

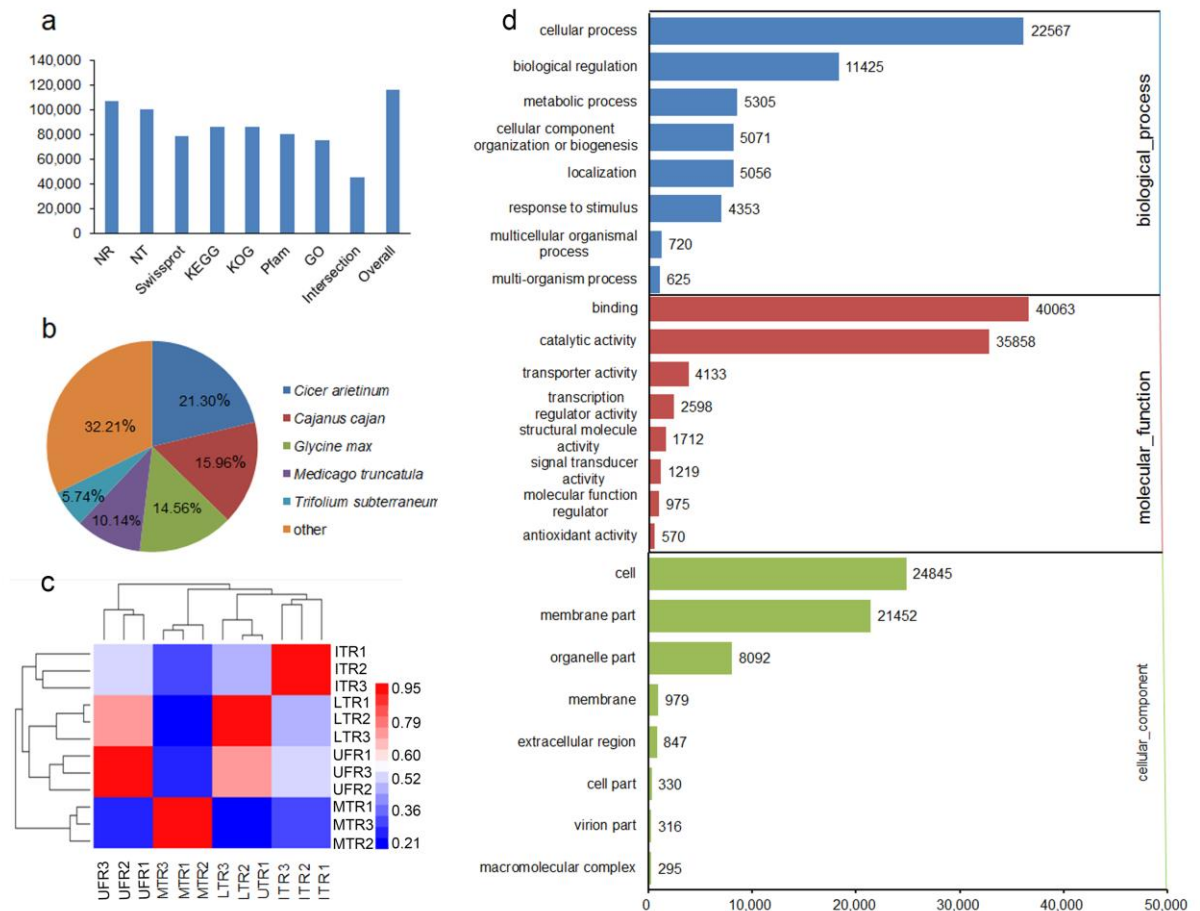


Fig. S2. Annotation of the assembled transcriptome and gene expression profiling. a. Number of transcripts aligned to different databases. b. Species aligned by the assembled genes. c. Heat map of sample correlation based on the gene expression profile. d. The eight-top for each category of GO annotation.