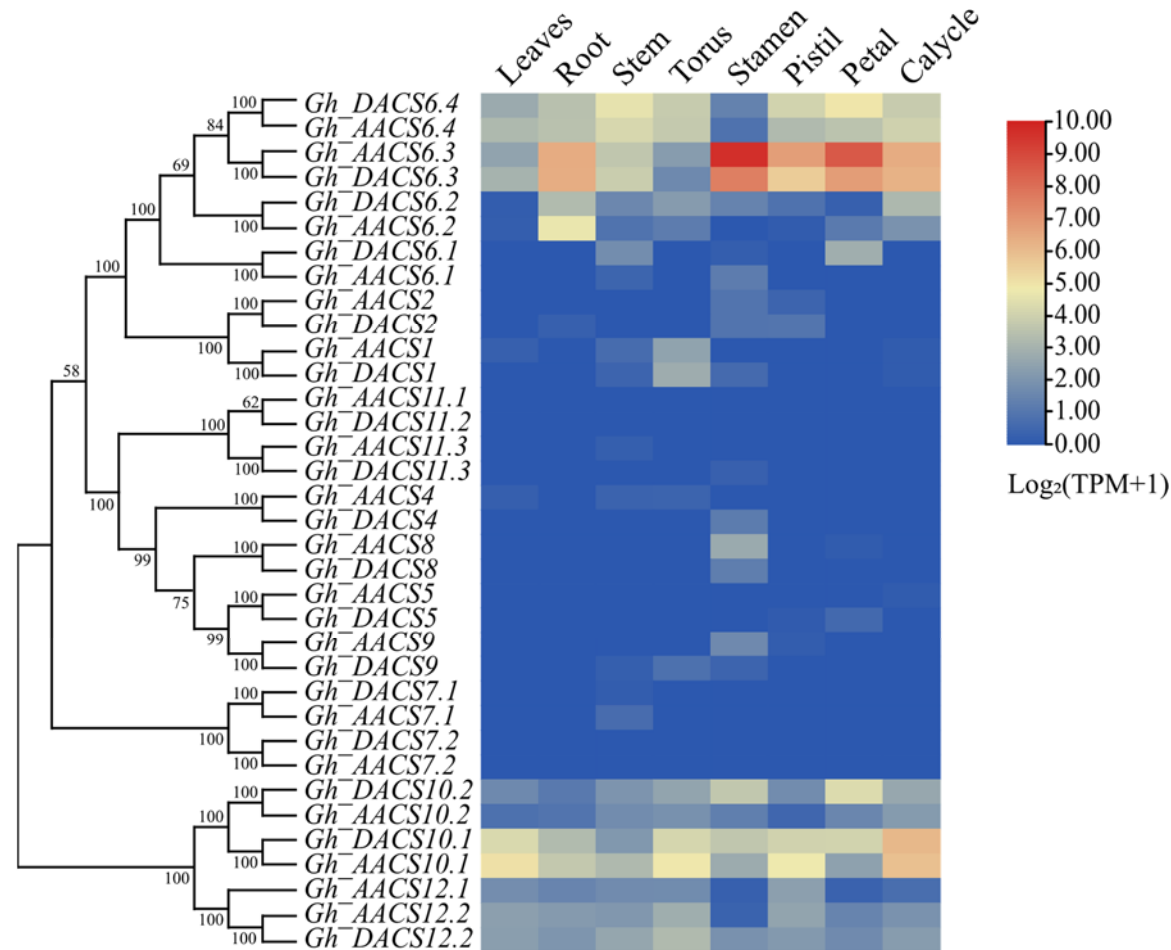


Supplementary Table S1: The primer used in this study.

