

Supplementary Data

A cytosine base editor toolkit with varying activity windows and target scopes for versatile gene manipulation in plants

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hAID	1	MDSL	LLMNRRKFLYQFKNVRWAKGRRETYLCYVVKRRDSATSFS	SLDFGYLR	50
hAID*Δ	1	MDSL	LLMNRR E FLYQFKNVRWAKGRRETYLCYVVKRRDSATSFS	SLDFGYLR	50
AID10	1	MDSL	LLMNRR E FLYQFKNVRWAKGRRETYLCYVV ERRD CATSFS	SLDFGYLR	50
hAID	51	NKNG	CHVELLFLRYISDWDLDPGRCYRVTWFTSWSPCYDCARHVADFLRG	100	
hAID*Δ	51	NKNG	CHVELLFLRYISDWDLDPGRCYRVTWF I SWSPCYDCARHVADFLRG	100	
AID10	51	NKNG	CHVELLFLRYISDWDLDPGRCYRVTWF I SWSPCYDCARHVADFLRG	100	
hAID	101	NP	NLSLRIFTARLYFCEDRKAEPGLRRLHRAGVQIAIMTFKDYFYCWNT	150	
hAID*Δ	101	NP	NLSLRIFTARLYFCEDRKAEPGLRRLHRAGVQIAIMTFKDYFYCWNT	150	
AID10	101	NP	NLSLRIF A ARLYFCEDRKAEPGLRRL R RAGVQIAIMTFKDYFYCWNT	150	
hAID	151	FV	ENHERTFKAWEGLHENSVRLSRQLRRILLPLYEVDDLRFRTLGL	198	
hAID*Δ	151	FV	ENH G RTFKAWEGLHENSVRLSRQLRRILLPLYEVDDLRFRT---	195	
AID10	151	F A ENH G RTFKAWEGLHENSVRLS G QLRRIL-----		180	

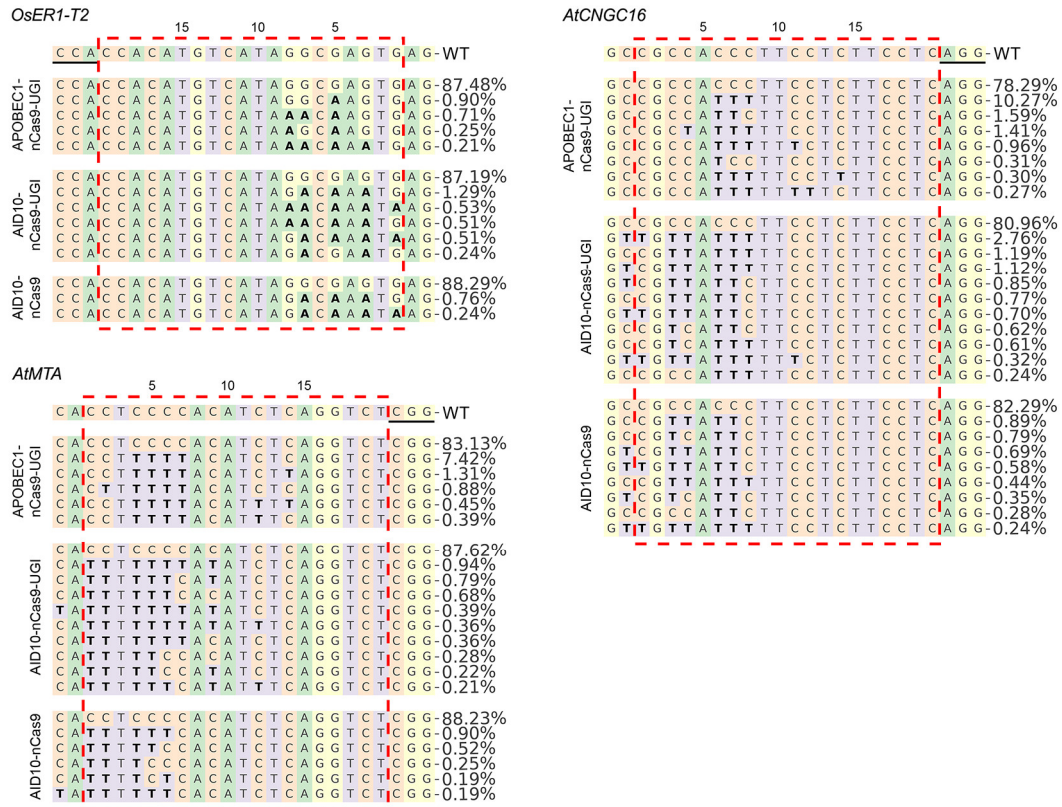
Supplementary Figure S1. Protein sequence alignment of wild-type hAID, hAID*Δ, and AID10.

Amino acid mutations are shadowed in yellow and truncations are indicated by dash lines.

<i>OsER1-T1</i>		
WT	5' -- <u>AGAACTCGAGTCGCAAGTCG</u> AGG --3'	Clone number
APOBEC1-nCas9-UGI	5' --AGAA TT TGAGTCGCAAGTCG AGG --3'	6/9
	5' --AGAA T TGAGTCGCAAGTCG AGG --3'	2/9
	5' --AGAA CT TGAG T TGCAAGTCG AGG --3'	1/9
AID10-nCas9-UGI	5' --AGAA T TCGAGTCGCAAGTCG AGG --3'	9/14
	5' --AGAA TT TGAGTCGCAAGTCG AGG --3'	3/14
	5' --AGAA TT TGAG T TGCAAGTCG AGG --3'	1/14
	5' --AGAA CT TGAGTC G T A AGTCG AGG --3'	1/14
AID10-nCas9	5' --AGAA T TCGAGTCGCAAGTCG AGG --3'	9/12
	5' --AGAA TT TGAGTCGCAAGTCG AGG --3'	2/12
	5' --AGAA G TCGAGTCGCAAGTCG AGG --3'	1/12

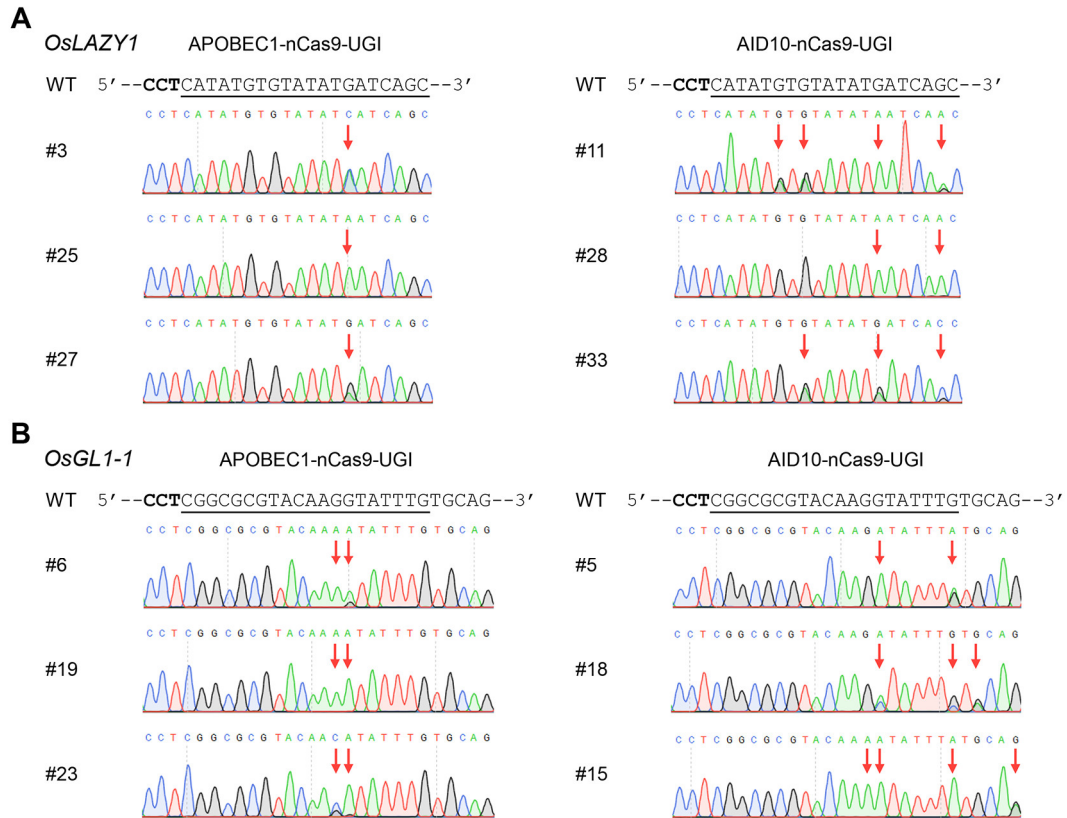
Supplementary Figure S2. *Xho*I-resistant mutant alleles of the *OsER1-T1* locus generated by APOBEC1-nCas9-UGI, AID10-nCas9-UGI, or AID10-nCas9 in protoplasts.

*Xho*I-resistant amplicons of the *OsER1-T1* locus induced by APOBEC1-nCas9-UGI, AID10-nCas9-UGI, or AID10-nCas9, were cloned and randomly selected for Sanger sequencing. The abundances of individual mutant alleles are indicated by the corresponding clone numbers divided by the total sequenced clone numbers. The target sequence and the PAM are underlined and in bold, respectively. The *Xho*I restriction site is marked in green and the C-to-T substitutions in mutant alleles are highlighted in red.



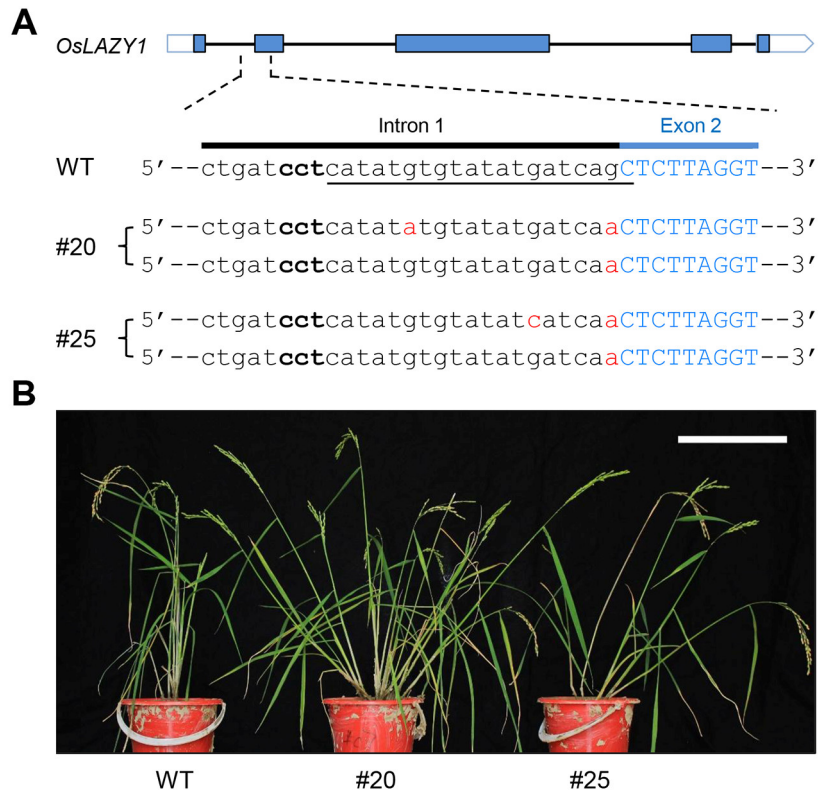
Supplementary Figure S3. Mutant allele compositions of three target sites edited by APOBEC1-nCas9-UGI, AID10-nCas9-UGI, or AID10-nCas9 in protoplasts.

C-to-T (or G-to-A) conversions are highlighted in bold and the frequencies of individual alleles are shown on the right. Dashed-line box marks the target sequence and the PAM is underlined. The numbers on the top indicate the protospacer positions. Data are collected from one biological replicate in Figure 1C.



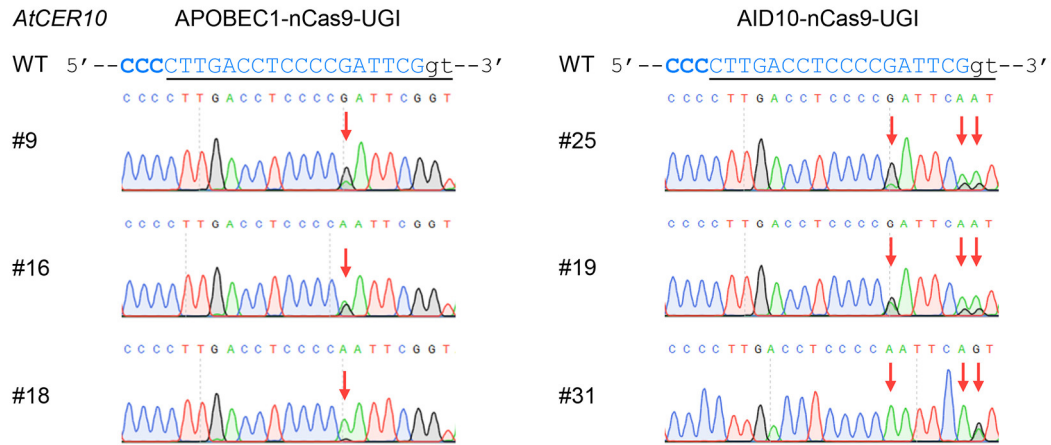
Supplementary Figure S4. Base editing at two genomic loci by APOBEC1-nCas9-UGI or AID10-nCas9-UGI in transgenic rice plants.

