

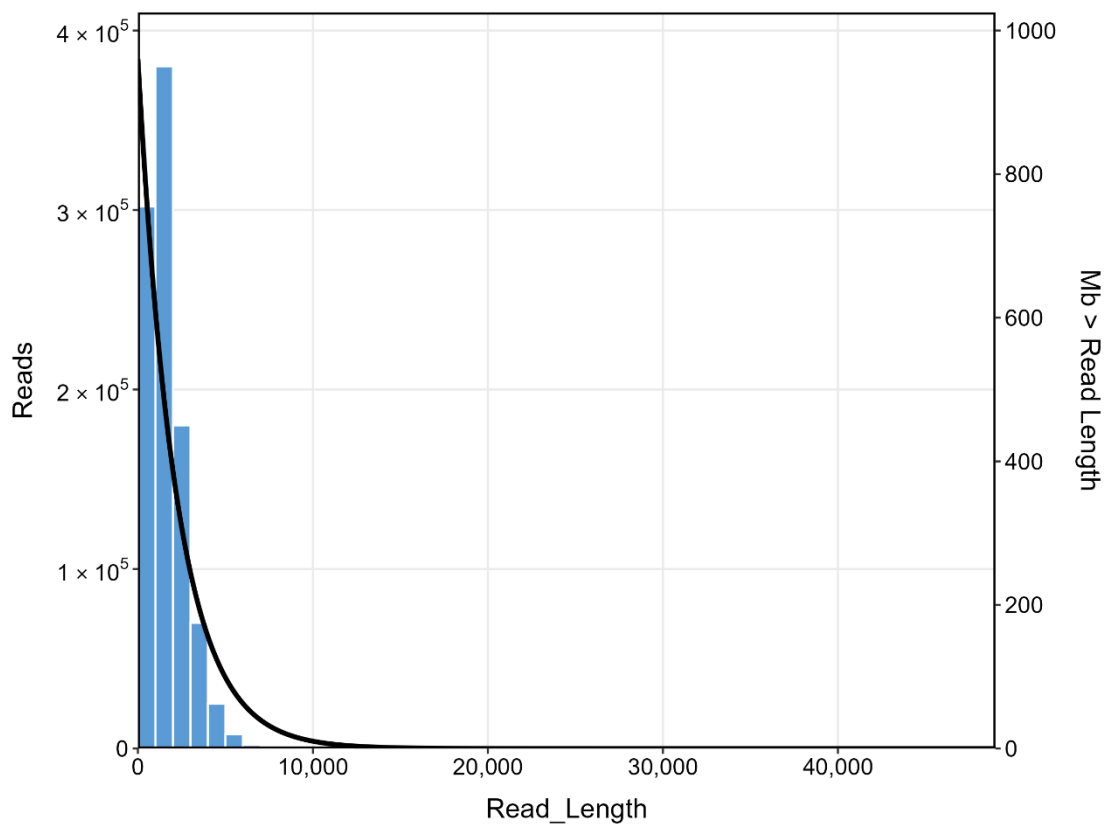


Figure S1. Histogram of ROI read lengths. The black curve indicates the distribution trend relative to read length.

