

Table S1 Strains used in the work

Insertions are shown by yellow. Sequences of FLAG are underlined. In the frame stop codons are red

Strain	Mutation		Comments
	Gene and position of a mutation	Sequence of exon containing an insert	
Δ KU80 -C4 ^a	Cre10.g42 3800, <i>KU80</i> Exon 3, position 958	CTCCTGTTCAAGCCACTGCACGAGGTGG CCGTG ctagagtatgactagaattgacacgtcagcgtgct gtacggcactgagggtgagagacacctagagtatgactag aattgacacgtcagc GCTGCTGTACGGCACTGAG GGTGAGAGACACCGCAGCACTGCAGCAG ATAGGGAGCGGGCGGACTCGTGCGGC GCAGCCATGTGGCATAGCGTGTGTGATA TCTACCCGCCACCCCTGCACGGCCGCAG	The 90 bp insertion
Δ KU80 -C6	Cre10.g42 3800, <i>KU80</i> Exon 3, position 958	CTCCTGTTCAAGCCACTGCACGAGGTGG CCGTG ctaaagtatgactagaattgacacgtcaccgggtt taatgtctgaacaccaagggctgaagcggtagcttacctcc ccgtttcgggctgatcagtttttcaaacgtaaaaagcggga ggagtttgcaatttttggtgtaacaatcctccttgattttggc cttttctccatgggctgggggtattgaaagcgggtacc agctttgttcccttagggagggtaattcaagctgggggta atcatggtcatagcttttctgtggggaattgtgagcggaaa acaattcccactgttcaagcccctgcacaagggggccgtg ctaaagtatgactagaattgacacgtcagcgg GCTGTA CGGCACTGAGG	The 371 bp insertion. The vector DNA is shown by italics
Δ KU70 -C8	Cre13.g60 7500, <i>KU70</i> Exon 5, Position 1773	GTCGCTCAACACCATT ctagagtatgactagaatt gacacgtcagc GCTGGTGTCTCAAACGACCC CGAGCCCTGCGGACCCGCCACCGCACC CGGCTTCAAGGCCGCAGT	The 30 bp insertion

ΔKU70 -D10	Cre13.g60 7500, <i>KU70</i> Exon 5, Position 1775	GTCGCTCAACACCATTGTctagagtatgactaga attgacacgtcagcgtggtgttctcaaacgacccccgagccct gcccgatccccctcaggctcgtcaacaccattctagagtatg actagaattgacacgtcagcatggcggatcatcctctacaaca cggcgttGGTGTCTCAAACGACCCCGAG CCCTGCGGACCCGCCACCGCACCCGGC TTCAAGGCCGCAGT	The 151 bp insertion
ΔPOL Q-E2	Cre16.g66 4300, <i>POLQ</i> Exon 1, position 1357	GCGCCCATGCTGGTGCCGCGGGGTC AGGCACCTGCTGCGCATCAGTTGATGGT Ggctagagtatgactagaattg nnnnnnnnnnnnnnnnnnnn nnngctagagtatgactagaattgACGGCGGCTCC C	Insertion > 3 kb. It is shown exon 1 fragment. Unidentified DNA sequence, probably vector DNA, is shown by italics
ΔPOL Q-G2 ^a	Cre16.g66 4300, <i>POLQ</i> Exon 1, position 1373	TCAGTTGATGGTGACGGCGGCTCCAGC Afatgaccacgctcctttagtcgatgctggtcattatgctg ggagccgcccgtcaccatcgactacaaggacATGTGGA TGGCGCGGCGGCATGCCGCA	The 74 bp insertion. It is shown exon 1 fragment
D5- ΔKU80 -E4	Cre10.g42 3800, <i>KU80</i> Exon 2, position 322	GACCTGCATGTGTTGGTGCTGGACGTGG GGCCGCACATGCAGCCCTACCTCCCGCT GCTGCACCGCCTGctagagtatgactagaattgac acgtcagcgtgttaatgtctgaacaccaaggcaaggcag ccctacctcccgtgctgcaccgctgctagagtatgactag aattgacacgtcagcGTGTTTAATGTCTTGAACA CCAAG	The 120 bp insertion
D5- ΔKU80 -G4	Cre10.g42 3800, <i>KU80</i> Exon 2, position	GACCTGCATGTGTTGGTGCTGGACGTGG GGCCGCACATGCAGCCCTACCTCCCGCT GCTGCACCGCCTGctagagtatgactagaattgac acgtcagcGTGTTTAATGTCTTGAACACCAA G	The 30 bp insertion

