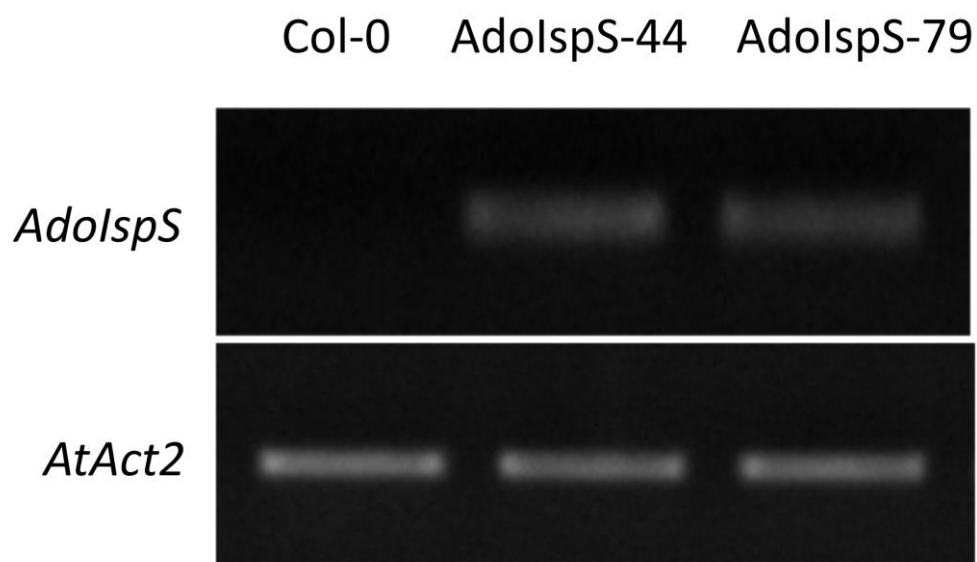
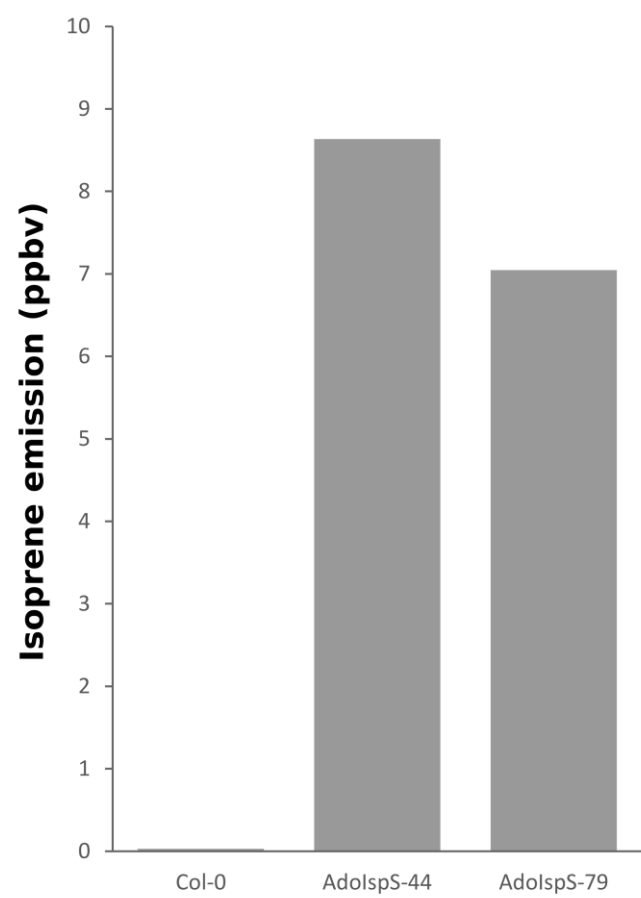


