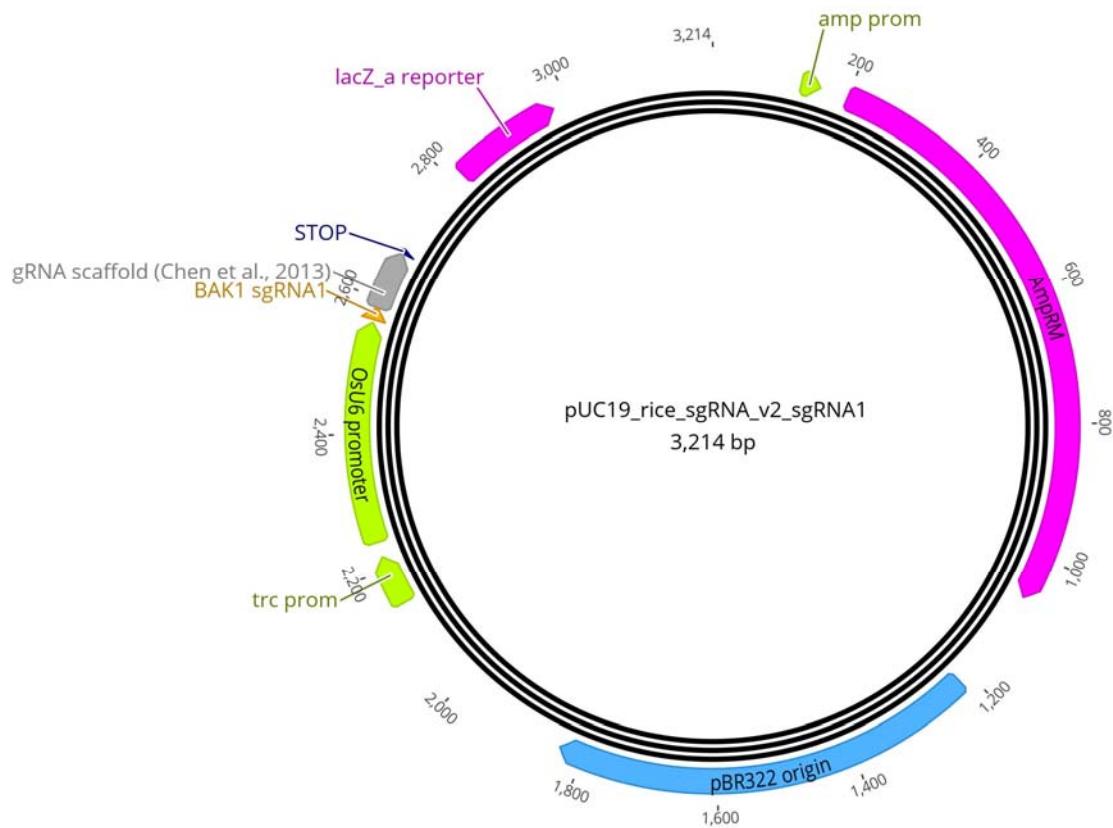


Table S1

Primers used for genotyping of transgenic lines.

Primer	5'-3' Sequence
UbiPro4	TTTAGCCCTGCCTTCATACG
WheatCas9R1	GGATTAAGGTGCCCTCGATGAGG
M13F	GTAAAACGACGCCAGT
M13R	CAGGAAACAGCTATGAC
Bar1	GTCTGCACCATCGTCAACC
Bar2	GAAGTCCAGCTGCCAGAAC
FH41	GAGATTCTGCTGAGATCCTACAT
FH42	GGATTATTACCAAAACTGTGACAAT
FH43	CTGAAAGAGAAGAAGGTGGAGAT
FH44	GCTATCTGTCGGTCATCATGTAC
FH46	TCAAACGGTGTAGCGGTTCTT
FH56	GTATGATCAGATTTCCGTCCG
FH57	TGAACAGCTCGTTACTGGCAG
FH59	TGTCCAAAAGCAATCCGACC
FH147	GATGCGGAAGGTCAAGGATCT
FH168	AGCAAGTTGAATGTGGGAGC
FH187	GTGGTCTCCGGCAACAAAGCACAGTGGTCT
FH188	TAGGTCTCAATGTGGGAGCTGCACCAGCCGGGAATC
FH189	GTGGTCTCCACATTCAACTTGCTGTTCAGAGCTATGCTGGGAACA
FH190	TAGGTCTCAGTCGACAACCTGCACCAGCCGGGAATC
FH191	GTGGTCTCCGAACCAGAAGGTCCGTTTCAGAGCTATGCTGGGAACA
FH192	TAGGTCTCACCAACACCTCTGCACCAGCCGGGAATC
FH193	GTGGTCTCCGTGGATGGGGTGGAGTTTCAGAGCTATGCTGGGAACA
FH194	TAGGTCTCAATGGACCATCTGCACCAGCCGGGAATC
FH195	GTGGTCTCCCATTACGCCATGTTTCAGAGCTATGCTGGGAACA
FH196	TAGGTCTCAAACCTCTCTGCACCAGCCGGGAATC
FH197	GTGGTCTCCAGTTCTGGACTACAGTTTCAGAGCTATGCTGGGAACA
FH198	GTGCGGTCTCCAAACAAAAAAAGCACCGACTCGGTGCCACT
FH199	TAGGTCTCACGAAGAGTTCTGCACCAGCCGGGAATC
FH200	GTGGTCTCCTCGACGGTGTGAGTTTCAGAGCTATGCTGGGAACA
FH201	TAGGTCTCATACCCCAGCCTGCACCAGCCGGGAATC
FH202	GTGGTCTCCGGTAGAACCAAAGTGTTCAGAGCTATGCTGGGAACA
FH203	TAGGTCTCATTATCCTGTCACCAGCCGGGAATC
FH204	GTGGTCTCCATAAGCTTCATTAGTTTCAGAGCTATGCTGGGAACA
FH205	TAGGTCTCACATCCAGACCTGCACCAGCCGGGAATC
FH206	GTGGTCTCCGATGTCGTACCAAGAGTTTCAGAGCTATGCTGGGAACA
FH207	TAGGTCTCAGCTCGACCTGCACCAGCCGGGAATC
FH208	GTGGTCTCCAAGCTGCGCTCCGGGTTTCAGAGCTATGCTGGGAACA
FH209	TGAAGCCTTCAGGACATGTAT
FH210	CACTATAGGGCGAATTGGAGA
FH221	TAGAAAAGCCCGCGACTTTC
FH224	ATTAGCTGAGGGCGGTTCGAATCT
FH227	TGTAAAACGACGCCAGTTTGGCGCTCTCATTATGTAT
FH228	CCTCTCTATGGGCAGTCGGTGATAGGAATCGCAACTTAAGAGTT
FH230	CCTCTCTATGGGCAGTCGGTGATCATGCCACAGCATATCCT
FH431	TCCCCATCCAAAACCCCTCG
FH445	TGTTCACCAATCATTGCCAGC
FH447	ATTTACCAAGATAAGCATTGGCAA



AAGAACGAACTAAGCCGGACAAAAAAAGGAGCACATATAACAAACCGTTTATTCA
TGAAATGGTCACGATGGATGATGG
GGCTCAGACTTGAGCTACGAGGCCGAGGCAGAGAAGCCTAGTGTGCTCTGCTTGGCCGTAACGGAGGATA
CGGCCGACGAGCGTGTACTACCGCGCGGATGCCGCTGGCGCTGCCGCTGGGGGGCCGTTGGATGGGGATCGGTGGGTCGCGG
GAGCGTTGAGGGGGAGACAGGTTAGTACCAACCTCGCCTACCGAACAA
TGAAAGAACCACCTATAACCCCGCGCGCTGC
CGCTTGTTGTTGTCAGTTCCCGAGTTCAA
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OsU6 promoter

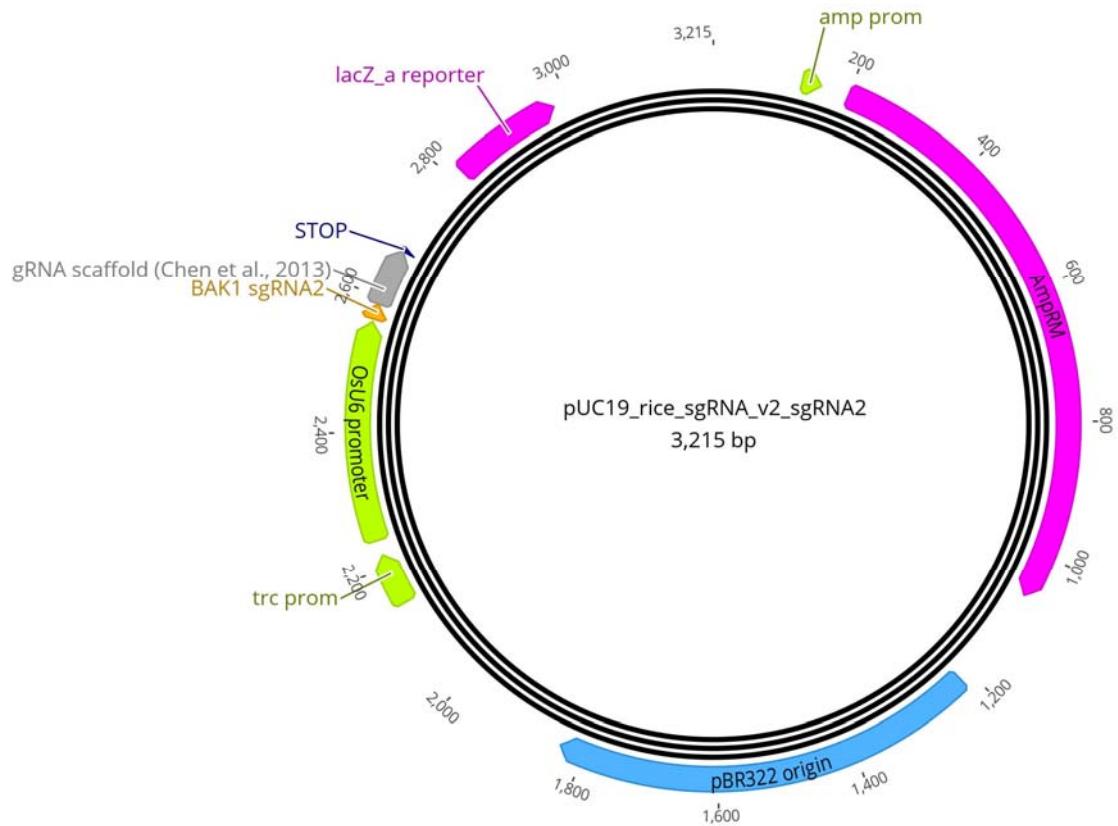
gRNA scaffold (Chen et al., 2013)

PolyT STOP

Target sequence

Figure S1

pUC19_rice_sgRNA_v2_sgRNA1 construct map and insert sequence.



AAGAACGAACTAAGCCGGACAAAAAAAGGAGCACATATAACAACCGGTTTATTGATGAATGGTCACGATGGATGATGG
 GGCTCAGACTTGAGCTACGAGGCCGAGGCAGAGAAGCCTAGTGTGCTCTGCTTGGGCCGTAACGGAGGATA
 CGGCCGACGAGCGTGTACTACCGCGCGGATGCCGCTGGCGCTGCCGCTGGGGGCCGTTGGATGGGGATCGGTGGGTCGCGG
 GAGCGTTGAGGGGAGACAGGTTAGTACCACTCGCCTACCGAACAAATGAAGAACCCACCTTATAACCCCGCGCGCTGC
 CGCTTGTTGAACTTGGAGGGTGCTAATATGTTAAGAGCTATGCTGGAAACAGCATAGCAAGTTAAATAAGGCTAG
 TCCGTTATCAACTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTT

OsU6 promoter

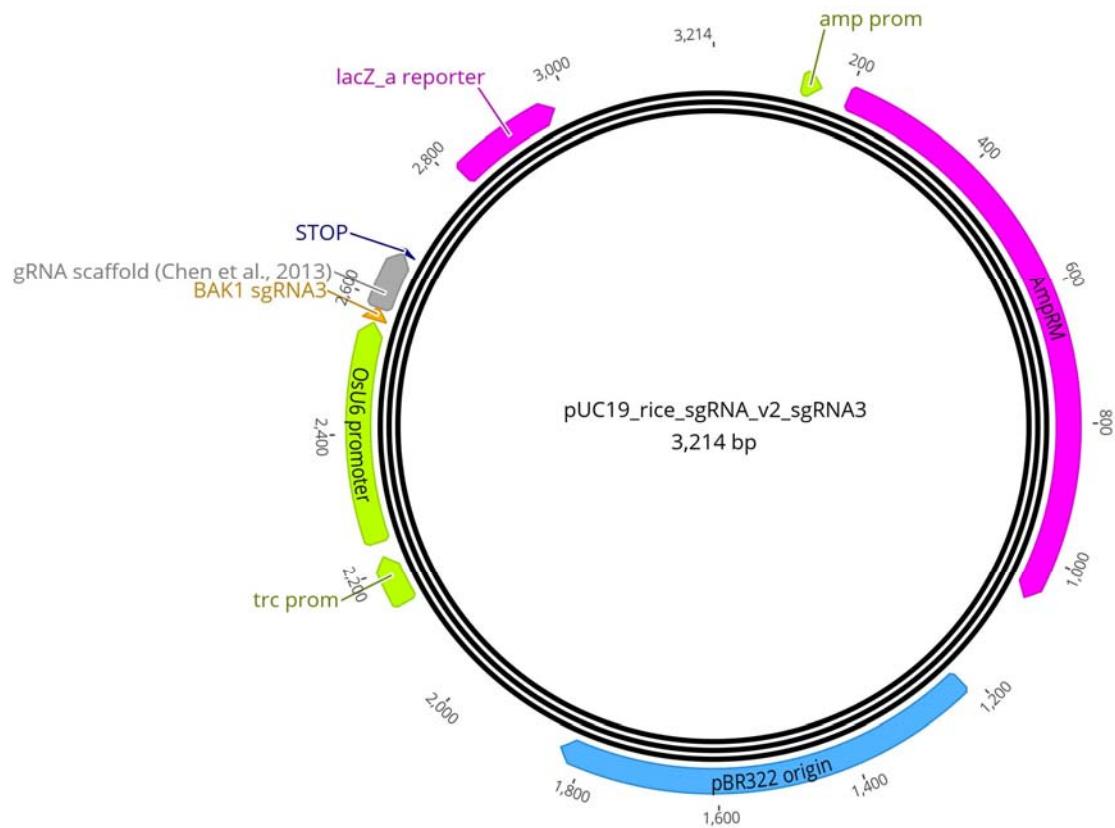
gRNA scaffold (Chen et al., 2013)

PolyT STOP

Target sequence

Figure S2

pUC19_rice_sgRNA_v2_sgRNA2 construct map and insert sequence.



