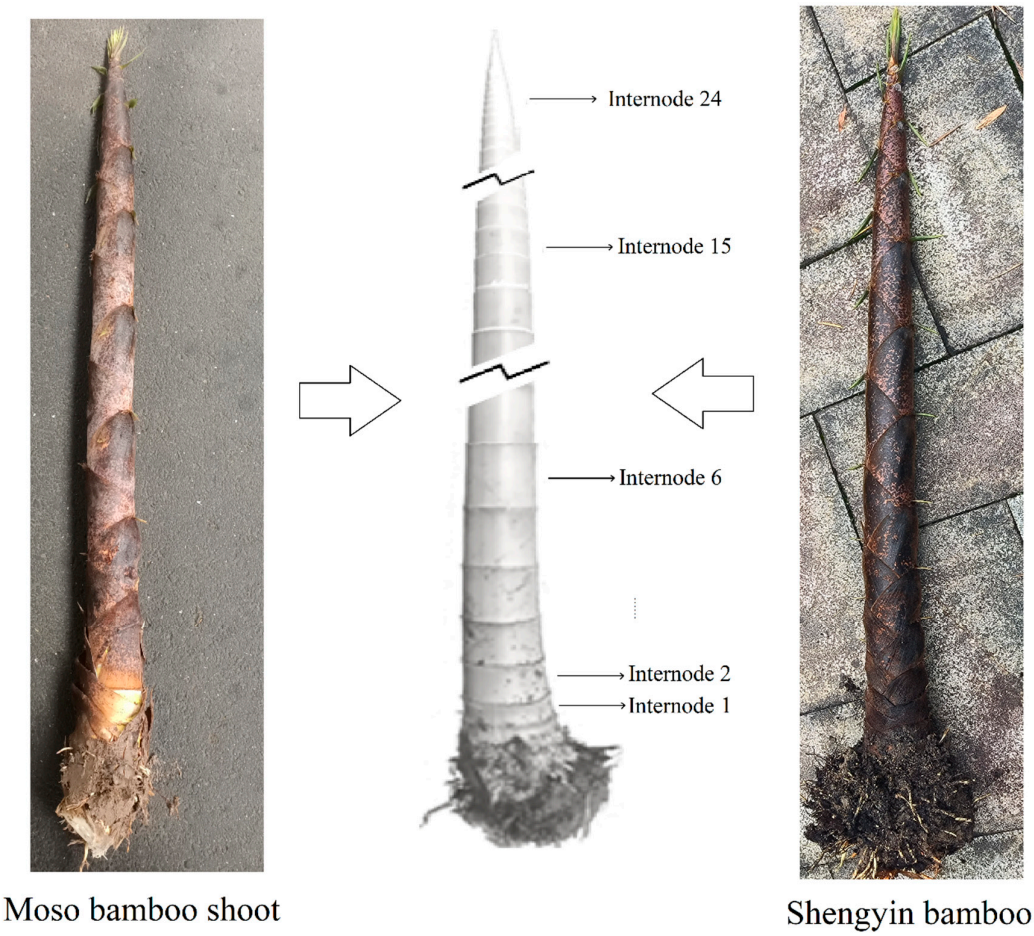


Figure S1. sampling strategy of Moso bamboo shoot (Left panel) and Shengyin bamboo shoot (Right panel), and the middle showing a schematic of bamboo shoots with the sheath removed. The internodes marked as 6, 15, and 24 are used for subsequent transcriptome sequencing.