SUPPLEMENTARY LEGENDS

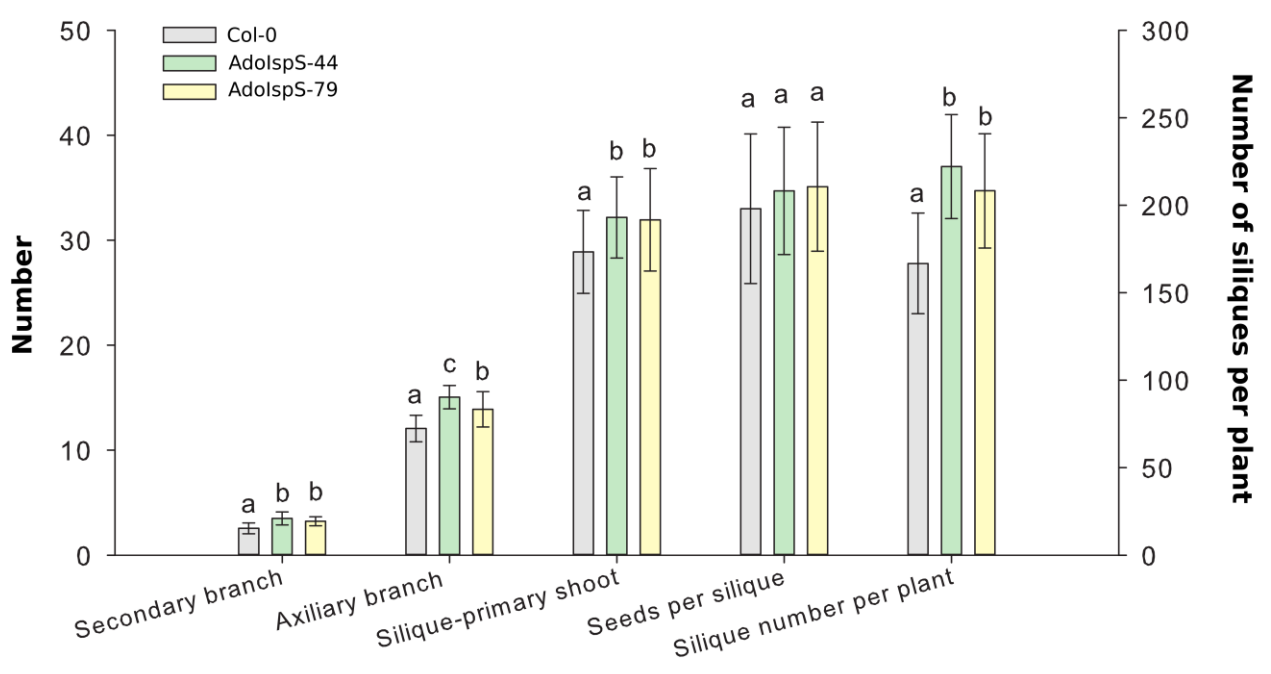
Supplementary Figure 1. Semi-quantitative PCR of *AdoIspS* expression in transgenic *AdoIspS* lines and Col-0 WT. *AtACT2*: *Arabidopsis thaliana* Actin 2 housekeeping gene. In total, 26 cycles and 28 PCR amplification cycles were used for *AtACT2* and *AdoIspS*, respectively.



Supplementary Figure 2. Isoprene emission of transgenic AdoIspS lines and Col-0 WT. ppbv: parts per billion volume.



Supplementary Figure 3. Inflorescence architecture comparison between transgenic AdoIspS lines and Col-0 WT. The left y-axis refers to the number of secondary branches, axillary branches, siliques in the primary shoot and seeds per silique. Histogram bars marked with the same letter do not significantly differ from each other (Tukey–Kramer test, $P>0.05$). Error bars represent the SD of the means.



Table_S1_R1

qPCR OF ABA-RELATED GENES - TWO-WAY ANOVA TABLES SUMMARY

Fig. 3A - ABA2 leaf

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	0.64500	2	15.6109	0.000117 ***
Genotype	0.01532	2	0.3708	0.695314
Time:Genotype	0.03675	4	0.4447	0.774790
Residuals	0.37186	18		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 3B - NCED3 leaf

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	499.34	2	233.971	1.313e-13 ***
Genotype	74.89	2	35.088	6.156e-07 ***
Time:Genotype	124.40	4	29.145	1.205e-07 ***
Residuals	19.21	18		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 3C - RAB18 leaf

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	123327	2	161.6364	3.159e-12 ***
Genotype	2419	2	3.1705	0.06613 .
Time:Genotype	4499	4	2.9480	0.04895 *
Residuals	6867	18		

Fig. 3D - RD29B leaf

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	39887710	2	589.714	< 2.2e-16 ***
Genotype	1797311	2	26.572	4.248e-06 ***
Time:Genotype	3654785	4	27.017	2.149e-07 ***
Residuals	608752	18		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 3E - ABA2 root

