Supplementary Data

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>*SlGAD3* (Solyc01g005000)

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ATGGTTCTCTCAAAAACTCCTTCTGATGATTCTGTACACTCCACATTTGCTTCTCGCTATGTTCGAACTT
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                SlGAD3-F
CACTACCAAGGTTTGAGATGCTAGAGAAGTCTATACCCAAAGAGGCAGCATACCAAATGATTAATGATGA

GTTAATGCTTGATGGGAATCCAAGGTTAAATTTGGCATCATTTGTAACCACATGGATGGAACCAGAATGT

GATAAGCTTATGATGGCTTCAATTAACAAGAATTATGTTGACATGGATGAATACCCTGTCACCACTGAGC

TTCAGAATCGATGTGTAAACATGATAGCGCGTTTATTCAATGCGCCTTTGAAAGAGGAAGAAATAGGAAT

TGGTGTGGGGACAGTGGGGTCATCAGAGGCCATAATGTTAGCAGGGCTGGCCTTCAAGAGGAACTGGCAA

AACAAACGCAAAGCTGAGGGAAAGCCTTATGATAAGCCCAACATTGTCACTGGTGCTAATGTTCAGGTGT

GTTGGGAGAAATTTGCAAACTACTTTGAAGTGGAATTGAAACAAGTCAAGTTAAGTGAAGGGTACTATGT

GATGGACCCAATCAAAGCTGTGGAAATGGTAGATGACAACACTATTTGTGTTGCTGCTATTTTGGGTTCA

ACACTTAATGGAGAATTTGAAGATGTCAAACTCTTGAATGATCTTTTGATTGAAAAGAATAAACAAACTG

GATGGGACACACCTATTCATGTGGATGCAGCAAGTGGTGGATTCATTGCACCATTTATCTATCCAGAGTT

