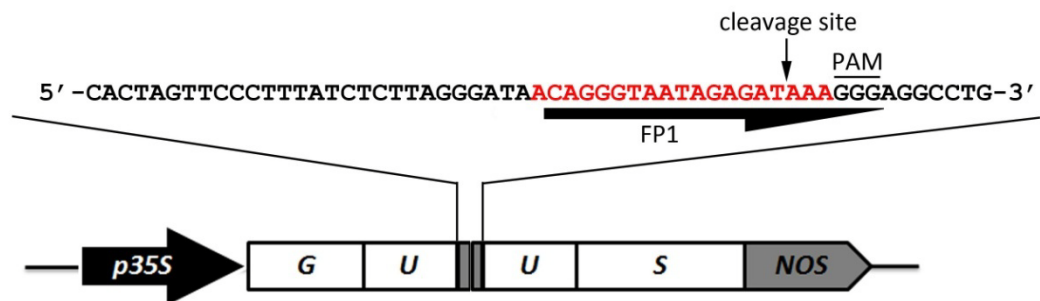
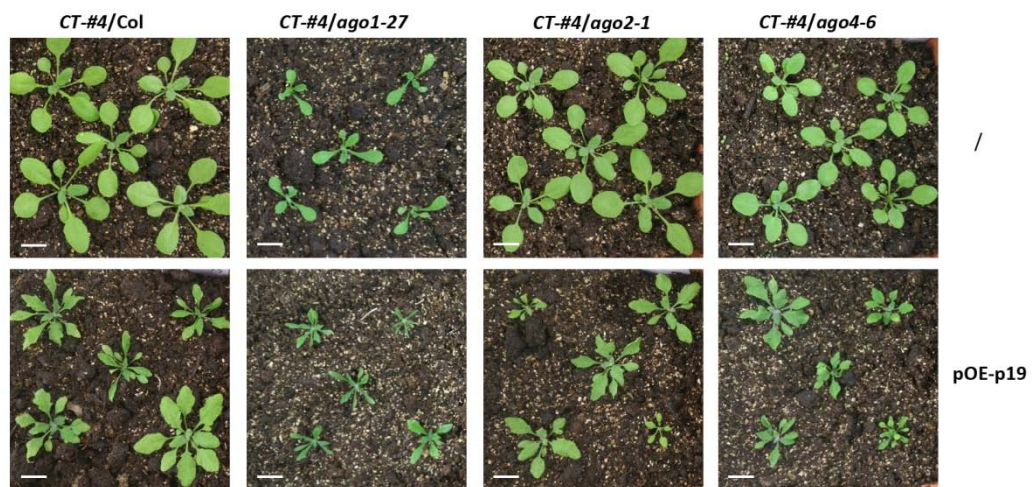


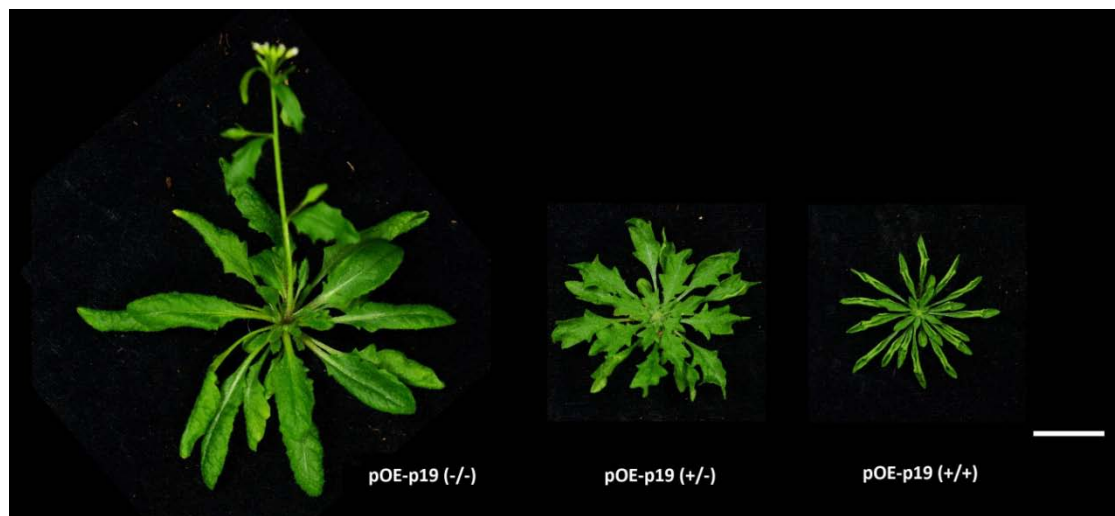
Additional file 1: Figure S1. A schematic showing the sequences of the sgRNA targeting site and FP1 in GUUS reporter gene.



Additional file 1: Figure S2. Phenotypes of the pOE-p19 T2 lines in CT-#4 of mutant backgrounds. Bar=1 cm.



