Supplementary Materials

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Supplementary Table S1. List of amino acid sequences used as queries in BLASTp searches [Available at http://www.e-algae.org].

Supplementary Table S2. List of amino acid sequences used in the phylogenetic analysis of bestrophins [Available at http://www.e-algae.org].

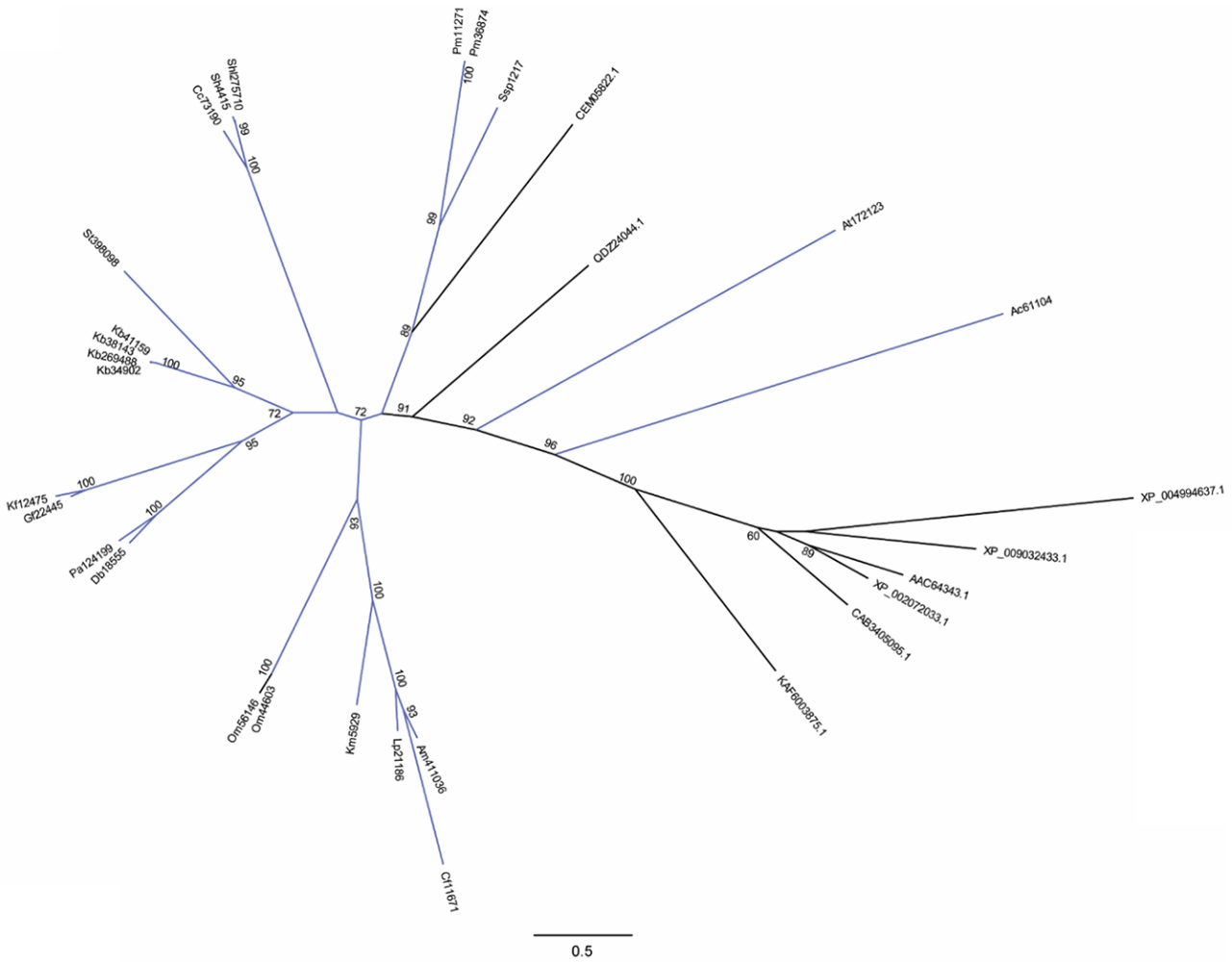
Supplementary Table S3. List of amino acid sequences used in the phylogenetic analysis of large-conductance calcium-activated potassium channels (BK) [Available at http://www.e-algae.org].

Supplementary Table S4. List of amino acid sequences used in the phylogenetic analysis of inositole-1,4,5-trisphosphate receptors (IP_3R) [Available at http://www.e-algae.org].

