

Figure S1. Inflorescence phenotype of *jointless* (*j*) mutants in different genetic backgrounds

Inflorescences of wild type and *j* mutants in (A, B) Ailsa Craig (AC), (C, D) Gardener (GRD), (E, F) Fireball (FB) and (G, H) Heinz (Hz) accessions. The composition of > 15 inflorescences in each genotype is shown. Each line represents a single inflorescence and each box represents a flower (white) or a leaf (gray). X-axis shows the position along the proximal-distal axis of the inflorescences; Y-axis is the stacking of the inflorescences that were characterized. Black dots indicate that flower initiation was not finished.

All plants were in the same growth chamber in 16-h long days, 300 $\mu\text{E m}^{-2} \text{s}^{-1}$ light.

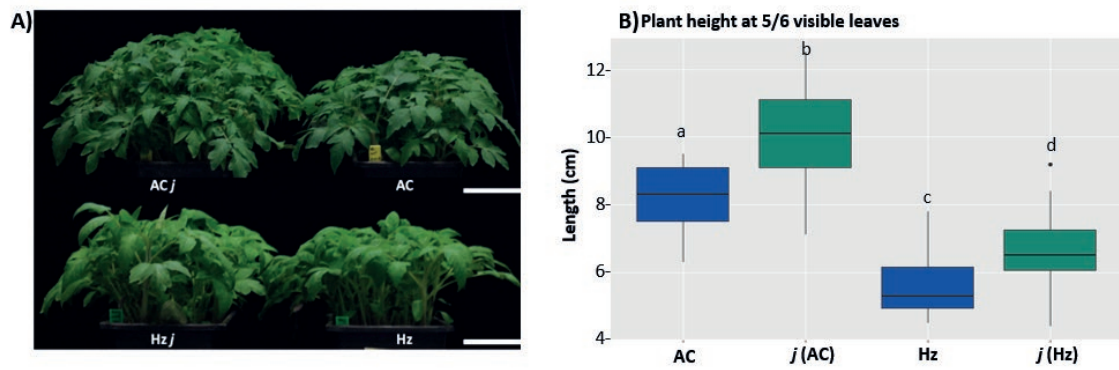


Figure S2. Shoot phenotype of *jointless* (*j*) mutants in different genetic backgrounds.

(A) Pictures of *j* mutants in Ailsa Craig (AC) and Heinz (Hz) backgrounds, compared to AC and Hz accessions. Plants are at the 5-6 visible leaf stage and the increased plant height of the mutants is already visible. Scale bars = 5 cm.

(B) Plant height measured as the addition of the first four internodes. Measurements were done on fifteen plants per genotype. Error bars represent standard deviation. Means with different letters are statistically different (Tukey-test, $p < 0.05$).

