

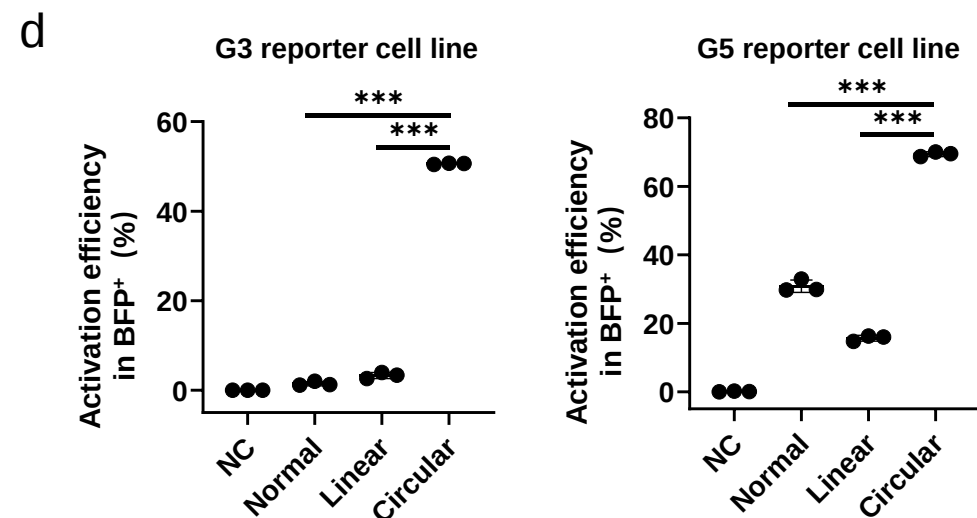
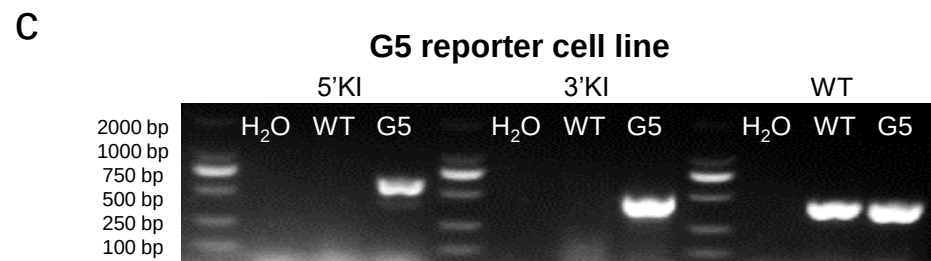
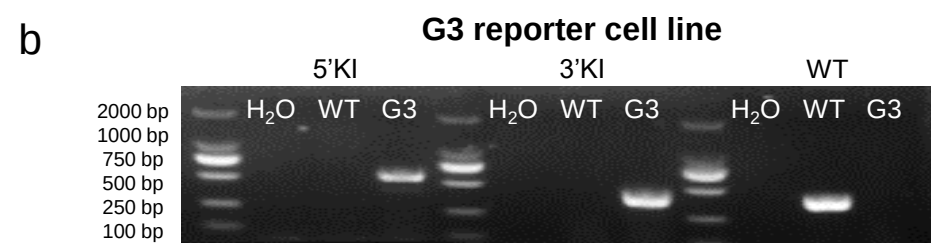
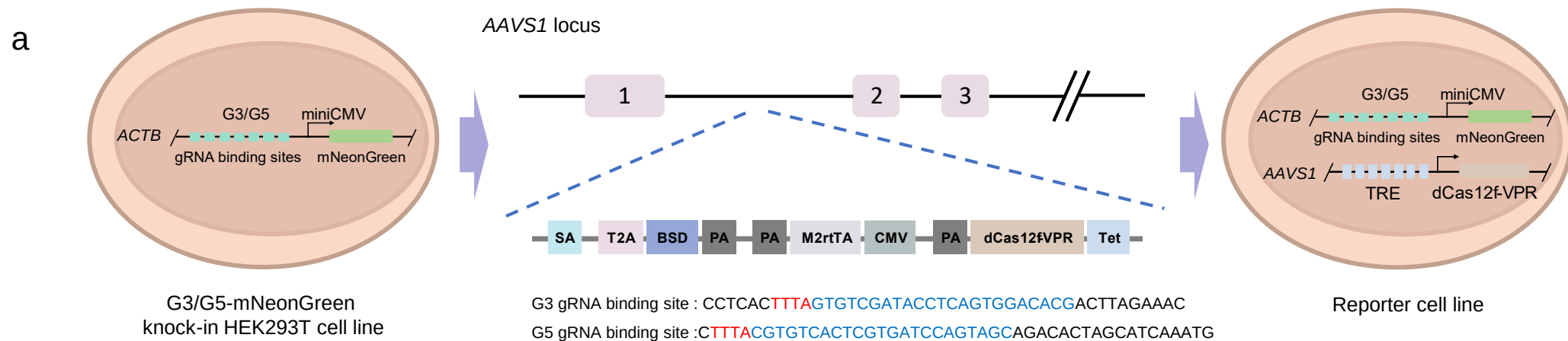
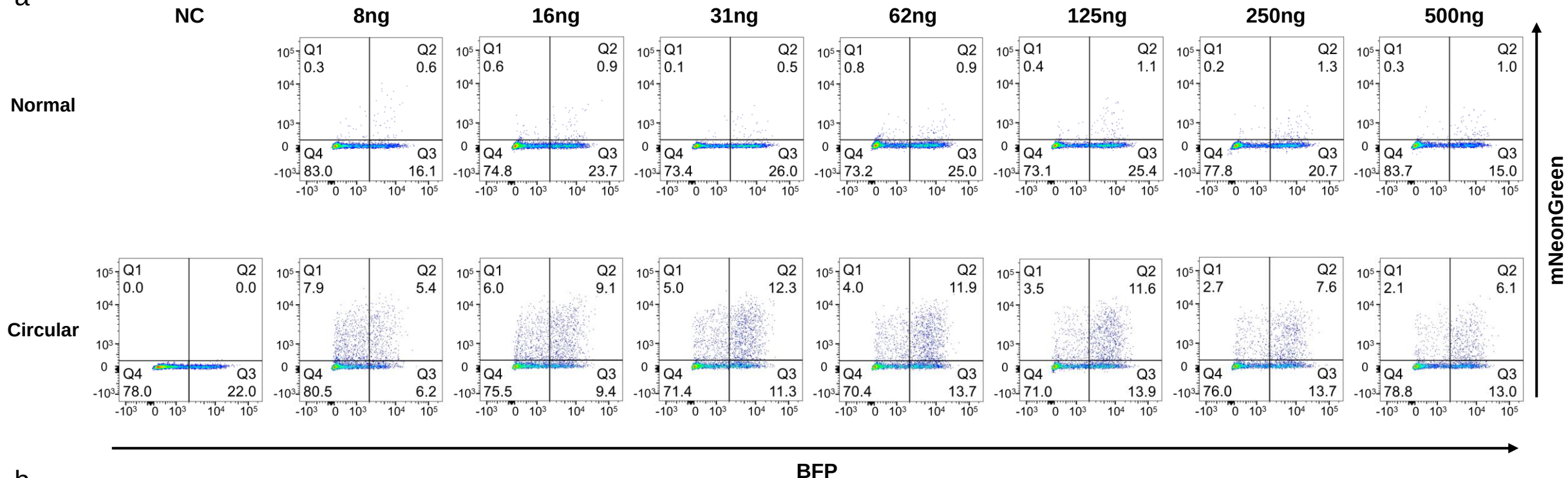


Fig. S1 Establishment of the reporter cell line

Fig. S1 Establishment of the reporter cell line. **a**, Schematic representation of the dCas12f-VPR knock-in strategy at the *AAVS1* locus, The original G3/G5-mNeonGreen knock-in HEK293T cell line includes 7 G3 /G5-gRNA binding sites, which gRNA spacer sequences are marked in blue, and PAM sequences are marked in red. **b** & **c**, Identification of knock-in (KI) clones by genomic PCR. The G3 reporter cell clone involves dCas12f-VPR and Cas/G3 gRNA-activatable mNeonGreen in the HEK293T cells (**b**). The G5 reporter cell clone involves dCas12f-VPR and Cas/G5 gRNA-activatable mNeonGreen in the HEK293T cells (**c**). **d**, Statistical analysis of activation efficiency was quantified using the ratio of mNeonGreen-positive to BFP-positive cells (mNeonGreen+ BFP+ / BFP+) in the FACS assays. n = 3 independent experiments. *p <0.05, **p <0.01, ***p <0.001, Student's t-test.

a



b

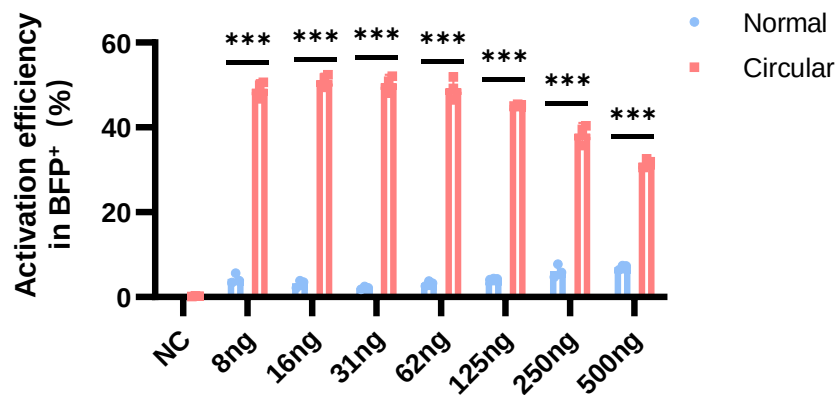


Fig. S2: Dose-dependent analysis of cgRNA-directed gene activation in the G3 reporter cells

Fig. S2: Dose-dependent analysis of cgRNA-directed gene activation in the G3 reporter cells. **a**, FACS analysis showed mNeonGreen expression in the G3 reporter cells 2 days post-transfection with different dosages of G3 gRNA plasmids. **b**, Statistical analysis of activation efficiency was quantified using the ratio of mNeonGreen-positive to BFP-positive cells ($\text{mNeonGreen}^+ \text{BFP}^+ / \text{BFP}^+$) in the FACS assays. $n = 3$ independent experiments. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, Student's t -test.

