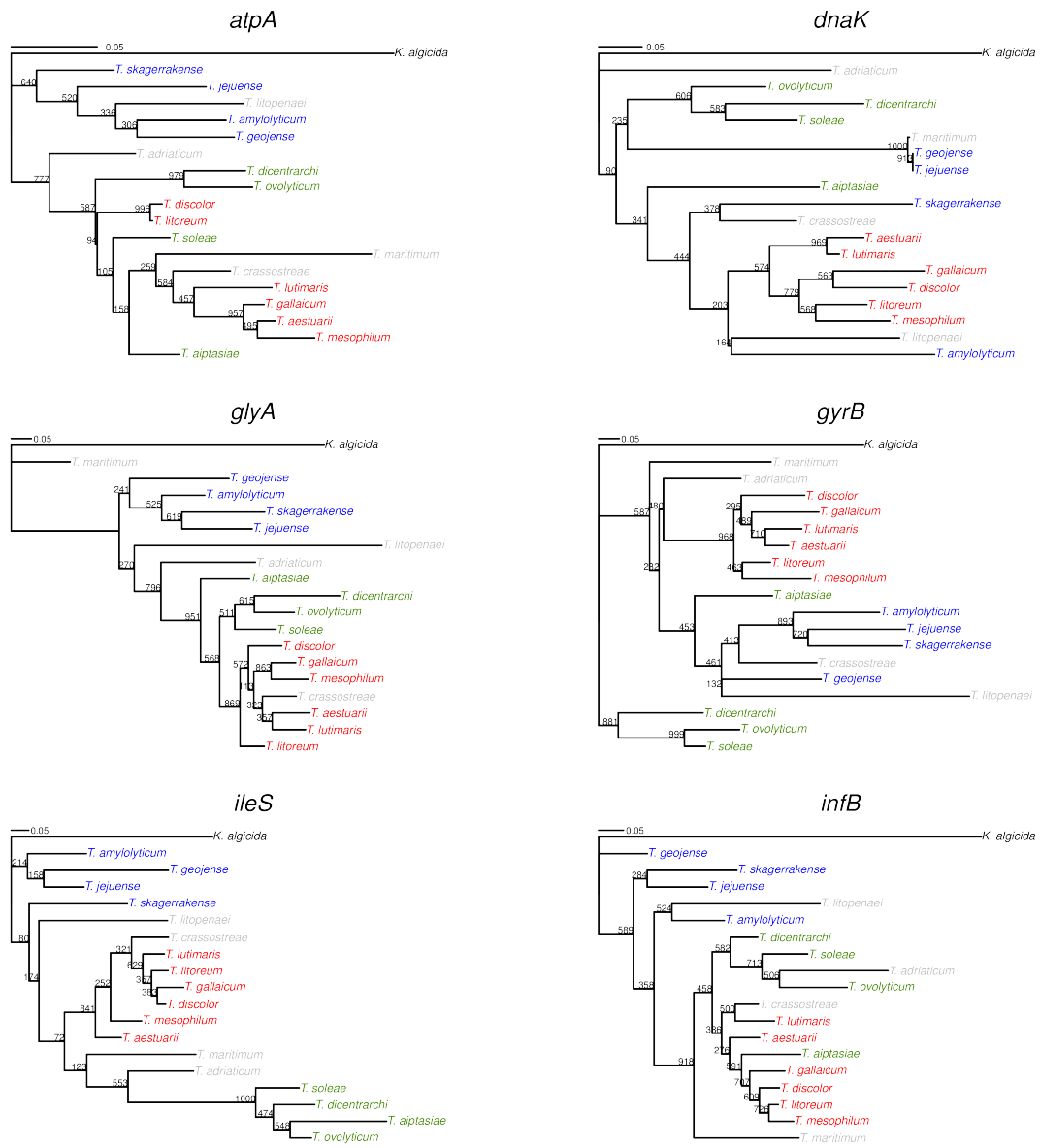