Additional file 1: Figure S3. Segregation of pOE-p19 transgenic plants in T2 generation. Bar=1cm



Additional file 1: Table S1. Primers used in this study

	Primer	Sequences 5'-3'
pLUC-p19	p19-F-Sall	AGGTCGACCATGGAACGAGCTATACAAGGAAACG
	2A-R-Bsal	TTTGGTCTCCCATGCCAGGTCCAGGGTTCTCCT
pRNAi-Cas9	PDK intron-F	CCAATTGGTAAGGAAATAATTATTTTCTTTTTCCTTTTA
	PDK intron-R	CAACTGTAATCAATCCAAATGTAAGATCAATGATAACACA
	AGO1 5'UTR-36F	GAGAGGACACTGCAGGTCGACTCGTTTGTTCGGAGTTAGA G
	AGO1 5'UTR-166R	ATTATTTCTTACCAATTGGAAAAGCAATCTCTCGCCGGA
	AGO1 5'UTR reverse-166F	ATTTGGATTGATTACAGTTGAAAAGCAATCTCTCGCCGGA
	AGO1 5'UTR reverse-36R	TGAACGCCTGAGCTCGGTACCTCGTTTGTTCGGAGTTAGAG
	AGO1-926F	TTTGGAGAGGACACGCTCGAGACAATCAGATGCCCCACAG G
	AGO1-1520R	ATTATTTCTTACCAATTGGTACCGCTGGCCTTCAACAAT
	AGO1 reverse-1520F	ATTTGGATTGATTACAGTTGGTACCGCTGGCCTTCAACAA
	AGO1 reverse-926R	CATTAAAGCAGGACTCTAGAACAATCAGATGCCCCACAGG
	DCL1 3'UTR-F	GAGAGGACACTGCAGGTCGACTCTTTACTCTCTTCAACGA
	DCL1 3'UTR-R	ATTATTTCTTACCAATTGGACCAATTAAACTCGAATAAC
	DCL1 3'UTR reverse-F	ATTTGGATTGATTACAGTTGACCAATTAAACTCGAATAAC
	DCL1 3'UTR reverse-R	TGAACGCCTGAGCTCGGTACCTCTTTACTCTCTTCAACGA
	DCL1 CDS-309F	GAGAGGACACTGCAGGTCGACTGGGTTGCAAAGAATGGC G
	DCL1 CDS-691R	ATTATTTCTTACCAATTGGCTGCCTTGACATCGCATTCTG
	DCL1 CDS reverse-691F	ATTTGGATTGATTACAGTTGCTGCCTTGACATCGCATTCTG
	DCL1 CDS reverse-309R	TGAACGCCTGAGCTCGGTACCTGGGTTGCAAAGAATGGCG
Probes	anti-sgR	AGCACCGACTCGGTGCCACT-3'biotin
	anti-U6	TCATCCTTGCGCAGGGGCCA-3'biotin
	anti-167	TAGATCATGCTGGCAGCTTCA-3'biotin
	anti-168	TTCCCGACCTGCACCAAGCGA-3'biotin
Realtime PCR	Cas9-92F	GGTCGGTATCCACGGAGTCCCAGC
	Cas9-471R	GATGGGGTGCCGCTCGTGCTTC
	p19-380F	GCGAACTCTTCAGCATCTCT
	p19-483R	AGGGCATCCTCTTGATACATTAC
	DCL1-2022F	GGTTGCTGCTTTGGTTCTTC
	DCL1-2123R	TTCATCTCTGGCTGTTATTGT
	AGO1-1548F	CACTGCTTTGCTGAAGGTTAC

	AGO1-1693R	CCTCAACAGAAGCCAGAGAA
	Actin-F	TGGCATCAYACTTTCTACAA
	Actin-R	CCACCACTDAGCACAATGTT
RI Value	TT4-65F	AGAGAGCTGATGGACCTGC
	TT4-296R	AATTGTCGACTTGTCGCCT
	Actin-GF	GACTCTGGAGATGGTGTGAG
	Actin-R	CCACCACTDAGCACAATGTT
	GUUS-FP1	AACAGGGTAATAGAGATAAAG
	GUUS-RP1	TTTGCCGTAATGAGTGACC
	GUUS-FP0	CTGAAGAGATGCTCGACTG
	GUUS-RP0	CAGCTCTTTAATCGCCTGTA

Note S. Sequences of the TBSV p19-2A, pRNAi-Cas9 cassettes, the pIUC-p19 cassettes and the GUUS cassette.

> TBSV p19-2A

ATGGAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAACGTTGGGATGGAGGATCAG
GAGGAACCACTTCTCCCTTCAAACCTCCTGACGAAAGTCCGAGTTGGACTGAGTGGCGGCTACATAACGAT
GAGACTAATTCTGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTCGGGAAAGTTGTATTTAAG
AGATATCTCAGATACGACAGGACGGAGGCTTCACTGCACAGAGTCCTTGGATCTTGGACGGGAGATTTCGGT
TAACTATGCAGCATCTCGATTTTTCGGTTTCGACCAGATCGGATGTACCTATAGTATTCGGTTTCGAGGAGTTA
GTATCACCGTTTCTGGAGGGTCGCGAACTCTTCAGCATCTCTGTGAGATGGCAATTCGGTCTAAGCAAGAAC
TGCTACAGCTTGCCCCAATCGAAGTGGAAGTAATGTATCAAGAGGATGCCCTGAAGGTAAGTAAACCTTCG
AAAAAGAAAGCGAGGGAAGCGGAGCTACTAACTTCAGCCTGCTGAAGCAGGCTGGTGACGTGGAGGAGA
ACCCTGGACCT

