Table S1 RNA-Seq clean data from materials treated with 7d and 14d.

Samples	CK_7G	CK_7Y	NaCl_7G	NaCl_7Y	CK_14G	CK_14Y	NaCl_14G	NaCl_14Y
Total reads	41536271	38187089	41276229	40834729	40247362	39245175	42796309	40679483
Reads mapped	30299747 (72.95%)	28083241 (73.54%)	30581516 (74.09%)	27151803 (66.49%)	29213524 (72.58%)	29352139 (74.79%)	32060343 (74.91%)	31661551 (77.83%)

Note: CK_7G, CK_7Y, NaCl_7G, NaCl_7Y represent the roots and leaves treated with water and those treated with 400mM NaCl for 7 days, respectively; CK_14G, CK_14Y, NaCl_14G, NaCl_14Y represent the roots and leaves treated with water and those treated with 400mM NaCl for 14 days, respectively.

Table S2. Isoform annotation

Database	Annotated Number	Number of isoforms contained in different length intervals				
		0≤length<1k	1k≤length<2k	2k≤length<3k	3k≤length<6k	Length≥6k
GO	21 445	2 862	10 009	6 079	2 457	38
KEGG	14 457	1 940	6 731	3 969	1 785	32
KOG	12 116	1 138	5 651	3 707	1 594	26
NR	27 086	3 607	12 313	7 748	3 358	60
NT	22 419	2 526	10 039	6 817	2 978	59
Swiss-prot	22 495	2 626	10 259	6 694	2 868	48
All	27 233	3 685	12 351	7 769	3 368	60

Table S3 Information of *TIFY* gene family members in *S. portulacastrum*

Gene	**Gene ID**	**CDs**	**Protein**			
			Size/aa	**（MW/kD）**	**pI**	**Subcellular localization**
SpJAZ1	BDLW_1-10k_transcript/52437	522	173	183.64	9.94	Nuclear
SpJAZ2	BDLW_1-10k_transcript/50558	549	182	203.23	8.99	Nuclear
SpJAZ3	BDLW_1-10k_transcript/44318	702	233	261.22	9.18	Nuclear
SpJAZ4	BDLW_1-10k_transcript/46815	702	233	260.05	9.07	Nuclear
SpJAZ5	BDLW_1-10k_transcript/46388	750	249	269.08	9.79	Nuclear
SpJAZ6	BDLW_1-10k_transcript/40702	798	265	284.87	9.81	Nuclear
SpJAZ7	BDLW_1-10k_transcript/37680	801	266	285.35	9.72	Nuclear
SpPPD1	BDLW_1-10k_transcript/28788	675	224	241.76	9.73	Nuclear
SpPPD2	BDLW_1-10k_transcript/29236	1071	356	385.42	8.73	Nuclear
SpZML1	BDLW_1-10k_transcript/31804	699	232	257.91	8.76	Nuclear
SpZML2	BDLW_1-10k_transcript/33174	822	273	301.82	9.57	Nuclear
SpZML3	BDLW_1-10k_transcript/28502	906	301	330.23	6.09	Nuclear
SpZML4	BDLW_1-10k_transcript/37056	1032	343	376.85	5.70	Nuclear

SpZML5	BDLW_1-10k_transcript/28142	1059	352	385.66	5.08	Nuclear
SpTIFY	BDLW_1-10k_transcript/31097	345	114	117.86	5.53	Nuclear

