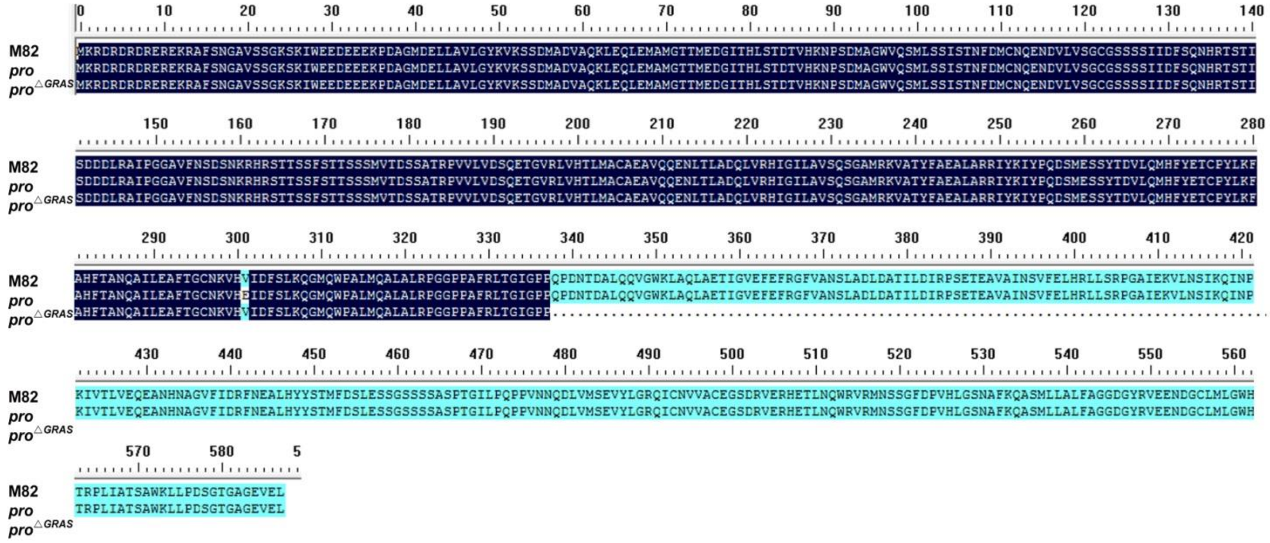
Supplemental Data



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         0         10        20        30        40        50        60        70        80        90        100       110       120       130       140
M82      MKRDRDRDREREKRAFSNGAVSSGKSKIWEEDEEEKPDAGMDELLAVLGYKVKSSDMADVAQKLEQLEMAMGTTMEDGITHLSTDTVHKNPSDMAGWVQSMLSSISTNFDMCNQENDVLVSGCGSSSSIIDFSQNHRTSTI
pro      MKRDRDRDREREKRAFSNGAVSSGKSKIWEEDEEEKPDAGMDELLAVLGYKVKSSDMADVAQKLEQLEMAMGTTMEDGITHLSTDTVHKNPSDMAGWVQSMLSSISTNFDMCNQENDVLVSGCGSSSSIIDFSQNHRTSTI
pro∆GRAS MKRDRDRDREREKRAFSNGAVSSGKSKIWEEDEEEKPDAGMDELLAVLGYKVKSSDMADVAQKLEQLEMAMGTTMEDGITHLSTDTVHKNPSDMAGWVQSMLSSISTNFDMCNQENDVLVSGCGSSSSIIDFSQNHRTSTI

                  150       160       170       180       190       200       210       220       230       240       250       260       270       280
M82      SDDDLRAIPGGAVFNSDSNKRHRSTTSSFSTTSSSMVTDSSATRPVVLVDSQETGVRLVHTLMACAEAVQQENLTLADQLVRHIGILAVSQSGAMRKVATYFAEALARRIYKIYPQDSMESSYTDVLQMHFYETCPYLKF
pro      SDDDLRAIPGGAVFNSDSNKRHRSTTSSFSTTSSSMVTDSSATRPVVLVDSQETGVRLVHTLMACAEAVQQENLTLADQLVRHIGILAVSQSGAMRKVATYFAEALARRIYKIYPQDSMESSYTDVLQMHFYETCPYLKF
pro∆GRAS SDDDLRAIPGGAVFNSDSNKRHRSTTSSFSTTSSSMVTDSSATRPVVLVDSQETGVRLVHTLMACAEAVQQENLTLADQLVRHIGILAVSQSGAMRKVATYFAEALARRIYKIYPQDSMESSYTDVLQMHFYETCPYLKF

                  290       300       310       320       330       340       350       360       370       380       390       400       410       420
M82      AHFTANQAILEAFTGCNKVHVIDFSLKQGMQWPALMQALALRPGGPPAFRLTGIGPPQPDNTDALQQVGWKLAQLAETIGVEFEFRGFVANSLADLDATILDIRPSETEAVAINSVFELHRLLSRPGAIEKVLNSIKQINP
pro      AHFTANQAILEAFTGCNKVHEIDFSLKQGMQWPALMQALALRPGGPPAFRLTGIGPPQPDNTDALQQVGWKLAQLAETIGVEFEFRGFVANSLADLDATILDIRPSETEAVAINSVFELHRLLSRPGAIEKVLNSIKQINP
pro∆GRAS AHFTANQAILEAFTGCNKVHVIDFSLKQGMQWPALMQALALRPGGPPAFRLTGIGPP....................................................................................

