Supplemental Data. David-Schwartz et al. (2009). *LYRATE* is a key regulator of leaflet initiation and lamina outgrowth in tomato.

Supplemental figure 1

AtJAG	(1)	1 NLS 50 MRHEENYLDLNNLPDDFSKDGNKOALEEGSSSGORKKKGSKEGKDESGKV
SIJAG	(1)	MSPERNPLDLNNLPHEEFCRDGKQVLEGGGYRKKKNGGKEDCGKV
		51 C2H2-type zinc finger domain 100
AtJAG	(51)	YECRFC SLKFCKSQALGGHMNRHRQERETET LNQARQLVYRNDT I TPPGI
SIJAG	(46)	YECRFCSLKFCKSQALGGHMNRHRQERETETLNRARQLVFNNDNIIPP
		101 proline-rich motif 150
AtJAG	(101)	SPFGY <mark>HH</mark> TTD <mark>P</mark> TIYRSVYSSPMIYP <mark>G</mark> SSSTNLVPQPPMPPPPPYPYSSN
SIJAG	(94)	<mark>HH</mark> LSCPPIPHGGGYHQSTNI <mark>G</mark> DPTLSYRPPPPPPPSL <mark>Y</mark> PTG
		151 200
AtJAG	(151)	QYSPHNHFNDYYLNPSFRGSRSISPSPNLPTTTTVDYMADSPVEPGYTCV
SIJAG	(135)	L <mark>FS</mark> GNPTQP <mark>P</mark> HQ <mark>P</mark> SYMYA
	:	250
AtJAG	(201)	GAPIGPTGFPIRGPSIVRAPLEPPQGRDGDASRQRLDHSLRFPINRFQDH
SIJAG	(162)	SP <mark>P</mark> RMV <mark>S</mark> FSSHQY <mark>PA</mark> QTNDYFLGHVLS <mark>E</mark> SNTHSTSTTNNFMGSSALGP <mark>DH</mark>
	2	1
AtJAG	(251)	H <mark>S</mark> L-
SIJAG	(212)	G <mark>S</mark> N-

Supplemental Figure 1. Protein alignment of JAG and SIJAG. Identical residues shaded in yellow and similar residues are shaded in green. A predicted EAR motif is shaded in light blue. A putative Nuclear Localization Sequence (NLS) is underlined. A C2H2-type zinc finger domain is shaded in pink and a proline-rich motif is shaded in gray. Dashes indicate gaps. Numbers on the left and right indicate amino acid position. The red arrowhead indicates the cysteine residue that is substituted to an arginine in the *lyr2* allele.



Supplemental figure 2. Southern blot analysis of *SlJAG* in tomato. Southern blot analysis of BspHI, SpeI and SwaI digests of DNA isolated from VF36 tomato cultivar. BspHI, SpeI cut outside of *SlJAG* sequence, while SwaI cuts in the middle of the gene. Band sizes of the DNA ladder indicated on the right and left are in Kb.



Supplemental figure 3. Function of *SlJAG* in *A. thaliana* transgenic plants. (A) and (B) Wild-type and *jag-3* young plants, respectively. (C) to (L) Phenotypes of 35S:SLJAG in jag-3 background. 35S:LYR displayed similar phenotypes in jag-2, jag-3 and wild-type which were similar to 35S: JAG plants. Many of the plants had retarded overall development compared to wild-type, jag-2 or jag-3. (C) Fused first true leaves with no meristem (arrowhead). (D) Fused tri-cotyledons (arrowhead) and fused first leaves. (E) Ectopic blade on petiole growth (bracket) and a divided leaf (arrowhead). Ectopic blade on petiole phenotype resembled the *blade on petiole* (*bop*) and *lettuce* (*let*) mutant phenotypes (van der Graaff et al., 2000; Hepworth et al., 2005; Norberg et al., 2005). (F) Folded leaf with extra growth along the margin. (G) A leaf fused to a stem with ectopic leaves growing on the joint (arrowheads). (H) SEM image of ectopic leaves (arrowheads) on the leaf-stem joint showing trichomes. (I) Leaf-like structure forming on the adaxial side of a pedicel of a wild-type looking flower in a T2 transgenic line. All plants that produced flowers showed suppression of the jag flower phenotype. (J) Ectopic tissue forming on the adaxial side of a pedicel. Bract formation was not evident. (K) SEM image of (J) showing stomata (arrowheads) but no trichome development. The developing tissue resembles sepal epidermal cells (Bowman, 1993). (L) A petiole of a rosette leaf with ectopic growth of leaves (arrowhead), resembling JAG gain-of-function allele *jag-5D* (Dinneny et al., 2004). hyp, hypocotyl; cot, cotyledons; L, leaves; S, stem. Bars: 1 cm in (A), (B) and (E), 1 mm in (C), (D), (F), (G) and (J), 100µ m in (H), 500 μ m in (I), 30 μ m in (K), 2 mm in (L).



