

**Figure S2.** (A) Neighbour-joining (NJ) tree using Nei's genetic distance of 24 *Iberodorcadion fuliginator* populations sampled in the border region Switzerland, France and Germany and in the wider distribution area of the species. Values at the nodes (in green) are bootstrapping percentages from 10,000 replicates. (B) Principal Coordinate Analysis (PCoA) based on pairwise genetic distances ( $D_{ST}$ ) of the same populations.