Table S4 Primers used in this real-time PCR

Primer Name	Sequence（5' to 3'）	Product（bp）	bp
SpJAZ1 Forward Primer	GGATGGCTAATGCCAGTGGAA	115	21
SpJAZ1 Reverse Primer	TTATCGGCCGGCAAGTCGTTG		
SpJAZ2 Forward Primer	TGAGCAGAAAGTTGAAAAAAC	127	21
SpJAZ2 Reverse Primer	TTAGATATCATCGGATGGATG		
SpJAZ3 Forward Primer	TCAACAATTCTTTATAGACCC	125	21
SpJAZ3 Reverse Primer	AGGAGGAAATATGTAGGTAGG		
SpJAZ4 Forward Primer	TGGATAAGATTTTGCATAATG	111	21
SpJAZ4 Reverse Primer	GGATCTATAAAGAATCGTCGA		
SpJAZ5 Forward Primer	AGAGCTGACGTTTTTGTGAG	122	20
SpJAZ5 Reverse Primer	TAAGGGAATAGATATTTGTA		
SpJAZ6 Forward Primer	CATAAACCCCTCTCCAAAAAG	121	21
SpJAZ6 Reverse Primer	TTCAATAACGACCCACAAATC		
SpJAZ7 Forward Primer	GAAGCATGTCAACACATCGGC	137	21
SpJAZ7 Reverse Primer	GGTTATTGGGGGTGATGGAAA		
SpPPD1 Forward Primer	AACGACAACAACCAAAACAGG	131	21
SpPPD1 Reverse Primer	GCCATCAAAGGACTAAACCCA		
SpPPD2 Forward Primer	ACAAACAACTCAAAGCAACAG	115	21
SpPPD2 Reverse Primer	ATTAAGATCAACCGACAAGCC		
SpZML1 Forward Primer	AAAATGGCTGTTGTCATCTTC	125	21
SpZML1 Reverse Primer	ATCCAATTAACGTCCACTTAA		
SpZML2 Forward Primer	CAAGAAGCAGTTGCAGCCA	109	19
SpZML2 Reverse Primer	TCCCCTACTAACCCCCAGA		
SpZML3 Forward Primer	GATGCAACGAAATAAAGGC	145	19
SpZML3 Reverse Primer	ACAATGTCGGCAGCAAACT		
SpZML4 Forward Primer	CTGGGACCGTAGCAGATATTAA	142	22
SpZML4 Reverse Primer	GAAATCTTGTCATGAGGTTGAT		
SpZML5 Forward Primer	ATGACCATTGGTGACCCTT	135	19
SpZML5 Reverse Primer	TTGAGCAACTTCTTTTCGG		
SpTIFY Forward Primer	CTACCTGGTGACTCTTCCTTG	137	21
SpTIFY Reverse Primer	GATTCTCCTGCTTGATTTGGA		
GAPDH Forward Primer	TTGGCATCGTTGAGGGTCT	180	19
GAPDH Reverse Primer	CAGTGGGAACACGGAAAGC		

Table S5 Target gene primer information and overexpression vectors construction

Primer Name	Sequence（5' to 3'）
SpJAZ1-F	ATGGCTAATGCCAGTGGAA
SpJAZ1-R	CTAGAGCTGCTGTTGCTGA

SpJAZ5-F	ATGACCTTTTCTCAGACTT
SpJAZ5-R	CTAGAGCTGCTGTTGCTGA
SpJAZ7-F	ATGTCAACCACATCGGCAG
SpJAZ7-R	CTAGAGCTGCTGTTGCTGA
G-SpJAZ1-F	GGGGACTCTTGAGGATCCATGGCTAATGCCAGTGGAA
G-SpJAZ1-R	GACAGATCCCCGGGTACCCTAGAGCTGCTGTTGCTGA
G-SpJAZ5-F	GGGGACTCTTGAGGATCCATGACCTTTTCTCAGACTT
G-SpJAZ5-R	GACAGATCCCCGGGTACCCTAGAGCTGCTGTTGCTGA
G-SpJAZ7-F	GGGGACTCTTGAGGATCCATGTCAACCACATCGGCAG
G-SpJAZ7-R	GACAGATCCCCGGGTACCCTAGAGCTGCTGTTGCTGA

Table S6 Identification primers for transgenic *Arabidopsis*.

Primer Name	Sequence（5' to 3'）
G418-F	CGGCTATGACTGGGCACAACAGACAAT
G418-R	CTCGGCAGGAGCAAGGTGAGATGAC
G-JAZ1-F	CGTAAGGGATGACGCACAA
G-JAZ1-R	TCTGGGTCGGATTAGGACA
G-JAZ5-F	TGACGCACAATCCCACTAT
G-JAZ5-R	CCATCAAAGGACTAAACCC
G-JAZ7-F	ACGCACAATCCCACTATCC
G-JAZ7-R	AGCCATCAAAGGACTAAAC

Table S7 Silent sequence primers for transgenic *Arabidopsis*.