Sanger sequencing chromatograms evidence cytosine editing at the *OsLAZY1* (**A**) or *OsGL1-1* (**B**) locus by APOBEC1-nCas9-UGI (left) or AID10-nCas9-UGI (right) in transgenic T0 rice lines. Reverse complements of the target sequences and PAMs are underlined and in bold, respectively. Red arrows mark base substitutions.



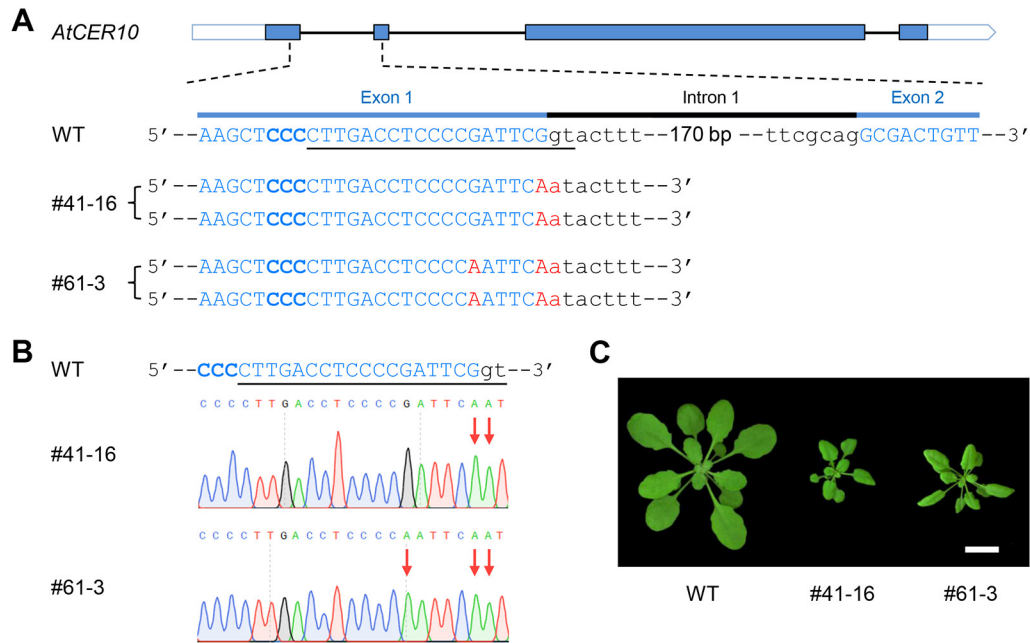
Supplementary Figure S5. Disruption of the intron splice site in *OsLAZY1* by AID10-nCas9-UGI produces gene knockout phenotype in transgenic rice plants.

(A) Two rice *lazy1* mutant alleles (lines #20 and #25) generated by AID10-nCas9-UGI. Sequences of the intron 1 and exon 2 are shown as black lowercase and blue uppercase letters, respectively. Reverse complements of the target sequence and PAM are underlined and in bold, respectively. Base conversions are highlighted in red. (B) Disruption of the intron splice site in *OsLAZY1* leads to increased tiller angle, resembling the reported rice *lazy1* null plants. Two-month-old plants are shown. Scale bar = 20 cm.



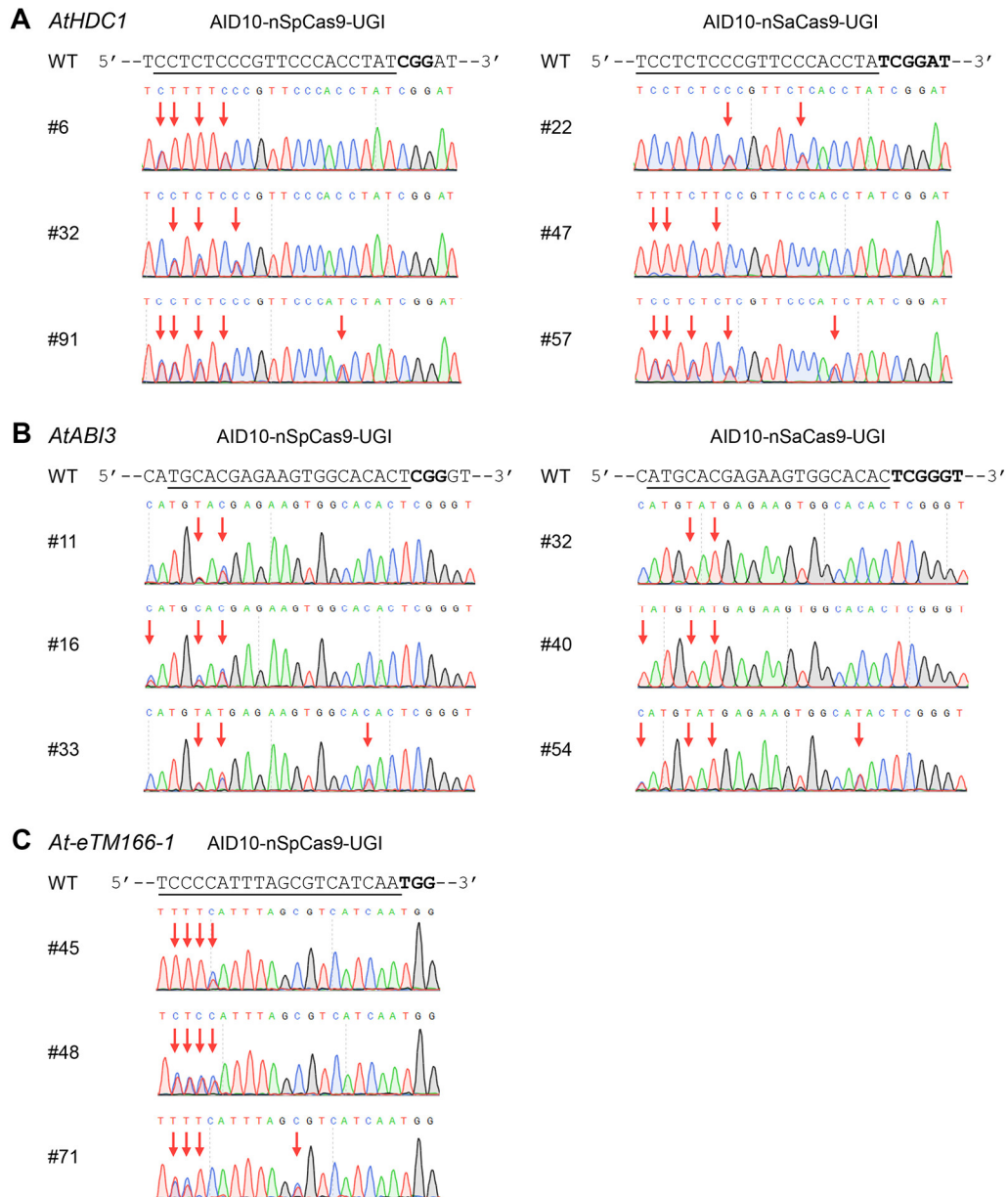
Supplementary Figure S6. Base editing at the *AtCER10* locus by APOBEC1-nCas9-UGI or AID10-nCas9-UGI in transgenic *Arabidopsis* plants.

Sanger sequencing chromatograms evidence cytosine editing at the *AtCER10* locus by APOBEC1-nCas9-UGI (left) or AID10-nCas9-UGI (right) in multiple transgenic T1 *Arabidopsis* lines. The expression of base editors was driven by the *ZmUbi* promoter. Reverse complements of the target sequence and PAM are underlined and in bold, respectively. Intronic and exonic sequences are shown as black lowercase and blue uppercase letters, respectively. Red arrows mark base substitutions.



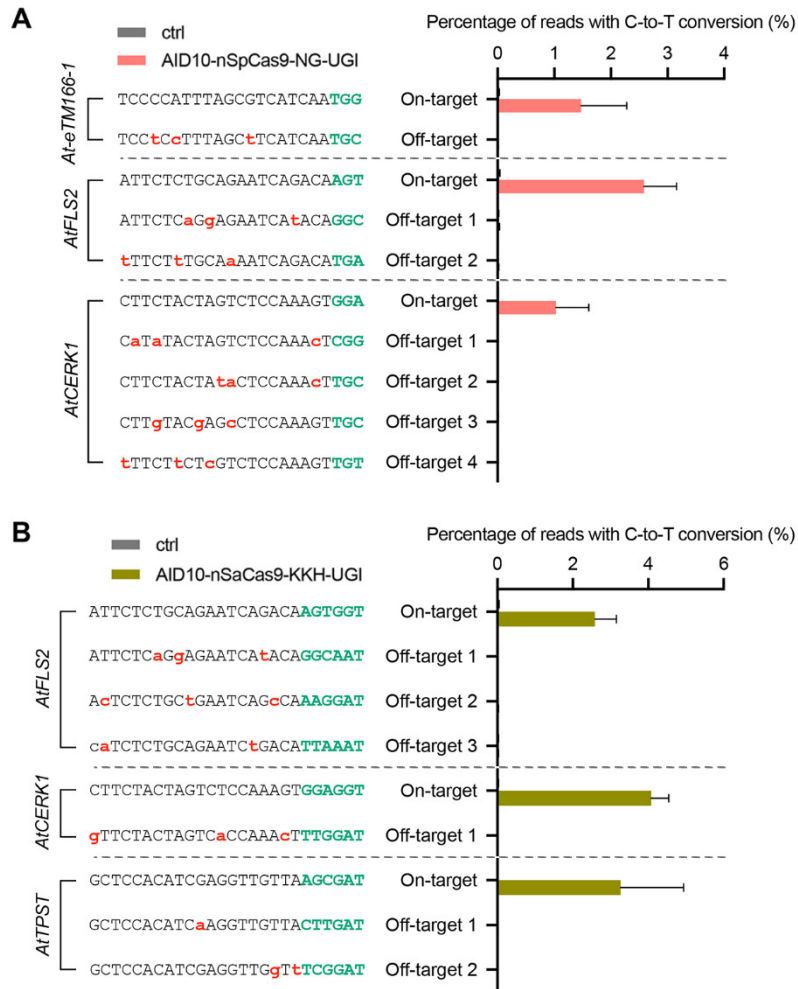
Supplementary Figure S7. Disruption of the intron splice site in *AtCER10* by AID10-nCas9-UGI produces gene knockout phenotype in transgenic *Arabidopsis* plants.

(A) Two T2 homozygous mutant alleles (lines #41-16 and #61-3) generated by AID10-nCas9-UGI. The expression of the base editor was driven by the egg cell-specific *EC1.2en-EC1.1p* promoter. Sequences of the intron 1 and neighboring exons are shown as lowercase and uppercase letters, respectively. Reverse complements of the target sequence and PAM are underlined and in bold, respectively. Base conversions are highlighted in red. (B) Sanger sequencing chromatograms show base substitutions (marked by red arrows) at the *AtCER10* target site in the two T2 mutant lines. (C) Disruption of the intron splice site in *AtCER10* leads to dwarfism, resembling the reported *Arabidopsis cer10* null plants. Four-week-old plants are shown. Scale bar = 1 cm.



Supplementary Figure S8. Base editing at three genomic loci by AID10-nSpCas9-UGI or AID10-nSaCas9-UGI in transgenic *Arabidopsis* plants.

Sanger sequencing chromatograms for the *AtHDC1* (A), *AtABI3* (B) or *At-eTM166-1* (C) locus in representative transgenic T1 lines edited by AID10-nSpCas9-UGI (left) or AID10-nSaCas9-UGI (right). In (C), AID10-nSaCas9-UGI (not shown) failed to induce any detectable base change at the *At-eTM166-1* locus. The expression of base editors was driven by the egg cell-specific *EC1.2en-EC1.1p* promoter. The target sequences are underlined and the PAMs are in bold. Red arrows mark base substitutions.



Supplementary Figure S9. Amplicon deep sequencing reveals no guide-dependent off-target editing by AID10-nSpCas9-NG-UGI and AID10-nSaCas9-KKH-UGI in protoplasts.

(A) No guide-dependent (no more than 3 base mismatches) off-target editing is detected for AID10-nSpCas9-NG-UGI when targeting the *At-eTM166-1*, *AtFLS2*, and *AtCERK1* sites. No potential off-target site was identified for the *AtTPST* site. (B) No guide-dependent (no more than 3 base mismatches) off-target editing is detected for AID10-nSaCas9-KKH-UGI when targeting the *AtFLS2*, *AtCERK1*, and *AtTPST* sites. No potential off-target site was identified for the *At-eTM166-1* site. Mismatches between off-target and on-target sites are highlighted in red. The PAM is shown in green. Data are shown as mean \pm s.d. of two biological replicates performed at different times.

