

Fig. 1 The flowchart of *A. nanchuanensis* genome assembly and annotation process.



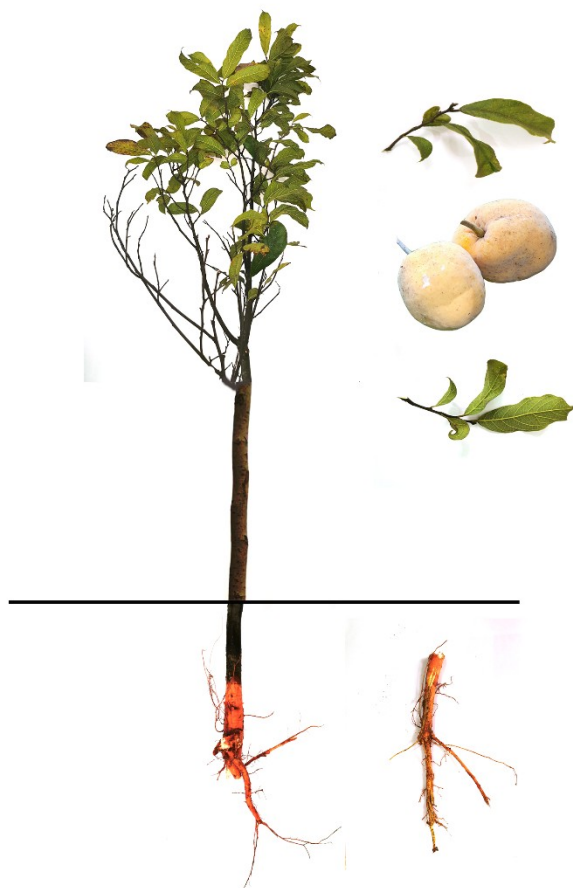


Fig. 2 The *A. nanchuanensis* tree used in this study.

Note: This picture was taken in 2019.

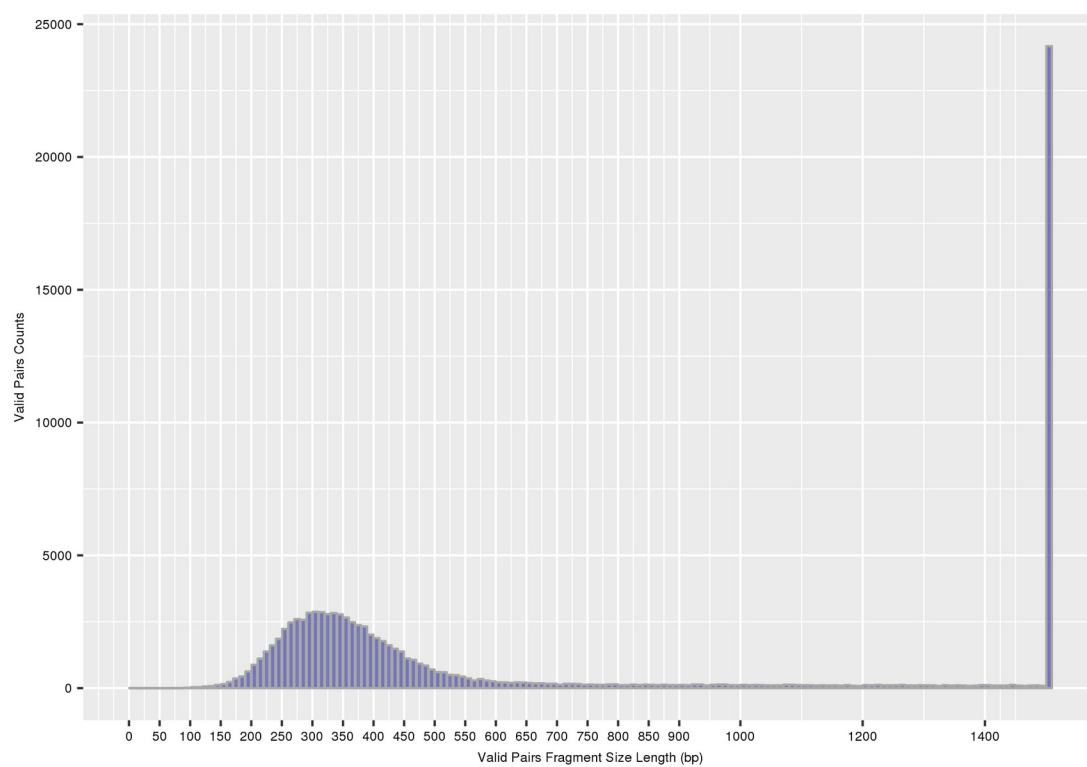


Fig. 3 The length distribution of library insert fragment.

Note: The abscissa axis is the sum of the distance between double ends Reads on the assembly genome and the nearest enzyme-cutting site. The vertical coordinate is the number of random extracted 100,000 pairs of Reads corresponding to the insert fragment of different length.