AAGAACGAACTAAGCCGGACAAAAAAAGGAGCACATATAACAACCGGTTTATTCA
TGAAATGGTCACGATGGATGATGG
GGCTCAGACTTGAGCTACGAGGCCGAGGCAGAGAAGCCTAGTGTGCTCTGCTTGGCGTAACGGAGGATA
CGGCCGACGAGCGTGTACTACCGCGCGGATGCCGCTGGCGCTGCCGCTGGGGGCCGTTGGATGGGGATCGGTGGGTCGCGG
GAGCGTTGAGGGGAGACAGGTTAGTACCAACCTCGCCTACCGAACAA
TGAAGAACCACCTATAACCCCGCGCGCTGC
CGCTTGTTGATCCAGTCGTTGTTGCGGTTAACAGAGCTATGCTGGAAACAGCATAGCAAGTTAAATAAGGCTAGT
CCGTTATCAACTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTT

OsU6 promoter

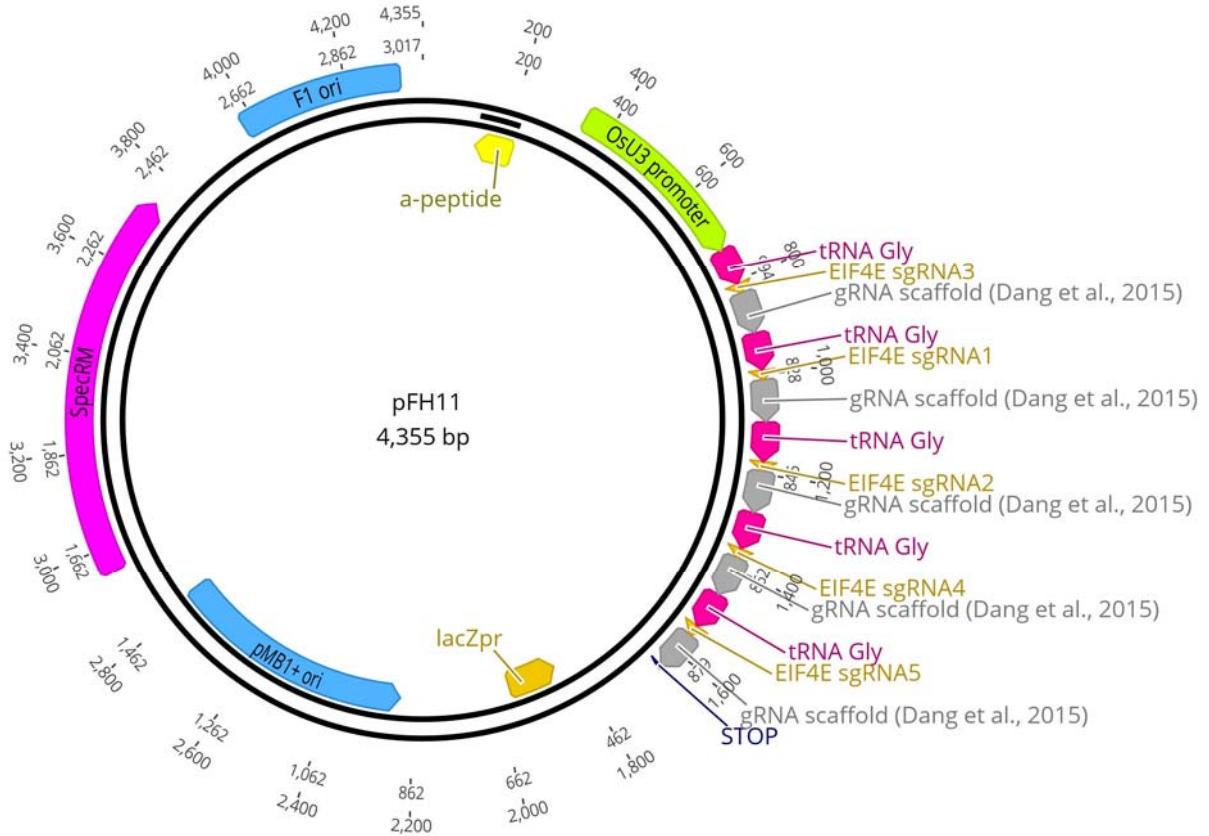
gRNA scaffold (Chen et al., 2013)

PolyT STOP

Target sequence

Figure S3

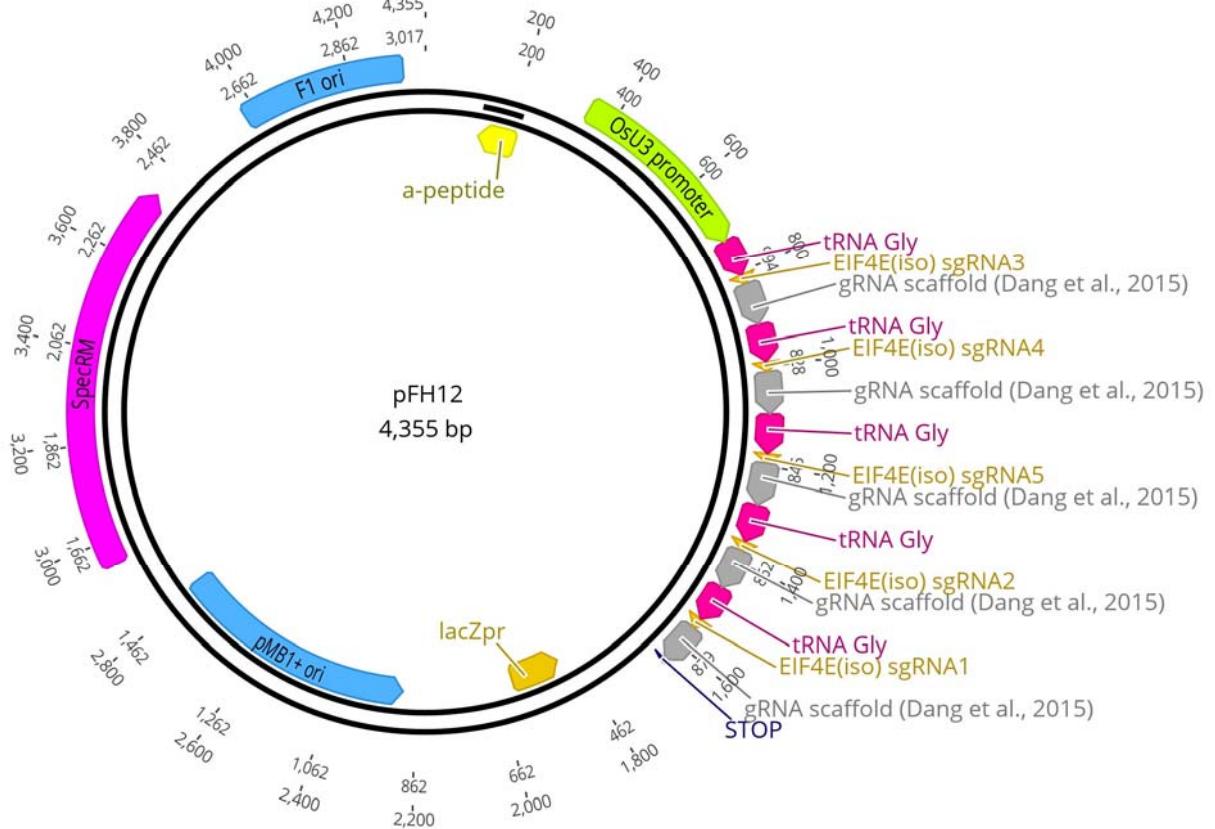
pUC19_rice_sgRNA_v2_sgRNA3 construct map and insert sequence.



AAGCTTAAGGAATCTTAAACATAACGAAACAGATCACTAAAGTTCTCTGAAGCAACTAAAGTTATCAGGCATGCATG
 GATCTTGAGGAATCAGATGTGCAGTCAGGGACCATAGCACAAGACAGGCCTTCTACTGGTGCTACCAGCAAATGCT
 GGAAGCCGGAACACTGGGTACGGTACGGAAACCACGTGATGTGAAGAAGTAAGATAAAACTGTAGGAGAAAAGCATTGCT
 AGTGGGCCATGAAGCCTTCAGGACATGTATTGCAGTATGGGCCGCCATTACGCAATTGGACAGACAACAAAGACTAG
 TATTAGTACCACTCGGCTATCCACATAGATCAAAGCTGATTTAAAAGAGTTGTGCAGATGATCCGTGGCAACAAAGCA
 CCAGTGGCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGATTCCCGCTGGTGCAGCTCCCACATT
 CAAACTTGCTGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT
 GGCACCGAGTCGGTGCACAAAGCACCAGTGGCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGAT
 TCCCGGCTGGTGCAGTTGTCGAACCAGAAGGTCCGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGC
 TAGTCGGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAAAGCACCAGTGGCTAGTGGTAGAATAGTACCC
 GCCACGGTACAGACCCGGTTCGATTCCCGCTGGTGCAGAAGGTGTGGATGGGTTGGAGTTTCAGAGCTATGCTGGGA
 ACAGCATAGCAAGTTGAAATAAGGCTAGTCGGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCACAAAGCACCAG
 TGGTCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGATTCCCGCTGGTGCAGATGGTCCATTAC
 GCCATGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA
 CCGAGTCGGTGCACAAAGCACCAGTGGCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGATTCCC
 GGCTGGTGCAGAAGGAGTTCTGGACTACAGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGCTAGT
 CCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCCTTTTTTTT

OsU3 promoter
 tRNA Gly
 gRNA scaffold (Dang et al., 2015)
 PolyT STOP
 Target sequences

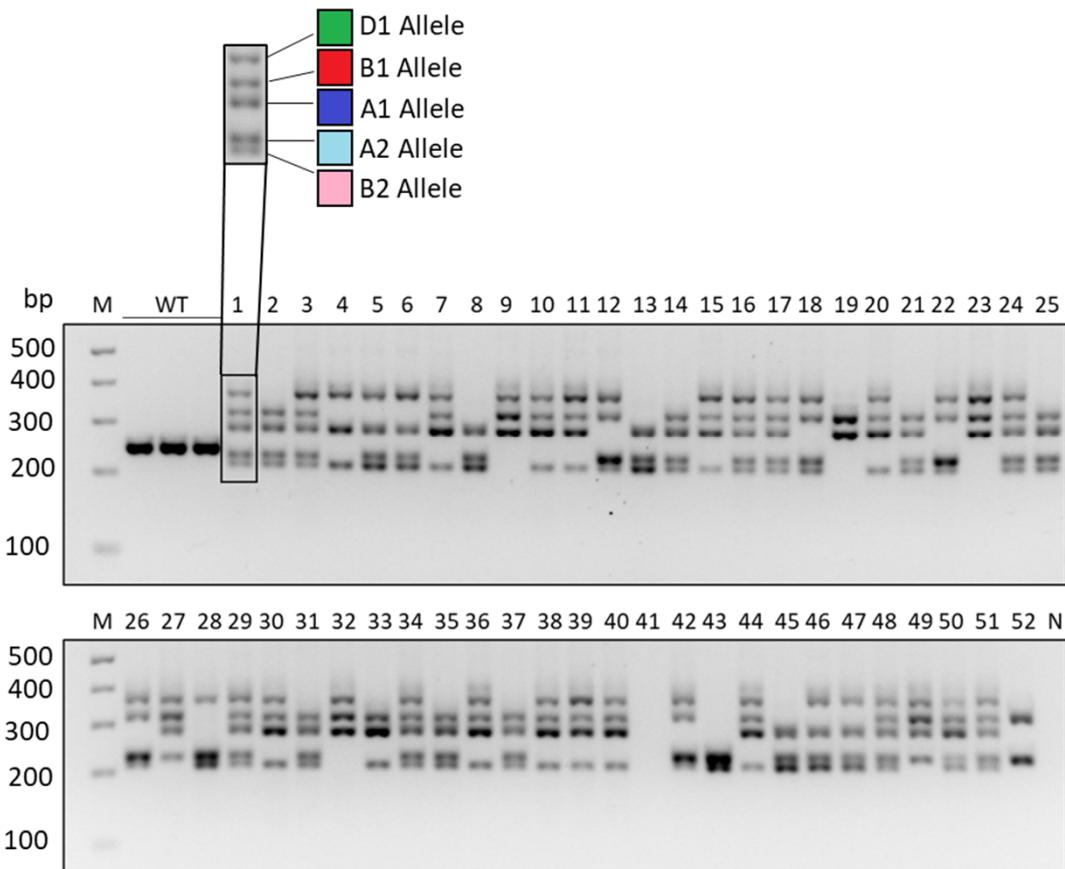
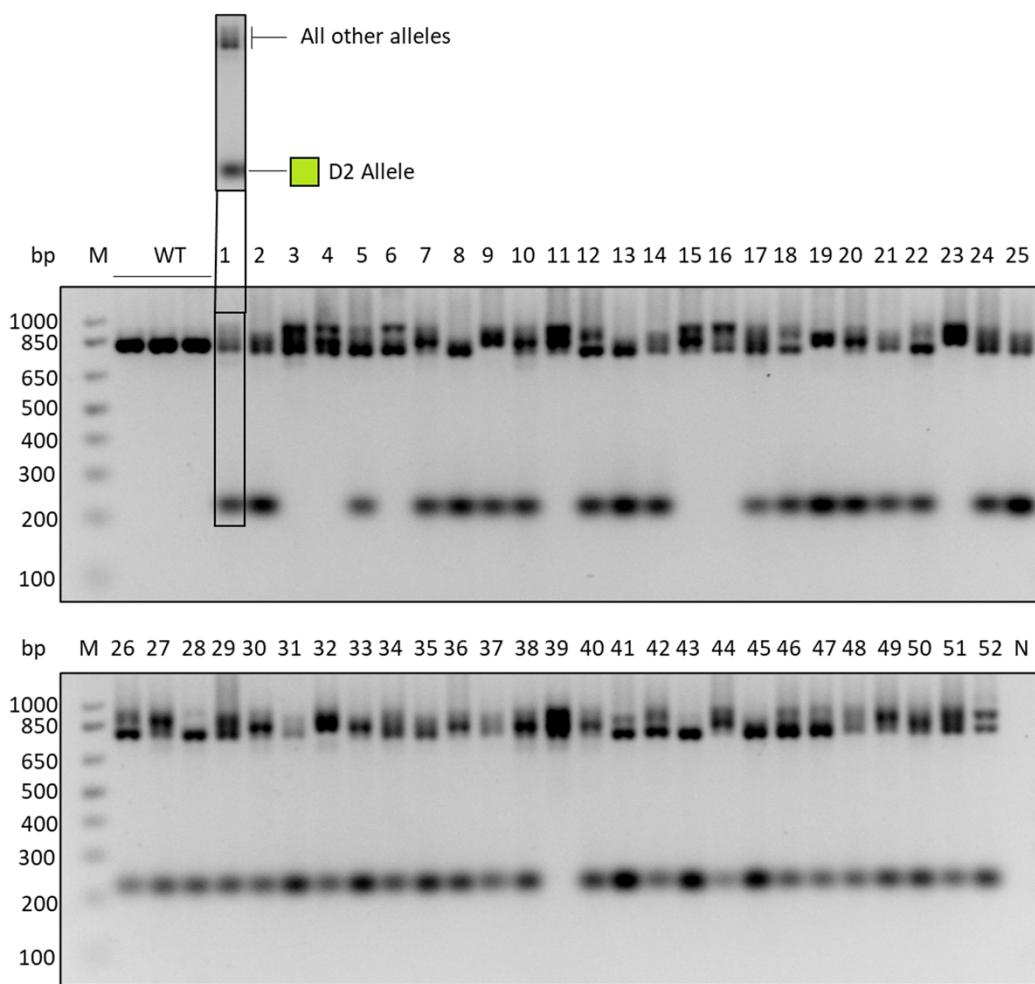
Figure S4
 pFH11 construct map and insert sequence.