Primer Name	Sequence（5' to 3'）
JAZs-F	CTAATGCCAGTGGAAGCAA
JAZs-R	CTTTTCCCACAAGCCTGTC
V-JAZs-F	GTTACCGAATTCTCTAGACTAATGCCAGTGGAAGCAA
V-JAZs-R	CTCGAGACGCGTGAGCTCCTTTTCCCACAAGCCTGTC

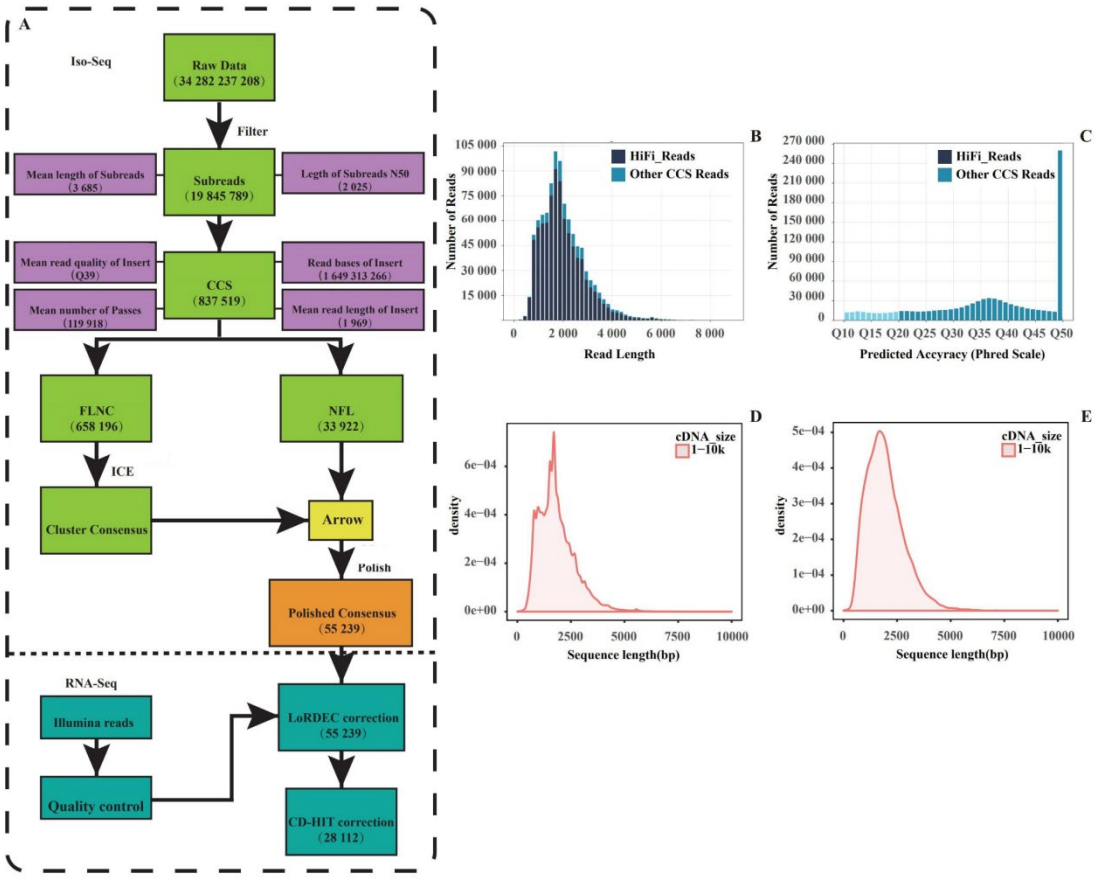


Figure S1. Full-length transcriptome characteristics of *S. portulacastrum*. (A) Distribution of circular consensus sequencing (CCS) reads (n = 837,519) generated from PacBio sequencing. (B) Length distribution and (C) quality metrics of filtered Reads of Insert (ROI). (D) Size profile of full-length non-chimeric (FLNC) transcripts. (E) Length distribution of ICE-clustered consensus isoforms. Raw data yield = 34.28 Gb; 19,845,789 subreads (mean length = 3,685 bp; N50 = 2,025 bp).