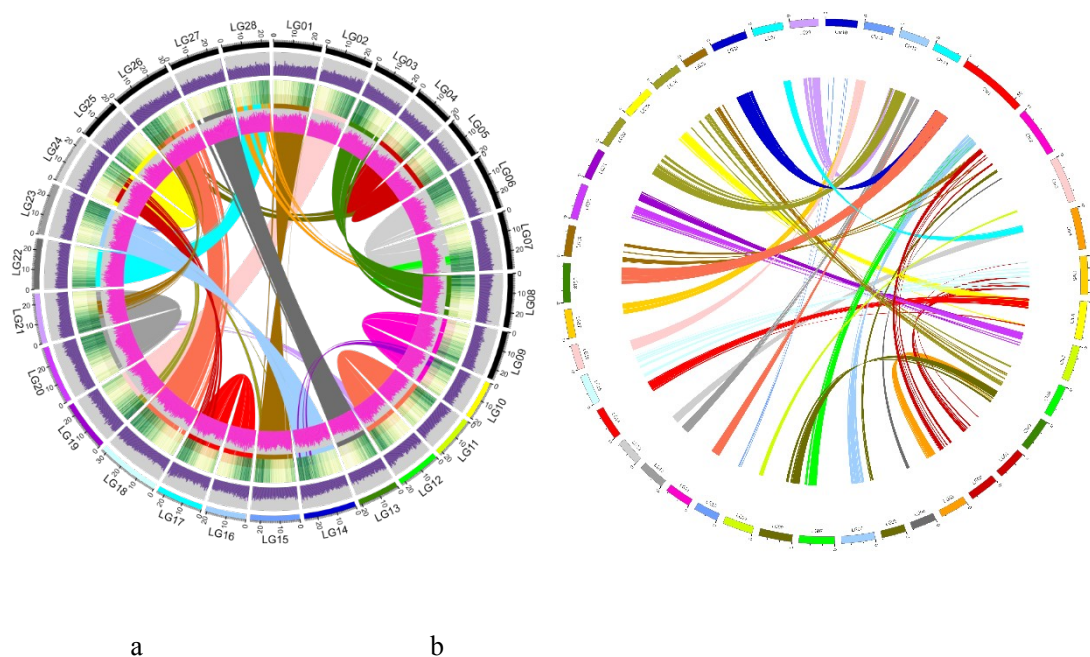


Fig. 4 Circos plot of the reference genome of *A. Nanchuanensis* and syntenic relationship with the *Ficus_microcarpa* genome.

Note: (a) Circos plot of *A. Nanchuanensis* 28 chromosomes. The tracks from outside to inside are 28 chromosome-level scaffolds, the GC content of chromosomes (purple), the gene density of chromosomes (green), the TE ratio of chromosomes (pink), and the lines of different colors in the innermost circle represent the collinearity within themselves. (b) Genes collinearity circle of *A. Nanchuanensis* and *F. microcarpa*. Each coloured represents a collinear block of each chromosome, with at least five collinearity genes in each block.

