



Figure S5. The phylogram built by MEGA-X software and its utility for ML-gene tree reconstruction based on 13 PCG-sequences of 26 analyzed flounder representatives of the family Pleuronectidae with the out-group taxon *Paralichthys olivaceus*.

The ML tree and topology support scores obtained through n=1000 replications throughout the tradition mode of the bootstrap test; the scores given besides the nodes. Numerals below the branches indicate the composition distance, CD (bias) calculated for 26 sequences in the analysis.

CD is a measure of the difference in nucleotide composition for a given pair of sequences. It is one half the sum of squared difference in counts of bp or residues. MEGA computes and presents the CD per site, which is given by the total CD between two sequences divided by the number of positions compared, excluding gaps and missing data (MEGA-X help).