

**Fig. S1** Flowchart of the experimental design and analysis for PacBio sequencing and RNA sequencing. This pipeline includes the workflow for the quality control of the raw data, the classification of the reads of the insert, isoform clustering, correction, and transcriptome analysis.



**Fig. S2** Read length with different ploidy hybrids. **a** F01. **b** F02. **c** F03



**Fig. S3** The number of isoforms of functional annotation of with different ploidy hybrids. **a** Number of isoforms of KOG enrichment. **b** Number of isoforms of KOG enrichment (GO) term. **c** Number of isoforms of KEGG enrichment (GO) terms