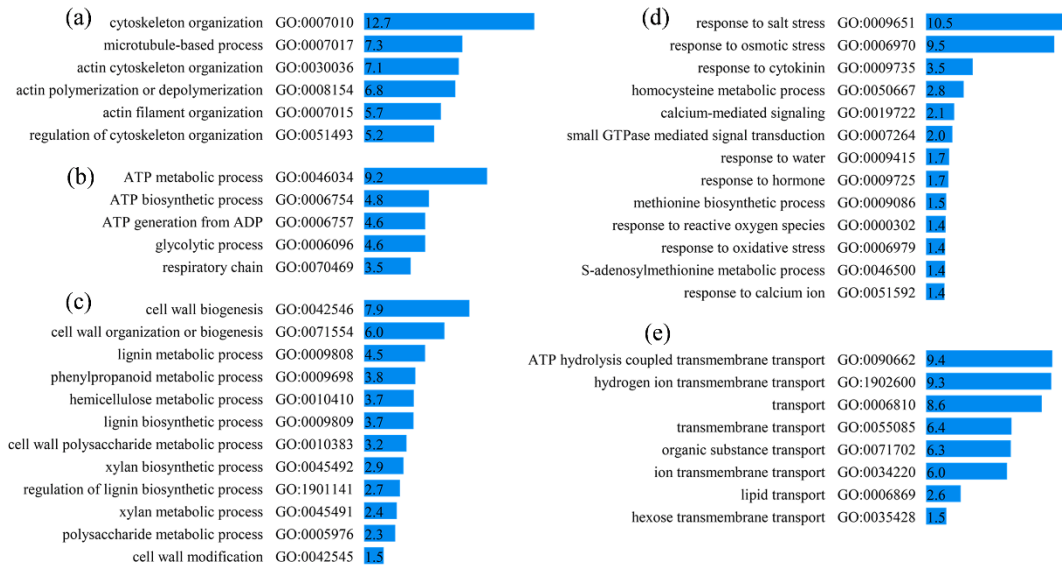
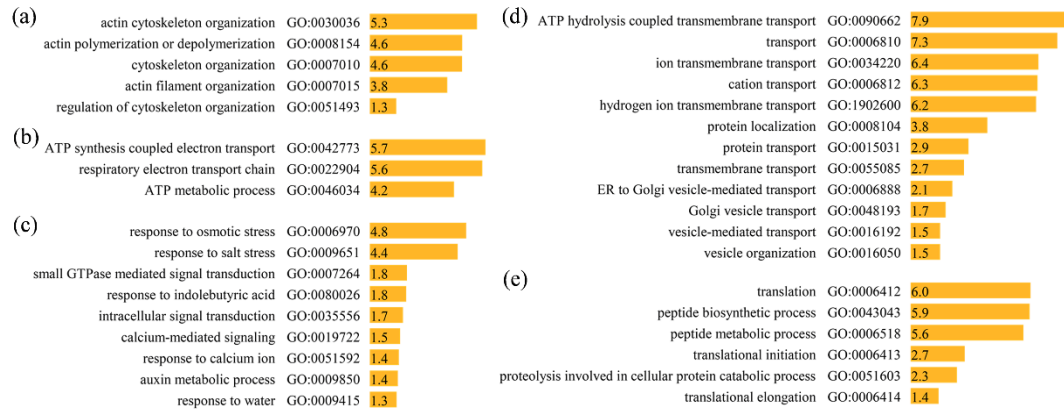


