



**Figure S4: Phylogenetic tree using COX2 gene.** Maximum likelihood tree of COX2 rooted on *D. melanogaster* (Dmel01) using the Tamura 3-parameter model + G, with bootstrap fractions greater than 0.5 from 500 replicate runs displayed next to branch points. Branch lengths measure number of substitutions per site. 70 variable sites were analyzed from a total of 720 positions in the alignment.