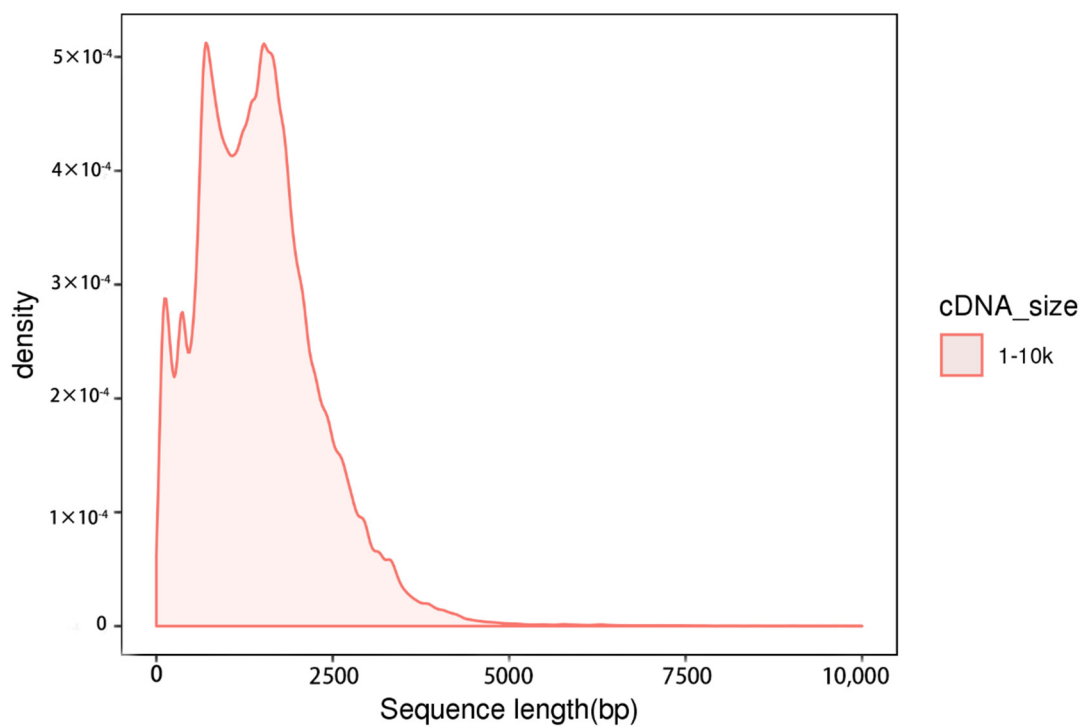


Figure S2. Density distribution of FLNC read lengths.