	322		
D5- ΔKU70 -B6	Cre13.g60 7500, KU70 Exon 5, Position 1773	GTCGCTCAACACCATTctagagtatgactagaatt gacacgctcagcgtggtgttctcaaacaacccaagccattct agagtatgactagaattgacacgctcagcgtggtgttctcaa caacccaagccattctagagtatgactagaattgacactt caccgtggtgttctcaaacgaccccgatcccctcaggtcgc tcaacaccatttagagtatgactagaattgacacttcagcG TGGTGTCTCAAACGACCCCGAGCCCTG CGGACCCGCCACCGCACCCGGCTTCAAG GCCGCAGT	The 228 bp insertion
D5- ΔPOL Q-A6	Cre16.g66 4300, POLQ Exon 1, position 1357	CGGCGGGTCAGGCACCTGCTGCGCATCA GTTGATGGTGctagagtatgactagaattgacacgctc agcACGGCGGCTCCCAGCAATGTGGATG GCGCGGCGGCGCATGCCGG	The 30 bp insertion. It is shown the exon 1 fragment

^a Mutants ΔKU80-C4 and ΔPOLQ-G2 were prepared by Greiner and colleagues (2017)

Table S2 Mutations generated in the *APT* gene

Strain/nam e of a clone	Mutation		Notes
	Gene and position	Sequence of exon containing an insert	
wt, APT ins 132	<i>APT</i> Exon 1 Position 101	ATGGCTGACGTTGAGGCCAAGAAGG AGATTATCAAGAATGCCATTCGTGGC ATTCCTGACTTTCCCACAAGGGTAT TCTGTTCTGGGATGTCA <u>CCACCA</u> ttga cgcggggcagccacatgacgtgcatgtcctcggcgt ctgcttccgctgaccattgccggaatgcgccagctg atgcagcgttacgccgtacgagttggtggcctcgtcg aaatcgacaaccgtgacTCATGCTGAACC	It is shown the exon 1 fragment. The 132 bp insertion of the <i>DHC2</i> fragment is shown by yellow. The 5 bp homology between <i>APT</i> and <i>DHC2</i> is underlined. PAM is red. Protospacer is green