Supplemental figure 4. Southern blot analysis revealing altered *SlJAG* gene in *lyr* and *lyr3* tomato mutants. Genomic DNA of VF36 (first WT from left), wild-type (second WT from left), *lyr*, M82 and *lyr3* was digested with SwaI and hybridized with *SlJAG* probe. White arrows indicate three bands of *lyr3* allele. The two lanes on the right are the DNA ladder. Numbers on the left indicate band size in kb.



Supplemental figure 5. *lyrate* flower phenotype. (A) Floral developmental series in wild-type (upper row) and *lyr* (lower row). Mature flowers of wild-type (B) and *lyr* (C). *lyr* flowers open prematurely and have reflexed petals. (D) and (E) Stamen of wild-type (D) and *lyr* (E) with the two outer whorls peeled away. Wild-type tomato stamens are fused to form a cone surrounding the carpel, but *lyr* anthers are narrow and unfused curving inwardly towards the carpel. (F) Carpel of wild-type (left) and *lyr* (right). *lyr* carpel are composed of a thickened style with unfused carpel sand an enlarged ovary containing disorganized ovules. (G) and (H) Longitudinal section of ovaries of wild-type (G) and *lyr* (H). Bars: 1 cm in (A), 0.5 cm in (B) and (C), 3 mm in (D) to (F) and 1 mm in (G) and (H).



Suplemental Figure 6. Representative examples of wild type (A) and *lyr* (B) leaves used for area measurements and cell counts. Laminar tissue cell density was higher in wild type (C) when compared to *lyr* (D). Quantitation of terminal leaflet area (E) (n=9 for wild type and n=10 for *lyr*) and cell density (F) (n=12 for wild type and n=13 for *lyr*) in wild type and *lyr* leaves. Error bars in (E-F) indicate standard error. Scale bars are 2 cm (A-B) and 2.5 μ m (C-D).



Supplemental figure 7. *LYR* expression pattern in an apex of wild-type tomato. (A) to (I) *in situ* hybridization on serial sections of a wild-type tomato apex showing expression in distal tissue of the leaf primordium (LP, [B] to [E]) but not in the shoot apical meristem (SAM [G] to [I]). Arrows in (A) and (B) indicate leaflet initiation site. Bars = $250 \mu m$.



Supplemental figure 8. Additional *35S:LYRATE* phenotypes. (A) Bifurcated leaf. (B) WT flower. (C) Enlarged *lyr* flower. Bars are equivalent to 1 cm.

Supplemental Table 1:

Transcript	Forward primer	Reverse Primer
GAPDH	GGTGCTGACTTCGTTGTTG	GCTCTGGCTTGTATTCATTCTC
SIJAG	TGAACCGCCACCGTCAAGAG	CATGAGGAATTGGAGGACAACTAAGG
IAA4	TATGAAGACAAGGATGGTGATTG	ACCTTTAGCTTCAGATCCTTTG
IAA9	GCCTTCTGCTGTGAATGATGCCTC	TTCCGTCAACCTCTTCGTTATTCTTCG
LeT6	GGCTCATCCTCACTACCATCGTCTC	ATTCCACCACCACTACTACTACTGCTAC
TKN1	TGAAGGCCCTTTTCGTTTGGGT	CCTTGTGCTTAGGCCTATAAGGCTTG
PIN1	CTCAAGAAGAGACCAAGGCAACTG	AGAGACCAAGGACCAAGTTAGGC
IAA3	GTTAGCATGGATGGAGCACCTTATTTG	CCTTCTCTTTCTGAATACACTCCAATAG

Supplemental Table 1 Primers used in this study

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