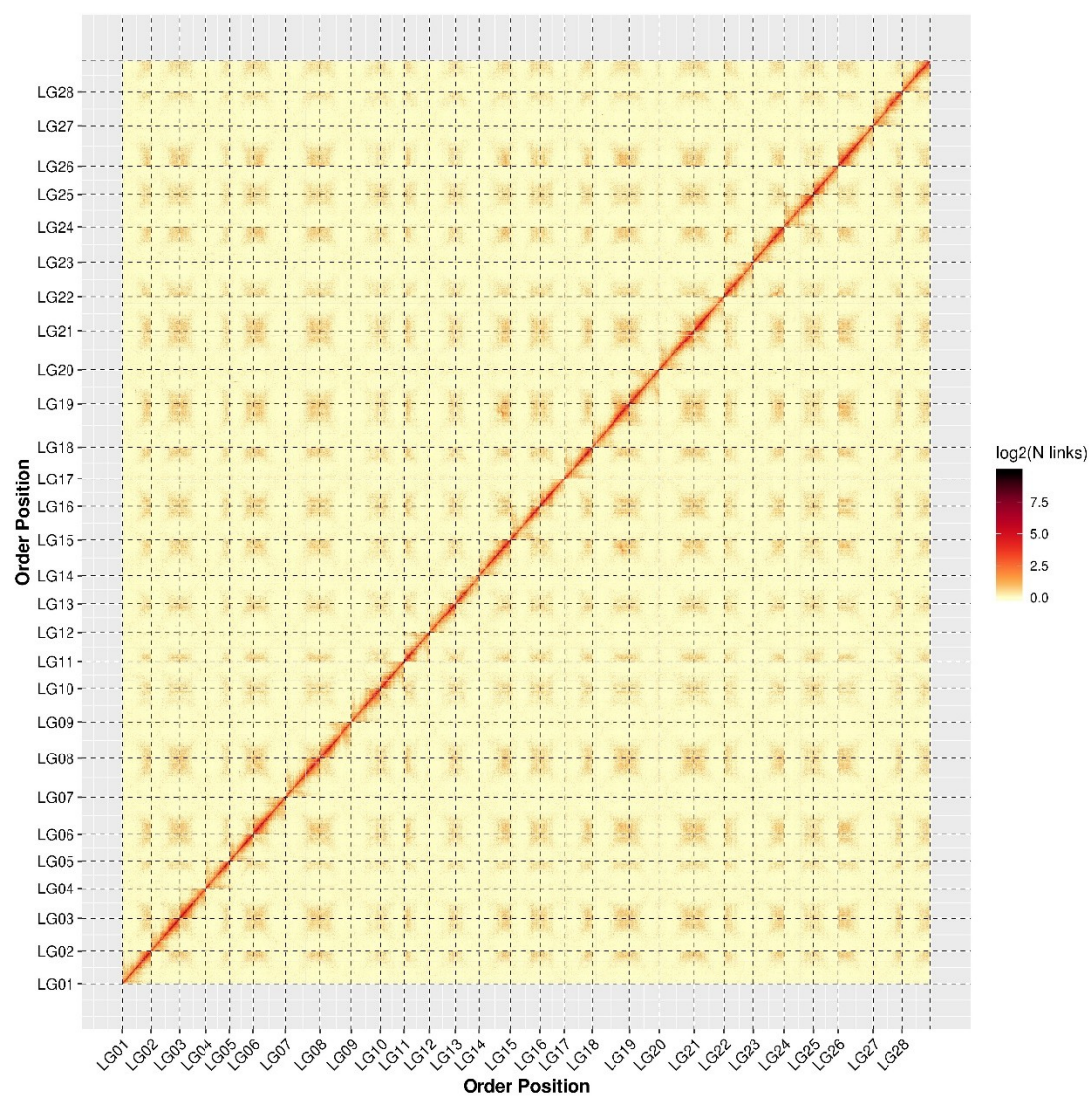


Fig. 5 The interaction heat map of Hi-C assembly chromosome.

Note: The LG01-LG28 represents Lachesis group 01-28; The abscissa axis and vertical coordinates represent the Order of each bin on the corresponding chromosome group.

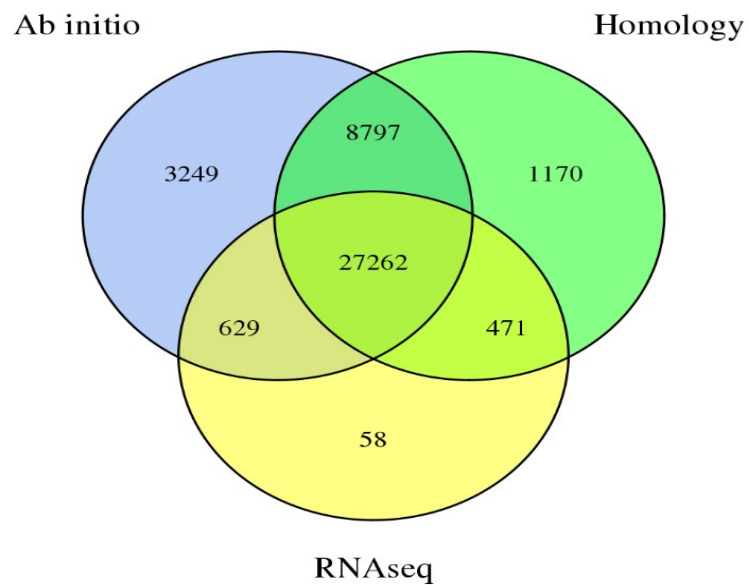


Fig. 6 The integrated genes were derived from the distribution of the three prediction methods.

Nr Homologous Species Distribution

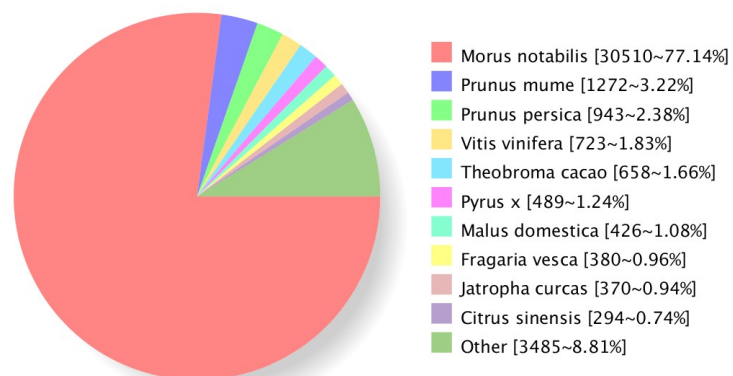


Fig. 7 The Nr homologous species distribution.