Primer Name	Sequence (5'-3')
<i>GhACS6.3-F</i>	CCTGGTTTCAGAGTCGGCAT
<i>GhACS6.3-R</i>	ATGCTGAGTTTGCGAGGACA
<i>GhACS10.1-F</i>	AGCCTGCTAGACTTTGCCAG
<i>GhACS10.1-R</i>	CGATTTCTGCCATGCTCACG
<i>GhMML3-F</i>	ATCGACCCTGCAACTCACAG
<i>GhMML3-R</i>	TCGAGGCATTGCGGTTTAGT
<i>GhMML4-F</i>	TTGAACGATGTGGGAAGAGC
<i>GhMML4-R</i>	GGAGGTTGAGGGCTTGTGAG
<i>GhMML7-F</i>	CTGGTTCGTGAGTCCAAGCT
<i>GhMML7-R</i>	GCCATGCTTTGAGTACGTCG
<i>GhSUT1-F</i>	TATCAACCCGGCACCAGTC
<i>GhSUT1-R</i>	GCCAAATGAAAGCAGCCCAA
<i>GhSUT2-F</i>	CACCACCACGAAAGCTTGTG
<i>GhSUT2-R</i>	AGGTTACCGGCATTTCCAGG
<i>GhSWEET2-F</i>	TCACTGTTCAGTGCGATGCT
<i>GhSWEET2-R</i>	AGACAAGTCCGAACCCGAAA
<i>GhSWEET5-F</i>	ATCGGCTCAGCAAGTAGTCG
<i>GhSWEET5-R</i>	CGGTTCCGTCACCATTGTTG
<i>GhSuSy1-F</i>	GATTCCACACTTACCGCCCA
<i>GhSuSy1-R</i>	GATGGCTTCCTGACTGGCTT
<i>GhSuSy3-F</i>	ATCAGCGGCTGGAAAGAGTC
<i>GhSuSy3-R</i>	CGTCCTCCGCATAAGTCTCC
<i>GhUBQ7-F</i>	CGGCAAGCAACTCGAAGATG
<i>GhUBQ7-R</i>	GACAGCGAGCTTGACCTTCT

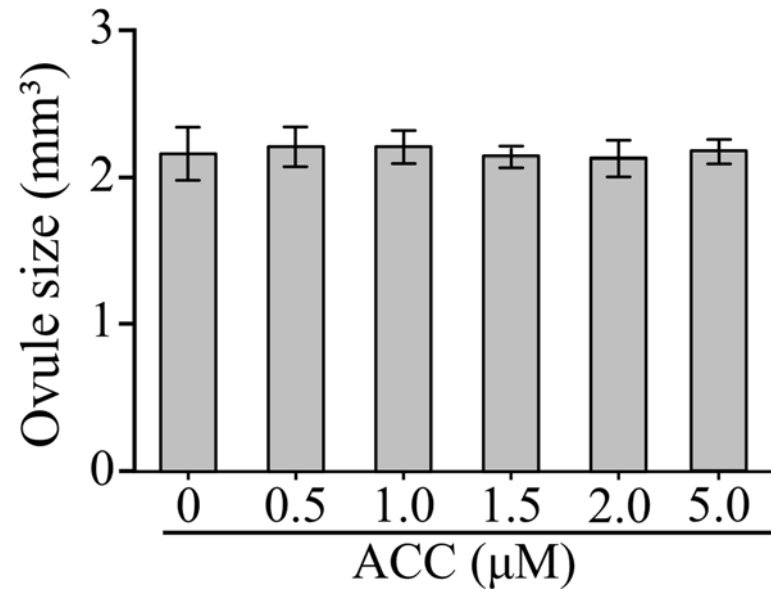
Supplementary Figure S1 Expression profiles of *GhACS*s in leaves, root, stem, torus, stamen, pistil, petal and calycle.



Supplementary Figure S1: Expression profiles of *GhACS*s in leaves, root, stem, torus, stamen, pistil, petal and calycle.

Phylogenetic analysis of 35 *GhACS*s in *G. hirsutum* were used to construct the neighbor-joining tree using MEGA 7.0 software. Heatmap generated from RNA-seq data (SRA:PRJNA248163) of *GhACS*s in leaves, root, stem, torus, stamen, pistil, petal and calycle of *G. hirsutum*. Different columns in the figure represent various samples, and rows represent genes.

Supplementary Figure S2: The size of culture ovules with ACC treatment.