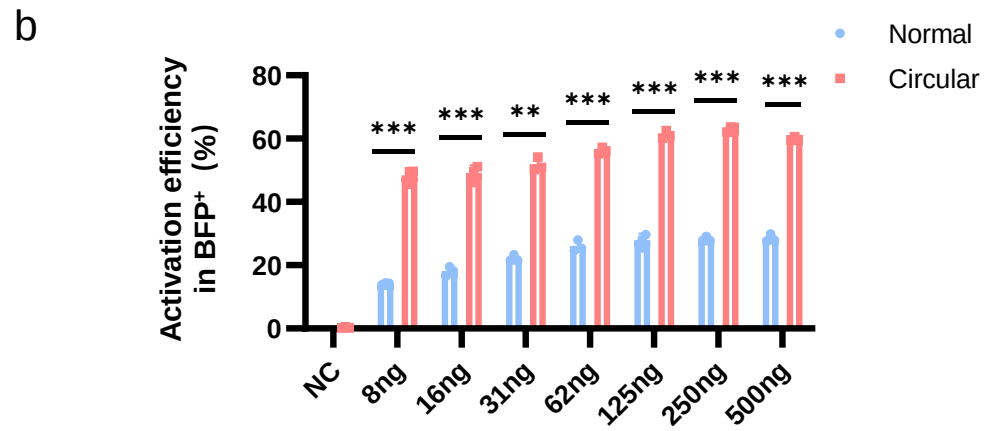
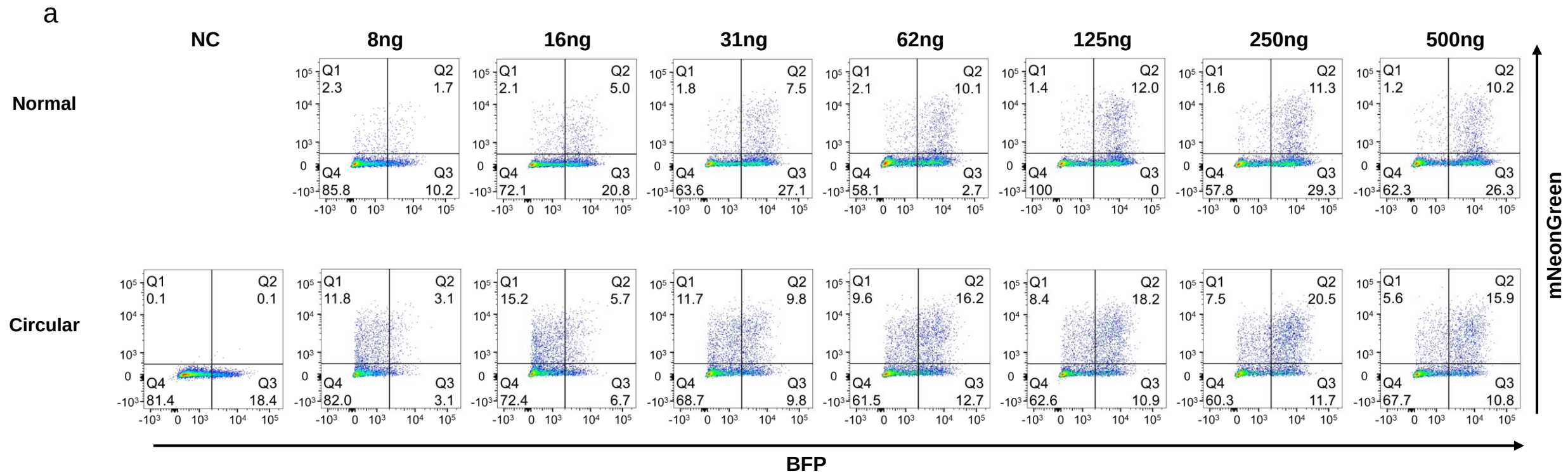


Fig. S3: Dose-dependent analysis of cgRNA-directed gene activation in the G5 reporter cells

Fig. S3: Dose-dependent analysis of cgRNA-directed gene activation in the G5 reporter cells. **a**, FACS analysis revealed mNeonGreen expression in the G5 reporter cells 2 days post-transfection with various dosages of G5 gRNA plasmids. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, Student's t -test.

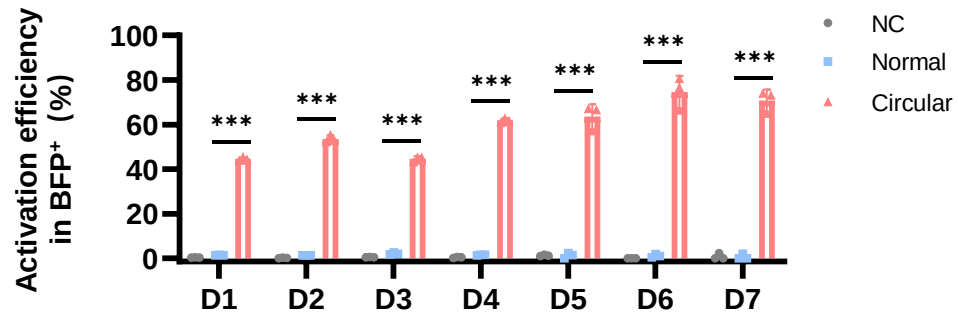
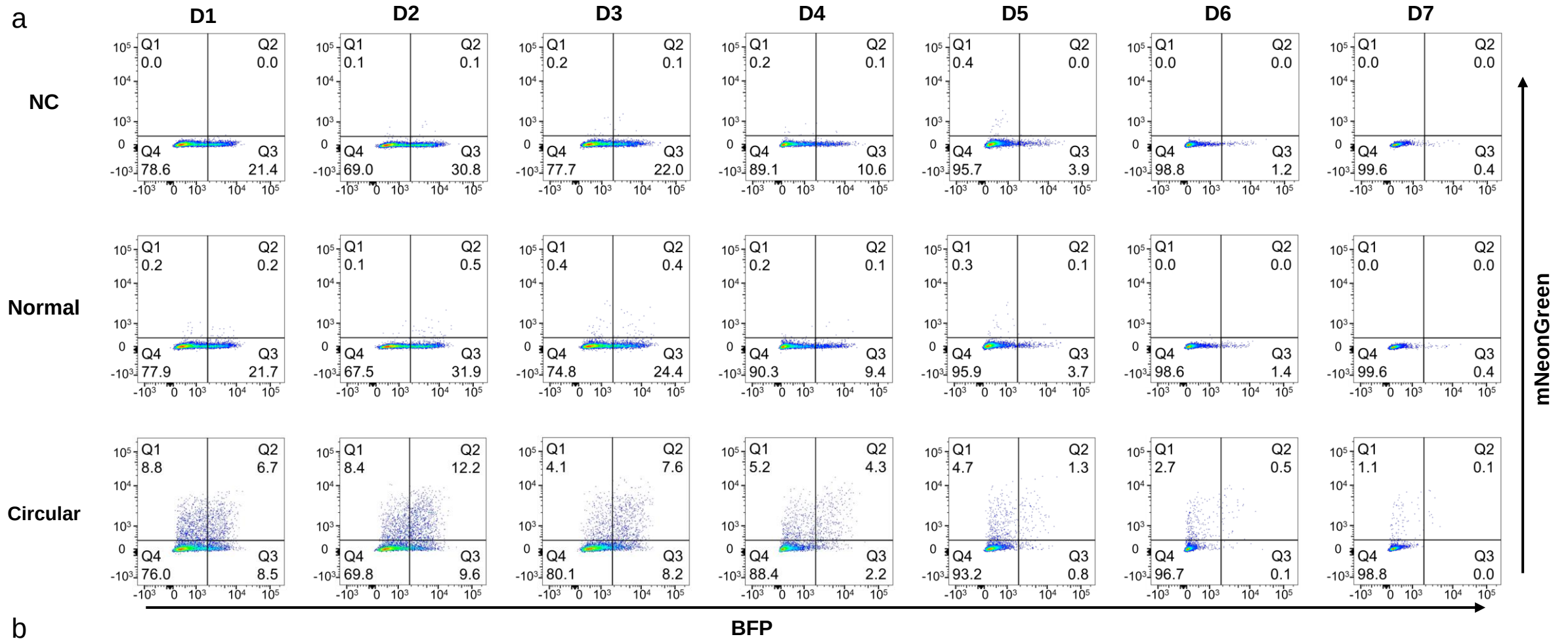
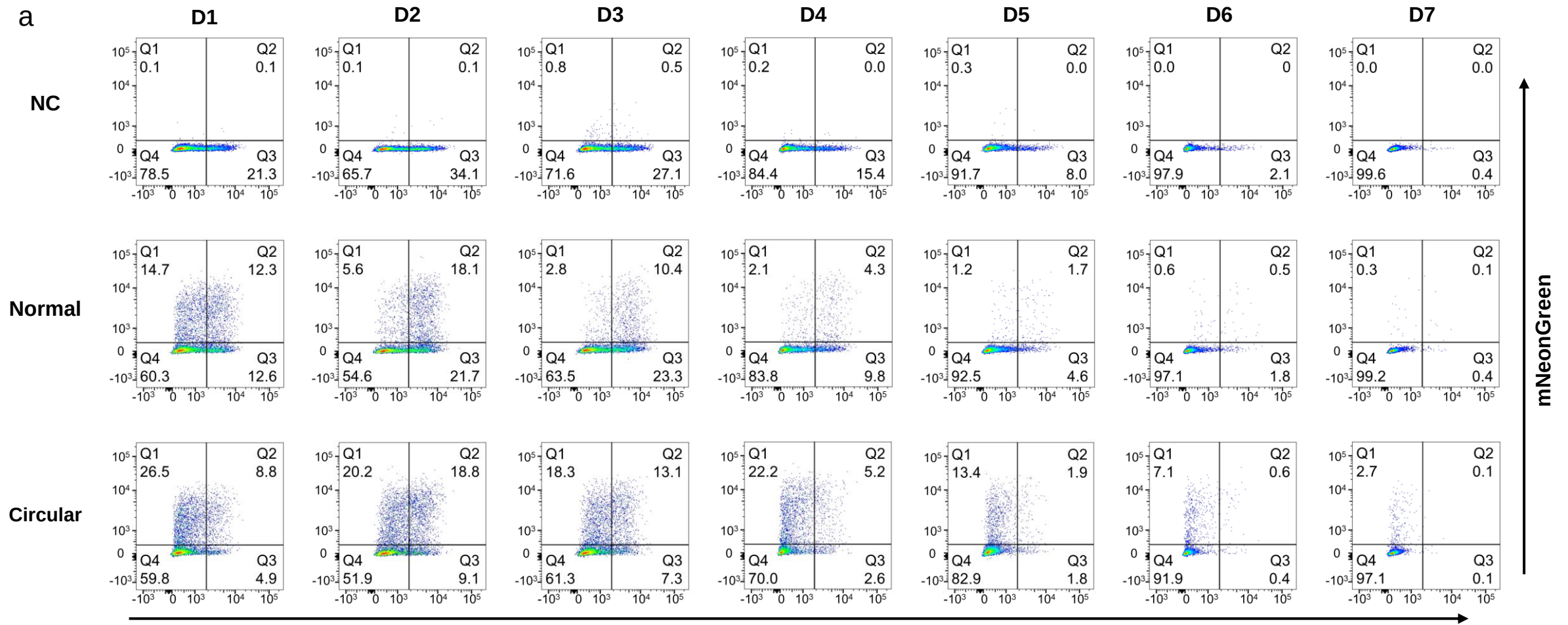