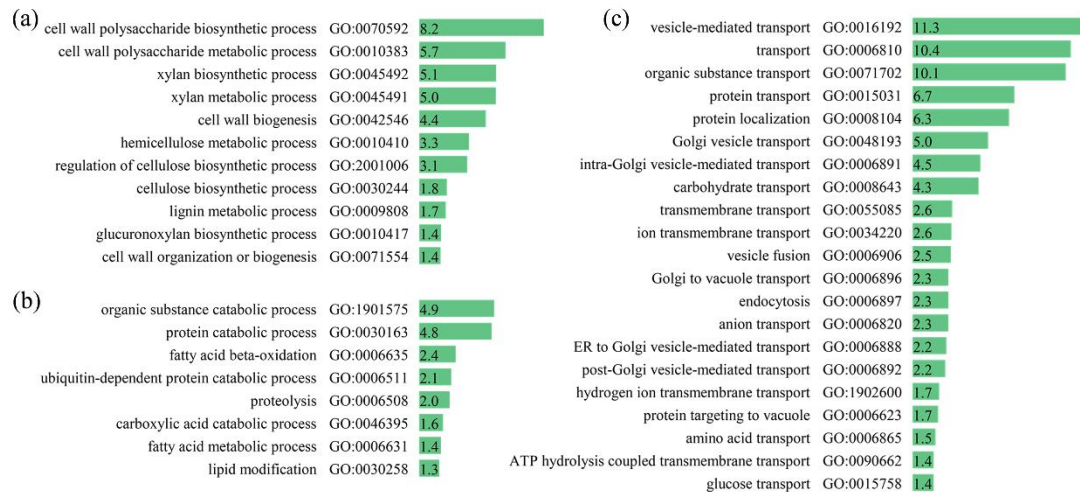
Supplementary Figure S2 Functional analysis of *GbTWS1* in *Arabidopsis*. **(a)** Expression of *GbTWS1* in *GbTWS1*-overexpressed *Arabidopsis* plants, detected by qRT-PCR. **(b)** Western blot of GbTWS1 in *GbTWS1*-overexpressed *Arabidopsis* plants. **(c-d)** *Arabidopsis* plants with overexpression of *GbTWS1*, compared with wild type, showed significantly longer dark-grown hypocotyls. **(e)** Microscopic inspection of hypocotyl epidermal cells. The arrows mark the ends of representative epidermal cells.



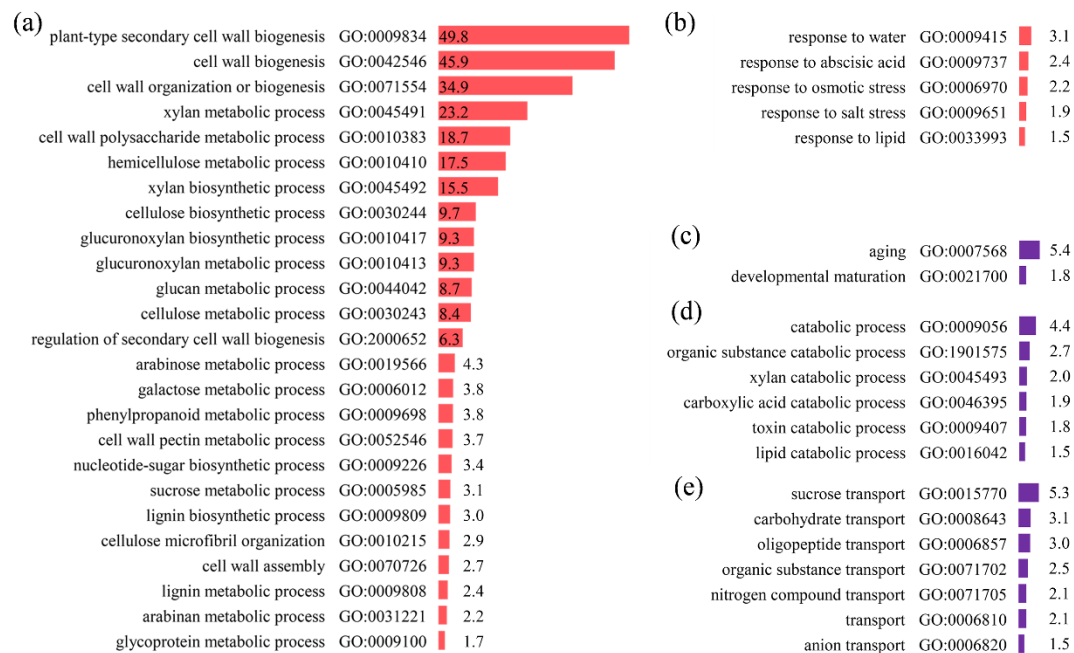
Supplementary Figure S3 GO enrichment analysis of the group I preferentially expressed genes during SCW biosynthesis. The significantly enriched GO terms were mainly classified into five categories: cytoskeleton organization **(a)**, ATP metabolism **(b)**, cell wall development **(c)**, gene expression regulation **(d)**, and transport **(e)**. GO terms with Q -value < 0.05 were considered significantly enriched. The bars show Q -value with a $-\log_{10}$ transformation.



