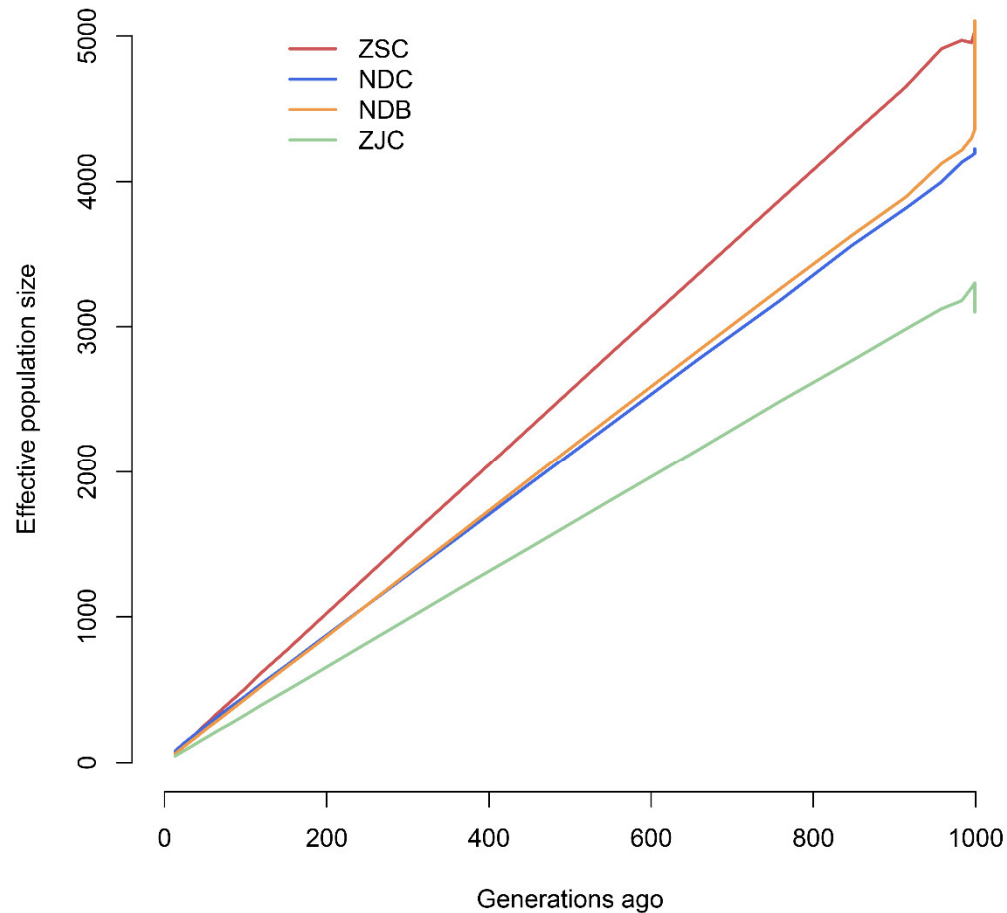
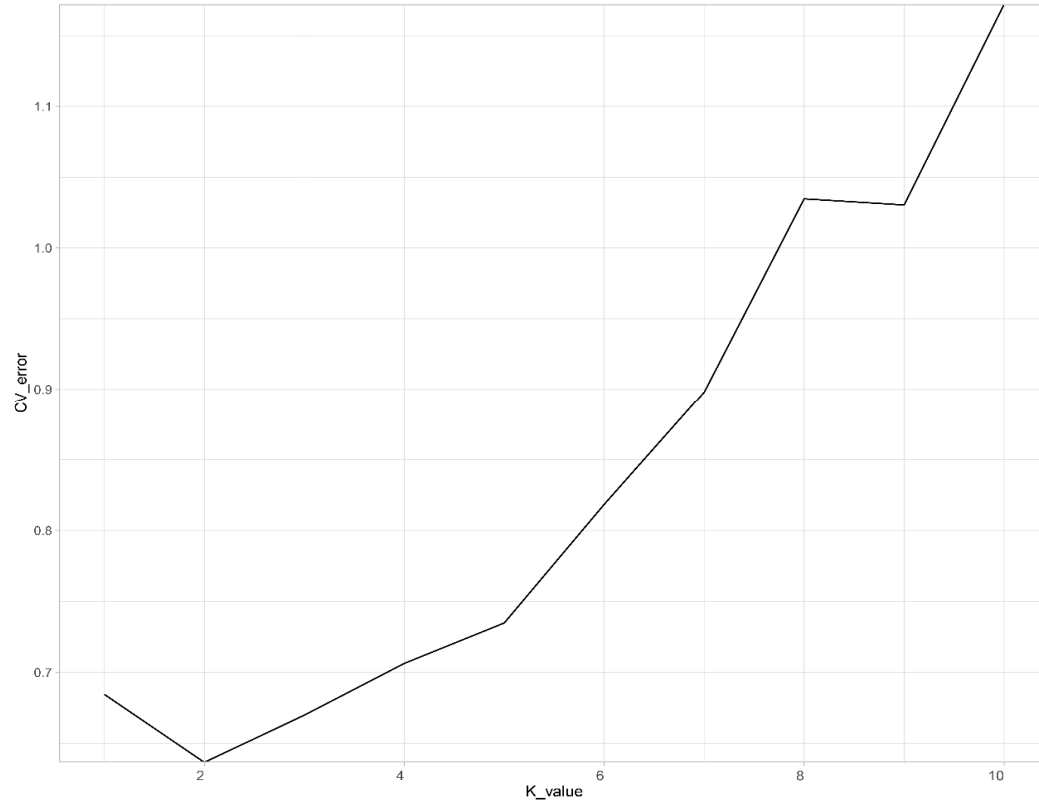