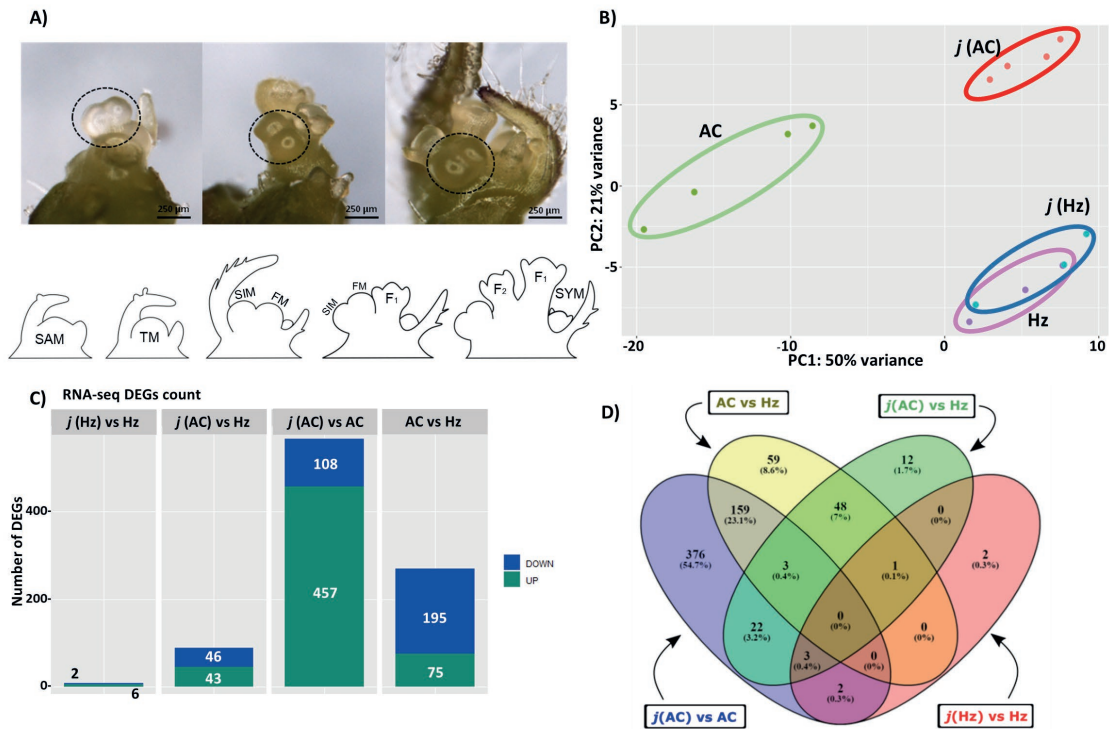


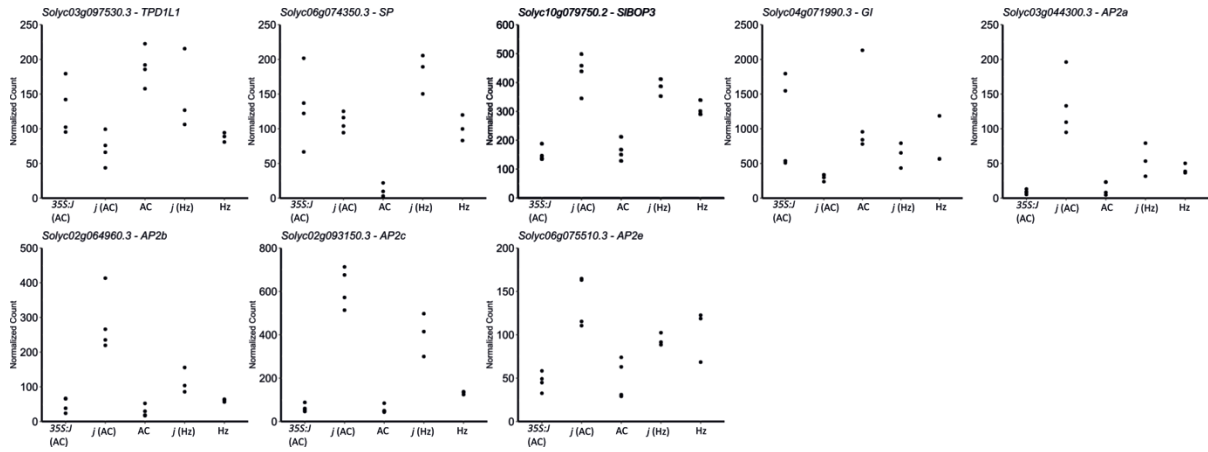
Figure S3. RNA-seq analysis of *jointless* (*j*) mutant inflorescence meristems

(A) Pictures and schematic representation of young inflorescences. Circles show the two meristems that were harvested, which were the last SIM and FM. F, Flower; FM, Floral Meristem; SAM, Shoot Apical Meristem; SIM, Sympodial Inflorescence Meristem; SYM, Sympodial shoot Meristem; TM, Transitional Meristem. (B) PCA showing the distribution and clustering of RNA-seq samples. (C) Number of Differentially Expressed Genes (DEGs) in *j* mutants in Ailsa Craig (AC) and Heinz (Hz) backgrounds. Genes were considered as DEGs when $|\text{Log}_2\text{FoldChange}| > 0.5$ or < -0.5 and the adjusted p-value after False Discovery Rate (FDR) was < 0.05 . (D) Venn diagram of DEGs between *j*(AC), *j*(Hz) and their genetic backgrounds.

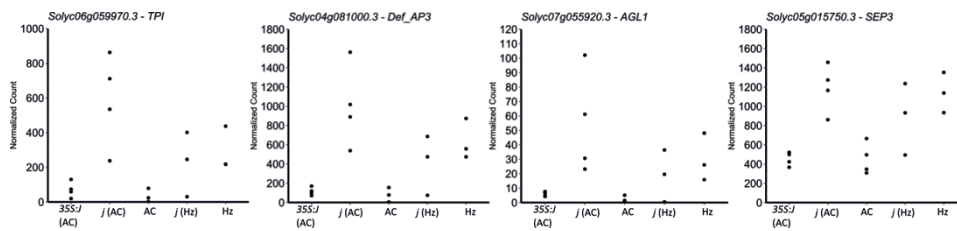
Figure S4. Expression (as DESeq2 normalized read counts) of differentially expressed genes from Figure 3.