Fig. S4: Time-course analysis of cgRNA-directed gene activation in the G3 reporter cells

Fig. S4: Time-course analysis of cgRNA-directed gene activation in the G3 reporter cells. **a**, FACS analysis showed mNeonGreen expression in the G3 reporter cells post-transfection with 16 ng G3 gRNA plasmids at various time points. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, Student's t -test.



b

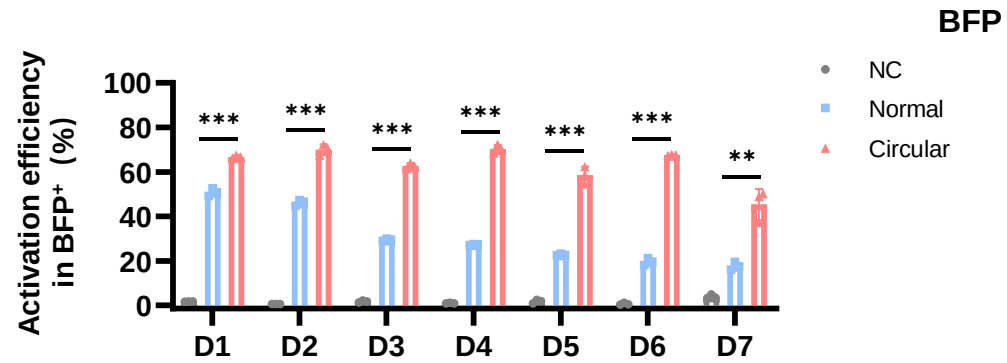


Fig. S5: Time-course analysis of cgRNA-directed gene activation in the G5 reporter cells

Fig. S5: Time-course analysis of cgRNA-directed gene activation in the G5 reporter cells. **a**, FACS analysis showed mNeonGreen expression in the G5 reporter cells post-transfection with 16 ng G5 gRNA plasmids at various time points. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$ Student's *t*-test.

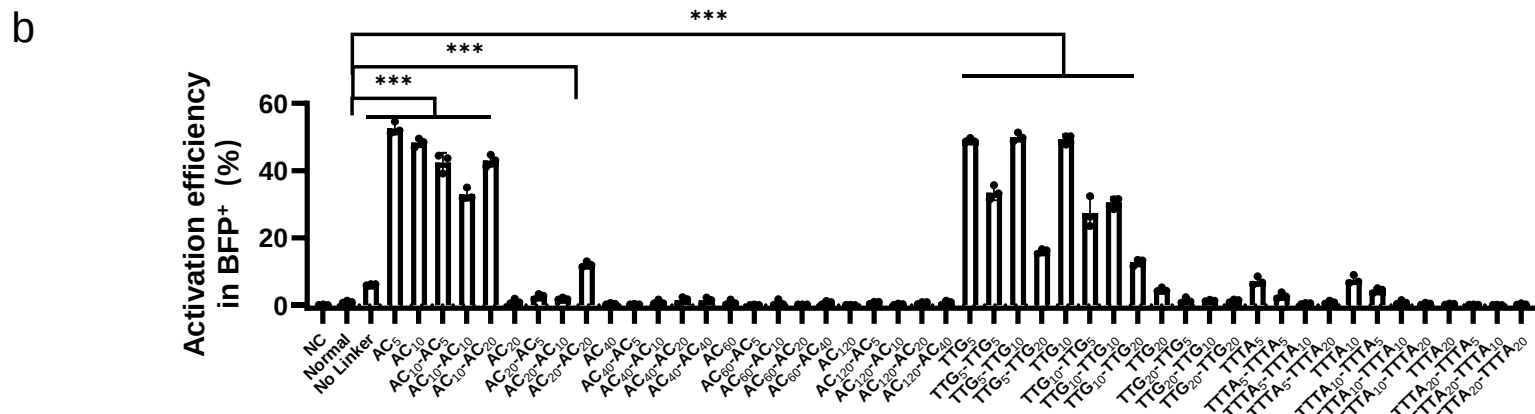
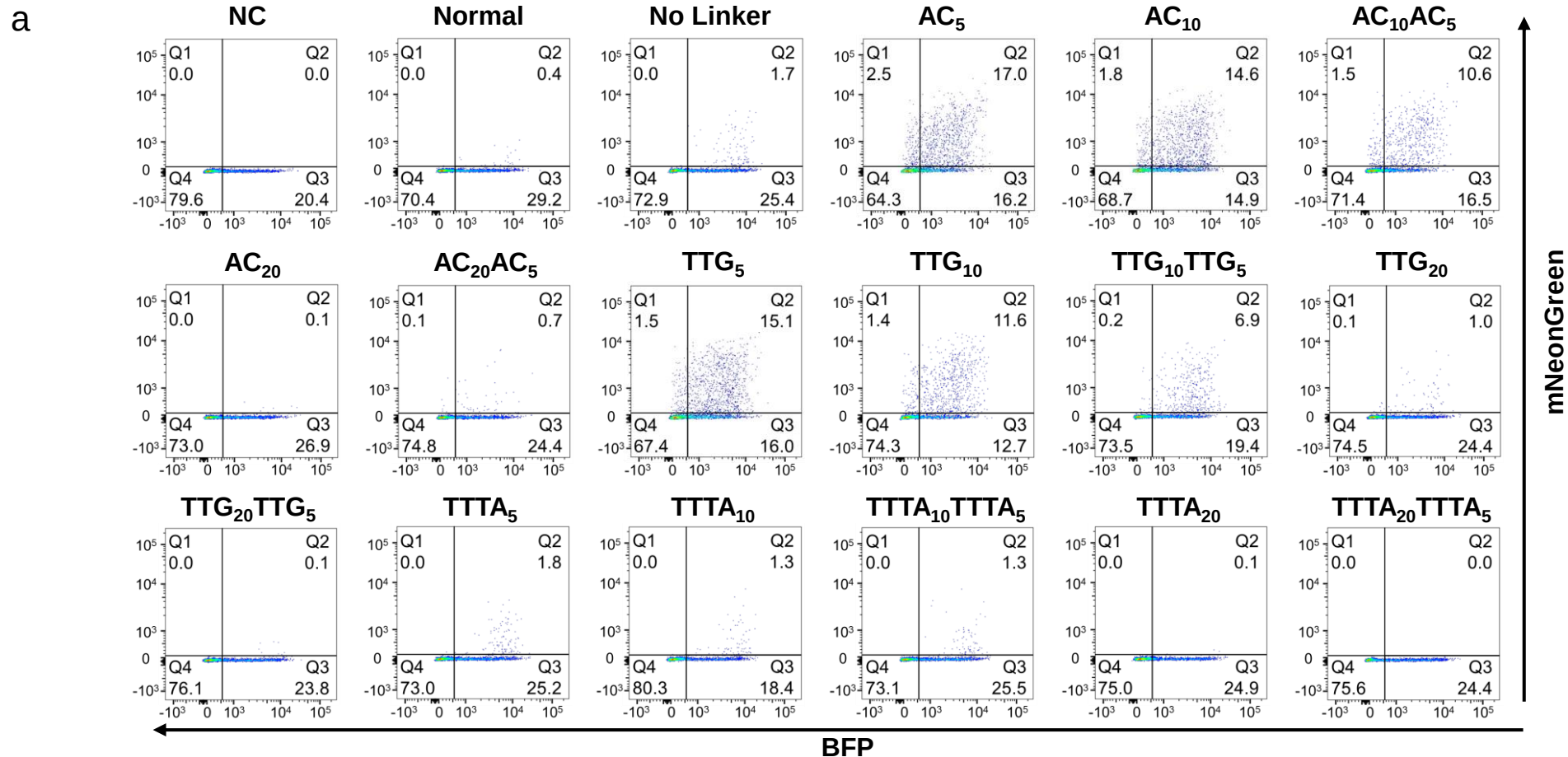
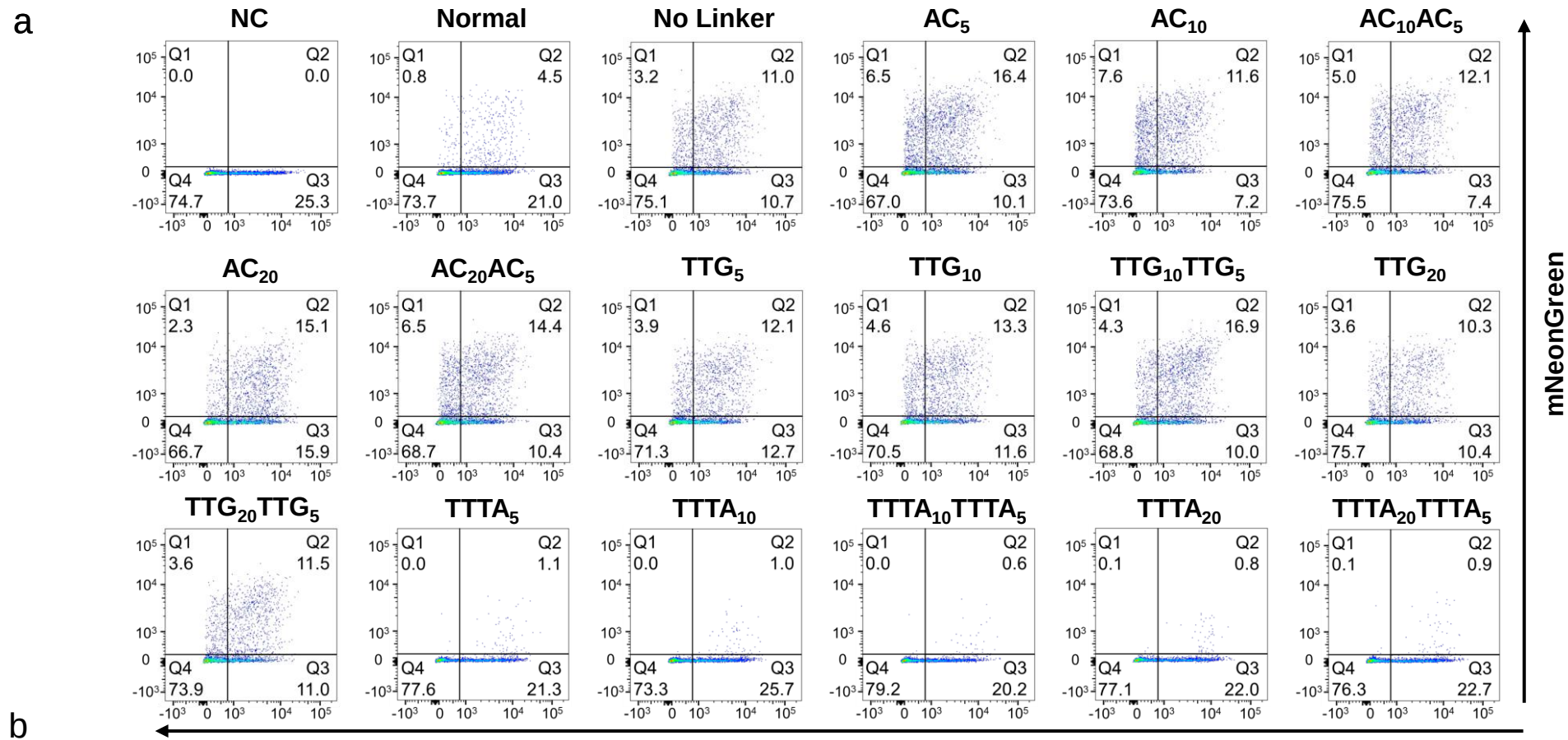


