**Figure S2** ML tree obtained based on mitochondrial genes for a set of species similar to that used for the nuclear markers. The best-fit evolutionary models for aa mt matrix as JTT+G+F (lnL -36081.99) was used for the ML analyses with a discrete Gamma (+G) distribution for 100 replicates. This analysis is consistent with the naked coral hypothesis, as in the case of previous analyses based on mitochondrial amino acid sequences.

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