

Figure S1. Cluster analysis of partial COI gene sequences, representing European populations of *Anopheles algeriensis*, based on Maximun Likelihood method. The tree was built using the T92+G model and rooted with *An. superpictus* and *Culex pipiens molestus*. Statistical support of taxa clustering was assessed by 1000 bootstrap iterations and support values $\geq 70\%$ are displayed at tree nodes. Tree scale indicates the amount of genetic divergence in substitution per site.*Original sequences obtained in the present study.