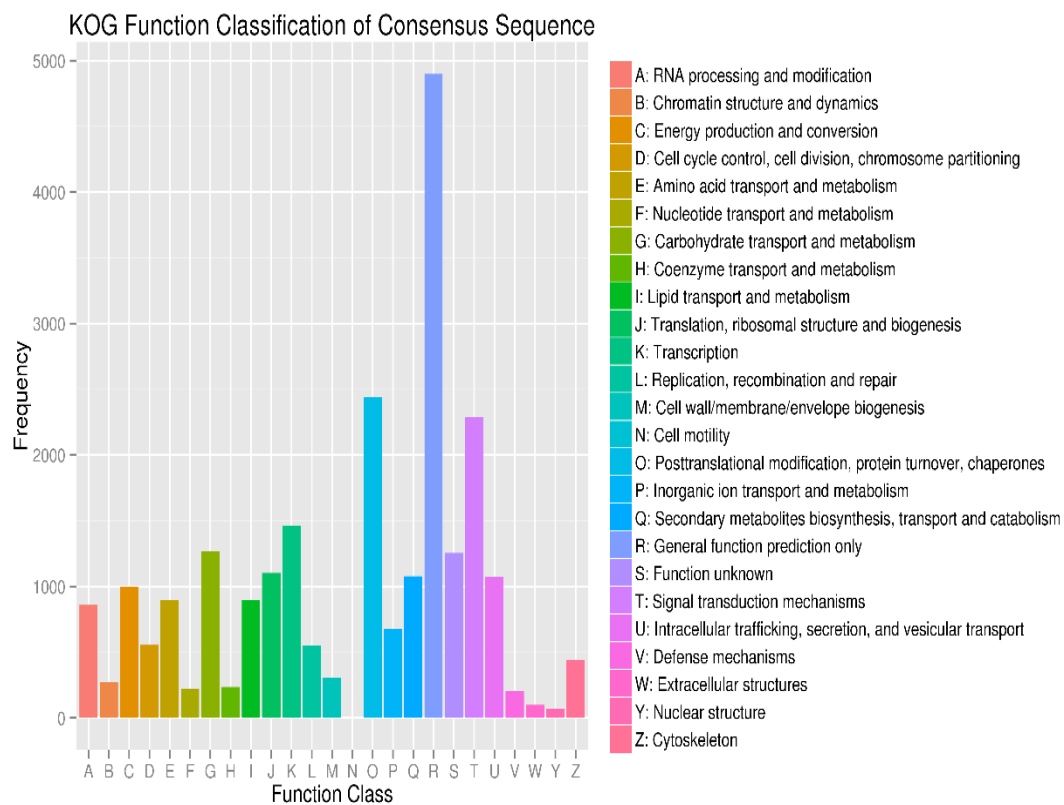


Fig. 8 The statistical graph of KOG functional annotation classification.

Note: The abscissa axis is the contents of each KOG classification, and the vertical coordinate is the number of genes.

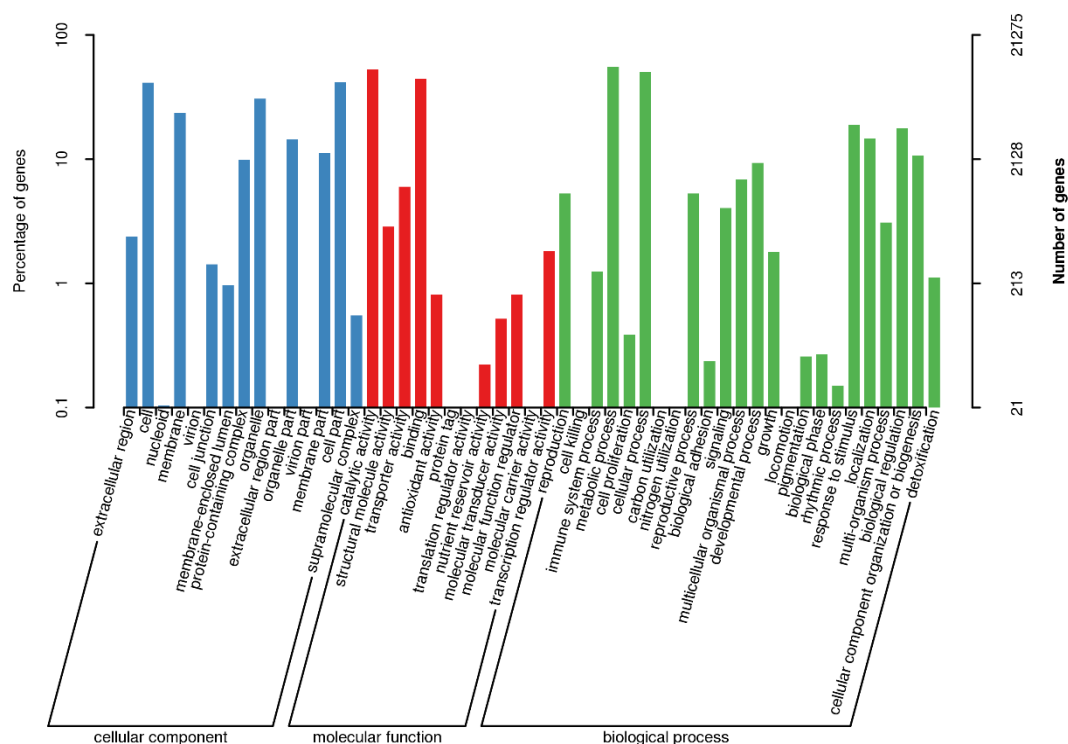


Fig. 9 The GO secondary node annotation classification statistics diagram.

Note: The abscissa axis is the contents of each category of GO; The vertical coordinates mean the percentage of the number of genes; And the right side is the number of genes. This figure shows the enrichment of each secondary function of gene GO.

