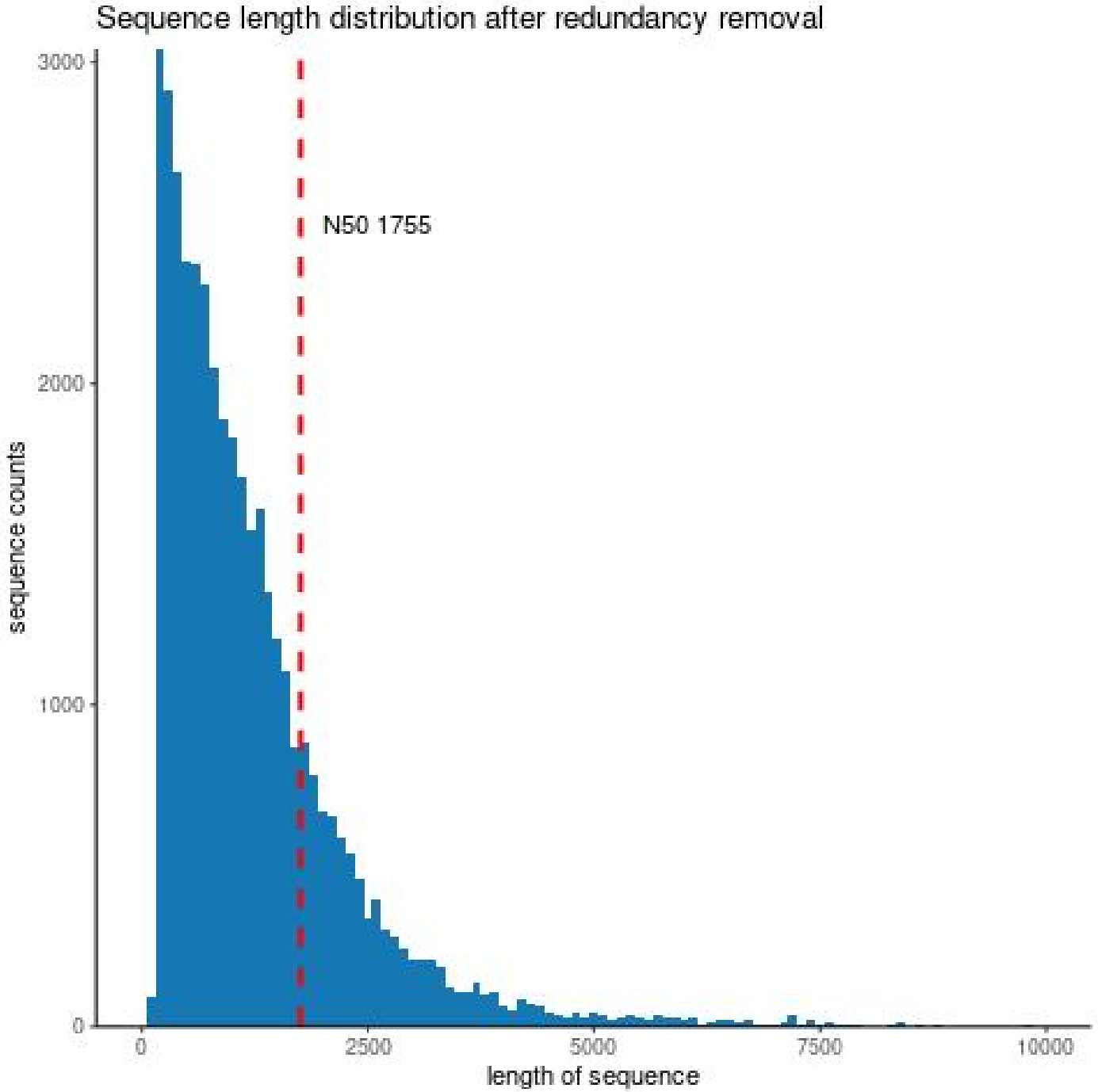


Figure S1. Distribution Chart of CDS Length of New Transcripts. The horizontal axis represents the length of the new transcripts; the vertical axis represents the number of new transcripts within each length range, with the red dotted line indicating the length of N50.