AAGCTTAAGGAATCTTAAACATAACGAAACAGATCACTTAAAGTTCTCTGAAGCAACTTAAAGTTATCAGGCATGCATG
GATCTTGAGGAATCAGATGTGCAGTCAGGGACCATAGCACAAGACAGGCCTTCTACTGGTGCTACCAGCAAATGCT
GGAAGCCGGAACACTGGGTACGGTGGAAACCACGTGATGTGAAGAAGTAAGATAAAACTGTAGGAGAAAAGCATTGCT
AGTGGGCCATGAAGCCTTCAGGACATGTATTGCAGTATGGGCCGCCATTACGCAATTGGACAGACAACAAAGACTAG
TATTAGTACCACTCGGCTATCCACATAGATCAAAGCTGATTTAAAAGAGTTGTGCAGATGATCCGTGGCAACAAAGCA
CCAGTGGCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGATTCCCGCTGGTGAGAACTCTCGA
CGGTGTCGAGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGT
GGCACCGAGTCGGTGCAACAAAGCACCAGTGGTCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGAT
TCCCGGCTGGTGCAGGCTGGGTTAGAACCAAAGTGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGC
TAGTCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACAAAGCACCAGTGGTCTAGTGGTAGAATAGTACCC
GCCACGGTACAGACCCGGGTTCGATTCCCGCTGGTGCAGACAGGATAAGCTTCATTAGTTTCAGAGCTATGCTGGGA
ACAGCATAGCAAGTTGAAATAAGGCTAGTCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCAACAAAGCACCAG
TGGTCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGATTCCCGCTGGTGCAGGTCTGGATGTCGTA
CCAGAGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGCTAGTCCGTTATCAACTTGAAAAAGTGGCA
CCGAGTCGGTGCAACAAAGCACCAGTGGTCTAGTGGTAGAATAGTACCCGCCACGGTACAGACCCGGTTCGATTCCC
GGCTGGTGCAGGTCGAAGGCTGCGCTCCGGTTTCAGAGCTATGCTGGAACAGCATAGCAAGTTGAAATAAGGCTAGT
CCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTTT

OsU3 promoter
tRNA Gly
gRNA scaffold (Dang et al., 2015)
PolyT STOP
Target sequences

Figure S5
pFH12 construct map and insert sequence.

A**B****Figure S6**

PCR-genotyping of T1 progeny of *tabak1-2* T0 plant 1 with FH227 + FH228 primers (A) and FH227 + FH230 primers (B).

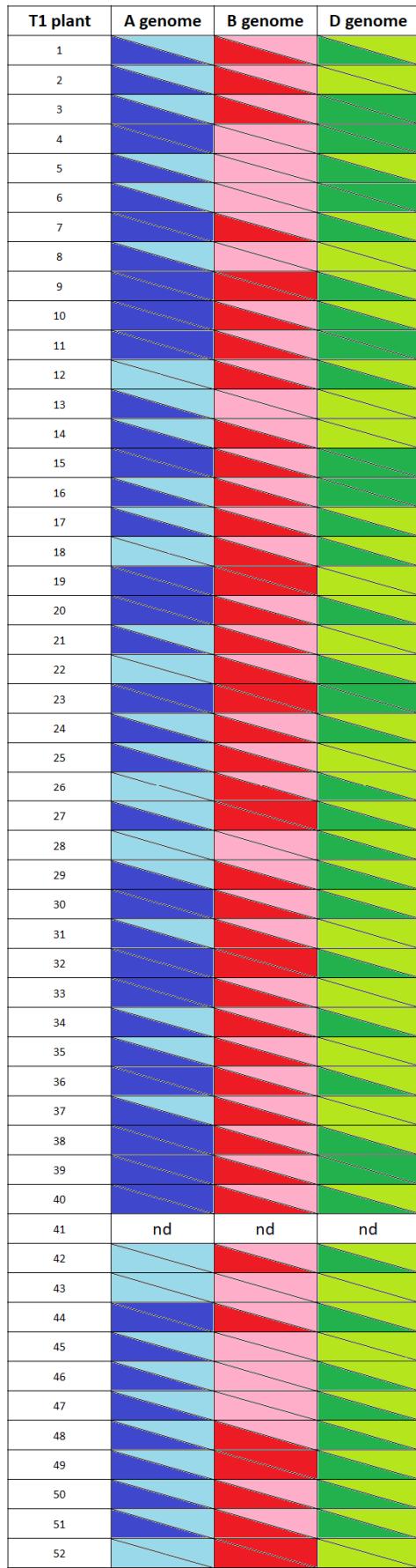


Figure S7

TaBAK1-2 allele distribution among T1 progeny of *tabak1-2* T0 plant 1.

TaBAK1-2_A(WT)	1	MAASPEMLRRCWAAAVALSAVLTVSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_T0-1_A1	1	MAASPEMLRRCWAAAVALSAVLTVSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_A(WT)	61	PCTWFHVTCTNDNSVIRVDSLGNAGLSQLGQLNLQYLELYSNNISGTIPLGN-	119
		PCTWFHVTCTNDNSVIRVDSLGNAGLSQLGQLNLQYLELYSNNISGTIPL +	
TaBAK1-2_T0-1_A1	61	PCTWFHVTCTNDNSVIRVDSLGNAGLSQLGQLNLQYLELYSNNISGTIPLRRQS*	120
TaBAK1-2_A(WT)	120	-LTNLVSLDLYLNKFTGGIPDTLGLKLLKLRLFLRLNNNSLSGQIPQS-----LTNISTLQ	172
	L +	G ++ + + R+ R +L IP S +N + LQ	
TaBAK1-2_T0-1_A1	121	VLGCRKAGG*TRELDKPGQFGSVPEQIHWRYSRHIGETLKVAIPPS*QQQSFWSNSTILQ	180
TaBAK1-2_A(WT)	173	VLDLSNNNLSGAVPSTGSFSLFTPISFGNNPNLCGPFTTKPCPGAPPFSPPPFNPPTPP	232
	VLDLSNNNLSGAVPSTGSFSLFTPISFGNNPNLCGPFTTKPCPGAPPFSPPPFNPPTPP		
TaBAK1-2_T0-1_A1	181	VLDLSNNNLSGAVPSTGSFSLFTPISFGNNPNLCGPFTTKPCPGAPPFSPPPFNPPTPP	240
TaBAK1-2_A(WT)	233	AAQGDPKTGAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKR	292
	AAQGDPKTGAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKR		
TaBAK1-2_T0-1_A1	241	AAQGDPKTGAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKR	300
TaBAK1-2_A(WT)	293	FSLRELQVASDNFSNKNILGRGGFGKVYKGRLTDGLVAVKRLKEERTPGGELQFQTEVE	352
	FSLRELQVASDNFSNKNILGRGGFGKVYKGRLTDGLVAVKRLKEERTPGGELQFQTEVE		
TaBAK1-2_T0-1_A1	301	FSLRELQVASDNFSNKNILGRGGFGKVYKGRLTDGLVAVKRLKEERTPGGELQFQTEVE	360
TaBAK1-2_A(WT)	353	MISMAVHRNLLRLRGFCMTPTERLLVYPYMANGVASRLRERGPNEPALEWEKRTRIALG	412
	MISMAVHRNLLRLRGFCMTPTERLLVYPYMANGVASRLRERGPNEPALEWEKRTRIALG		
TaBAK1-2_T0-1_A1	361	MISMAVHRNLLRLRGFCMTPTERLLVYPYMANGVASRLRERGPNEPALEWEKRTRIALG	420
TaBAK1-2_A(WT)	413	SARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTI	472
	SARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTI		
TaBAK1-2_T0-1_A1	421	SARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTI	480
TaBAK1-2_A(WT)	473	GHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEK	532
	GHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEK		
TaBAK1-2_T0-1_A1	481	GHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEK	540
TaBAK1-2_A(WT)	533	KVEMLVDPLDLQSVYVEHEVEALIQVALCLTGQSPMDRPMSEVVRMLEGDGLAERWEEWQ	592
	KVEMLVDPLDLQSVYVEHEVEALIQVALCLTGQSPMDRPMSEVVRMLEGDGLAERWEEWQ		
TaBAK1-2_T0-1_A1	541	KVEMLVDPLDLQSVYVEHEVEALIQVALCLTGQSPMDRPMSEVVRMLEGDGLAERWEEWQ	600
TaBAK1-2_A(WT)	593	KVEVVRQEAEELAPRNNDWIVDSTYNLRAVELSGPR- 627	
	KVEVVRQEAEELAPRNNDWIVDSTYNLRAVELSGPR		
TaBAK1-2_T0-1_A1	601	KVEVVRQEAEELAPRNNDWIVDSTYNLRAVELSGPR* 636	

Figure S8

Protein alignment of the *tabak1-2* T0 plant 1 A1 allele to the WT.

TaBAK1-2_A(WT)	1	MAASPEMLRRCWAAAAVLSAVLTVSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_T0-1_A2	1	MAASPEMLRRCWAAAAVLSAVLTVSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_A(WT)	61	PCTWFHVCNTDNSVIRVDLGNAGQLSGALVSQLGQLKNLQYLELYSNNISGTIPLELGNL	120
		PCTWFHVCNTDNSVIRVDLGNAGQLSGALVSQLGQLKNLQYLELYSNI ELGNL	
TaBAK1-2_T0-1_A2	61	PCTWFHVCNTDNSVIRVDLGNAGQLSGALVSQLGQLKNLQYLELYSN---NISGELGNL	116
TaBAK1-2_A(WT)	121	TNLVSLDLYNKFTGGIPDTLGKLLKLRFLRLNNNSLSGQIPQSLTNISTLQVLDLSNNN	180
		TNLVSLDLYNKFTGGIPDTLGKLLKLRFLRLNNNSLSGQIPQSLT +VLDLSNNN	
TaBAK1-2_T0-1_A2	117	TNLVSLDLYNKFTGGIPDTLGKLLKLRFLRLNNNSLSGQIPQSLT---NKVLDLSNNN	172
TaBAK1-2_A(WT)	181	LSGAVPSTGSFSLFTPISFGNNPNLCGPGTTKPCPGAPPFSPPPFNPPTPPAAQGDPKT	240
		LSGAVPSTGSFSLFTPISFGNNPNLCGPGTTKPCPGAPPFSPPPFNPPTPPAAQGDPKT	
TaBAK1-2_T0-1_A2	173	LSGAVPSTGSFSLFTPISFGNNPNLCGPGTTKPCPGAPPFSPPPFNPPTPPAAQGDPKT	232
TaBAK1-2_A(WT)	241	GAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	300
		GAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	
TaBAK1-2_T0-1_A2	233	GAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	292
TaBAK1-2_A(WT)	301	ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVR	360
		ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVR	
TaBAK1-2_T0-1_A2	293	ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVR	352
TaBAK1-2_A(WT)	361	NLLRLRGFCMTPTERLLVYPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	420
		NLLRLRGFCMTPTERLLVYPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	
TaBAK1-2_T0-1_A2	353	NLLRLRGFCMTPTERLLVYPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	412
TaBAK1-2_A(WT)	421	HDHCDPKI IHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTAVRGTIGHIAPEYL	480
		HDHCDPKI IHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTAVRGTIGHIAPEYL	
TaBAK1-2_T0-1_A2	413	HDHCDPKI IHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTAVRGTIGHIAPEYL	472
TaBAK1-2_A(WT)	481	STGKSSEKTDVFGYGINLLELITGQRFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	540
		STGKSSEKTDVFGYGINLLELITGQRFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	
TaBAK1-2_T0-1_A2	473	STGKSSEKTDVFGYGINLLELITGQRFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	532
TaBAK1-2_A(WT)	541	DLQSVYVEHEVEALIQVALLCTQGSPMDRPMSEVVRMLEGDGLAERWEWQKVEVVRQE	600
		DLQSVYVEHEVEALIQVALLCTQGSPMDRPMSEVVRMLEGDGLAERWEWQKVEVVRQE	
TaBAK1-2_T0-1_A2	533	DLQSVYVEHEVEALIQVALLCTQGSPMDRPMSEVVRMLEGDGLAERWEWQKVEVVRQE	592
TaBAK1-2_A(WT)	601	AELAPRNNDWIVDSTYNLRAVELSGPR	627
		AELAPRNNDWIVDSTYNLRAVELSGPR	
TaBAK1-2_T0-1_A2	593	AELAPRNNDWIVDSTYNLRAVELSGPR	619

Figure S9

Protein alignment of the *tabak1-2* T0 plant 1 A2 allele to the WT.