                  430       440       450       460       470       480       490       500       510       520       530       540       550       560
M82      KIVTLVEQEANHNAGVFIDRFNEALHYYSTMFDSLESSGSSSSASPTGILPQPPVNNQDLVMSEVYLGRQICNVVACEGSDRVERHETLNQWRVRMNSSGFDPVHLGSNAFKQASMLLALFAGGDGYRVEENDGCLMLGWH
pro      KIVTLVEQEANHNAGVFIDRFNEALHYYSTMFDSLESSGSSSSASPTGILPQPPVNNQDLVMSEVYLGRQICNVVACEGSDRVERHETLNQWRVRMNSSGFDPVHLGSNAFKQASMLLALFAGGDGYRVEENDGCLMLGWH
pro∆GRAS

                  570       580       5
M82      TRPLIATSAWKLLPDSGTGAGEVEL
pro      TRPLIATSAWKLLPDSGTGAGEVEL
pro∆GRAS
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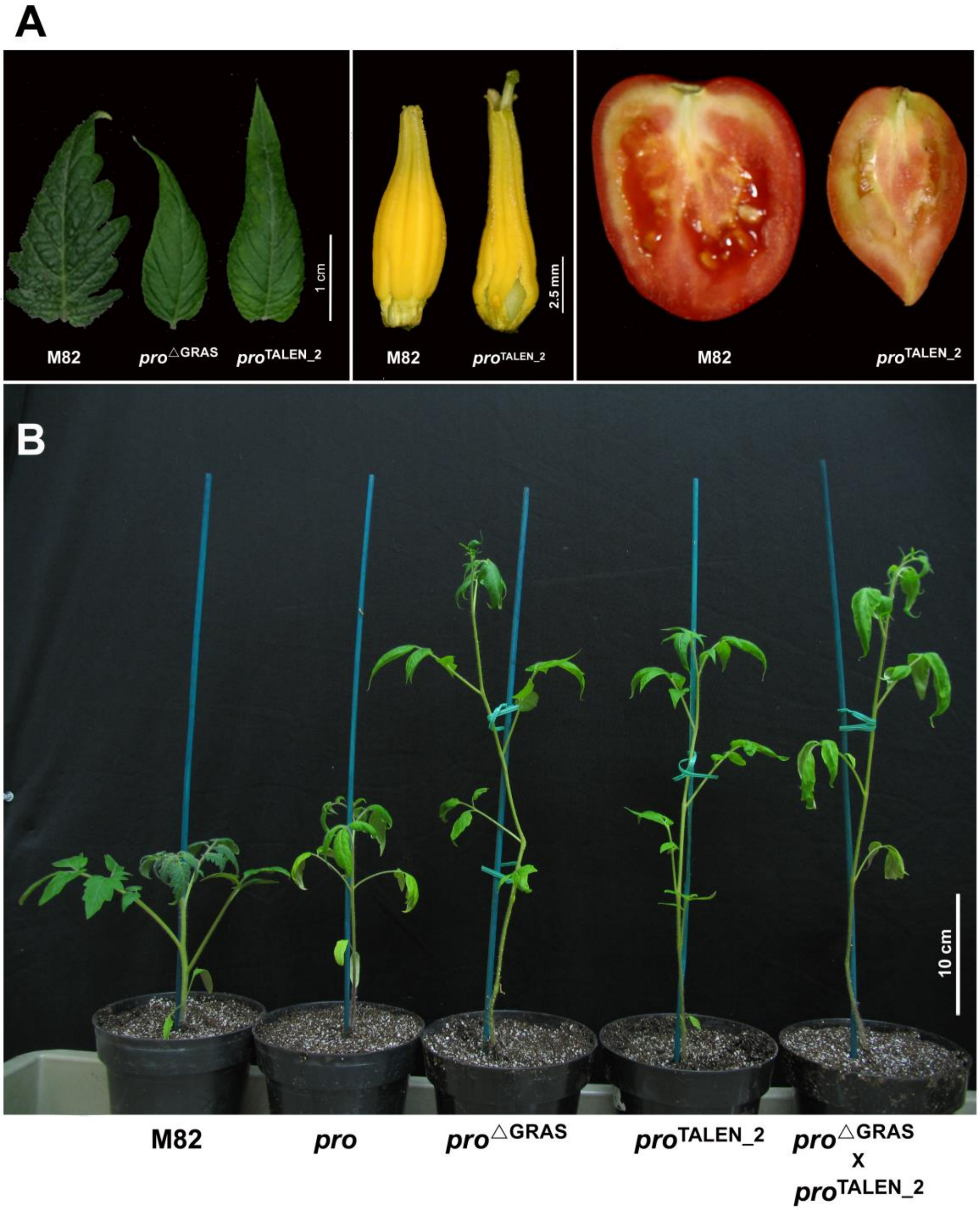
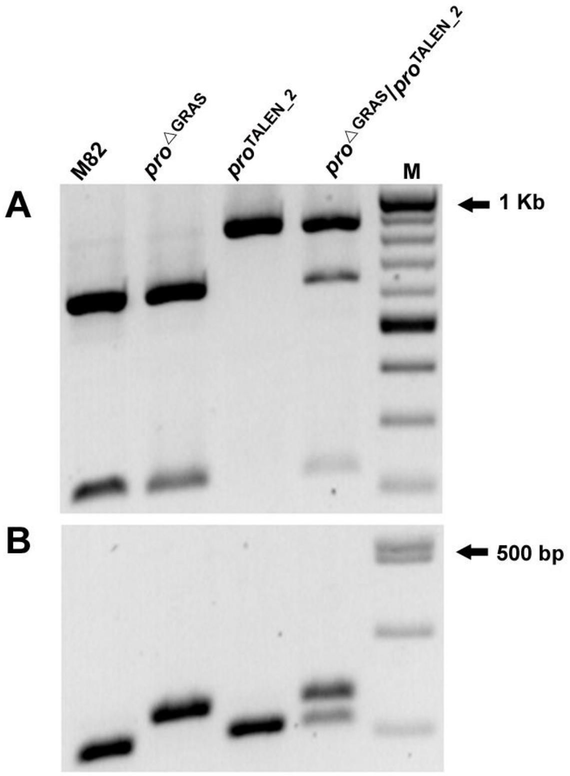
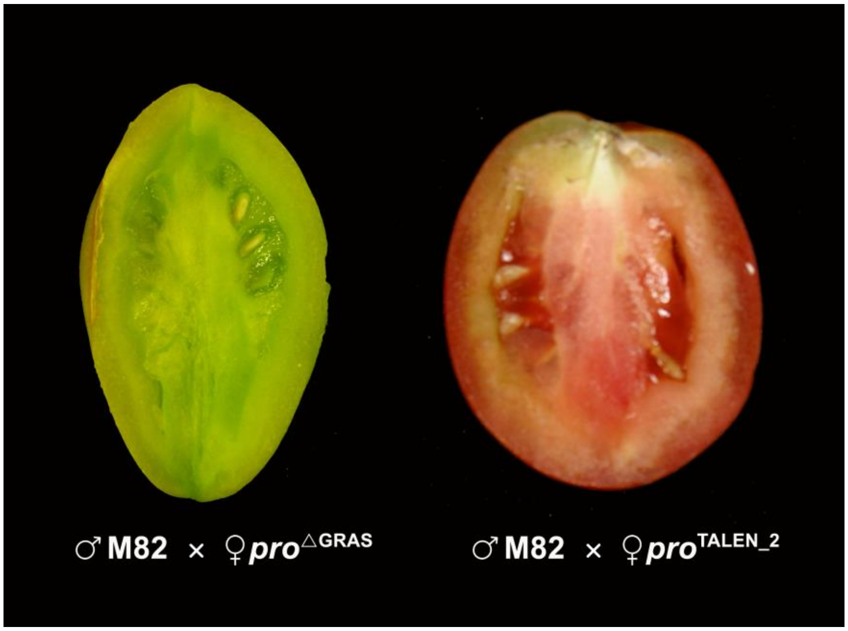
Supplemental Figure 1. Predicated amino acid sequence of PRO from M82, *pro* and *pro*$^{\Delta GRAS}$. Dark blue indicates predicted amino acid sequence present in M82, *pro* and *pro*$^{\Delta GRAS}$. Light blue indicates amino acid sequence present in some but not all genetic backgrounds. The entire C' terminal region of PRO is missing from *pro*$^{\Delta GRAS}$.



