

Fig. S1. Horizontal gene transfer from plastome to nuclear genome of wile jujube. A, Visualization of the distribution of transfer fragments from the plastome to the nuclear genome. Distinct colors indicate varying lengths of transfer fragments. B, Density map illustrating the identity of transferred fragments. Areas of high density (> 0.05) are shaded in light red. C, Collinearity analysis between the chloroplast and nuclear genome. The outermost circle depicts genome size, with the plastome unit as kb and the nuclear genome unit as Mb. The second circle portrays comparison density, using a 1 kb window for the plastome and a 10 kb window for the nuclear genome. The innermost circle depicts a collinearity plot between the nuclear genome and plastome, wherein high-density and low-density fragments are denoted by red and blue colors, respectively. D, Bar chart illustrating the quantity of three types of gene-affecting mutations across all NUPTs.

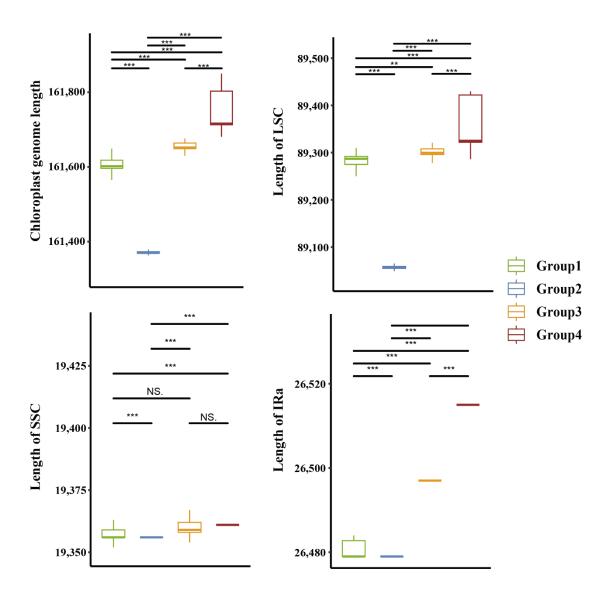


Fig. S3. Boxplots comparing the lengths (bp) of the entire chloroplast genome, as well as the LSC, SSC, and IRa for the four categorized groups of 326 jujube individuals. Statistically significant differences from the student's t-test are denoted with asterisks (\* p<0.05, \*\* p<0.01, \*\*\*\* p < 0.001, \*\*\*\* p < 0.001, NS, not significant).

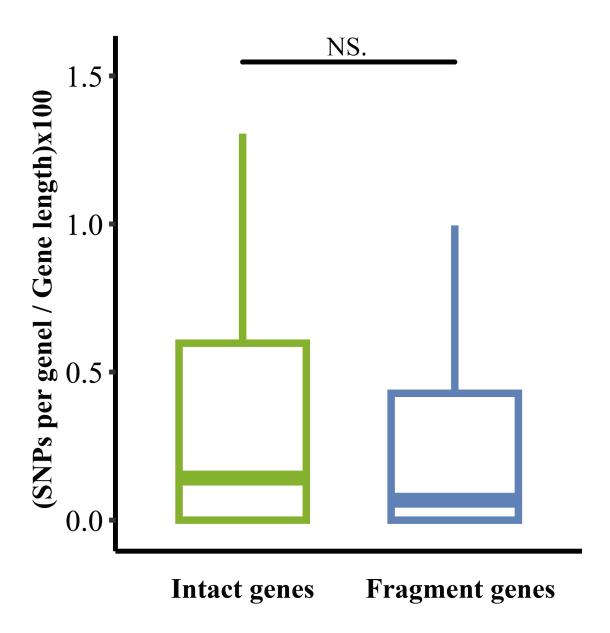


Fig. S4. Boxplots comparing the SNP density between intact and fragment HGT genes of 326 jujube individuals based on 'Dongzao' jujube. Statistically significant differences from the student's t-test are denoted with asterisks (\* p<0.05, \*\* p<0.01, \*\*\* p<0.001, \*\*\*\* p<0.0001, NS, not significant).