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**Table S1** The profiles of RNA deep sequencing for VF36, *Pts*, CR, *tf2*, AC, *entire*

Sample	Raw Read Number	Raw Q30 rate	Trimmed Read Number	Useful read%	Clean Reads	Uniquely Mapped%
VF36-1	47429216	92.5	41989416	88.53	41989416	95.04
VF36-2	38867902	91.9	34598214	89.01	34598214	94.78
VF36-3	41163226	92.28	36463972	88.58	36463972	95.14
Pts-1	39541314	91.88	34797720	88	37954732	95.77
Pts-2	43494104	91.98	37954732	87.62	38875492	94.01
Pts-3	44665608	92.14	38875492	87.03	34797720	93.84
CR-1	38674246	92.29	35420234	91.58	35394168	94.84
CR-2	45094878	92.63	40695638	90.24	35420234	94.16
CR-3	39455908	91.87	35394168	89.7	40695638	95.19
tf2-1	44666134	92.56	40306878	90.24	40306878	95.27
tf2-2	39755182	92.19	33382472	83.97	33382472	95.84
tf2-3	38234284	91.78	34266664	89.62	34266664	95.60
AC-1	46930312	92.62	42060712	89.62	42060712	95.66
AC-2	41162622	91.96	36089572	87.67	36089572	95.70
AC-3	45496202	92.81	40427608	88.85	40427608	96.26
entire-1	47962200	92.13	42276226	88.14	42276226	97.05
entire-2	46075944	92.63	40971144	88.92	40971144	97.23
entire-3	46207452	92.56	40776746	88.24	40776746	96.16

**Table S2** Primers used in this study.

Gene	Purpose	sequence (5'-3')
<i>SIGA2ox7</i>	VIGS	Forward (KpnI) CCTCCATGGGGATCCGGTACCATGTACTTAG CCACCTCCAC TTCTC Reverse (Infusion) GAGACGCATGAGCTCGGTACCGCATTCTTCT CTCTCAAATT CTCTT
<i>SIGA20ox</i>	VIGS	Forward (KpnI) CCTCCATGGGGATCCGGTACCAGCTGCATAACAATTGTCTAT Reverse (Infusion) GAGACGCATGAGCTCGGTACCAAGTTTAAATAGTCAGAGCAA
<i>SIIAA-aah</i>	VIGS	Forward (KpnI) CCTCCATGGGGATCCGGTACCATGGGTACTA AGAAAGTTTT GGTCT Reverse (Infusio) GAGACGCATGAGCTCGGTACCAACGACACCGGTTTTAGCCA CCGGC
<i>SlbHLH079</i>	VIGS	Forward (KpnI) CCTCCATGGGGATCCGGTACCATGGAGCAGCAGTACTGTTCTAACA Reverse (Infusion) GAGACGCATGAGCTCGGTACCAGTGTTACTG CTTGAATTTG AATTC
<i>SIWRKY44</i>	VIGS	Forward (KpnI) CCTCCATGGGGATCCGGTACCATGGCGATTACTGCCATAAGACCA Reverse (Infusion) GAGACGCATGAGCTCGGTACCATGATGTTGTTTAGCTTCTTT
<i>SIWRKY76</i>	VIGS	Forward (KpnI) CCTCCATGGGGATCCGGTACCGCTAAGGAAAGATAGAGCAATGG Reverse (Infusion) GAGACGCATGAGCTCGGTACCTCTCCCTAAGCTCAAAGAAACA
Actin	reference	Forward TGTCCCTATTTACGAGGGTTATGC Reverse AGTTAAATCACGACCAGCAAGAT
<i>SIGA2ox7</i>	RT-qPCR	Forward CTTGTACACAGCAGCCAAACC Reverse CCCCATTCTTGTGAAGCTTGTG
<i>SIGA20ox</i>	RT-qPCR	Forward GCAAGCTTGGAGCAATGACA Reverse CCAGAGGTAGGTGGAGCCT
<i>SIIAA-aah</i>	RT-qPCR	Forward GGGCGCGAAGAAGAATGTTT Reverse AACGACACCGGTTTTAGCCA
<i>SlbHLH079</i>	RT-qPCR	Forward TCAACTTGAAGAAGCCGCGA

<i>SlWRKY44</i>	RT-qPCR	Reverse GTGGCAATGGCAATGTATTTTCC
		Forward AGAGCACAGAAGAGGTCCCA
<i>SlWRKY76</i>	RT-qPCR	Reverse GACAAGTTGCGCTTTGGAGG
		Forward TGATGTAAACGCCAGGTGCT
		Reverse TCAGTGGGAACCAAAGTGGG