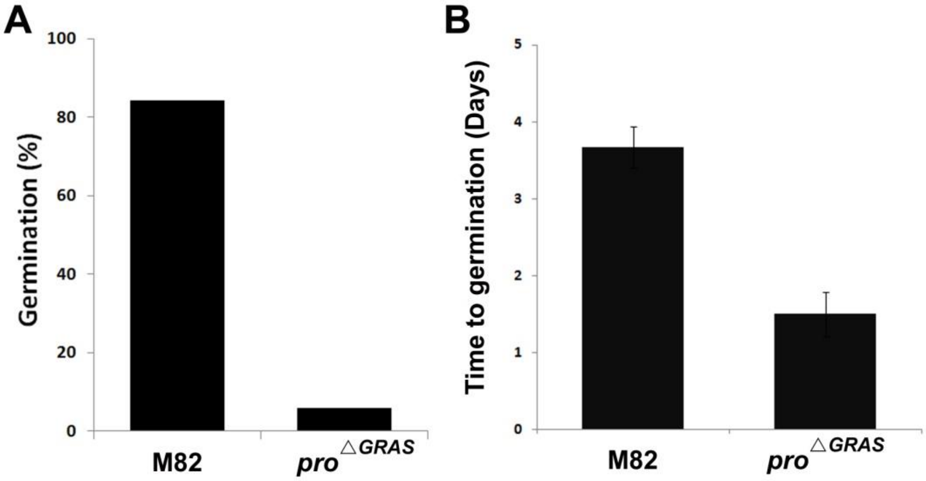
Supplemental Figure 2. Phenotypic characterization of *pro*$^{TALEN\_2}$ plants. A. Leaves, flowers and fruits of M82 and *pro*$^{TALEN\_2}$. B. Four week old M82, *pro, pro*$^{\Delta GRAS}$, *pro*$^{TALEN\_2}$ and *pro*$^{TALEN\_2}$/*pro*$^{\Delta GRAS}$ plants.



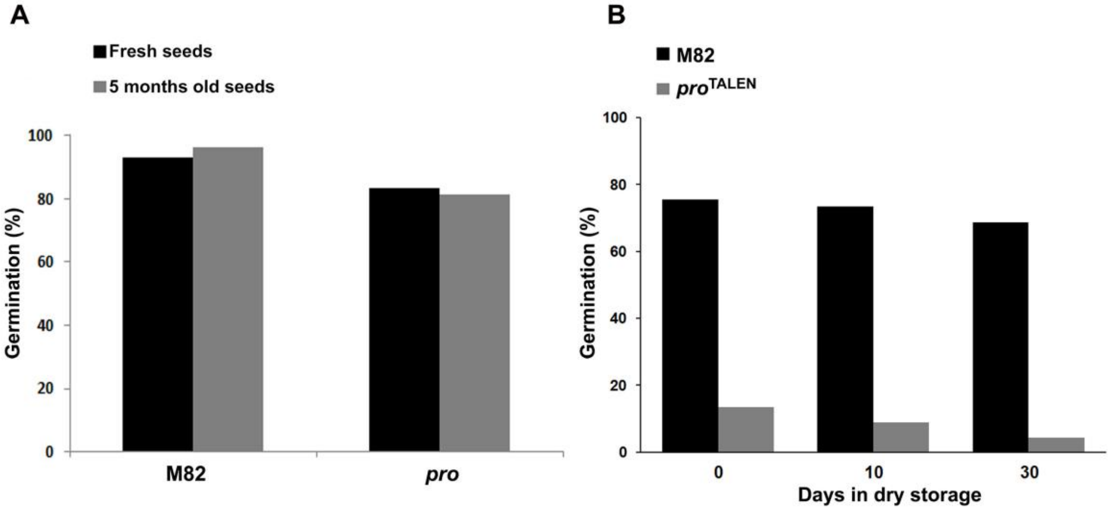
Supplemental Figure 3. Genotyping of plants shown in Supplemental Figure 2B. A) Genotyping for the *pro*$^{TALEN\_2}$ allele. The regions of the TALEN-induced mutation was PCR amplified and digested with *Sm1*I. *Sm1*I cleaves M82 (WT) amplicons producing 647bp and 225bp products. The *pro*$^{TALEN\_2}$ allele is resistant to *Sm1*I digestion. (M) indicates the marker lane. B) Genotyping for the *pro*$^{\Delta GRAS}$ allele. PCR amplification was performed using *pro*$^{\Delta GRAS}$ Derived Cleaved Amplified Polymorphic Sequences (dCAPs) primers and the amplicons were digested with *Pvu*II. *Pvu*II digests wild-type amplicons producing 302bp and 27bp products, while *pro*$^{\Delta GRAS}$ are resistant to digestion.



