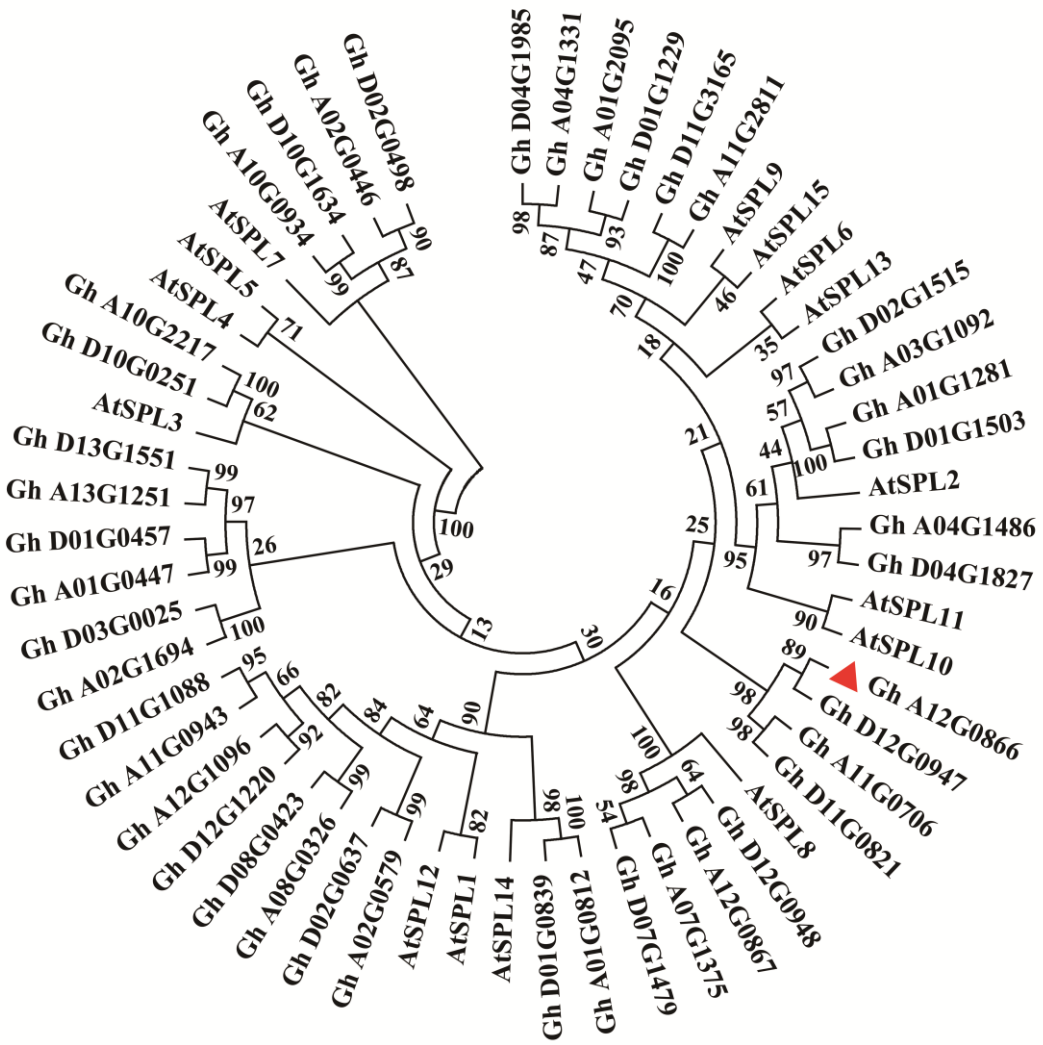

Fig. S1. Phylogeny of SPL proteins based on alignment of 42 SPL protein sequences in *Gossypium hirsutum* TM-1 and 15 SPLs in *Arabidopsis*. Unrooted phylogram was generated by MEGA7 software based on the neighbor-joining algorithm, with number of bootstrap replications set as 500. The red triangle indicates the *GhSPL10* focused in this study.