**Table S3** RNA-Seq analysis of DEGs in *Pts*/VF36.

Gene ID( <i>Pts</i> /VF36)	TF	Description	Regulation
Solyc05g052040.1	ERF	PREDICTED:ethylene-responsive transcription factor 5 [Solanum lycopersicum]	Down Regulation
Solyc10g084380.1	WRKY	PREDICTED:WRKY transcription factor 44 [Solanum lycopersicum]	Down Regulation
Solyc05g007110.2	WRKY	PREDICTED: probable WRKY transcription factor 72 isoform X1 [Solanum lycopersicum]	Up Regulation
Solyc10g009290.1	bHLH	PREDICTED: transcription factor MYC3-like [Solanum lycopersicum]	Up Regulation
Solyc04g006980.1	TCP	TCP transcription factor 22 [Solanum lycopersicum]	Down Regulation
Solyc06g065190.1	TCP	TCP transcription factor 13 [Solanum lycopersicum]	Down Regulation
Solyc06g075670.1	MYB	PREDICTED: transcription factor MYB48-like [Solanum pennellii]	Up Regulation
Solyc08g074860.1	bZIP	PREDICTED: stress response protein NST1-like [Solanum lycopersicum]	Up Regulation
Solyc06g066540.1	ERF	PREDICTED: dehydration-responsive element-binding protein 3-like [Solanum lycopersicum]	Up Regulation
Solyc02g030460.2	Trihelix	PREDICTED: uncharacterized protein LOC101256819 [Solanum lycopersicum]	Down Regulation
Solyc02g077590.1	HD-ZIP	PREDICTED: homeobox-leucine zipper protein ATHB-52 [Solanum lycopersicum]	Up Regulation
Solyc02g092570.1	GRAS	PREDICTED: scarecrow-like protein 32 [Solanum lycopersicum]	Down Regulation

**Table S4** RNA-Seq analysis of DEGs in *tf2/CR*.

Gene ID( <i>tf2/CR</i> )	TF	Description	Regulation
Solyc10g052470.1	MYB	PREDICTED: protein RADIALIS-like 1 [Solanum pennellii]	Down Regulation
Solyc10g078610.1	ERF	PREDICTED: ethylene-responsive transcription factor RAP2-11-like [Solanum lycopersicum]	Up Regulation
Solyc10g084380.1	WRKY	PREDICTED: WRKY transcription factor 44 [Solanum lycopersicum]	Down Regulation
Solyc11g020670.1	TCP	TCP transcription factor 12 [Solanum lycopersicum]	Up Regulation
Solyc10g086380.1	GRAS	PREDICTED: DELLA protein GAI-like [Solanum lycopersicum]	Up Regulation
Solyc05g051200.1	ERF	ethylene-responsive factor 1 [Solanum lycopersicum]	Up Regulation
Solyc05g007110.2	WRKY	PREDICTED: probable WRKY transcription factor 72 isoform X1 [Solanum lycopersicum]	Down Regulation
Solyc08g014030.1	GRAS	PREDICTED: protein SHORT-ROOT-like [Solanum lycopersicum]	Up Regulation
Solyc03g062750.1	NAC	PREDICTED: NAC transcription factor 56-like [Solanum pennellii]	Down Regulation
Solyc01g109690.1	MYB	PREDICTED: protein RADIALIS-like 4 [Solanum lycopersicum]	Down Regulation
Solyc06g065440.1	C2H2	protein SENSITIVE TO PROTON RHIZOTOXICITY 1-like [Solanum lycopersicum]	Up Regulation
Solyc10g080960.1	G2-like	PREDICTED: transcription factor PCL1-like [Solanum lycopersicum]	Down Regulation
Solyc05g052040.1	ERF	ethylene-responsive transcription factor 5 [Solanum lycopersicum]	Down Regulation
Solyc05g054650.1	C2H2	PREDICTED: zinc finger protein ZAT11-like [Solanum lycopersicum]	Up Regulation