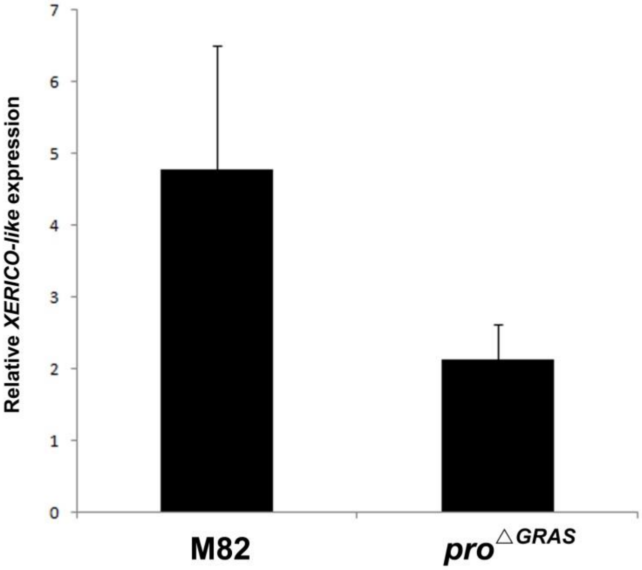
Supplemental Figure 4. Seed set in tomato fruits following hand pollination of *pro*$^{\Delta GRAS}$ and *pro*$^{TALEN\_2}$ emasculated flowers with M82 pollen grains.



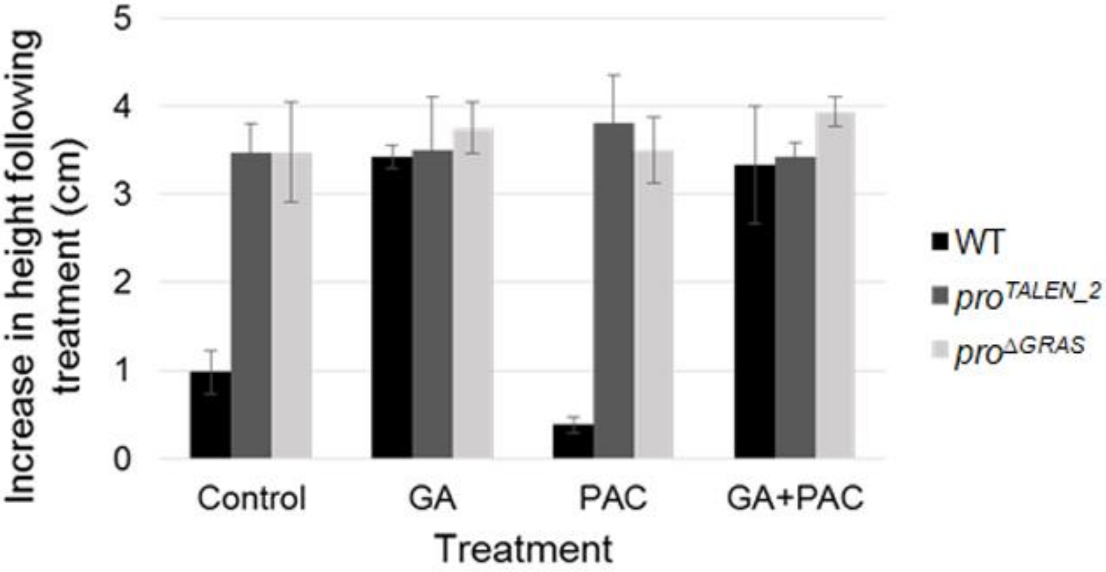
Supplemental Figure 5. *pro*$^{\Delta GRAS}$ seeds are sensitive to desiccation and have weak dormancy. (**A**) Germination of M82 and *pro*$^{\Delta GRAS}$ seeds stored dry for one month. Seeds were sown on soil and the number of seedlings with M82 or *pro*$^{\Delta GRAS}$ phenotypes was counted. **(B)** Germination time of M82 and *pro*$^{\Delta GRAS}$ fresh seeds. Seeds from heterozygous fruits were harvested and sown immediately on soil. Time to germination (days) was measured. Values are average of 15 seedlings ± SE.



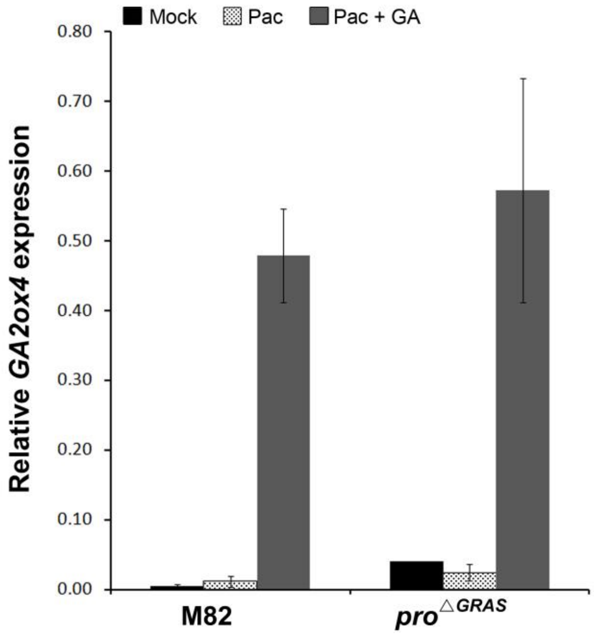
Supplemental Figure 6. *pro*$^{TALEN\_2}$ but not *pro* seeds are sensitive to desiccation. (**A**) M82 and *pro* seeds were sown fresh (black columns) or stored at room temperature for 5 months and then sown (grey columns). (**B)** M82 and *pro*$^{\Delta TALEN}$ seeds were sown on soil after different periods of dry storage.



