

Figure S1 Identification of the *GhCYP710A1*-overexpression transgenic cotton

(A) GUS staining results of *GhCYP710A1*-overexpression transgenic cotton. (B) PCR amplification results of *GhCYP710A1*-overexpression transgenic cotton, primers are gene upstream primer (*GhCYP710A1*-R) with NOS terminal primer; M: DNA Marker. P: positive control, template is sense *GhCYP710A1* plasmid; N: negative control, template is gDNA of wild-type cotton leave; W: blank control, water is template; OE-1~OE-8 represent different transgenic cottons. (C) Relative expression levels of *GhCYP710A1* in leaves of transgenic cotton. Error bars represent SD of three independent replicates. ** represent $P < 0.01$, *** represent $P \leq 0.001$.

Figure S2 Identification of VIGS-induced *GhCYP710A1* gene silencing in cotton

(A) Diagram of TRV: *GhCYP710A1* vector. LB: The left border of T-DNA; CaMV35S: promoter; RB: The right border of T-DNA; TRV-RNA2 5': 5' noncoding region; TRV-RNA2 3': 3' noncoding region; Nos-T: terminator; EcoRI and BclI indicate multiple cloning sites for *GhCYP710A1* insertion. (B) Silencing *GhCYP710A1* cotton phenotype. TRV:00 represent negative control of pTRV1+pTRV2. (C) Relative transcription level of *GhCYP710A1* gene in TRV: *GhCYP710A1* plants. Error bars represent the standard deviation of three independent replicates.