GGAATGGGATTTTAGGCTTCCTTTAGTGAAAAGTATTAATGTGAGTGGACACAAATATGGGCTTGTTTAT

GCTGGTATTGGTTGGGTTATTTGGAGAACTAAACAAGACTTGCCTCAACAACTCATTTTTCATATCAATT

ATCTTGGTGCTGATCAGCCTACTTTTACTCTCAATTTCTCTAAAGGTTCAAGTCAAGTCATTGCTCAATA

TTATCAGCTTATCCGCTTGGGCTATGAGGGATATCGAAATGTAATGGAAAATTGTCGTGAAAATGCAATT

GTGCTAAGAAAAGGACTTGAAAAAACAGGACGTTTCAATATAATCTCCAAAGATGAAGGTATACCCTTGG

TGGCATTTTCCCTCAAAGACAATAGCCTCCACAACGAATTCGAGGTCTCTGAGACCCTCCGTAGGTTTGG

GTGGATTGTCCCAGCCTACACTATGCCAGCTGACCTGCAACATGTTACAGTGTTGCGCGTTGTGATTAGA

GAGGACTTCTCCCGAACCCTAGCAGATCGTCTTGTCTCTGACATCGTCAAGGTCCTCCACGAGCTCCCGA

ATGCCAAAAAAGTGGAGGATAATTTGATGATCAAT`AATGAGAAGAAAACAGAAATTGAAGTTCAAAGGGC`
            ◀──────────────────────
                SlGAD3ΔC-R
`AATTGCTGAGTTTTGGAAGAAATATGTTTTAGCTAGGAAAGCATCTATTTGT`TAG
                                    ◀───────────────────
                                          SlGAD3-R
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Fig. S1