OsSLR1

WT 5' --ACAACCCTCGGACCTCTCCTCCT**GGG**--3'

#11 { 5' --ACAACCCTCGGACCT**T**TCCTCCT**GGG**--3'
5' --ACAACCCTCGGACCTCTCCTCCT**GGG**--3'

#15 { 5' --ACAA**T**TTCCTCGGACCTCTCCTCCT**GGG**--3'
5' --ACAACCCTCGGACCTCTCCTCCT**GGG**--3'

#20 { 5' --ATAACCCTCGGACCTCTCCTCCT**GGG**--3'
5' --ACAACCCTCGGACCTCTCCTCCT**GGG**--3'

Supplementary Figure S10. Base editing at the *OsSLR1* locus by AID10-nCas9-AID10-UGI in transgenic rice plants.

Three transgenic T0 rice lines containing cytosine changes at the *OsSLR1* target site were generated by AID10-nCas9-AID10-UGI. The target sequence is underlined and the PAM is in bold. C-to-T base substitutions are highlighted in red.

OsCKX2

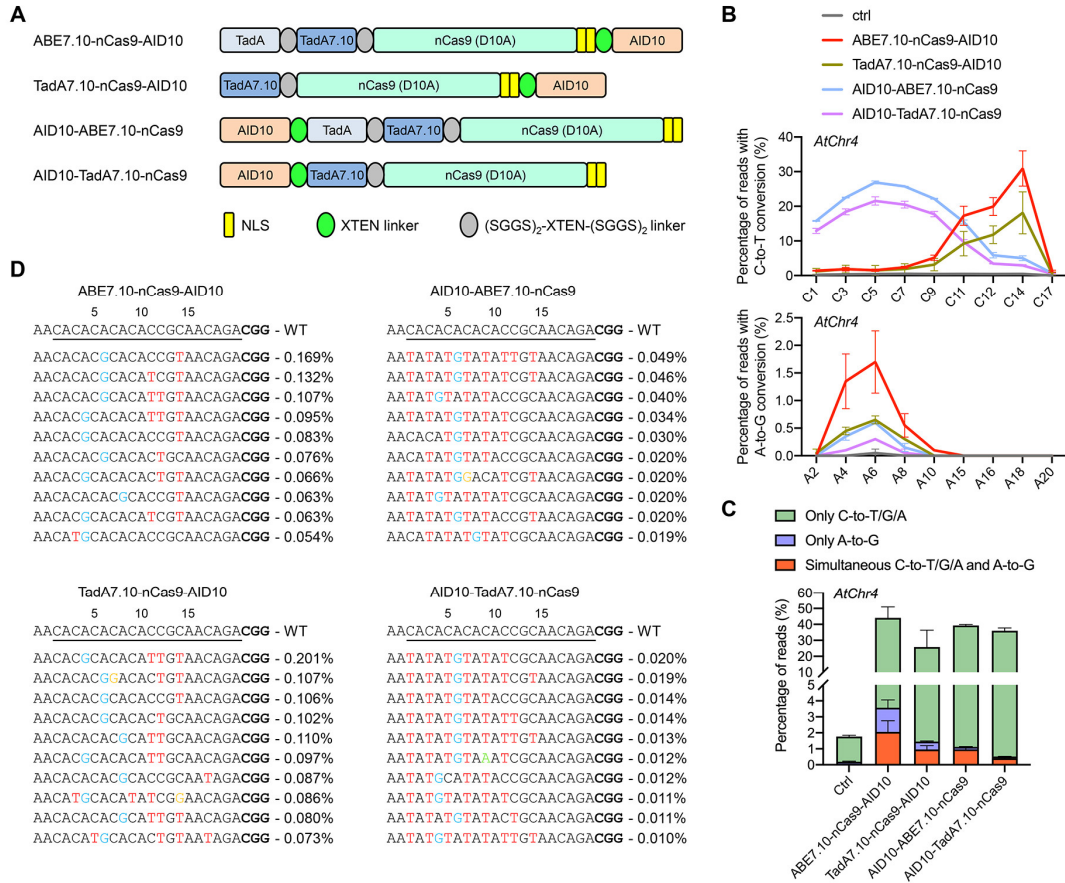
WT 5' --GAGCTCAAGCTCCGCGCCGC**GGG**--3'

#3 { 5' --GAGCTCAAGCTCCG**T**GCCGC**GGG**--3'
 5' --GAGCTCAAGCTCCGCGCCGC**GGG**--3'

#19 { 5' --GAGCTCAAGCTCCG**T**GCCGC**GGG**--3'
 5' --GAGCTCAA-----GCGCCGC**GGG**--3'
 5' --GAGCTCAAGCTCCGCGCCGC**GGG**--3'

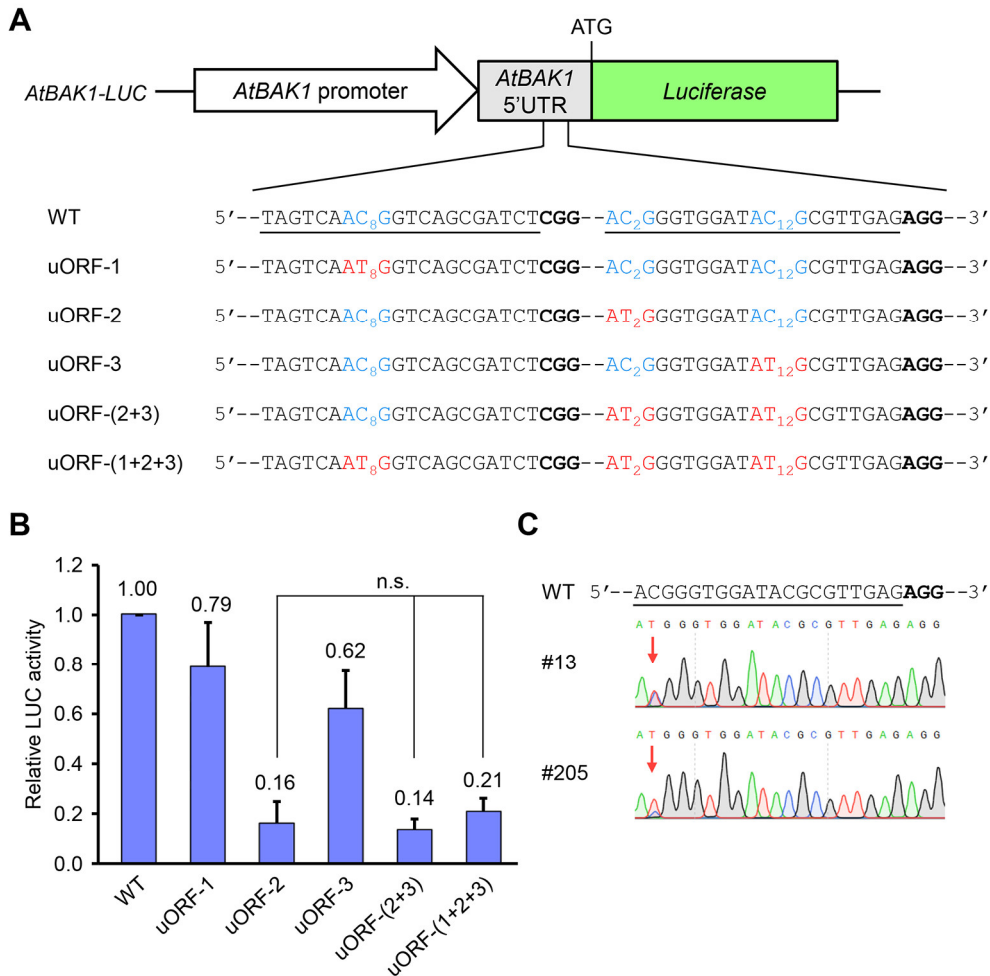
Supplementary Figure S11. Base editing at the *OsCKX2* locus by ABE7.10-nCas9-AID10 in transgenic rice plants.

Two transgenic T0 rice lines edited by the dual base editor ABE7.10-nCas9-AID10 only contained cytosine changes at the *OsCKX2* target site. The line #19 contained chimeric mutations. The target sequence is underlined and the PAM is in bold. Base substitutions or deletions are highlighted in red.



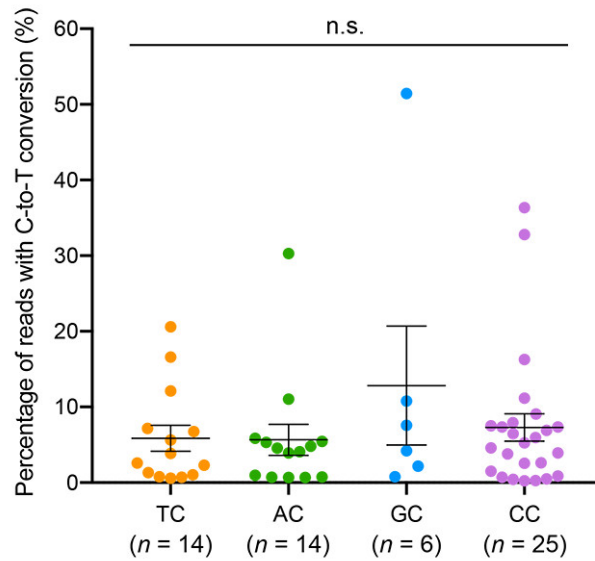
Supplementary Figure S12. Simultaneous editing of cytosines and adenines at the same target sequence by AID10- and TadA7.10-based dual base editors.

(A) Schematic diagram of four AID10- and TadA7.10-based dual base editors with different protein architectures. (B) Comparison of C-to-T (top) and A-to-G (bottom) editing efficiencies between the four dual base editors at the *AtChr4* locus in *Arabidopsis* protoplasts by amplicon deep sequencing. Data are shown as mean \pm s.d. of two biological replicates performed at different times. (C) Comparison of editing product compositions at the *AtChr4* locus generated by the four dual base editors. (D) The ten most abundant mutant alleles with concurrent C-to-T/G/A and A-to-G substitutions by individual dual base editors. Data of one replicate in (C) are shown. The A-to-G, C-to-T, C-to-G, and C-to-A substitutions are highlighted in blue, red, orange, and green, respectively.



Supplementary Figure S13. Luciferase reporter assay reflects inhibitory effects of different *AtBAK1* uORF mutations on the primary ORF.

(A) Schematic diagram of six *AtBAK1-LUC* reporters containing no uORF (WT) or different combinations of uORF mutations in the 5' UTR of *AtBAK1*. Two possible target sequences in the 5' UTR that can be used to introduce the uORF mutations through base editing are underlined. Their PAMs are indicated in bold. The native ACG trinucleotides and the artificially created start codons are highlighted in blue and red, respectively, with subscripted numbers indicating the protospacer positions. (B) Inhibition of luciferase expression by different uORFs. The reporter constructs were transiently expressed in *Arabidopsis* protoplasts. Data are presented as means \pm s.d. of three biological replicates. n.s., not significant (two-tailed Student's *t* test). (C) Sanger sequencing chromatograms evidence the creation of uORF-2 in the 5' UTR of *AtBAK1* by AID10-nCas9-UGI in two transgenic T1 lines. Red arrows mark base substitutions.



Supplementary Figure S14. AID10 cytosine deaminase shows no sequence context bias in plant cells.

C-to-T editing frequencies are shown as mean \pm s.e.m. with individual data points representing the average editing frequency of a single cytosine within the optimal activity window (positions -1–9) of each protospacer. Data shown in Figures 1C, 2B, and 3B for AID10-nCas9-UGI and in Figure 2D for AID10-nCas9-NG-UGI are used for this analysis. n.s., not statistically significant (one-way ANOVA with Tukey’s multiple comparisons test).