Fig. S6: Gene activation guided by cgRNAs with various linkers in the G3 reporter cells

Fig. S6: Gene activation guided by cgRNAs with various linkers in the G3 reporter cells. **a**, FACS analysis showed mNeonGreen expression in the G3 reporter cells 3 days post-transfection with G3 gRNA plasmids containing various linkers. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, one-way ANOVA test, tested sample versus Normal sample.



b

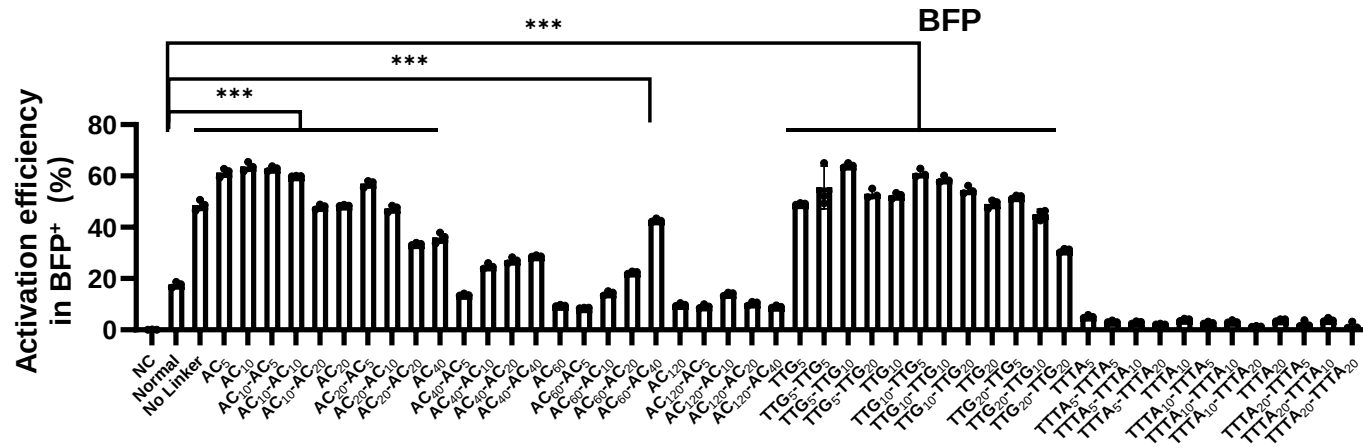


Fig. S7: Gene activation guided by cgRNAs with various linkers in the G5 reporter cells

Fig. S7: Gene activation guided by cgRNAs with various linkers in the G5 reporter cells. **a**, FACS analysis showed mNeonGreen expression in the G5 reporter cells 3 days post-transfection with G5 gRNA plasmids containing various linkers. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, one-way ANOVA test, tested sample versus Normal sample.