Supplementary Table S5. List of amino acid sequences used in the phylogenetic analysis of two-pore domain potassium channels (K_{2P}) [Available at http://www.e-algae.org].

Supplementary Table S6. List of amino acid sequences used in the phylogenetic analysis of voltage-dependent anion channels (VDAC) [Available at http://www.e-algae.org].

Supplementary Table S7. The best results of BLASTp search in the translated combined assembles of dinoflagellate transcriptomes in marine microbial eukaryote transcriptome sequencing project (MMETSP) [Available at http://www.e-algae.org].



Supplementary Fig. S1. Maximal likelihood inference of unrooted phylogenetic tree (LG + F + R3, 10,000 ultrafast bootstrap replicates, bootstrap values <60 are not shown) of bestrophins. Branches of the dinoflagellate sequences are blue. The list of sequences is provided in Supplementary Table S2.

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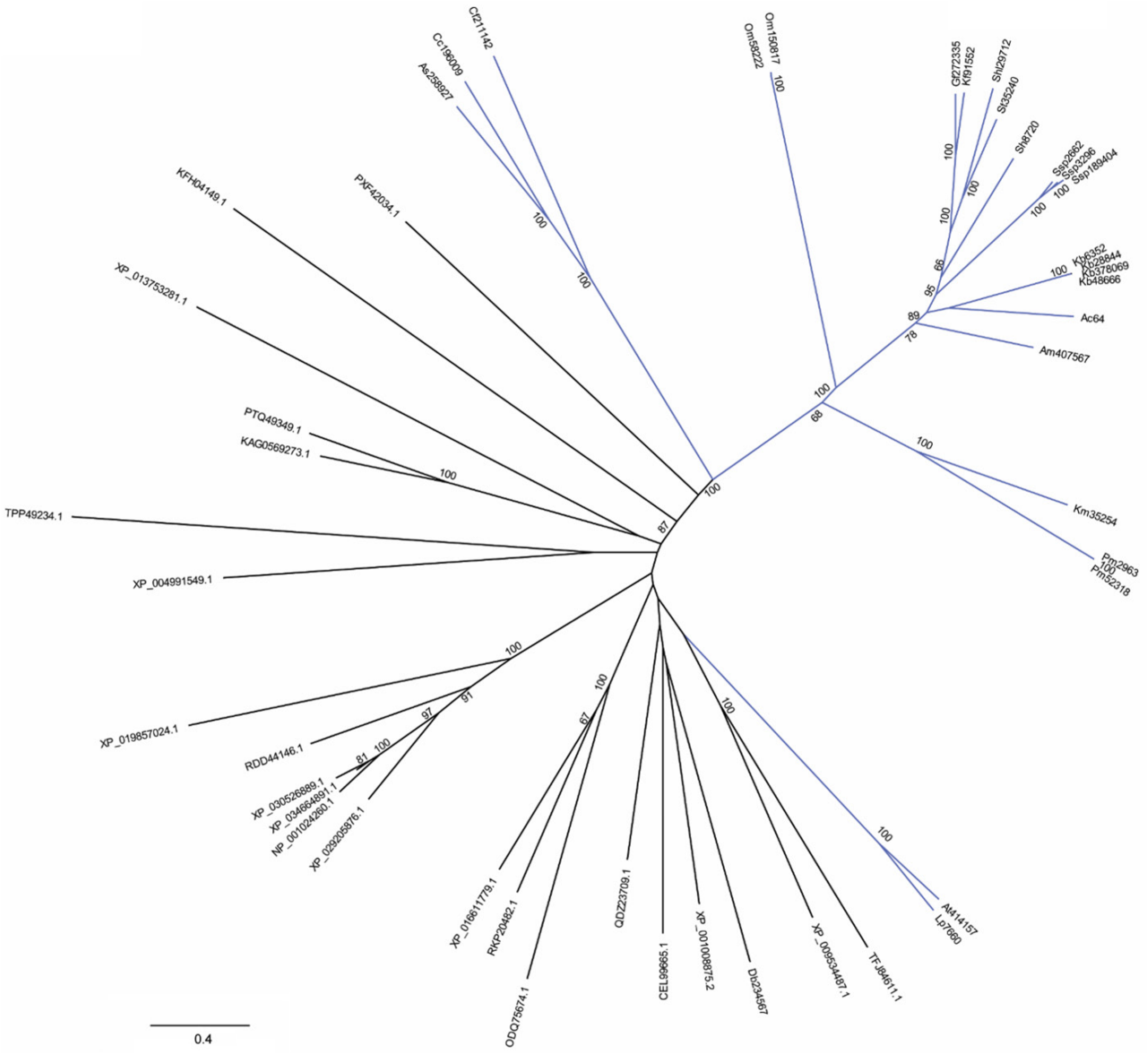
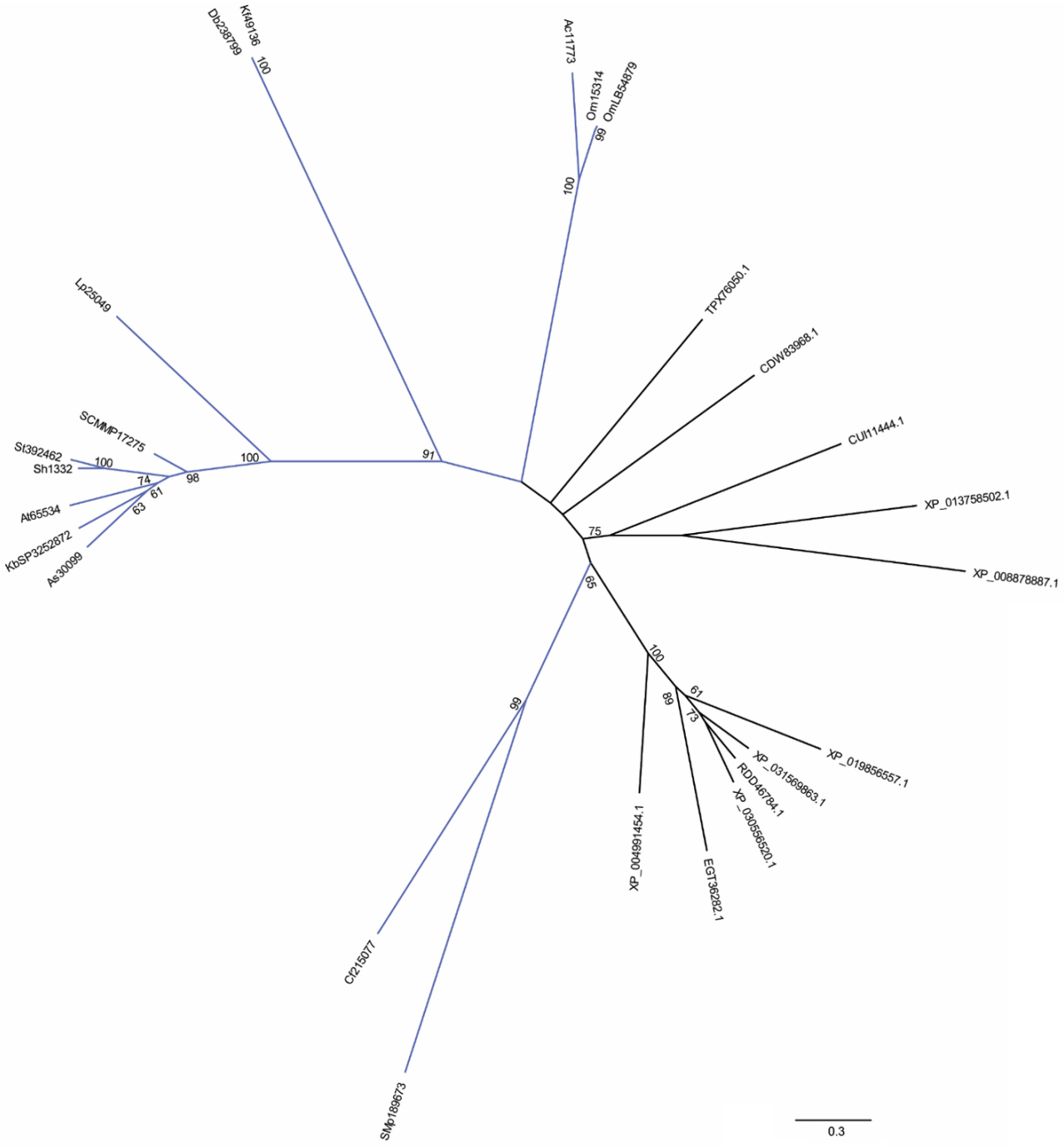
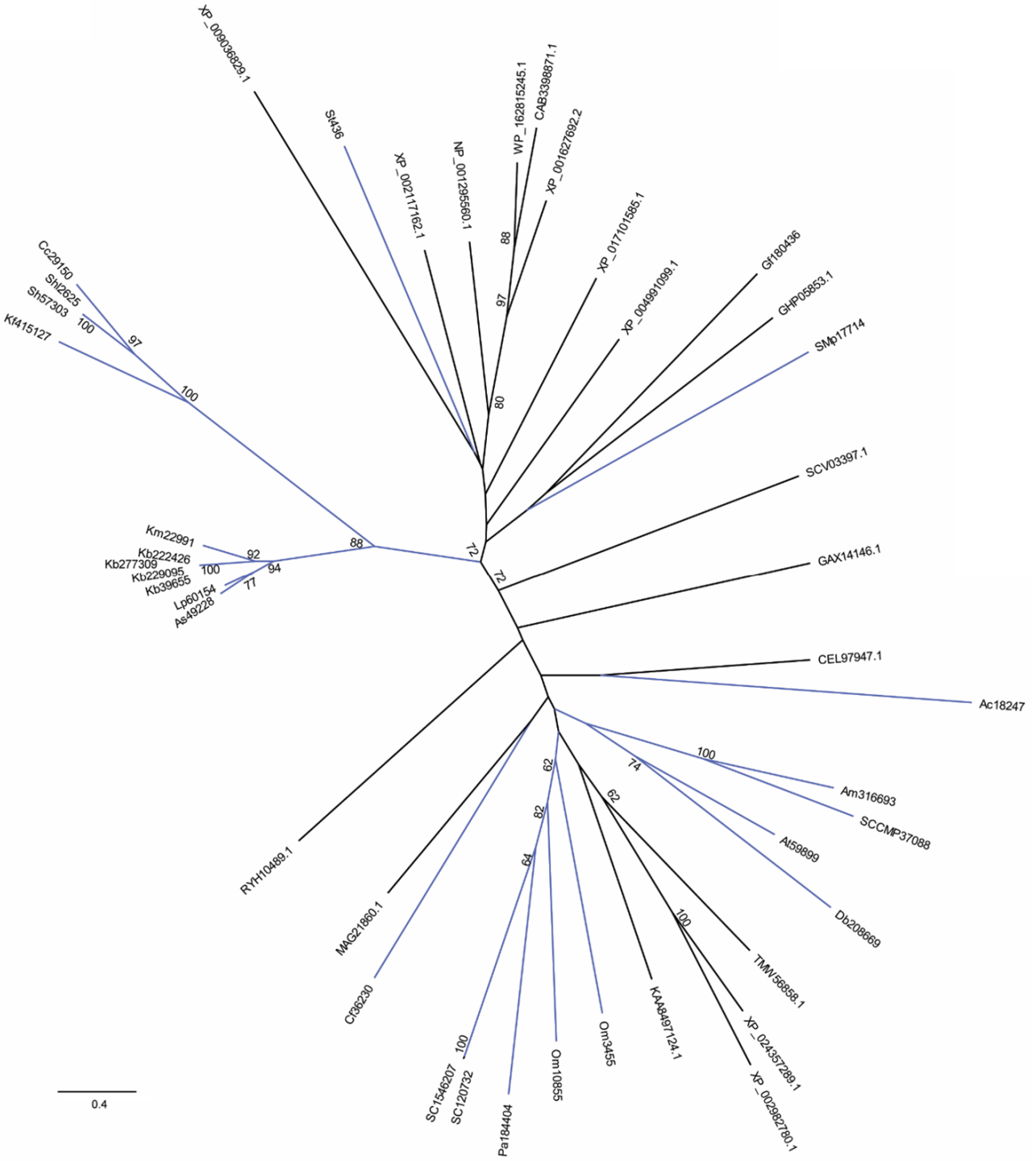


