

SUPPLEMENTARY MATERIAL

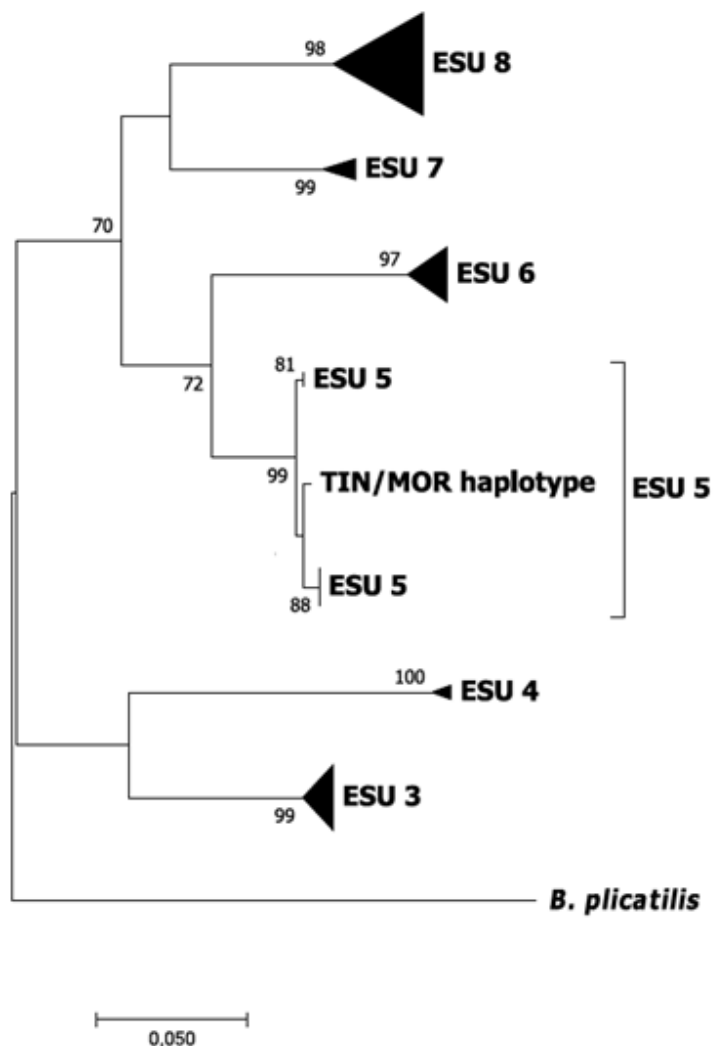


FIGURE S1. Molecular Phylogenetic analysis by Maximum Likelihood method of two *K. cochlearis* clones isolated from Tinaja (TIN) lake and Cueva Morenilla (MOR) lake. The evolutionary history was inferred by using the Maximum Likelihood method based on the Tamura-Nei model (Tamura and Nei, 1993). The tree with the highest log likelihood (-2101.35) is shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site. The analysis involved 92 nucleotide sequences. Codon positions included were 1st+2nd+3rd+Noncoding. All positions containing gaps and missing data were eliminated. There were 392 positions in the final dataset. Evolutionary analyses were conducted in MEGA7 (Kumar et al., 2016).

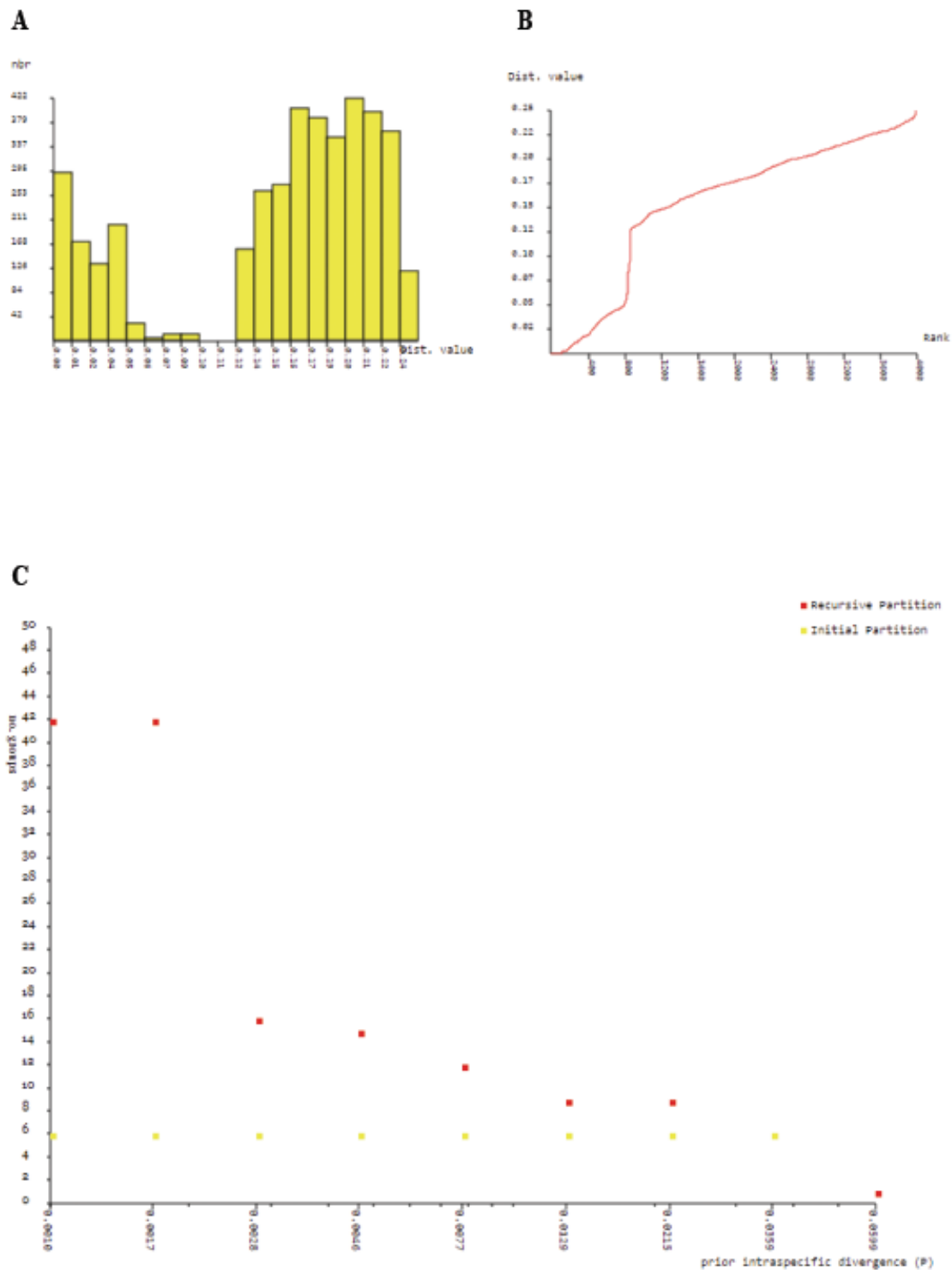


FIGURE S2. Barcode gap analysis generated by Automatic Barcode Gap Discovery (ABGD) (Puillandre *et al.*, 2012). (A) Histogram with distributions of Jukes-Cantor distances (Jukes and Cantor, 1969) between each pair of *K. cochlearis* COI sequences, (B) ranked distances and (C) automatic partition based on our *K. cochlearis* COI dataset.