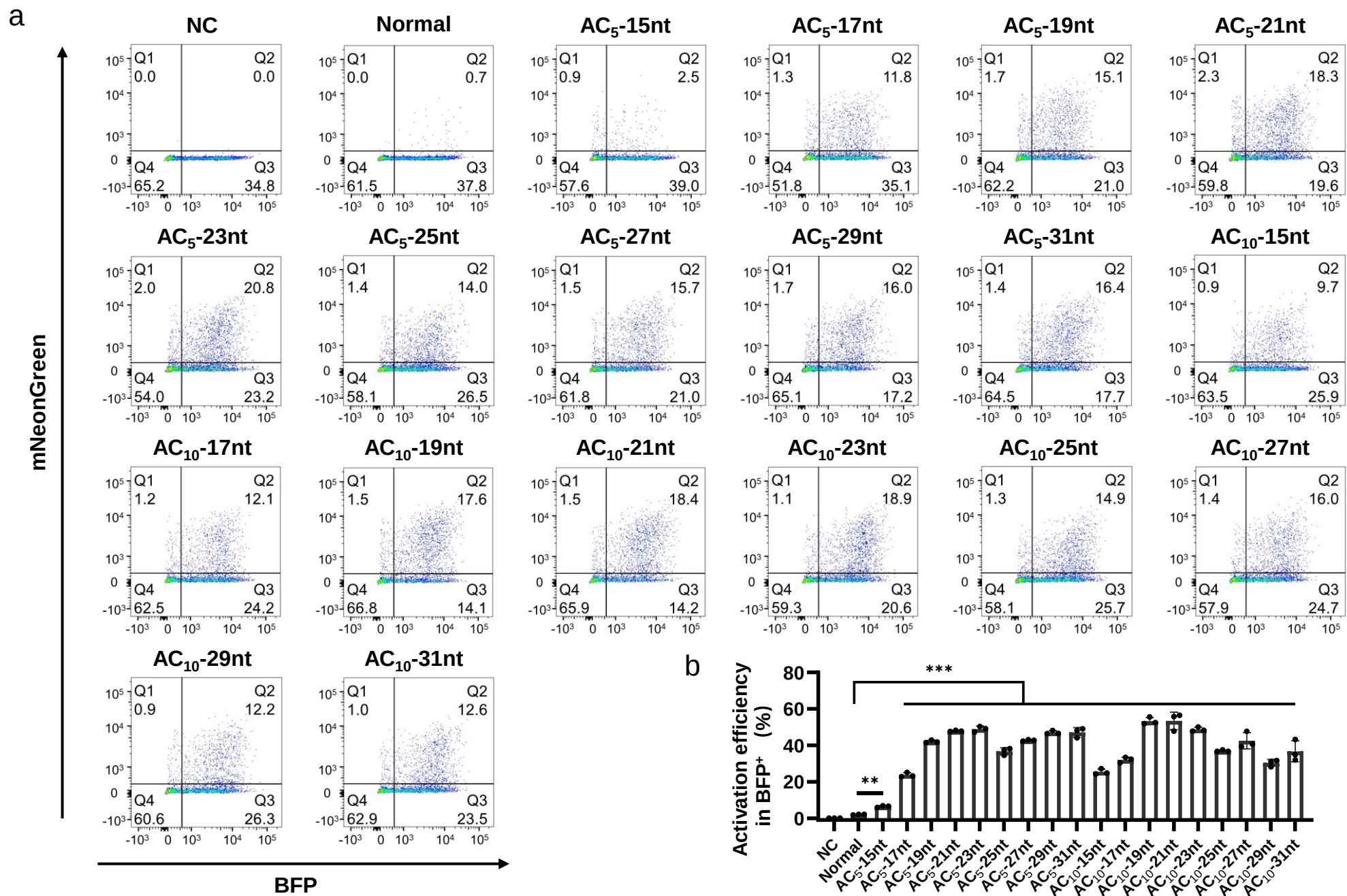


Fig. S8: Gene activation guided by crRNAs with different lengths in the G3 reporter cells

Fig. S8: Gene activation guided by cgRNAs with different lengths in the G3 reporter cells. **a**, FACS analysis showed mNeonGreen expression in the G3 reporter cells 3 days post-transfection with G3 gRNA plasmids containing different lengths. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, one-way ANOVA test, tested sample versus Normal sample.

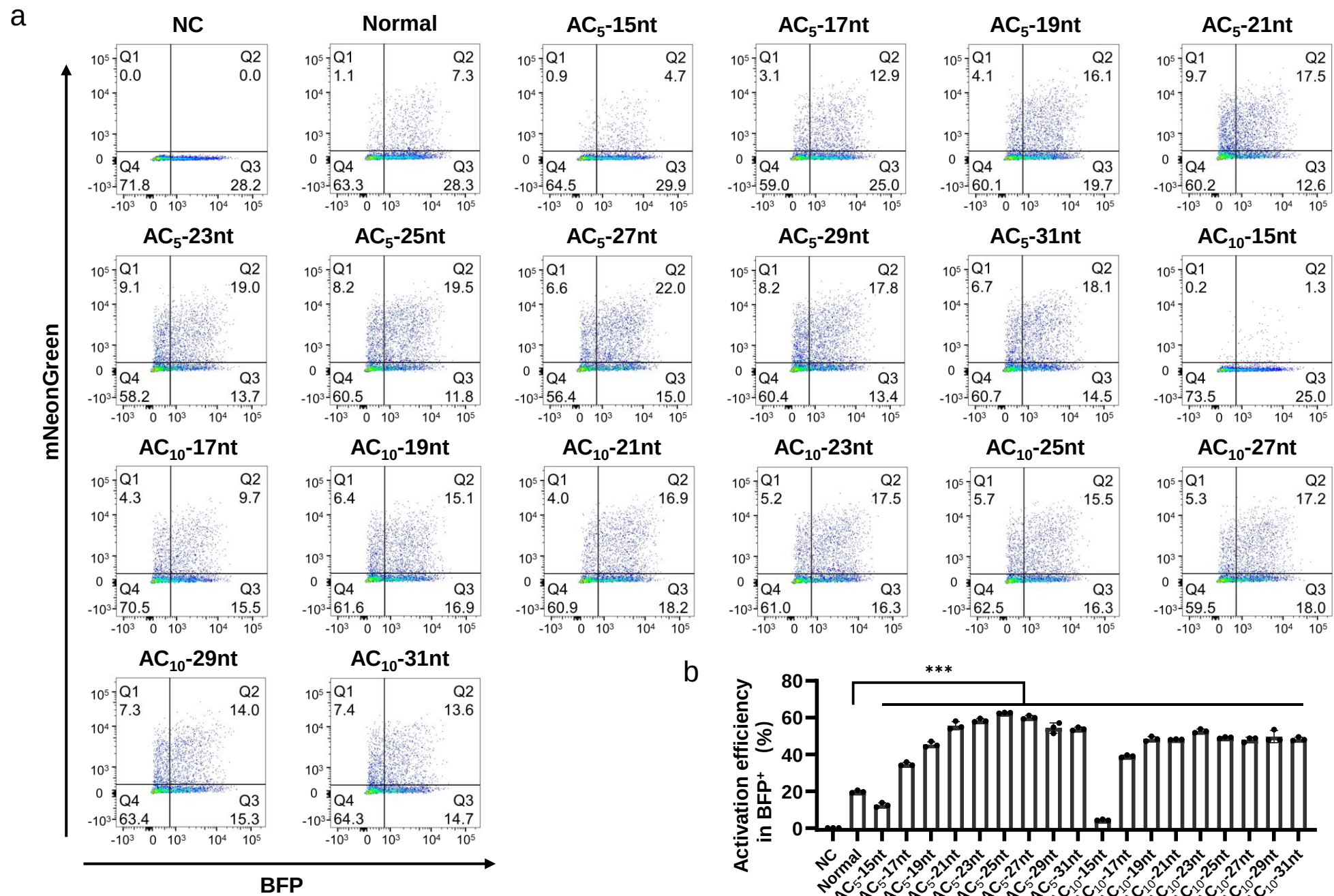
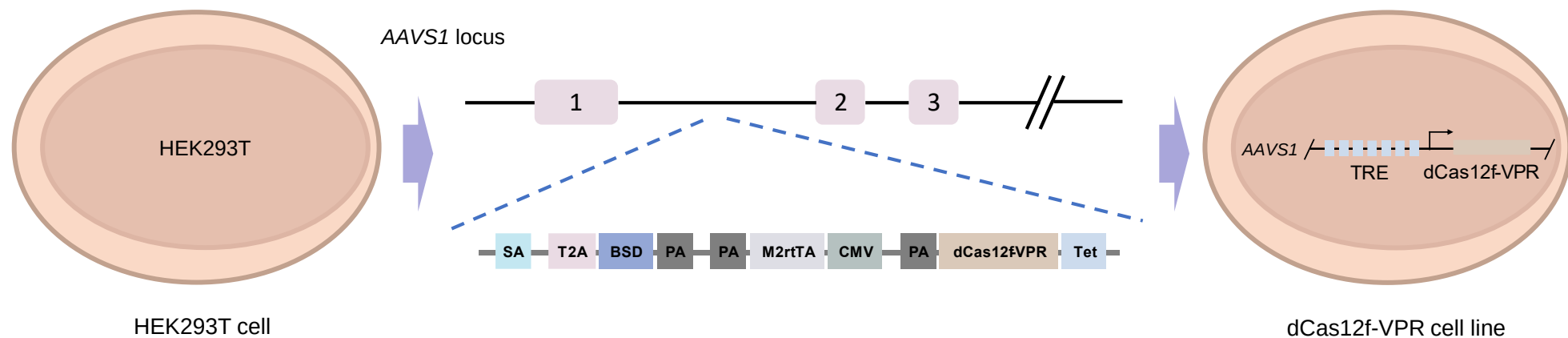


Fig. S9: Gene activation guided by cgRNAs with different lengths in the G5 reporter cells

Fig. S9: Gene activation guided by cgRNAs with different lengths in the G5 reporter cells. **a**, FASC analysis showed mNeonGreen expression in reporter the G5 cells 3 days post-transfection with G5 gRNA plasmids containing different lengths. **b**, Statistical analysis of activation efficiency was performed using the ratio of mNeonGreen⁺ BFP⁺ / BFP⁺ in the FACS assays. n = 3 independent experiments. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, one-way ANOVA test, tested sample versus Normal sample.

a



b

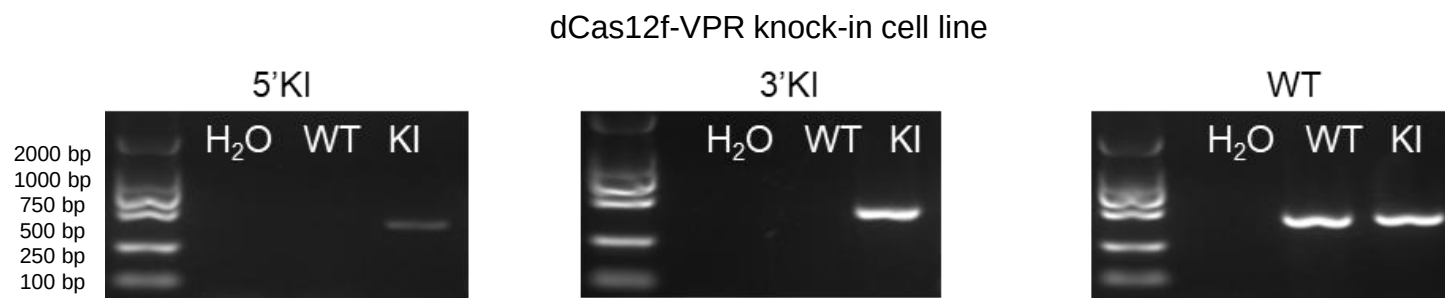


Fig. S10: Establishment of the dCas12f-VPR knock-in cell line

Fig. S10: Establishment of dCas12f-VPR knock-in cell line. **a**, Schematic representation of the dCas12f-VPR knock-in strategy at the *AAVS1* locus in the HEK293T cell . **b**, Identification of knock-in (KI) clones by genomic PCR.