Flowering and Transcription Factors

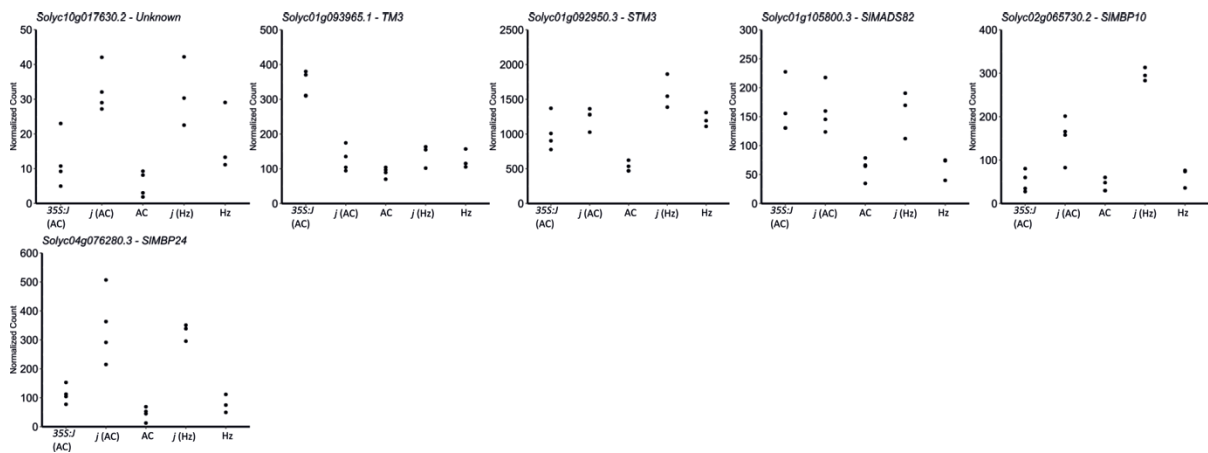
Flowering



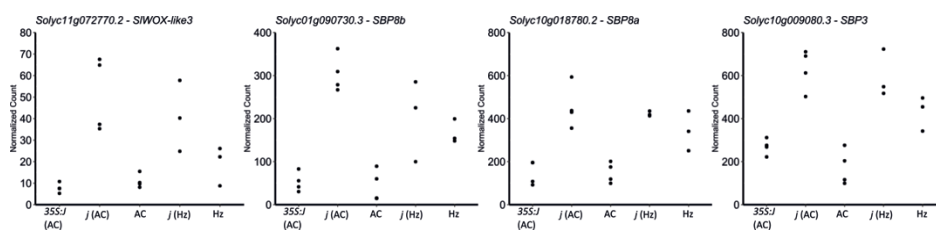
BCDE model



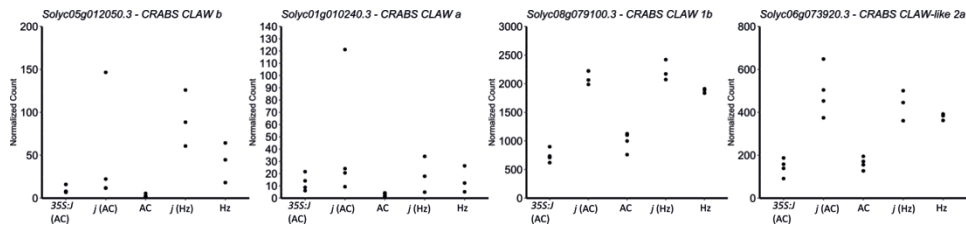
MADS box



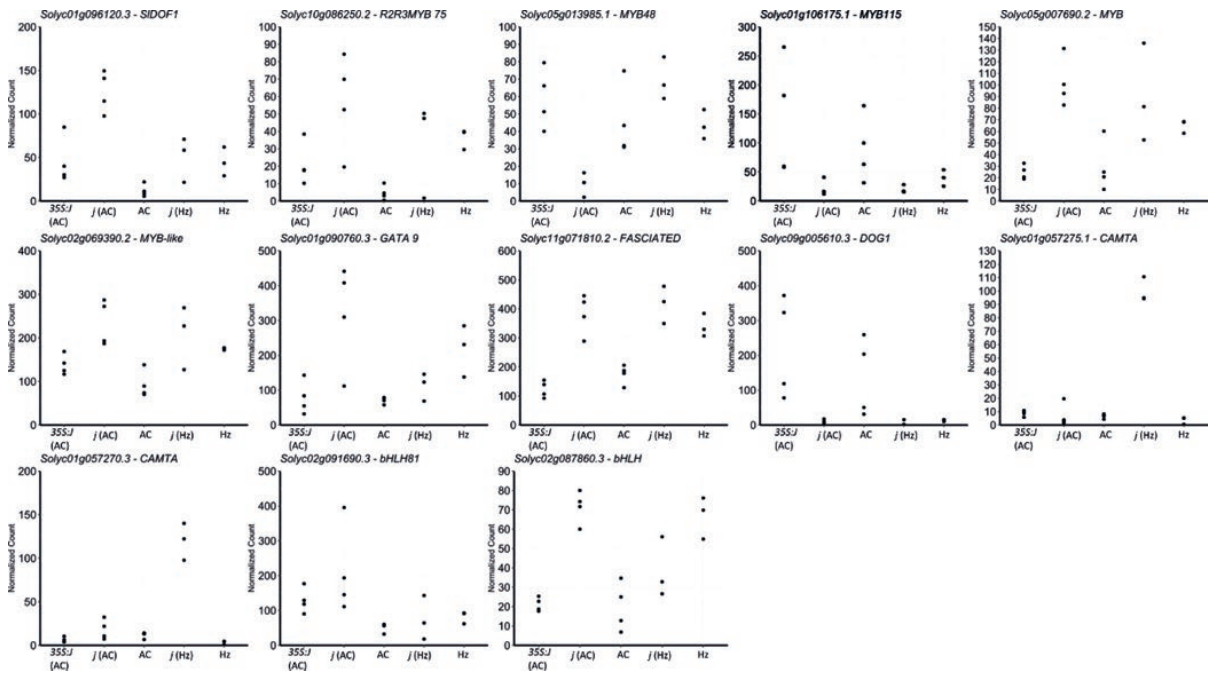
SPLs



CRABS CLAWS

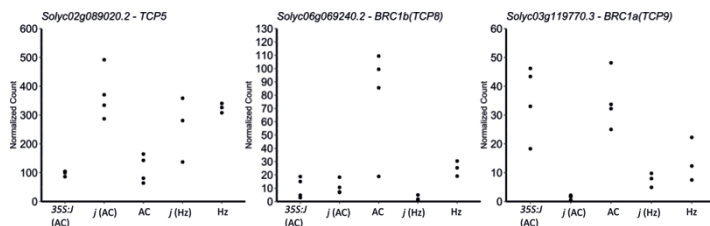


Other families

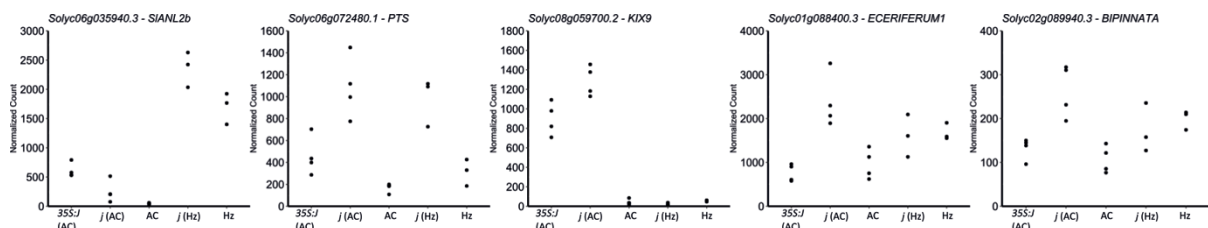


Branching and Leaf Growth

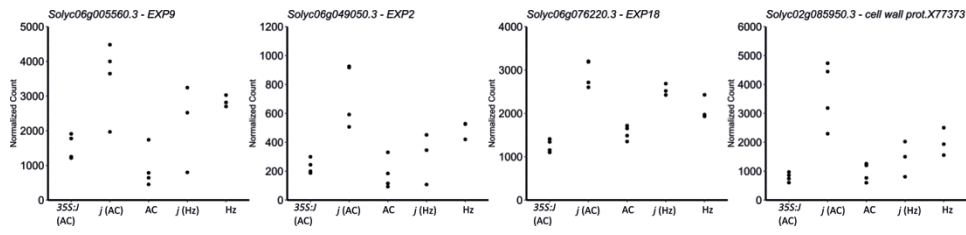
TCPs



Leaf polarity and growth

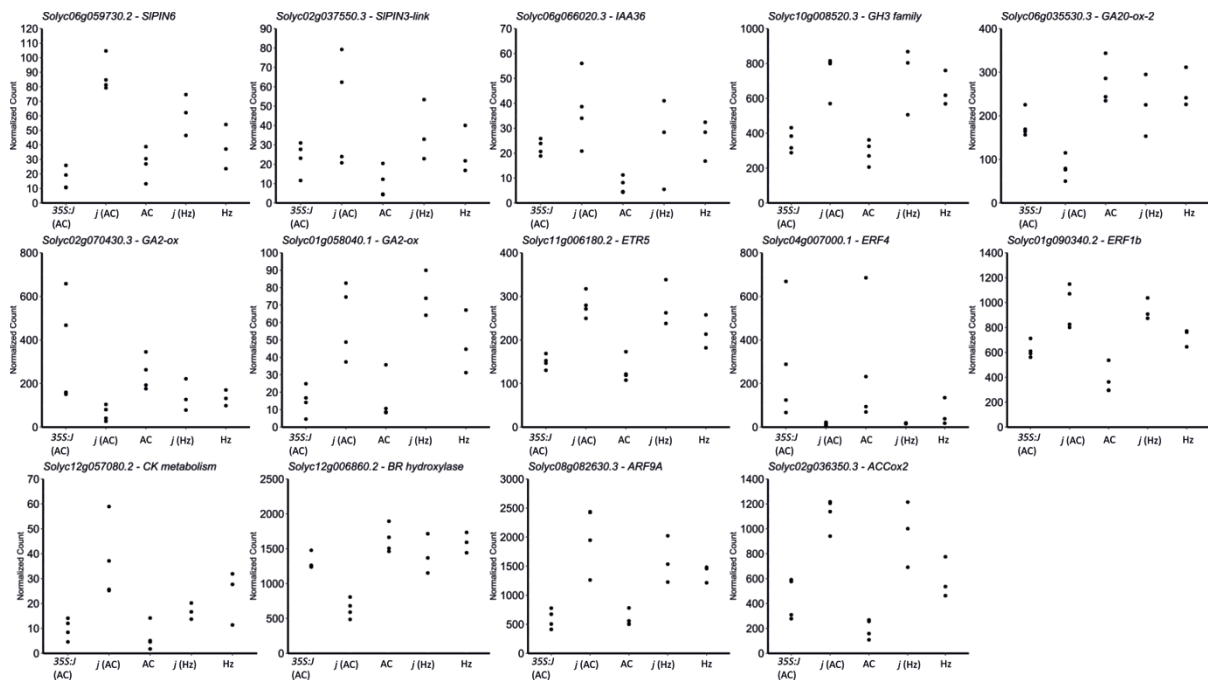


Expansins and Cell Wall related

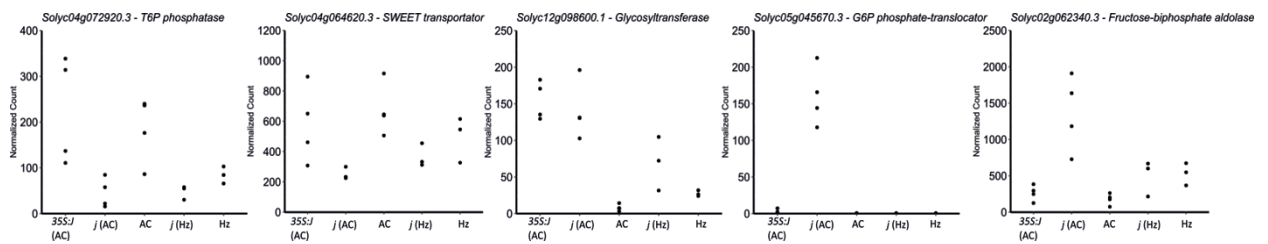