TaBAK1-2_B(WT)	1	MAASPEMLRRRWAAAVAVLSVVLAVSRVAANTEGDALYSLRQLSKDANNVLQSWDPTLVN	60
TaBAK1-2_T0-1_B1	1	MAASPEMLRRRWAAAVAVLSVVLAVSRVAANTEGDALYSLRQLSKDANNVLQSWDPTLVN	60
TaBAK1-2_B(WT)	61	PCTWFHVTCTNDNSVIRVLDGNAQLSGALVSQQLQNLQYLELYSNNISGTIPLELG--	118
TaBAK1-2_T0-1_B1	61	PCTWFHVTCTNDNSVIRVLDGNAQLSGALVSQQLQNLQYLELYSNNISGTIPL L	
TaBAK1-2_B(WT)	119	-----NLTNLVSLLYLNKFTGGIPDTLQQLKLRLFLRN	154
TaBAK1-2_T0-1_B1	121	HTHTTRSPPNPPVGETSASRYAALGNLTNLVSLDLYLNKFTGGIPDTLQQLKLRLFLRN	180
TaBAK1-2_B(WT)	155	NSLSGQIPQSNTNISTLQVLDLSNNNLGAVPSTGSFSLFTPISFGNNPNLCGPGTSKPC	214
TaBAK1-2_T0-1_B1	181	NSLSGQIPQSNTNISTLQVLDLSNNNLGAVPSTGSFSLFTPISFGNNPNLCGPGTSKPC	240
TaBAK1-2_B(WT)	215	PGAPPFSPPPPPFPNPPTPGDPKTGAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHF	274
TaBAK1-2_T0-1_B1	241	PGAPPFSPPPPPFPNPPTPGDPKTGAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHF	300
TaBAK1-2_B(WT)	275	FDVPAEEDPEVHLGQLKRFSLRELQVASDNFSNKNILGRGGFGKVKGR LTDGTLVAVKR	334
TaBAK1-2_T0-1_B1	301	FDVPAEEDPEVHLGQLKRFSLRELQVASDNFSNKNILGRGGFGKVKGR LTDGTLVAVKR	360
TaBAK1-2_B(WT)	335	LKEERTPGGELQFQTEVEMISMAVHRNLLRLRGFCMTPTERLLVVPYMANGSVASRLRER	394
TaBAK1-2_T0-1_B1	361	LKEERTPGGELQFQTEVEMISMAVHRNLLRLRGFCMTPTERLLVVPYMANGSVASRLRER	420
TaBAK1-2_B(WT)	395	GPNEPALEWEKRTRIALGSARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLA	454
TaBAK1-2_T0-1_B1	421	GPNEPALEWEKRTRIALGSARGLSYLHDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLA	480
TaBAK1-2_B(WT)	455	KLMDYKDTHVTTAVRGTIGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLA	514
TaBAK1-2_T0-1_B1	481	KLMDYKDTHVTTAVRGTIGHIAPEYLSTGKSSEKTDVFGYGIMLLELITGQRAFDLARLA	540
TaBAK1-2_B(WT)	515	NDDDVMLLDWVKGLLKEKKVEMLVDPDLQSVYVEHEVEALIQVALLCTQGSPMDRPMSE	574
TaBAK1-2_T0-1_B1	541	NDDDVMLLDWVKGLLKEKKVEMLVDPDLQSVYVEHEVEALIQVALLCTQGSPMDRPMSE	600
TaBAK1-2_B(WT)	575	VVRMLEGDGLAERWEEWQKVEVVRQEAEALAPRNNNDIVDSTYNLRAVELSGPR	627
TaBAK1-2_T0-1_B1	601	VVRMLEGDGLAERWEEWQKVEVVRQEAEALAPRNNNDIVDSTYNLRAVELSGPR	653

Figure S10

Protein alignment of the *tabak1-2* T0 plant 1 B1 allele to the WT.

TaBAK1-2_B(WT)	1	MAASPEMLRRRWAAAVAVLSVVLAVSRVAANTEGDAlysLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_T0-1_B2	1	MAASPEMLRRRWAAAVAVLSVVLAVSRVAANTEGDAlysLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_B(WT)	61	PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQIQLGQLKLNQYLELYSNNISGTIPLELGNL	120
		PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQIQLGQLKLNQYLELYSNNISGT	
TaBAK1-2_T0-1_B2	61	PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQIQLGQLKLNQYLELYSNNISGTN-----	113
TaBAK1-2_B(WT)	121	TNLVSLDLYLNKFTGGIPDTLGQLLKLRFLRLNNNSLSGQIPQSLTNISTLQVLDLSNNN	180
		LVSLDLYLNKFTGGIPDTLGQLLKLRFLRLNNNSLSGQIPQSLT +TLQVLDLSNNN	
TaBAK1-2_T0-1_B2	114	--LVSLDLYLNKFTGGIPDTLGQLLKLRFLRLNNNSLSGQIPQSLT--NTLQVLDLSNNN	169
TaBAK1-2_B(WT)	181	LSGAVPSTGSFSLFTPISFGNNPNLCGPGTSKPCPGAPPFSPPPFNPPTPPTPGDPKT	240
		LSGAVPSTGSFSLFTPISFGNNPNLCGPGTSKPCPGAPPFSPPPFNPPTPPTPGDPKT	
TaBAK1-2_T0-1_B2	170	LSGAVPSTGSFSLFTPISFGNNPNLCGPGTSKPCPGAPPFSPPPFNPPTPPTPGDPKT	229
TaBAK1-2_B(WT)	241	GAIAGGVAAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	300
		GAIAGGVAAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	
TaBAK1-2_T0-1_B2	230	GAIAGGVAAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	289
TaBAK1-2_B(WT)	301	ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVHR	360
		ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVHR	
TaBAK1-2_T0-1_B2	290	ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVHR	349
TaBAK1-2_B(WT)	361	NLLRLRGFCMTPTERLLVYPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	420
		NLLRLRGFCMTPTERLLVYPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	
TaBAK1-2_T0-1_B2	350	NLLRLRGFCMTPTERLLVYPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	409
TaBAK1-2_B(WT)	421	HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYL	480
		HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYL	
TaBAK1-2_T0-1_B2	410	HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYL	469
TaBAK1-2_B(WT)	481	STGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	540
		STGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	
TaBAK1-2_T0-1_B2	470	STGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	529
TaBAK1-2_B(WT)	541	DLQSVYVEHEVEALIQVALLCTQGSPMDRPMKSEVVRMLEGDGLAERWEWQKVEVVRQE	600
		DLQSVYVEHEVEALIQVALLCTQGSPMDRPMKSEVVRMLEGDGLAERWEWQKVEVVRQE	
TaBAK1-2_T0-1_B2	530	DLQSVYVEHEVEALIQVALLCTQGSPMDRPMKSEVVRMLEGDGLAERWEWQKVEVVRQE	589
TaBAK1-2_B(WT)	601	AELAPRNNDWIVDSTYNLRAVELSGPR	627
		AELAPRNNDWIVDSTYNLRAVELSGPR	
TaBAK1-2_T0-1_B2	590	AELAPRNNDWIVDSTYNLRAVELSGPR	616

Figure S11

Protein alignment of the *tabak1-2* T0 plant 1 B2 allele to the WT.

TaBAK1-2_D (WT)	1	MAASPEMLRRRWAAAALSVVLAWSRVSANTEGDALYSLRQLSKDANNVLQSWDP TLVN	60
TaBAK1-2_T0-1_D1	1	MAASPEMLRRRWAAAALSVVLAWSRVSANTEGDALYSLRQLSKDANNVLQSWDP TLVN	60
TaBAK1-2_D (WT)	61	PCTWFHVT CNTDNS VIRVDLGN AQLSGALVSQLGQLKNLQYLELYSNNISGTIPL EGNL	120
TaBAK1-2_T0-1_D1	61	PCTWFHVT CNTDNS VIRVDLGN AQLSGALVSQLGQLKNLQYLELYSNNISGTIPL+ G L	120
TaBAK1-2_D (WT)	121	TNLVSL DLYLN KFTGGIPDTLGQLLKL RFLRLNNNSLSG-----	159
TaBAK1-2_T0-1_D1	121	*ENRVL *LCGD KRR *GSLQ RL A GNV PRLA QDH *G *RL PR *RT *QTWS VWI CT*TNSL AVF	180
TaBAK1-2_D (WT)	160	-----QIPQS LTNISTLQVLDLSNNNLSGAVPSTGSFSLFTP I	197
TaBAK1-2_T0-1_D1	181	+ + + F QTHWGNS *SCDSSVLT TVFLVKFHNP *PILAPSKFWIYQTTISLERFHQLARFHSLPL *	240
TaBAK1-2_D (WT)	198	SFGNNPNL CPGPTT KPCPGAPPFS PPPPFN PPAQGD PKTGAIAGGV AAGA ALIF AV	257
TaBAK1-2_T0-1_D1	241	G F P + K + + VLVI IQIF VARV LRNHVL GHLLFLHLHHSILQHHPRHKVTLKPEQ LLEV LLRVLH *YLLF	300
TaBAK1-2_D (WT)	258	PAIGF ALWRRK PEEH FF DVPAEEDP E VHLGQLKRF SRL RELQ VASDN FSNK N ILGRGG FG	317
TaBAK1-2_T0-1_D1	301	+ + + + + + L + ++ + + + + LQDL LHCG GDVN LKSISLMSL RRIQ KCTL AS *RG SH *GSFK LLAITS AIRT F *EEVALE	360
TaBAK1-2_D (WT)	318	KVYKG RLTD GTLV AVKRLKEERTPG GELQ F QT EVEM ISMAVHRNLLRLRGFCMTP TERLL	377
TaBAK1-2_T0-1_D1	361	+ + G + K K + + + + RCTRG D *RMVHW *QLKD *KKNVLLVANSNSKQSK *LWQCIGTCFD SVDSA *HLQNGY *	420
TaBAK1-2_D (WT)	378	VYPYMANGSVASRLRERGPNEPALEWEKRTRIALG SARG LSYLHDHC DP KII HRDVKAAN	437
TaBAK1-2_T0-1_D1	421	++ G L + K + + + P + K SIHTWLTV ALHHVCESEGQMSRLLNGKKELGLHWDLPEDCLTC M ITV I PRSFIV MSKP QT	480
TaBAK1-2_D (WT)	438	ILLDED FEA VVGDF GLAKLMDYKD THVTTA VRG TIGHIA PEYL STG KSE KTDVFGY GIM	497
TaBAK1-2_T0-1_D1	481	+ + L + G + P + + FSWMKTLRRLWVTLDWPSLWTT RTLM *PQPSVERSGILLPSTYPPESPPRRM FS VTASC	540
TaBAK1-2_D (WT)	498	LLELITGQRAFDLARL ANDDDVM LLDWVKG LLKEKKV EMLVDP DLQSVY VHEVEALIQV	557
TaBAK1-2_T0-1_D1	541	L G+ L L KG K ++ ++ + FW SLSL GRGH STSHVLQTTM SCCL TG *KGC *KRR RWRCWWTR TCA RCTW STRW RR *SRW	600
TaBAK1-2_D (WT)	558	ALLCTQGSPMDR PKMSEVVRM LEGD GLAERWE EWQKV E VVRQ EAELAPRN NDWIVD STYN	617
TaBAK1-2_T0-1_D1	601	+ G P + G ++ + RCCARRGRRWTGPRC RRW *GCWRATG WRSAGRSGR WRWS GR RRSW PRETT GSST PPTT	660
TaBAK1-2_D (WT)	618	LRAVEL SGPR 627	
TaBAK1-2_T0-1_D1	661	SGRWSSP ARG 670	

Figure S12

Protein alignment of the *tabak1-2* T0 plant 1 D1 allele to the WT.