**Table S5** RNA-Seq analysis of DEGs in *e/AC*.

Gene ID( <i>entire/AC</i> )	TF	Description	Regulation
Solyc10g084380.1	WRKY	PREDICTED: WRKY transcription factor 44 [Solanum lycopersicum]	Down Regulation
Solyc10g054010.1	bZIP	PREDICTED: ocs element-binding factor 1-like [Nicotiana sylvestris]	Up Regulation
Solyc01g109690.1	MYB	PREDICTED: protein RADIALIS-like 4 [Solanum lycopersicum]	Down Regulation
Solyc10g009290.1	bHLH	PREDICTED: transcription factor MYC3-like [Solanum lycopersicum]	Down Regulation
Solyc02g092570.1	GRAS	PREDICTED: scarecrow-like protein 32 [Solanum lycopersicum]	Down Regulation
Solyc04g006980.1	TCP	TCP transcription factor 22 [Solanum lycopersicum]	Down Regulation

**Table S6.** RNA-Seq analysis of DEGs in *Pts*/VF36 and *tf2*/CR.

Gene ID	<i>Pts</i> /VF36	Log <sub>2</sub> (FC)	<i>tf2</i> /CR	Log <sub>2</sub> (FC)	Description
Solyc05g006220.3	Upregulation	1.57	Downregulation	−1.95	IAA-amino acid hydrolase
Solyc02g078130.3	Upregulation	2.29	Downregulation	−2.44	<i>SibHLH079</i> is part of the 159 member basic helix-loop-helix gene family
Solyc06g083900.3	Upregulation	2.28	Downregulation	−6.30	<i>SIMYB13</i> is a member of <i>SIR2R3</i> MYB gene family
Solyc05g007110.2	Upregulation	4.49	Downregulation	−4.82	<i>SIWRKY76</i> is a member of WRKY transcription factor gene family
Solyc02g080120.3	Upregulation	2.46	Downregulation	−1.64	Gibberellin 2-beta-dioxygenase 7

**Table S7.** RNA-Seq analysis of DEGs in *Pts*/VF36 and *entire*/AC.

Gene ID	<i>Pts</i> /VF36	Log <sub>2</sub> (FC)	<i>tf2</i> /CR	Log <sub>2</sub> (FC)	Description
Solyc10g009290.1	Upregulation	1.54	Downregulation	−1.53	bHLH transcription factor <i>SlbHLH155</i>
Solyc01g094590.4	Downregulation	−1.55	Upregulation	1.05	Gibberellin 20-oxidase-like protein

**Table S8.** RNA-Seq analysis of DEGs in *tf2*/CR and *entire*/AC.

Gene ID	<i>tf2</i> /CR	Log <sub>2</sub> (FC)	<i>entire</i> /AC	Log <sub>2</sub> (FC)	Description
Solyc10g084380.1	Downregulation	−2.38	Downregulation	−3.51	<i>SlWRKY44</i> is a member of WRKY transcription factor gene family
Solyc01g105800.4	Downregulation	−2.38	Downregulation	−1.92	MADS box transcription factor



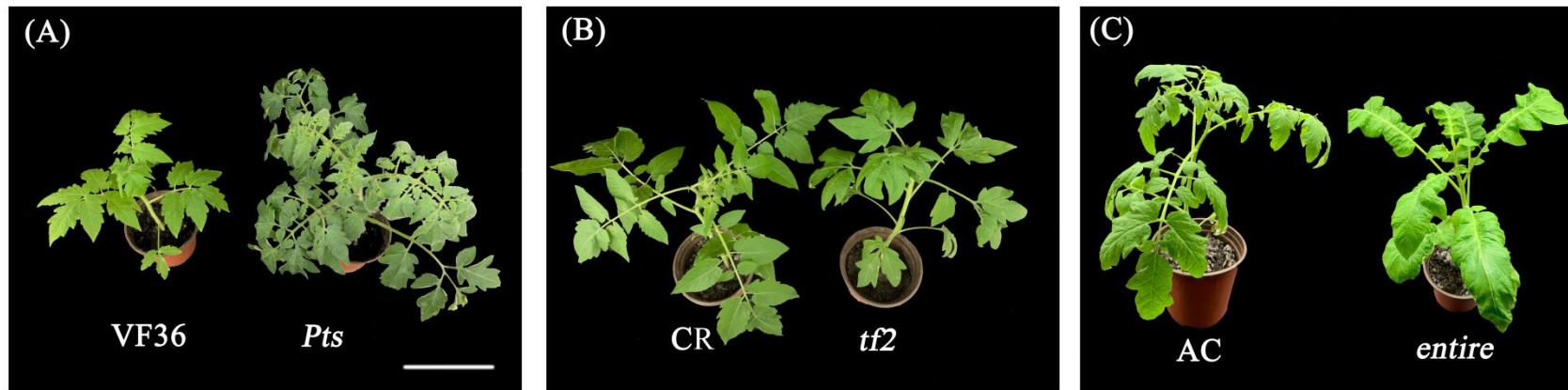


Figure S1. Morphological differences between mutant and wild-type plants. (A–C) 45-d-old plants. Bars=500  $\mu$ m in (A–F).