Full-length coding sequence (CDS) of *SlGAD3*. Arrows indicate the position of primers that were used for vector construction of *SlGAD3ox* and *SlGAD3ΔCox*. The sequence deleted in SlGAD3ΔCox construct is highlighted in yellow.
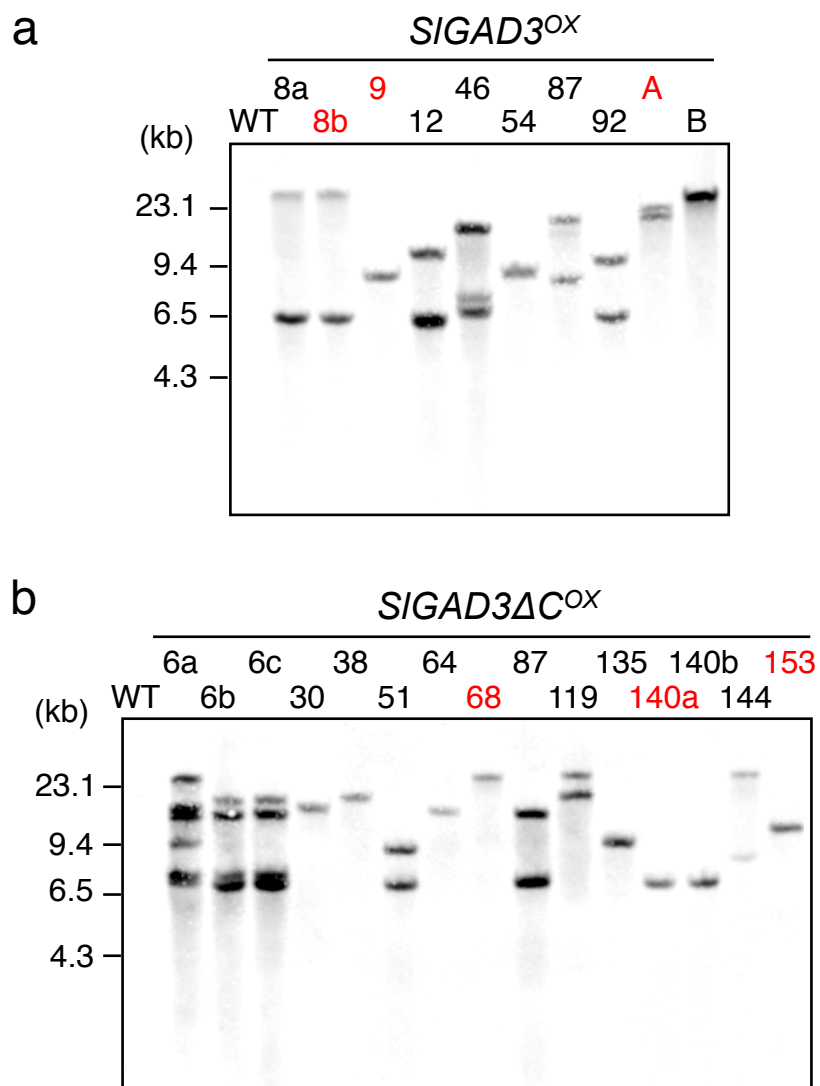
Fig. S2
Southern blot analysis of T$_0$ transgenic plants. (a) *SlGAD3^{OX}*. (b) *SlGAD3ΔC^{OX}*. Genomic DNA (10 μg) was digested with *Eco*RI and detected with the *NPTII* probe. WT was also tested as a negative control. The lines used for more detailed analyses are shown in red.
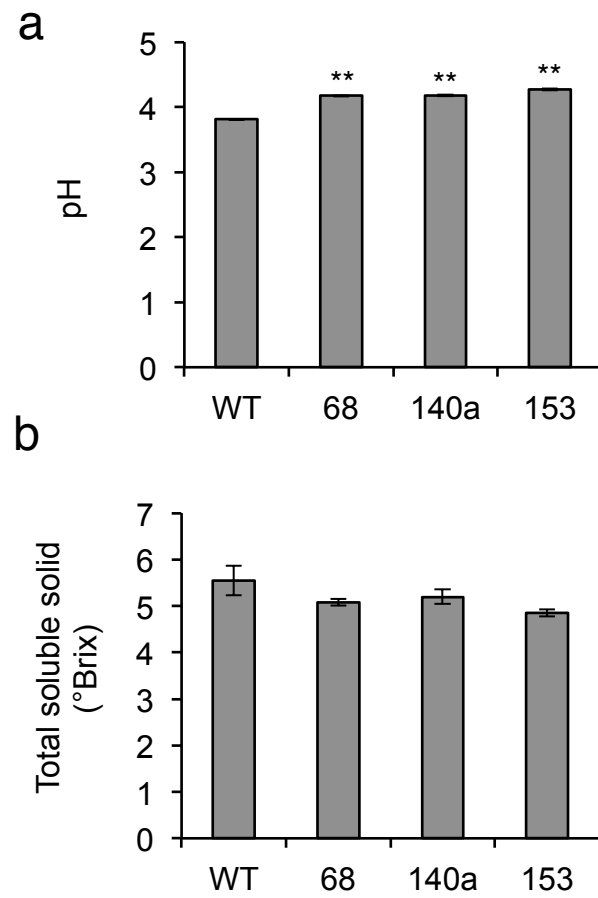
Fig. S3
Effects of SlGAD3ΔC over expression on the fruit pH and total soluble solid in T_1 *SlGAD3ΔC^{OX}*
lines. pH (a) and total soluble solids (b) were determined using Br+10 fruits of WT and in T_1
SlGAD3ΔC^{OX} lines. The mean ± SE of three biological replicates are shown. Asterisks indicate
a significant difference between WT and transgenic lines according to Student's *t*-test (**P* <
0.05 and ***P* < 0.01).
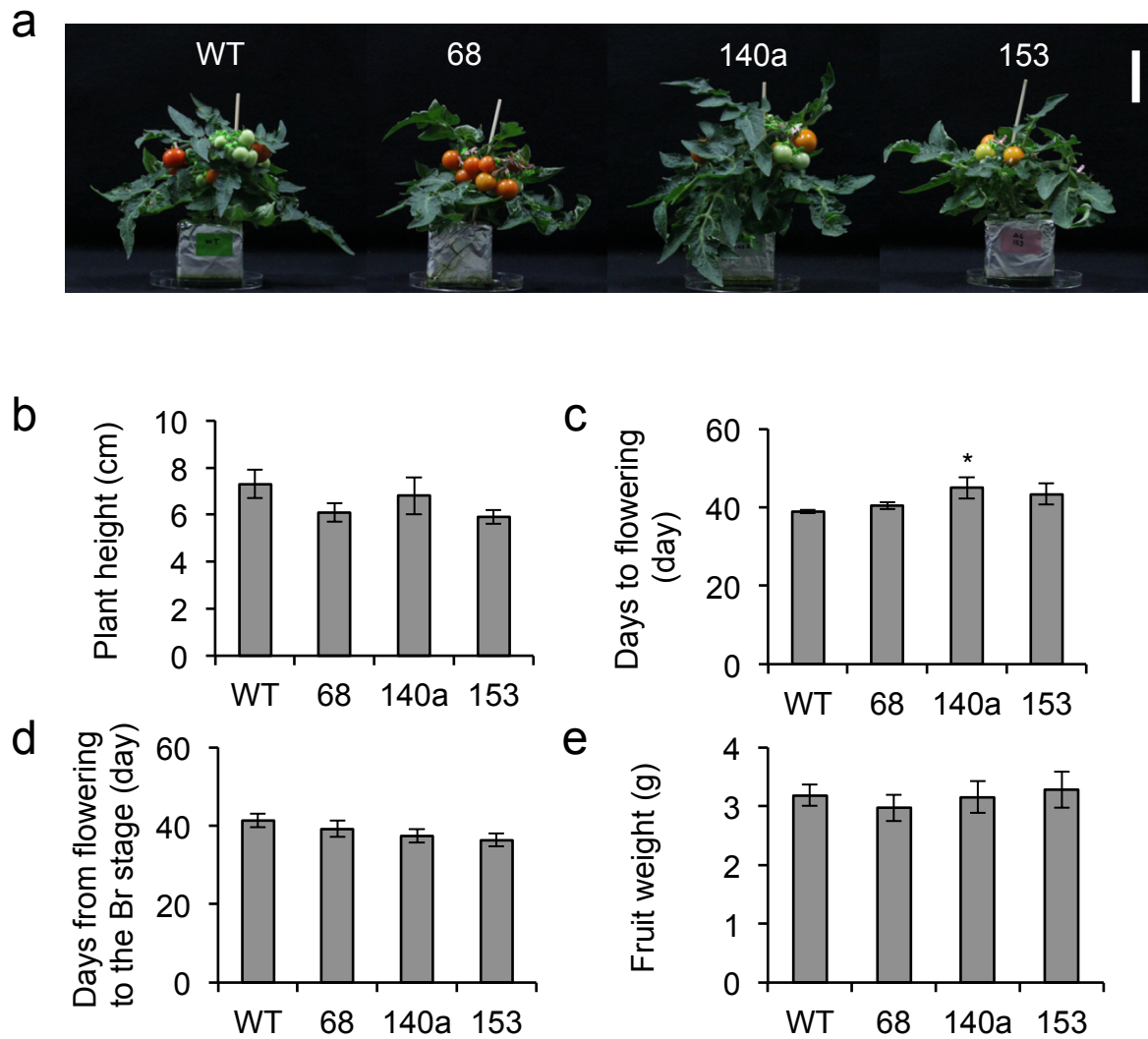
Fig. S4

