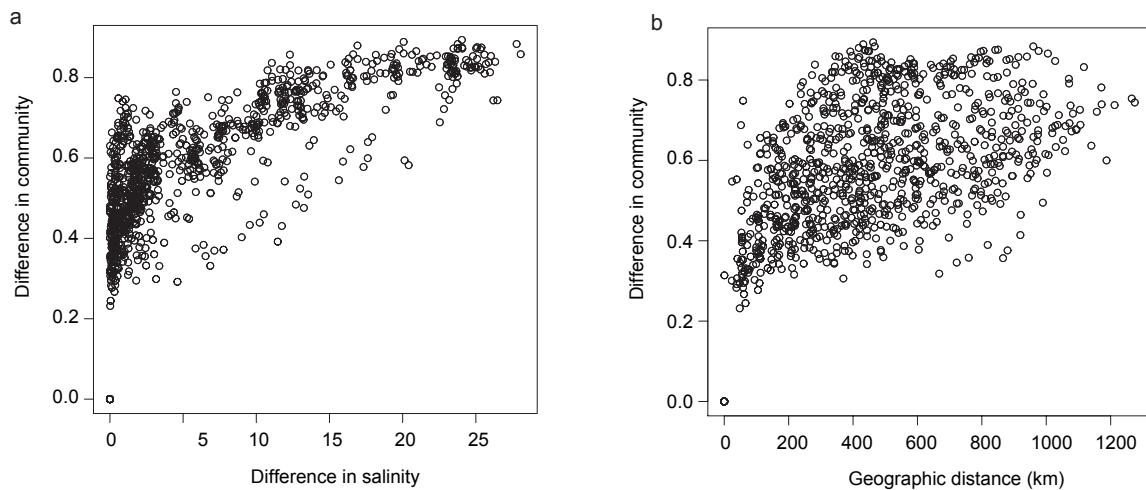
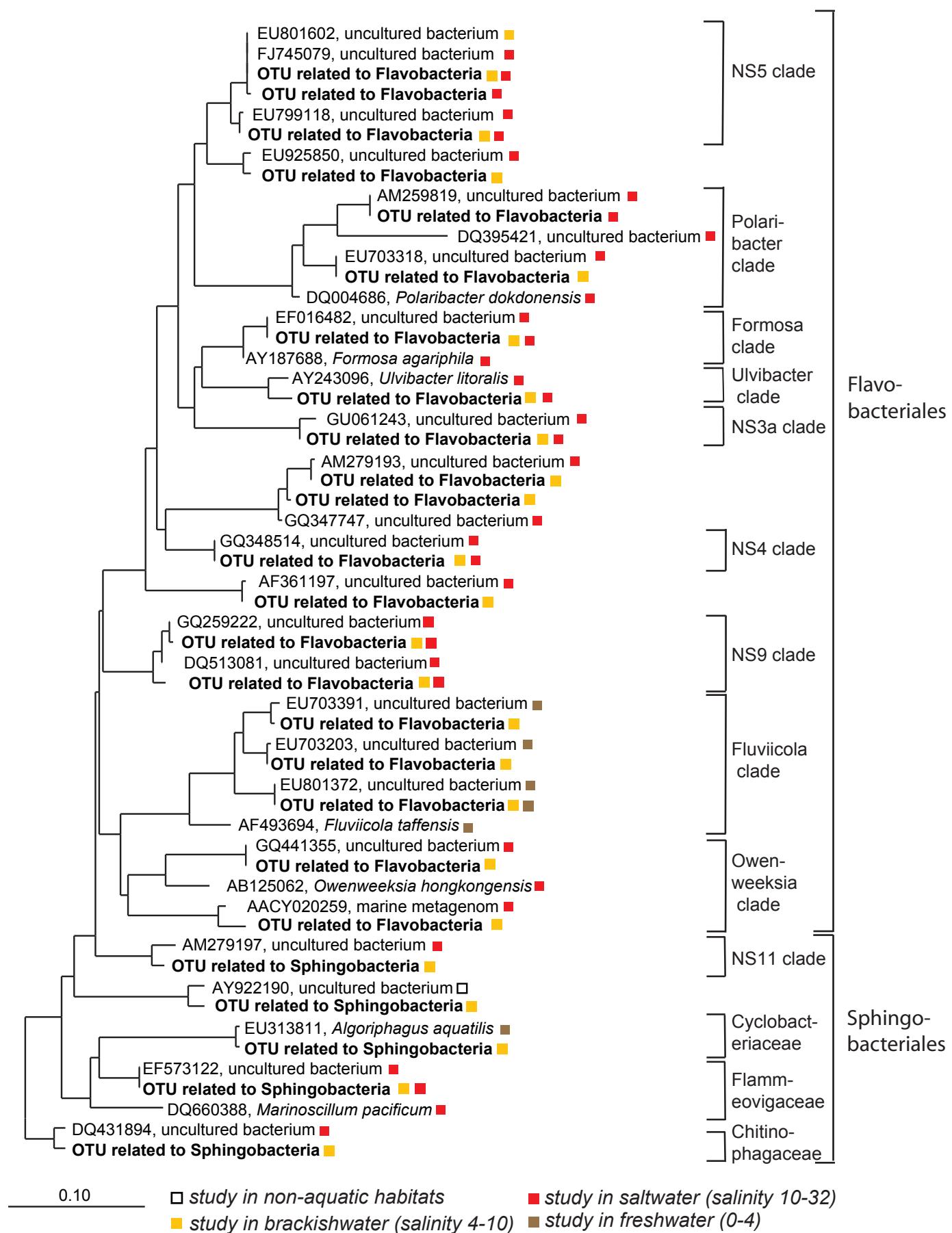
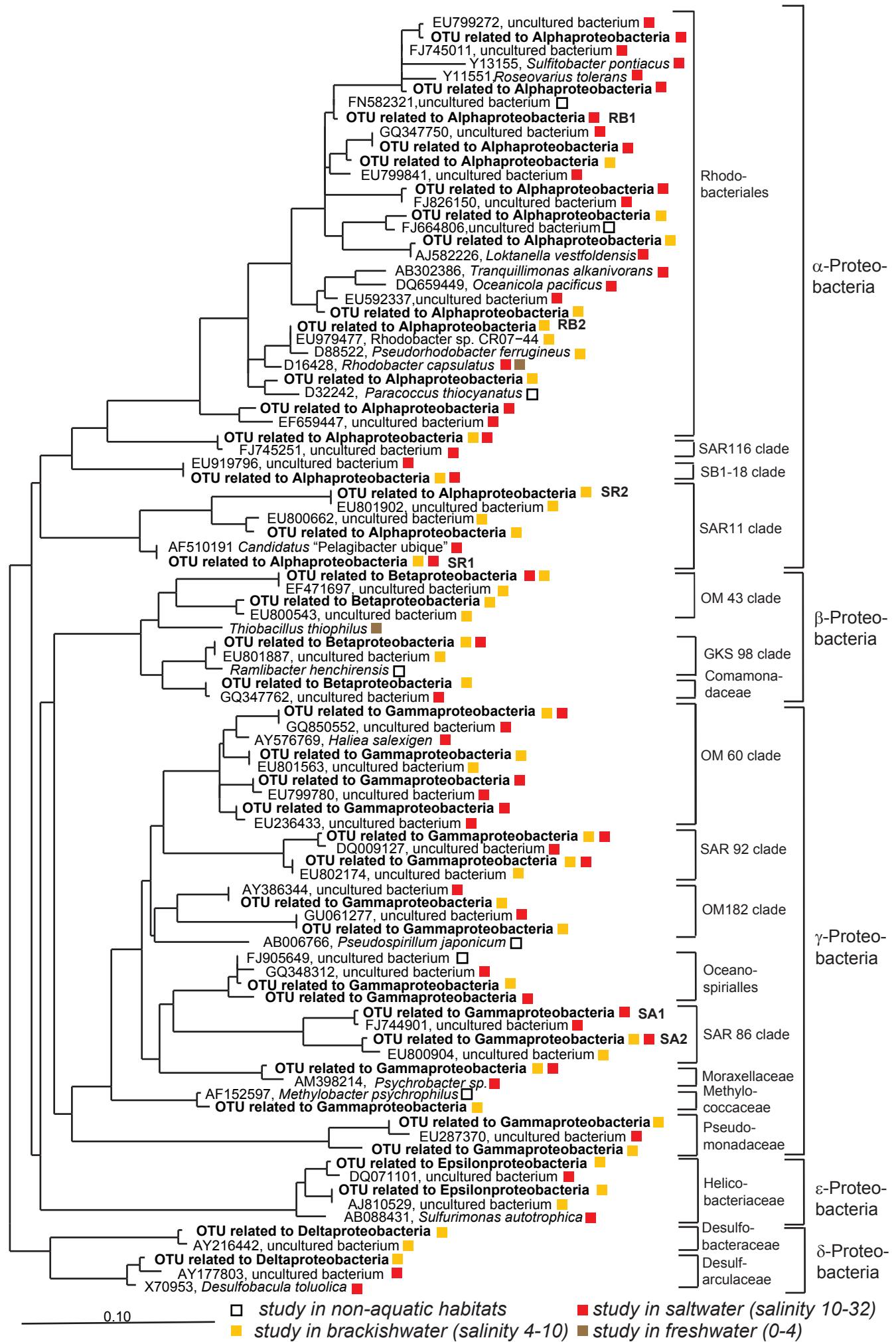


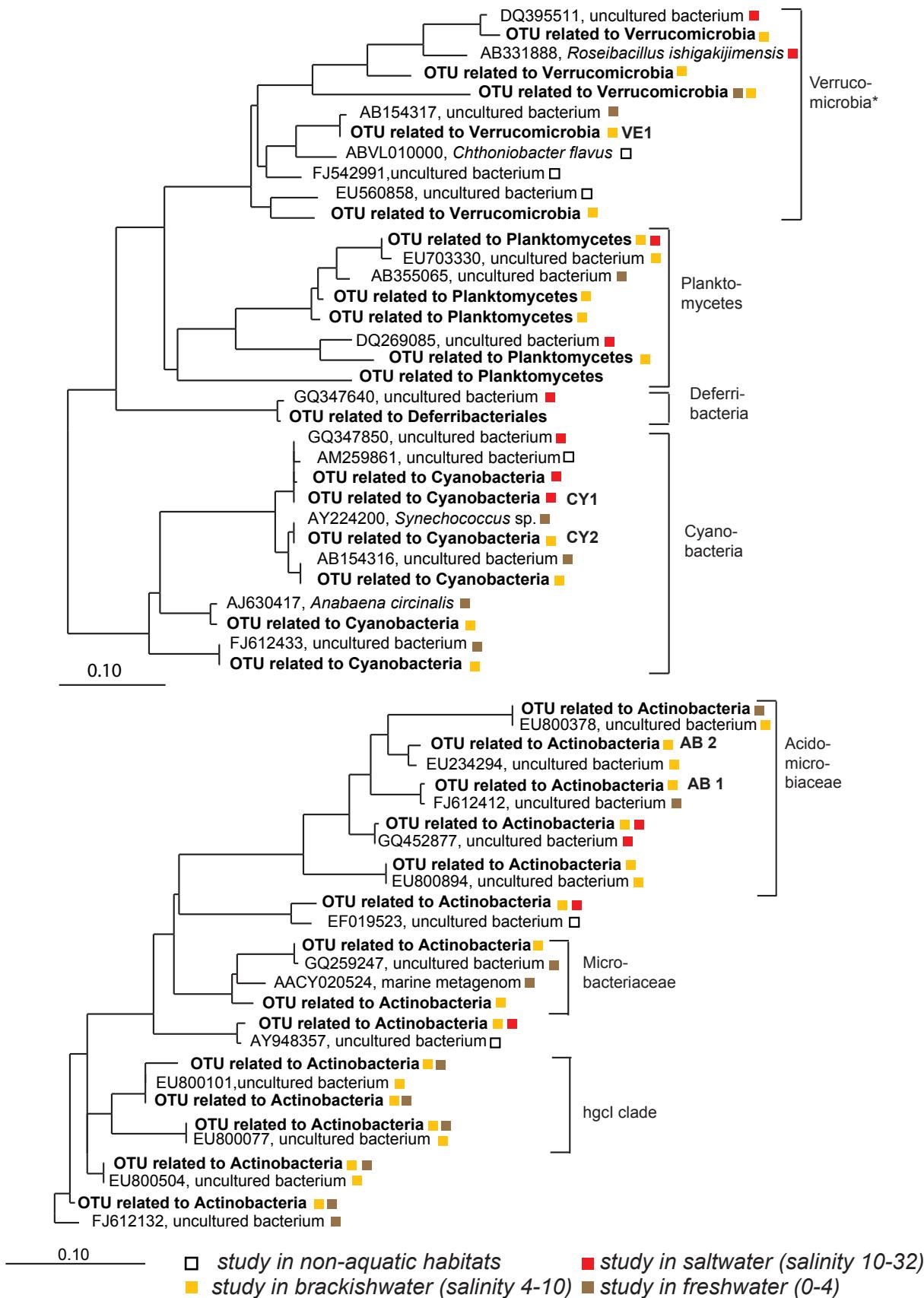
**Supplementary Figure 1.** Bacterial community composition along depth profiles of two of the deepest sampling stations: (a) Gotland Deep ( $57^{\circ} 18.33' \text{N}, 20^{\circ} 4,47' \text{E}$ ) and (b) the Åland Deep ( $60^{\circ} 11.50' \text{N}; 19^{\circ} 7.03' \text{E}$ ). The composition of the bacterial community shifted at broad phylogenetic levels below the oxygen chemocline in the Gotland Deep, but did not change considerably in the deep water layers of the Åland Deep, which are not anoxic.