Hormone and Sugar Signaling

Hormone

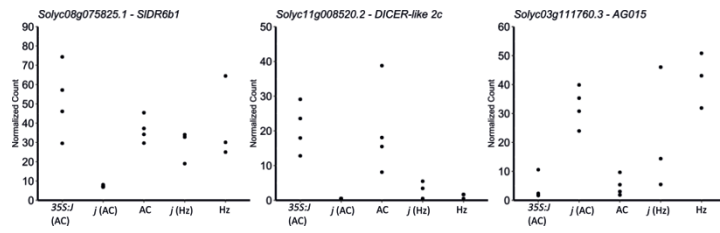


Sugar

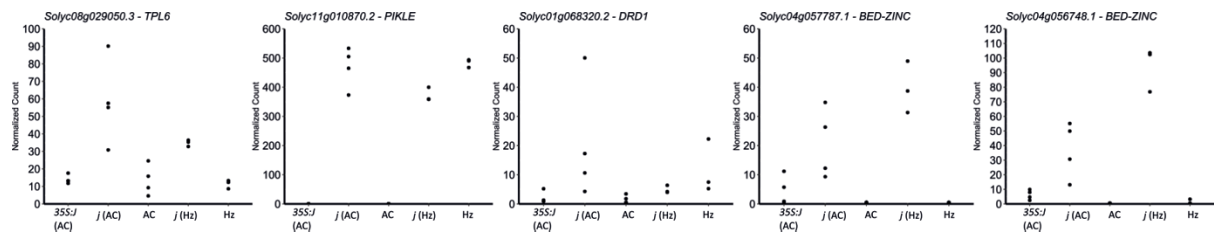


Small RNA Machinery & Chromatin Remodeling

Small RNA



Chromatin modelers/transcription



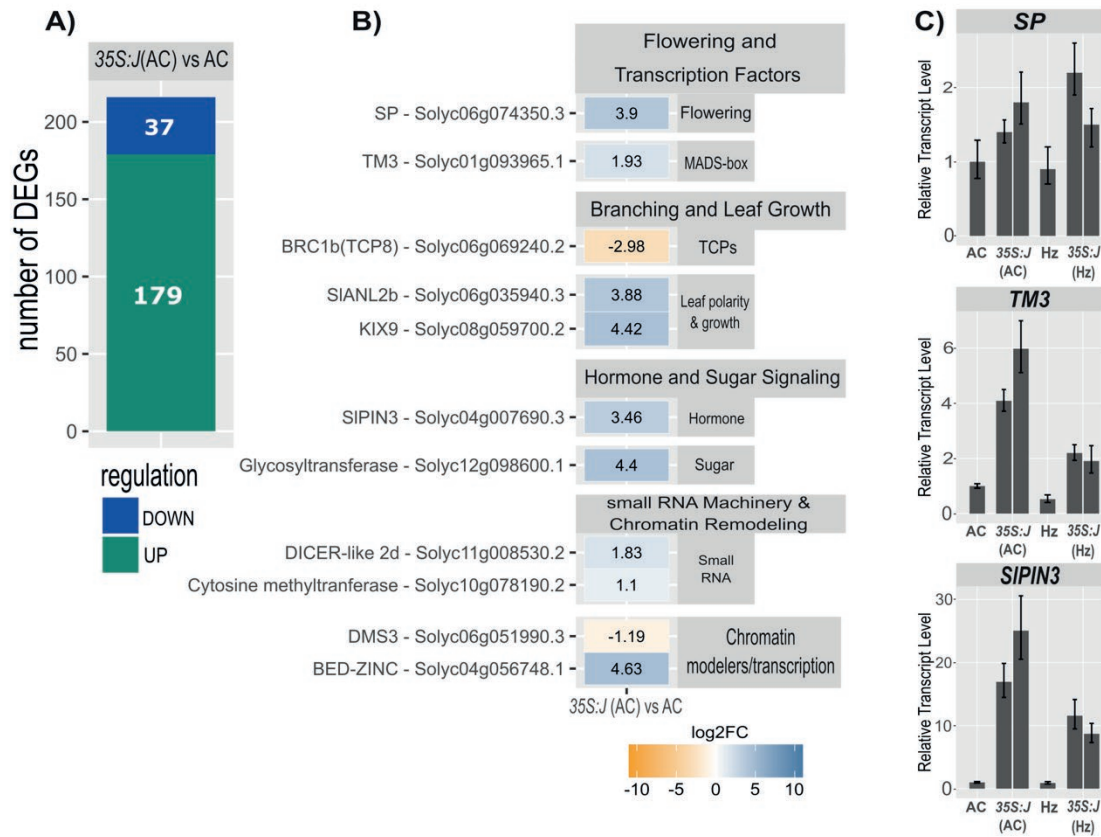


Figure S5. Transcriptomic analysis of inflorescence meristems in 35S:J (AC) plants

(A) Number of Differentially Expressed Genes (DEGs) in 35S:J (AC) inflorescence meristems as compared to AC meristems. (B) HeatMap of DEGs and their functional classification. Numbers and colors represent the log₂FC of the DEG. Grey shows non-significant