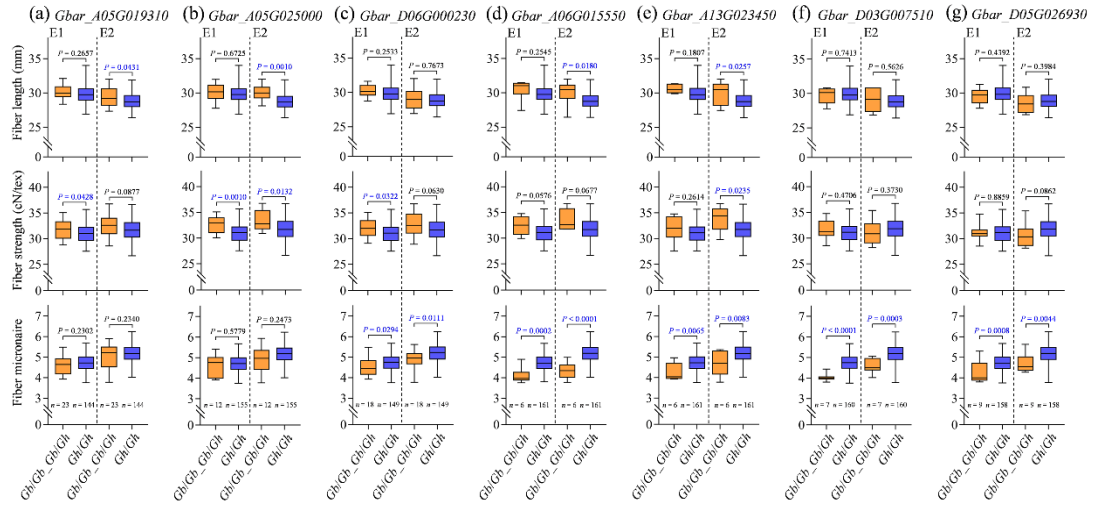
Supplementary Figure S4 GO enrichment analysis of the group II preferentially expressed genes during SCW biosynthesis. The significantly enriched GO terms were mainly classified into five categories: cytoskeleton organization **(a)**, ATP metabolism **(b)**, gene expression regulation **(c)**, transport **(d)**, and protein metabolism **(e)**.



Supplementary Figure S5 GO enrichment analysis of the group III preferentially expressed genes during SCW biosynthesis. The significantly enriched GO terms were mainly classified into three categories: cell wall development **(a)**, protein and lipid metabolism **(b)**, and transport **(c)**.



Supplementary Figure S6 GO enrichment analysis of the group IV (a-b) and V (c-e) preferentially expressed genes during SCW biosynthesis. Diagram exhibits the significantly enriched GO terms related to cell wall development (a), gene expression regulation (b), maturation (c), catabolism (d) and transport (e).



Supplementary Figure S8 The influence on cotton fiber quality with the introgression of *Gbar_A05G019310* (a), *Gbar_A05G025000* (b), *Gbar_D06G000230* (c), *Gbar_A06G015550* (d), *Gbar_A13G023450* (e), *Gbar_D03G007510* (f) and *Gbar_D05G026930* (g).