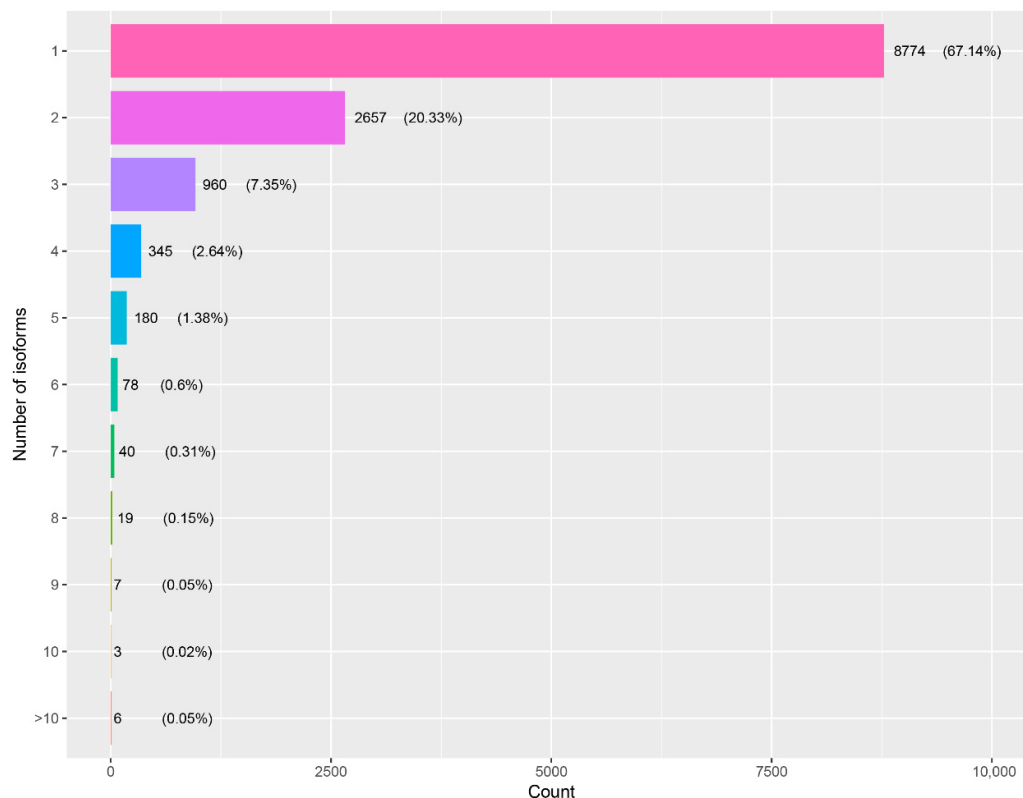


Figure S3. Distribution of isoform counts per UniTransModel. The bar chart illustrates the number of isoforms generated by each full-length UniTransModel.

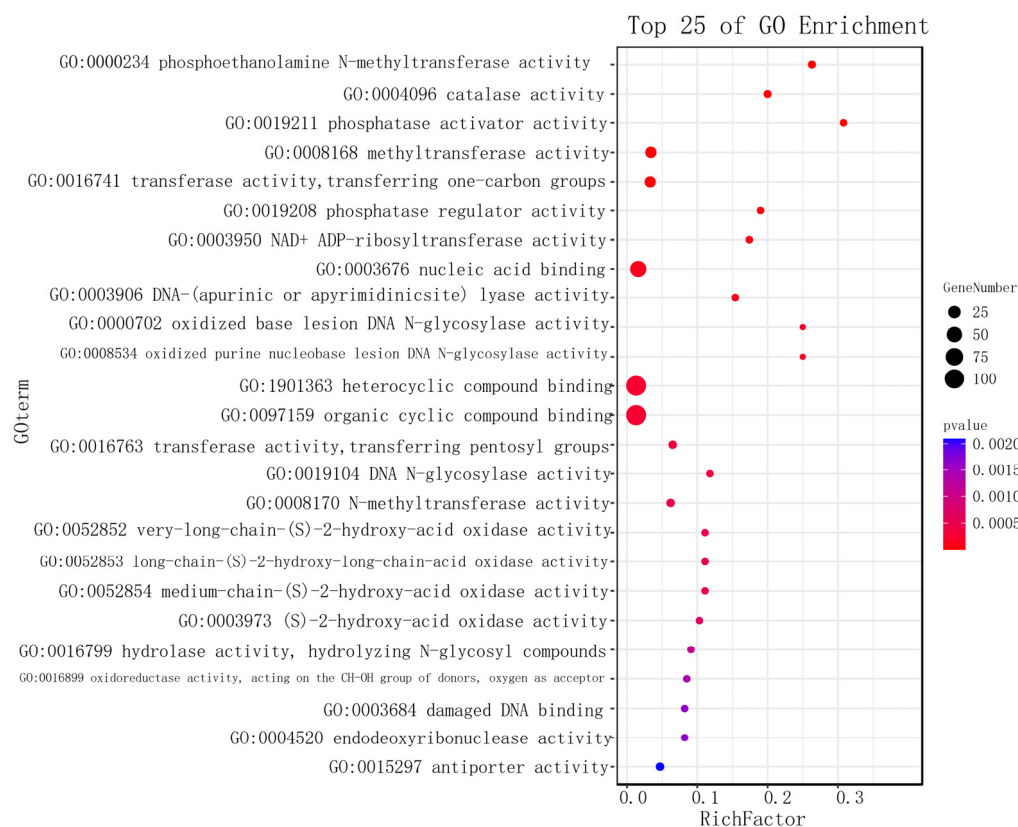


Figure S4. Top 25 GO enrichment terms for genes undergoing Alternative Splicing (AS).