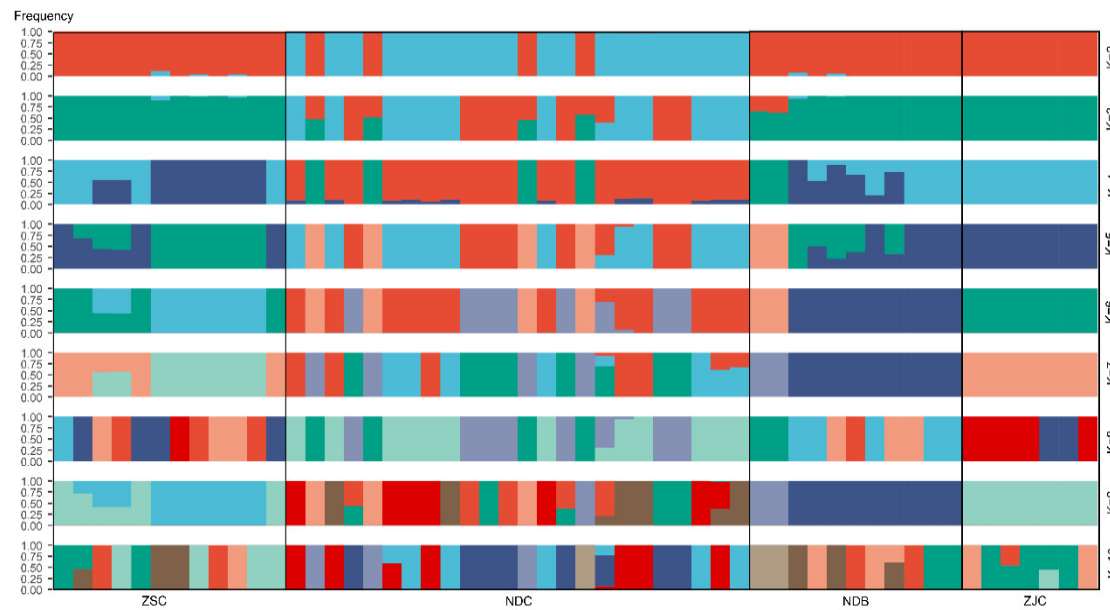
**Figure S1.** Density distribution of SNPs on different chromosomes. The horizontal lines represent the total length of the chromosomes, and different colors or grayscales represent different SNP densities.



