



Figure S5. Admixture plots for two–six population subdivisions for each individual *B. microptera* from Washington (WA), the Monterey Bay area (NorCal), San Luis Obispo–Santa Barbara basin, CA (SoCal) and progeny from the cross experiment of WA and CA (WAXCA). Each bar represents the probability of genotypic assignment for mitochondrial (upper plot; 440 sites) and nuclear (lower plot; 8,034,973 sites) genome SNP analyses. (A) NGSadmix results for mitochondrial (upper plot; 440 sites) and nuclear (lower plot; 8,034,973 sites) genome SNP analyses. (B) STRUCTURE results based on Sanger-sequenced fragments (COI, PK, H3, LDH1, and LDH2).