		ACCAGGCGTTCCAGTACAGCA	
wt, APT ins 500 Δ1	APT Exon 1 Position 101	<p>CCCACAAGGGTATTCTGTTCTGGGAT</p> <p>GTCACCACTGGTACC GCCACTGCCTATGTTA</p> <p>ATACTCCAAGTTACTGCCC GAAGGGAAGGAGG</p> <p>CAGTTGGCAGGCAACTGCCACTGACGTCCTAAGG</p> <p>GGACGTCCACTAAAATTCATTGCCTCGGCAGTTGGCA</p> <p>GGACGTCCCCTCGGGCAAATAAATTTAGTGGCAGTG</p> <p>GGACCATAAAAATATAAATTTCCCTACGGGTGT</p> <p>AAATAACATAAATCCCTTATGACTACAAAAAAC</p> <p>AATACAATTTATGCTAATATAGCTCAGGTTCTAATCAC</p> <p>GACTAATTTCTTAGTAACATCCAACAATCTTAA</p> <p>ACTTACAAGTAAGTATGCTAGGACCCTGTCAAAATGC</p> <p>ATTTAAATTAAGAAGCGGGTTAAATAAAGGTATT</p> <p>GGTTATTATAAAATGGCGTTCCCGTGGCTAAGCTGAT</p> <p>AACATTTGGCTATATAAATCCGTGAAGCGCTAAAA</p> <p>ATTATATAATCGAAATCATGCTGAACCACC</p> <p>AGGCGTTCCAGTACAGCATTGAC</p>	It is shown the exon 1 fragment. The 500 bp insert of the chloroplast DNA is shown by yellow. PAM is red. Protospacer is green
wt, APT ins 182 Δ421	APT Exon 1 Position 103	<p>ATGGCTGACGTTGAGGCCAAGAAGG</p> <p>AGATTATCAAGAATGCCATTCGTGGC</p> <p>ATTCCTGACTTTCCCACAAGGGTAT</p> <p>TCTGTTCTGGGATGTCACTCATCTC</p> <p>AGGGCTCCTATCTAATGTCTCCAGACATAATTGGCCA</p> <p>TTTGGCGTTTCTAGACATTCTCTGGGACTAATGT</p> <p>GTGAGGCAAGACATTGTCGCCGTTTGGGGCGGGT</p> <p>TTGTCCAATCCTATGGAGAAGCCCCAAACCGCC</p> <p>ATGTGCCAGACAAAAGACGGCGGCCA</p> <p>CCCGG</p> <p>CCG(G)TTAAACCGCTGCACTGCGAG</p> <p>GGCCGCGGGCCGACCCTGTTG</p>	It is shown exon 1 and intron 2 fragments. The 182 bp insert containing a fragment of the unnamed transposon Tc 238 bp is shown by yellow and italics. APT deletion Δ421 bp is from 103 to 523 bp. The 11 bp homology between APT and Tc 238 bp is underlined. In brackets it is shown the mismatch G/T. PAM is red. Protospacer is green

<p>wt, APT ins 246</p>	<p>APT Exon 1 Position 103</p>	<p>ATGGCTGACGTTGAGGCCAAGAAGG AGATTATCAAGAATGCCATTTCGTGGC ATTCCTGACTTTCCCCACAAGGGTAT TCTGTTCTGGGATGTCACCACCATC<u>c</u> <i>agggtcctatcttaatgtctccagacattaattggcca</i> <i>tttggccgttcttagacattcctcctgggactaatgt</i> <i>gtgaggcaagacattgtcgcccggtttggggcgggt</i> <i>ttgtccaattcctatggagaagccccaaaccgcc</i> <i>atgtgccagacaaaagacggcgccaccggcc</i> <i>ggtttctctgagcctagacattgccctgaaaacaag</i> <i>atacgaccctgccaccatc</i>ATGCTGAACCA CCAGGCGTTCAGTACAGCA</p>	<p>It is shown the exon 1 fragment. The 246 bp insert is shown by yellow. Sequence of the unnamed transposon Tc 238 bp is shown by italics. Sequence of the 8 bp repeat of the transposon insertion site is underlined. PAM is red. Protospacer is green</p>
<p>ku80, APT ins 246</p>	<p>APT Exon 1 Position 128</p>	<p>ATGGCTGACGTTGAGGCCAAGAAGG AGATTATCAAGAATGCCATTTCGTGGC ATTCCTGACTTTCCCCACAAGGGTAT TCTGTTCTGGGATGTCACCACCATCA TGCTGAACCACCAGGCGTTCAGT<u>ca</u> <i>ggggtcgtatcttgttgggtaatgtctagctccaga</i> <i>caaaaacggtcgggtggccgcctcttctgtctgggc</i> <i>acatggcggtttgggggcttccataggaatacggga</i> <i>caaaacccgccccaaaccggcccaacgaagtctc</i> <i>accccagacattagccccgggaggaatgtctagga</i> <i>aacggccaaaatggccagttaatgtctggagacatta</i> <i>agataggagccctggtccagt</i>ACAGCATTGA CCTGTT</p>	<p>It is shown the exon 1 fragment. The 246 bp insert is shown by yellow. Sequence of the unnamed transposon Tc 238 bp is shown by italics. Sequence of the 8 bp repeat of the transposon insertion site is underlined. PAM is red. Protospacer is green.</p>
<p>polQ, APT ins 85</p>	<p>APT Exon 1 Position 102</p>	<p>ATGGCTGACGTTGAGGCCAAGAAGG AGATTATCAAGAATGCCATTTCGTGGC ATTCCTGACTTTCCCCACAAGGGTAT TCTGTTCTGGGATGTCACCACCAT<u>tgc</u> <i>gttggggtgcatgaaatgaaggcattgcgttgcgtgt</i> <i>gcatggaatgaaggctcctgcttgtgtccgccattgcc</i></p>	<p>It is shown the exon 1 fragment. The 85 bp insert of the <i>GTR14</i> gene (Cre14.g616200.t1.2) is shown by yellow. PAM is red. Protospacer is green</p>