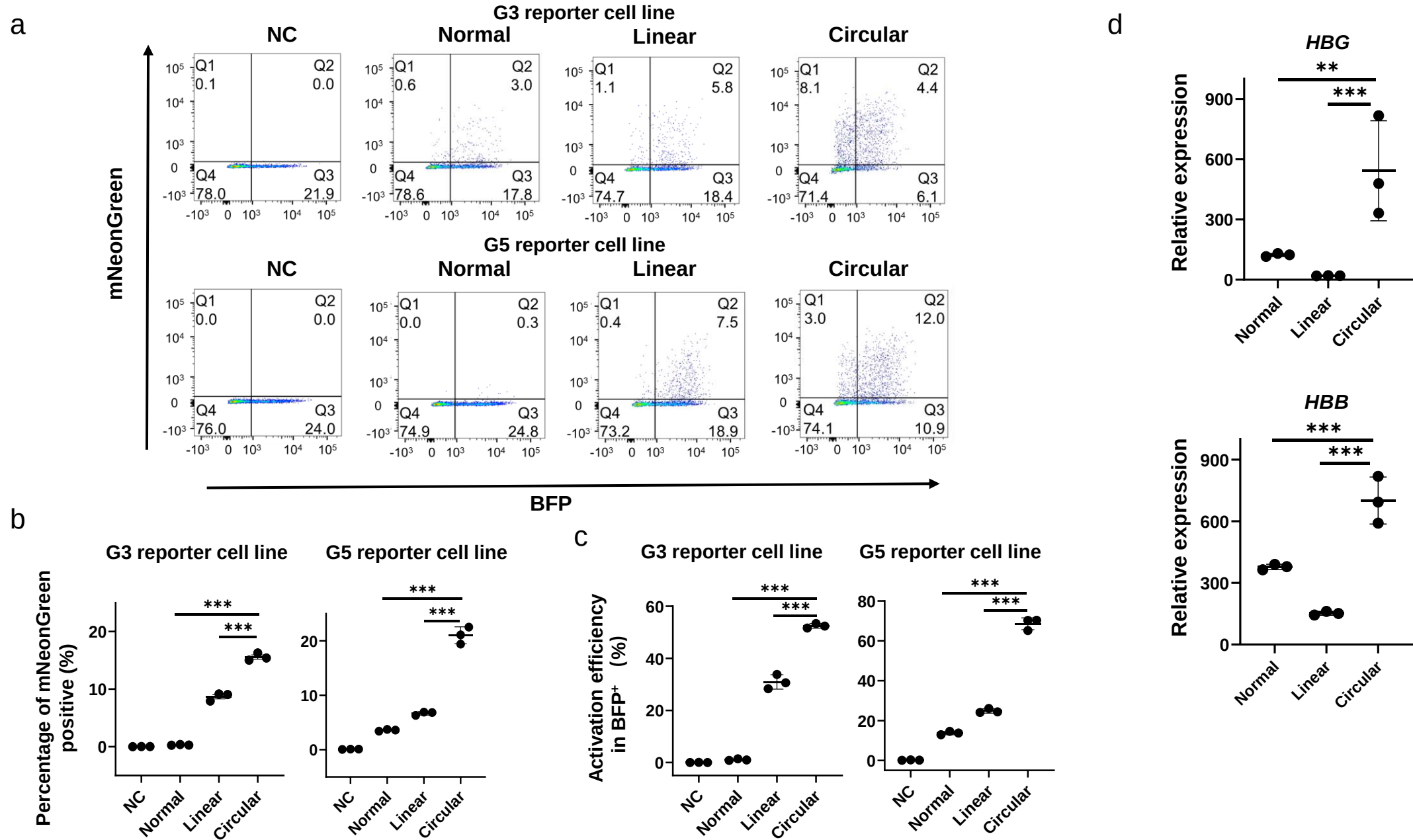


Fig. S11: Circular gRNAs improve the gene expression in Cas12f/ge4.1.

Fig. S11: Circular gRNAs improve the gene expression in Cas12f/ge4.1. **a**, FACS analysis showed mNeonGreen expression in reporter cells 3 days post-transfection with G3 or G5 gRNA plasmids. **b**, Quantification of activation efficiency by the ratio of mNeonGreen-positive cells in FACS assays. **c**, Statistical analysis of activation efficiency was quantified using the ratio of mNeonGreen-positive to BFP-positive cells ($\text{mNeonGreen}^+\text{BFP}^+/\text{BFP}^+$) in the FACS assays. **d**, Targeted gene activation guided by Normal, linear and circular gRNAs in the dCas12f-VPR knock-in (KI) HEK293T cell line transfected with 16 ng gRNAs. For a-d, n = 3 independent experiments. **p < 0.01, ***p < 0.001,, one-way ANOVA test.

a

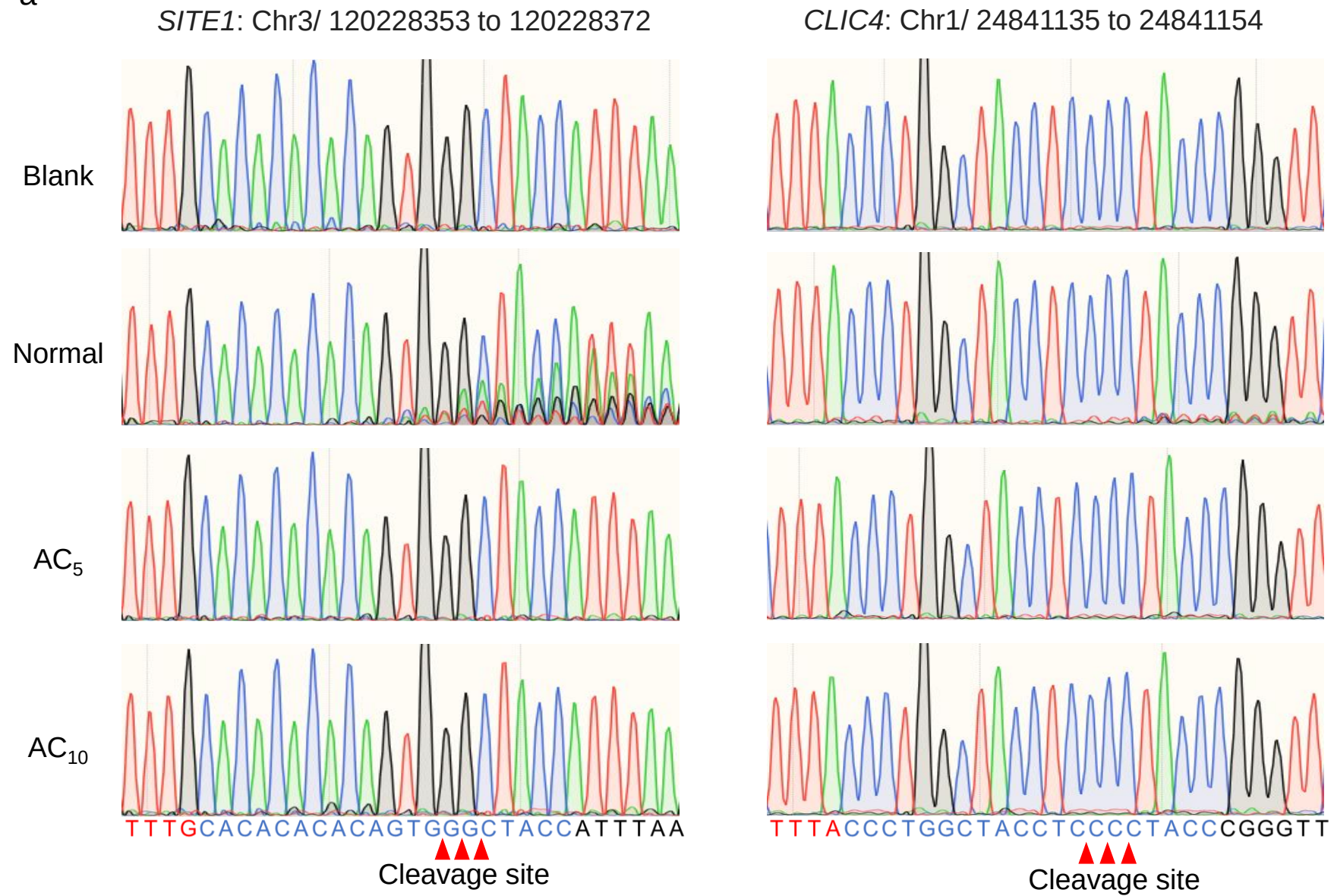


Fig. S12: Circular gRNAs failed to guide Cas12f-dependent DNA cleavage

Fig. S12: Circular gRNAs failed to guide Cas12f-dependent DNA cleavage. a, Sanger-seq revealed the DNA cleavage activity at the *SITE1* and *CLIC4* target sites in the HEK293T cell. The PAM sequences were marked in red, while the spacer sequences were marked in blue.