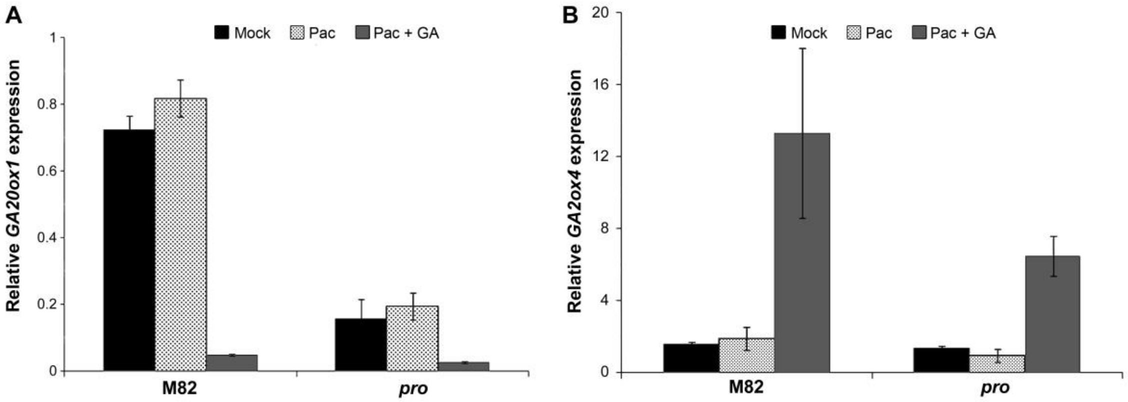
Supplemental Figure 7. Expression analyses (qRT-PCR) of the putative *XERICO* gene in tomato. RNA was extracted from fresh M82 and *pro*$^{\Delta GRAS}$ homozygous seeds. Values are the average of three biological replicas ± standard error (SE).



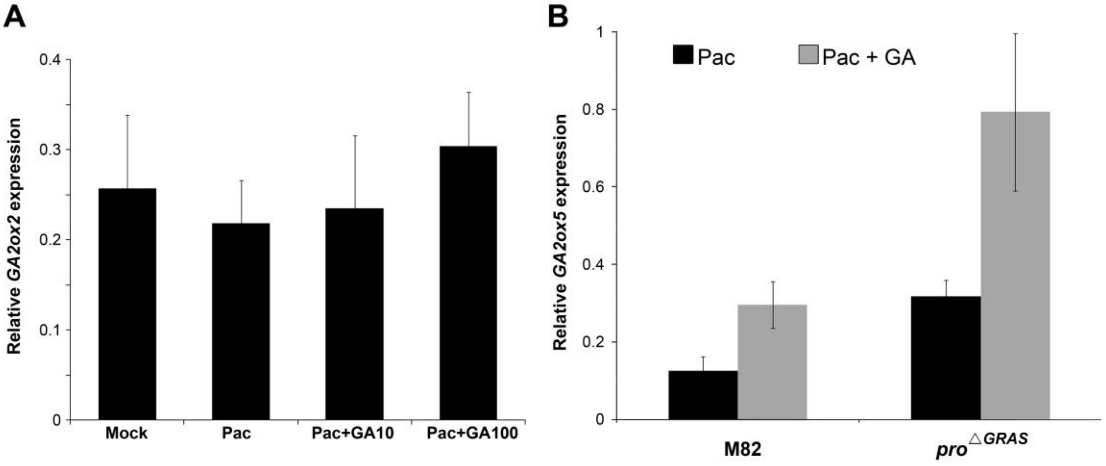
Supplemental Figure 8. Average increase in plant height of M82 (WT), *pro*$^{TALEN\_2}$ and *pro*$^{\Delta GRAS}$ seedlings following five days of daily treatments with GA_3 (50μM), PAC (100mg/L) or GA+PAC solutions. Values are average of five to eight plants ± SE.



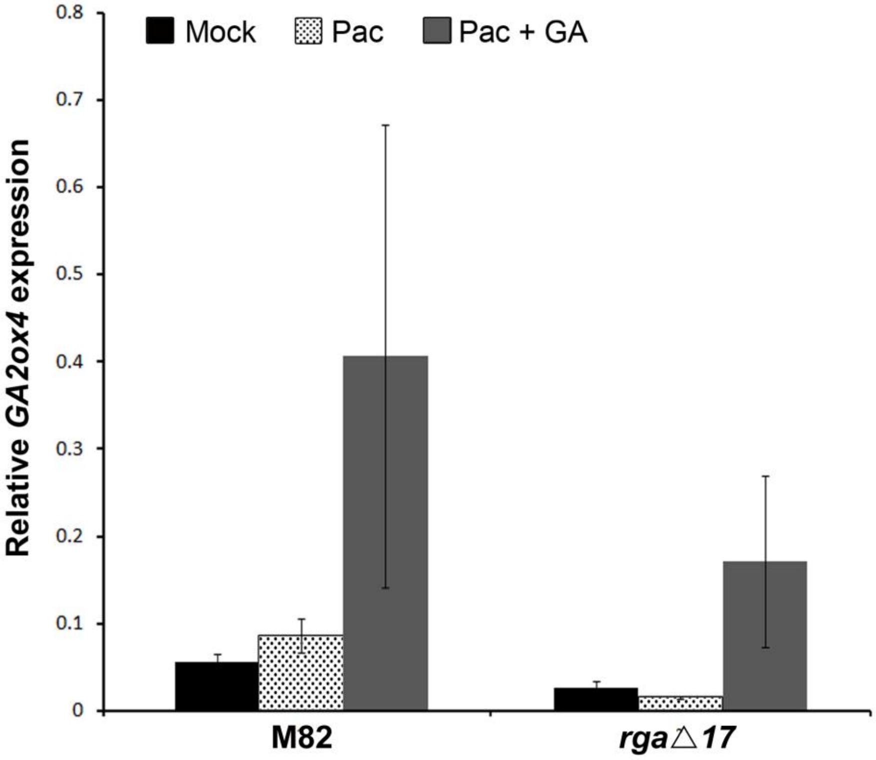
Supplemental Figure 9. Regulation of *GA2ox4* expression by GA in *pro*$^{\Delta GRAS}$. qRT-PCR analysis of *GA2ox4* expression. Seedlings were treated with 10mg/l PAC for three days, followed by one application of GA_3 (100µM). RNA was extracted from young leaves 3 hours after the application of GA and analyzed. Values (gene-to-*TUBULIN* ratios) are means of three biological replicates ± SE.