		ccgcct CATGCTGAACCACCAGGCGTT CCAGTACAGCATTGACCTGTTCGCT GAGCAGTACA	
--	--	--------------------------------------------------------------------------------	--

Table S3 Donor DNA used in the work

FLAG sequences are indicated in red, left homology arms are highlighted in yellow, phosphorothioate bonds are indicated by asterisks

Construct name, the length of homology	Sequence
Gene-specific homology insertions inside plasmids used as HDR-Donors	
pHDR-APHVIII ^{Δ120} , 1350 bp	GTCAAGGTGGCAGCTCTGGGGGCCGGGGTGGGCTTGTGGGTGAGGCTGAGCG GCTGGTGTGGTTGGCGGAGGTGGGGATTCCCGTACCTCGTGTGTTGTGGAGGGTGG TGGGGACGAGAGGGTCGCTGTTGGTCACCGAAGCGTTCCGGGGCGTCCGG CCAGTGCGCGGTGGCCGCGGAGCAGCGGCTGGACGTGGCGGTGGCGCTCGCG GGGCTCGCTCGTTCGCTGCACGCGCTGGACTGGGAGCGGTGTCCGTTTCGATCGC AGTCTCGCGGTGACGGTGCCGCAGGCGGCCCGTGCTGTGCTGAAGGGAGCGT CGACTTGGAGGATCTGGACGAGGAGCGGAAGGGGTGGTCCGGGGAGCGGCTTC TCGCCGAGCTGGAGCGGACTCGGCCTGCGGACGAGGATCTGGCGGTTTGCCACG GTGACCTGTGCCCGACAACGTGCTGCTCGACCCTCGTACCTGCGAGGTGACCG GGCTGATCGACGTGGGGCGGGT CGGCCGTGCGGACCGGCACTCCGATCTCGCG CTGGTGCTGCGCGAGCTGGCCACGAGGAGGACCCGTGGTTCGGGCCGGAGTG TTCCGCGGCGTTCCCTGCGGGAGTACGGGCGCGGGTGGGATGGGGCGGTATCGG AGGAAAAGCTGGCGTTTTACCGGCTGTTGGACGAGTTCTTCTGAGGGACCTGATG GTGTTGGTGGCTGGGTAGGTTGCGTCGCGTGGGTGACAGCACAGTGTGGACGT TGGGATCGCACCTACCTGGCGGCGGAGGGACAGCACTGAGAATTCTGGCAGCAG CTGGACCGCCTGTACCATGGAGAAGAGCTTTACTTGCCGGGATGGCCGATTTTCG TGATTGATACGGGATCGGAGCTCGGAGGCTTTCGCGCTAGGGGCTAGGCGAAGG GCAGTGGTGACCAGGGTCGGTGTGGGGTTCGGCCACGGTCAATTAGCCACAGGA

