

Fig S1. Plot of Delta K values as a function of K, averaged over five independent runs of STRUCTURE, after setting the *Admixture* and *Independent Allele Frequencies* models, and K genetic clusters ranging from 1 to 10. Optimal K values (red dotted lines) were identified using the Evanno et al. (2005) method and were shown for: samples genotyped at 10 loci including a) two (Fca Ref and Fly Ref) or b) three (Fca Ref, Fly Ref, Fsi Ref) reference populations, and samples genotyped at 29 loci including c) two (Fca Ref and Fly Ref) or d) three (Fca Ref, Fly Ref, Fsi Ref) reference populations.