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
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Time	2.57328	2	25.9686	4.955e-06	***
Genotype	0.00721	2	0.0728	0.9301	
Time:Genotype	0.03692	4	0.1863	0.9425	
Residuals	0.89183	18			

Fig. 3F - NCED3 root

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	1020771	2	92.0017	3.542e-10 ***
Genotype	21738	2	1.9592	0.1699
Time:Genotype	44725	4	2.0155	0.1353
Residuals	99856	18		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 3G - RAB18 root

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	97561825	2	448.1078	4.446e-16 ***
Genotype	747532	2	3.4335	0.05456 .
Time:Genotype	1446898	4	3.3228	0.03326 *
Residuals	1959476	18		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 3H - RD29B root

Response: Relative expression

	Sum Sq	Df	F value	Pr(>F)
Time	1.0205e+11	2	85.9297	6.188e-10 ***
Genotype	6.8308e+08	2	0.5752	0.5726
Time:Genotype	1.3626e+09	4	0.5737	0.6852
Residuals	1.0688e+10	18		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table_S2_R1

qPCR OF DEHYDRATION-RELATED GENES - TWO-WAY ANOVA TABLES SUMMARY

Fig. 7A - *COR15A*

Response: Relative gene expression

	Sum Sq	Df	F value	Pr(>F)	
FactorA	94363	2	330.9552	6.388e-15	***
FactorB	4236	2	14.8557	0.0001548	***
FactorA:FactorB	4849	4	8.5037	0.0004900	***
Residuals	2566	18			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 7B - *P5CS*

Response: DependentVariable

	Sum Sq	Df	F value	Pr(>F)	
FactorA	18279.4	2	347.764	4.138e-15	***
FactorB	1797.5	2	34.197	7.398e-07	***
FactorA:FactorB	1288.2	4	12.254	5.518e-05	***
Residuals	473.1	18			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 7C - *RD20*

Response: DependentVariable

	Sum Sq	Df	F value	Pr(>F)	
FactorA	54777	2	34.6934	6.675e-07	***
FactorB	655	2	0.4148	0.6666	
FactorA:FactorB	360	4	0.1140	0.9759	
Residuals	14210	18			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Fig. 7D - *RD29A*

Response: DependentVariable

	Sum Sq	Df	F value	Pr(>F)	
FactorA	99070	2	86.6067	5.805e-10	***
FactorB	314	2	0.2743	0.7632	
FactorA:FactorB	583	4	0.2549	0.9029	
Residuals	10295	18			

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Table_S3_R1

Primer name	Sequence (5' - 3')	Tm *	PCR cycles
<i>ABA2_Fw</i>	AAGCATGAAACATGCAGCTCG	60°C	40
<i>ABA2_Rv</i>	AAGAATGTGGACCAACGCCTC	60°C	40
<i>NCED3_RT_Fw</i>	ACATGGAAATCGGAGTTACAGATAG	60°C	40
<i>NCED3_RT_Rv</i>	AGAAACAACAAACAAGAAACAGAGC	60°C	40
<i>RAB18_RT_Fw</i>	GGAAGAAGGGAATAACACAAAAGAT	60°C	40
<i>RAB18_RT_Rv</i>	GCGTTACAAACCCTCATTATTTTAA	60°C	40
<i>RD29B_RT_Fw</i>	GTGAAGATGACTATCTCGGTGGTC	60°C	40
<i>RD29B_RT_Rv</i>	TACCAAGAGACTCAGCAATCTCTG	60°C	40
<i>COR15A_RT_Fw</i>	GATACATTGGGTAAAGAAGCTGAGA	60°C	40
<i>COR15A_RT_Rv</i>	ACATGAAGAGAGAGGATATGGATCA	60°C	40
<i>RD20_RT_Fw</i>	GCTTTCAAACAAAGTTGAATGGATAC	60°C	40
<i>RD20_RT_Rv</i>	TAGTCTTGTTTGCGAGAATTGGCC	60°C	40
<i>RD29A_RT_Fw</i>	GGAAGTGAAAGGAGGAGGAGGAA	60°C	40
<i>RD29A_RT_Rv</i>	CACCACCAAACCAGCCAGATG	60°C	40
<i>AtActII_RT_Fw</i>	GCACCCTGTTCTTCTTACC	60°C	40
<i>AtActII_RT_Rv</i>	AACCCTCGTAGATTGGCACA	60°C	40

* Annealing temperature