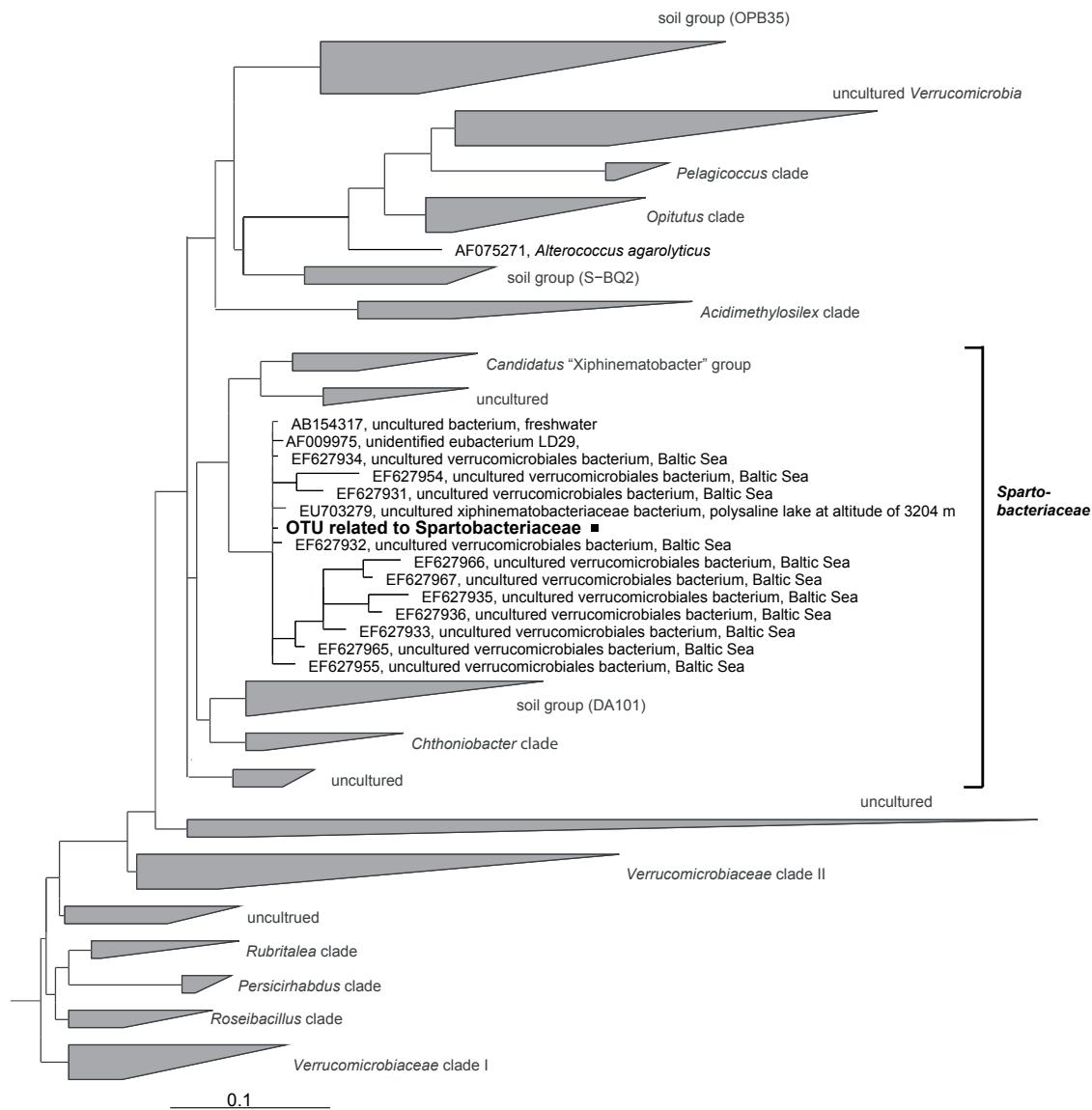
**Supplementary Figure 2.** Scatter-plots displaying  $\beta$ -diversity *vs.* (a) absolute difference in salinity (Spearman correlation  $\rho = 0.81$ ,  $P < 10^{-16}$ ) and (b) geographic distance ( $\rho = 0.51$ ,  $P < 10^{-16}$ ), for all pairs of surface water samples.







**Supplementary Figure 3.** Phylogenetic trees of the 100 most-abundant operational taxonomic units (OTUs) from our study. The scale bar is only approximate because the procedure disorts branch lengths. Sequences from our study are in bold, strains are in italics. Original sequence definition in Genbank were replaced by SILVA taxonomy and neutral name. An asterik indicates that the group is resolved in more detail in Supplementary Figure 4, and abbreviations indicate that the OTU is displayed in Figure 3.



**Supplementary Figure 4.** Phylogeny of the most abundant taxonomic unit in our study (black square), which belong to the *Verrucomicrobia*. Original sequence definitions and GenBank accession numbers of sequences closely related to the *Verrucomicrobia* sequence detected in our study are given.