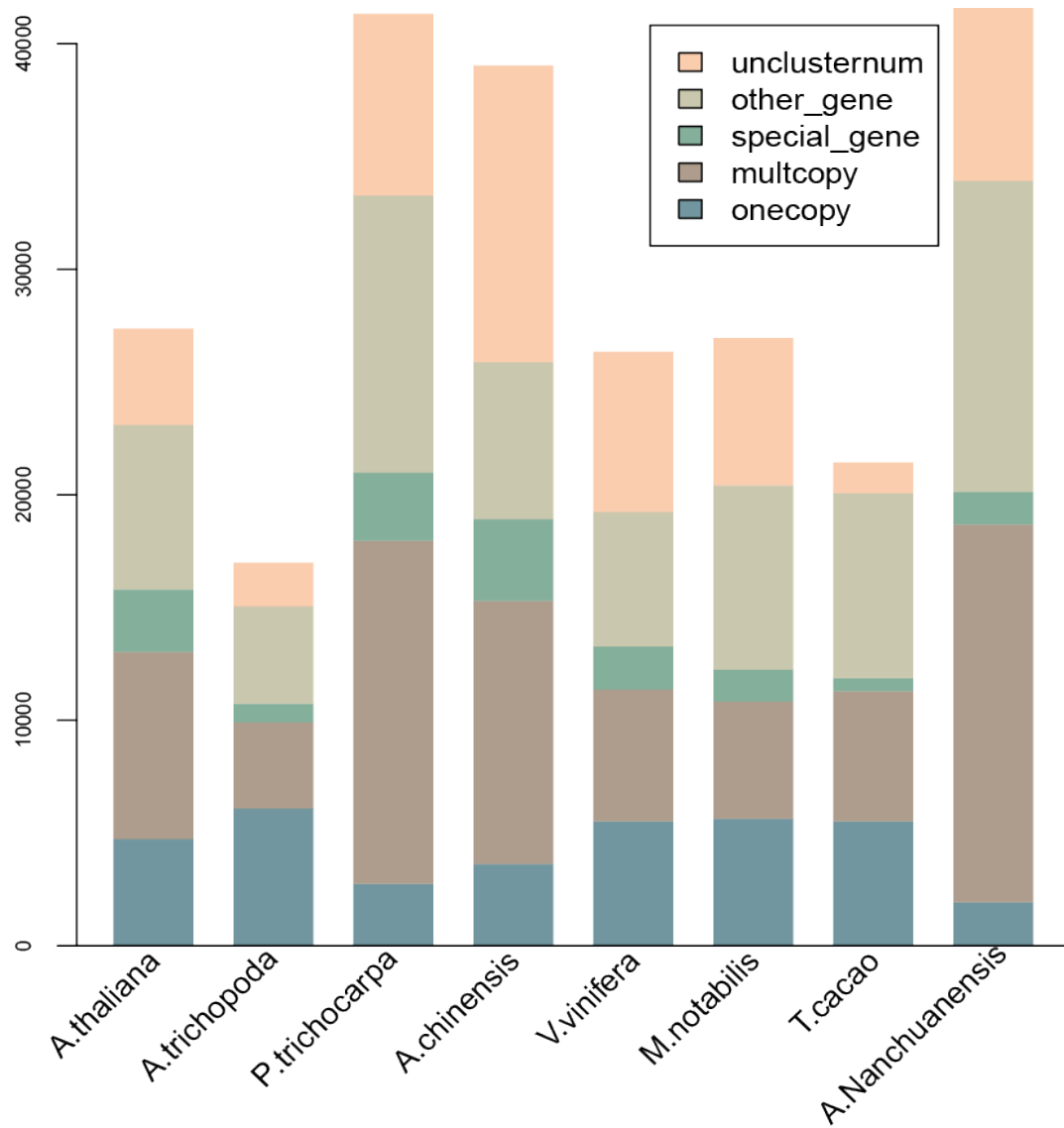


Fig. 10 The histogram of family clustering statistics.

Note: The abscissa axis mean the species name; The vertical coordinates mean the number of genes; Unclusternum mean the gene of unclustered to any family; Other gene mean all other genes; Special gene: the species specific genes in the family; Multcopy: the number of multiple copies of homologous genes in a common gene family; Onecopy: the number of single-copy homologous genes in the family of genes shared by species.