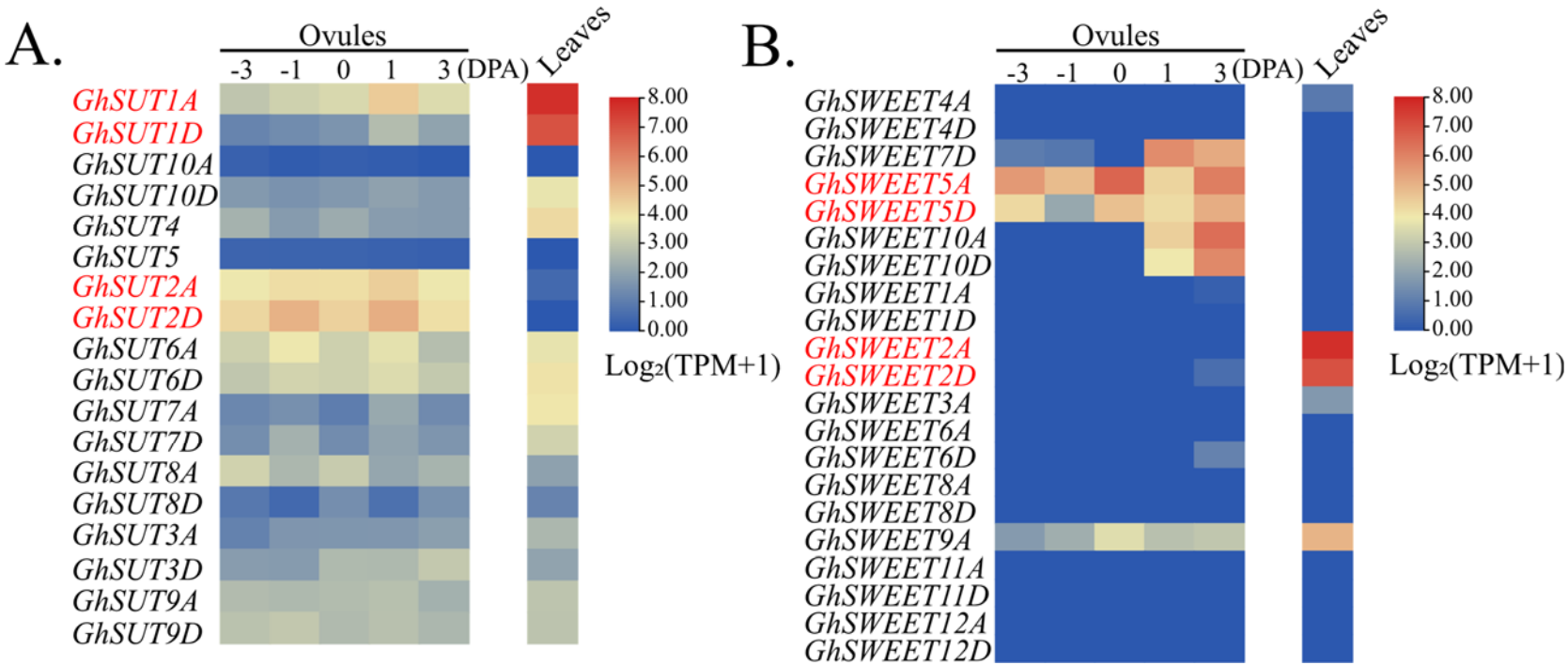


Supplementary Figure S2: The size of culture ovules with ACC treatment. Statistics of the size of ovules cultured in vitro for 48 h with 0, 0.5, 1.0, 1.5, 2.0 and 5.0 μM ACC treatment.

Differences between groups were compared using Student's *t*-test (*, $P < 0.05$, **, $P < 0.01$).

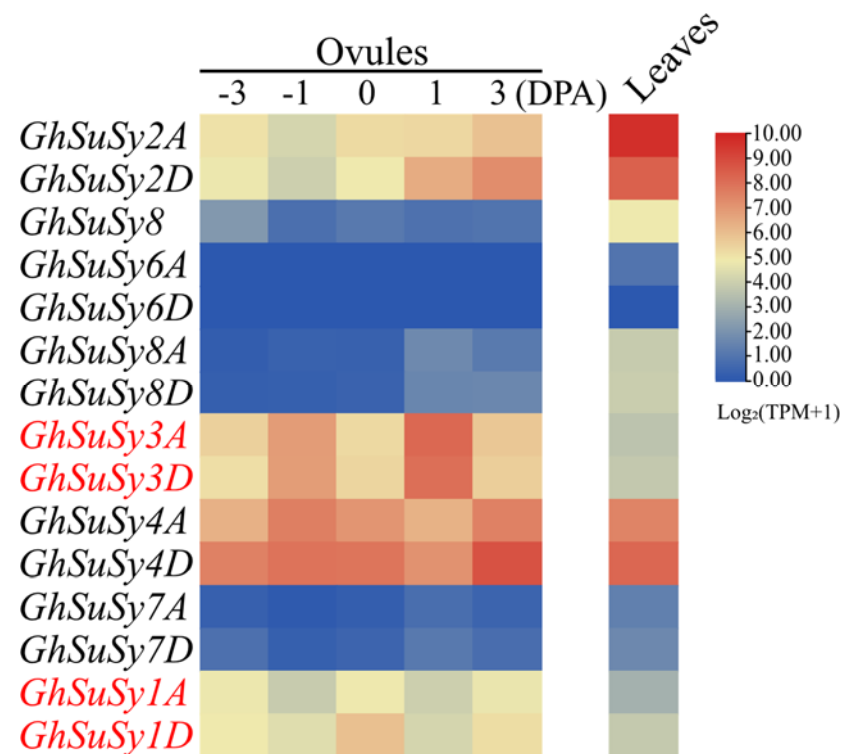
Experiments were repeated five times with similar results, Error bars represent \pm SD.