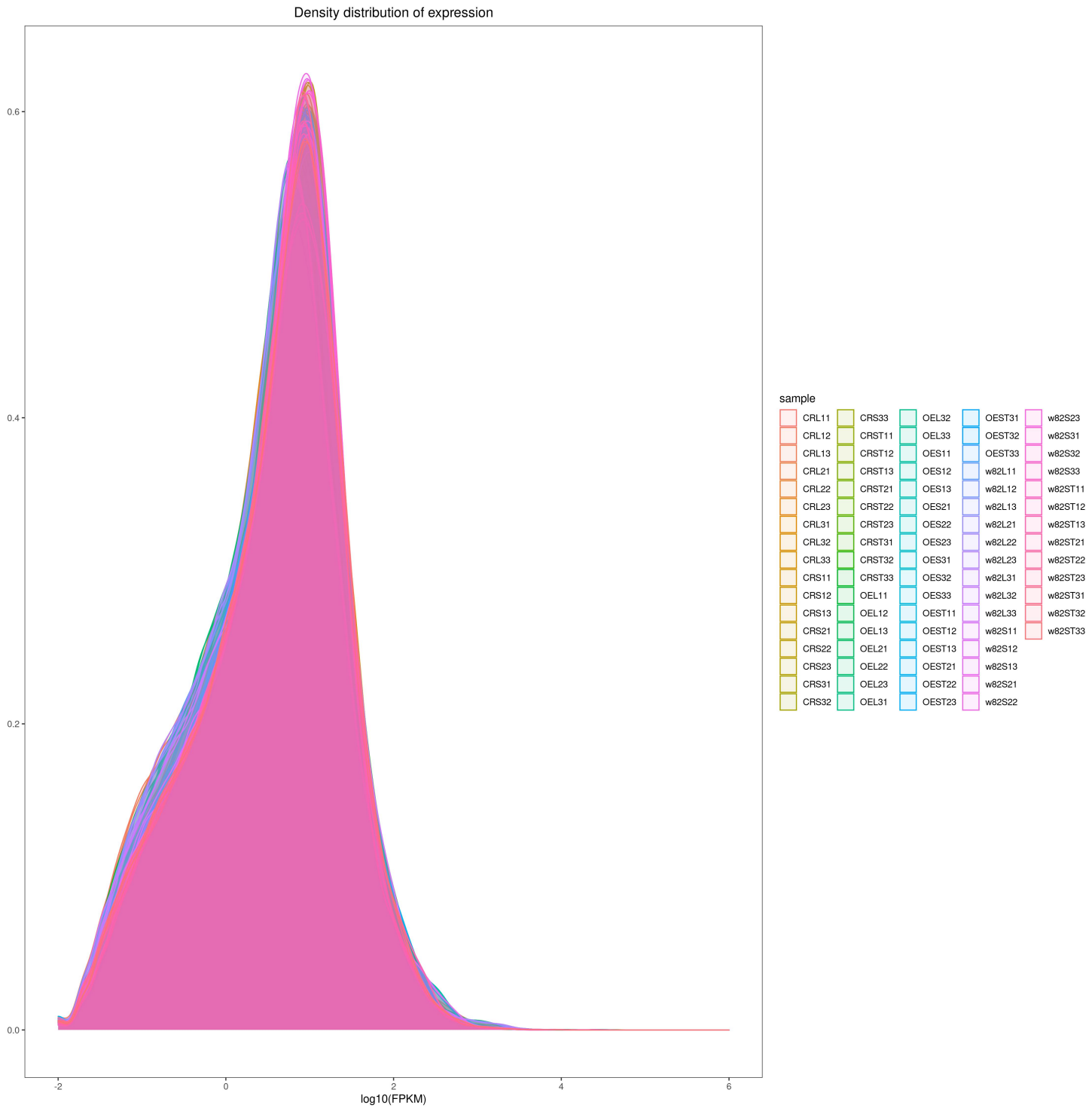
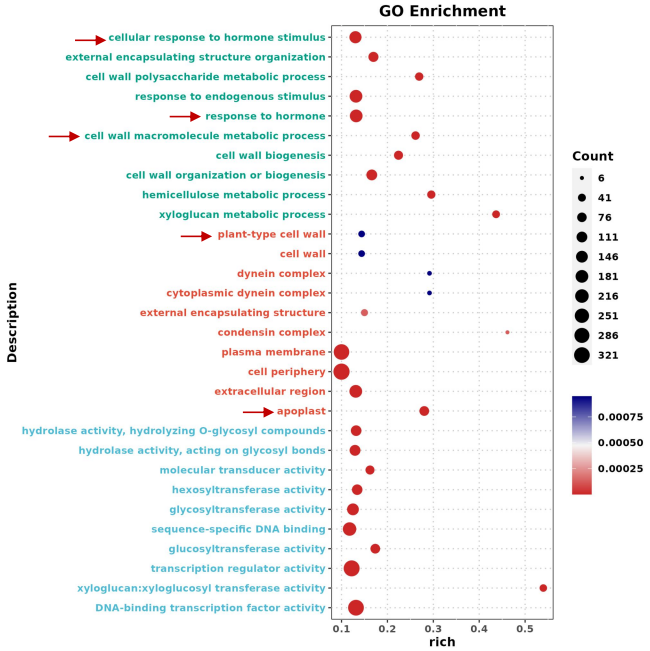