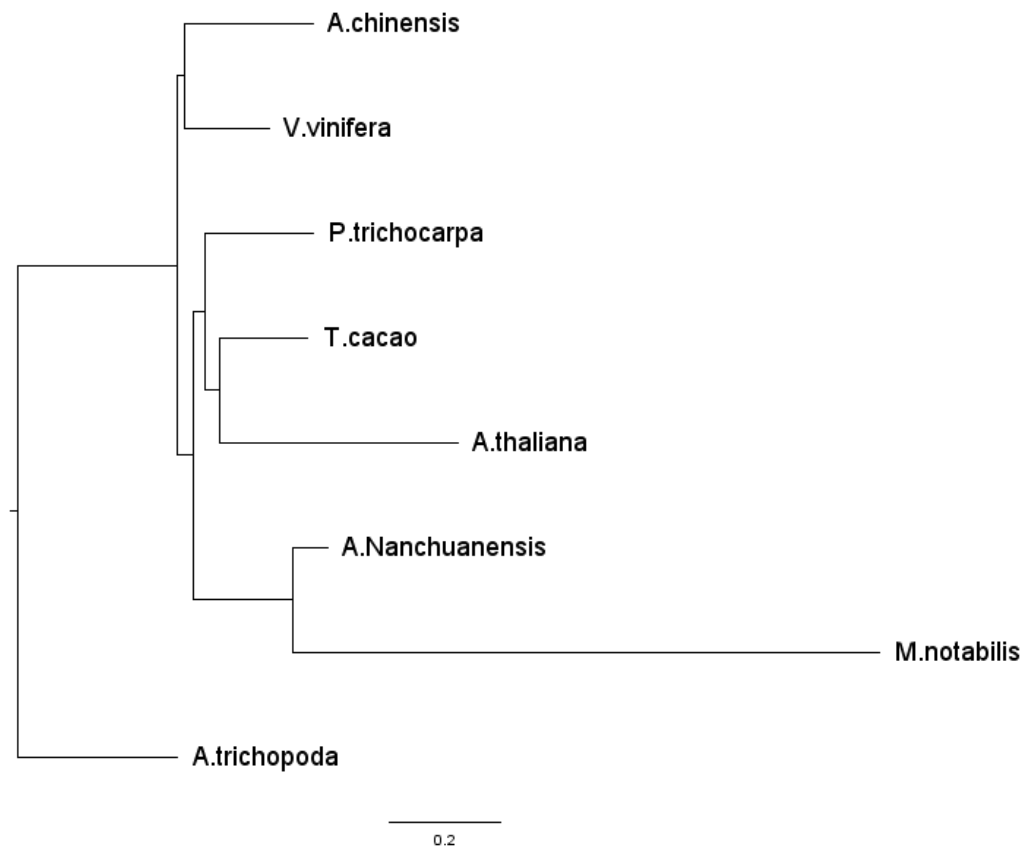


Fig. 11 The evolutionary relationships among species.

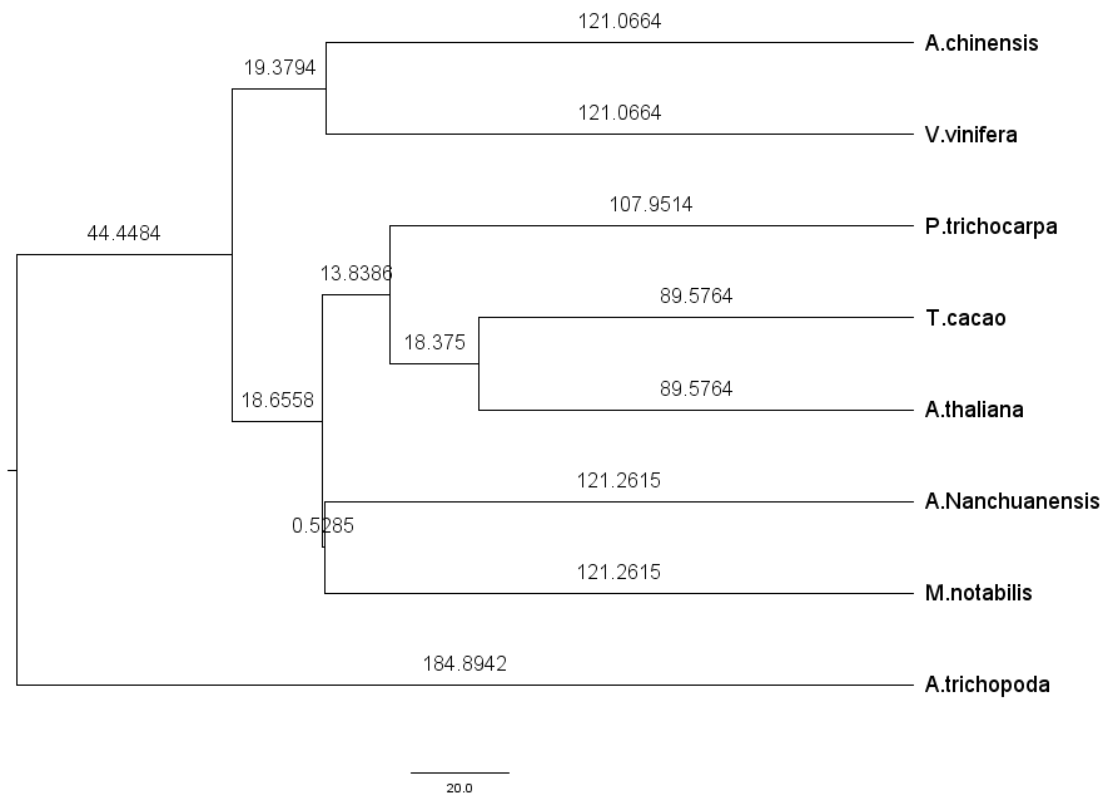
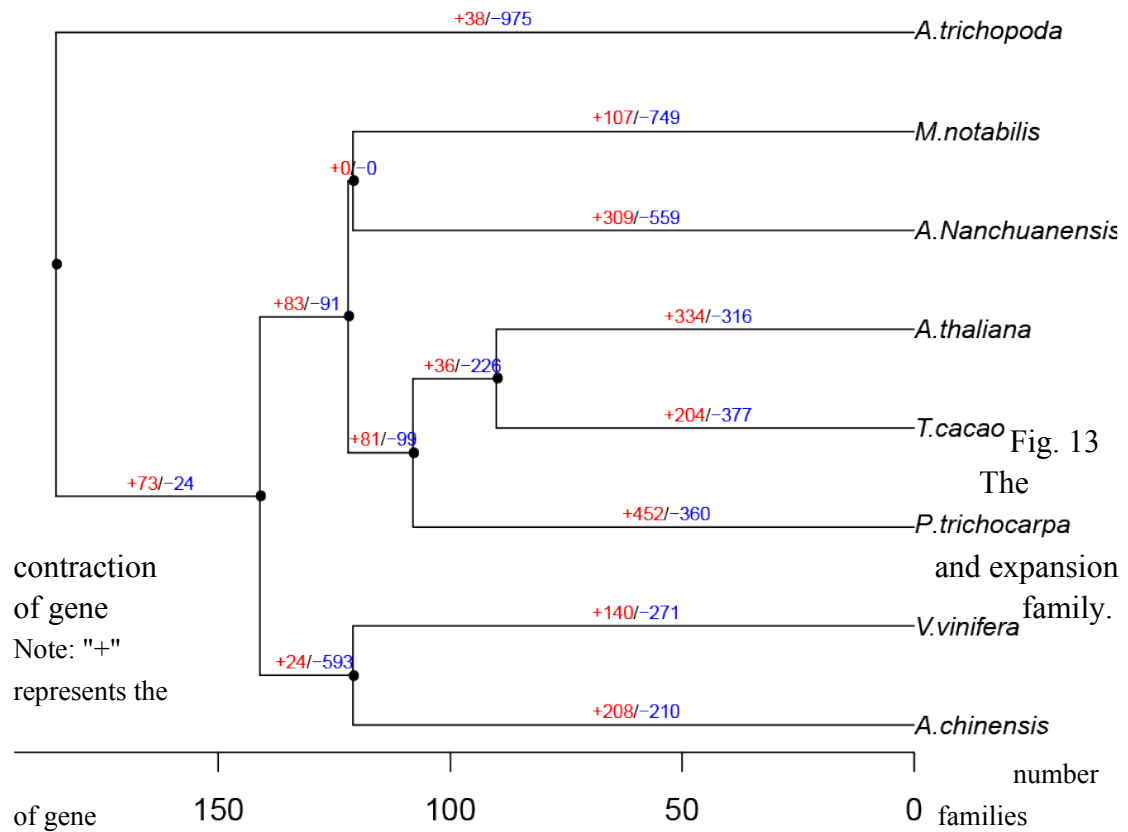