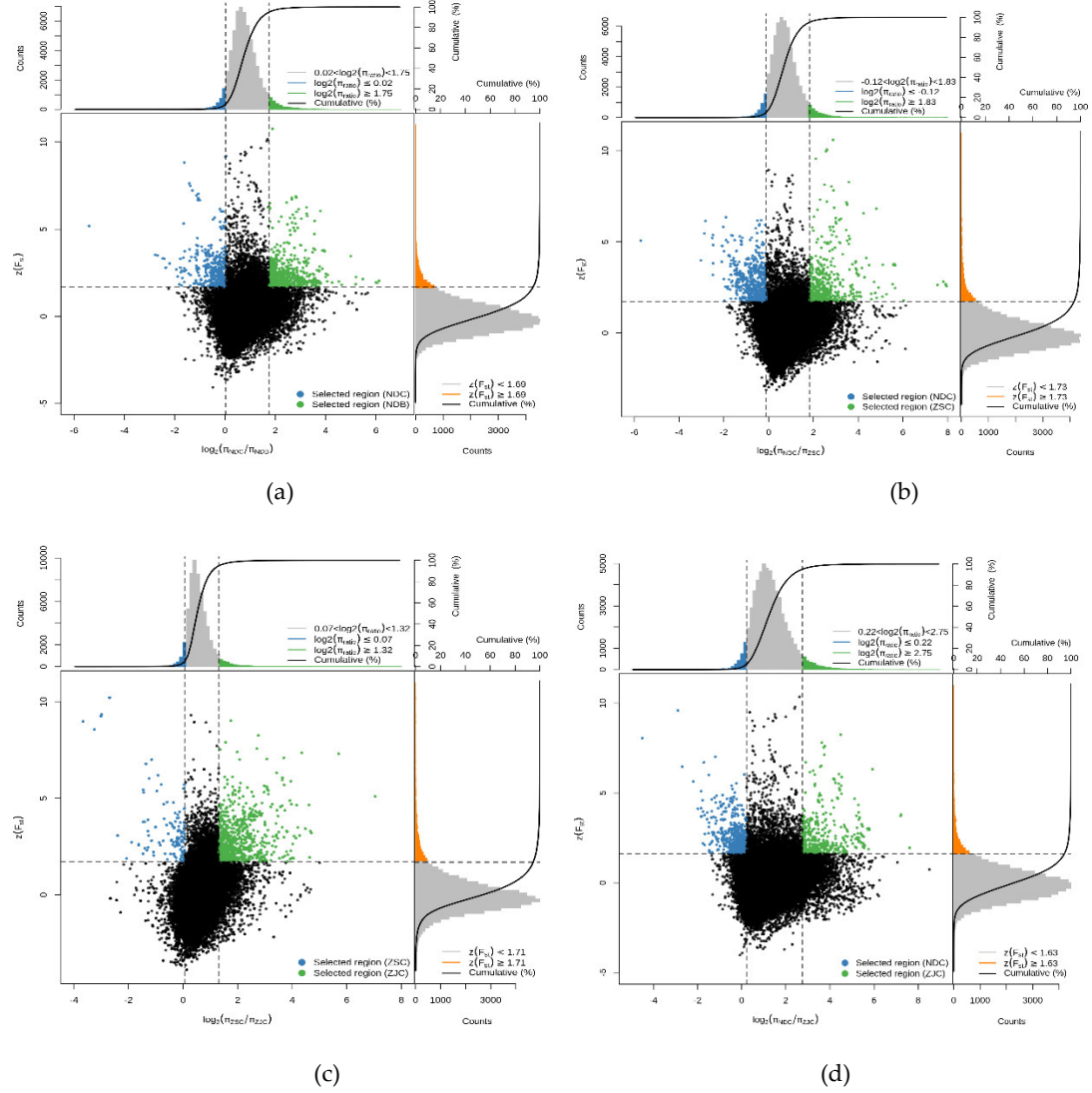
**Figure S2.** Effective population sizes of four populations over the past 1000 generations. All of the four populations showed decreasing trends.



**Figure S3.** The Cross-Validation error distribution according to the number of clusters (K) by ADMIXTURE.



**Figure S4.** Admixture analysis of four *L. crocea* populations. Length of each colored segment represents proportion of individual genome inferred from ancestral populations (K=2-10).



**Figure S5.** Genomic regions with strong selective signals in populations of *L. crocea*. **(a)** Distribution of  $\log_2(\theta\pi \text{ ratios})$  and  $Z(F_{ST})$  values calculated in 100 kb sliding windows with 10 kb increments between NDC/NDB populations. Data points in green (corresponding to top 5% of empirical  $\log_2[\pi \text{ ratio}]$  distributions with values  $>1.75$  and  $Z(F_{ST})$  distributions with values  $>1.69$ ) are genomic regions under selection in NDB population; **(b)** Distribution of  $\log_2(\theta\pi \text{ ratios})$  and  $Z(F_{ST})$  values calculated in 100 kb sliding windows with 10 kb increments between NDC/ZSC populations; **(c)** Distribution of  $\log_2(\theta\pi \text{ ratios})$  and  $Z(F_{ST})$  values calculated in 100 kb sliding windows with 10 kb increments between ZSC/ZJC populations; **(d)** Distribution of  $\log_2(\theta\pi \text{ ratios})$  and  $Z(F_{ST})$  values calculated in 100 kb sliding windows with 10 kb increments between NDC/ZJC populations.