TaBAK1-2_D(WT)	1 MAASPEMLRRRWAAAALSVVLAWSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_T0-1_D2	1 MAASPEMLRRRWAAAALSVVLAWSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_D(WT)	61 PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQLGQLKNLQYLELEYSNNISGTIPL	120
TaBAK1-2_T0-1_D2	61 PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQLGQLKNLQYLELEYSNNISGTIPL	120
TaBAK1-2_D(WT)	121 TNLVSLDLYLNKFTGGIPDTLQQLLKLRLRLNNNSLSQIPQSNTNISTLQVLDLSNNN	180
	++ L + + + + + L + L + +	
TaBAK1-2_T0-1_D2	121 IYQTTISLERFHQLARFHSLPL*VLVIIQIFVARVLRNHLGHLLFLHLHHSILQHHPRH	180
TaBAK1-2_D(WT)	181 LSGAVPSTGSFSLFTPISFGNNPNLCGPGTTKPCPGAPPFSPPPFNPPTPAAQGDPKT	240
	P L +	
TaBAK1-2_T0-1_D2	181 KVTLKPEQLLEVLLRVLH*-----	199
TaBAK1-2_D(WT)	241 GAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	300
	+ + + + L + + ++	
TaBAK1-2_T0-1_D2	200 -----YLLFLQLDLHCDDVNLSISLMSLLRRIQKCTLAS*RGSH*GSFKL	246
TaBAK1-2_D(WT)	301 ASDNFNSKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISAVHR	360
	+ + + + G + K K+ + + + +	
TaBAK1-2_T0-1_D2	247 LAITSAIRTF*EEVALERCTRGD*RMVHW*QLKD*KKNVLLVANSNSKQSK*LWQCIG	306
TaBAK1-2_D(WT)	361 NLLRLRGFCMTPTERLLVYPYMANGVASRILRERGPNEPALEWEKRTRIALGSARGLSYL	420
	++ G L +K +	
TaBAK1-2_T0-1_D2	307 TCFDSVDSA*HLQNGY*SIHTWLTVLHHVCESEGQMSRLLNGKELGLHWDLPEDCLTC	366
TaBAK1-2_D(WT)	421 HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIIGHIAPEYL	480
	P+ K + + L + G + P	
TaBAK1-2_T0-1_D2	367 MITVIPRSFIVMSKPQTFSWMKTLRRLWVTLDWPSLWTTRTLM*PQPSVERSGILLPSTY	426
TaBAK1-2_D(WT)	481 STGKSSEKTDVFGYGINLLEITGQRAFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	540
	+ L G+ L L KG K ++	
TaBAK1-2_T0-1_D2	427 PPESPPRRRMFSVTASCFWSLSLGRGHSTSHVLQTTMSCCLTG*KGC*KRRRWRCWWTR	486
TaBAK1-2_D(WT)	541 DLQSVYVEHEVEALIQVALLCTQGSPMDRPMSEVVRMLEGDGLAERWEWQKVEVVRQE	600
	++ + +G P+ G ++ +	
TaBAK1-2_T0-1_D2	487 TCRACTWSTRWRR*SRWRCCARRGRRWTGPRCRRW*GCWRATGWRSGRSRRWRSGRR	546
TaBAK1-2_D(WT)	601 AELAPRNNDWIVDSTYNLRAVELSGPR	627
TaBAK1-2_T0-1_D2	547 RSWPRETTTGSSTPPTSGRWSPPARG	573

Figure S13

Protein alignment of the *tabak1-2* T0 plant 1 D2 allele to the WT.

TaBAK1-2_A (WT)	1 MAASPEMLRRCWWAAAVALSAVLTVSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
BAK1-2A_T0-2_A1	1 MAASPEMLRRCWWAAAVALSAVLTVSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_A (WT)	61 PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQGLQKLNLQYLELYSNNISGTIPL	120
BAK1-2A_T0-2_A1	61 PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQGLQKLNLQYLELYSNNISGTIPL	117
TaBAK1-2_A (WT)	121 TNLVSLDLYLNKFTGGIPDTLGKLLKLRFLRLNNNSLSQIIPQSLTNISTLQVLDLSNNN	180
BAK1-2A_T0-2_A1	118 -----	TLQVLDLSNNN 128
TaBAK1-2_A (WT)	181 LSGAVPSTGSFSLFTPISFGNNPNLCGPGTTKPCPGAPPFSPPPFNPPTPPAAQGDPKT	240
BAK1-2A_T0-2_A1	129 LSGAVPSTGSFSLFTPISFGNNPNLCGPGTTKPCPGAPPFSPPPFNPPTPPAAQGDPKT	188
TaBAK1-2_A (WT)	241 GAIAGGVAAGAACIFAVPAIGFALWRRRKPEEHHFDVPAEEDPEVHLGQLKRFSLRELQV	300
BAK1-2A_T0-2_A1	189 GAIAGGVAAGAACIFAVPAIGFALWRRRKPEEHHFDVPAEEDPEVHLGQLKRFSLRELQV	248
TaBAK1-2_A (WT)	301 ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVR	360
BAK1-2A_T0-2_A1	249 ASDNFSNKNILGRGGFGKVYKGRLTDGTLVAVKRLKEERTPGGELQFQTEVEMISMAVR	308
TaBAK1-2_A (WT)	361 NLLRLRGFCMTPTERLLVVPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	420
BAK1-2A_T0-2_A1	309 NLLRLRGFCMTPTERLLVVPYMANGSVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	368
TaBAK1-2_A (WT)	421 HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYL	480
BAK1-2A_T0-2_A1	369 HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYL	428
TaBAK1-2_A (WT)	481 STGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	540
BAK1-2A_T0-2_A1	429 STGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLLKEKKVEMLVDP	488
TaBAK1-2_A (WT)	541 DLQSVYVEHEVEALIQVALLCCTQGSPMDRPKMSEVVRMLEGDGLAERWEEWQKVEVVRQE	600
BAK1-2A_T0-2_A1	489 DLQSVYVEHEVEALIQVALLCCTQGSPMDRPKMSEVVRMLEGDGLAERWEEWQKVEVVRQE	548
TaBAK1-2_A (WT)	601 AELAPRNNDWIVDSTYNLRAVELSGPR	627
BAK1-2A_T0-2_A1	549 AELAPRNNDWIVDSTYNLRAVELSGPR	575

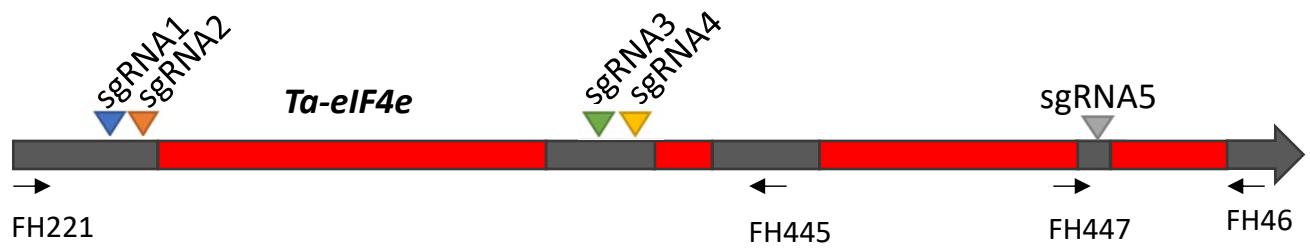
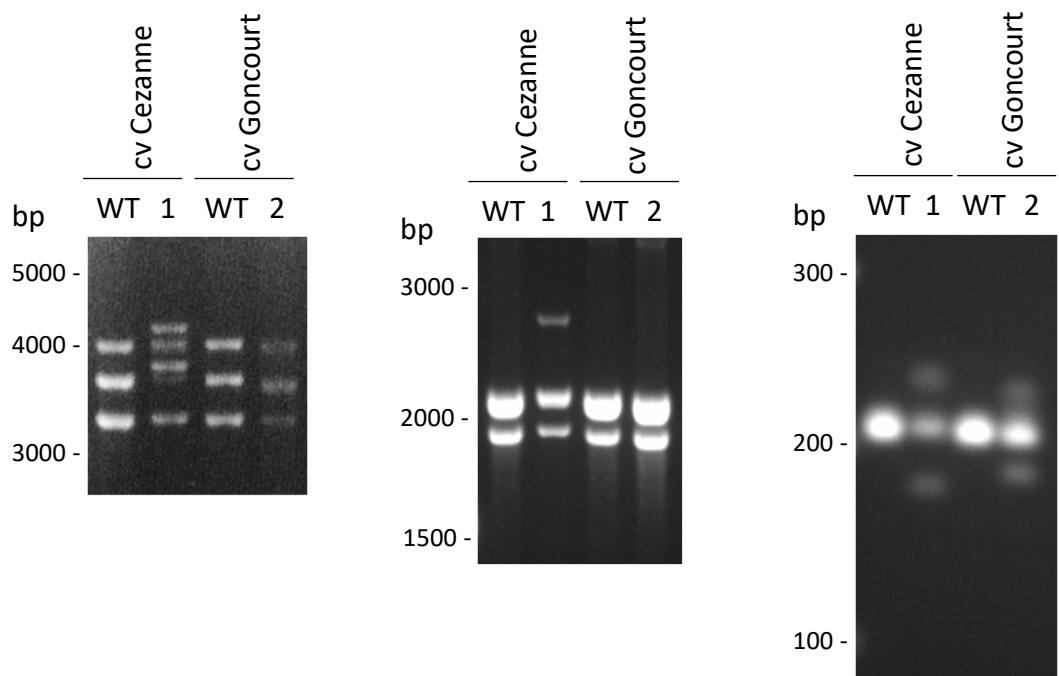
Figure S14

Protein alignment of the *tabak1-2* T0 plant 2 A1 allele to the WT.

TaBAK1-2_D(WT)	1 MAASPEMLRRRWAAAALSVVLAWSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_T0-2_D1	1 MAASPEMLRRRWAAAALSVVLAWSRVSANTEGDALYSLRQSLKDANNVLQSWDPTLVN	60
TaBAK1-2_D(WT)	61 PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQLGQLKNLQYLELYSNNISGTIPLGNL	120
TaBAK1-2_T0-2_D1	61 PCTWFHVTCTNDNSVIRVDLGNAQLSGALVSQLGQLKNLQYLELYSNNISGTIPL	119
TaBAK1-2_D(WT)	121 TNLVSLDLYLNLKFTGGIPDTLQQLLKLRLRLNNNSLSQIIPQSLTNISTLQVLDLSNNN	180
	G L + ++ +	
TaBAK1-2_T0-2_D1	120 QTWSVWICT*TNSLAVFQTHWGNS*SCDSSVLTTTVFLVKFHNP*PILAPSKFWIYQTTI	179
TaBAK1-2_D(WT)	181 LSGAVPSTGSFSLFTPISFGNNPNLCGPPTKPCPGAPPFSPPPFNPPTPPAAQGDPKT	240
	F G F P + K	
TaBAK1-2_T0-2_D1	180 SLERFHQLARFHSLPL*VLVIIQIFVARVLRNHVLGHLLFLHLHHHSILQHHPRHKVTLKP	239
TaBAK1-2_D(WT)	241 GAIAGGVAAGAALIFAVPAIGFALWRRRKPEEHFFDVPAEEDPEVHLGQLKRFSLRELQV	300
	+ + + + + + L + ++	
TaBAK1-2_T0-2_D1	240 EQLLEVLLRVLH*YLLFLQLDLHCGGDVNLSISLMSLLRIQKCTLAS*RGSH*GSFKL	299
TaBAK1-2_D(WT)	301 ASDNFSNKNILGRGGFGKVYKGR LTDGLVAVKRLKEERTPGGELQFQTEVEMISMAVHR	360
	+ + + + + K K+ + + + +	
TaBAK1-2_T0-2_D1	300 LAITSAIRTF*EEVALERCTRGD*RMVHW*QLKD*KKNVLLVANSNSKQKSK*LVWQCIG	359
TaBAK1-2_D(WT)	361 NLLRLRGFCMTPTERLLVYPYMANGVASRLRERGPNEPALEWEKRTRIALGSARGLSYL	420
	++ G L +K +	
TaBAK1-2_T0-2_D1	360 TCFDSVDSA*HLQNGY*SIHTWLTVLHVCESEGQMSRLLNGKKEGLHWDLPEDCLTC	419
TaBAK1-2_D(WT)	421 HDHCDPKIIHRDVKAANILLDEDFEAVVGDFGLAKLMDYKDTHVTTAVRGTIGHIAPEYL	480
	P+ K + + L + G + P	
TaBAK1-2_T0-2_D1	420 MITVIPIRSFIVMSKPQTFSWMKTLRRLWVTLDWPSLWTTRTLM*PQPSVERSGILLPSTY	479
TaBAK1-2_D(WT)	481 STGKSSEKTDVFGYGIMLLELITGQRAFDLARLANDDDVMLLDWVKGLKEKKVEMLVDP	540
	+ L G+ L L KG K ++	
TaBAK1-2_T0-2_D1	480 PPESPPRRMF SVTASCFWSLISLGRGHSTSHVLQTTTMSCCLTG*KGC*KRRRWRCWWTR	539
TaBAK1-2_D(WT)	541 DLQSVYVEHEVEALIQVALLCTQGSPMDRPMKSEVVRMLEGDGLAERWEEWQKVEVVRQE	600
	++ + +G P+ G ++ +	
TaBAK1-2_T0-2_D1	540 TCRACTWSTRWRR*SRWRCCARRGRRWTGPRCRRW*GCWRATGWRSGRSRRWRSGRR	599
TaBAK1-2_D(WT)	601 AELAPRNNDWIVDSTYNLRAVELSGPR	627
TaBAK1-2_T0-2_D1	600 RSWPRETTTGSSTPPTTSGRWSSPARG	626

Figure S15

Protein alignment of the *tabak1-2* T0 plant 2 D1 allele to the WT.