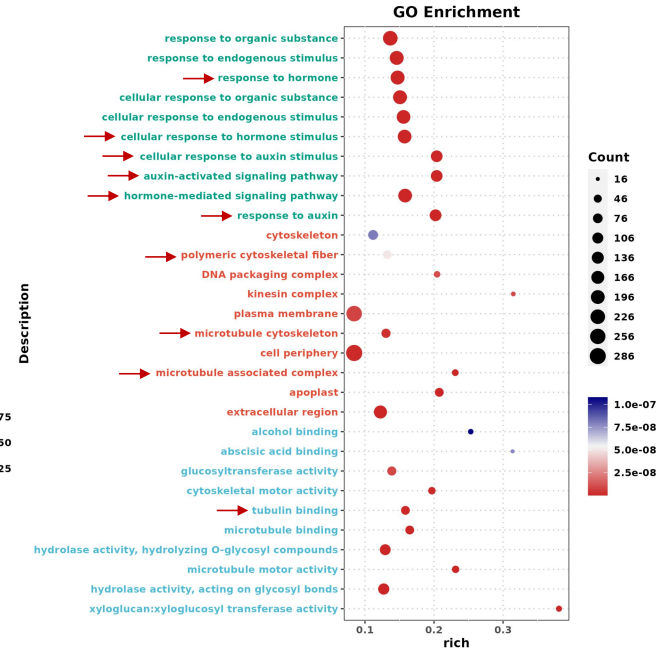