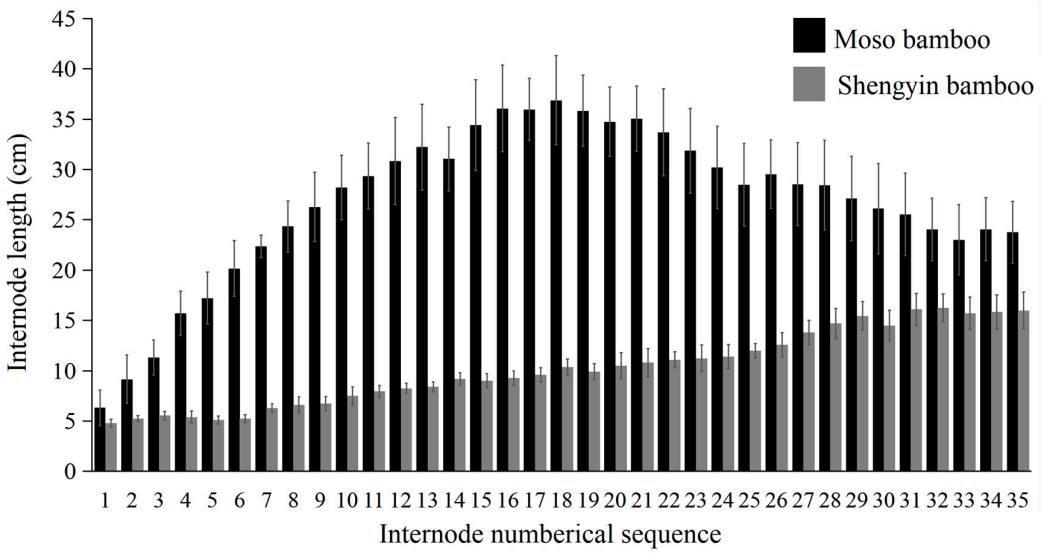


Figure S2. Statistical analysis of internode lengths of mature culms of Moso bamboo and Shengyin bamboo. The X-axis represents the number of internodes counting up from the base, and the Y-axis

represents the internode length.

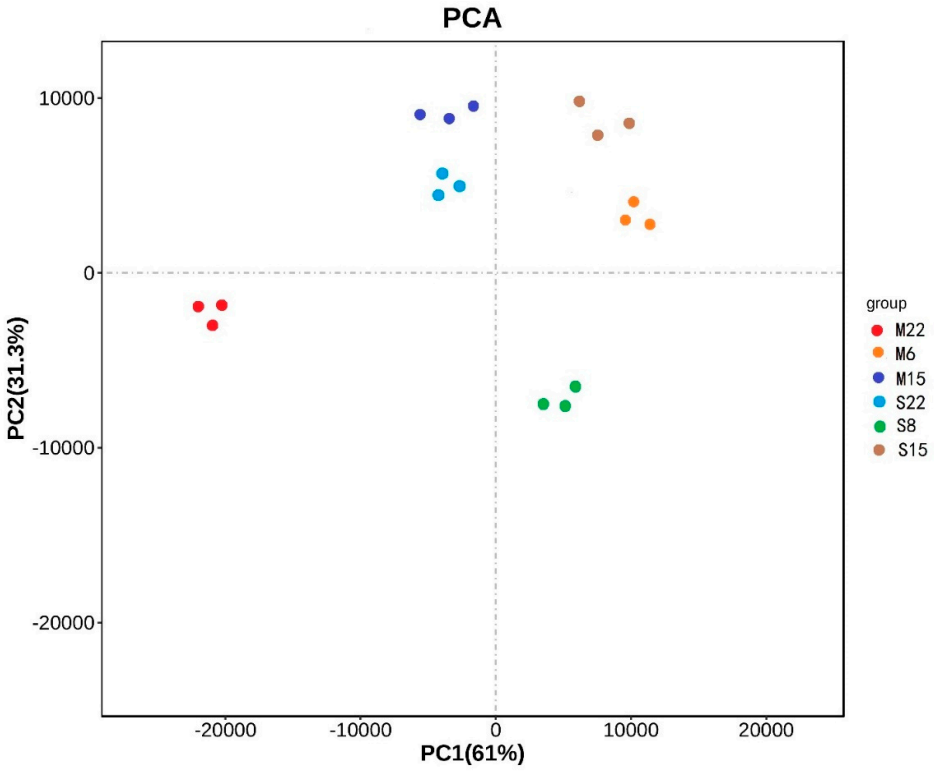


Figure S3. Principal component analysis based on isoform expression level.