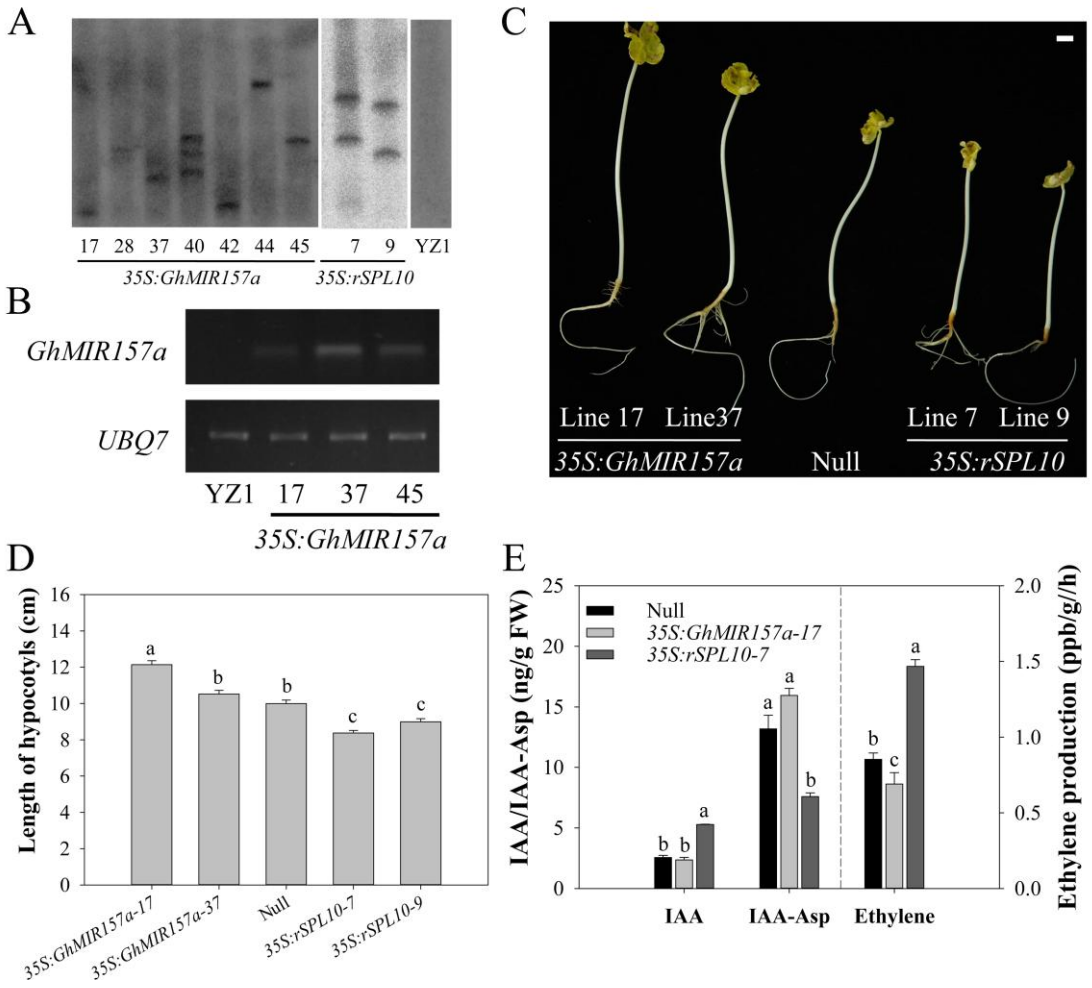

Fig. S2. Molecular and seedling phenotype characterization of *GhmiR157a* and *GhSPL10* overexpression lines. **(A)** Copy number identification of *GhmiR157a* and *GhSPL10* overexpression lines by Southern blotting, with YZ1 as a negative control and PCR products of *NPTII* gene as probe. **(B)** *GhmiR157a* precursor (*GhMIR157a*) detection in leaves of YZ1 and *GhmiR157a* overexpression lines by RT-PCR. *UBQ7* was used as the endogenous reference gene. **(C)** Etiolated seedling phenotype in *GhmiR157a* and *GhSPL10* overexpression lines. Scale bars = 1 cm. **(D)** Hypocotyl length of etiolated seedlings in *GhmiR157a* and *GhSPL10* overexpression lines germinated for 4 days. Error bars = mean + SE (n = 12-20). **(E)** IAA and IAA-Asp content and ethylene production in null, *35S:GhMIR157a-17* and *35S:rSPL10-7*. IAA and IAA-Asp was determined in hypocotyls of 4 d-old seedlings, and ethylene production was determined using 1 d-old germinated seeds. Error bars = mean + SE (n = 2-4). Statistical significances in **(D)** and **(E)** were determined by multiple comparison, $p < 0.05$.