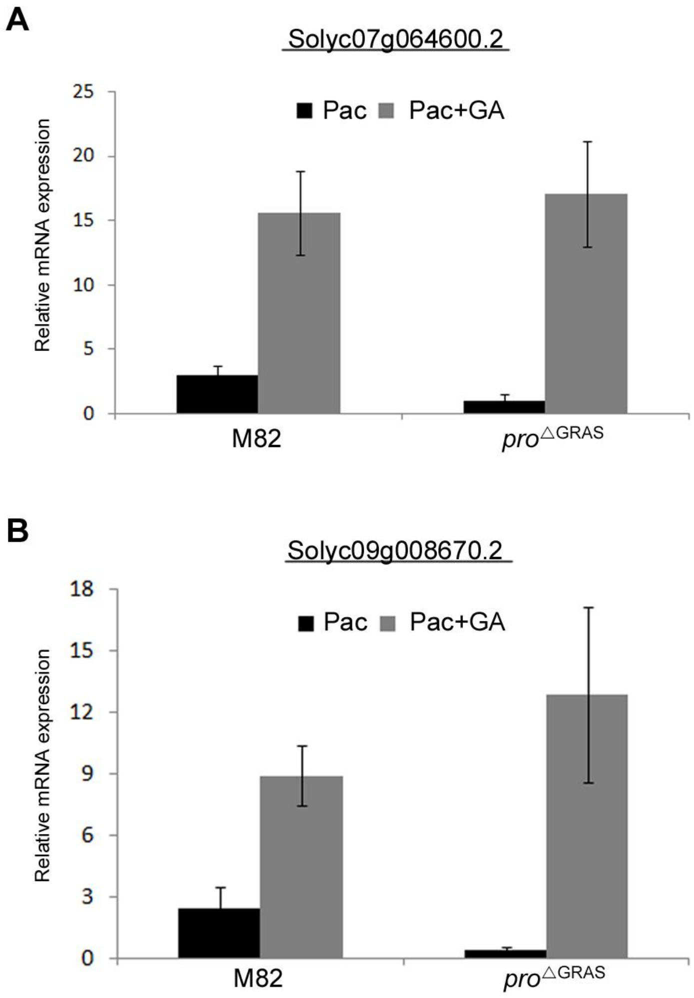
Supplemental Figure 10. Expression analyses of *GA20ox1* and *GA2ox4* in M82 and *pro*. (**A**) qRT-PCR analysis of *GA20ox1* expression and (**B**) qRT-PCR analysis of *GA2ox4* expression. Seedlings were treated with PAC followed by GA_3 application. RNA was extracted from young leaves and analyzed. Values (gene-to-*TUBULIN* ratios) are means of three biological replicates ± standard error (SE).



Supplemental Figure 11. Expression analyses (qRT-PCR) of *GA2ox2* and *GA2ox5*. **(A)** M82 seedlings were treated with PAC followed by 10µM or 100µM GA_3 application. RNA was extracted from young leaves 3 hours after the application of the hormone and analyzed for *GA2ox2* expression. Values (gene-to-*TUBULIN* ratios) are means of three biological replicates ± standard error (SE). **(B)** M82 and *pro*$^{\Delta GRAS}$ seedlings were treated with PAC followed by application of 10µM GA_3. RNA was extracted from young leaves 3 hours after the application of the hormone and analyzed. Values (gene-to-*TUBULIN* ratios) are means of three biological replicates ± standard error (SE).



Supplemental Figure 12. qRT-PCR analyses of *GA2ox4* expression in M82 and *rgaΔ17* leaves treated with 10mg/l PAC for three days or PAC for three days followed by one application of 100µM GA_3. Values (gene-to-*TUBULIN* ratios) are means of three biological replicates ± SE.



Supplemental Figure 13. qRT-PCR analyses of Endoribonuclease and Threonine ammonia lyase. M82 and *pro*$^{\Delta GRAS}$ seedlings were treated with 10mg/l PAC for three days and then part of them with 10µM GA$_3$. RNA was extracted from young leaves 3 hours after the GA treatment and analyzed for (**A**) Endoribonuclease (Solyc07g064600.2) and (**B**) Threonine ammonia lyase (Solyc09g008670.2) expression. Values (gene-to-*TUBULIN* ratios) are means of three or four biological replicates ± SE.

Supplemental Table 1. *pro*$^{TALEN\_2}$ plants are male, but not female sterile.

M82 x *pro*^{TALEN} crossses[a]	**M82 (♂) x M82 (♀)**	**M82 (♂) x *pro*^{TALEN} (♀)**	***pro*^{TALEN} (♂) x M82 (♀)**	***pro*^{TALEN} (♂) x *pro*^{TALEN} (♀)**
Flowers corssed	**10**	**10**	**10**	**10**
Fruits developed	**10**	**9**	**0**	**8***
%	**100**	**90**	**0**	**80**

[a] All flowers were emasculated and then crossed with the respective pollen. Flowers from the *pro*$^{TALEN\_2}$ (♂) x M82 (♀) senesced one week after the cross, therefore, no fruits were developed.