A**B**

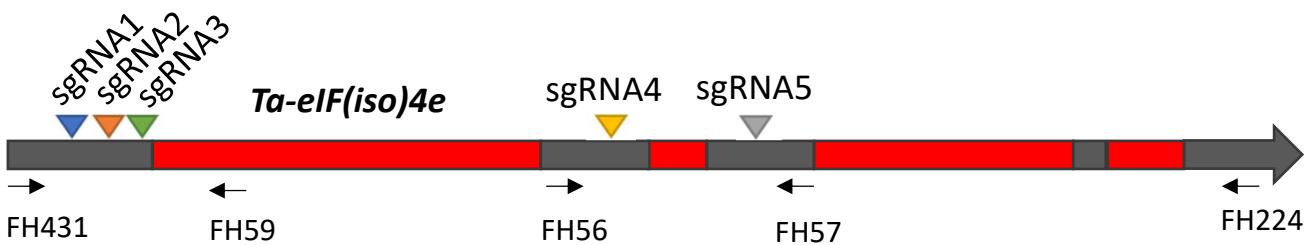
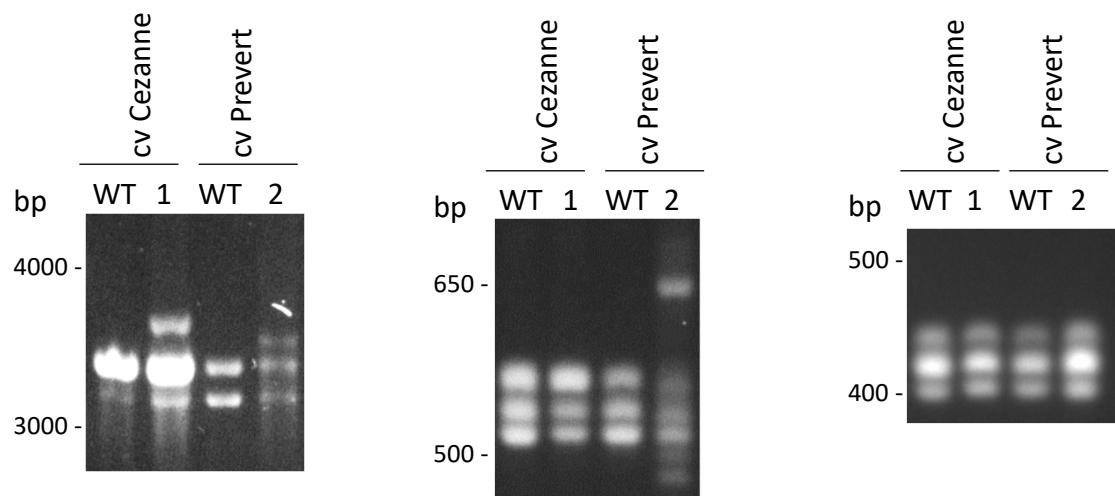
PCR primers: FH221/
 FH46

 FH221/
 FH445

 FH447/
 FH46

Figure S16

PCR genotyping of the *ta-eif4e* T0 plants 1 and 2 (cvs Cezanne and Goncourt, respectively). (A) A cartoon showing positions of sgRNA target sites and PCR primer binding sites within the *Ta-eIF4e* gene. Exons are shown in grey, while introns – in red. (B) Results of PCR genotyping with three primer sets.

A**B**

PCR primers: FH431/
 FH224

FH431/
FH59

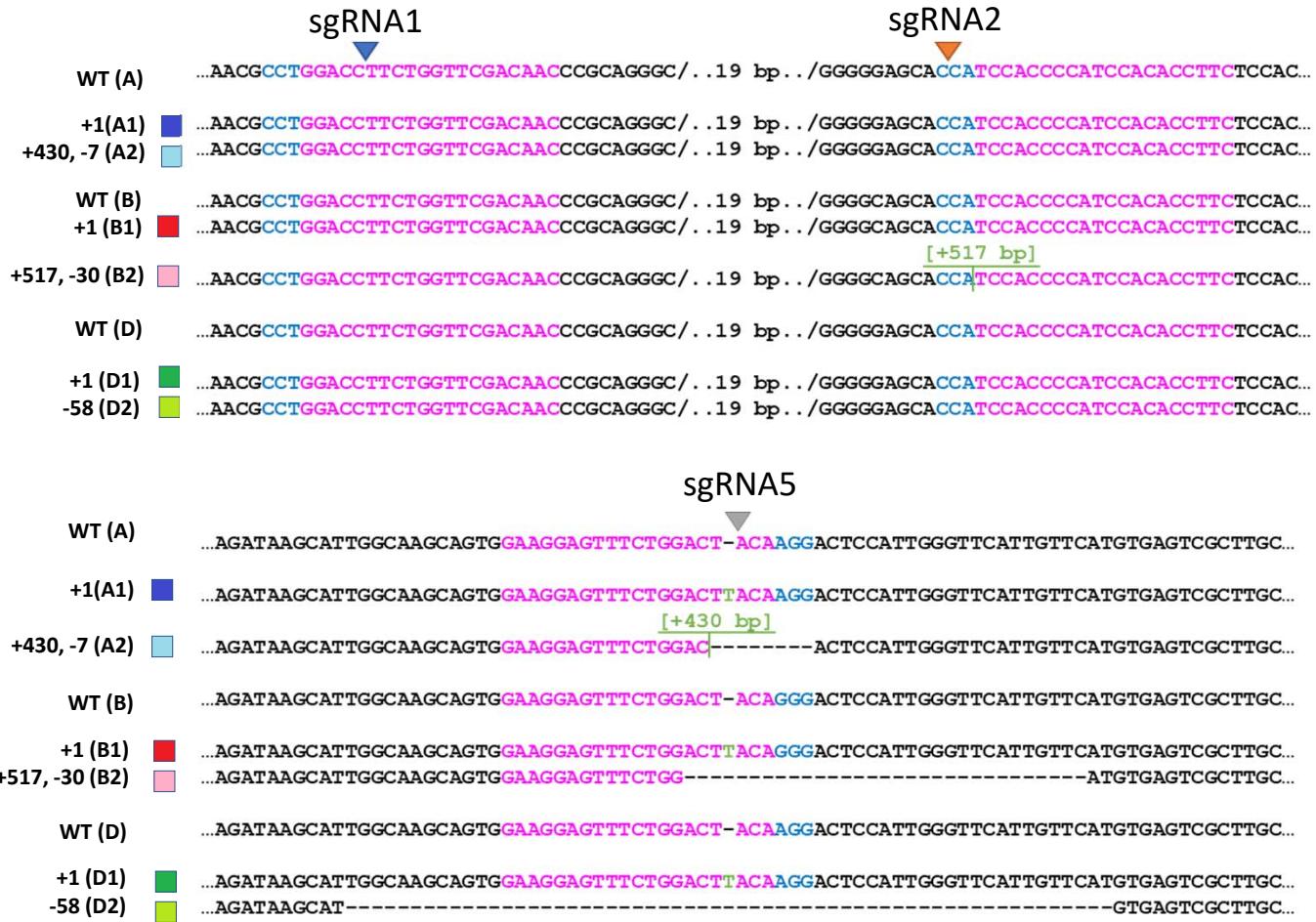
FH56/
FH57

Figure S17

PCR genotyping of the *ta-eif(iso)4e* T0 plants 1 and 2 (cvs Cezanne and Prevert, respectively). (A) A cartoon showing positions of sgRNA target sites and PCR primer binding sites within the *Ta-eIF(iso)4e* gene. Exons are shown in grey, while introns – in red. (B) Results of PCR genotyping with three primer sets.

ta-eif4e

T0 Plant 1 (cv Cezanne)



T0 Plant 2 (cv Goncourt)

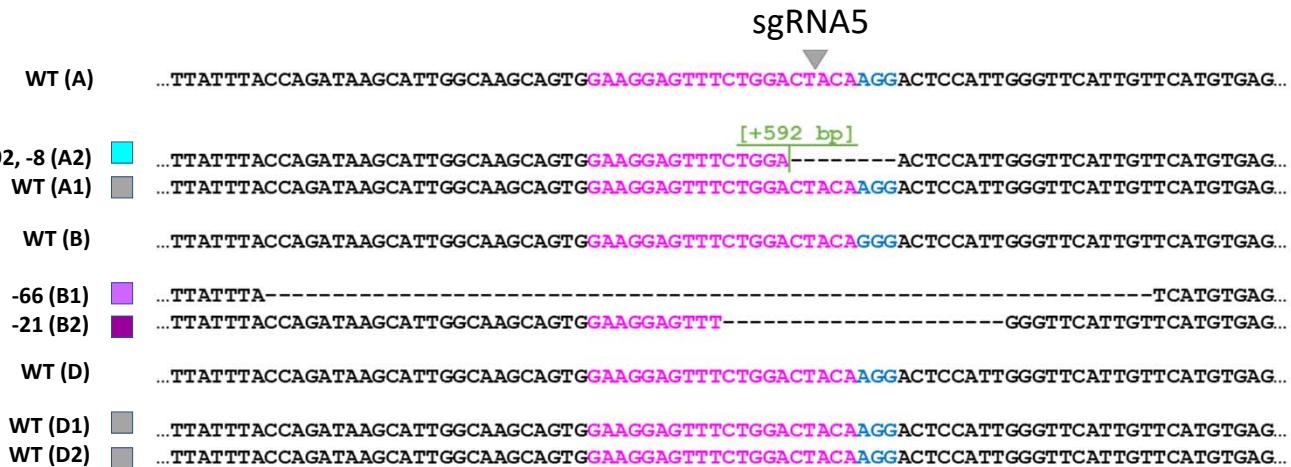


Figure S18

Alignments showing CRISPR/Cas-induced indels in *Ta-eif4e* homoeologues in two *ta-eif4e* T0 plants (cvs Cezanne and Goncourt).

A

Ta-eIF4e_A(WT)	1 MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITAHPLEN AWT FWFDNPQGKSRQV	60
Ta-eIF4e_T0-1_A1	1 MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITAHPLEN AWT FWFDNPQGKSRQV	60
Ta-eIF4e_A(WT)	61 AWGSTIHIPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHC FKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_T0-1_A1	61 AWGSTIHIPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHC FKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_A(WT)	121 ISCGRGKSDTFWLHLLAMIGEQFDFGDEICGAVVSVRQKQERVAIWTKNAANEAQISI	180
	ISCGRGKSDTFWLHLLAMIGEQFDFGDEICGAVVSVRQKQERVAIWTKNAANEAQISI	
Ta-eIF4e_T0-1_A1	121 ISCGRGKSDTFWLHLLAMIGEQFDFGDEICGAVVSVRQKQERVAIWTKNAANEAQISI	180
Ta-eIF4e_A(WT)	181 GKQWKEFLDYKDSIGFIVHEDAKRS DKGPKNRYTV*	216
	GKQWKEFLD + K + P+	
Ta-eIF4e_T0-1_A1	181 GKQWKEFLDLQGLHWVHCS*GCKEV*QRPQEPLHRL	216

B

Ta-eIF4e_A(WT)	1 MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITAHPLEN AWT FWFDNPQGKSRQV	60
Ta-eIF4e_T0-1_A2	1 MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITAHPLEN AWT FWFDNPQGKSRQV	60
Ta-eIF4e_A(WT)	61 AWGSTIHIPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHC FKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_T0-1_A2	61 AWGSTIHIPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHC FKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_A(WT)	121 ISCGRGKSDTFWLHLLAMIGEQFDFGDEICGAVVSVRQKQERVAIWTKNAANEAQISI	180
	ISCGRGKSDTFWLHLLAMIGEQFDFGDEICGAVVSVRQKQERVAIWTKNAANEAQISI	
Ta-eIF4e_T0-1_A2	121 ISCGRGKSDTFWLHLLAMIGEQFDFGDEICGAVVSVRQKQERVAIWTKNAANEAQTPL	180
Ta-eIF4e_A(WT)	181 GKQWKEFLDYKDSIGFIVHEDAKRS DKGPKNRYTV*	216
	G + + +	
Ta-eIF4e_T0-1_A2	181 GSLFMRMRQGLTKAPRTATPFE*ALASSGRSFW---	213

Figure S19Protein alignments of the *ta-eif4e* T0 plant 1 A1 (A) and A2 (B) alleles to the WT.

A

Ta-eIF4e_B(WT)	1 MAEDTETR PASAGAE EERE EGE IADDGDGSAAAAGRISAHPLENAWTFWFDNPQGKSRQV	60
	MAEDTETR PASAGAE EERE EGE IADDGDGSAAAAGRISAHPLENAWTFWFDNPQGKSRQV	
Ta-eIF4e_T0-1_B1	1 MAEDTETR PASAGAE EERE EGE IADDGDGSAAAAGRISAHPLENAWTFWFDNPQGKSRQV	60
Ta-eIF4e_B(WT)	61 AWGSTI HPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
	AWGSTI HPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	
Ta-eIF4e_T0-1_B1	61 AWGSTI HPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_B(WT)	121 ISCGRGKS DTFWLH TLLAMIGEQ FDFGDEICGAVV SVRQ KQER VAI WTKNAAN EA AQISI	180
	ISCGRGKS DTFWLH TLLAMIGEQ FDFGDEICGAVV SVRQ KQER VAI WTKNAAN EA AQISI	
Ta-eIF4e_T0-1_B1	121 ISCGRGKS DTFWLH TLLAMIGEQ FDFGDEICGAVV SVRQ KQER VAI WTKNAAN EA AQISI	180
Ta-eIF4e_B(WT)	181 GK QWKEFL DYRDSIG FIVHEDA KRS DKGP KNRY TV*	216
	GK QWKEFLD + K + P+	
Ta-eIF4e_T0-1_B1	181 GK QWKEFL DLQGLHWVHCS*GC KEV*QRPQEPLHRL	216

B

Ta-eIF4e_B(WT)	1 MAEDTETR PASAGAE EERE EGE IADDGDGSAAAAGRISAHPLENAWTFWFDNPQGKSRQV	60
	MAEDTETR PASAGAE EERE EGE IADDGDGSAAAAGRISAHPLENAWTFWFDNPQGKSRQV	
Ta-eIF4e_T0-1_B2	1 MAEDTETR PASAGAE EERE EGE IADDGDGSAAAAGRISAHPLENAWTFWFDNPQGKSRQV	60
Ta-eIF4e_B(WT)	61 AWGSTI HPIHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
	AWGSTI S L + A F + E +	
Ta-eIF4e_T0-1_B2	61 AWGSTI QW*TGQSGPCRLASLASCPATAQYRTRKAAPF*SAAYLEVTIVVHDDEYFTVYN	120
Ta-eIF4e_B(WT)	121 ISCGRGKS DTFWLH TLLAMIGEQ FDFGDEICGAVV SVRQ KQER VAI WTKNAAN EA AQISI	180
	++ D + V + +++ +A	
Ta-eIF4e_T0-1_B2	121 ELTKVKYVTEGMRKPAFLSGEQQKAIVDLLFKTNRKVTDET K KIMKSIPS AERLEPSQDS	180
Ta-eIF4e_B(WT)	181 GK QWKEFL DYRDSIG FIVHEDA KRS DKGP KNRY TV*-----	216
	K+ L R + + H S	
Ta-eIF4e_T0-1_B2	181 PKRNTGKLAIRTC LTYRSHPCTN ASSTDLTQTRI*HKHEQK*NYRALIMDRNA DLEKVEP	240
Ta-eIF4e_B(WT)	-----	
Ta-eIF4e_T0-1_B2	241 HPHLLHRRG L LGHLLHRRG L L GPLQQYP*P*QVECGSRLPLLQE*D*A*MGRPHLCQWR*	300
Ta-eIF4e_B(WT)	-----	
Ta-eIF4e_T0-1_B2	301 MDHQLWQREI*HILVAYFAGNDW*TIRLW*RNLWSSR*RASETGKSSYLD*ECCQ*SCSD	360
Ta-eIF4e_B(WT)	-----	
Ta-eIF4e_T0-1_B2	361 KHWQAVEGVSG*GC KEV*QRPQEPLHRL	388

Figure S20Protein alignments of the *ta-eif4e* T0 plant 1 B1 (A) and B2 (B) alleles to the WT.