Supplementary Figure S3: Expression profile of *GhSUTs* and *GhSWEETs* in ovules and leaves.



Supplementary Figure S3 Expression profiles of *GhSUTs* and *GhSWEETs* in ovules during fiber initiation and in leaves. **A and B.** Expression profile of *GhSUTs* and *GhSWEETs* in ovules at -3, -1, 0, 1 and 3 DPA developmental stages and in leaves of *G. hirsutum*. Heatmap generated from RNA-seq data (SRA:PRJNA248163). The color represents the level of expression of the gene ($\log_2(\text{TPM}+1)$) in the sample.

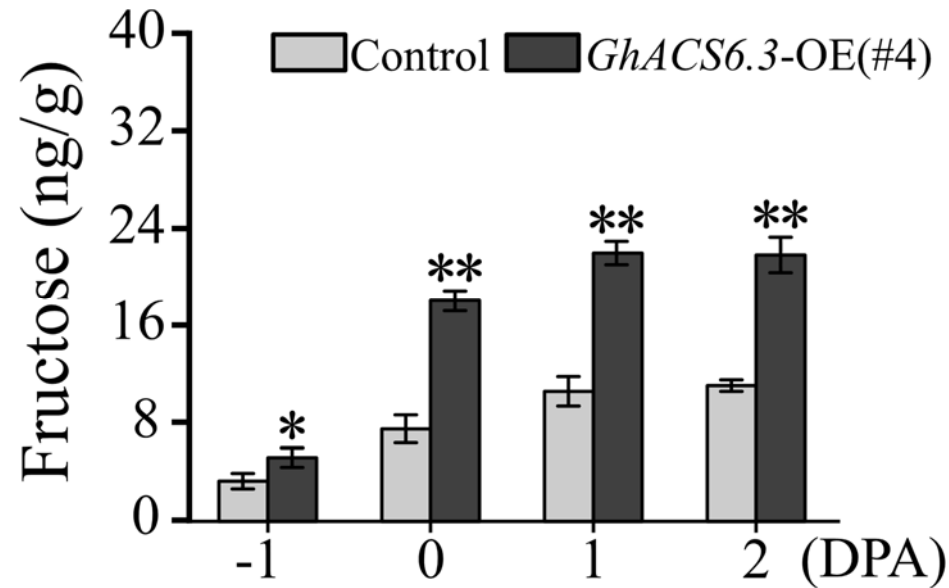
Supplementary Figure S4: Expression profile of *GhSuSy* in ovules and leaves.



Supplementary Figure S4: Expression profile of *GhSuSy* in ovules and leaves during fiber initiation.

Heatmap generated from RNA-seq data (SRA:PRJNA248163) of *GhSuSy* in ovules at -3, -1, 0, 1 and 3 DPA developmental stages and in leaves of *G. hirsutum*. Different columns in the figure represent various samples, and rows represent genes. The color represents the level of expression of the gene ($\log^2(\text{TPM}+1)$) in the sample.

Supplementary Figure S5: Fructose content in ovules of the *GhACS6.3*-OE lines.



Supplementary Figure S5: Fructose content in ovules of the *GhACS6.3*-OE lines.

HPLC analysis fructose in ovules at -1 to 2 DPA development stages of the control and *GhACS6.3*-OE(#4) lines.

Differences between groups were compared using Student's *t*-test (*, $P < 0.05$, **, $P < 0.01$). Experiments

were repeated three times with similar results, Error bars represent \pm SD.