*parthenocarpic fruits

Supplemental Table 2. Complete list of GA up-regulated genes

GA up-regulated genes

		M82				$pro^{\Delta GRAS}$			
SolyC	Description	Mean Pac[a]	Mean Pac +GA[a]	Fold change[b]	Adj P Value[c]	Mean Pac[a]	Mean Pac +GA[a]	Fold change[b]	Adj P Value[c]
Solyc05g007950.2	Ribonuclease T2	68	1068	15.78	5.62E-08	189	763	4.05	0.115224
Solyc12g010800.1	BZIP transcription factor	10	106	10.29	7.15E-06	41	87	2.15	0.999968
Solyc03g025380.2	Peroxidase	24	243	9.98	0.000267	121	226	1.87	0.999968
Solyc03g005320.2	Fatty acid elongase 3-ketoacyl-CoA synthase	60	379	6.36	1.64E-06	120	127	1.06	0.999968
Solyc01g110630.2	Auxin-induced SAUR-like	18	108	5.95	0.000945	36	39	1.08	0.999968
Solyc04g017720.2	Gibberellin regulated protein	55	312	5.71	1.22E-07	220	232	1.06	0.999968
Solyc12g056250.1	Glutathione S-transferase	341	1917	5.62	2.76E-06	603	1304	2.16	0.999968
Solyc07g062710.2	BZIP transcription factor	64	342	5.38	6.02E-08	214	210	-1.02	0.999968
Solyc04g081790.2	GDSL esterase/lipase	54	290	5.38	6.02E-08	262	410	1.57	0.999968
Solyc04g016190.1	Glucosyltransferase	87	465	5.33	0.001001	246	326	1.32	0.999968
Solyc03g097170.2	Cinnamoyl-CoA reductase-like	140	739	5.29	8.31E-07	379	495	1.31	0.999968
Solyc03g078090.2	Pectinesterase	19	89	4.80	0.033812	104	144	1.38	0.999968
Solyc10g005210.2	DNA-3-methyladenine glycosylase I	42	195	4.60	1.64E-06	132	195	1.48	0.999968
Solyc10g011730.2	Arabinogalactan	49	219	4.49	3.75E-05	107	171	1.60	0.999968
Solyc03g006100.2	Receptor like kinase, RLK	144	633	4.41	0.000322	113	96	-1.18	0.999968
Solyc08g075210.1	Acyltransferase-like protein	60	259	4.31	0.011786	210	127	-1.66	0.999968
Solyc03g114710.2	Glucosyltransferase	33	141	4.30	0.00217	38	34	-1.13	0.999968
Solyc10g052530.1	Auxin-responsive protein	20	84	4.29	0.018011	77	67	-1.16	0.999968
Solyc07g064600.2	Endoribonuclease L-PSP	544	2301	4.23	0.00546	415	2378	5.73	0.000413
Solyc11g069960.1	Receptor like kinase, RLK	32	137	4.22	0.000267	124	129	1.04	0.999968
Solyc04g081870.2	Expansin	467	1964	4.20	1.98E-07	2153	1814	-1.19	0.999968
Solyc02g088100.2	Expansin	659	2740	4.16	6.02E-08	1878	2823	1.50	0.999968
Solyc09g083440.2	Proteinase inhibitor I	297	1232	4.14	0.000293	264	1064	4.03	0.001424
Solyc07g008560.2	Purple acid phosphatase	25	103	4.04	0.010653	26	53	2.08	0.999968
Solyc02g088740.1	Genomic DNA chromosome 5 TAC clone K3	84	332	3.94	1.16E-05	159	183	1.15	0.999968
Solyc05g005960.2	Peptide transporter 1	291	1133	3.89	0.000576	741	534	-1.39	0.999968
Solyc04g007690.2	Auxin efflux carrier	126	486	3.86	6.06E-06	362	377	1.04	0.999968
Solyc10g074540.1	Expressed protein	137	521	3.79	5.66E-06	107	254	2.37	0.103198
Solyc05g006510.1	Glycosyltransferase	107	396	3.70	1.54E-05	136	261	1.92	0.942727
Solyc01g105360.2	UDP-glucuronosyltransferase	207	743	3.60	0.000154	553	349	-1.58	0.999968
Solyc03g123620.2	Pectinesterase	160	566	3.53	0.006902	379	370	-1.02	0.999968
Solyc02g077110.2	Lipase-like protein	157	555	3.53	0.000267	279	561	2.01	0.897338
Solyc07g043000.2	Unknown Protein	86	305	3.52	0.00921	81	78	-1.03	0.999968
Solyc02g089350.2	Gibberellin regulated protein	1585	5413	3.41	0.003145	6174	5415	-1.14	0.999968
Solyc04g005660.2	Transcription factor style2.1	61	204	3.33	0.00245	98	90	-1.09	0.999968
Solyc02g069490.2	FAD linked oxidase domain	319	1050	3.29	0.025107	339	352	1.04	0.999968
Solyc02g087960.2	MYB transcription factor	108	356	3.28	0.000616	444	332	-1.34	0.999968
Solyc09g091430.2	Pectate lyase 1-27	1025	3326	3.24	1.22E-07	3198	3375	1.06	0.999968
Solyc06g060830.2	Homeobox-leucine zipper	147	477	3.24	0.00921	253	166	-1.52	0.999968
Solyc03g111120.2	Malate synthase	467	1508	3.23	4.17E-05	336	270	-1.24	0.999968
Solyc03g113250.2	Nitrate transporter	51	163	3.22	0.045512	167	75	-2.24	0.999968
Solyc01g100660.2	Transcription factor	137	440	3.21	4.14E-05	273	296	1.08	0.999968
Solyc09g008670.2	Threonine ammonia-lyase biosynthetic	122	390	3.21	0.013414	45	532	11.89	7.53E-13
Solyc03g114720.2	Transcription factor BIM2	156	496	3.18	0.000647	169	157	-1.07	0.999968
Solyc01g090760.2	GATA transcription factor 9	68	215	3.16	0.02203	44	67	1.52	0.999968
Solyc09g065560.2	Sulfate transporter	49	152	3.13	0.012949	83	173	2.07	0.999968