A

Ta-eIF4e_D(WT)	1	MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITA HPLEA WTFWFDNPQGKSRQV	60
Ta-eIF4e_T0-1_D1	1	MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITA HPLEA WTFWFDNPQGKSRQV	60
Ta-eIF4e_D(WT)	61	AWGSTIHP IHTFSTVEDFW GLYNNIHNPSKLNVGADFHC FKNKIEPKWEDP ICANGG KWT	120
Ta-eIF4e_T0-1_D1	61	AWGSTIHP IHTFSTVEDFW GLYNNIHNPSKLNVGADFHC FKNKIEPKWEDP ICANGG KWT	120
Ta-eIF4e_D(WT)	121	ISCGRGKS DTFWLH TLAMIGEQ FDFG DEICGA VSVR QKQERVAI WTKNAAN EAQISI	180
Ta-eIF4e_T0-1_D1	121	ISCGRGKS DTFWLH TLAMIGEQ FDFG DEICGA VSVR QKQERVAI WTKNAAN EAQISI	180
Ta-eIF4e_D(WT)	181	GKQWKEFLDYKD SIGFIVHEDA KRS DKGP KNRYTV*	216
		GKQWKEFLD + K + P+	
Ta-eIF4e_T0-1_D1	181	GKQWKEFLDLQGLHWVHCS*GC KEV*QRPQEPLHRL	216

B

Ta-eIF4e_D(WT)	1	MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITA HPLEA WTFWFDNPQGKSRQV	60
Ta-eIF4e_T0-1_D2	1	MAEDTETR PASAGAE EERE EGE IADDGDGSSAAAAGRITA HPLEA WTFWFDNPQGKSRQV	60
Ta-eIF4e_D(WT)	61	AWGSTIHP IHTFSTVEDFW GLYNNIHNPSKLNVGADFHC FKNKIEPKWEDP ICANGG KWT	120
Ta-eIF4e_T0-1_D2	61	AWGSTIHP IHTFSTVEDFW GLYNNIHNPSKLNVGADFHC FKNKIEPKWEDP ICANGG KWT	120
Ta-eIF4e_D(WT)	121	ISCGRGKS DTFWLH TLAMIGEQ FDFG DEICGA VSVR QKQERVAI WTKNAAN EAQISI	180
Ta-eIF4e_T0-1_D2	121	ISCGRGKS DTFWLH TLAMIGEQ FDFG DEICGA VSVR QKQERVAI WTKNAAN EAQISM	180
Ta-eIF4e_D(WT)	181	GKQWKEFLDYKD SIGFIVHEDA KRS DKGP KNRYTV*	216
		Q + + F	
Ta-eIF4e_T0-1_D2	181	RMQRGLTKAPRTATPF-----	196

Figure S21Protein alignments of the *ta-eif4e* T0 plant 1 D1 (A) and D2 (B) alleles to the WT.

Ta-eIF4e_A(WT)	1 MAEDTETRPASAGAEEREEGEIADDGDGSSAAAAGRITAHPLENAWTFWDNPQGKSRQV	60
Ta-eIF4e_T0-2_A2	1 MAEDTETRPASAGAEEREEGEIADDGDGSSAAAAGRITAHPLENAWTFWDNPQGKSRQV	60
Ta-eIF4e_A(WT)	61 AWGSTIHP1HTFSTVEDFWGLYNNIHNP SKLNVGADFHC FKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_T0-2_A2	61 AWGSTIHP1HTFSTVEDFWGLYNNIHNP SKLNVGADFHC FKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_A(WT)	121 ISCGRGKSDTFWLHTLLAMIGEQFDGFDEICGA VSVRQKQERVAIWTKNAANEAQISI	180
Ta-eIF4e_T0-2_A2	121 ISCGRGKSDTFWLHTLLAMIGEQFDGFDEICGA VSVRQKQERVAIWTKNAANEAQISI	180
Ta-eIF4e_A(WT)	181 GKQWKEFLDYKDSIGFIVHEDA KRS DKG PKN RYTV*-----	216
Ta-eIF4e_T0-2_A2	181 GKQWKEFL+ + + S ++ *	
Ta-eIF4e_A(WT)	-----	
Ta-eIF4e_T0-2_A2	241 LNP KP*TLKP*QP*TLNP KP*TLNLKP*TLNP NPNP KP*TLNP KP*TLNP NPKP*TLNP K	300
Ta-eIF4e_A(WT)	-----	
Ta-eIF4e_T0-2_A2	301 P*TQP*TLNP KP*TLNP KP*TLTLNP KP QTLNP NPMAA Q*HSCRYL RASHDRH*SGYLAD	360
Ta-eIF4e_A(WT)	-----	
Ta-eIF4e_T0-2_A2	361 KSKRT*RCLGRSSGGT L*SGS*TGSTPLGSLFMRMQRGLTKAPRTATPF	410

Figure S22

Protein alignment of the *ta-eif4e* T0 plant 2 A2 allele to the WT.

A

Ta-eIF4e_B(WT)	1 MAEDTETR PASAGAEEREEGEIADDGDGSSAAAAGRISAHPLENAWTFWFDPQGKSRQV	60
Ta-eIF4e_T0-2_B1	1 MAEDTETR PASAGAEEREEGEIADDGDGSSAAAAGRISAHPLENAWTFWFDPQGKSRQV	60
Ta-eIF4e_B(WT)	61 AWGSTIHP IHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_T0-2_B1	61 AWGSTIHP IHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_B(WT)	121 ISCGRGKSDTFWLHTLLAMIGEQFDGDEICGAVSVRQKQERVAIWTKNAANEAQISI	180
Ta-eIF4e_T0-2_B1	121 ISCGRGKSDTFWLHTLLAMIGEQFDGDEICGAVSVRQKQERVAIWTKNAANEAQ	
Ta-eIF4e_B(WT)	181 GKQWKEFLDYRDSIGFIVHEDAKRS DKGPKNRYTV*	216
	K+ +	
Ta-eIF4e_T0-2_B1	181 CKEV*QRPQEPLHRL-----	195

B

Ta-eIF4e_B(WT)	1 MAEDTETR PASAGAEEREEGEIADDGDGSSAAAAGRISAHPLENAWTFWFDPQGKSRQV	60
Ta-eIF4e_T0-2_B2	1 MAEDTETR PASAGAEEREEGEIADDGDGSSAAAAGRISAHPLENAWTFWFDPQGKSRQV	60
Ta-eIF4e_B(WT)	61 AWGSTIHP IHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_T0-2_B2	61 AWGSTIHP IHTFSTVEDFWGLYNNIHNP SKLNVGADFHCFKNKIEPKWEDPICANGGKWT	120
Ta-eIF4e_B(WT)	121 ISCGRGKSDTFWLHTLLAMIGEQFDGDEICGAVSVRQKQERVAIWTKNAANEAQISI	180
Ta-eIF4e_T0-2_B2	121 ISCGRGKSDTFWLHTLLAMIGEQFDGDEICGAVSVRQKQERVAIWTKNAANEAQISI	180
Ta-eIF4e_B(WT)	181 GKQWKEFLDYRDSIGFIVHEDAKRS DKGPKNRYTV*	216
	GKQWKEF FIVHEDAKRS DKGPKNRYTV	
Ta-eIF4e_T0-2_B2	181 GKQWKEFG-----FIVHEDAKRS DKGPKNRYTV-	208

Figure S23Protein alignments of the *ta-eif4e* T0 plant 2 B1 (A) and B2 (B) alleles to the WT.

ta-eif(iso)4e

T0 Plant 1 (cv Cezanne)

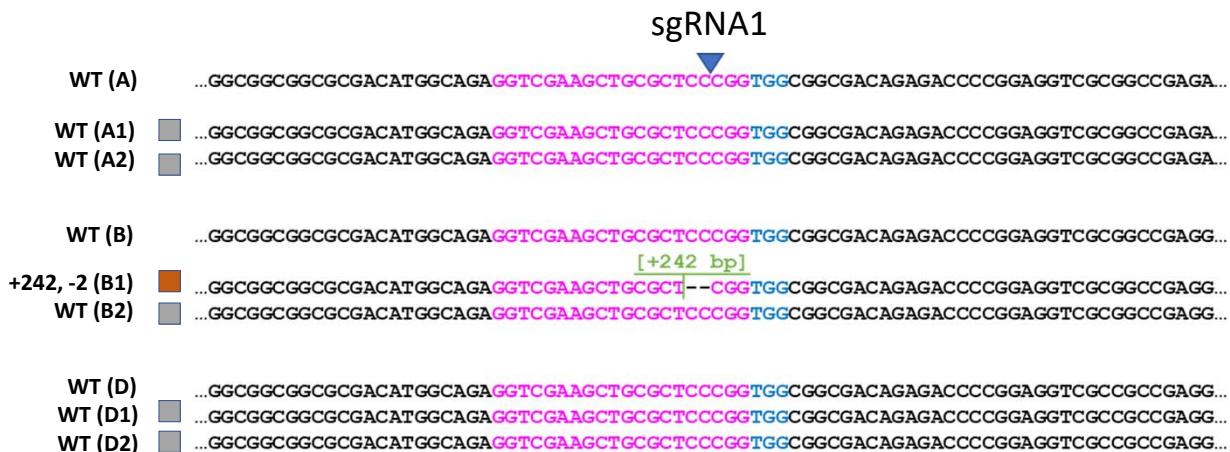


Figure S24

Alignment showing CRISPR/Cas-induced indels in *Ta-eif(iso)4e* homoeologues in the *ta-eif(iso)4e* T0 plant 1 (cv Cezanne).

ta-eif(iso)4e

T0 Plant 2 (cv Prevert)

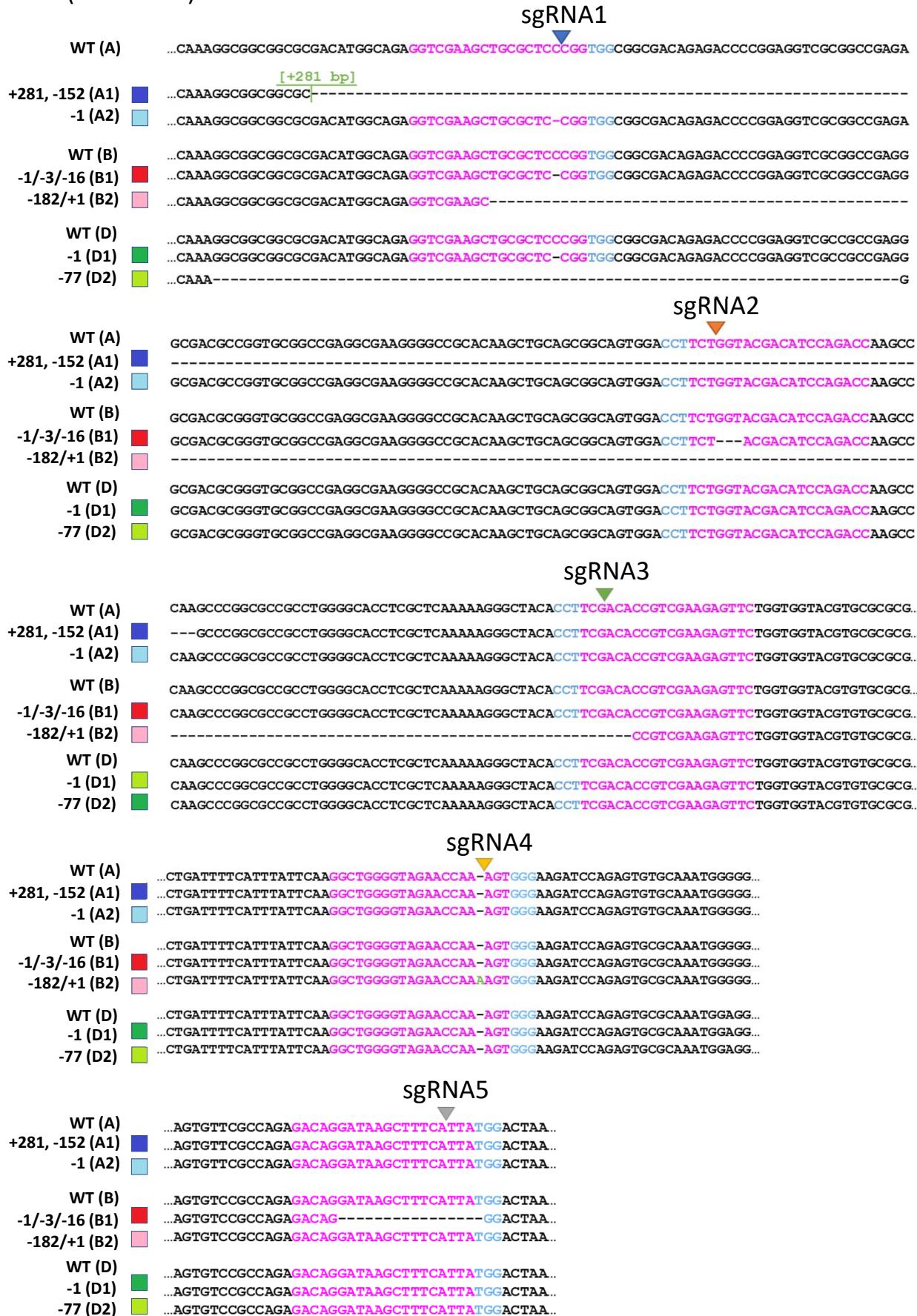


Figure S25

Alignment showing CRISPR/Cas-induced indels in *Ta-eif(iso)4e* homoeologues in the *ta-eif(iso)4e* T0 plant 2 (cv Prevert).