	<p>GGATCAGGGGGAGGTAGGCACGTGCGACTTGGTTTGCACCCCGCAGTTTTGGCG GACGTGCTGTTGTAGATGTTAGCGTGTGCGTGAGCCAGTGGCCAACGTGCCACAC CCATTGAGAAGACCAACCAACTTACTGGCAATATCTGCCAATGCCATACTGCATGT AATGGCCAGGCCATGTGAGAGTTTGCCGTGCCTGCGCGCGCCCCGGGGGCGCA GTTTAGCTGACCAGCCGTGGGATGATGCACGCATTTGCAAGGACAGGGTAATCAC AGCAGCAACATGGTGGGCTTAGGACAGCTGTGGGTGAGTGGACGGACGGCAGGG GAGGGACGGCGCAGCTCGGGAGACAGGGGGAGACAGCGTGACTGTGCAATCAA GCTT</p>
pSNRK- FLAG,1113+ 770 bp	<p>GGAACCCACGACGAAGCCTGTGCGCACGCTCAGTGGCACCGCCAGTGCCAC GGCTGCTGTGCGCTTGTAATTTGCATGTTTCAATAGTCCTATGAGGATGGATATG CAGACGTTGACGCGGTGCCCGGACCAATACCAACACGGTACAGCACGGGCCCG CCCTGCCGCCCTGCGCCCCGGGCCCAACGGCGGACCTTCACATACTAGCCCAG ACAGCTTTACTTTGAGAAGTAGAGGCAGAACACGTGCTGCTTGGCGTCGCTGCCA CGTGTGCGGCCACGTCCGCCTCCGGCAGGCAGCGATACTTGAAGCCTCACGC ACGCGCTCCACCTGCCGCCCGCCGCCGCGGCCAGGCTGCGGCACTGACGCACT CATCTCCGGCCGGACCAGTAGTTGACATCACCACCACCGCCGCGGGCCGCTAG CTCCTTTTGTAGCGTGGCATCGTGCACCTGTGCATCGGCATACCGACGTCAGCGG CTCAACGTGGCCCTTTGGAGCGCTGGAGAGGTGCGGTGCGTGGCGTGCCCTTCC GGAACCAAACACACCTGCCTCCGGGCCGGCCGCGACAGCCACTCCACCCGGTTG GGTACTGCGGATCTCGCGGGTTAAGCTGCATGATATTGTTTCAGCGAATGCAAAT GATGGACAGGCCGGAAGGAATGCACTTGGCGCGCTTCTAGTTGGTTCCAGTTTGC AGTCCAGTTTGTAGTCGCTCAACCTATTCTACATGGCGAAAAGTCTGTAACTGTGA GCGTTGACACAGCATCAAAAGTATTACTATGAGCCAGGGGGCAGCAAGGTCAGCC CCATCCGGCTTGCCCTGGGCGTGGGGCTCACGTGCGGTTGCTCCCAACGCACAT TGCAACACACTAATTCACAAGCCGAAACAACACATTTTGCCTGCTGGTTAACTGTC ACTTGTTGGAGCTAGTGACGCGAACCACGACCGGTCCAAAGGTTCTTCTGAGC CCCACCAACACGTTCTACTAGCTTGTAGTTCTTTCTAGGGCGGGGTGTGGCTGC CAGACCCCAAAAGCTCTCCTCCATGGCAGCGGCGAACCACAAAAGCCGGGTCCAGC AGGCCGACCAGAGCCCCTGACTCCGTTGTAACCTTTTCTTCAATCGAAATTGGACA TCCTCGCTATGAAAAGTTGGTAATTCTCAGGGTGCATAGAGGTGCTGTCTCTCGC CCAACCGGGCGCAGGGGCCAACGCGATGCTGCGTGGGCGGCCTCGGCTTCGCA</p>