“ _ ” : 2A-peptide; “**ATG**”: Start codon

>p35s-PDK-tNOS

AAGCTTAGTCAAAGATTCAAATAGAGGACCTAACAGAACTCGCCGTAAAGACTGGCGAACAGTTCATACAG
AGTCTCTTACGACTCAATGACAAGAAGAAAATCTTCGTCAACATGGTGGAGCACGACACGCTTGTCTACTCC
AAAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGG
AAACCTCCTCGATTCCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAGGAAGGTGGCTC
CTACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGA
TGGACCCCCACCCACGAGGAGCATCGTGGAAGAAAGAACGTTCCAACCACGTCTTCAAAGCAAGTGGAT
TGATGTGATATCTCCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCCTTCCTCTATATA
AGGAAGTTCATTTCAATTTGGAGAGGACACTGCAGGTGACCCCAATTGGTAAGGAAATAATTATTTCTTTTTT
CCTTTTAGTATAAAATAGTTAAGTGATGTTAATTAGTATGATTATAATAATATAGTTGTTATAATTGTGAAAAAAT
AATTTATAATATATTGTTTACATAAACAACATAGTAATGTAAAAAATATGACAAGTGATGTGTAAGACGAAG
AAGATAAAAGTTGAGAGTAAGTATATTATTTTAATGAATTTGATCGAACATGTAAGATGATATACTAGCATTAA
TATTTGTTTTAATCATAATAGTAATTCTAGCTGGTTTGATGAATTAAATATCAATGATAAAATACTATAGTAAAAA
TAAGAATAAAATAAATAAATAATATTTTTTATGATTAATAGTTTATATATAATTAAATATCTATACCATTACTAA
ATATTTTAGTTTTAAAGTTAATAAATATTTTGTAGAAATTCGAATCTGCTGTAATTTATCAATAAACAAAATAT
TAAATAACAAGCTAAAGTAACAAATAATCAAATAATAGAAACAGTAATCTAATGTAACAAAACATAATCTA
ATGCTAATATAACAAAGCGCAAGATCTATCATTTTATATAGTATTATTTCAATCAACATTCTTATTAATTTCTAAA
TAATACTTGATGTTTTATTAACCTCTAAATGGATTGACTATTAATTAATGAATTAGTCGAACATGAATAAACAA
GGTAACATGATAGATCATGTCATTGTGTTATCATTGATCTTACATTTGGATTGATTACAGTTGCTGGTACCGAG
CTCAGGCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGCGATGATTATCAT
ATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATGAGATGGGTTTT
TATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAAACCTAGGATAAAT
TATCGCGCGGGTGTCTATGTTACTAGATCGGGAATTGCCAATAGCTT

“ _ ” : PDK intron

>pAtU6-sgR-IR

TAGCTTCATTCGGAGTTTTTGTATCTTGTTTCATAGTTTGTCCCAGGATTAGAATGATTAGGCATCGAACCTTC
AAGAATTTGATTGAATAAAACATCTTCATTCTTAAGATATGAAGATAATCTTCAAAGGGCCCTGGGAATCTG
AAAGAAGAGAAGCAGGCCCATTTATATGGGAAAGAACAATAGTATTTCTTATATAGGCCCATTTAAGTTGAA

AACAATCTTCAAAAAGTCCCATCGCTTAGATAAGAAAACGAAGCTGAGTTTATATACAGCTAGAGTCGAAG
TAGTGATT**GAACAGGGTAATAGAGATAAA**GTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTAGTCCG
TTATCAACTTGAAAAAGTGGCACCGAGTCGGTGTCTTTTTGTTTTAGAGCTAGAAATAGCAAGTTAAAATAA
GGCTAGTCCGTAGCGCGTGCGCCAATTCTGCAGACAAATGGCCCCGGG