Figure S2. The FPKM density distribution graph shows a non-standard normal distribution. The area of each region is 1, indicating that the total probability is 1. The X-axis represents the logarithm of the expression level (FPKM value) to the base 10, and the Y-axis shows the density of genes with different expression level values. Different colors represent different samples.

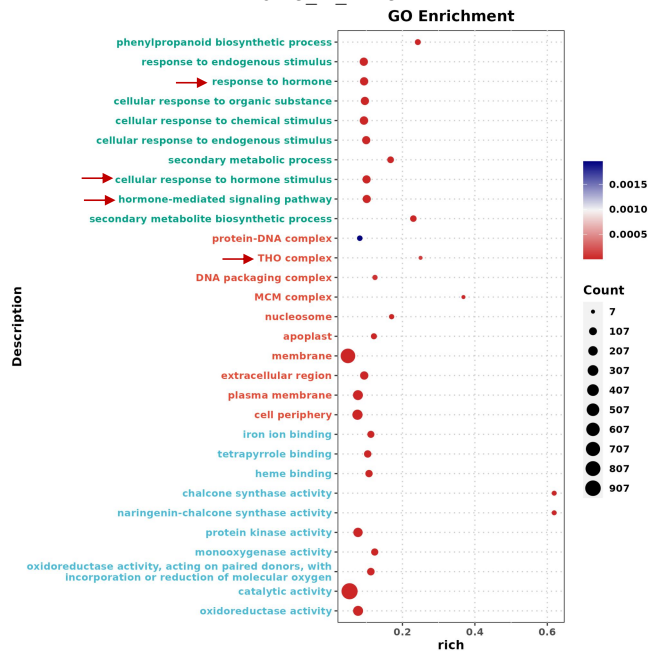
w82L1_vs_CRL1



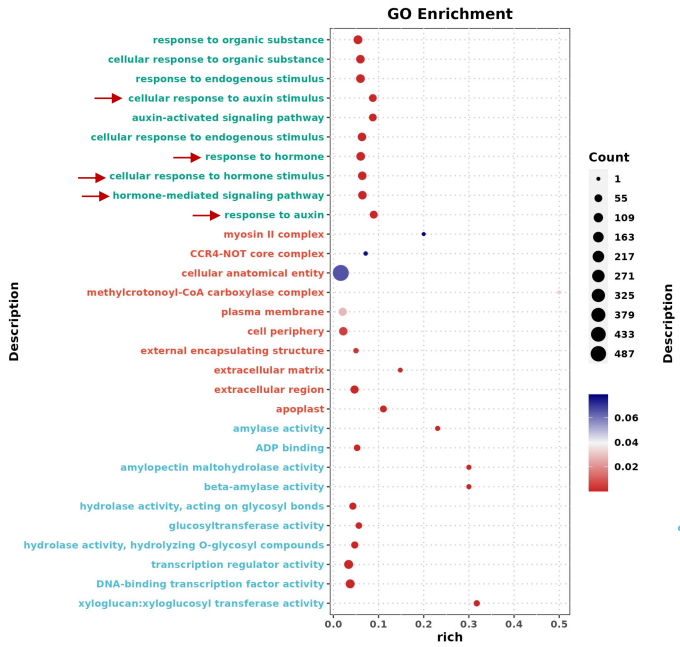
w82L2_vs_CRL2



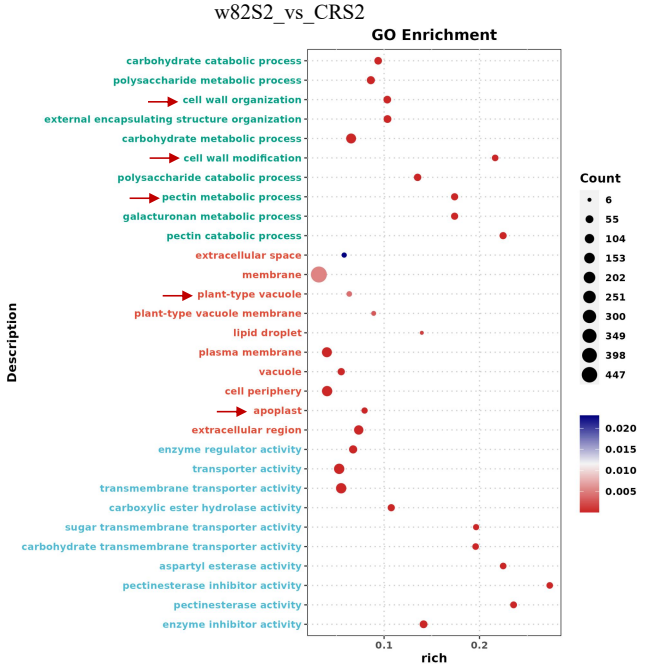
w82L3_vs_CRL3



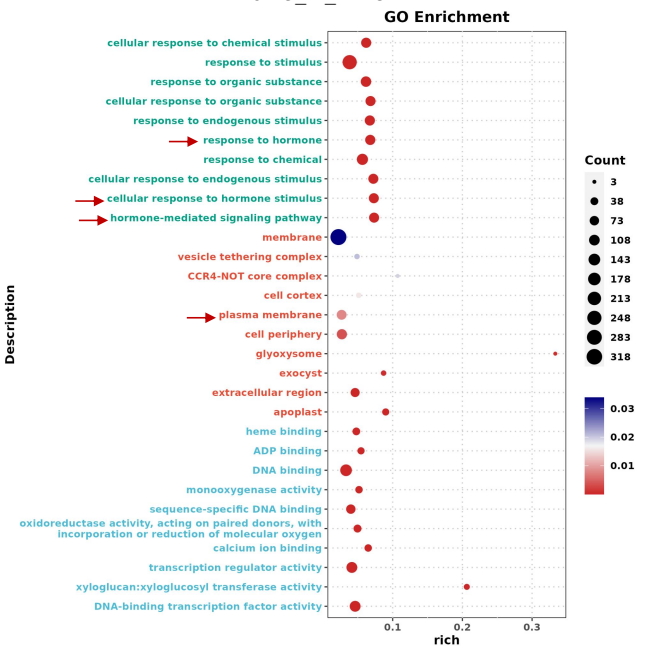
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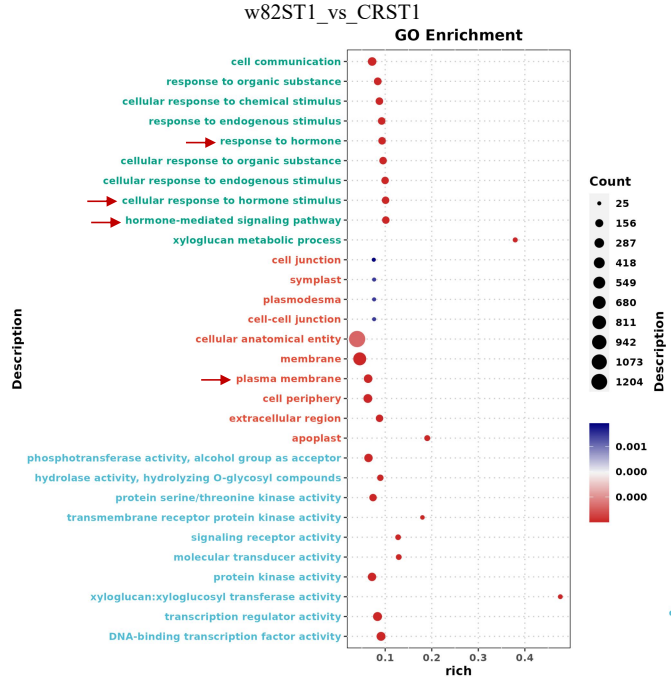
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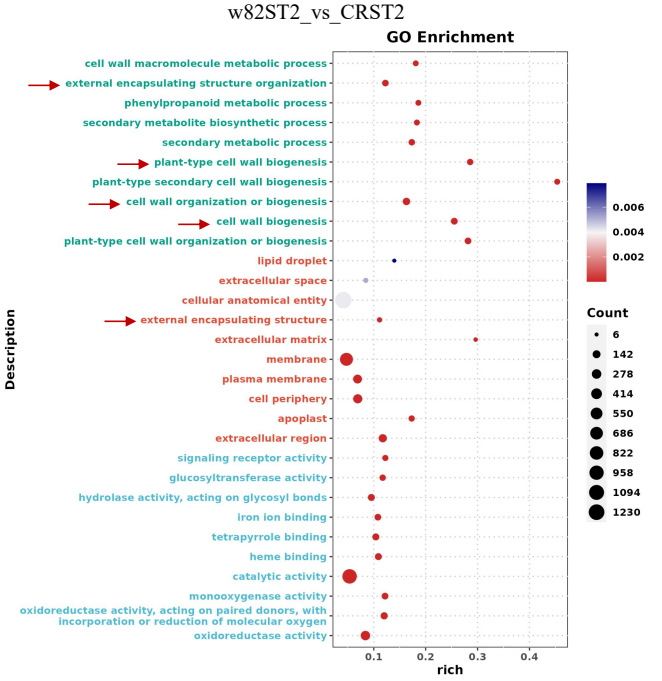
w82S3_vs_CRS3