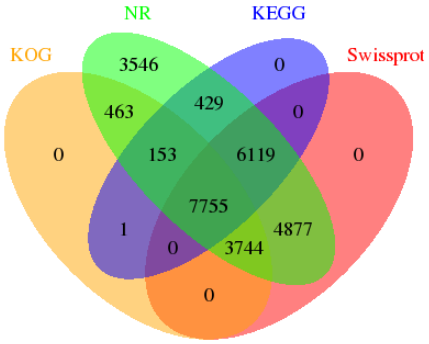


Figure S2. Venn diagram of Cd transcriptome annotation results in *S.portulacastrum* in different databases.

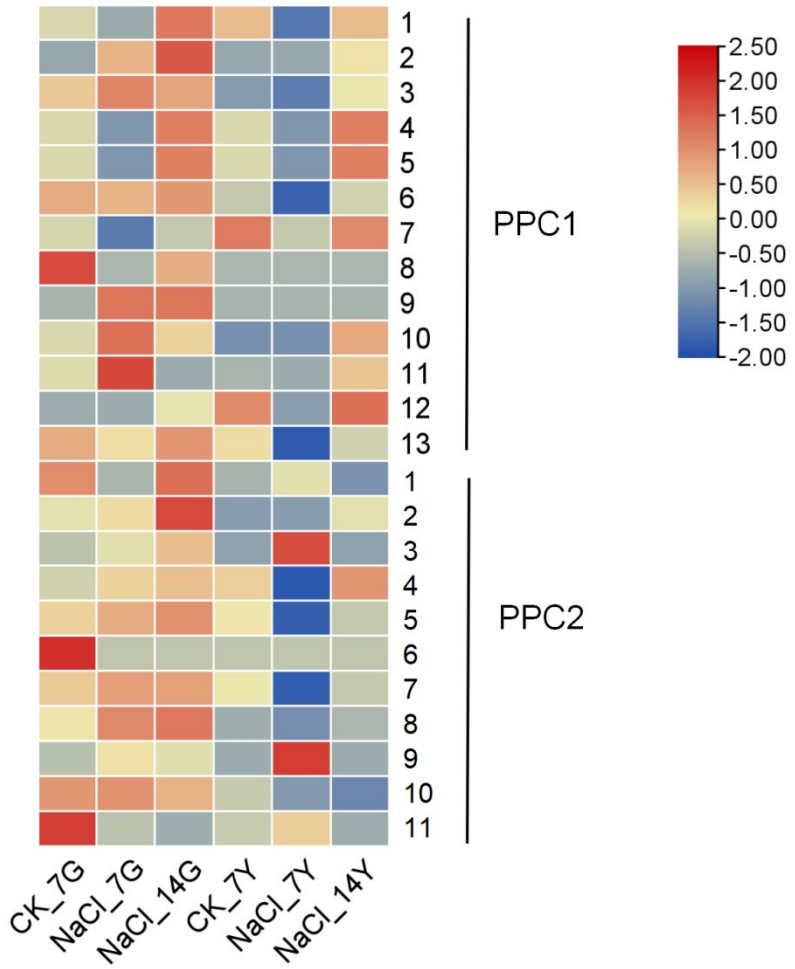


Figure S3. The expression levels of PPC1/PPC2 on the CAM pathway after 7d and 14d NaCl treatment groups.