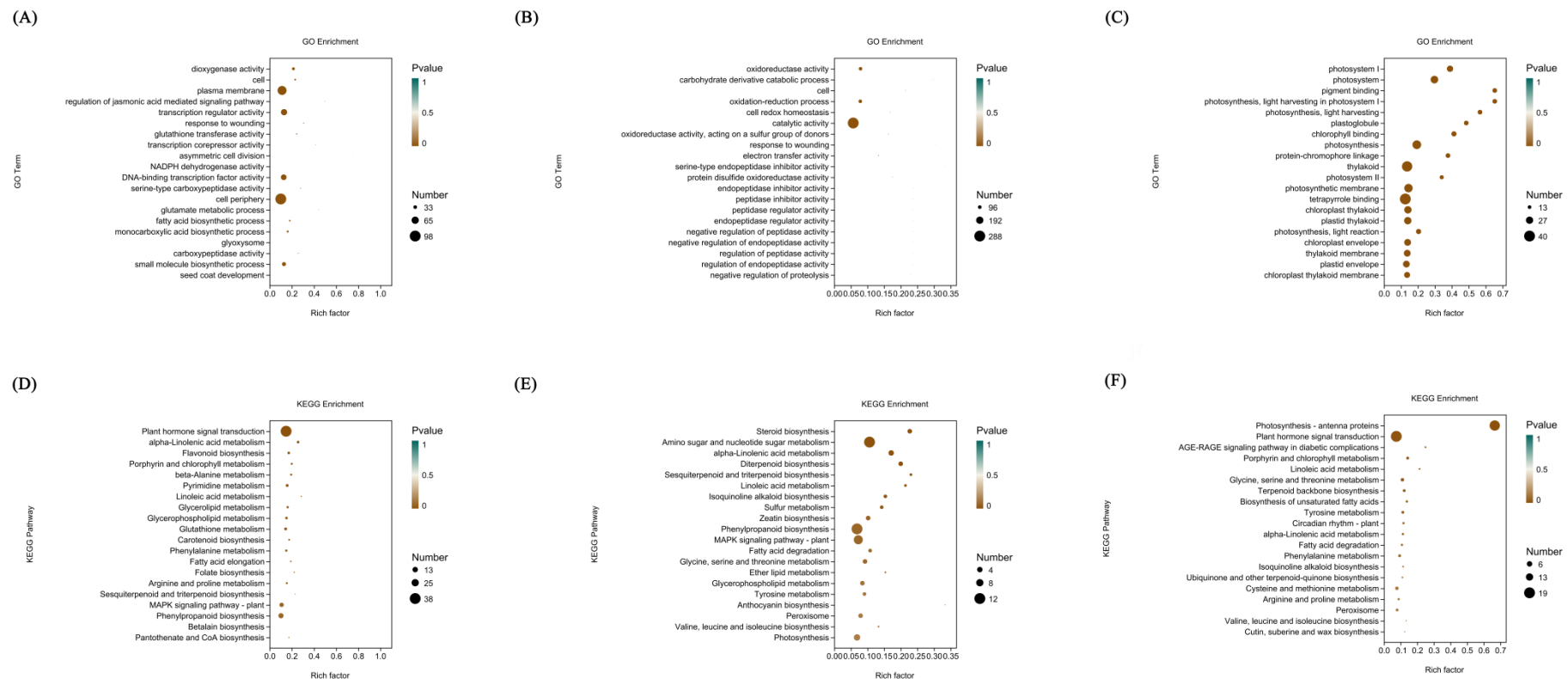


Figure S2. Go and KEGG enrichment analysis. (A–C) The abscissa is the rich factor (number of differentially annotated genes to the GO Term/total number of genes annotated to the GO Term), and the ordinate is the GO Term. The size of the midpoint in the figure represents the number of differentially annotated genes (upregulated or downregulated, which is related to the gene set selected during analysis) in the corresponding Term. The depth of the color indicates the level of significance. (A–C) Pts/VF36, tf2/CR, e/AC, respectively. (D–F) The abscissa is the Rich factor (number of differentially annotated genes into Pathway/total number of genes annotated into Pathway), and the ordinate is the Pathway. The size of the midpoint in the figure represents the number of differentially annotated genes (upregulated or downregulated, which is related to the gene

set selected during analysis) in the corresponding Pathway. The depth of the color indicates the level of significance. (D–F) Pts/VF36, tf2/CR, e/AC, respectively.