“ _ ” : sgR-IR; “**Bold**”: IR guide sequences

> pAtUBQ-NLS-SpCas9-BPNLS-tUBQ

CCCCGGATATTTCACAAATTGAACATAGACTACAGAATTTTAGAAAACAACTTCTCTCTTATCTCACCTT
TATCTTTTAGAGAGAAAAAGTTCGATTTCCGGTTGACCGGAATGTATCTTTGTTTTTTGTTTTGTAACATAT
TTCGTTTTCCGATTTAGATCGGATCTCCTTTCCGTTTTGTGCGACCTTCTCCGGTTTATCCGGATCTAATAAT
ATCCATCTTAGACTTAGCTAAGTTTGATCTGTTTTTGGTTAGCTCTTGCAATCGCCTCATCATCAGCAAGA
AGGTGAAATTTTGACAAATAAATCTTAGAATCATGTAGTGTCTTTGGACCTTGGGAATGATAGAAACGATTT
GTTATAGCTACTCTATGTATCAGACCCTGACCAAGATCCAACAATCTCATAGGTTTTGTGCATAGAAACCTTC
GACTAACGAGAAGTGGTCTTTAATGAGAGAGATATCTAAATGTTATCTTAAAGCCCACTCAAATCTCAAG
GCATAAGGTAGAAATGCAAATTTGGAAAGTGGGCTGGGCCTTTGTGGTAAAGGCCTGTAACTAGCCCAA
TATTAGCAAAACCTAGACGCTACATTGACATATATAAACCCGCTCCTCTGTTTAGGGTTTCTACGTGAG
AGAGACGAAACACAAAC**ATG**GACTATAAGGACCACGACGGAGACTACAAGGATCATGATATTGATTACAA
AGACGATGACGATAAGATGGCCCCAAAGAAGAAGCGGAAGGTCGGTATCCACGGAGTCCCAGCAGCCGAC
AAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGATCACCGACGAGTACAA
GGTGGCCAGCAAGAAATTCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAAGAAGAACCTGATCGGA
GCCCTGCTGTTGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAACCGCCAGAAGAAGATAC
ACCAGACGGAAGAACCGGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATGGCCAAGGTGGACGACA
GCTTCTTCCACAGACTGGAAGAGTCCTTCTGCTGGAAGAGGATAAGAAGCACGAGCGGCACCCCATCTTC
GGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCACCATCTACCACCTGAGAAAGAACTGGT
GGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCACATGATCAAGTTCCGGGGCC
ACTTCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTGTTTCATCCAGCTGGTGCAG
ACCTACAACCGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCGTGACGCCAAGGCCATCTGTCTGC
CAGACTGAGCAAGAGCAGACGGCTGGAATCTGATCGCCAGCTGCCGGCGAGAAGAAGAATGGCCT
GTTTCGGCAACCTGATTGCCCTGAGCCTGGGCTGACCCCAACTTCAAGAGCAACTTCGACCTGGCCGAGG
ATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCTGCTGGCCCAGATCGGCGA
CCAGTACGCCGACCTGTTCTGGCCGCAAGAACCTGTCCGACGCCATCCTGCTGAGCGACATCCTGAGAGT
GAACACCGAGATACCAAGGCCCCCTGAGCGCCTCTATGATCAAGAGATACGACGAGCACCACAGGACC
TGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAGAGATTTTCTTCGACCAGAGC
AAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTTCTACAAGTTCATCAAGCCCAT
CCTGGAAGAGATGGACGGCACCGAGGAATGCTCGTGAAGCTGAACAGAGAGGACCTGCTGCGGAAGCA
GCGGACCTTCGACAACGGCAGCATCCCCACCAGATCCACCTGGGAGAGCTGCACGCCATTCTGCGGCGGC
AGGAAGATTTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAAGATCCTGACCTTCCGCATCCCTT
ACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTGCGCTGGATGACCAGAAAGAGCGAGGAAACCAT
CACCCCTGGAATTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCAGAGCTTCATCGAGCGGATGACC
AACTTCGATAAGAACCTGCCCAACGAGAAGGTGTGCCCCAAGCACAGCCTGCTGTACGAGTACTTCACCGT
GTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGGAATGAGAAAGCCCGCCTTCTGAGCGGCGAG
CAGAAAAAGGCCATCGTGGACCTGCTGTTCAAGACCAACCGGAAAGTGACCGTGAAGCAGCTGAAAGAG
GACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTGGAAGATCGGTTCAACGCCTC
CCTGGGCACATACCAGATCTGCTGAAAATTATCAAGGACAAGGACTTCTGGACAATGAGGAAAACGAGG

ACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGATGATCGAGGAACGGCTGAAA
 ACCTATGCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGGAGATACACCGGCTGGGGCA
 GGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAGACAATCCTGGATTTCTGAA
 GTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGCCTGACCTTTAAAGAGGACA
 TCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTGCCAATCTGGCCGGCAGCCC
 CGCCATTAAGAAGGGCATCTGCAGACAGTGAAGGTGGTGGACGAGCTCGTGAAAGTGATGGGCGGGCAC
 AAGCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCAGAAGGGACAGAAGAACAGC
 CGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCCAGATCCTGAAAGAACACCCC
 GTGGAACACCCAGCTGCAGAACGAGAAGCTGTACTGTACTACCTGCAGAATGGGCGGGATATGTACGT
 GGACCAGGAAGTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATCGTGCCTCAGAGCTTTCTGA
 AGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGGCAAGAGCGACAACGTGC
 CCTCCGAAGAGGTCTGTAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGAACGCCAAGCTGATTACCCA
 GAGAAAGTTCGACAATCTGACCAAGGCCGAGAGAGGGCGCTGAGCGAACTGGATAAGGCCGGCTTCATC
 AAGAGACAGCTGGTGAAACCCGGCAGATCACAAGCACGTGGCACAGATCCTGGACTCCCGGATGAACA
 CTAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCTGAAGTCCAAGCTGGTGTCC
 GATTTCCGGAAGGATTTCCAGTTTTACAAAGTGCGCGAGATCAACAACCTACCACCACGCCACGACGCCTAC
 CTGAACGCCGTCTGTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAAAGCGAGTTCTGTGTACGGCG
 ACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAATCGGCAAGGCTACCGCCAA
 GTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGGCCAACGGCGAGATCCGGAA
 GCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATAAGGGCCGGGATTTTGCCACC
 GTGCGGAAAGTGCTGAGCATGCCCAAGTGAATATCGTGA AAAAGACCGAGGTGCAGACAGGCGGCTTCA
 GCAAAGAGTCTATCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGAAAGAAGGACTGGGACCCTAA
 GAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGTGGCCAAAGTGGA AAAAGGC
 AAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCATGGAAAGAAGCAGCTTCGAGA
 AGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAAGGACCTGATCATCAAGCTGCCT
 AAGTACTCCCTGTTTCGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCTCTGCCGGCGAACTGCAGAAGG
 GAAACGAACTGGCCCTGCCCTCCAAATATGTGAACCTCCTGTACCTGGCCAGCCACTATGAGAAGCTGAAGG
 GCTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACAAAGCACTACCTGGACGAGATCATC
 GAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAATCTGGACAAAGTGCTGTCCGCCTA
 CAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCATCCACCTGTTTACCCTGACCAATCT
 GGGAGCCCTGCCGCTTCAAGTACTTTGACACCACCATCGACCGGAAGAGGTACACCAGCACCAAAGAG
 GTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAGACACGGATCGACCTGTCTCAGCT
 GGGAGGCGACAAGAGAACCGCCGACGGAAGCGAGTTCGAGAGCCCTAAGAAAAAGCGGAAAGTGGAGT
 AAGGATCCAGAGACTCTTATCAAGAATCCCATCTCTTGCTTGCTTTTTTTGTTGCTTCCCTTTGATAGGGTTT
 GTTTTTCTGTTTCACTGACTTTCTATGTTAAAAGATAATGTCAGTAAAAGGATTTGGTTTTCTATTATTCTGAA
 TCGATTACGGAAGATTCTTGCTTAATTCCAATCTATACAAGTATCGTGAAATAATGACCGTTTATGTGGTACC
 “_” : SpCas9; “_” : NLS-BPNLS; “ATG”: Start codon; “TAA”: Stop codon