Supplemental Table 2. Continued

Solyc03g110990.1	Unknown Protein	39	120	3.09	0.035798	194	208	1.07	0.999968
Solyc04g074450.1	Phi-1 protein	245	746	3.05	0.000322	217	440	2.02	0.494203
Solyc01g079580.2	DNAJ heat shock protein	775	2342	3.02	0.000322	986	1059	1.07	0.999968
Solyc06g083650.2	GDSL esterase/lipase	100	302	3.02	0.006675	664	661	-1.01	0.999968
Solyc07g041920.2	Cathepsin L-like cysteine proteinase	232	692	2.99	0.049131	28	37	1.34	0.999968
Solyc04g074410.1	Os06g0220000 protein	369	1076	2.92	0.000614	728	1186	1.63	0.999968
Solyc03g120380.2	Auxin response factor 9	56	164	2.91	0.048072	97	93	-1.04	0.999968
Solyc01g097520.2	Annexin 11	870	2501	2.88	0.005886	1727	2553	1.48	0.999968
Solyc03g111690.2	Pectate lyase	172	493	2.87	8.98E-05	810	1085	1.34	0.999968
Solyc11g072030.1	Non-specific lipid-transfer	590	1688	2.86	0.00189	1323	2097	1.58	0.999968
Solyc04g080820.2	Cytokinin oxidase/dehydrogenase	90	253	2.81	0.040156	61	38	-1.63	0.999968
Solyc08g079740.2	Receptor like kinase, RLK	90	250	2.78	0.013414	202	202	-1.00	0.999968
Solyc07g006300.2	CER1 protein	369	1024	2.78	0.00733	1009	1012	1.00	0.999968
Solyc05g005950.2	Solute carrier family	687	1901	2.76	0.025107	1252	1066	-1.17	0.999968
Solyc05g014120.1	Os08g0119500 protein	95	258	2.71	0.012855	182	297	1.63	0.999968
Solyc07g054470.1	Unknown Protein	133	358	2.70	0.008722	299	379	1.27	0.999968
Solyc01g073640.2	oxidoreductase Mb1385	1526	4106	2.69	0.014012	1415	1745	1.23	0.999968
Solyc05g014000.2	Pectate lyase	464	1230	2.65	0.00373	1851	2422	1.31	0.999968
Solyc01g110680.2	Auxin-induced SAUR-like protein	72	190	2.63	0.047453	80	97	1.21	0.999968
Solyc10g083170.1	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	167	437	2.61	0.01348	538	521	-1.03	0.999968
Solyc05g051240.1	Aspartic proteinase nepenthesin I	669	1728	2.58	0.02339	1077	1278	1.19	0.999968
Solyc03g121270.2	IAA-amino acid hydrolase	1347	3429	2.55	0.015785	1240	4191	3.38	0.00038
Solyc01g005430.2	UBX domain protein 6	83	208	2.52	0.047453	128	101	-1.26	0.999968
Solyc02g087870.2	Uncharacterized ABC transporter ATP-binding protein/permease	213	521	2.44	0.013313	328	421	1.28	0.999968
Solyc06g054320.1	Disease resistance response	115	277	2.41	0.048072	372	576	1.55	0.999968
Solyc03g120790.1	Unknown Protein	151	363	2.40	0.012949	450	452	1.01	0.999968
Solyc05g051280.2	Calmodulin-binding heat-shock protein	111	266	2.40	0.035798	179	225	1.25	0.999968
Solyc06g007620.2	POT family domain containing	464	1096	2.36	0.003969	813	1035	1.27	0.999968
Solyc02g082120.2	DNA-3-methyladenine glycosylase I	725	1699	2.34	0.031042	999	1024	1.02	0.999968
Solyc02g089640.2	Cellulose synthase-like C1-2 glycosyltransferase family 2	291	679	2.34	0.018011	502	540	1.08	0.999968
Solyc03g111550.2	GDSL esterase/lipase	413	923	2.23	0.040156	1209	1196	-1.01	0.999968
Solyc01g005990.2	Non-specific lipid-transfer	878	1904	2.17	0.004863	2374	2378	1.00	0.999968
Solyc07g053540.1	Fasciclin-like arabinogalactan	2563	5550	2.17	0.017273	3113	4058	1.30	0.999968
Solyc11g019910.1	Pectinesterase	624	1294	2.07	0.018112	1131	1240	1.10	0.999968
Solyc06g049050.2	Expansin	2349	4834	2.06	0.041436	5728	4585	-1.25	0.999968

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[a] Mean value of two biological replicates.

[b] Fold change is the ratio Mean Pac+GA/ Mean Pac

[c] Corrected P-values were calculated using the Benjamini–Hochberg (1995) false discovery rate approach

Supplemental Table 3. Primers used in this study.

Clone		sequence (5'-3')
GA2ox4	qRT-PCR	Forward- CCAACAACACTTCCGGTCTT Reverse- CATTCGTCATCACCTGTAATGAG
GA20ox1	qRT-PCR	Forward- AGATTGTGTTGGTGGACTTCAA Reverse- TAGCGCCATAAATGTGTCG
GA2ox2	qRT-PCR	Forward- ATAGCGACTCCGTTTTCAGG Reverse- TTTTCATCAGGTGGGACAGA
GA2ox5	qRT-PCR	Forward- TTCTCCTCTCCCCTCTCTGA Reverse- TAATCCCTCCGCCAACTTTT
TUB	qRT-PCR	Forward- CACATTGGTCAGGCCGGTAT Reverse- CGCGAGATGAGATAAACCA
At-*RGA*	qRT-PCR	Forward- GTAACATGGACGAGGTTGCT Reverse- CGCGAGATGAGATAAACCA
At-*GA2ox1*	qRT-PCR	Forward- CACACTTCCTTCTTCTTCAACG Reverse- ATGTCAACGGAGCGATTCTC
At-*GA2ox4*	qRT-PCR	Forward- CACTATCCACCAGCACCGTA Reverse- AGGCAGTCACCGACCAATAC
At-*GA20ox2*	qRT-PCR	Forward- TATCCTCCATGCCAAACACC Reverse- TCGCGCTCTCTCTATTCACA
At-*TUB*	qRT-PCR	Forward- AAACTCACTACCCCCAGCTTT Reverse- GAGAGGAGCAAAACCAACCA
ABI3	qRT-PCR	Forward- TCCGCAATCACTTCCTATGG Reverse- TGACTTTCTGCTTCTTTCTTTGG
LE25	qRT-PCR	Forward- GGAGAAAACCAAAGCCAATG Reverse- CCAGTAGTTCCAGTTCCAGTG
FUS3-like	qRT-PCR	Forward- AGGCGTTCTTCCCTCAACTT Reverse- ATTCGGCTGCTGTTATTTGG
XERICO-like	qRT-PCR	Forward- TCGTTTGAATGTCGCAGAAG Reverse- GGCCACATGAGAGATGGTTT
GOLS	qRT-PCR	Forward- TCTTTCAGCCAAATCCGTCT Reverse- AGCCCCTGGAGAACAGTAGT
Endoribonuclease	qRT-PCR	Forward- TCTTATTCCTGAGACTGGAGAACT Reverse- GGTAATCCTGCTGCTTGA AAA
Threonine ammonia lyase	qRT-PCR	Forward- AACCACCCCACAAATCAAGA Reverse- GCTATCAAACCCCCACCAC