Fig. 12 The temporal relationship of species differentiation (unit: million years).



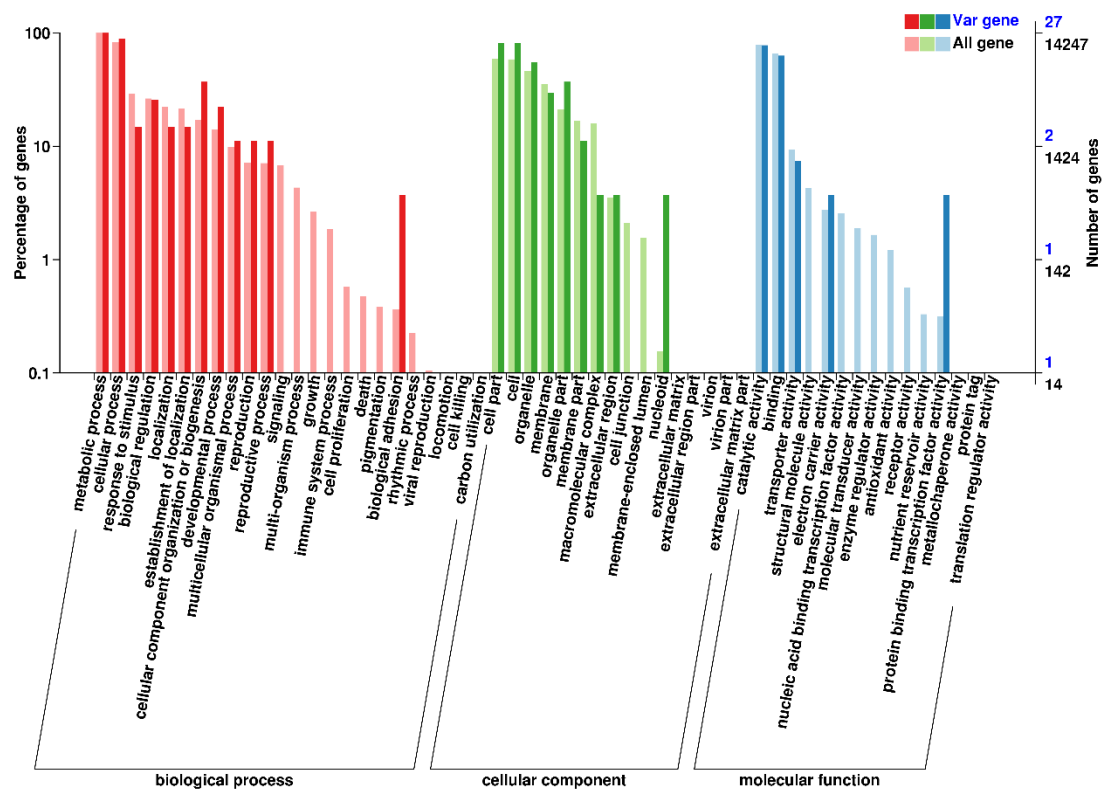


Fig. 14 The classification annotation statistics for GO.