	<p>CGAGGGCATCATGCGCGATGTTGCTTGCCTTGGCGAACCTGGTGTGGT ACTGTGTGCAGCAACTGACTCATGATTTCTGGGCTCCTGTGCAGATCAAGGACCTA AACAGCGGCACCTTCGGCTTCGTGCAGCTTGCACGCGACAAGCTGACAGGGGAA ACATGGGCTGTGAAGTTCATTGAGCGCGGGGACAAGGTGAACGCTGCTTGGGGG AGCCTGAACTTCGAGCGGGGGTTCGGGGTTGGGGGATGGGTAACGACGCGGCTC CGACCCGATGTTGGCGAACACTGCCCGGGCGGGGGCCTGAGGCGTCGATGCGG GTGACAAGTGGCCTGGTGCACCCTAGGAACGGCCGTTGGCCTTGGGATGCAGGC CGGTTTGCACCTCCATGGGGGCGCCCAAGCCCTCATCCGTCCGCTGGCCAGTGC GGTGGCCCTCACACGCGAACGGTGGGTGGGATATCGCCTAACCGCGCGTAACCC GGCCCGCATCGCTGTCTGACACACAGATTACGAAGTACGTGGAGCGCGAGATCAT CAACCACCGGTGTCTAGTGCACCCACACATTGTGCAGGTGCGTGGGAGAGGCTTG GGATTGCCAGTGCAGGGCAGGAGCGGGGGCTTGGTGGCTTGGCGTTGCATGTT CCT</p>
	Oligonucleotides used as HDR-Donors
<i>KU80-1</i> S-ssODN 30+30 nt	<p>C*T*G*TTCAAGCCACTGCACGAGGTGGCCGTGCTAGAGTATGACTAGAAATTGACAC GTCAGCGTGCTGTACGGCACTGAGGGTGAGAGA*C*A*C</p>
<i>KU80-1</i> P-ssODN 30+30 nt	<p>G*T*G*TCTCTCACCCCTCAGTGCCGTACAGCACGCTGACGTGTCAATTCTAGTCATA CTCTAGCACGGCCACCTCGTGCAGTGGCTTGAA*C*A*G</p>
<i>KU80-2</i> S-ssODN 30 nt	<p>G*T*C*CTTGTAGTCGATGTCGTGGTCaTTATAggctggctcctgccgccgcccctoga*a*c*a</p>
<i>KU80-2</i> P-ssODN 30 nt	<p>T*A*T*AAtGACCACGACATCGACTACAAGGACtggatggcgccgccgccggaaggcg*a*c*g</p>
<i>KU70</i> S-ssODN 30+30 nt	<p>C*C*G*GATCCCCTCAGGTGCTCAACACCATTCTAGAGTATGACTAGAAATTGACAC GTCAGCGTGGTGTCTCAAACGACCCCGAGCCC*T*G*C</p>
<i>KU70</i>	<p>G*C*A*GGGCTCGGGTTCGTTTGAAGAACACCACGCTGACGTGTCAATTCTAGTCAT</p>