a

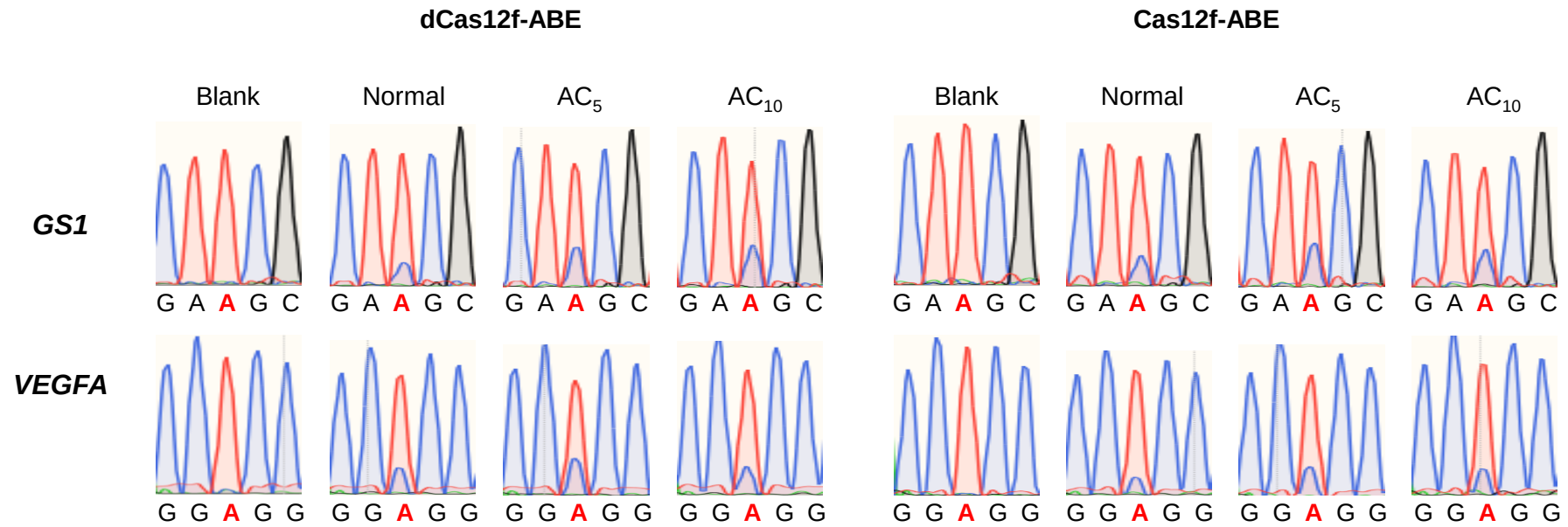


Fig. S13: Circular gRNAs improve the efficiency of A-to-G base editing

Fig. S13: Circular gRNAs improve the efficiency of A-to-G base editing . a, Sanger-seq revealed A-to-G base editing efficiency at targeted gene sites in HEK293T cells using dCas12f-ABE design or Cas12f-ABE design at the A3 location which was marked in red. The R in the TTTR PAM was defined as site 0.

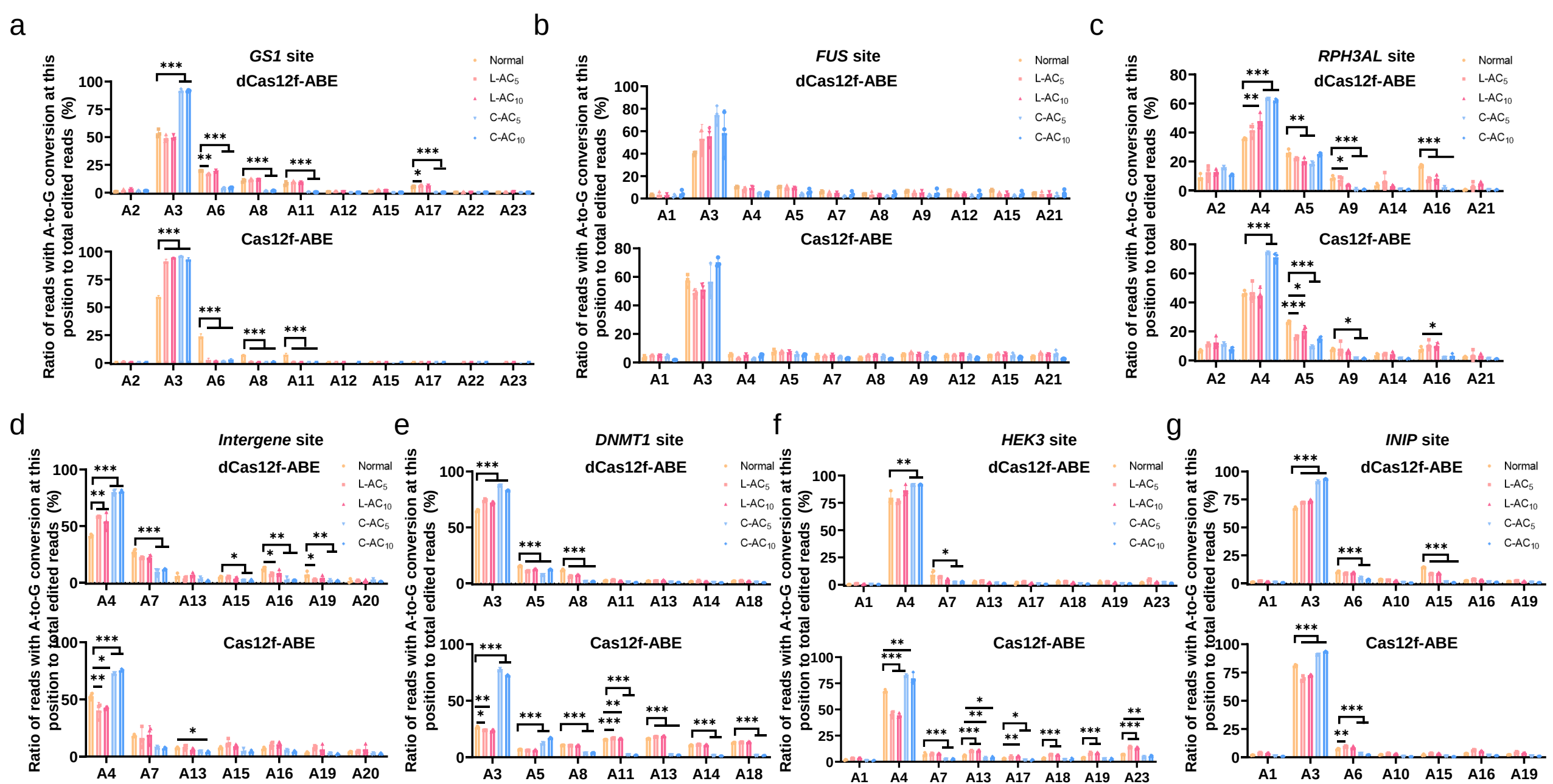


Fig. S14: Circular gRNAs narrow the editing window of A-to-G base editing

Fig. S14: Circular gRNAs narrow the editing window of A-to-G base editing . a-g, Deep-seq analysis of base editing efficiency at each A site in HEK293T cells. The histogram showed the ratio of reads with A-to-G conversion at a specific position to all the edited positions at the indicated 7 target sites. The R in the TTTR PAM was defined as site 0. n = 3 independent experiments. *p <0.05, **p <0.01, ***p <0.001, one-way ANOVA test, tested sample versus Normal gRNA sample.

a

GS1		dCas12f-ABE																						
		G ₁	A ₂	A ₃	G ₄	C ₅	A ₆	C ₇	A ₈	T ₉	C ₁₀	A ₁₁	A ₁₂	G ₁₃	G ₁₄	A ₁₅	C ₁₆	A ₁₇	T ₁₈	T ₁₉	C ₂₀	T ₂₁	A ₂₂	A ₂₃
Blank	A	0.0	99.9	99.7	0.0	0.1	100	0.1	100	0.1	0.1	99.9	99.9	0.0	0.0	100	0.1	99.8	0.1	0.1	0.1	0.0	99.9	99.8
	T	0.1	0.0	0.0	0.2	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.2	0.1	0.0	0.0	0.0	99.6	99.9	0.0	99.9	0.0	0.1
	C	0.0	0.0	0.1	0.0	99.8	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	99.9	0.0	0.1	0.0
	G	99.9	0.0	0.2	99.8	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	99.8	99.9	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0
Normal	A	0.0	99.8	87.7	0.1	0.1	95.5	0.0	97.5	0.1	0.1	98.0	99.8	0.0	0.0	99.8	0.1	98.6	0.1	0.1	0.1	0.0	99.9	99.8
	T	0.1	0.0	0.1	0.2	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.2	0.1	0.0	0.0	0.0	99.6	99.8	0.0	99.7	0.0	0.1
	C	0.0	0.0	0.1	0.0	99.8	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.1	0.1	99.9	0.2	0.1	0.0
	G	99.8	0.2	12.2	99.7	0.0	4.5	0.0	2.5	0.0	0.0	1.9	0.1	99.8	99.9	0.2	0.0	1.2	0.2	0.0	0.0	0.0	0.0	0.0
L-AC ₅	A	0.0	99.6	93.0	0.0	0.0	97.5	0.0	98.3	0.0	0.0	98.6	99.8	0.1	0.0	99.7	0.0	99.0	0.0	0.0	0.0	0.0	99.9	99.9
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	99.9	99.9	0.0	99.8	0.0	0.0
	C	0.0	0.1	0.0	0.0	100	0.0	100	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.1	0.1	100	0.2	0.0	0.0
	G	100	0.3	6.9	100	0.0	2.4	0.0	1.7	0.0	0.0	1.4	0.2	99.9	100	0.3	0.0	1.0	0.0	0.0	0.0	0.0	0.1	0.1
L-AC ₁₀	A	0.0	99.5	91.6	0.0	0.0	96.8	0.0	98.0	0.0	0.0	98.5	99.9	0.0	0.0	99.7	0.0	99.0	0.0	0.0	0.0	0.0	100	99.9
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	99.9	99.9	0.0	99.6	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.1	0.1	100	0.3	0.0	0.0
	G	100	0.4	8.4	100	0.0	3.2	0.0	2.0	0.0	0.0	1.5	0.1	100	100	0.3	0.0	1.0	0.0	0.0	0.0	0.0	0.0	0.1
C-AC ₅	A	0.0	99.5	75.5	0.1	0.1	98.9	0.1	99.6	0.1	0.1	99.8	99.9	0.0	0.0	100	0.1	99.8	0.1	0.1	0.1	0.0	99.9	99.9
	T	0.1	0.1	0.1	0.2	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.2	0.1	0.0	0.0	0.0	99.7	99.9	0.0	99.9	0.0	0.1
	C	0.0	0.0	0.0	0.0	99.8	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	99.9	0.0	0.1	0.0
	G	99.9	0.4	24.4	99.7	0.0	1.1	0.0	0.4	0.0	0.0	0.2	0.0	99.8	99.9	0.0	0.0	0.1	0.2	0.0	0.0	0.0	0.0	0.0
C-AC ₁₀	A	0.0	99.5	73.5	0.1	0.1	98.7	0.1	99.5	0.1	0.1	99.9	99.9	0.0	0.0	100	0.1	99.8	0.1	0.1	0.1	0.0	99.9	99.8
	T	0.1	0.1	0.1	0.2	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.2	0.1	0.0	0.0	0.0	99.7	99.9	0.0	99.9	0.0	0.1
	C	0.0	0.0	0.1	0.0	99.7	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	99.9	0.0	0.1	0.0
	G	99.8	0.4	26.3	99.8	0.0	1.2	0.0	0.5	0.0	0.0	0.1	0.0	99.8	99.9	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0