Plant growth and fruit development of WT and T_1 *SlGAD3ΔC*^{OX} lines. (a) Appearance of 3-month-old plants. Bar = 5 cm. (b) Plant height when the first flower opened. Values are the mean ± SE (n = 5). (c) Days to flowering. (d) Days from flowering to the Br stage. (e) Fruit weight. (c–e) Values are the mean ± SE (n = 13). Asterisks indicate a significant difference between WT and transgenic lines according to Student's *t*-test (*P < 0.05 and **P < 0.01). Br, breaker
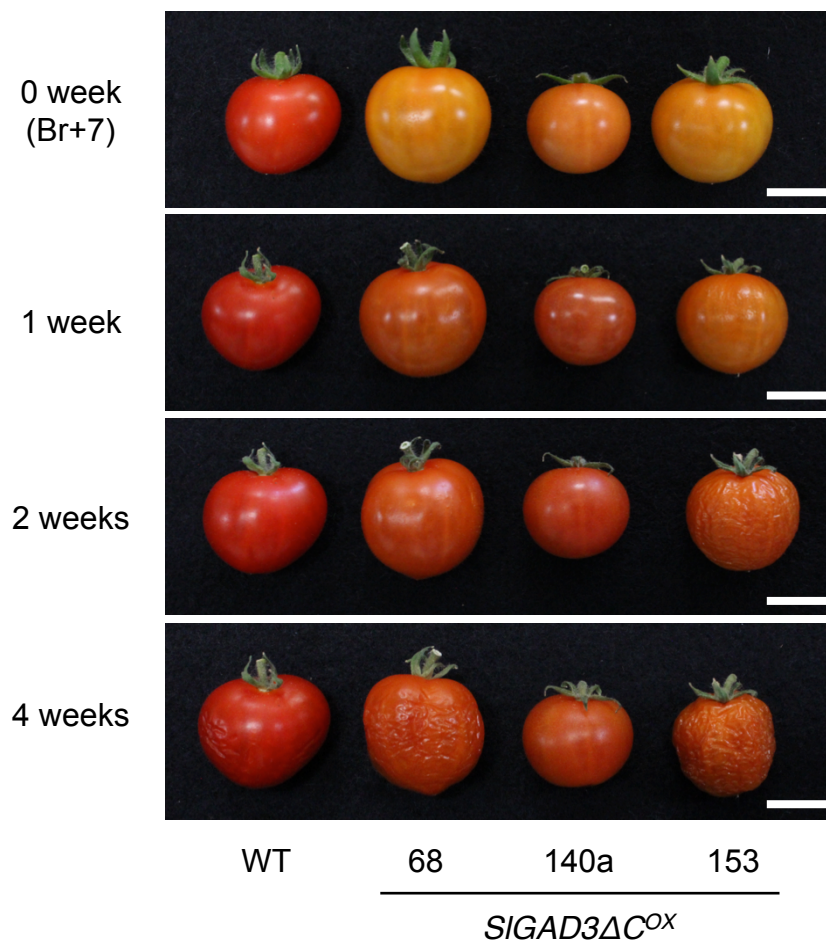
Fig. S5
Fruit shelf life of WT and T$_1$ *SlGAD3ΔC^{OX}* lines. Fruits were harvested at the Br+7 stage and stored at 25°C for 4 weeks. Bar = 1 cm.