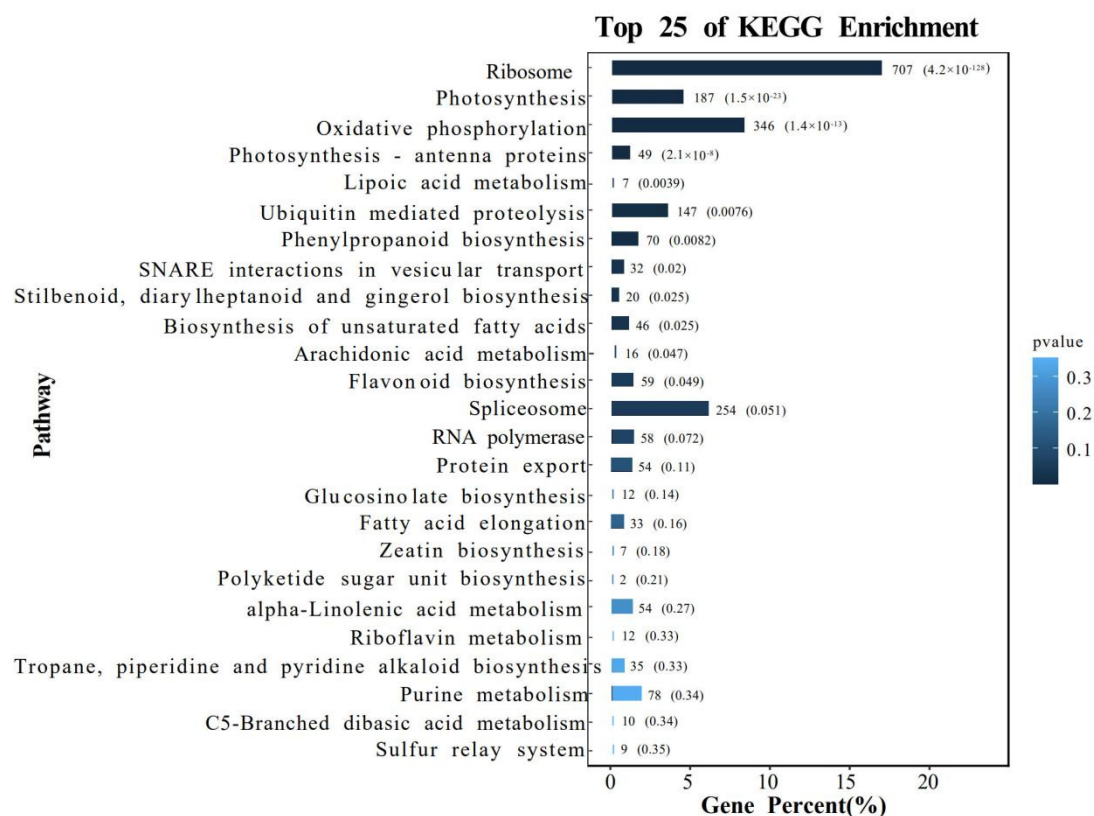


Figure S5. Top 25 KEGG enrichment in LncRNA.