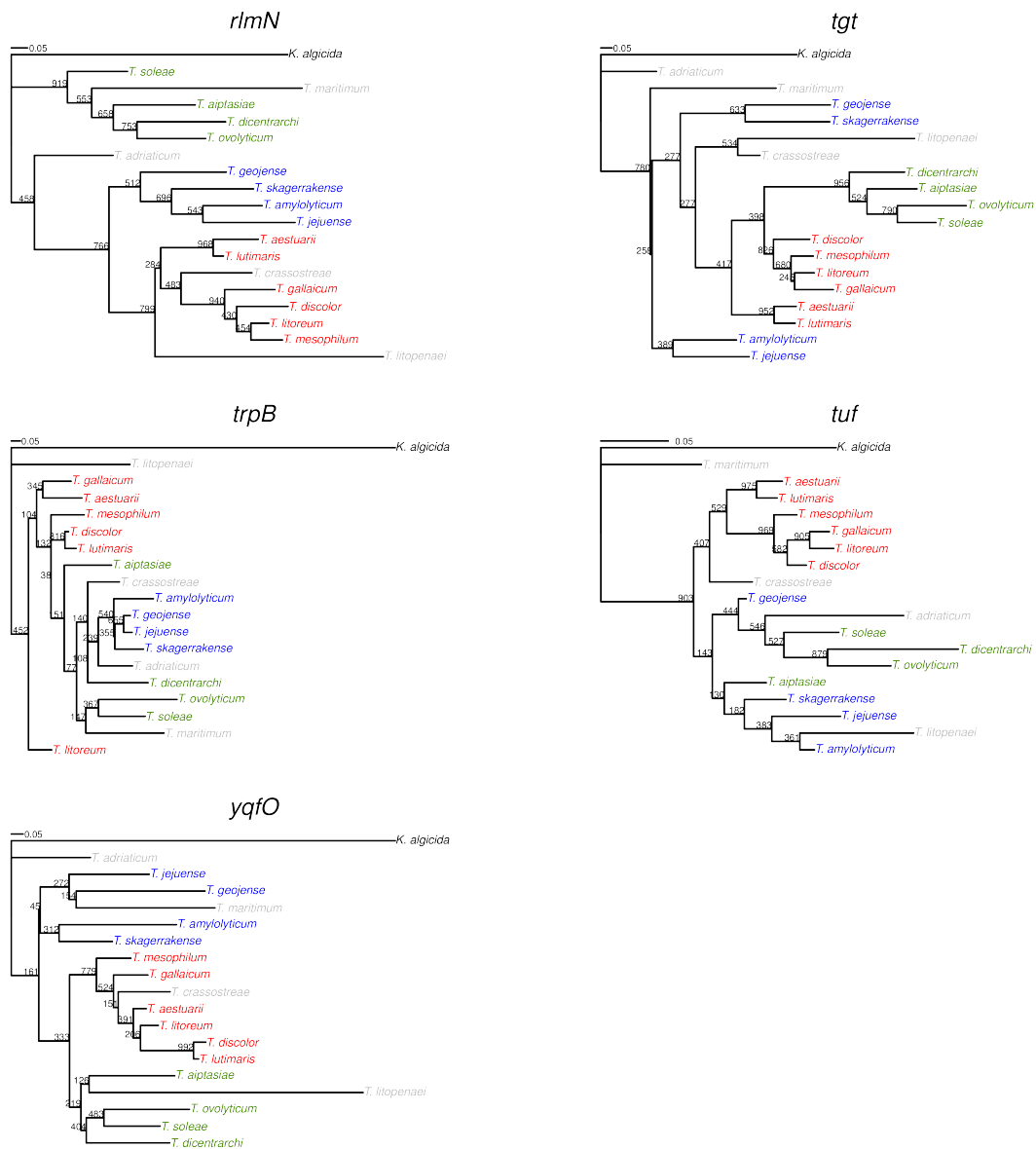