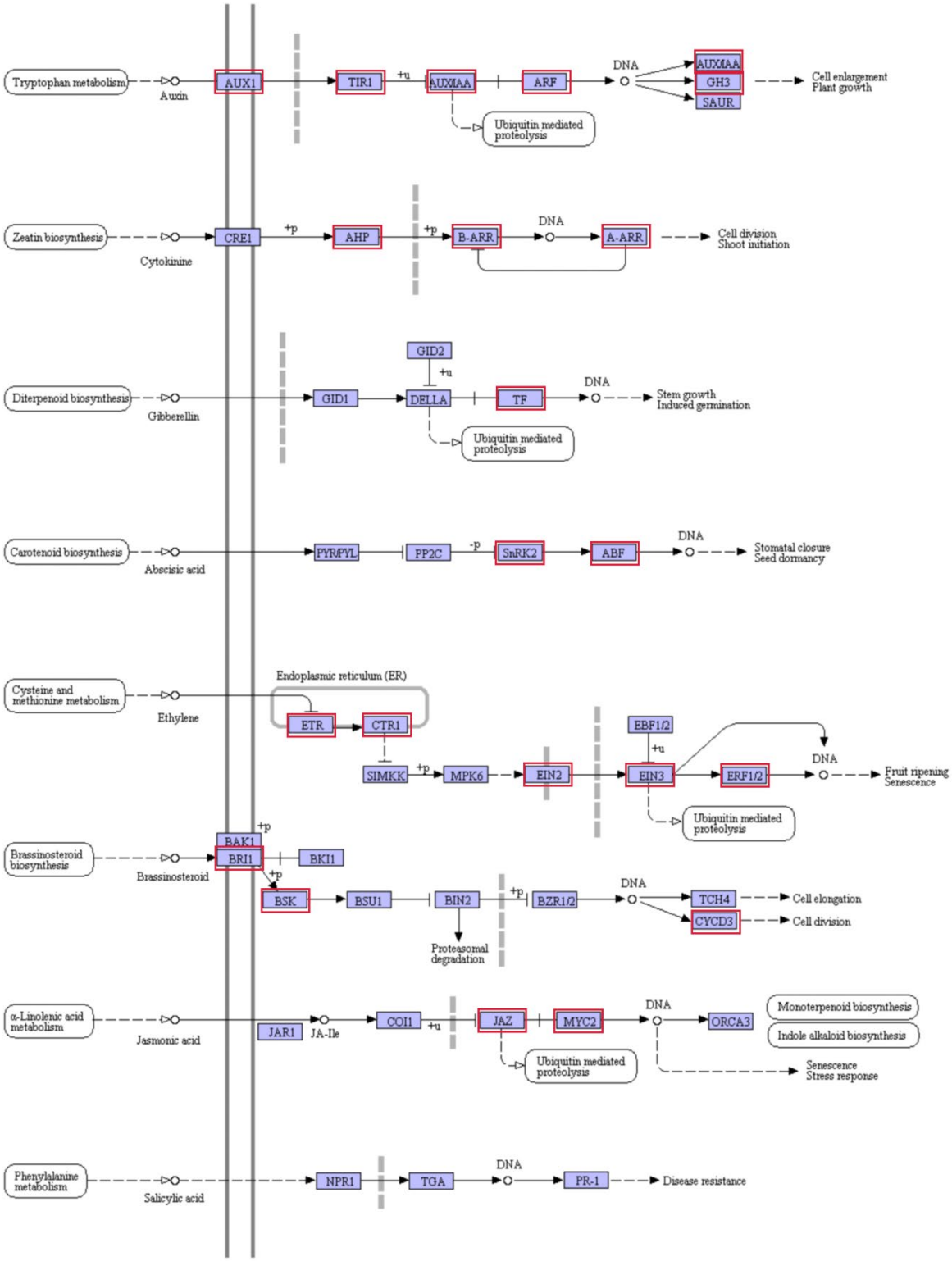


Figure S4. Changes in differentially related genes involved in plant hormone synthesis and signal transduction in the transcriptome after NaCl stress (red means up-regulated).