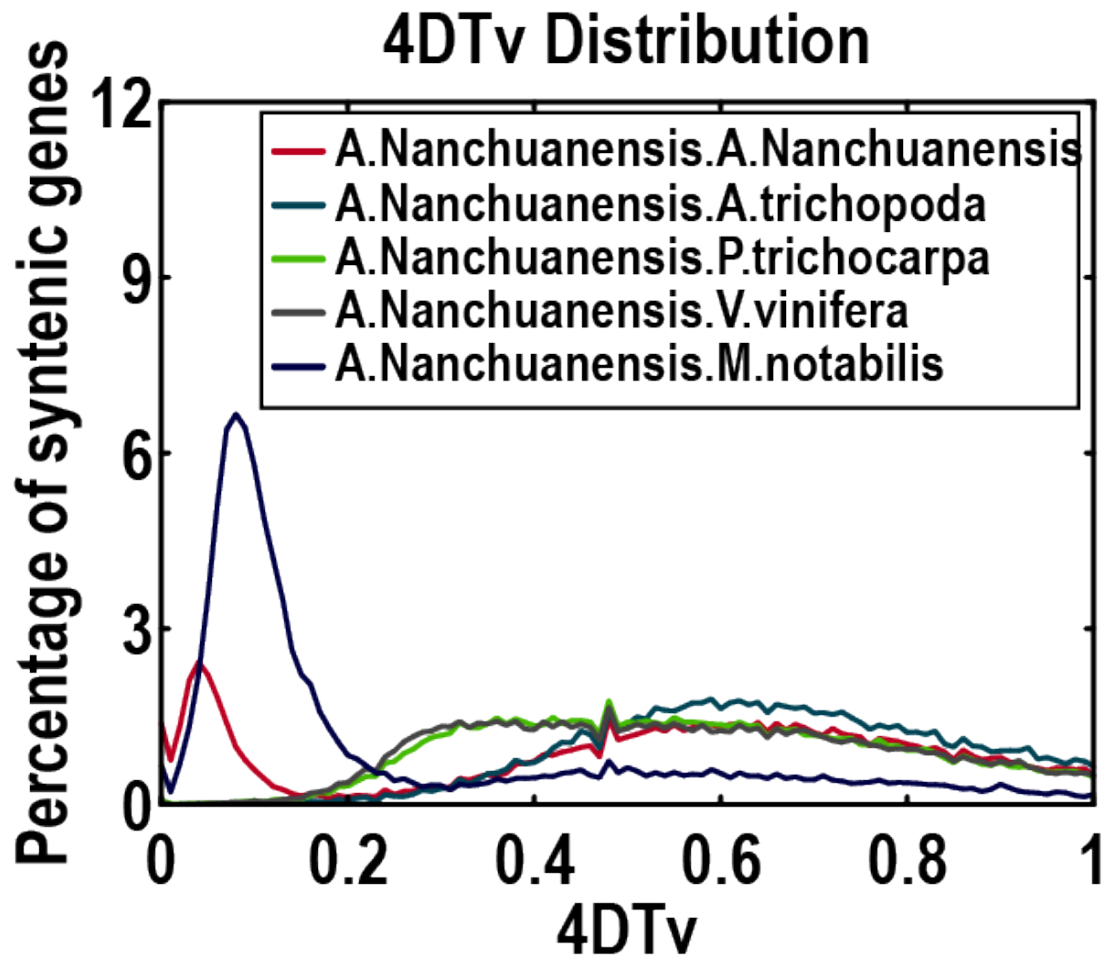


Fig. 15 The 4DTV distribution graphic.

Note: The abscissa axis represents the mutation rate of homologous genes to 4DTV, and the vertical coordinates represents the proportion of homologous gene pairs.

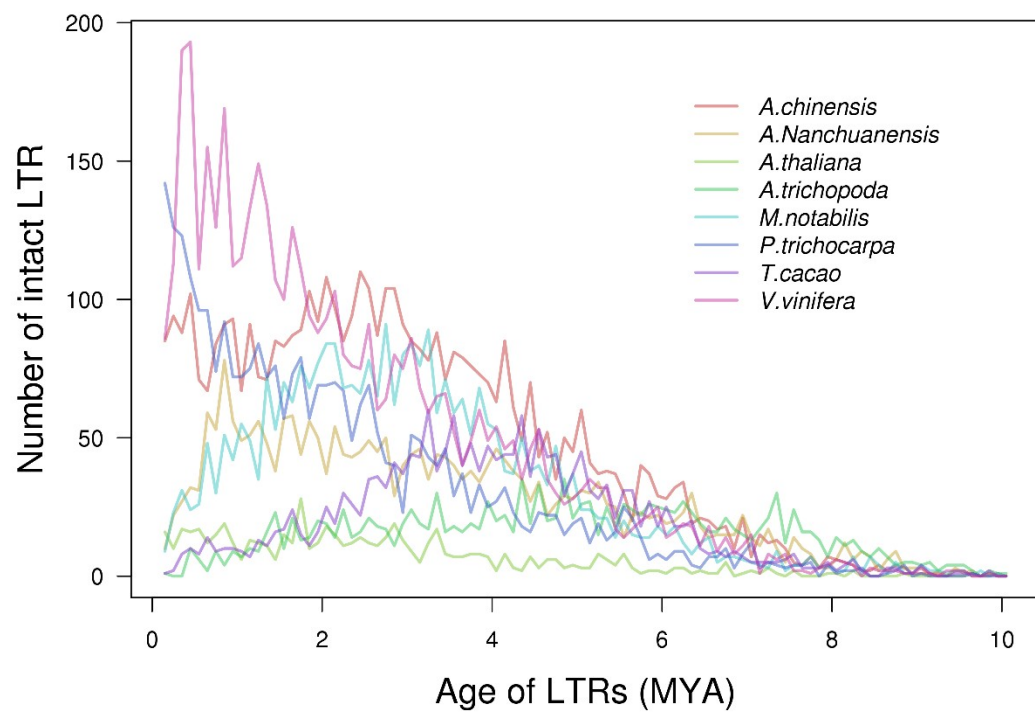


Fig. 16 The analysis graphic of LTR insertion time.