

Fig. S1. Phylogenetic tree showing the relationships between *Tetramitus* sp. (clone H16/15T), isolated from the gills of farmed salmon suffering from gill disease, and other members of genus *Tetramitus*. Sequences of SSU rRNA gene ((Accession no: AJ224887) from *Valkampfia inornata* has been used as outgroup. The analysis is based on 1418 nucleotides from the SSU rRNA gene. The scale bar shows the number of nucleotide substitutions as a proportion of branch length

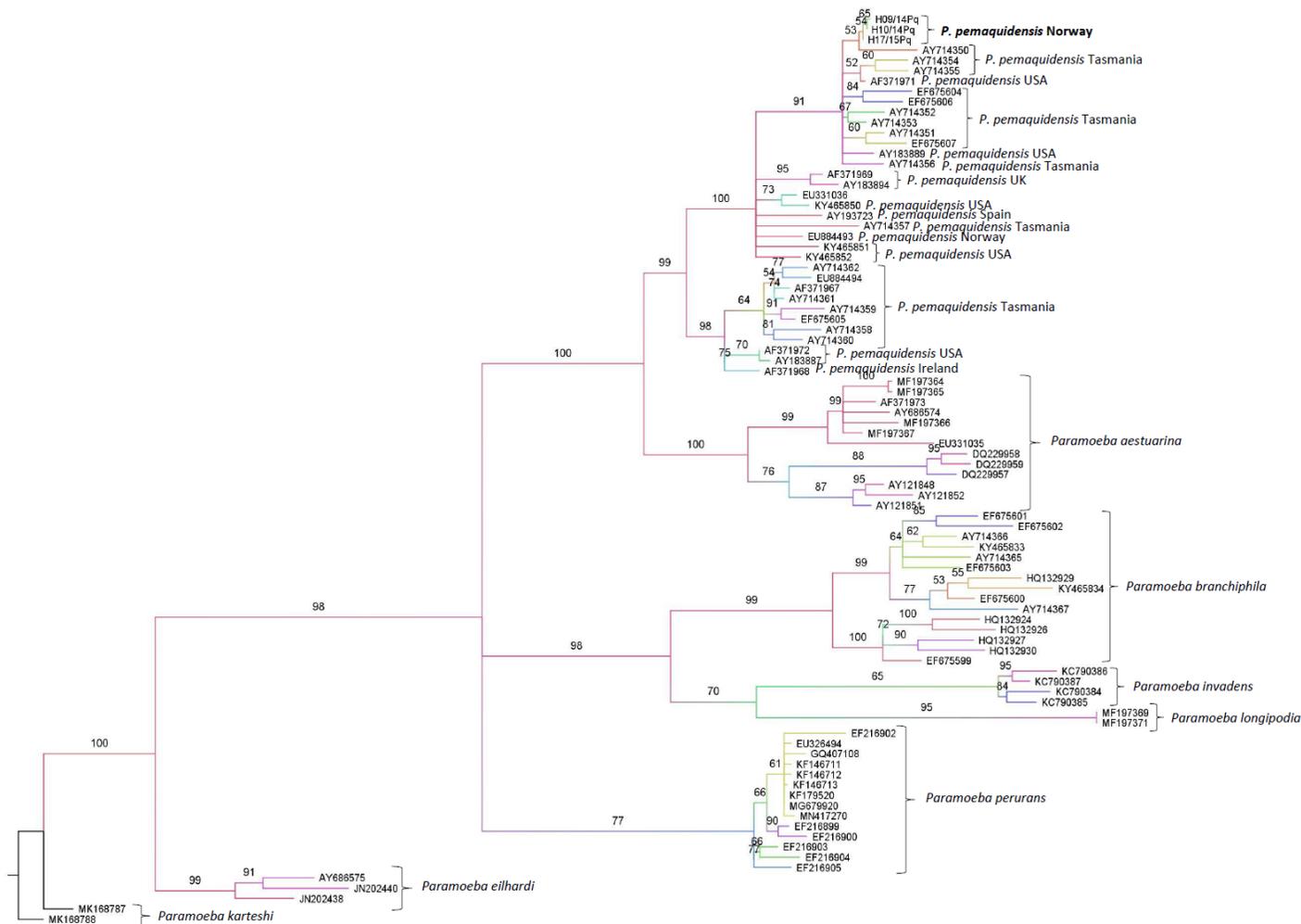


Fig. S2. Phylogenetic tree showing the relationships between *Paramoeba pemaquidensis* (clones H09/14Pq, H10/14Pq, H17/15Pq), isolated from the gills of ballan wrasse, saithe, and farmed salmon suffering from gill disease, and other members of genus *Paramoeba*. Sequences of SSU rRNA gene ((Accession no: MK168788) from *Paramoeba karteshi* has been used as outgroup. The analysis is based on 1865 nucleotides from the SSU rRNA gene. The scale bar shows the number of nucleotide substitutions as a proportion of branch lengths.