## Content of the Supplementary Information

- **Figure S1.** The 11 maximum-likelihood phylogenetic trees reconstructed on the basis of the nucleotide sequence of each individual locus.
- **Figure S2.** Same as Figure 2 but based on the 7 selected loci instead of the 11 loci.
- **Figure S3.** Same as Figure 3 but based on the 7 selected loci instead of the 11 loci.

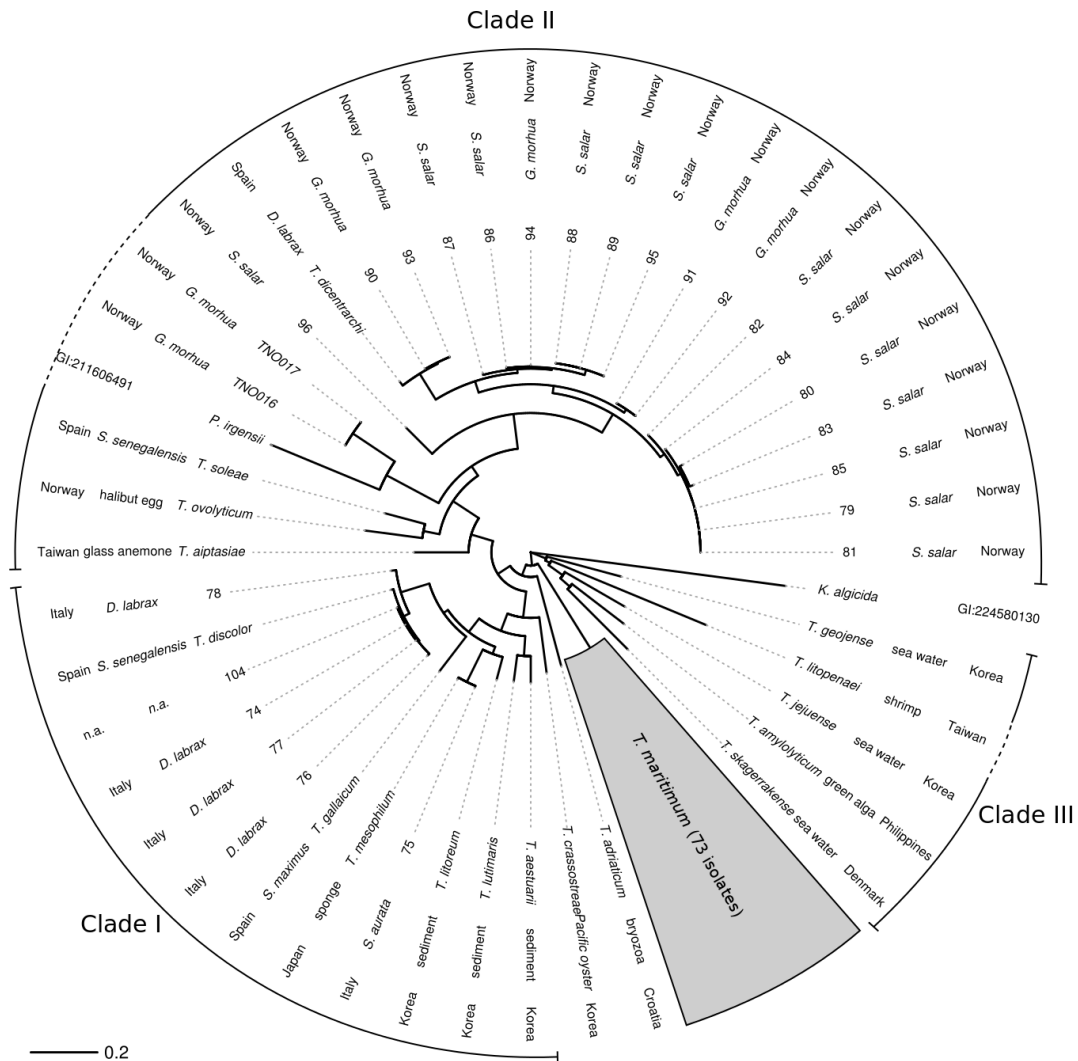
Figure S1.