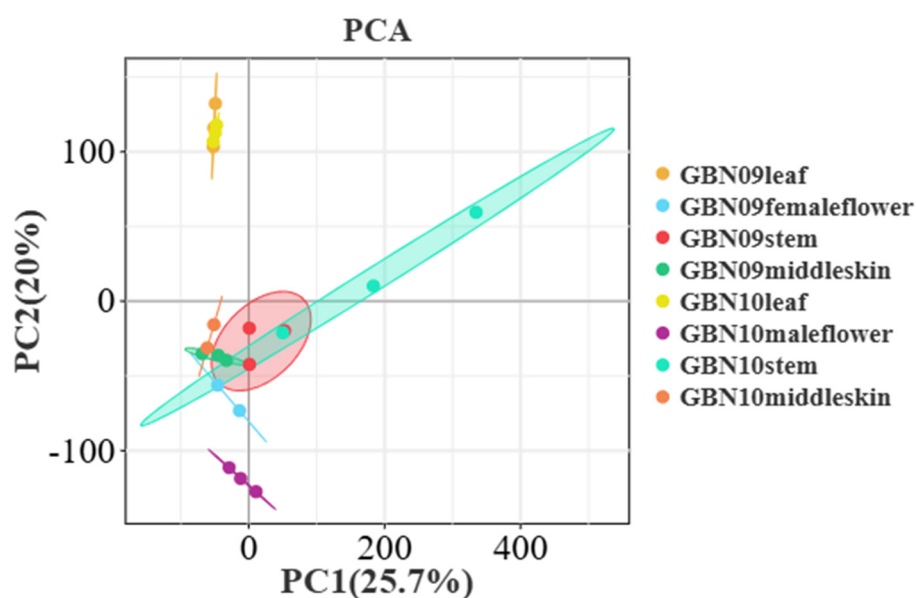


Figure S6. All_gene.PCA

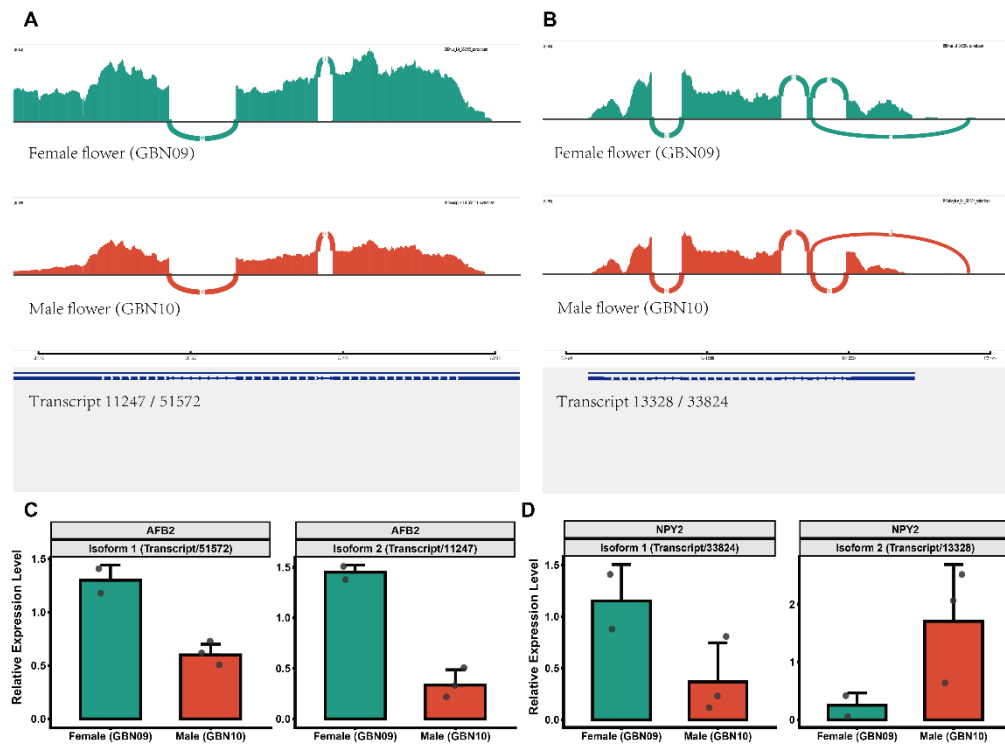


Figure S7. Transcriptomic evidence for sex-biased splicing of AFB2 and NPY2. (A, B) Sashimi plots visualizing the mapping of full-length sequencing reads and alternative splicing junctions for the AFB2 (A) and NPY2 (B) loci in female (GBN09, green tracks) and male (GBN10, red tracks) flowers. The arcs represent the splice junctions, providing solid physical evidence of differential splicing patterns between sexes. The corresponding gene models and specifically identified transcript isoforms are aligned below. (C, D) Isoform-specific expression levels of AFB2 (C) and NPY2 (D) in female and male flowers, matching the structural variations observed in the Sashimi plots. The bar plots display the relative expression levels of distinct transcript isoforms, providing robust quantitative validation of the sex-biased AS events and demonstrating clear isoform switching in male and female development.