Fig. S3. Correlation analysis and identified differentially expressed *SPLs* by RNA-SEQ. **(A)** Correlation analysis between samples, using the Pearson method. The blue circles represent Pearson correlation coefficient (R) between each sample pair. **(B)** Differentially expressed *SPL*s between *35S:rSPL10-7* and null, shown as heat map. Scale bar displayed as gradual color change from black to red represents log2 (*35S:rSPL10-7*/Null) values from -3 to 3. **(C)** Alignment of *GhmiR157a* reverse complementary sequences (GhmiR157aRC) with differentially expressed *SPLs* identified by RNA SEQ. The purple star shows the potential *SPL* target of *GhmiR157a*. The alignment was generated by clustalX (version 1.83).

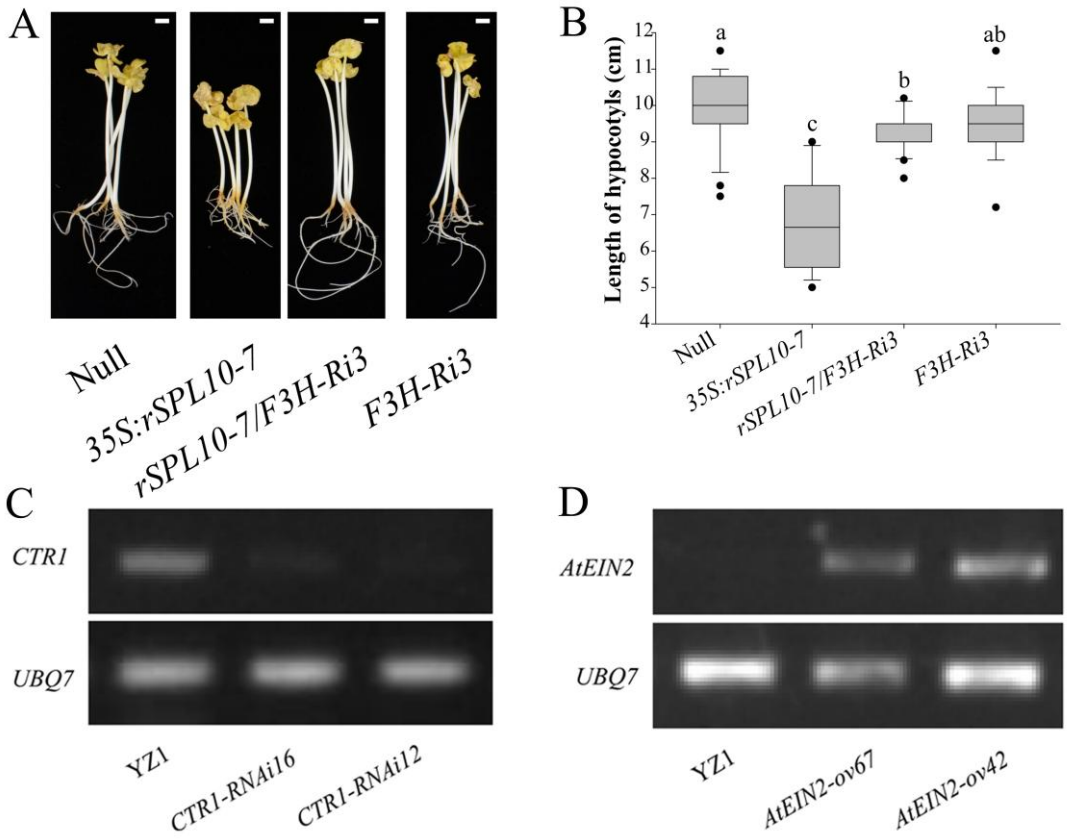

Fig. S4. Hypocotyl phenotype restoration in *35S:rSPL10-7* by inhibiting F3H activity, and transcription detection in *AtEIN2* overexpression and *CTR1* RNAi cotton plants. **(A)** Seedling phenotype of 5d-old etiolated seedlings of null, 35S:*rSPL10-7*, *rSPL10-7/F3H-Ri3* and *F3H-Ri3* cotton plants. Scale bars = 1 cm. **(B)** Hypocotyl length of 5d-old etiolated seedlings of null, 35S: *rSPL10-7*, *rSPL10-7/F3H-Ri3* and *F3H-Ri3* cotton plants. Error bars = mean + SE (n = 19-23). **(C)** Relative expression levels of *AtEIN2* in leaves of *EIN2-ov67* and *42* cotton plants, and **(D)** *CTR1* in *CTR1-RNAi16* and 12 cotton plants by RT-PCR, with YZ1 as control. *UBQ7* was used as an endogenous reference gene. Statistical significance in **(B)** and **(C)** was determined by multiple comparison, $p < 0.05$.