>pAtUBQ-p19-2A-NLS-SpCas9-NLS-tUBQ

CCCGGGATATTTCAAAATTGAACATAGACTACAGAATTTTAGAAAACAACTTTCTCTCTTATCTCACCTT
 TATCTTTTAGAGAGAAAAAGTTCGATTTCCGGTTGACCGGAATGTATCTTTGTTTTTTGTTTTGTAACATAT
 TTCGTTTTCCGATTTAGATCGGATCTCCTTTCCGTTTTGTCCGACCTTCTCCGGTTTATCCGGATCTAATAAT
 ATCCATCTTAGACTTAGCTAAGTTTGGATCTGTTTTTGGTTAGCTCTTGTCATCGCCTCATCATCAGCAAGA
 AGGTGAAATTTTACAAATAAATCTTAGAATCATGTAGTGTCTTTGGACCTTGGAATGATAGAAACGATTT

GTTATAGCTACTCTATGTATCAGACCCTGACCAAGATCCAACAATCTCATAGGTTTTGTGCATATGAAACCTTC
GACTAACGAGAAGTGGTCTTTTAATGAGAGAGATATCTAAAATGTTATCTTAAAAGCCCACTCAAATCTCAAG
GCATAAGGTAGAAATGCAAATTTGGAAAAGTGGGCTGGGCCTTTTGTGGTAAAGGCCTGTAACTAGCCCAA
TATTAGCAAAACCCTAGACGCGTACATTGACATATATAAACCCGCTCCTCCTGTTTAGGGTTTCTACGTGAG
AGAGACGAAACACAAACCATGGAACGAGCTATACAAGGAAACGACGCTAGGGAACAAGCTAACAGTGAAC
GTTGGGATGGAGGATCAGGAGGAACCACTTCTCCCTTCAAACCTCCTGACGAAAGTCCGAGTTGGACTGAG
TGGCGGTACATAACGATGAGACTAATTCGAATCAAGATAATCCCCTTGGTTTCAAGGAAAGCTGGGGTTTC
GGGAAAGTTGTATTTAAGAGATATCTCAGATACGACAGGACGGAGGCTTCACTGCACAGAGTCCTTGGATC
TTGGACGGGAGATTTCGGTAACTATGCAGCATCTCGATTTTTCGGTTTCGACCAGATCGGATGTACCTATAGT
ATTCGGTTTCGAGGAGTTAGTATCACCGTTTCTGGAGGGTCGCGAACTTTCAGCATCTCTGTGAGATGGCA
ATTCGGTCTAAGCAAGAACTGCTACAGCTTGCCCCAATCGAAGTGGAAGTAATGTATCAAGAGGATGCCCT
GAAGGTACTGAAACCTTCGAAAAAGAAAGCGAGGGAAGCGGAGCTACTAACTTCAGCCTGCTGAAGCAG
GCTGGTGACGTGGAGGAGAACCCTGGACCTGGCATGACTATAAGGACCACGACGGAGACTACAAGGATC
ATGATATTGATTACAAAGACGATGACGATAAGATGGCCCCAAGAAGCGGAAGGTCGGTATCCACGGA
GTCCCAGCAGCCGACAAGAAGTACAGCATCGGCCTGGACATCGGCACCAACTCTGTGGGCTGGGCCGTGA
TCACCGACGAGTACAAGGTGCCAGCAAGAAATCAAGGTGCTGGGCAACACCGACCGGCACAGCATCAA
GAAGAACCTGATCGGAGCCCTGCTGTTGACAGCGGCGAAACAGCCGAGGCCACCCGGCTGAAGAGAAC
CGCCAGAAGAAGATACACCAGACGGAAGAACC GGATCTGCTATCTGCAAGAGATCTTCAGCAACGAGATG
GCCAAGGTGGACGACAGCTTCTTCACAGACTGGAAGAGTCCTTCTGGTGGAAAGAGGATAAGAAGCACG
AGCGGCACCCCATCTTCGGCAACATCGTGGACGAGGTGGCCTACCACGAGAAGTACCCACCATCTACCAC
CTGAGAAAGAACTGGTGGACAGCACCGACAAGGCCGACCTGCGGCTGATCTATCTGGCCCTGGCCACAT
GATCAAGTTCGGGGCCACTTCTGATCGAGGGCGACCTGAACCCCGACAACAGCGACGTGGACAAGCTG
TTCATCCAGCTGGTGCAGACCTACAACCAGCTGTTTCGAGGAAAACCCCATCAACGCCAGCGGCTGGACGC
CAAGGCCATCTGTCTGCCAGACTGAGCAAGAGCAGACGGCTGGAAAATCTGATCGCCAGCTGCCCGGC
GAGAAGAAGAATGGCCTGTTTCGGCAACCTGATTGCCCTGAGCCTGGGCCTGACCCCAACTTCAAGAGCA
ACTTCGACCTGGCCGAGGATGCCAACTGCAGCTGAGCAAGGACACCTACGACGACGACCTGGACAACCT
GCTGGCCAGATCGGCGACCAGTACGCCGACCTGTTTCTGGCCGCAAGAACCTGTCCGACGCCATCCTGC
TGAGCGACATCCTGAGAGTGAACACCGAGATACCAAGGCCCCCTGAGCGCCTCTATGATCAAGAGATAC
GACGAGCACCAACAGGACCTGACCCTGCTGAAAGCTCTCGTGCGGCAGCAGCTGCCTGAGAAGTACAAAG
AGATTTTCTTCGACCAGAGCAAGAACGGCTACGCCGGCTACATTGACGGCGGAGCCAGCCAGGAAGAGTT
CTACAAGTTCATCAAGCCCATCTGGAAAAGATGGACGGCACCGAGGAAGTCTCGTGAAGCTGAACAGA
GAGGACCTGCTGCGGAAGCAGCGGACCTTCGACAACGGCAGCATCCCCACCAGATCCACCTGGGAGAGC
TGCACGCCATTCTGCGGCGGCAGGAAGATTTTACCCATTCTGAAGGACAACCGGGAAAAGATCGAGAA
GATCCTGACCTCCGCATCCCCTACTACGTGGGCCCTCTGGCCAGGGGAAACAGCAGATTGCCTGGATGAC
CAGAAAGAGCGAGGAAACCATCACCCCTGGAACCTCGAGGAAGTGGTGGACAAGGGCGCTTCCGCCCA
GAGCTTCATCGAGCGGATGACCAACTTCGATAAGAACCTGCCAACGAGAAGGTGCTGCCAAGCACAGCC
TGCTGTACGAGTACTTCACCGTGTATAACGAGCTGACCAAAGTGAAATACGTGACCGAGGGAATGAGAAAG
CCCGCCTTCTGAGCGGCGAGCAGAAAAAGGCCATCGTGACCTGCTGTTCAAGACCAACCGGAAAAGTGA
CCGTGAAGCAGCTGAAAGAGGACTACTTCAAGAAAATCGAGTGCTTCGACTCCGTGGAAATCTCCGGCGTG
GAAGATCGGTTCAACGCCTCCCTGGGCACATACCACGATCTGCTGAAAATTATCAAGGACAAGGACTTCCTG
GACAATGAGGAAAACGAGGACATTCTGGAAGATATCGTGCTGACCCTGACACTGTTTGAGGACAGAGAGAT
GATCGAGGAACGGCTGAAAACCTATGCCACCTGTTTCGACGACAAAGTGATGAAGCAGCTGAAGCGGCGG
AGATACACCGGCTGGGGCAGGCTGAGCCGGAAGCTGATCAACGGCATCCGGGACAAGCAGTCCGGCAAG
ACAATCCTGGATTCTCTGAAGTCCGACGGCTTCGCCAACAGAACTTCATGCAGCTGATCCACGACGACAGC