differences while orange-blue color chart shows DEGs with log₂FC > 0.5 (blue) or < -0.5 (orange) and a p_{adj} < 0.05. (C) RT-qPCR validation of differential expression of three DEGs in independent biological replicates. As a validation of the RNA-seq, only one sample was used for each genotype except for the over-expressors where two samples were used. Error bars represent standard deviation on technical replicates.

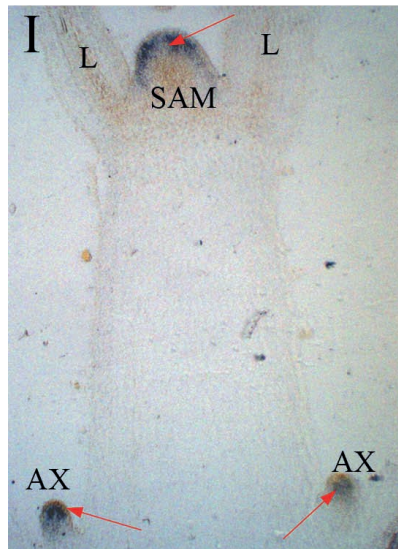


Figure S6. Expression of *JOINTLESS* (*J*) in the shoot apical meristem (SAM) and axillary buds of vegetative tomato plant (Ailsa Craig accession).

The red arrows point to the expression zones. AX, axillary bud; L, leaf; SAM, shoot apical meristem.

Image extracted with permission from Thouet (2011). Experimental procedure described in Thouet *et al.* (2012).

References

- Thouet J. 2011.** Contribution à l'étude du contrôle génétique de la croissance sympodiale et de l'architecture inflorescentielle chez la tomate. PhD thesis, University of Liège.
- Thouet J, Quinet M, Lutts S, Kinet JM, Périlleux C. 2012.** Repression of floral meristem fate is crucial in shaping tomato inflorescence. *PLoS One* 7: e31096.