w82ST1_vs_CRST1



w82ST2_vs_CRST2



w82ST3_vs_CRST3

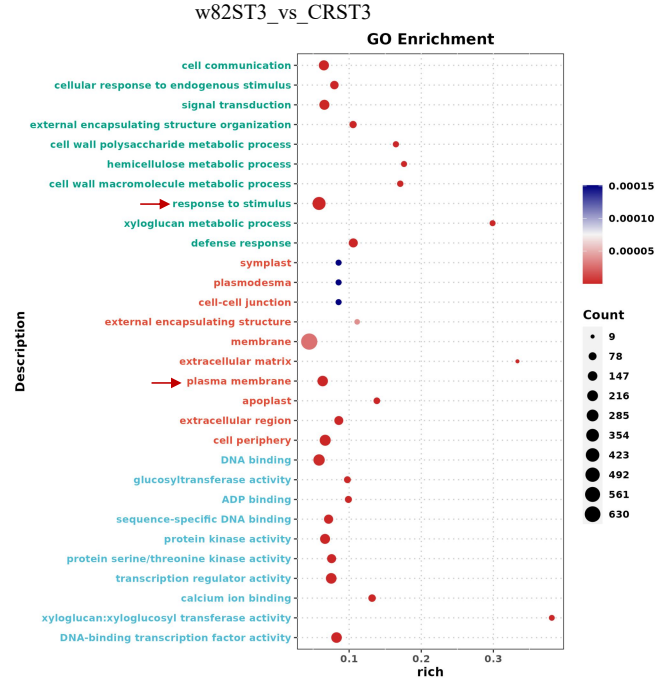


Figure S3. GO functional enrichment analysis of differentially expressed genes based on RNA-Seq sequencing results. W82, Williams 82; L, leaf; S, shoot apical meristem; ST, stem; 1, the stage when the first trifoliate leaf of soybean unfolds and flattens; 2, the stage when the second trifoliate leaf of soybean unfolds and flattens; 3, the stage when the third trifoliate leaf of soybean unfolds and flattens; the red arrow, the enriched pathway related to hormone metabolism; CR, the CRISPR/Cas9 gene edited mutants.

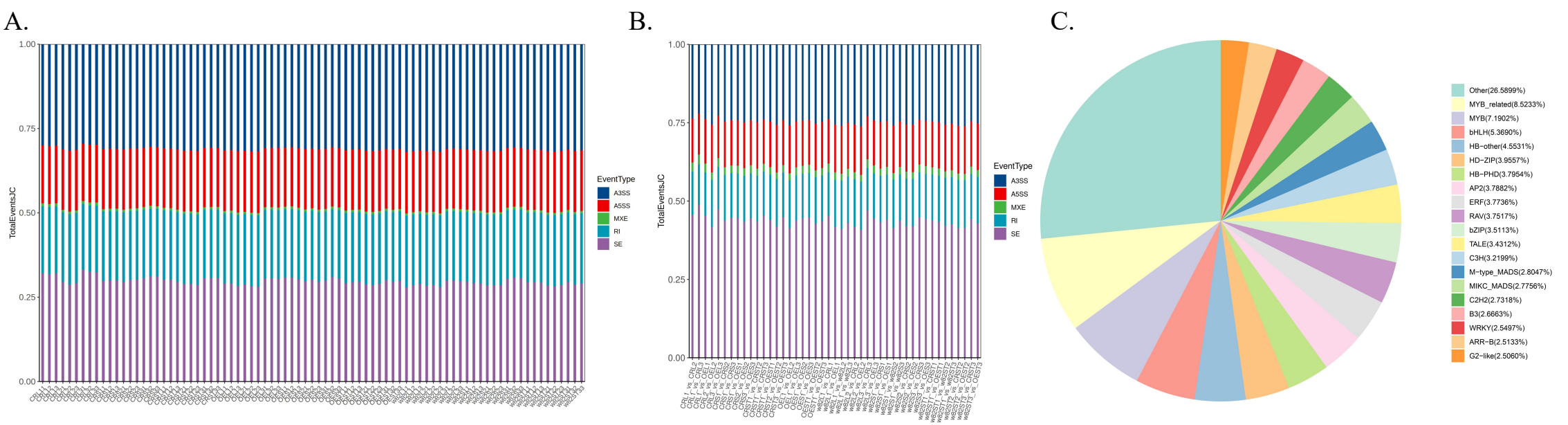


Figure S4. Analysis of alternative splicing and transcription factors in all comparison groups. Distribution map of all variable splicing event types in all samples (A); Distribution map of all comparison group variable splicing event types (B); Proportion chart of transcription factor families (C), and the different colors represent different families of transcription factors.



Figure S5. Growth conditions of soybean for the expression level analysis of light response. PPFD, photosynthetic photon flux density. SD, short day condition for 8 h light/16 h dark.