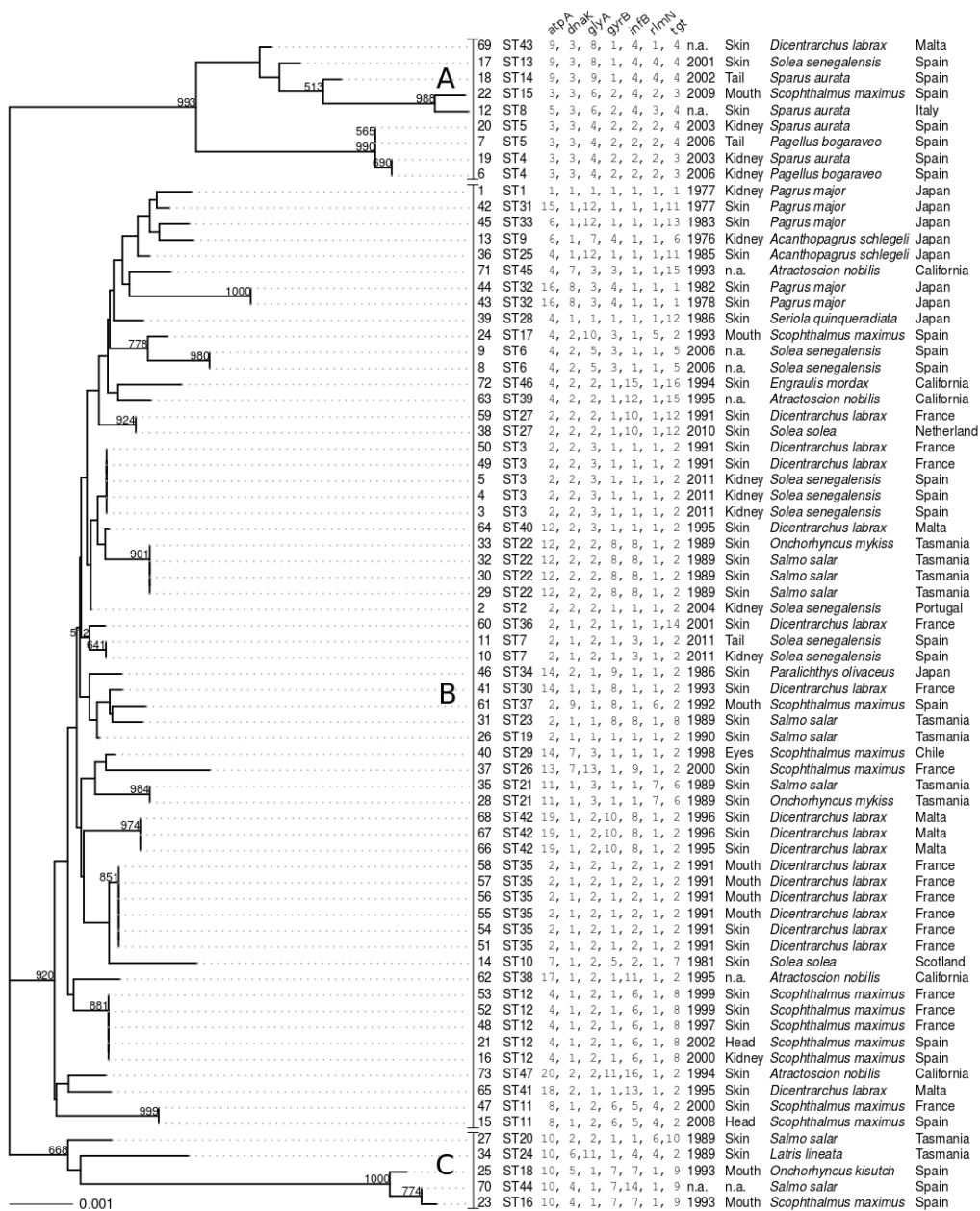
The 11 maximum likelihood phylogenetic trees reconstructed on the nucleotide sequences of each individual locus. The *Kordia algicida* type strain was included as an outgroup. Bootstrap supports estimated on 1,000 replicate data-sets are reported above each internal node. Colours indicate the three clades identified based on high bootstrap support in the concatenated MLSA tree (I in red, II in green, III in blue); the four isolated lineages that branch more deeply in the concatenated MLSA tree are represented in grey. The same branch-length scale (measured in expected number of nucleotide substitutions per site) is used in all trees. The branch leading to *K. algicida* in the 16S rRNA tree has been shortened by a factor 3 for the sake of representation.

Figure S2



Concatenated MLSA tree based reconstructed on 7 loci (*atpA*, *dnaK*, *glyA*, *gyrB*, *infB*, *rlmN*, and *tgt*) by maximum likelihood for the 114 *Tenacibaculum* isolates included in this study. A condensed representation (grey area) is used for the 73 isolates that group with the type strain of *T. maritimum*. For each other *Tenacibaculum* strain the following information is reported: isolate identifier or bacterial species for type strains, isolation source (binomial names for fish species), and country of origin. Dotted lines indicate isolates that do not belong to the clade according to Figure 1. The type strains of *Polaribacter irgensii* and *Kordia algicida* (accession numbers are indicated in the tree) were included to help rooting but only *K. algicida* could easily be used as an outgroup. Branch-length is measured in expected number of nucleotide substitutions per site.

Figure S3



Genotype and background information for the 73 *Tenacibaculum maritimum* isolates based on 7 loci (*atpA*, *dnaK*, *glyA*, *gyrB*, *infB*, *rlmN*, and *tgt*). From left to right: tentative phylogenetic tree; isolate identification numbers (see Table S2); sequence types; allele-types at the 7 loci; information on the isolation source (year, tissue, host fish, country; n.a, not available). The tree was obtained by neighbor joining with a simple Jukes-Cantor substitution model. Branch-length is measured in expected number of nucleotide substitutions per site. Bootstrap support was estimated on 1,000 replicate data-sets, and only values greater than 500 are shown. The three sub-groups of isolates designated A, B and C are labelled and delineated by vertical bars.