Table S1: List of DEGs identified by RNA-seq of inflorescence meristems of *jointless (j)* mutant in Ailsa Craig (AC) background, and which are part of the 288 meristem stage-anchor genes identified and classified by Meir et al. (2021).

- Class I: vegetative meristems;
- Classes II and III: early transition stages (meristem doming);
- Class IV: late transition stage (“first signs of bifurcation”, i.e. initiation of first sympodial inflorescence meristem), characterized by the up-regulation of structural and enzymatic factors;
- Class V: flower initiation phase

gene_ID	class	gene_name	gene_annotation	in <i>j</i> (AC)
Solyc02g093150	I	AP2c	Solyc02g093150_YE_Fals_direct_target_APETALA2c	UP
Solyc02g064960	I	AP2	Solyc02g064960	UP
Solyc08g014130	I	NA	Solyc08g014130_SG_Isopropylmalate_synthase	UP
Solyc03g120930	I	UNC03-2	Solyc03g120930_SG_Avr9/Cf-9_rapidly	UP
Solyc10g085950	I	NA	Solyc10g085950_SG_aluminum_sensitive	UP
Solyc02g090540	I	NA	Solyc02g090540_SG_NAD(P)-binding_Rossmann-fold	UP
Solyc08g082630	I	ARF9	Solyc08g082630_SG_Auxin_Response	UP
Solyc12g009050	I	NA	Solyc12g009050_SG_Nuclear_transcription	UP
Solyc04g080130	I	NA	Solyc04g080130_SG_Zinc_finger	UP
Solyc01g096040	I	NA	Solyc01g096040_SG_Eukaryotic_aspartyl	UP
Solyc01g111600	I	NA	Solyc01g111600_SG_Heavy_metal	UP
Solyc11g016970	I	MATE45	Solyc11g016970_SG_Protein_DETOXIFICATION	DOWN
Solyc06g054070	III	NA	Solyc06g054070_SG_Lipid_transfer	DOWN
Solyc08g066880	IV	PSP	Solyc08g066880_SG_Bark_storage	UP
Solyc12g010030	IV	LAP1	Solyc12g010030_SG_Leucine_aminopeptidase	UP
Solyc07g064600	IV	NA	Solyc07g064600_SG_inducible_plastid-lipid	UP
Solyc12g010020	IV	LAP2	Solyc12g010020_SG_Leucine_aminopeptidase	UP
Solyc07g006570	IV	RNS3	Solyc07g006570_SG_Ribonuclease	UP
Solyc05g005150	IV	NA	Solyc05g005150_SG_Kelch_repeat-containing	UP
Solyc02g093180	IV	HAT2	Solyc02g093180_SG_HXXXD-type_acyl-transferase	UP
Solyc01g073640	IV	SDR5-173	Solyc01g073640_SG_alcohol_dehydrogenase-3,Pfam:PF13561	UP
Solyc05g005920	IV	NA	Solyc05g005920_SG_Major_facilitator	UP
Solyc07g006380	IV	LCR	Solyc07g006380_SG_Defensin-like_protein	UP
Solyc08g074683	IV	NA	Solyc08g074683_SG_polyphenol_oxidase	UP
Solyc08g074630	IV	PPO	Solyc08g074630_SG_polyphenol_oxidase	UP
Solyc09g061860	IV	NA	Solyc09g061860_SG_UDP-glucose:sterol_3-O-glucosyltransferase	UP
Solyc08g014000	IV	LOX1	Solyc08g014000_SG_lipoxygenase_A	DOWN
Solyc12g006860	IV	CYP734A1	Solyc12g006860_SG_brassinosteroid_hydroxylase	DOWN
Solyc04g074770	V	NA	Solyc04g074770	UP
Solyc05g015750	V	SEP3	Solyc05g015750_YE_SEP_TM5/SEP3	UP

Reference

Meir Z, Aviezer I, Chongloi GL, Ben-Kiki O, Bronstein R, Mukamel Z, Keren-Shaul H, Jaitin D, Tal L, Shalev-Schlosser G, Harel TH, Tanay A, Eshed Y. 2021. Dissection of floral transition by single-meristem transcriptomes at high temporal resolution. *Nat Plants* 7: 800-813.