Table S1 List of primers used in this study

Primer name	Primer sequence (5'→3')	Note
SlGAD3-F (SlGAD3ΔC-F)	GCAAAAGAAG**GGATCC**ATGGTTCTCTCAA AAACTCCTTCTG	Used for vector construction. The last 10 bases of the E8 promoter sequence (Underlined) and the *Bam*HI site (Bold letters) were added.
SlGAD3-R	CTTCATCTTCATAT**GAGCTC**CTAACAAATAG ATGCTTT	Used for vector construction. The first 14 bases of the HSP terminator sequence (Underlined) and the *Sac*I site (Bold letters) were added.
SlGAD3ΔC-R	CTTCATCTTCATAT**GAGCTC**CTAATTGATCA TCAAATTATCCTCCAC	Used for vector construction. The first 14 bases of the HSP terminator sequence (Underlined) and the *Sac*I site (Bold letters) were added.
SlUbiquitin-F SlUbiquitin-R	CACCAAGCCAAAGAAGATCA TCAGCATTAGGGCACTCCTT	Used for qRT-PCR of *SlUbiquitin* (Takayama et al. 2015)
SlGAD3-F SlGAD3-R	CAGGACGTTTCAATATAATC CCTACGGAGGGTCTCAGAG	Used for qRT-PCR of *SlGAD3* (Takayama et al. 2015)
ACS2-F ACS2-R	GGAGGTTCGTAGGTGTTGAG TAATGGTGAGGGAGGAATAGGT	Used for qRT-PCR of *ACS2* (Mantelin et al. 2013)
ACS4-F ACS4-R	AACAAGCACAATGGAAGAGGA CGCACTACGAGCAAGGAAT	Used for qRT-PCR of *ACS4* (Mantelin et al. 2013)
ACO1-F ACO1-R	ACCATGTCCTAAGCCCGATTT ATTCGTGTCCCGTCTGTTTGT	Used for qRT-PCR of *ACO1* (Shinozaki et al. 2015)
PSY1-F PSY1-R	AACTTGTTGATGGCCCAAAC CTGTATCGGACAAAGCACCA	Used for qRT-PCR of *PSY1* (Ariizumi et al. 2014)
PDS-F PDS-R	AGCCGGTGACTACACGAAAC GCTTGCTTCCGACAACTTCT	Used for qRT-PCR of *PDS* (Ariizumi et al. 2014)
ZDS-F ZDS-R	CATGTCAAAGGCCACTCAGA ACGGTAACAACAGGCACTCC	Used for qRT-PCR of *ZDS* ((Ariizumi et al. 2014)
CRTISO-F CRTISO-R	CCTGGGAATGCCTTTCAATA AACTCAGCTGCAACACGATG	Used for qRT-PCR of *CRTISO* (Ariizumi et al. 2014)
LCYB-F LCYB-R	GGACCCCATTTGAAGTTTTC AACCATGATGTGGGTTCAGA	Used for qRT-PCR of *LCY-B* (Guo et al. 2013)
CYCB-F CYCB-R	CTTTTCGGACATGGCTCAAAC GCTAGATTGCCAATCAGTCTAACCA	Used for qRT-PCR of *CYC-B* (Guo et al. 2013)
RIN-F RIN-R	ATGGCATTGTGGTGAGCAAAG GTTGATGGTGCTGCATTTTCG	Used for qRT-PCR of *RIN* (Shima et al. 2013)
TAGL1-F TAGL1-R	TGCCTGTAAATCTCCTGGAACC AGAATACCTGCTCCATGATTATCAGA	Used for qRT-PCR of *TAGL1* (Itkin et al. 2009)
FUL1-F FUL1-R	CAACAACTGGACTCTCCTCACCTT TCCTTCCACTTCCCCATTATCTATT	Used for qRT-PCR of *FUL1* (Shima et al. 2013)
FUL2-F FUL2-R	CACACCCCTTTAACAATCTTCACA GCGATGATCCTTCTACTTCTCCAT	Used for qRT-PCR of *FUL2* (Shima et al. 2013)
SlERF6-F SlERF6-R	CCATGGAAATGCCCATAGTT TCAGTAGAACTGATGATGAGTTG	Used for qRT-PCR of *SlERF6* (Lee et al. 2012)