CTGACCTTTAAAGAGGACATCCAGAAAGCCCAGGTGTCCGGCCAGGGCGATAGCCTGCACGAGCACATTG
CCAATCTGGCCGGCAGCCCCGCCATTAAGAAGGGCATCCTGCAGACAGTGAAGGTGGTGGACGAGCTCGT
GAAAGTGATGGGCCGGCACAAGCCCCGAGAACATCGTGATCGAAATGGCCAGAGAGAACCAGACCACCCA
GAAGGGACAGAAGAACAGCCGCGAGAGAATGAAGCGGATCGAAGAGGGCATCAAAGAGCTGGGCAGCC
AGATCCTGAAAGAACACCCCGTGAAAAACACCCAGCTGCAGAACGAGAAGCTGTACCTGTACTACCTGCAG
AATGGGCGGGATATGTACGTGGACCAGGAAGTGGACATCAACCGGCTGTCCGACTACGATGTGGACCATATC
GTGCTCAGAGCTTTCTGAAGGACGACTCCATCGACAACAAGGTGCTGACCAGAAGCGACAAGAACCGGG
GCAAGAGCGACAACGTGCCCTCCGAAGAGGTCGTGAAGAAGATGAAGAACTACTGGCGGCAGCTGCTGA
ACGCCAAGCTGATTACCCAGAGAAAAGTTCGACAATCTGACCAAGGCCGAGAGAGCGGCCTGAGCGAACT
GGATAAGGCCGGCTTCATCAAGAGACAGCTGGTGGAAACCCGGCAGATCACAAAGCACGTGGCACAGATC
CTGGAATCCCGGATGAACATAAGTACGACGAGAATGACAAGCTGATCCGGGAAGTGAAAGTGATCACCT
GAAGTCCAAGCTGGTGTCCGATTTCCGGAAGGATTTCAGTTTTACAAAGTGC GCGAGATCAACAACCTACC
ACCACGCCACGACGCCTACCTGAACGCCGTCTGGGAACCGCCCTGATCAAAAAGTACCCTAAGCTGGAA
AGCGAGTTCTGTACGGCGACTACAAGGTGTACGACGTGCGGAAGATGATCGCCAAGAGCGAGCAGGAAA
TCGGCAAGGCTACCGCCAAGTACTTCTTCTACAGCAACATCATGAACTTTTTCAAGACCGAGATTACCCTGG
CCAACGGCGAGATCCGGAAGCGGCCTCTGATCGAGACAAACGGCGAAACCGGGGAGATCGTGTGGGATA
AGGGCCGGGATTTTGCCACCGTGC GGAAGTGTGAGCATGCCCAAGTGAATATCGTAAAAAGACCGA
GGTGCAGACAGGCGGCTTCAGCAAAGAGTCTATCTGCCCAAGAGGAACAGCGATAAGCTGATCGCCAGA
AAGAAGGACTGGGACCCTAAGAAGTACGGCGGCTTCGACAGCCCCACCGTGGCCTATTCTGTGCTGGTGGT
GGCCAAAGTGGAAGAGGGCAAGTCCAAGAACTGAAGAGTGTGAAAGAGCTGCTGGGGATCACCATCAT
GGAAAGAAGCAGCTTCGAGAAGAATCCCATCGACTTTCTGGAAGCCAAGGGCTACAAAGAAGTGAAAAA
GGACCTGATCATCAAGCTGCCTAAGTACTCCCTGTTCTGAGCTGGAAAACGGCCGGAAGAGAATGCTGGCCT
CTGCCGGCGAAGTGCAGAAAGGGAAACGAACTGGCCCTGCCCTCAAATATGTGAACCTCTGTACCTGGCC
AGCCACTATGAGAAGCTGAAGGGTCCCCGAGGATAATGAGCAGAAACAGCTGTTTGTGGAACAGCACA
AGCACTACCTGGACGAGATCATCGAGCAGATCAGCGAGTTCTCCAAGAGAGTGATCCTGGCCGACGCTAAT
CTGGACAAAGTGCTGTCCGCCTACAACAAGCACCGGGATAAGCCCATCAGAGAGCAGGCCGAGAATATCAT
CCACCTGTTTACCCTGACCAATCTGGGAGCCCCTGCCGCCTTCAAGTACTTTGACACCACCATCGACCGGAA
GAGGTACACCAGCACCAAGAGGTGCTGGACGCCACCCTGATCCACCAGAGCATCACCGGCCTGTACGAG
ACACGGATCGACCTGTCTCAGCTGGGAGGCGACAAAAGGCCGGCGGCCACGAAAAAGGCCGGCCAGGCA
AAAAAGAAAAAGTAAAGGATCCAGAGACTCTTATCAAGAATCCCATCTCTTGCTTGCTTTTTTTTGTGCTTCC
CTTTGATAGGGTTTGTCTTTCTGTTTCAGTGACTTTCTATGTTAAAGATAATGTCAGTAAAGGATTTGGTT
TTCTATTATTCTGAATCGATTACGGAAGATTCTTGCTTAATTCCAATCTATACAAGTATCGTGAAATAATGACCG
TTTATGTGGTACCGAGCTCGAATTC