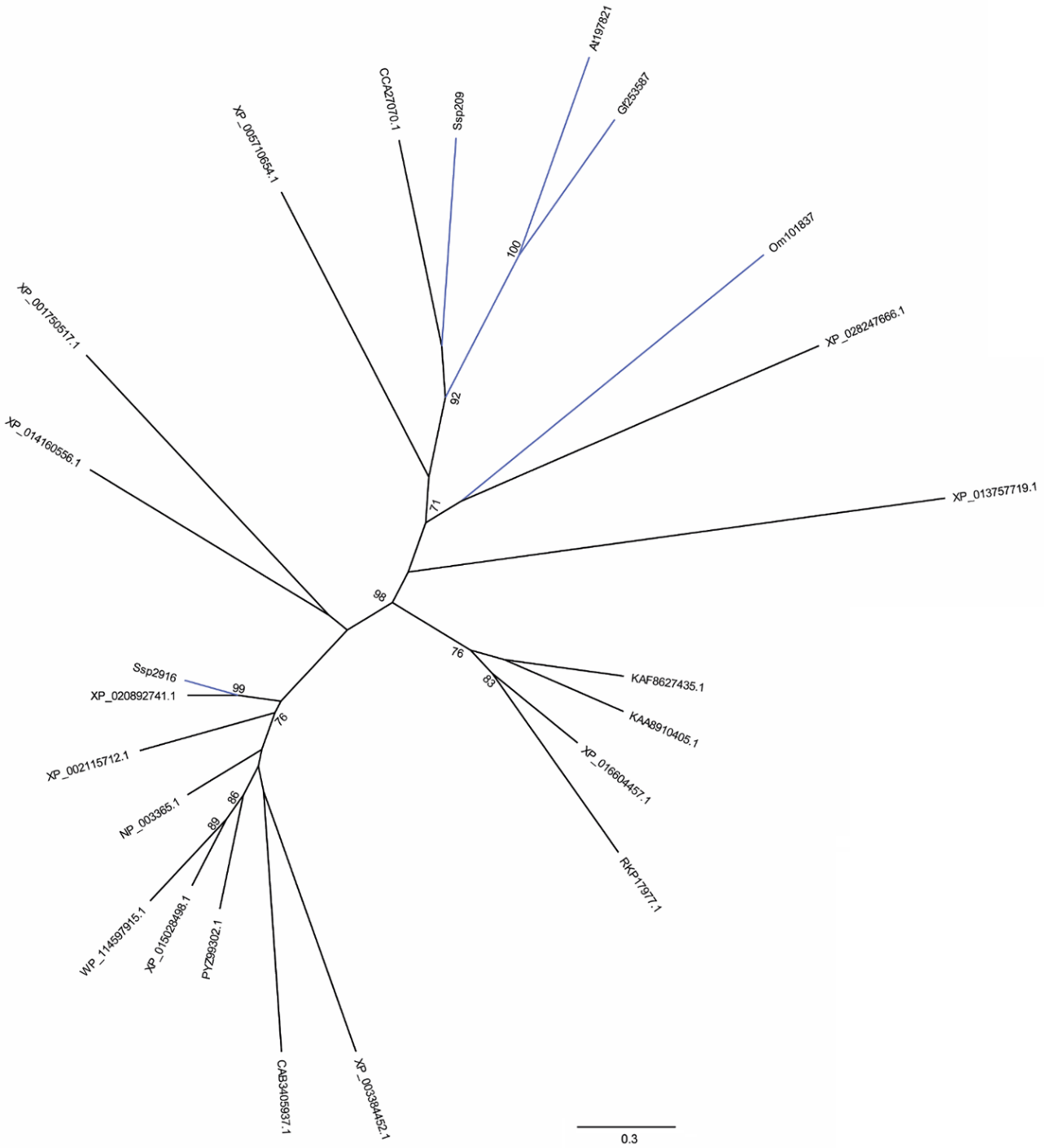
Supplementary Fig. S2. Maximal likelihood inference of unrooted phylogenetic tree (LG + F + R5, 10,000 ultrafast bootstrap replicates, bootstrap values <60 are not shown) of large-conductance calcium-activated potassium channels (BK). Branches of the dinoflagellate sequences are blue. The list of sequences is provided in Supplementary Table S3.



Supplementary Fig. S3. Maximal likelihood inference of unrooted phylogenetic tree (LG + I + Γ4, 10,000 ultrafast bootstrap replicates, bootstrap values <60 are not shown) of inositole-1,4,5-trisphosphate receptors (IP_3R). Branches of the dinoflagellate sequences are blue. The list of sequences is provided in Supplementary Table S4.



Supplementary Fig. S4. Maximal likelihood inference of unrooted phylogenetic tree (LG + F + R4, 10,000 ultrafast bootstrap replicates, bootstrap values <60 are not shown) of of two-pore domain potassium channels (K_{2P}). Branches of the dinoflagellate sequences are blue. The list of sequences is provided in Supplementary Table S5.



Supplementary Fig. S5. Maximal likelihood inference of unrooted phylogenetic tree (LG + F + I + Γ4, 10,000 ultrafast bootstrap replicates, bootstrap values <60 are not shown) of of voltage-dependent anion channels (VDAC). Branches of the dinoflagellate sequences are blue. The list of sequences is provided in Supplementary Table S6.