Supplementary Table S1. Summary of editing targets in this study

Target site	Gene ID or genomic location	Target sequence (5'-3') ¹
<i>OsER1-T1</i>	<i>LOC_Os06g10230</i>	AGAACTCGAGTCGCAAGTCG <u>AGG</u>
<i>OsER1-T2</i>		CACTCGCCTATGACATGTGG <u>TGG</u>
<i>OsLAZY1</i>	<i>LOC_Os11g29840</i>	GCTGATCATATACACATATG <u>AGG</u>
<i>OsGLI-1</i>	<i>LOC_Os09g25850</i>	CAAATACCTTGTACGCGCCG <u>AGG</u>
<i>OsNAL1</i>	<i>LOC_Os04g52479</i>	ACCGTCACGACTGTAGTTAG <u>GGG</u>
		ACCGTCACGACTGTAGTTAG <u>GGGAGT</u>
		<u>TTTC</u> CACCGTCACGACTGTAGTTAGG
<i>OsTCP21</i>	<i>LOC_Os07g05720</i>	ACCACACCCCTCCCTACGTTG <u>GGG</u>
		TAACCACACCCCTCCCTACGT <u>TGGGGT</u>
		<u>TTTG</u> TTGTAACCACACCCCTCCCTACGT
<i>OsALS</i>	<i>LOC_Os02g30630</i>	ATCTCCATGGACGCGCCGCC <u>CGG</u>
<i>OsSWEET11</i>	<i>LOC_Os08g42350</i>	TGTACACCACCAAAGTGG <u>AGG</u>
<i>OsSWEET13</i>	<i>LOC_Os12g29220</i>	GGAGTTGTGGTGCTTTATAT <u>AGG</u>
<i>OsSWEET14</i>	<i>LOC_Os11g31190</i>	GCTTAGCACCTGGTTGGAGG <u>GGG</u>
<i>OsSLR1</i>	<i>LOC_Os03g49990</i>	CCCCTCGGACCTCTCCTCCT <u>GGG</u>
<i>OsIPA1</i>	<i>LOC_Os08g39890</i>	AGAGAGAGCACAGCTCGAGT <u>CGG</u>
<i>OsCKX2</i>	<i>LOC_Os01g10110</i>	GAGCTCAAGCTCCGCGCCGC <u>GGG</u>
<i>AtCNGC16</i>	<i>At3g48010</i>	CGCCACCCCTTCCTCTTCCTC <u>AGG</u>
<i>AtMTA</i>	<i>At4g10760</i>	CCTCCCCACATCTCAGGTCT <u>CGG</u>
<i>AtCER10</i>	<i>At3g55360</i>	ACCGAATCGGGGAGGTCAAG <u>GGG</u>
<i>AtBIK1</i>	<i>At2g39660</i>	CGCCGGAAAAATGTCCATCC <u>TGG</u>
		CGCCGGAAAAATGTCCATCC <u>TGGAAT</u>
		<u>TTTC</u> AAGTAAACCGCCGGAAAAATGTC
<i>AtHDC1</i>	<i>At5g08450</i>	CCTCTCCCGTTCCCACCTAT <u>CGG</u>
		TCCTCTCCCGTTCCCACCTA <u>TCGGAT</u>
		<u>TTTC</u> TGCTCCATCCTCTCCCGTTCCCA
<i>AtABI3</i>	<i>At3g24650</i>	TGCACGAGAAGTGGCACACT <u>CGG</u>
		ATGCACGAGAAGTGGCACACT <u>TCGGGT</u>
<i>At-eTM166-1</i>	<i>chr5:25327627..25327649</i>	TCCCCATTTAGCGTCATCAAT <u>TGG</u>
	<i>chr5:25327624..25327649</i>	TCCCCATTTAGCGTCATCAAT <u>TGGAAT</u>
<i>AtFLS2</i>	<i>At5g46330</i>	ATTCTCTGCAGAATCAGACA <u>AGT</u>
		ATTCTCTGCAGAATCAGACA <u>AGTGGT</u>
<i>AtCERK1</i>	<i>At3g21630</i>	CTTCTACTAGTCTCCAAAGT <u>GGA</u>
		CTTCTACTAGTCTCCAAAGT <u>GGAGGT</u>

<i>AtTPST</i>	<i>At1g08030</i>	GCTCCACATCGAGGTTGTTA <u>AGC</u>
		GCTCCACATCGAGGTTGTTA <u>AGCGAT</u>
<i>AtBAK1</i>	<i>At4g33430</i>	CCTACACCGCCATCACCTGC <u>AGG</u>
<i>AtBAK1-5'UTR</i>		ACGGGTGGATACGCGTTGAG <u>AGG</u>
<i>AtChr3</i>	<i>Chr3: 951091..951113</i>	ACACACACACACACTCCTCT <u>AGG</u>
<i>AtChr4</i>	<i>Chr4: 18302232..18302254</i>	CACACACACACCGCAACAG <u>CGG</u>

¹ The PAM sequence is in bold and underlined. Sequences with a 3'-NGG or 3'-NGN PAM, a 3'-NNGRRT or 3'-NNNRRT PAM, and a 5'-TTTN PAM are targets for base editors derived from SpCas9, SaCas9 and LbCas12a, respectively, where "N" refers to any type of nucleotide and "R" stands for "A" or "G".

Supplementary Table S2. Primers used for amplification of target sites in this study

Primer name	Primer sequence (5'-3')	Application
OsER1-T1-F	TTGAATACCGGAGTAAGGTGGTG	RFLP assay analysis of the <i>OsER1-T1</i> site
OsER1-T1-R	ATGGCCGATGGACACTGAGA	
OsER1-T2-NGS-F	NNNNNNCAGCTACTCGTAAGCTACACTTAT	Amplicon deep sequencing of the <i>OsER1-T2</i> site
OsER1-T2-NGS-R	TGGCCGATGGACACTGAGAT	
OsNAL1-NGS-F	NNNNNNTTGTACGAGCTGACGGTGCATT	Amplicon deep sequencing of the <i>OsNAL1</i> site
OsNAL1-NGS-R	GCATAGGCCATCACAGTCCCAG	
AtCNGC16-NGS-F	NNNNNNGTGAAATCGCTATCCGTTAC	Amplicon deep sequencing of the <i>AtCNGC16</i> site
AtCNGC16-NGS-R	AAACCAAATCATTATCTGAGA	
AtMTA-NGS-F	NNNNNNTGCATTTCCTCTTGGTGCATTC	Amplicon deep sequencing of the <i>AtMTA</i> site
AtMTA-NGS-R	GCCTAGGATCATGGTTTTAGC	
OsTCP21-NGS-F	NNNNNNGCCAATCGCACGGTTTCTGC	Amplicon deep sequencing of the <i>OsTCP21</i> site
OsTCP21-NGS-R	GACATTGGGGGTTAGCGTCC	
AtBIK1-NGS-F	NNNNNNCACGTTTGTCCAGAACCGC	Amplicon deep sequencing of the <i>AtBIK1</i> site
AtBIK1-NGS-R	ACAACAACCTTCAGGACAACCTGGGA	
AtHDC1-NGS-F	NNNNNNAGTCCTTGGCTCTCTTTTGATATGATCTTT	Amplicon deep sequencing of the <i>AtHDC1</i> site
AtHDC1-NGS-R	AAGGTTGATGCCAAAAACGAAGATAGATT	
At-eTM166-NGS-F	NNNNNNCGATGATGATGATGATGGAAGCTA	Amplicon deep sequencing of the <i>At-eTM166-1</i> site
At-eTM166-NGS-R	TAGTTCGACGATACATTCCATGAG	
AtFLS2-NGS-F	NNNNNNACAAAGGTCAGCTAGAAGATGGG	Amplicon deep sequencing of the <i>AtFLS2</i> site
AtFLS2-NGS-R	AATGGTGTCTCCAAGTTTCCAT	
AtCERK1-NGS-F	NNNNNNTGTCTCTTTTGTTAGCTGGGAGT	Amplicon deep sequencing of the <i>AtCERK1</i> site
AtCERK1-NGS-R	TGCATAGTAAACAGCCCCAAAAC	
AtTPST-NGS-F	NNNNNNTCTAACAGACGCGTACAAGAGTT	Amplicon deep sequencing of the <i>AtTPST</i> site
AtTPST-NGS-R	TTAGACTGCACACGAATCATGGA	
AtBAK1-NGS-F	NNNNNNGTTTTGCCAACACCAAGTTGACT	Amplicon deep sequencing of the <i>AtBAK1</i> site
AtBAK1-NGS-R	TAGAAGTGCAGCACCTGCAG	
AtC3-NGS-F	NNNNNNTCTTAATGTTGAACAAACCATCTAACC	Amplicon deep sequencing of the <i>AtChr3</i> site
AtC3-NGS-R	TATTGGCTAAGTGAAGTAATTTGAGATTAT	
AtC4-NGS-F	NNNNNNCATTCAAACAAAAAGTTTTATCTACATCAC	Amplicon deep sequencing of the <i>AtChr4</i> site
AtC4-NGS-R	GAATTGTTTGTTTTTCTTTTTTACATGTACT	
AtCERK1-Sp-OT1-F	NNNNNNGGACTTAGCCCTCTCAAACCA	Amplicon deep sequencing of the <i>AtCERK1</i> off-target site 1 of SpCas9-NG
AtCERK1-Sp-OT1-R	GCCCGTGATGCATTAAGCTTTTA	
AtCERK1-Sp-OT2-F	NNNNNNCAGTAGCGACGTGGTCTTGA	Amplicon deep sequencing of the <i>AtCERK1</i> off-target site 2 of SpCas9-NG
AtCERK1-Sp-OT2-R	GCCGAATTCGATACGGATTACC	

AtCERK1-Sp-OT3-F	NNNNNNTGCTGTAGACTCTTGGTTTGCT	Amplicon deep sequencing of the <i>AtCERK1</i> off-target site 3 of SpCas9-NG
AtCERK1-Sp-OT3-R	ATTGGTCATGGCGTAGCTGT	
AtCERK1-Sp-OT4-F	NNNNNNCAAGACCCAGCCTAGCGAAG	Amplicon deep sequencing of the <i>AtCERK1</i> off-target site 4 of SpCas9-NG
AtCERK1-Sp-OT4-R	AAGCAGCAGACTCGTCATCTC	
AtCERK1-Sa-OT1-F	NNNNNNTCGAGTTTACCCGCATGTTTC	Amplicon deep sequencing of the <i>AtCERK1</i> off-target site 1 of SaCas9-KKH
AtCERK1-Sa-OT1-R	GATGCATAGACTTAAAATTCCACC	
AtFLS2-Sa_Sp-OT1-F	NNNNNNTGCCAGAGATTTCCAGAGGC	Amplicon deep sequencing of the <i>AtFLS2</i> off-target site 1 of SpCas9-NG and SaCas9-KKH
AtFLS2-Sa_Sp-OT1-R	TCTCCAGTTTCTTGGAACGCA	
AtFLS2-Sp-OT2-F	NNNNNNTTATCTTCATCGACTCTTCTCCTT	Amplicon deep sequencing of the <i>AtFLS2</i> off-target site 2 of SpCas9-NG
AtFLS2-Sp-OT2-R	AGCTTCCATCGTTAGTCACAA	
AtFLS2-Sa-OT2-F	NNNNNNTCGTTTAGGGGAATCGGACAA	Amplicon deep sequencing of the <i>AtFLS2</i> off-target site 2 of SaCas9-KKH
AtFLS2-Sa-OT2-R	TCGTCTGTTAATTAGCACCATTCA	
AtFLS2-Sa-OT3-F	NNNNNNTGTCATCGAGATCACACTTGAAGA	Amplicon deep sequencing of the <i>AtFLS2</i> off-target site 3 of SaCas9-KKH
AtFLS2-Sa-OT3-R	CACACTCTCATTCTATCTTTCTTCTCTT	
At-eTM166-Sp-OT1-F	NNNNNNCTGTCCTCACCAACCACCAG	Amplicon deep sequencing of the <i>At-eTM166-1</i> off-target site 1 of SpCas9-NG
At-eTM166-Sp-OT1-R	GAGAGGTTGCAGGAGAACCC	
AtTPST-Sa-OT1-F	NNNNNNTGACACAGGTGAGTGAGAGC	Amplicon deep sequencing of the <i>AtTPST</i> off-target site 1 of SaCas9-KKH
AtTPST-Sa-OT1-R	CGACAAACAGGGACGCAATG	
AtTPST-Sa-OT2-F	NNNNNNGTGGATTTGCAGTTTCCGACC	Amplicon deep sequencing of the <i>AtTPST</i> off-target site 2 of SaCas9-KKH
AtTPST-Sa-OT2-R	AAAGCGACGTCGTCTCGG	
OsLAZY1-HiTOM-F	GGAGTGAGTACGGTGTGCCCTCCGGTGTGAACTCTT TGAA	HiTOM sequencing of the <i>OsLAZY1</i> site
OsLAZY1-HiTOM-R	GAGTTGGATGCTGGATGGTAGCTGATCATGCTTTCTG GGTTGAAT	
OsLAZY1-F	TCTTAGCACGCTAAACCGGC	Sanger sequencing of the <i>OsLAZY1</i> site
OsLAZY1-R	AGTGCGTTTGTGTTACGAGC	

OsGL1-1-HiTOM-F	GGAGTGAGTACGGTGTGCAGGACGAAGAAGAAGATC AAGC	HiTOM sequencing of the <i>OsGL1-1</i> site
OsGL1-1-HiTOM-R	GAGTTGGATGCTGGATGGCACATACTGCGCACACACA AT	
OsGL1-1-F	AACATCTTCTAACTCCCCTCACG	Sanger sequencing of the <i>OsGL1-1</i> site
OsGL1-1-R	TGCACCTGCAGTATCAAGAAGTT	
AtCER10-HiTOM-F	GGAGTGAGTACGGTGTGCTTAAGCACCATGAAGGTCA CCG	HiTOM sequencing of the <i>AtCER10</i> site
AtCER10-HiTOM-R	GAGTTGGATGCTGGATGGCGAAGCACAAAACACACG AAAT	
AtCER10-F	GGTGGATCCTTAAAACAAAGCCA	Sanger sequencing of the <i>AtCER10</i> site
AtCER10-R	CGAAGCACAAAACACACGAAATC	
AtHDC1-HiTOM-F	GGAGTGAGTACGGTGTGCCCCAAAGAGATTGGAAGA GAAG	HiTOM sequencing of the <i>AtHDC1</i> site
AtHDC1-HiTOM-R	GAGTTGGATGCTGGATGGTTCTCAGCACCAGTCCTTG G	
AtHDC1-F	CCCAAAGAGATTGGAAGAGAAG	Sanger sequencing of the <i>AtHDC1</i> site
AtHDC1-R	TTCTCAGCACCAGTCCTTGG	
AtABI3-HiTOM-F	GGAGTGAGTACGGTGTGCGTACCAAATAAGAAAGAG GG	HiTOM sequencing of the <i>AtABI3</i> site
AtABI3-HiTOM-R	GAGTTGGATGCTGGATGGCCAGAAATATAACACAAA CACC	
AtABI3-F	GTACCAAATAAGAAAGAGGG	Sanger sequencing of the <i>AtABI3</i> site
AtABI3-R	ACGATATGTAAGCTCGACTC	
At-eTM166-HiTOM -F	GGAGTGAGTACGGTGTGCATTTCCTTTCAAATAAAGG TCG	HiTOM sequencing of the <i>At-eTM166-1</i> site
At-eTM166-HiTOM -R	GAGTTGGATGCTGGATGGATGATGATGATGATGGAAG C	
At-eTM166-F	ATTCCTTTCAAATAAAGGTGC	Sanger sequencing of the <i>At-eTM166-1</i> site
At-eTM166-R	ATGATGATGATGATGGAAGC	
OsALS-HiTOM-F	GGAGTGAGTACGGTGTGCCGCCGCGAACGCCTCG	HiTOM sequencing of the <i>OsALS</i> site
OsALS-HiTOM-R	GAGTTGGATGCTGGATGGCGGCCGAGCCCCGCAA	
OsALS-F	CACCACCCACCATGGCT	Sanger sequencing of the <i>OsALS</i> site
OsALS-R	GTCCTCCACATCAAGGACAAGGTAA	
OsSWEET11-HiTO M-F	GGAGTGAGTACGGTGTGCAGTGAAAAAGAAATATCA AGCACAAG	HiTOM sequencing of the <i>OsSWEET11</i> site
OsSWEET11-HiTO M-R	GAGTTGGATGCTGGATGGAGGTGTTAATCAGTGAGAA GGTTAG	
OsSWEET11-F	TGATTGCACACGAACACTACTCTG	Sanger sequencing of the <i>OsSWEET11</i> site
OsSWEET11-R	GCAATGGTGCAGACAACAATA	