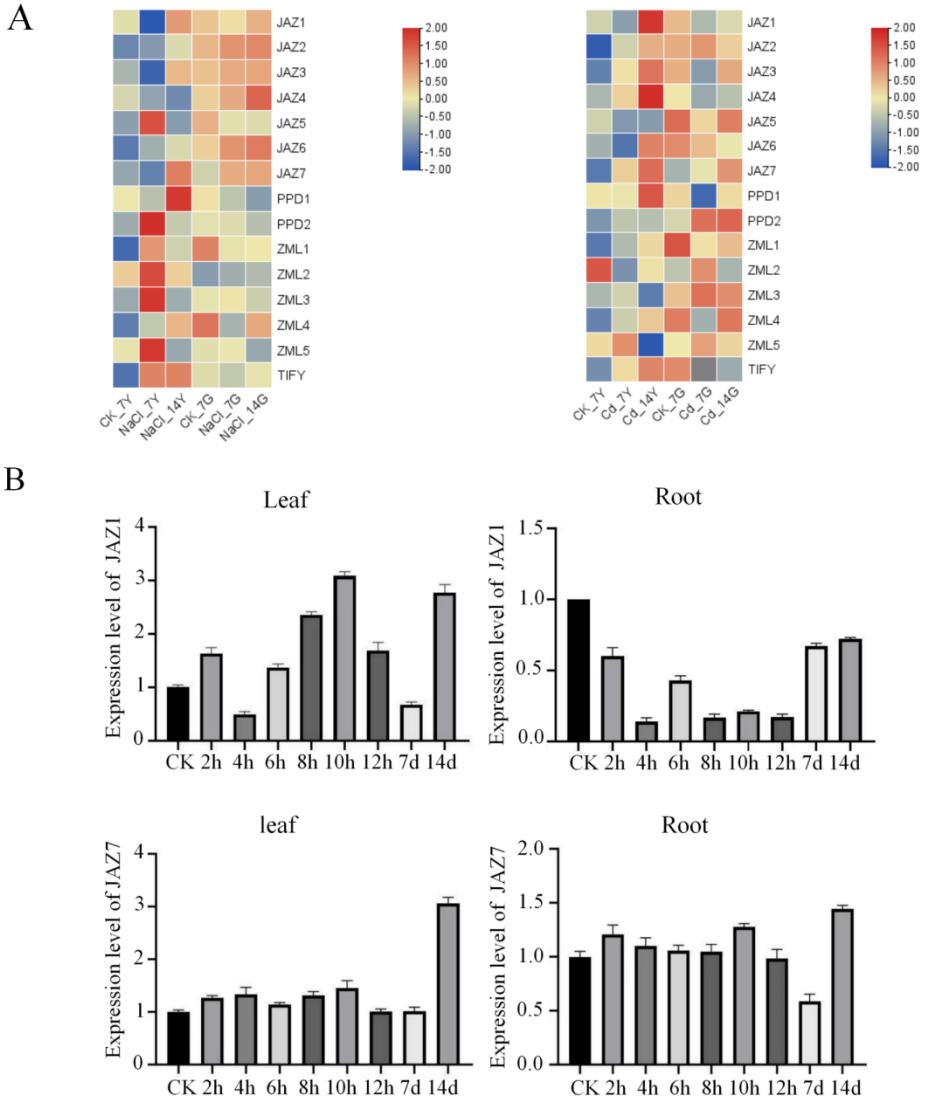


Figure S5. Genetic quantification of TIFY family. A. Expression profiling of TIFY family under salt stress and Cd stress. B. Expression levels of the *SpJAZ1* and *SpJAZ7* genes according to qRT-PCR under Cd stress.

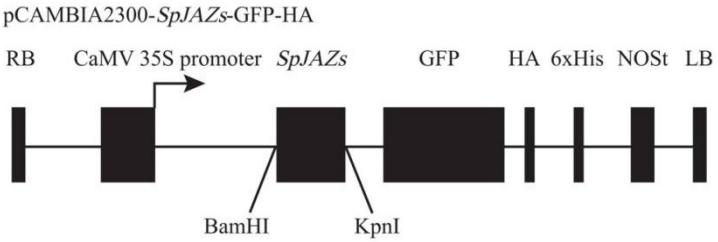


Figure S6. Structure of pCAMBIA2300-SpJAZs-GFP-HA.