P-ssODN 30+30 nt	ACTCTAGAATGGTGTTGAGCGACCTGAGGGGATC*C*G*G
POLQ-1 S-ssODN 30+30 nt	C*G*C*GCCATCCACATTGCTGGGAGCCGCCGTGCTGACGTGTCAATTCTAGTCAT ACTCTAGCACCATCAACTGATGCGCAGCAGGTGC*T*G
POLQ-1 P-ssODN 30+30 nt	C*A*G*GCACCTGCTGCGCATCAGTTGATGGTGCTAGAGTATGACTAGAATTGACAC GTCAGCACGGCGGCTCCCAGCAATGTGGATGGC*G*C*G
POLQ-2 S-ssODN 30 nt	T*A*T*AATGACCACGACATCGACTACAAGGACATGTGGATGGCGCGGCGGCGCAT GCCG*G*C*A
POLQ-2 P-ssODN 30 nt	G*T*C*CTTGTAGTCGATGTCGTGGTCATTATATGCTGGGAGCCGCCGTCACCATCA ACT*G*A*T
APHVIII S-ssODN, 100 nt	C*C*C*TCGTACCTGCGAGGTGACCGGGCTGATCGACGTGGGGCGGGTCGGCCGT GCGGACCGGCACTCCGATCTCGCGCTGGTGTGCGCGAGCTGGCC*C*A*C
APHVIII P-ssODN, 100 nt	G*T*G*GGCCAGCTCGCGCAGCACCAGCGCGAGATCGGAGTGCCGGTCCGCACGG CCGACCCGCCCCACGTGATCAGCCCGGTACCTCGCAGGTACGA*G*G*G
SNRK2.2 S-ssODN- FLAG, 90 nt, 33+28 nt	A*G*C*CGGGTCCAGCAGGCCGACCAGAGCCCCTGACTCCGTTGTAACTTTTCTT CAATCGAAATTGGACATCCTCGCTATGAAtAGGT*T*G*G
SNRK2.2 P-ssODN- FLAG, 90 nt 33+28 nt	C*C*A*ACCTaTTCATAGCGAGGATGTCCAATTTTCGATTGAAGGAAAAGTTACAACG GAGTCAGGGGCTCTGGTCGGCCTGCTGGACCCG*G*C*T

Table S4 Oligonucleotides used for screening and sequencing

Oligo Name	Sequence (5'3')
KU70 F	AAGTGGATGGTGGCAGGCTGG
KU70 R	CATTGGGAGCGCGGTTAGAAGCG
KU80-1 F	GTGGACGGCGTACCGAGCAA
KU80-1 R	TGTAGCGGCAGCGACATGGG
KU80-2 F	AGGCGCTGCTCAACACCACG
KU80-2 R	GGCATGGACTTGAAAGGCACGTAGG
POLQ-1 F	GGCCAGCGGTGGTTAACAGTG
POLQ-1 R	TCGTCATCAAAGGGCGTGCTGT
APHVIII F	GACGGTGCCGCAGGCGGCCCGTG
APHVIII R	CCCTCCGCCGCCAGGTAGGTGCGATCCC
SNRK2.2-1 F	TCCGGAACCAAACACACCTGCCT
SNRK2.2-2 F	TGGCTGCCAGACCCCAAAGC
SNRK2.2-3 R	GGGCGAGGACAGCACCTCTATG
SNRK2.2-4 R	CCAAGCCACCGCAAGCGAACAT
APT-1 F	GACCCCTCCTTGCAGCGGGAT
APT-2 F	CAGCACAGCAGCAGCAGGACATTC
APT-3 R	CCTACCCGCCACCACGTCAATC
APT-4 F	CGCCTTTGGTCATGGGATTCATGCAGG
APT-5 R	TGGTTGCTCATGCTGCCGTCT

Table S5 Protospacer sequences

Target Gene name	Endonuclease	Protospacer	PAM
<i>KU80-1</i>	SpCas9	CTCAGTGCCGTACAGCACCA	CGG
<i>KU80-2</i>	SpCas9	GGCGGCAGGACCAGCCTGGA	TGG
<i>KU70</i>	SpCas9	GTCGTTTGAGAACCACAA	TGG
<i>POLQ-1</i>	SpCas9	GCATCAGTTGATGGTGACGG	CGG
<i>POLQ-2</i>	SpCas9	GCCGCGCCATCCACATTGCT	GGG

<i>EMX1</i> mut- <i>aphVIII</i>	SpCas9	GCCTCCCCAAAGCCTGGCCA	GGG
mut- <i>aphVIII</i>	LbCas12a	GGGAGGCCCCCTCCGCCATGAGC	TTTG
<i>SNRK2.2</i>	SpCas9	TAGCGAGGATGTCCAATCAG	GGG
<i>APT</i>	SpCas9	CTGGTGGTTCAGCATGATGG	TGG