OsSWEET13-HiTOM-F	GGAGTGAGTACGGTGTGCGAGGGAGAGCTCTGAAGAA GA	HiTOM sequencing of the <i>OsSWEET13</i> site
OsSWEET13-HiTOM-R	GAGTTGGATGCTGGATGGCTCCAACAGTAGCTCATT TTGTAA	
OsSWEET13-F	TCGATCTCTACTGACAATGCAC	Sanger sequencing of the <i>OsSWEET13</i> site
OsSWEET13-R	AGTACCATCCATATTGCCTTCG	
OsSWEET14-HiTOM-F	GGAGTGAGTACGGTGTGCGCTGGTAATCAGCTACTAC TTG	HiTOM sequencing of the <i>OsSWEET14</i> site
OsSWEET14-HiTOM-R	GAGTTGGATGCTGGATGGGTGCTGATGATTATCTT	
OsSWEET14-F	GCCCAACTCTAGATCCCTTAAC	Sanger sequencing of the <i>OsSWEET14</i> site
OsSWEET14-R	CCACTCACAATTGCATCCAAAA	
OsSLR1-HiTOM-F	GGAGTGAGTACGGTGTGCCGCGGATGACGGGTTTCG	HiTOM sequencing of the <i>OsSLR1</i> site
OsSLR1-HiTOM-R	GAGTTGGATGCTGGATGGTGAAGCATGGCGGG	
OsSLR1-F	GCCGCGGATGACGGGTTTCG	Sanger sequencing of the <i>OsSLR1</i> site
OsSLR1-R	GGTGAAGCATGGCGGG	
OsCKX2-HiTOM-F	GGAGTGAGTACGGTGTGCGCGCGGGTTCGTGTTTCG	HiTOM sequencing of the <i>OsCKX2</i> site
OsCKX2-HiTOM-R	GAGTTGGATGCTGGATGGGATGCCGTGGAAGACGC	
OsCKX2-F	ATCCGAGAAGATCCTGCATG	Sanger sequencing of the <i>OsCKX2</i> site
OsCKX2-R	CTTAGTACACACTATTTGCAGTCAA	
OsIPA1-HiTOM-F	GGAGTGAGTACGGTGTGCGCTGGTGGTAGTGGACATG G	HiTOM sequencing of the <i>OsIPA1</i> site
OsIPA1-HiTOM-R	GAGTTGGATGCTGGATGGTCGCTGGCCCAAATCTCCC T	
OsIPA1-F	GTTCCAAGCAGCGTAAGGAATG	Sanger sequencing of the <i>OsIPA1</i> site
OsIPA1-R	AGACTTCATGTGGTAGCTGGTG	
AtBAK1-5'UTR-HiTOM-F	GGAGTGAGTACGGTGTGCGGAAATATCTTCTTCCTCC TTTCG	HiTOM sequencing of the <i>AtBAK1-5'UTR</i> site
AtBAK1-5'UTR-HiTOM-R	GAGTTGGATGCTGGATGGTCGATTAAGCTACCACCCA CA	
AtBAK1-5'UTR-F	GGAAATATCTTCTTCCTCCTTTCG	Sanger sequencing of the <i>AtBAK1</i> site
AtBAK1-5'UTR-R	TATCCTCAAGAGATTA AAAACAAACCC	

Supplementary Table S3. Primers used for qPCR analysis in this study

Primer name	Primer sequence (5'-3')
AtPHV-qPCR-F	CTGAGTGTTGACAAGCTCGA
AtPHV-qPCR-R	TCTTCTCTCGATTGCGGA
AtPHB-qPCR-F	AGGAGCATACATCTGCGTGT
AtPHB-qPCR-R	TTTCTATAGCAGAGGAGGCC
AtCNA-qPCR-F	CAGCCAGAAATCGCGTGGT
AtCNA-qPCR-R	CAGCACCAATTGGCATCTCAA

Supplementary Table S4. Summary of base editing outcomes in transgenic *Arabidopsis* T1 and rice T0 plants

Target gene	Base editor (BE)	Promoter for BE expression	No. of transgenic plants	Genotype and No. ¹	Base editing efficiency ²	Indel ratio ³
<i>OsLAZY1</i>	APOBEC1-nCas9-UGI	<i>ZmUbi</i>	40	11WT/7Homo/3Het/15Bi/4Chi	65.0% (26/40)	42.5% (17/40)
	AID10-nCas9-UGI	<i>ZmUbi</i>	33	8WT/4Homo/1Het/14Bi/6Chi	72.7% (24/33)	21.2% (7/33)
<i>OsGL1-1</i>	APOBEC1-nCas9-UGI	<i>ZmUbi</i>	27	12WT/4Homo/2Het/8Bi/1Chi	51.9% (14/27)	11.1% (3/27)
	AID10-nCas9-UGI	<i>ZmUbi</i>	47	7WT/5Homo/16Het/18Bi/1Chi	83.0% (39/47)	14.9% (7/47)
<i>AtCER10</i>	APOBEC1-nCas9-UGI	<i>ZmUbi</i>	42	14WT/28Chi	64.3% (27/42)	4.8% (2/42)
	AID10-nCas9-UGI	<i>ZmUbi</i>	34	2WT/32Chi	94.1% (32/34)	0% (0/34)
	AID10-nCas9-UGI	<i>EC1.2en-EC1.1p</i>	157	153WT/4Het	2.5% (4/157)	0% (0/157)
<i>AtHDC1</i>	AID10-nCas9-UGI	<i>EC1.2en-EC1.1p</i>	118	108WT/8Het/2Bi	8.5% (10/118)	0% (0/118)
	AID10-nSaCas9-UGI	<i>EC1.2en-EC1.1p</i>	57	54WT/1Homo/2Het	5.3% (3/57)	0% (0/57)
<i>AtABI3</i>	AID10-nCas9-UGI	<i>EC1.2en-EC1.1p</i>	107	103WT/4Het	3.7% (4/107)	0% (0/107)
	AID10-nSaCas9-UGI	<i>EC1.2en-EC1.1p</i>	101	75WT/2Homo/16Het/6Bi/2Chi	17.8% (18/101)	9.9% (10/101)
<i>At-eTM166-1</i>	AID10-nCas9-UGI	<i>EC1.2en-EC1.1p</i>	71	63WT/3Het/5Bi	11.3% (8/71)	0% (0/71)
	AID10-nSaCas9-UGI	<i>EC1.2en-EC1.1p</i>	139	139WT	0% (0/139)	0% (0/139)
<i>OsALS</i>	nCas9-AID10-UGI	<i>ZmUbi</i>	39	33WT/5Het/1Bi	12.8% (5/39)	2.6% (1/39)
<i>OsSWEET11</i>	AID10-nCas9-AID10-UGI	<i>ZmUbi</i>	77	38WT/3Homo/14Het/20Bi/2Chi	36.4% (28/77)	26.0% (20/77)
<i>OsSWEET13</i>	AID10-nCas9-AID10-UGI	<i>ZmUbi</i>	77	69WT/1Homo/6Het/1Bi	9.1% (7/77)	0% (0/77)

<i>OsSWEET14</i>	AID10-nCas9-AID10-UGI	<i>ZmUbi</i>	77	38WT/2Homo/11Het/21Bi/5Chi	41.6% (32/77)	26.0% (20/77)
<i>OsSLR1</i>	AID10-nCas9-AID10-UGI	<i>ZmUbi</i>	56	52WT/4Het	5.4% (3/56)	1.8% (1/56)
<i>OsIPA1</i>	ABE7.10-nCas9-AID10	<i>ZmUbi</i>	29	29WT	0% (0/29)	0% (0/29)
<i>OsCKX2</i>	ABE7.10-nCas9-AID10	<i>ZmUbi</i>	23	21WT/1Het/1Chi	8.7% (2/23)	4.3% (1/23)
<i>AtBAK1-5'UTR</i>	AID10-nCas9-UGI	<i>ECl.2en-ECl.1p</i>	325	320WT/5Het	1.5% (5/325)	0% (0/325)

¹ Homo, Het, Bi, and Chi represent homozygote, heterozygote, biallele, and chimera, respectively.

² Base editing efficiency is defined as the ratio of the number of transgenic lines with base substitution(s) to the number of total lines.

³ Indel ratio is the percentage of transgenic lines with nucleotide insertion or deletion (indel). Numbers of plants with indels to total transgenic plants are given in parentheses.

Supplementary Table S5. Summary of base editors developed in this study

Base editor	Cas effector	PAM	Optimal editing window¹	Possible editing window¹
AID10-nCas9-UGI	nSpCas9	NGG	C ₋₁ -C ₉	C ₋₅ -C ₁₅
AID10-nCas9-NG-UGI	nSpCas9-NG	NG	C ₋₁ -C ₉	C ₋₅ -C ₁₅
AID10-nSaCas9-UGI	nSaCas9	NNGRRT	C ₋₂ -C ₁₂	C ₋₅ -C ₁₆
AID10-nSaCas9-KKH-UGI	nSaCas9-KKH	NNNRRT	C ₋₂ -C ₁₂	C ₋₅ -C ₁₆
nCas9-AID10-UGI	nSpCas9	NGG	C ₁₂ -C ₁₄	C ₁₂ -C ₁₄
AID10-nCas9-AID10-UGI	nSpCas9	NGG	C ₋₁ -C ₁₄	C ₋₁ -C ₁₄
ABE8e-nCas9-AID10-UGI	nSpCas9	NGG	A ₄ -A ₈ , C ₁₁ -C ₁₄	A ₂ -A ₈ , C ₉ -C ₁₄
AID10-ABE8e-nCas9-UGI	nSpCas9	NGG	A ₄ -A ₈ , C ₋₁ -C ₁₁	A ₂ -A ₈ , C ₋₁ -C ₁₄

¹ The subscripted numbers represent the protospacer positions, counting the PAM as 21–23.

Supplementary Sequence. Amino acid sequences of base editors tested in this study.