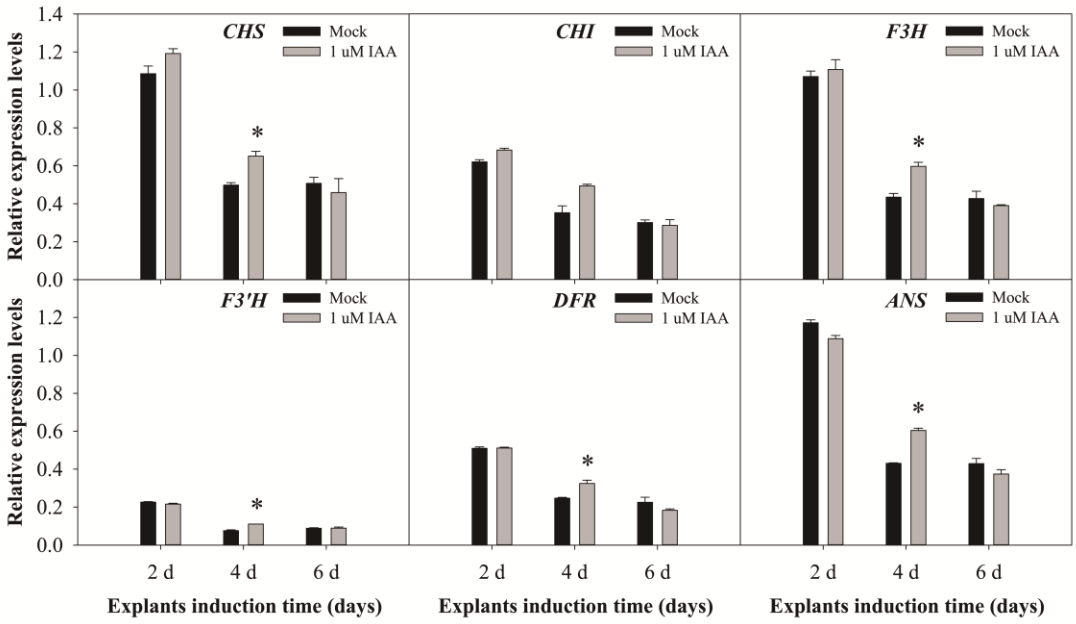

Fig. S5. IAA treatment promotes flavonoid biosynthesis-related gene expression. qRT-PCR of *CHS*, *CHI*, *F3H*, *F3'H*, *DFR* and *ANS* in explants of YZ1 cultured on MSB medium supplemented with 1 uM IAA for 2, 4 and 6 d respectively. Error bars represent mean and SE, statistical significance was determined by multiple comparison, *$p < 0.05$.

Table S1. List of primers used in this study.

Category	Gene annotation	Gene ID	Primer	Primer Sequence
5' RACE	SPL10	Gh_A12G0866	3' primer	GTTCCTTGCAGGGAATGCCACAAC
			3' nested primer	TAATGTGACTTGACCACCGATTTCC
In situ hybridization probe	SPL10 frag1	Gh_A12G0866	forward	ATGGAACATGATGATATGTTCATGGG
			reverse	TGACTAGTGTAACATTACACCCTTCAAC
	SPL10 frag2		forward	ACGCTAAAGACTATCACCGGAGAC
			reverse	CCACAATCAGCTCACGCAAGG
	SPL10 frag3		forward	AAAACCGTGCTGCTGTCCTC
			reverse	AATCACTTGGCATTTATGGTTCA
Overexpression	SPL10	Gh_A12G0866	5' forward	GGGGACAAGTTTGTACAAAAAAGCAGGCTGAAAGAAAAAAAA AGGAGAGACAA
			bridged-reverse	CCTTGGAAGAGAGGAGTGACAGTGCTCGTCCTGTTGGCGACGA
			bridged-forward	CAGGACGAGCACTGTCACTCCTCTCTTCCAAGGTTGATTCTTG GATC
			3'reverse	GGGGACCACTTTGTACAAGAAAGCTGGGTTTCCATGTGTTCCT TGCAGGGA
RT-PCR	AtEIN2	AT5G03280	forward	AGTTGCTCCTGCGCTTTATTGT
			reverse	TTGATTCGTCTTCGTTCCTCCT
	CTR1	Gh_D09G1340	forward	CCTTAGCCAGTATCCCGACG