Table S2: Primers used in this study**Primers used for RT-qPCR**

Gene name		Direction	Sequence 5'-3'
<i>UBI</i>	Solyc01g056940	FOR	CGTGGTGGTGCTAAGAAGAG
		REV	ACGAAGCCTCTGAACCTTTC
<i>AP2c</i>	Solyc02g093150	FOR	GCAAGGAAGTCAAGAATTGGGG
		REV	AATTAAGGCAGATTGCTTCTCAGG
<i>BL</i>	Solyc11g069030	FOR	TCCTCAAAAAGCAGGACTAAGG
		REV	TCTTCATCATCAGAAAAATCACCAT
<i>BRC1a</i>	Solyc03g119770	FOR	TGCTGATTTCGGACAACTAGA
		REV	GTCCTACACCAGCACTACCACT
<i>BRC1b</i>	Solyc06g069240	FOR	CTGACAGCTGCACCGAGATT
		REV	TTTCTTTTCGCCTCGGCCTT
<i>FA</i>	Solyc03g118160	FOR	AATGCCCTACGAAGGTGACG
		REV	GGCAGTGAAGTCATAGCAA
<i>GA20ox2</i>	Solyc06g035530	FOR	AGGTGACACATTTATGGCGCTT
		REV	GCAAGAGATTTTCTAGGTGTTTTGT
<i>J</i>	Solyc11g010570	FOR	CTGTGATGCTGATGTTGCTCTC
		REV	TGCAAATCACGCCTCTCAAG
<i>MC</i>	Solyc05g056620	FOR	CCTCAAAGGAACCACAAGC
		REV	GCTGTTGTTCCAAGTTTTCG
<i>MADSa - MBP10</i>	Solyc02g065730	FOR	GGACGCCTTTAATCTGCGTG
		REV	CTCGTGCATCAGTTGGTTCTTC
<i>SIMADS82</i>	Solyc01g105800	FOR	AGAATCGGGAGTTAAGGCAACT
		REV	ACGACTTATTCCTCCCTCGAC
<i>SIMBP24</i>	Solyc04g076280	FOR	AAGCTGGTTTCAACCGTGTG
		REV	TCAGCTCAGCACCTTTCTT
<i>SIPIN3</i>	Solyc06g059730	FOR	TGGAATGTGGGGATGCCAAG
		REV	TGCCATGAACAACCCTAAACTG
<i>SIPIN6</i>	Solyc04g007690	FOR	GTGCCAACGAACAGTCTTGT
		REV	ACCAAAATCTTGAGAAACGTCTTTA
<i>SP</i>	Solyc06g074350	FOR	GTGCACCAGTGTCCAGAGAT
		REV	CGGCAGTTTCCCTCTGACAA
<i>STM3 (SOC1-like)</i>	Solyc01g092950	FOR	AAGCAATTGGAGCAGAGTGTC
		REV	CTGTAAGGGCTCTCTCCCTTT
<i>TM3 (SOC1-like)</i>	Solyc01g093965.1	FOR	TTGCAGCACGCAGGAGATAA
		REV	TGCCTCATGCTGCATATACTGT
<i>WUS</i>	Solyc02g083950	FOR	TGGAGAAGAGCTTTAGGGAGTG
		REV	GATCAACACCAACCCATGTC

Primers used for riboprobes synthesis

Probe	Sense		
<i>SP</i>	antisense	FOR	ATGGCTTCCAAAATGTGTGA
		REV	<u>TGTAATACGACTCACTATAGGGCTCAACGCCTTCTAGCGG</u>

	sense	FOR	<u>TGTAATACGACTCACTATAGGGCATGGCTTCCAAAATGTGTGA</u>
		REV	TCAACGCCTTCTAGCGG
<i>BRC1a</i>	antisense	FOR	CGGTGAACGATCTGGTTCA
		REV	<u>TGTAATACGACTCACTATAGGGCATTGTTCTTCCCTGCCCTT</u>
	sense	FOR	<u>TGTAATACGACTCACTATAGGGCCGGTGAACGATCTGGTTCA</u>
		REV	ATTGTTCTTCCCTGCCCTT
<i>BRC1b</i>	antisense	FOR	TGAAGAGCTTGTGCGCGCTAA
		REV	<u>TGTAATACGACTCACTATAGGGCTCGTAAGAGGTTCTAACACAGC</u>
	sense	FOR	<u>TGTAATACGACTCACTATAGGGCTGAAGAGCTTGTGCGCGCTAA</u>
		REV	TCGTAAGAGGTTCTAACACAGC
T7 promoter			<u>TGTAATACGACTCACTATAGGGC</u>

Primers used for cloning of *JOINTLESS* coding sequence in GateWay vectors

<i>J</i>	Nested PCR 1st set of primers	FOR	TCTGGTTTATTCTTTGTTCCCTCT
		REV	TAGCCACACCTTGCTTTTGA
	Nested PCR 2nd set of primers + adapters	FOR	GGGGACAAGTTTGTACAAAAAAGCAGGCTTCATGGCTAGAGAAAAAATTCAGAT
		REV	GGGGACCACTTTGTACAAGAAAGCTGGGTCTCAGCCTGAGTAAGGTAGCC

Primers used for 35S :*J* plant genotyping

35S Promoter		FOR	TCCTTCGCAAGACCCTTCCT
		REV	CAACACATGAGCGAAACCCT