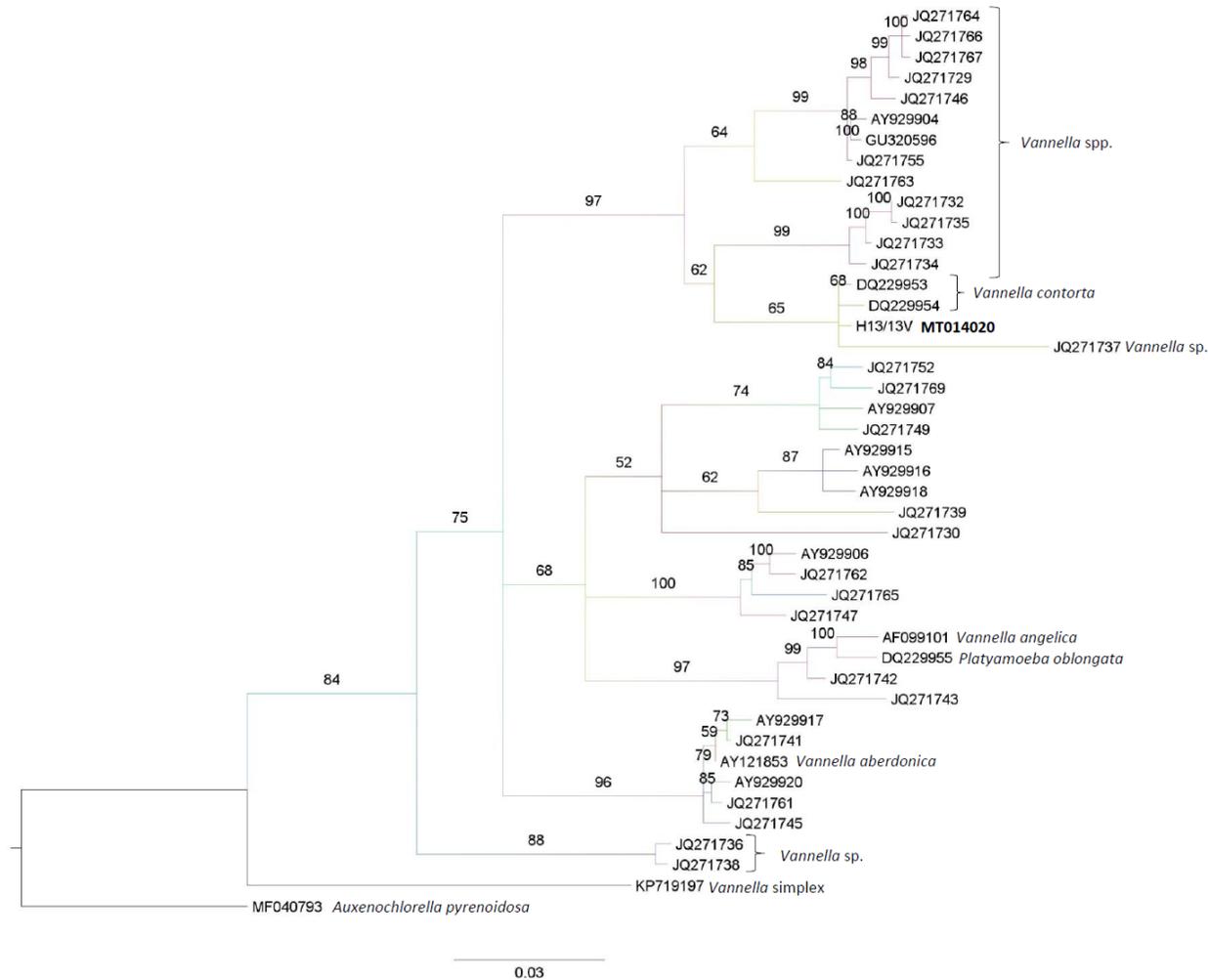


Fig. S3. Phylogenetic tree showing the relationships between *Vannella* sp. (H13/13V), isolated from salmon louse attached to farmed salmon suffering from gill disease, and other members of genus *Vannella*. Sequences of SSU rRNA gene (Accession no: MF040793) from *Auxenochlorella pyrenoidosa* has been used as outgroup. The analysis is based on 1897 nucleotides from the SSU rRNA gene. The scale bar shows the number of nucleotide substitutions as a proportion of branch lengths.