			reverse	AAAGCCAACGCCAACTGC
qRT-PCR	SPL10	Gh_A12G0866	forward	GACTGGGAGTTTTCCGTATGTATCG
			reverse	CCACAATCAGCTCACGCAAGG
	ACO	Gh_D07G1899	forward	TGGATTGGGAAAGCACATTC
			reverse	TTTGGACATGGTGGGTAGTTG
		Gh_A07G0773	forward	TACCTTCTATTTGCGCCATC
			reverse	TGCCCCATAGAAAGCCTTTT
		Gh_A06G1341	forward	GCTGGCTGAGAAACTTTTGGA
			reverse	AGGGACATCAATCCATTGGT
	CHS	Gh_A10G1079	forward	TGTGTGCTCGGAGATTACTGCT
			reverse	GTTCAAACATGGGCTTCTCGAT
	CHI	Gh_A13G0197	forward	TGATGCAGAAGCAAAAGCCAT
			reverse	TCCCACCTTCTGGTACTGAGCT
	F3H	Gh_D12G0566	forward	GGGCCTAGCTTGCAAGCTTCTT
			reverse	AAGCAAGAGTGTGATGGTGCCTGG
	F3'H	Gh_D12G1798	forward	AGTGGGAGTTGGCTGATGGATT
			reverse	CTCCTCACCCTGAAACGACAAC
	FLS	Gh_D05G2212	forward	CAAGTTGTGAACCATGGCATTC
			reverse	GCCTTCAATGGATTGAGATCCT
	DFR	Gh_A05G1647	forward	CGAGGACCCTGAGAATGAAGT
			reverse	GGCTTTTGTTGTTCTGCAACAT
	ANS	Gh_D08G1902	forward	GAGGCCTAGCGAGCAAAATAC
			reverse	GTGAGCTTCGACACCGAGAG
	CYCA2;2	Gh_D06G0428	forward	ACTGTTGGCCTTCAGCCTAAA
			reverse	TTCTTCAACCGATGGAATCC
	CYCA3;2	Gh_D06G0190	forward	ATGGCGGGTCAGGAGAATT

		reverse	GGCTGTTGTTGTTGCTGTTGT
CYCA3;4	Gh_A12G0183	forward	AGTTGATCAAGAGAACCGCGT
		reverse	ACTTGGGCATTTCTCGATCT
CYCB1;2	Gh_D11G3346	forward	CCTATTGTTCCTCAACAACCC
		reverse	AACTGTGCGCAAAAGGACCTA
CYCB1;4	Gh_A09G1018	forward	GCTATTGTTCCTCAGCATGAA
		reverse	TGTCAACCTGCTTTCTTTGG
CYCB2;4	Gh_D01G0881	forward	TCCACACATGTGCATAGACCA
		reverse	ATCCGGTCAATCTCCTCCAA
CYCB3;1	Gh_A08G0724	forward	TCAAAGAAAGGCACTGTCAGA
		reverse	GCACCTTGATTTAGATGGTCC
CYCD1;1	Gh_A03G1593	forward	TCCATCAGCCGCATCTTTAT
		reverse	CTCATCGGGATTGGGATAAT
CDKB1;2	Gh_Sca005019G02	forward	TACTCACTACTCCACCGCCGT
		reverse	AACAGCGCGTTCCAAGTTCT
CDKB2;2	Gh_D01G0840	forward	AGGCAAATCTCAGCAATGGA
		reverse	CATCAATCTGACGACATGAGG
Dpa	Gh_A11G2912	forward	AATCAAACGAAACCAGCGGA
		reverse	TCATGCAAACTGAATGGCGT
KRP7	Gh_A03G1676	forward	ATGGGCGATTGTATGAGAAGC
		reverse	AGTCTGCAACACTTTTCACCG
LEC1	Gh_D05G1686	forward	GCCAACCATACGAACAGCCAC
		reverse	GGACACACATTCTTGGATCGTTT
LEC2	Gh_A09G0695	forward	CGAAGAAGGCAACGACAACAG
		reverse	GTGAACCATAAGTAGAATCCATAGGC

GhUBQ7	Gh_A11G0969	forward	GAAGGCATTCCACCTGACCAAC
		reverse	CTTGACCTTCTTCTTCTTGTGCTTG

Table S2. Summary statistics of sequencing and mapping.

Sample Name	Clean reads	Genome map Rate	Gene map Rate	Expressed Gene
Null-1	12154146	86.87%	69.37%	50359
Null-2	12162581	86.60%	69.84%	51011
35S:rSPL10-7-1	12163262	86.74%	71.34%	50911
35S:rSPL10-7-2	12160933	86.56%	71.83%	51216