Ta-eIF(iso)4e_B(WT)	1 MAEVEAAL-----P-----	9
	MAEVEAAL P	
Ta-eIF(iso)4e_T0-1_B1	1 MAEVEAALSPVPVTSSLLSRRRADETLHQHSAGS*VRGTSLS*TCADHGGAVLFFLFH*	60
Ta-eIF(iso)4e_B(WT)	10 -----VAATETPEVAAEGDAGAAEAKGPHKLQRQWT	40
	VAATETPEVAAEGDAGAAEAKGPHKLQRQWT	
Ta-eIF(iso)4e_T0-1_B1	61 IWEHIV*ISEQF*KFHDLF*NQDFF*KNSVAATETPEVAAEGDAGAAEAKGPHKLQRQWT	120
Ta-eIF(iso)4e_B(WT)	41 FWYDIQTCKPKPGAAWGTSLKKGYTFDTVEEFWCLYDQIFRPSKLVGSADFHLFKAGVEPK	100
	FWYDIQTCKPKPGAAWGTSLKKGYTFDTVEEFWCLYDQIFRPSKLVGSADFHLFKAGVEPK	
Ta-eIF(iso)4e_T0-1_B1	121 FWYDIQTCKPKPGAAWGTSLKKGYTFDTVEEFWCLYDQIFRPSKLVGSADFHLFKAGVEPK	180
Ta-eIF(iso)4e_B(WT)	101 WEDPECANGGKWTVISSRKANLDTMWEETCMALIGEQFDESQEICGVVASVRQRQDKLSL	160
	WEDPECANGGKWTVISSRKANLDTMWEETCMALIGEQFDESQEICGVVASVRQRQDKLSL	
Ta-eIF(iso)4e_T0-1_B1	181 WEDPECANGGKWTVISSRKANLDTMWEETCMALIGEQFDESQEICGVVASVRQRQDKLSL	240
Ta-eIF(iso)4e_B(WT)	161 WTKTASNEAVQVDIGKKWKEVIDYNDKMVYSFHDDRSRSQKPSRGGRYTV*	210
	WTKTASNEAVQVDIGKKWKEVIDYNDKMVYSFHDDRSRSQKPSRGGRYTV*	
Ta-eIF(iso)4e_T0-1_B1	241 WTKTASNEAVQVDIGKKWKEVIDYNDKMVYSFHDDRSRSQKPSRGGRYTV*	290

Figure S26

Protein alignment of the *ta-eif(iso)4e* T0 plant 1 B1 allele to the WT.

A

Ta-eIF(iso)4e_A(WT)	1	-----MAEVEAALPVAATETPEVAAESDAGAAEAKGPHKLQRQWTFWYDIQTCKPKPG	52
		+ + S A Q	
Ta-eIF(iso)4e_T0-2_A1	1	MALMMSFLRKSIICRFSSSGKRR*TDRGTPSRLATSPAIRDSTNVQNAVSTTSAESFAFF	60
Ta-eIF(iso)4e_A(WT)	53	AAWGTSLKKGYTFDTVEEFWCFFGSLYDQIFRPSKLVGSADFHLFKAGVEPKWEDPECAN	112
	++W ++ ++	+ + + F +	
Ta-eIF(iso)4e_T0-2_A1	61	SSWASARRRLGHLAQKGLHLRHRRRLVLV*SDFPSE*AGRKC*FSFIQGWGRTKVGRSR	120
Ta-eIF(iso)4e_A(WT)	113	GGKWTVISSRKANLDTMWLETCMALIGEQFDESQEICGVVASVRQRQDKLSLWTKTASNE	172
	KW +	+ G + + G + R + +	
Ta-eIF(iso)4e_T0-2_A1	121	VCKWGQMDCDI*QEGQS*YHVA*NVYGSWRRAVR*EPGNLWCCR*CSPETG*AFIMD*DC	180
Ta-eIF(iso)4e_A(WT)	173	AVQVDIGKKWKEVIDYNDKMVYSFHDDRSRSQKPSRGGRYTV*---	214
	G W+E+ R + S +		
Ta-eIF(iso)4e_T0-2_A1	181	Q**SCSGGHWQEMEGGY*LQ**DGLQLPR*LEKSETKQRWTIHRV	225

B

Ta-eIF(iso)4e_A(WT)	1	MAEVEAALPVAATETPEVAAESDAGAAEAKGPHKLQRQWTFWYDIQTCKPKPGAAWGTSLK	60
	MAEVEAAL	+ +G + P P K	
Ta-eIF(iso)4e_T0-2_A2	1	MAEVEAALRWRQRPRRSRPRATPVPRRRGRTSCSGSGPSGTTSRPSPSPAPPGAPRSK	60
Ta-eIF(iso)4e_A(WT)	61	KGYTFDTVEEFWCFFGSLYDQIFRPSKLVGSADFHLFKAGVEPKWEDPECANGGKWTVIS	120
	+ + + L+ F + G + G		
Ta-eIF(iso)4e_T0-2_A2	61	RATPSTPSKSSGACMIRFSVRVSW*EVLI---FIYSRLG*NQSGKIQSVQMGANGL*YL	116
Ta-eIF(iso)4e_A(WT)	121	SRKANLDTMWLETCMALIGEQFDESQEICGVVASVRQRQDKLSLWTKTASNEAVQVDIGK	180
	+ + L L+ + +++ + + + + + + + +		
Ta-eIF(iso)4e_T0-2_A2	117	AGRPILIPCGLKRVWL*LESSSMRARKFVVLSLVFARDRISFYGLRLPVMKLFRWTIAR	176
Ta-eIF(iso)4e_A(WT)	181	KWKEVIDYNDKMVYSFHDDRSRSQKPSRGGRYTV*	214
	+ ++ + + + +		
Ta-eIF(iso)4e_T0-2_A2	177	NGRRLLLTMIRWSTASTMTREVRNQAEVDDPC-	209

Figure S27

Protein alignments of the *ta-eif(iso)4e* T0 plant 2 A1 (A) and A2 (B) alleles to the WT.

A

Ta-eIF(iso)4e_B(WT)	1 MAEVEAALPVAATETPEVAAEGDAGAAEAKGPHKLQRQWTFWYDIQTKPKPGAAWGTSLK	60	
	MAEVEAAL	+G	+ S +
Ta-eIF(iso)4e_T0-2_B1	1 MAEVEAALRWRQRPRRSRPRATVRPRRRGRTSCSGGPSTTSRPSPSPAPPGAPRSKR	60	
Ta-eIF(iso)4e_B(WT)	61 KGYTFDTVEEFWCLYDQIFRPSK-LVGSADFHLFKAGVEPKWEDPECANGGKWTVISSRK	119	
	+ + C+	R S V + K + + G ++ R	
Ta-eIF(iso)4e_T0-2_B1	61 ATPSTPSKSSGACMIRFSVRVSW*EVLIFIYSRLG*NQSGKIQSAQMGANGL*-YLAGRP	119	
Ta-eIF(iso)4e_B(WT)	120 ANLDTMWLETCKMALIGEQFDESQEICGVVASVRQRQDKLSLWTKTASNEAVQVDIGKKWK	179	
	+ + L + + ++ S R R ++ S G+ W+		
Ta-eIF(iso)4e_T0-2_B1	120 ILIPCGLKRVWL*LESSLMKARKFVVLLLVSARDRD*--DCQ*RSCS-----GRHWQ	169	
Ta-eIF(iso)4e_B(WT)	180 EVIDYN-DKMVYSFHDDSRSQKPSRGGRYTV*--	210	
	E+ + + +K R+T+		
Ta-eIF(iso)4e_T0-2_B1	170 EMEGGD*LQ**DGLQLPR*LKKSETKQRWTIHGV	203	

B

Ta-eIF(iso)4e_B(WT)	1 MAEVEAALPVAATETPEVAAEGDAGAAEAKGPHKLQRQWTFWYDIQTKPKPGAAWGTSLK	60
	MAEVEA V + +E A K + W + + A G	
Ta-eIF(iso)4e_T0-2_B2	1 MAEVearrrvvlvlv*SDFPSE*---AGRKC*FSFIQGWGRTKSGKIQSAQMGANGL*YL	56
Ta-eIF(iso)4e_B(WT)	61 KGYTFDTVEEFWCLYDQIFRPSKLVGSADFHLFKAGVEPKWEDPECANGGKWTVISSRKA	120
	G RP L G++ W E + ++ +R	
Ta-eIF(iso)4e_T0-2_B2	57 AG-----RP-----ILIPCGLKRVWL*LESS-----LMKAR--	82
Ta-eIF(iso)4e_B(WT)	121 NLDTMWLETCKMALIGEQFDESQEICGVVASVRQRQDKLSLWTKTASNEAVQVDIGKKWKE	180
	+ L + I + R + L+ T + +	
Ta-eIF(iso)4e_T0-2_B2	83 KFVVLLLVSARDRISFHYG-----LRLPVMKLFR*TLARNGRR*----LT	124
Ta-eIF(iso)4e_B(WT)	181 VIDYNDKMVYSFHDDSRSQKPSRGGRYTV*	210
	+I ++ + + R+Q R	
Ta-eIF(iso)4e_T0-2_B2	125 MIRWS--TASTMTQEVRNQAEVDDTRC---	149

Figure S28

Protein alignments of the *ta-eif(iso)4e* T0 plant 2 B1 (A) and B2 (B) alleles to the WT.

A

Ta-eIF(iso)4e_D(WT)	1 MAEVEAALPVAATETPEVAAEGDAGAAEAKGPHKLQRQWTFWYDIQTCKPKPGAAWGTSLK	60
	MAEVEAAL +G + P P K	
Ta-eIF(iso)4e_T0-2_D1	1 MAEVEAALRWRRQRPRRSPPRATVRPQQRTSCSGSGPSGTTSRPSPAPPAGAPRSK	60
Ta-eIF(iso)4e_D(WT)	61 KGYTFDTVEEFWCLYDQIFRPSKLVGSADFHLFKAG--VEPKWEDPECANGGKWTVISSR	118
	+ + + F + G K + + G ++ R	
Ta-eIF(iso)4e_T0-2_D1	61 RATPSTPSKSSGACMIRFSVRVSW*EVLIIFIYSLRG*NQSGKIQSQAQMEEANGL*-YLAGR	119
Ta-eIF(iso)4e_D(WT)	119 KTNLDTMWLETCMALIGEQFDESQEICGVVASVRQRQDKLSLWTKTASNEAVQVDIGKKW	178
	+ + L + + S R R + + + +	
Ta-eIF(iso)4e_T0-2_D1	120 PILIPCGLKRVWL*LESSSMKARKFVVLLVSARDRIS-FHYGLRLPVMKLFRWTLARNG	178
Ta-eIF(iso)4e_D(WT)	179 KEVIDYNDKMVYSFHDDSRSQKPSRGGRYTV*	210
	+ ++ + + + +	
Ta-eIF(iso)4e_T0-2_D1	179 RRLLTIRMIRWSTASTMTQEVRNQAEVDDTPS-	209

B

Ta-eIF(iso)4e_D(WT)	1 MAEVEAALPVAATETPEVAAEGDAGAAEAKGPHKLQRQWTFWYDIQTCKPKPGAAWGTSLK	60
	V + F Y + G ++	
Ta-eIF(iso)4e_T0-2_D2	1 ----MIRFSVRVSW*-----EVLIIFIYSLRG*NQSGKIQSQAUME	35
Ta-eIF(iso)4e_D(WT)	61 KGYTFDTVEEFWCLYDQIFRPSKLVGSADFHLFKAGVEPKWEDPECANGGKWTVISSRKT	120
	L G L G++ W E + S +	
Ta-eIF(iso)4e_T0-2_D2	36 ANGL*-----YLAGRP--ILIPCGLKRVWL*LESS-----SMKAR	68
Ta-eIF(iso)4e_D(WT)	121 NLDTMWLETCMALIGEQFDESQEICGVVASVRQRQDKLSLWTKTASNEAVQVDIGKKWKE	180
	+ L + I + +R KL WT + + + +W	
Ta-eIF(iso)4e_T0-2_D2	69 KFVVLLLVSARDRISFHYG-----LRLPVMKLFRWTLARNGRLLTTM-IRWST	116
Ta-eIF(iso)4e_D(WT)	181 VIDYNDKMVYSFHDDSRSQKPSRGGRYTV*	210
	++ D	
Ta-eIF(iso)4e_T0-2_D2	117 ASTMTQEVRNQAEVDDTPS-----	135

Figure S29

Protein alignments of the *ta-eif(iso)4e* T0 plant 2 D1 (A) and D2 (B) alleles to the WT.