“_”:p19-2A, “ ”: SpCas9-NLS; “ATG”: Start codon; “TAA”: Stop codon

>p35S-GU-IR-US-polyA

CATGGAGTCAAAGATTCAAATAGAGGACCTAACAGAACTCGCCGTAAAGACTGGCGAACAGTTCATACAGA
GTCTCTTACGACTCAATGACAAGAAGAAAATCTTCGTCAACATGGTGGAGCACGACACACTTGTCTACTCCA
AAAATATCAAAGATACAGTCTCAGAAGACCAAAGGGCAATTGAGACTTTTCAACAAAGGGTAATATCCGGA
AACCTCCTCGGATTCCATTGCCAGCTATCTGTCACTTTATTGTGAAGATAGTGGAAAAGGAAGGTGGCTCCT
ACAAATGCCATCATTGCGATAAAGGAAAGGCCATCGTTGAAGATGCCTCTGCCGACAGTGGTCCCAAAGAT
GGACCCCCACCCACGAGGAGCATCGTGAAAAAGAAGACGTTCCAACCACGTCTTCAAAGCAAGTGGATT
GATGTGATATCTCACTGACGTAAGGGATGACGCACAATCCCACTATCCTTCGCAAGACCTTCTCTATATAA
GGAAGTTCATTTCAATTGGAGAGAACACGGGGGACTCTTGACCATGGTAGATCTGAGGGTAAATTCTAGTT

