Supplementary Figure 5.

Bar plots displaying ancestry coefficients of individuals from monospecific populations and from the two sites of sympatry, for the best clustering solution (K=2). Individuals are arranged according to their sampling sites. In each sympatry, individuals were further arranged according to their ploidy level. "Other" refer to individuals that could not be undoubtedly assigned to a given ploidy level from their genome size. Each genetic cluster is represented by a specific colour (orange for the "serbica" genetic cluster, and yellow for the "nathaliae" genetic cluster).