**00\_Samples.xlsx**: Description of individual and population codes used in the different analyses.

**01\_FASTSTRUCTURE\_DAPC.str**: Input file (.STR format) used to perform genetic clustering analyses (FASTSTRUCTURE) and discriminant analyses of principal components (DAPC).

**02\_SVDQuartets.unlinked\_snps.nex**: Input file (.NEX format) used for phylogenomic analyses in SVDQuartets.

**03\_SNAPP.unlinked\_snps.nex**: Input file (.NEX format) used to perform phylogenomic analyses in SNAPP.

**04\_Dstatistics.zip**: This ZIP folder contains the input file (.LOCI format) used to perform D-statistic (ABBA/BABA) tests in PYRAD.

**05\_FASTSIMCOAL2.zip**: This ZIP folder contains input files for demographic analyses in FASTSIMCOAL2.

**06\_Morphology.zip:** This ZIP folder contains input files for morphological analyses, including forewing images (.JPG format) and the final dataset.