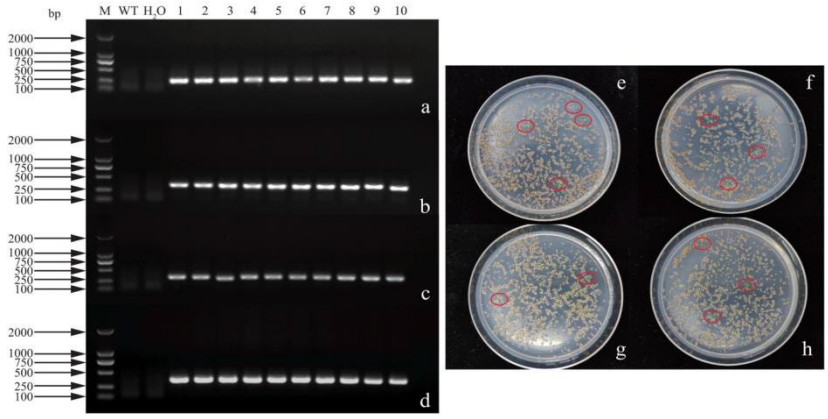


Figure S7. Screening of transgenic *Arabidopsis* positive seedlings. Note: a~d: PCR detection of 2300-GFP-HA empty vector, *SpGFP-JAZ1*, *SpGFP-JAZ5* and *SpGFP-JAZ7* transgenic *Arabidopsis*; 1~10: Transgenic *Arabidopsis*; M: Marker; e~h: Screening of *SpGFP-JAZ1*, *SpGFP-JAZ5*, *SpGFP-JAZ7* transgenic *Arabidopsis* T0 generation positive seedlings.

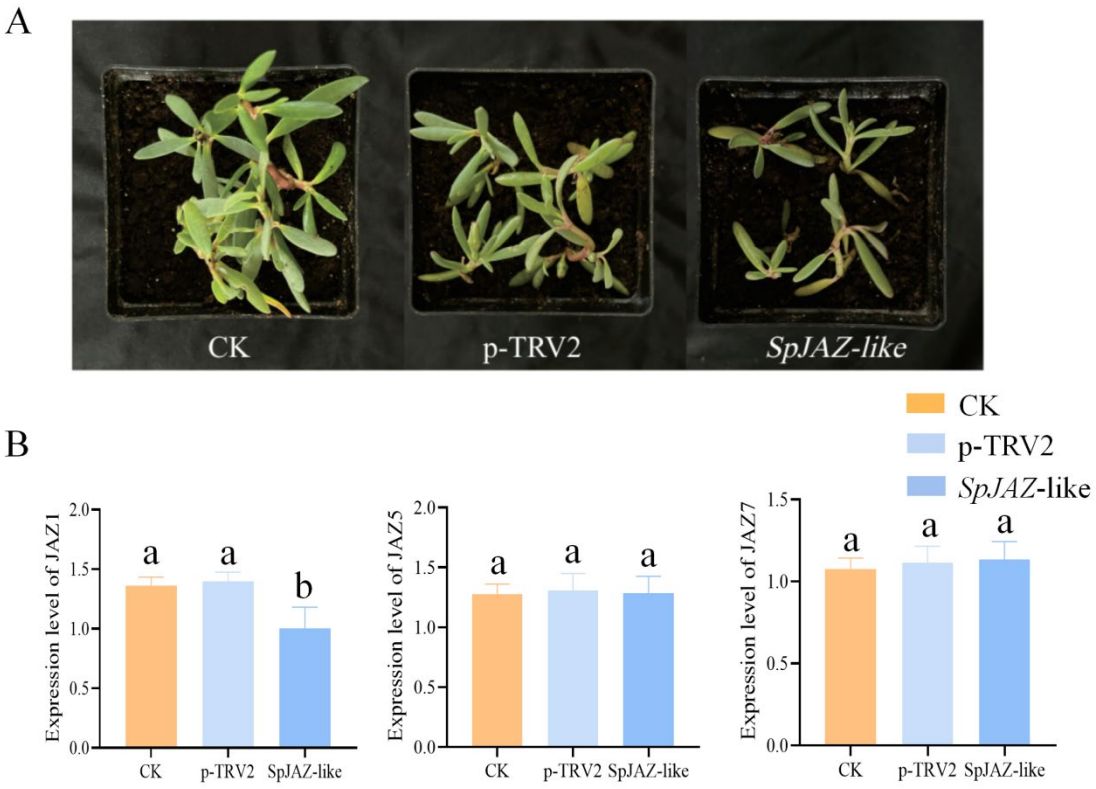


Figure S8. Virus-induced gene silencing of SpJAZ-like gene. A. CK: Leaf phenotype of control group; p-TRV2: Leaf phenotype of negative control group; SpJAZ-ike: Leaf phenotype after infection with recombinant virus vector SpTRV2-JAZ-ike; B. Relative expression of *SpJAZ1*, *SpJAZ5* and *SpJAZ7*. Different lowercase letters of a, b and c indicate significant differences at $p < 0.05$ among different treatments.