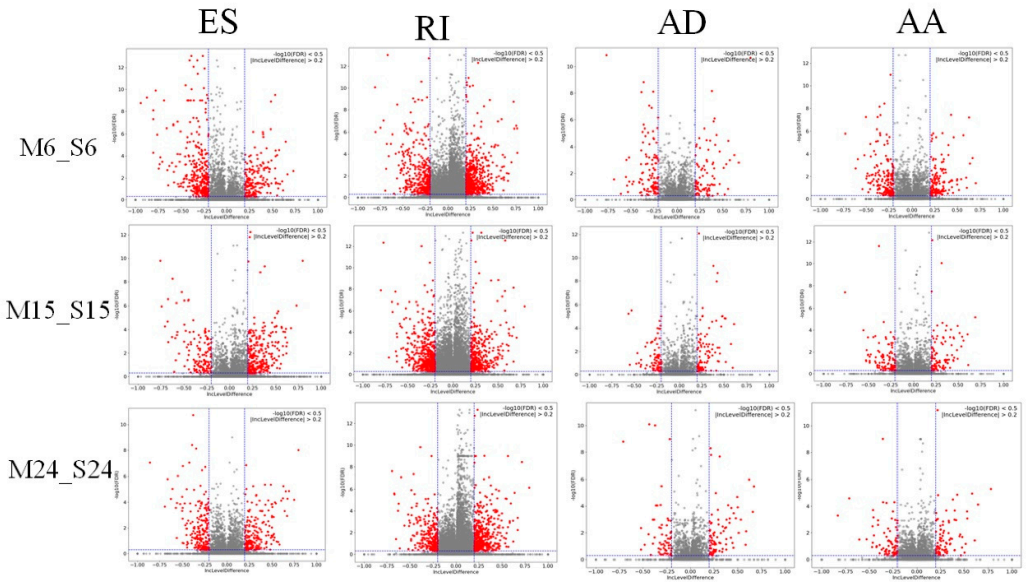


Figure S4. The volcano plot represents the differential alternative splicing (DAS) analysis. Inclevel diff = PSI1 (percent spliced in) – PSI2. A gene was considered as DAS, if it satified with FDR ≤ 0.05 and |IncLevelDiff|≥ 0.2

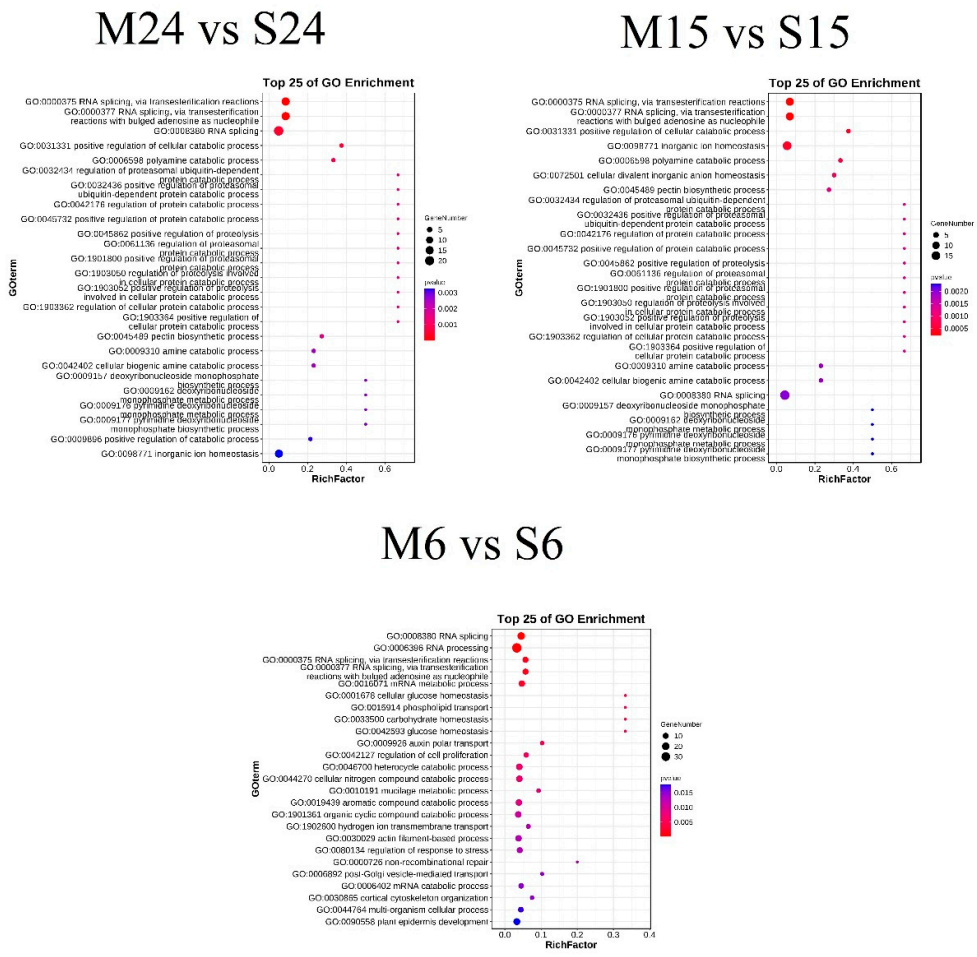


Figure. S5. GO enrichment (biological process) of differentially alternative spliced genes.