TTTCTCCTTCATTTTCTTGGTTAGGACCTTTTCTCTTTTATTTTTTGTAGCTTTGATCTTTCTTTAACTGATC
 TATTTTTTAATTGATTGGTTATGGTGAAATATTACATAGCTTTAACTGATAATCTGATTACTTTATTCGTGTGT
 CTATGATGATGATGATAGTTACAGAACCGACGACTCGTCCGTCCTGTAGAAAACCCCAACCCGTGAAATCAAA
 AAACCTCGACGGCCTGTGGGCATTAGTCTGGATCGCGAAAACCTGTGGAATTGATCAGCGTTGGTGGGAAA
 GCGCGTTACAAGAAAGCCGGGCAATTGCTGTGCCAGGCAGTTTTAACGATCAGTTGCGCGATGCAGATATTC
 GTAATTATGCGGGCAACGTCTGGTATCAGCGCGAAGTCTTTATACCGAAAGGTTGGGCAGGCCAGCGTATCG
 TGCTGCGTTTCGATGCGGTCACTCATTACGGCAAAGTGTGGGTCAATAATCAGGAAGTGATGGAGCATCAG
 GGCGGTATACGCCATTTGAAGCCGATGTCACGCCGTATGTTATTGCCGGGAAAAGTGTACGTATCACCGTTT
 GTGTGAACAACGAACCTGAACTGGCAGACTATCCCGCCGGGAATGGTGATTACCGACGAAAACGGCAAGAA
 AAAGCAGTCTTACTTCCATGATTTCTTTAACTATGCCGGAATCCATCGCAGCGTAATGCTCTACACCACGCCGA
 ACACCTGGGTGGACGATATCACCGTGGTGACGCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGG
 CAGGTGGTGGCCAATGGTGATGTCAGCGTTGAACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGAC
 AAGGCACTAGTTCCTTTATCTCTTAGGGATA**ACAGGGTAATAGAGATAAA****GGG**AGGCCTGAATTGCTGTG
 CCAGGCAGTTTTAACGATCAGTTGCGCGATGCAGATATCGTAATTATGCGGGCAACGTCTGGTATCAGCGC
 GAAGTCTTTATACCGAAAGGTTGGGCAGGCCAGCGTATCGTGCTGCGTTTCGATGCGGTCACTCATTACGGC
 AAAGTGTGGGTCAATAATCAGGAAGTGATGGAGCATCAGGGCGGCTATACGCCATTTGAAGCCGATGTCAC
 GCCGTATGTTATTGCCGGGAAAAGTGACGTATCACCGTTTGTGTGAACAACGAACCTGAACTGGCAGACTAT
 CCCGCCGGGAATGGTGATTACCGACGAAAACGGCAAGAAAAAGCAGTCTTACTTCCATGATTTCTTTAACTA
 TGCCGGAATCCATCGCAGCGTAATGCTCTACACCACGCCGAACACCTGGGTGGACGATATCACCGTGGTGAC
 GCATGTCGCGCAAGACTGTAACCACGCGTCTGTTGACTGGCAGGTGGTGGCCAATGGTGATGTCAGCGTTG
 AACTGCGTGATGCGGATCAACAGGTGGTTGCAACTGGACAAGGCACTAGCGGGACTTTGCAAGTGGTGAA
 TCCGCACCTCTGGCAACCGGGTGAAGGTTATCTCTATGAACTCGAAGTCACAGCCAAAAGCCAGACAGAGT
 CTGATATCTACCCGCTTCGCGTCGGCATCCGGTCAGTGGCAGTGAAGGGCCAACAGTTTCTGATTAACCACA
 AACCGTTCTACTTTACTGGCTTTGGTCGTCATGAAGATGCGGACTTACGTGGCAAAGGATTCGATAACGTGC
 TGATGGTGCACGACCACGCATTAATGGACTGGATTGGGGCCAACCTCCTACCGTACCTCGCATTACCCTTACGC
 TGAAGAGATGCTCGACTGGGCAGATGAACATGGCATCGTGGTGATTGATGAAACTGCTGCTGTCGGCTTTT
 AGCTGTCTTTAGGCATTGGTTTTGAAGCGGGCAACAAGCCGAAAGAACTGTACAGCGAAGAGGCAGTCAA
 CGGGGAAACTCAGCAAGCGCACTTACAGGCGATTAAAGAGCTGATAGCGCGTGACAAAAACCAACCAAGC
 GTGGTGATGTGGAGTATTGCCAACGAACCGGATACCCGTCCGCAAGGTGCACGGGAATATTTCGCGCCACT
 GGCGGAAGCAACGCGTAAACTCGACCCGACGCGTCCGATCACCTGCGTCAATGTAATGTTCTGCGACGCTC
 ACACCGATACCATCAGCGATCTTTGATGTGCTGTGCCTGAACCGTTATTACGGATGGTATGTCCAAAGCGG
 CGATTTGGAAACGGCAGAGAAGGTACTGGAAAAAGAACTTCTGGCCTGGCAGGAGAACTGCATCAGCCG
 ATTATCATCACCGAATACGGCGTGGATACGTTAGCCGGGCTGCACTCAATGTACACCGACATGTGGAGTGAA
 GAGTATCAGTGTGCATGGCTGGATATGTATCACCGCGTCTTTGATCGCGTCAGCGCCGTCGTCGGTGAACAG
 GTATGGAATTTGCGCGATTTTGCGACCTCGCAAGGCATATTGCGCGTTGGCGGTAACAAGAAAGGGATCTTC
 ACTCGCGACCGCAAACCGAAGTCGGCGGCTTTTCTGCTGCAAAAAACGCTGGACTGGCATGAACTTCGGTG
 AAAAACCGCAGCAGGGAGGCAAACAAGCTAGCCACCACCACCACCACCGT**TGA**ATTACAGGTGACCA
 GCTCGAATTTCCCGATCGTTCAAACATTTGGCAATAAAGTTTCTTAAGATTGAATCCTGTTGCCGGTCTTGC
 GATGATTATCATATAATTTCTGTTGAATTACGTTAAGCATGTAATAATTAACATGTAATGCATGACGTTATTTATG
 AGATGGGTTTTTATGATTAGAGTCCCGCAATTATACATTTAATACGCGATAGAAAACAAAATATAGCGCGCAA
 ACTAGGATAAATTATCGCGCGCGGTGTCATCTATGTTACTAGATCGGG

“_”: U fragment; “....”: G and S fragment; “ ”: IR region; “**Bold**”:sgRNA target site; “**GGG**”:PAM
 sequences; “**ATG**”: Start codon; “**TAG**”: Stop codon