

**Figure S1** The K\_mer distribution for GL1 survey analysis.



**Figure S2** The GL1 whole genome Hi-C linkage information with windows size of 500Kb.



**Figure S3** The GL1 Hi-C linkage information of every pseudo-chromosome with windows size of 500Kb.



**Figure S4** Insertion time analysis of long terminal repeat (LTR) sequences in GL1, CB5 and F153 genomes. A: The GL1 genome; B: The CB5 genome; C: The F153 genome.



**Figure S5** The cross-validation error for admixture analysis with K value ranging from two to seven. The x axis represents the K value and y axis represent cross-validation error value.