AID10-dCas9

(NLS-AID10-XTEN-dCas9-NLS-2×FLAG)

MAPKKKRKVG IHGVPAADSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDF
GYLRNKNKGCHVELLFLRYISDWDLDPGRCYRVTFWISWSPCYDCARHVADFLRGPNLSLRI
FAARLYFCEDRKAEPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENS
VRLSGQLRRILSGSETPGTSESATPESDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRKKNRICYLQEIFSNEMAKVDDSDFFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPNDSVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRL
NLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNREDLLRKQRTFDNGS
IPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGNSRFAMWTRKSEE
TITPWNFEVVDKASQAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT
YH DLLKI IKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERM
KRIIEGIKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVAIVP
QSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLT
KAER GGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKS
KLVSDFR KDFQFYKVREINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVR
KMIKSEQEI GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDF
ATVRKVL SMPQ VNIVKKTVEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPT
VAYSVLVVAKVEK GK SKKLKSVKELLGITIMERSSSFENPIDFLEAKGYKEVKKDLI
IKLPKYSLFELENGRKRMLA SAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQ
LFVEQHKHYLDEIIEQISEFS KRVI LADANL DKVLSAYNKHRDKPIREQAENI
IHLFTLTNLGAPAAFKYFDTTIDRKRYTST KEVL DATLIHQSI TGLYETRIDL
SQLGGDKRPAATKKAGQAKKKRPPPSDYKDDDDKDYKD DDDK*

AID10-dCas9-UGI

(NLS-AID10-XTEN-dCas9-(GGG)₆ linker-UGI-NLS-2×FLAG)

MAPKKKRKVG IHGVPAADSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDF
GYLRNKNKGCHVELLFLRYISDWDLDPGRCYRVTFWISWSPCYDCARHVADFLRGPNLSLRI
FAARLYFCEDRKAEPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENS
VRLSGQLRRILSGSETPGTSESATPESDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRKKNRICYLQEIFSNEMAKVDDSDFFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPNDSVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRL
NLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY

VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGGK
SKKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLI IKLPKYSLFELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
KRVILADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKRPPPSDYKDDDDKDYKD
DDDK*

AID10-nCas9-UGI

(NLS-AID10-XTEN-nCas9-(GGG)₆ linker-UGI-NLS-2×FLAG)

MAPKKRKRKVGIHGVPAADSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDF
GYLRNKNKGCHVELLFLRYISDWDLDPGRCYRVTFWISWSPCYDCARHVADFLRGNPNLSLRI
FAARLYFCEDRKAPEPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENS
RLSGQLRRILSGSETPGTSESATPESDKKYSIGLAIGTNSVGWAVITDEYKVPKPKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRKRNRYCYLQEIFSNEMAKVDDSDFFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPNDSVDKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLE
NLIAQLPGEKKNLFGNLIALSGLTPNFKSNFDLAEDAKLQLSKDITYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRQRTFDNGS
IPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYYVGPLARGNSRFAMWTRKSEE
TITPWNFEVVDKGSASQSFIERMTNFDKNLPNEKVLPHKSLLEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
DLLKIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFMLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIKKGI LQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERM
KRIIEGKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVP
QSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER
GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEI
GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQ
VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEKGGK
SKKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLI IKLPKYSLFELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
KRVILADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGDGGGGSGGGSGGGSGGGSGGGSGGGSGGGSTNL
SDIEKETGKQLVIQESILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYK
PWALVIQDSNGENKIKMLS GGSKRPAATKKAGQAKKKRPPPSDYKDDDDKDYKDDDDK*

AtCDA1-nCas9-UGI

(NLS-AtCDA1-XTEN-nCas9-NLS-UGI-NLS)

MPKKRKRKVMKPSFVIQSKEAESAAKQLGVSVIQLLPSLVKPAQSYARTPISKFNVAVVGLG
SSGRIFLGVNVEFPNLPLHHSIHAEQFLVTNLTLNGERHLNFFAVSAAPCGHCRQFLQEIRD
APEIKILITDPNNSADSDSAADSDFLRLGSLPHRFGPDDLKGDHPLLESHDNHLKISD

LDSICNGNTDSSADLKQTALAAANRSYAPYSLCPSGVSLVDCDGKVYRGWYMESAAYNPSMG
PVQAALVDYVANGGGGGYERIVGAVLVEKEDAVVRQEHTARLLETISPCKEFKVFHCYEAS
GSETPGTSESATPELKDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGNTDRHSIKKNL
IGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVEE
DKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLIE
GDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQLPGEK
KNGLFGNLIASLSGLTPNFKSNFDLAEDAKLQLSKDTYDDDLNLLAQIGDQYADLFLAAKN
LSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSKN
GYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRKQRTFDNGSIPHQIHLGEL
HAILRRQEDFYFPLKDNREKIEKILTFRIPIYVVGPLARGNSRFAWMTRKSEETITPWNFEEV
VDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLEYEFTVYNELTKVKYVTEGMRKPAFLSGE
QKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLKIKDKD
FLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKL
NGIRDKQSGKTIIDFLKSDGFANRNFMLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLAG
SPAIKKILQTVKVVDELVKVMGRHKPENIVIEARENQTTQKGQKNSRERMKRIEEGKEL
GSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSID
NKVLRSDKNRGKSDNVPSEEVVKMKNYWRQLLNAKLITQRKFDNLTKAERGGSELKAG
FIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVR
INNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVDVRKMIKSEQEIGKATAKYFFY
SNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSPQVNIKKTEVQ
TGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVAKVEKKGSKKLKSVKEL
LGITIMERSSEFKNPIDFLEAKGYKEVKKDLIKLPKYSLELENGRKRMLASAGELQKNE
LALPSKYVNFYLYASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIEQISEFSKRVILADANL
DKVLSAYNKHDKPIREQAENIHLFTLTNLGAPAAFYFDTTIDRKRYTSTKEVLDATLIH
QSITGLYETRIDLSQLGGDKRPAATKKAQAKKKKTRDSGGSTNLSDIIEKETGKQLVIQES
IILMLPEEVEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKM
LSGGS PKKKRKV*

APOBEC1-nCas9-UGI

(NLS-APOBEC1-XTEN-nCas9-NLS-UGI-NLS)

M P K K K R K V S S E T G P V A V D P T L R R R I E P H E F E V F F D P R E L R K E T C L L Y E I N W G G R H S I W R H T S
Q N T N K H V E V N F I E K F T T E R Y F C P N T R C S I T W F L S W S P C G E C S R A I T E F L S R Y P H V T L F I Y I A
R L Y H H A D P R N R Q G L R D L I S S G V T I Q I M T E Q E S G Y C W R N F V N Y S P S N E A H W P R Y P H L W V R L Y V
L E L Y C I I L G L P P C L N I L R R K Q P Q L T F F T I A L Q S C H Y Q R L P P H I L W A T G L K S G S E T P G T S E S A
T P E L K D K K Y S I G L A I G T N S V G W A V I T D E Y K V P S S K F K V L G N T D R H S I K K N L I G A L L F D S G E T
A E A T R L K R T A R R R Y T R R K N R I C Y L Q E I F S N E M A K V D D S F F H R L E E S F L V E E D K K H E R H P I F G
N I V D E V A Y H E K Y P T I Y H L R K K L V D S T D K A D L R L I Y L A L A H M I K F R G H F L I E G D L N P D N S D V D
K L F I Q L V Q T Y N Q L F E E N P I N A S G V D A K A I L S A R L S K S R R L E N L I A Q L P G E K K N G L F G N L I A L
S L G L T P N F K S N F D L A E D A K L Q L S K D T Y D D D L N L L A Q I G D Q Y A D L F L A A K N L S D A I L L S D I L
R V N T E I T K A P L S A S M I K R Y D E H H Q D L T L L K A L V R Q Q L P E K Y K E I F F D Q S K N G Y A G Y I D G G A S
Q E E F Y K F I K P I L E K M D G T E E L L V K L N R E D L L R K Q R T F D N G S I P H Q I H L G E L H A I L R R Q E D F Y
P F L K D N R E K I E K I L T F R I P Y Y V G P L A R G N S R F A W M T R K S E E T I T P W N F E E V V D K G A S A Q S F I
E R M T N F D K N L P N E K V L P K H S L L Y E Y F T V Y N E L T K V K Y V T E G M R K P A F L S G E Q K K A I V D L L F K

AID10-dLbCas12a-UGI

(NLS-AID10-XTEN-dLbCas12a-(GGG)₆ linker-UGI-NLS-2×FLAG)

MA**PKKKR**K**VG**I**HG**V**PA**AD**SLLMNR**REFLYQ**FKNVR**WAK**GRRE**TYLCYV**VERRD**CATS**FS**SLDF
GYLRN**KNGCH**VELL**FLRY**ISDWLD**PGRCYR**VTW**FIS**WSPCYDCARHVAD**FLRGNPN**LSLRI
FAARLY**FCEDR**KAE**PEGLRRL**RRAGVQ**IAIM**TFKDYFYCWNT**FAENH**GRT**FKAW**EGLHENS**V**
RL**SGQLRR**IL**SGSE**TP**GTSES**AT**PES**M**SKLE**KFTNCYSLSKTLRFKAI**PVG**KTQENIDNKRL
LVEDEKRAEDYKGVKLLDRYYLS**FIND**VLHSIKLKNLNNYISLFRKKTRTEKENKELENLE
INLRKEIAKAFK**NEGYK**SLFKKDI**IETIL**PEFLDDKDEIALVNSFNGFTTAFTGFFDNREN
MFSE**EAK**ST**SIA**FR**CINEN**LTRYIS**NMDI**FEKVD**AIF**DKHEVQ**EIKE**KILNSDYDVEDFFEG
EFFNFVLTQEGIDVYNAI**IGGF**V**TES**GEKIKGLNEYINLYNQ**TKQ**KLPKFKPLYKQVLSDR
ESLSFYGEGY**TSDEE**VLE**VRNT**LNK**NS**E**IF**SS**IKK**LEKLFK**NF**DEYSSAG**IF**VKNGPA**IST**
ISKDI**FG**EWN**VI**RD**KWNA**EYDDIHL**KKK**AVVTEKYEDDRRKS**FKK**IGSFSLEQLQEYADADL
SVVEKLKEII**I**Q**V**DEIYK**VY**GSSEKLFDA**DV**LEKSLK**KNDA**VVA**IMK**DL**LD**SVK**S**FENYI
KAFFGEGKETNRDES**FY**GDFV**LAY**DILLKVDHIYDAIRNYVTQ**KP**YSKDKFKLYFQ**NP**QFMG
GWDKDKETDYRATILRYGSKYYLA**IM**DKKYAKCLQKIDKDDVNGNYEKIN**YK**LLPGPNKMLP
KVFFSK**WM**AY**NP**SEDIQKIYK**NG**TFKK**GDM**FN**LN**DCHKLIDFFKDSISRYPKWSNAYDFN
FSETEKYKDIAGFYREVEEQYKVS**FES**ASKKEVDK**LVEE**GKLYMFQIYNKDFSDKSHGTPN
LHTMYFKLLFDENN**HGQ**IRLSGGAE**LF**MRRASL**KKEE**LVVHPANSPIANK**NP**DNPKKTTLS
YDVYKDKR**FS**EDQYELHIPIA**IN**KCPK**NI**FKINTEVRVLLKHDDNPYVIGI**A**RGERNLLYIV
VVDGKGNIVEQYSLNEI**INN**FNGIRIKTDYHSLLDKKEKERFEARQ**NW**TSIENIKELKAGYI
SQVVHKICELVEKYDAVIALED**LN**SGFKNSRVKVEKQVYQ**KFE**KMLIDKLN**YM**VDKKS**N**PCA
TGGAL**KY**QITNK**FES**FKSMSTQNGF**IF**YIPAWLTSKIDPSTGFVN**LL**KTKYTSIADSKKFI
SSFD**RIM**YVPEEDLFEFALDYK**NF**SRTDADYIKKW**KLY**SYGNRIRIFRNPK**NN**VFDWEEVC
LTSAYKELFNKYGIN**YQ**QDIRALLCEQSDKAFYSSFMALMSLMLQMRNSITGR**TD**VDFLIS
PVKNSDGI**FY**DSRNYEAQENAILPK**NAD**ANGAYNIARKV**LWA**IGQFKKAEDEKLDKVKIAIS
NKEWLEYAQTSVKH**GGGG**SGGGSGGGSGGGSGGGSGGGSGGG**ST**NLS**DI**IEKETG**KQ**L**VI**Q
ES**IL**MLPEEVEEVIG**NK**PESDILVHTAYDESTDEN**VML**LTS**DA**PEYK**PW**AL**VI**QDSNGENKI
KMLSGGS**KR**PAAT**KK**AG**QA**KKKKRPPPSDYKDDDDKDYKDDDDK*

AID10-nSpCas9-NG-UGI

(NLS-AID10-XTEN-nSpCas9-NG-(GGG)₆ linker-UGI-NLS-2×FLAG)

MA**PKKKR**K**VG**I**HG**V**PA**AD**SLLMNR**REFLYQ**FKNVR**WAK**GRRE**TYLCYV**VERRD**CATS**FS**SLDF
GYLRN**KNGCH**VELL**FLRY**ISDWLD**PGRCYR**VTW**FIS**WSPCYDCARHVAD**FLRGNPN**LSLRI
FAARLY**FCEDR**KAE**PEGLRRL**RRAGVQ**IAIM**TFKDYFYCWNT**FAENH**GRT**FKAW**EGLHENS**V**
RL**SGQLRR**IL**SGSE**TP**GTSES**AT**PES**D**KKY**SIG**LA**IGTNSVGWAVITDEYK**VPS**KKFKVLGN
TDRHSIKK**NLI**GALLFD**SGET**A**EAT**RLKRTARRRYTRRKNR**IC**YLQ**EI**FSNEMAKVDD**SFF**H
RLEESFLVEEDKKHERHPI**FG**NI**V**DEVAYHEKYPTIYHLR**KK**LVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNP**DS**DVDKLF**IQ**LVQTY**NQ**LFEENPINASGVDAKAIL**SAR**LSK**S**RRLE
NLIAQL**PGE**KK**NGL**FGN**LIAL**SLGLTP**NF**KS**NF**DLA**E**DAKLQLSKDTYDDDL**DN**LLAQIGDQ
YADLFLAAK**NLS**DA**ILL**SDILRVNTEITK**AP**LS**AS**MIKRYDEHHQDLTLLK**AL**VRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQ**E**EFYK**FI**KPILEKMDGTE**ELL**VKLNREDLLR**KQ**RTFDNGS
IPHQIHLGELHAILRRQ**ED**FYPFLKDNREKIEKIL**TF**RIPYYVG**PL**ARGNSRF**AW**M**TR**KSEE
TITPW**NF**E**EV**VDKGAS**AQ**S**FIER**MT**NF**DK**NL**PNEK**VL**PKHSLLYEYFTVYNELTKVKYVTEG

nCas9-AID10-UGI

(NLS-nCas9-NLS-XTEN-AID10-NLS-UGI-2×FLAG)

MAPKKKRKVGIIHGVPAAADKKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGNTDRHSIKKN
LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFHRLEESFLVE
EDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFRGHFLI
EGDLNPDNSDVKLFIQLVQTYNQLFEEENPINASGVDAKAILSARLSKSRLENLIAQLPGE
KKNGLFGNLIASLGLTPNFKSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQYADLFLAAK
NLSDAILLSLILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSK
NGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFDNGSIPHQIHLGE
LHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGNSRFAMTRKSEETITPWNFEE
VVDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLEYEFTVYNELTKVKYVTEGMRKPAFLSG
EQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLKIKDK
DFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKL
INGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDSLHEHIANLA
GSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE
LGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSI
DNKVLTRSDKNRGKSDNVPSEEVVKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDA
GFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVR
EINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVDVRKMIKSEQEIGKATAKYFF
YSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLVSMQVNIIVKKTEV
QTGGFSKESILPKRNSDKLIARKKDWDPKKGFFSPTVAYSVLVVAKVEKGSKLLKSVKE
LLGITIMERSSSFENPIDFLEAKGYKEVKKDLIKLPHYSLFELENGRKRMLASAGELQKGN
ELALPSKYVNFYLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIEQISEFSKRVIADAN
LDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVL DATLI
HQSITGLYETRIDLSQLGGDKRPAATKKAQAKKKRPSPSGSETPGTSESATPESDLSLLMN
RREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRNKNKGCHVELLFLRYISDWD
LDPGRCYRVTFWISWSPCYDCARHVADFLRGNPNLSLRIFAARLYFCEDRKAPEGLRRLRR
AGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGHENSVRSLGQLRRILGPKKKRKGSTNL
SDIEKETGKQLVIQESILMLPEEVEEVI GNKPESDILVHTAYDESTDENVMLLTSDAPEYK
PWALVIQDSNGENKIKMLRPPPSDYKDDDDKDYKDDDDK*

AID10-nCas9-AID10-UGI

(NLS-AID10-XTEN-nCas9-NLS-XTEN-AID10-NLS-UGI-2×FLAG)

MAPKKKRKVGIIHGVPAAADSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDF
GYLRNKNKGCHVELLFLRYISDWDLDPGRCYRVTFWISWSPCYDCARHVADFLRGNPNLSLRI
FAARLYFCEDRKAPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGHENS
RLSGQLRRILSGSETPGTSESATPESDKKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEEENPINASGVDAKAILSARLSKSRLE
NLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSLILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFDNGS

IPHQIHLGELHAILRRQEDFYPFLLKDNREKIEKILTFRIPIYYVGPLARGNSRFAMWTRKSEE
TITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLEYEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERM
KRIIEGKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVP
QSFLKDDSIDNKVLRSDKNRGSNDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER
GGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVREINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRKMIKSEQEI
GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSPQ
VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKGFFDSPTVAYSVLVAKVEKKG
SKKLSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
KRVILADANLNDKVL SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVLDTLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKRPSPSGSETPGTSESAT
PESDLSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRNKNNGCHVELL
FLRYSIDWDLDPGRCYRVTWFISWSPCYDCARHVADFLRGPNLSLRIFAARLYFCEDRKAE
PEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGHENSVRLSGQLRRILGPKK
KRKVGSTNLSDIIEKETGKQLVIQESILMLPEEVVEEVIIGNKPESDILVHTAYDESTDENVML
LTSDAPEYKPWALVIQDSNGENKIKMLRPPPSDYKDDDDKDYKDDDDK*

ABE7.10-nCas9

(TadA-32aa linker-TadA7.10-32aa linker-nCas9-NLS-NLS-2×FLAG)

MGSEVEFSHEYWMRHALTLAKRAWDEREVPVAVLVHNNRVIGEGWNRPIGRHDPTAHAEIM
ALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHH
PGMNRHVEITEGILADECAALLSDFFRMRQEIKAQKKAQSSTDSGGSSGGSSGSETPGTSE
SATPESSGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVAVLVHNNRVIGEGWNRPI
GLHDPTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGVRNAKT
GAAGSLMDVLHYPGMNRHVEITEGILADECAALLCYFFRMRQVFNAQKKAQSSTDSGGSSG
GSSGSETPGTSESATPESSGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVPKSKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLE
NLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAKLQLSKDXYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRQRTFDNGS
IPHQIHLGELHAILRRQEDFYPFLLKDNREKIEKILTFRIPIYYVGPLARGNSRFAMWTRKSEE
TITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPHKSLLEYEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKGQKNSRERM

KRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP
QSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER
GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVR EINNYYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEI
GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQ
VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEK GK
SKKLKSVKELLGITIMERSSSFENPIDFLEAKGYKEVKKDLI IKLPKYSLFELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
KRVILADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGKRPAAATKKAGQAKKKKSGGS PKKKRKVRPPPSD
YKDDDDKDYKDDDDK*

nCas9-AID10

(NLS-nCas9-NLS-XTEN-AID10-2xFLAG)

MAPKKKRKVG I HGVPAADKKYSIGLAIGTNSVGVAVITDEYKVP SKKFKVLGNTDRHS IKKN
LIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSDFFHRLEESFLVE
EDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLV DSTDKADLRLIYLALAHMIKFRGFHFLI
EGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIAQLPGE
KKNGLFGNLI ALSLGLTPNFKSNFDLAEDAQLSKD TYDDDLNLLAQIGDQYADFLFAAK
NLSDAILLSDILRVNTEITKAPLSAMIKRYDEHHQDLTLLKALVRQQLPEKYKEIFFDQSK
NGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNREDLLRKQRTFDNGSIPHQIHLGE
LHAILRRQEDFY PFLKDNREKIEKILTFRI PYYVGPLARGNSRFAMWTRKSEETITPWNFEE
VVDKGASAQSFIERMTNFDKNLPNEKVL PKHSLLEYFTVYNELTKVKYVTEGMRKPAFLSG
EQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLKI IKDK
DFLDNEENEDI LEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYTGWGRLSRKL
INGIRDKQSGKTILDFLKSDFANRNFMQLIHDDSLTFKEDIQKAQVSGQGD SLHEHIANLA
GSPAIAKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIEEGIKE
LGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFLKDDSI
DNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLSELDKA
GFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFRKDFQFYKVR
EINNYYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEI GKATAKYFF
YSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQVNIVKKTEV
QTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEK GKSKKLKSVKE
LLGITIMERSSSFENPIDFLEAKGYKEVKKDLI IKLPKYSLFELENGRKRMLASAGELQKGN
ELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIEQISEFSKRVILADAN
LDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVL DATLI
HQSI TGLYETRIDLSQLGGKRPAAATKKAGQAKKKKRP SGSETPGTSSESATPESDSL MNRR
EFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRNKGCHVELLFLRYISDWDL D
PGRCYRVTWFI SWSPCYDCARHVADFLRGPNLSLRI FAARLYFCEDRKAPEGLRRLRRAG
VQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENSVRLSGQLRRILRPPPSDYKDDDDKDY
KDDDDK*

ABE7.10-nCas9-AID10

(TadA-32aa linker-TadA7.10-32aa linker-nCas9-NLS-NLS-XTEN-AID10-2×FLAG)

MGSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVIGEGWNRPIGRHDPTAHAEIM
ALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHH
PGMNRHVEITEGILADECAALLSDFFRMRQEIKAQKKAQSSTDSGGSSGGSSGSETPGTSE
SATPESSGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNR
GLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKT
GAAGSLMDVLHYPGMNRHVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSG
GSSGSETPGTSESATPESSGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSSFFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAIL SARLSKSRLE
NLIAQLPGEKKNGLFGNLIALSGLTPNFKSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRQRTFDNGS
IPHQIHLGELHAILRRQEDFYPFKDNREKIEKILTFRIPIYYVGPLARGNSRFAMWTRKSEE
TITPWNFEVVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT
DYLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFMLIHDSDLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIKKGIHQTVKVVDELVKVMGRHKPENIVIAMARENQTTQKQKNSRERM
KRIIEGKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVP
QSFLKDDSIDNKVLRSDKNRGSNDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER
GGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVVREINNYHHAHDAYLNAVVGTAIIKKYPKLESEFVYGDYKVYDVRKMIAKSEQEI
GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQ
VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVAKVEK GK
SKKLSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
KRVILADANLNDKVL SAYNKHRDKPIREQAENIHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKKSGGSPKKKRKVRPSGSE
TPGTSESATPESD SLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRN
KNGCHVELLFLRYISDWDLDPGRCYRVTWFI SWSPCYDCARHVADFLRGNPNLSLRIFAARL
YFCEDRKAPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGHENSVRLSGQ
LRRILRPPPSDYKDDDDKDYKDDDDK*

TadA7.10-nCas9-AID10

(TadA7.10-32aa linker-nCas9-NLS-NLS-XTEN-AID10-2×FLAG)

MGSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVIGEGWNRPIGRHDPTAHAEIM
ALRQGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAGSLMDVLH
PGMNRHVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSGGSSGSETPGTSE
SATPESSGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGN TDRHSIKKNLIG
ALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSSFFHRLEESFLVEEDK

RQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRDILLRK
QRTFDNGSIPHQIHLGELHAILRRQEDFYPPFLKDNREKIEKILTFRIPIYYVGPLARGNSRFA
WMTRKSEETITPWNFEVVDK GASAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELT
KVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
NASLGTYHDLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMK
QLKRRRYTGWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKA
QVSGQGDSLHEHIANLAGSPAIIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKG
QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSD
YDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF
DNLTKAERGGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLK
SKLVSDFRKDFQFYKREINNYHHAHDAYLNAVGTALIKKYPKLESEFVYGDYKVYDVRKM
IAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATV
RKVLSMPQVNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLV
VAKVEKGSKKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLEFE
NGRKRMLASAGELQKGNELALPSKYVNFYLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEI
IEQISEFSKRVI LADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTI
DRKRYTSTKEVL DATLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKKSGGS PPKKR
KVRPPPSDYKDDDDKDYKDDDDK*

AID10-TadA7.10-nCas9

(AID10-XTEN-TadA7.10-32aa linker-nCas9-NLS-NLS-2×FLAG)

MDSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRNKNKGCHVELLFL
RYISDWDLDPGRCYRVTWFI SWSPCYDCARHVADFLRGNPNLSLRI FAARLYFCEDRKAPEE
GLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENSVRLSGQLRRILSGSETP
GTSESATPESSEVEFSHEYWMRHALLAKRARDEREVPPGAVLVLNRRVIGEGWNRAIGLHD
PTAHAEIMALRQGGGLVMQNYRLIDATLYVTFEPCVMCAGAMIHSRIGRVVFGVRNAKTGAAG
SLMDVLHYPGMNRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSGGSSG
SETPGTSESATPESGGSSGGSDKKYSIGLAIGTNSVGWAVITDEYKVPSKKFKVLGNTDRH
SIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSSFHRL
SFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHMIKFR
GHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRLENLIA
QLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAKLQLSKD TYDDDLNLLAQIGDQYADL
FLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKYKEIF
FDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNRDILLRKQRTFDNGSIPHQ
IHLGELHAILRRQEDFYPPFLKDNREKIEKILTFRIPIYYVGPLARGNSRFAWMTRKSEETITP
WNFEVVDK GASAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELTKVKYVTEGMRKPA
AFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYHDLLK
IIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKTYAHLFDDKVMKQLKRRRYTGWGR
LSRKLINGIRDKQSGKTILDFLKSDFANRNFQMQLIHDDSLTFKEDIQKAQVSGQGDSLHEH
IANLAGSPAIIKKGILQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERMKRIE
EGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVPQSFL
KDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAERGGLS
ELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSKLVSDFRKDFQ

FYKVVREINNYHHAHDAYLNAVVGTTALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEIGKAT
AKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSPQVNI
KKTEVQTTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVAKVEKSKKL
KSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLEFELNGRKRMLASAGE
LQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIIEQISEFSKRVI
LADANLDKVL SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTSTKEVL
DATLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKKSGGSPKKKRKVRPPPSDYKDD
DDKDYKDDDDK*

ABE7.10-nCas9-AID10-UGI

(TadA-32aa linker-TadA7.10-32aa linker-nCas9-NLS-NLS-XTEN-AID10-(GGG)₆ linker-UGI-2×FLAG)

MGSEVEFSHEYWMRHALTLAKRAWDEREVPVAVLVHNNRVIGEGWNRPIGRHDPTAHAEIM
ALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHH
PGMNHRVEITEGILADECAALLSDFFRMRQEIKAQKKAQSSTDSGGSSGGSSGSETPGTSE
SATPESSGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVAVLVHNNRVIGEGWNRPI
GLHDPTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGVRNAKT
GAAGSLMDVLHYPGMNHRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSSTDSGGSSG
GSSGSETPGTSESATPESSGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVPKSKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRL
NLIAQLPGEKKNGLFGNLIALLSGLTPNFKSNFDLAEDAKLQLSKDQYDDDLNLLAQIGDQ
YADFLAANKLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNLREDLLRKQRTFDNGS
IPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYVVGPLARGNSRFAMWTRKSEE
TITPWNFEVVDKASQAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGT
YHDLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFMLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIKKGIQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKQKNSRERM
KRIEELGKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVP
QSFLKDDSIDNKVLRSDKNRGSNDNVPSEEVVKKMKNYWRQLLNAKLITQRKFDNLTKAER
GGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVVREINNYHHAHDAYLNAVVGTTALIKKYPKLESEFVYGDYKVYDVRKMIKSEQE
IGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVLSPQ
VNIKKTEVQTTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVAKVEKSK
SKLKSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLEFELNGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIIEQISEFS
KRVI LADANLDKVL SAYNKHRDKPIREQAENIIHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKKSGGSPKKKRKVRPSGSE
TPGTSESATPESDSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRN
KNGCHVELLFLRYSIDWDLDPGRCYRVTFWISWSPCYDCARHVADFLRGNPNLSLRIFAARL

YFCEDRKAPEPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENSVRLSGQ
LRRILGGGGSGGGSGGGSGGGSGGGSGGGSGGGSTNLSDIIEKETGKQLVIQESILMLPEE
VEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLS GGSRP
PPSDYKDDDDKDYKDDDDK*

ABE8e-nCas9-AID10-UGI

(TadA-32aa linker-TadA8e-32aa linker-nCas9-NLS-NLS-XTEN-AID10-(GGG)₆ linker
-UGI-2×FLAG)

MGSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVI GEGWNRPIGRHDPTAHAEIM
ALRQGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLHH
PGMNRHVEITEGILADECAALLSDFFRMRQEIKAQKKAQSSTDSGGSSGGSSGSETPGTSE
SATPESSGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNRRVIGEGWNRAI
GLHDPTAHAEIMALRQGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGVRNSKR
GAAGSLMNVLNYPGMNRHVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINSGGSSG
GSSGSETPGTSESATPESSGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVPSSKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAIL SARLSKSRLE
NLIAQLPGEKKNLFGNLIALLSLGLTPNFKSNFDLAEDAQLQSKD TYDDDLNLLAQIGDQ
YADFLAAKNLSDAILLSDILRVNTEITKAPLSAMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNREDLLRQRTFDNGS
IPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYYVGPLARGNSRFAMWTRKSEE
TITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELTKVKYVTEG
MRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRFNASLGTYH
DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
GWGRLSRKLINGIRDKQSGKTILDFLKSDFANRNFMQLIHDDSLTFKEDIQKAQVSGQGDS
LHEHIANLAGSPAIKKGI LQTVKVDELVKVMGRHKPENIVIEMARENQTTQKGQKNSRERM
KRIEEGIKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSDYDVDHIVP
QSFLKDDSIDNKVLRSDKNRGSNDNVPSEEVVKMKNYWRQLLNAKLITQRKFDNLTKAER
GGLSELDKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEI
GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQ
VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLVVAKVEK GK
SKKLSVKELLGITIMERSSEFEKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIIEQISEFS
KRVI LADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGKRPAAATKKAGQAKKKKSGGSPKKKRKVRPSGSE
TPGTSESATPESD SLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRN
KNGCHVELLFLRYISDWLDPGRCYRVTWFISWSPCYDCARHVADFLRGNPNLSLRIFAARL
YFCEDRKAPEPEGLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGLHENSVRLSGQ
LRRILGGGGSGGGSGGGSGGGSGGGSGGGSGGGSTNLSDIIEKETGKQLVIQESILMLPEE
VEEVIGNKPESDILVHTAYDESTDENVMLLTSDAPEYKPWALVIQDSNGENKIKMLS GGSRP
PPSDYKDDDDKDYKDDDDK*

AID10-ABE7.10-nCas9-UGI

(AID10-XTEN-TadA-32aa linker-TadA7.10-32aa linker-nCas9-(GGS)₆ linker-UGI-NLS-NLS-2×FLAG)

MDSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRNKNKGCHVELLFL
RYISDWDLDPGRCYRVTWFISWSPCYDCARHVADFLRGNPNLSLRIFAARLYFCEDRKAEP
GLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGHENSVRSLSGQLRRILSGSETP
GTSESATPESSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVIGEGWNRPIGRHD
PTAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAG
SLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRQEIKAQKKAQSSSTDSGGSSGGSSG
SETPGTSESATPESGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVI
GEGWNRRAIGLHDPATAHAEIMALRQGGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRV
FGVRNAKTGAAGSLMDVLHYPGMNHRVEITEGILADECAALLCYFFRMPRQVFNAQKKAQSS
TDSGGSSGGSSGSETPGTSESATPESGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVP
KKFKVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMA
KVDDSFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRL
IYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSAR
LSKSRLENLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAKLQLSKDITYDDDLN
LLAQIGDQYADFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALV
RQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRK
QRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYVYVGPLARGNSRFA
WMTRKSEETITPWNFEEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELT
KVKYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
NASLGTYHDLKIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMK
QLKRRRYTGWGRLSRKLINGIRDKQSGKTIIDFLKSDGFANRNFQMQLIHDDSLTFKEDIQKA
QVSGQGDSLHEHIANLAGSPAIKKILQTVKVVDELVKVMGRHKPENIVIVEMARENQTTQKG
QKNSRERMKRIEEGIKELGSQILKEHPVENTQLQNEKLYLYLQNGRDMYVDQELDINRLSD
YDVDHIVPQSFLKDDSIDNKVLTRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF
DNLTKAERGGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLK
SKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVGTALIKKYPKLESEFVYGDYKVYDVRKM
IAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATV
RKVLSMPQVNIKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLV
VAKVEKGSKKLKSVKELLGITIMERSSEFKNPIDFLEAKGYKEVKKDLIIKLPKYSLFELE
NGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLGKSPEDNEQKQLFVEQHKHYLDEI
IEQISEFSKRVI LADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTI
DRKRYTSTKEVLDATLIHQ SITGLYETRIDLSQLGGDGGGGSGGGSSGGSSGGGGSSGGGS
GGGSSTNLSDIIEKETGKQLVIQESILMLPEEVEEVI GNKPESDILVHTAYDESTDENVMLL
TSDAPEYKPWALVIQDSNGENKIKMLSGGSKRPAATKKAGQAKKKKSGGSPKKRKRVRPPPS
DYKDDDDKDYKDDDDK*

AID10-ABE8e-nCas9-UGI

(AID10-XTEN-TadA-32aa linker-TadA8e-32aa linker-nCas9-(GGS)₆ linker-UGI-NLS-NLS-2×FLAG)

MDSLLMNRREFLYQFKNVRWAKGRRETYLCYVVERRDCATSFSLDFGYLRNKNKGCHVELLFL

RYISDWDLDPGRCYRVTWFI SWSPCYDCARHVADFLRGPNLRLRIFAARLYFCEDRKAEP
 GLRRLRRAGVQIAIMTFKDYFYCWNTFAENHGRTFKAWEGHENSVRLSGQLRRILSGSETP
 GTSESATPESSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVI GEGWNRPIGRHD
 PTAHAEIMALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAG
 SLMDVLHHPGMNHRVEITEGILADECAALLSDFFRMRRQEIKAQKKAQSSTDSGGSSGGSSG
 SETPGTSESATPESGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVI
 GEGWNRRAIGLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVV
 FGVNRNSKRGAAAGSLMNVLNYPGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSS
 INSGGSSGGSSGSETPGTSESATPESGGSSGGSSDKKYSIGLAIGTNSVGWAVITDEYKVP
 KKFVVLGNTDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMA
 KVDDSFHRLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRL
 IYLALAHMIKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSAR
 LSKSRLENLIAQLPGEKKNLFGNLIALSGLTPNFKSNFDLAEDAKLQLSKDITYDDDLN
 LLAQIGDQYADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALV
 RQQLPEKYKEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKLNREDLLRK
 QRTFDNGSIPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPIYYVGPLARGNSRFA
 WMTRKSEETITPWNFEVVVDKGASAQSFIERMTNFDKPNLNEKVLPHKSHLLYEYFTVYNELT
 KVYVTEGMRKPAFLSGEQKKAIVDLLFKTNRKVTVKQLKEDYFKKIECFDSVEISGVEDRF
 NASLGTYHDLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMK
 QLKRRRYTGWGRLSRKLINGIRDKQSGKTI LDFLKSDFANRNFMLIHDDSLTFKEDIQKA
 QVSGQGDSLHEHIANLAGSPAIKKGI LQTVKVDELVKVMGRHKPENIVIVEMARENQTTQKG
 QKNSRERMKRIE EGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSD
 YDVDHIVPQSFLKDDSIDNKVLRSDKNRGKSDNVPSEEVVKKMKNYWRQLLNAKLITQRKF
 DNLTKAERGGLSELKAGFIKRQLVETRQITKHVAQILDSRMNTKYDENDKLIREVKVITLK
 SKLVSDFRKDFQFYKVREINNYHHAHDAYLNAVVGTA LIKKYPKLESEFVYGDYKVYDVRKM
 IAKSEQEIGKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATV
 RKVLSMPQVNIVKKTVEVQTGGFSKESILPKRNSDKLIARKKDWDPKKYGGFDSPTVAYSVLV
 VAKVEKGSKKLKSVELLGITIMERSSEKPNIDFLEAKGYKEVKKDLIIKLPKYSLFELE
 NGRKRMLASAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQQLFVEQHKHYLDEI
 IEQISEFSKRVI LADANLDKVL SAYNKHDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTI
 DRKRYTSTKEVL DATLIHQ SITGLYETRIDLSQLGGDGGGGGGGGGGGGGGGGGGGGGGGG
 GGGGSTNLSDIIEKETGKQLVIQESILMLPEEVEEVI GNKPESDILVHTAYDESTDENVMLL
 TSDAPEYKPPALVIQDSNGENKIKMLSGGSKRPAATKKAGQAKKKKSGGS PKKKRKV RPPPS
 DYKDDDDKDYKDDDDK*

ABE8e-nCas9

(*TadA*-32aa linker-*TadA8e*-32aa linker-nCas9-NLS-NLS-2×FLAG)

MGSEVEFSHEYWMRHALTLAKRAWDEREVPVGAVLVHNNRVI GEGWNRPIGRHDPTAHAEIM
 ALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGARDAKTGAAGSLMDVLH
 PGMNHRVEITEGILADECAALLSDFFRMRRQEIKAQKKAQSSTDSGGSSGGSSGSETPGTSE
 SATPESGGSSGGSSSEVEFSHEYWMRHALTLAKRARDEREVPVGAVLVLNNRVI GEGWNRRAI
 GLHDPTAHAEIMALRQGGLVMQNYRLIDATLYVTLEPCVMCAGAMIHSRIGRVVFGVNRNSK
 GAAGSLMNVLNYPGMNHRVEITEGILADECAALLCDFYRMPRQVFNAQKKAQSSINSGGSSG

GSSGSETPGTSESATPESSGGSSGGSDKKYSIGLAIGTNSVGWAVITDEYKVPSSKKFKVLGN
TDRHSIKKNLIGALLFDSGETAEATRLKRTARRRYTRRKNRICYLQEIFSNEMAKVDDSFH
RLEESFLVEEDKKHERHPIFGNIVDEVAYHEKYPTIYHLRKKLVDSTDKADLRLIYLALAHM
IKFRGHFLIEGDLNPDNSDVKLFIQLVQTYNQLFEENPINASGVDAKAILSARLSKSRRE
NLIAQLPGEKKNGLFGNLIASLGLTPNFKSNFDLAEDAQLQSKDQYDDDLNLLAQIGDQ
YADLFLAAKNLSDAILLSDILRVNTEITKAPLSASMIKRYDEHHQDLTLLKALVRQQLPEKY
KEIFFDQSKNGYAGYIDGGASQEEFYKFIKPILEKMDGTEELLVKNREDLLRQRTFDNGS
IPHQIHLGELHAILRRQEDFYFPLKDNREKIEKILTFRIPYYVGPLARGNSRFAMTRKSEE
TITPWNFEVVDKGASAQSFIERMTNFDKNLPNEKVLPKHSLLEYFTVYNELTKVKYVTEG
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DLLKIIKDKDFLDNEENEDILEDIVLTLTLFEDREMIEERLKYAHLFDDKVMKQLKRRRYT
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LHEHIANLAGSPAIKKGIQTVKVVDELVKVMGRHKPENIVIEMARENQTTQKQKNSRERM
KRIEEGIKELGSQILKEHPVENTQLQNEKLYLYYLQNGRDMYVDQELDINRLSDYDVDHIVP
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GGLSELKAGFIKRQLVETRQITKHVAQILD SRMNTKYDENDKLIREVKVITLKSCLVSDFR
KDFQFYKVREINNYHHAHDAYLNAVVG TALIKKYPKLESEFVYGDYKVYDVRKMIKSEQEI
GKATAKYFFYSNIMNFFKTEITLANGEIRKRPLIETNGETGEIVWDKGRDFATVRKVL SMPQ
VNIVKKTEVQTGGFSKESILPKRNSDKLIARKKDWDPK KYGGFDSPTVAYSVLVVAKVEK GK
SKKLKSVKELLGITIMERSSEFKNPIDFLEAKGYKEVKKDLI IKLPKYSLFELENGRKRMLA
SAGELQKGNELALPSKYVNFLYLASHYEKLGSPEDNEQKQLFVEQHKHYLDEIIEQISEFS
KRVILADANLDKVL SAYNKHRDKPIREQAENI IHLFTLTNLGAPAAFKYFDTTIDRKRYTST
KEVL DATLIHQSI TGLYETRIDLSQLGGDKRPAATKKAGQAKKKKSGGS PKKKRKV RPPPSD
YKDDDDKDYKDDDDK*