**Figure S3.** Differences in leaf morphology of VIGS plants compared with that of pTRV2 plants. (A–G) Height of VIGS and pTRV2 plants at 45 d. pTRV2 plants were used as the control. Bars = 4 cm.

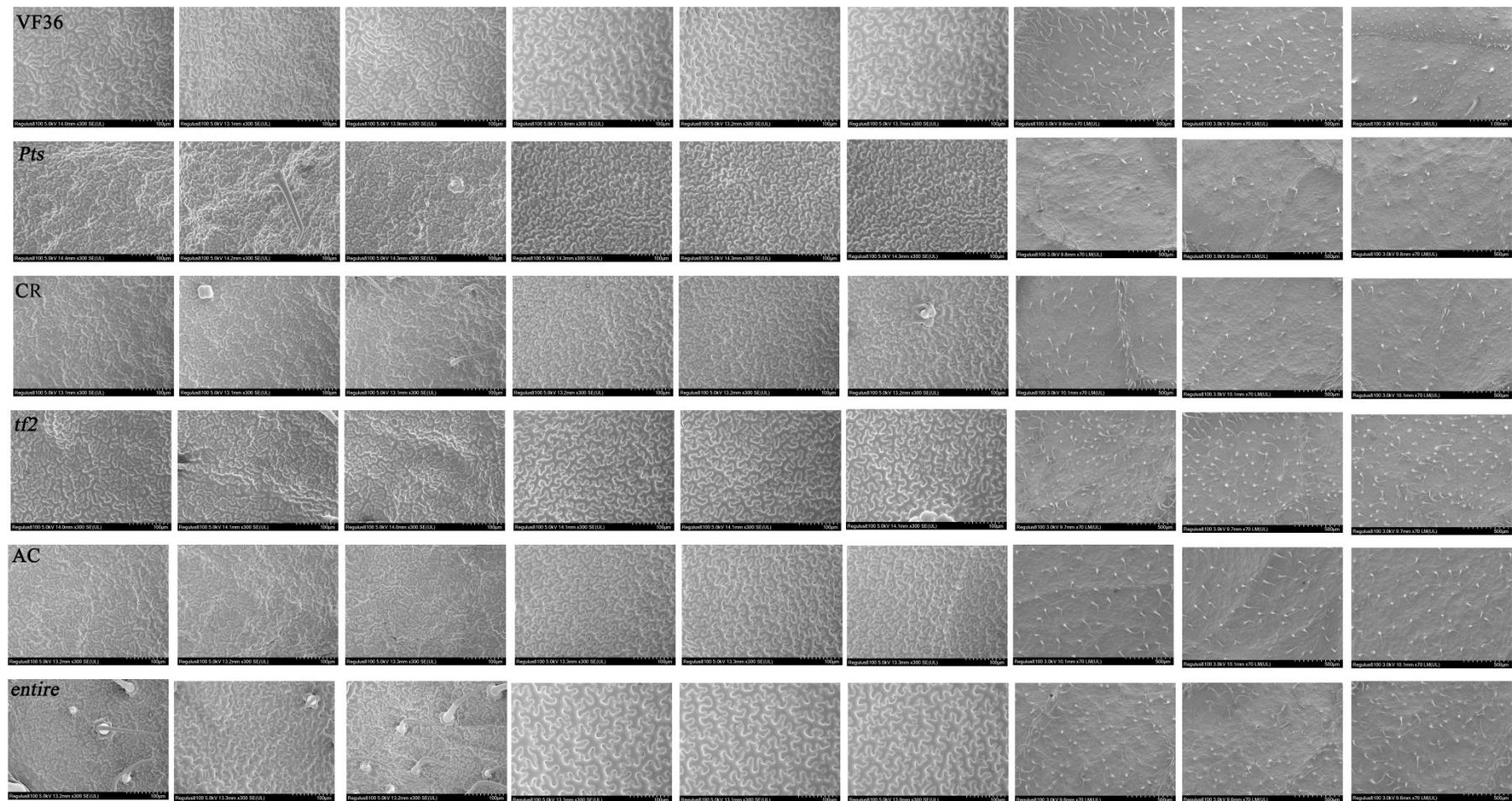


Figure S4. Stomata, epidermal cells, leaf hair supplement.