		Cas12f-ABE																						
		G ₁	A ₂	A ₃	G ₄	C ₅	A ₆	C ₇	A ₈	T ₉	C ₁₀	A ₁₁	A ₁₂	G ₁₃	G ₁₄	A ₁₅	C ₁₆	A ₁₇	T ₁₈	T ₁₉	C ₂₀	T ₂₁	A ₂₂	A ₂₃
Blank	A	0.0	99.9	99.7	0.0	0.1	99.9	0.1	99.9	0.1	0.1	99.9	99.9	0.0	0.0	100	0.1	99.8	0.1	0.1	0.1	0.0	99.9	99.9
	T	0.1	0.0	0.0	0.2	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.0	99.6	99.9	0.0	99.9	0.0	0.1
	C	0.0	0.0	0.0	0.0	99.8	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	99.9	0.0	0.1	0.0
	G	99.9	0.0	0.2	99.8	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	99.8	99.9	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0
Normal	A	0.0	100	92.2	0.0	0.0	96.8	0.0	99.0	0.0	0.0	99.0	99.9	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.1	99.9	99.9
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.8	99.8	0.0	99.1	0.1	0.1
	C	0.0	0.0	0.0	0.0	100	0.0	100	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	100	0.1	0.2	0.1	99.9	0.8	0.0	0.0
	G	100	0.0	7.8	100	0.0	3.2	0.0	1.0	0.0	0.0	1.0	0.1	100	100	0.1	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
L-AC ₅	A	0.0	100	98.4	0.0	0.0	100	0.0	100	0.0	0.0	100	100	0.0	0.0	100	0.0	100	0.0	0.0	0.0	0.0	100	100
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0	100	0.0	0.0
	C	0.0	0.0	0.0	0.0	100	0.0	100	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	100	0.0	0.0	0.0
	G	100	0.0	1.6	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
L-AC ₁₀	A	0.0	99.9	96.6	0.0	0.0	99.9	0.0	100	0.0	0.0	100	100	0.0	0.0	100	0.0	100	0.0	0.0	0.0	0.0	100	100
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0	100	0.0	0.0
	C	0.0	0.0	0.0	0.0	100	0.0	100	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	100	0.0	0.0	0.0
	G	100	0.0	3.4	100	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C-AC ₅	A	0.0	99.9	88.7	0.0	0.0	99.7	0.0	99.9	0.0	0.0	100	100	0.0	0.0	100	0.0	100	0.0	0.0	0.0	0.0	100	100
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0	99.9	0.0	0.0
	C	0.0	0.0	0.0	0.0	100	0.0	100	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	100	0.1	0.0	0.0
	G	100	0.1	11.3	100	0.0	0.3	0.0	0.1	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C-AC ₁₀	A	0.0	99.8	86.3	0.0	0.0	99.5	0.0	99.8	0.0	0.0	99.9	100	0.0	0.0	100	0.0	100	0.0	0.0	0.0	0.0	100	99.9
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	100	0.0	99.9	0.0	0.0
	C	0.0	0.0	0.0	0.0	100	0.0	100	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	100	0.0	0.1	0.0	100	0.1	0.0	0.0
	G	100	0.1	13.7	100	0.0	0.5	0.0	0.2	0.0	0.0	0.1	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

a

FUS

dCas12f-ABE

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃	
Blank	A	99.8	0.0	99.9	99.9	99.8	0.0	99.9	99.9	99.8	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	0.1	0.0	99.8	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
	C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
	G	0.1	0.0	0.1	0.0	0.2	100	0.1	0.1	0.2	0.0	0.0	0.1	99.9	0.0	0.2	100	0.0	100	99.9	0.0	0.2	100	99.9
Normal	A	99.8	0.0	97.1	99.2	99.2	0.0	99.5	99.7	99.5	0.0	0.0	99.4	0.1	0.0	99.4	0.1	0.0	0.1	0.1	0.0	99.6	0.1	0.1
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.7	0.0	0.0	0.2	0.0	0.0	0.0
	C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.8	0.0	0.0	0.3	0.0	0.0	99.8	0.0	0.0	0.0
	G	0.2	0.0	2.9	0.7	0.8	100	0.4	0.3	0.5	0.0	0.0	0.5	99.9	0.0	0.5	99.9	0.0	99.9	99.9	0.0	0.3	99.9	99.9
L-AC ₅	A	99.8	0.0	96.6	99.5	99.4	0.0	99.7	99.8	99.7	0.0	0.0	99.8	0.1	0.0	99.7	0.1	0.0	0.0	0.1	0.0	99.8	0.0	0.1
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
	C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
	G	0.2	0.0	3.3	0.5	0.6	100	0.3	0.2	0.3	0.0	0.0	0.2	99.9	0.0	0.2	99.9	0.0	99.9	99.9	0.0	0.2	100	99.9
L-AC ₁₀	A	99.8	0.0	95.8	99.3	99.3	0.0	99.7	99.8	99.6	0.0	0.0	99.7	0.1	0.0	99.7	0.1	0.0	0.1	0.1	0.0	99.7	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.2	0.0	0.0	0.0
	C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.8	0.0	0.0	0.0
	G	0.2	0.0	4.2	0.7	0.7	100	0.3	0.2	0.3	0.0	0.0	0.3	99.9	0.0	0.3	99.9	0.0	99.9	99.9	0.0	0.3	100	99.9
C-AC ₅	A	99.8	0.0	93.3	99.5	99.6	0.0	99.8	99.8	99.8	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	0.1	0.0	99.7	0.0	0.1
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
	C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
	G	0.2	0.0	6.7	0.4	0.3	100	0.2	0.2	0.2	0.0	0.0	0.2	99.9	0.0	0.2	100	0.0	99.9	99.9	0.0	0.2	100	99.9
C-AC ₁₀	A	99.8	0.0	96.1	99.7	99.6	0.0	99.8	99.8	99.7	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.1	0.1	0.0	99.7	0.0	0.1
	T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.7	0.0	0.0	0.2	0.0	0.0	0.0
	C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.3	0.0	0.0	99.8	0.0	0.0	0.0
	G	0.2	0.0	3.9	0.3	0.3	100	0.2	0.2	0.2	0.0	0.0	0.2	99.9	0.0	0.2	99.9	0.0	99.9	99.9	0.0	0.2	99.9	99.9

Cas12f-ABE

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃
A	99.9	0.0	99.7	99.9	99.8	0.0	99.9	99.9	99.8	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	0.1	0.0	99.8	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
G	0.1	0.0	0.2	0.1	0.2	100	0.1	0.1	0.1	0.0	0.0	0.1	99.9	0.0	0.2	100	0.0	100	99.9	0.0	0.2	100	100

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃
A	99.8	0.0	97.3	99.7	99.6	0.0	99.8	99.9	99.7	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	0.1	0.0	99.8	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.7	0.0	0.0	0.1	0.0	0.0	0.0
C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.3	0.0	0.0	99.9	0.0	0.0	0.0
G	0.2	0.0	2.7	0.2	0.4	100	0.2	0.1	0.3	0.0	0.0	0.2	99.9	0.0	0.2	100	0.0	99.9	99.9	0.0	0.2	99.9	99.9

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃
A	99.9	0.0	98.8	99.9	99.8	0.0	99.9	99.9	99.8	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	0.1	0.0	99.8	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
G	0.1	0.0	1.2	0.1	0.2	100	0.1	0.1	0.2	0.0	0.0	0.1	99.9	0.0	0.2	100	0.0	100	99.9	0.0	0.2	100	100

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃
A	99.8	0.0	98.5	99.8	99.8	0.0	99.8	99.8	99.8	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	0.1	0.0	99.8	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
G	0.1	0.0	1.5	0.1	0.2	100	0.1	0.2	0.2	0.0	0.0	0.2	99.9	0.0	0.2	100	0.0	100	99.9	0.0	0.2	100	99.9

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃
A	99.8	0.0	97.4	99.9	99.7	0.0	99.8	99.8	99.7	0.0	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.1	0.1	0.0	99.7	0.0	0.1
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
C	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.8	0.0	0.0	0.0
G	0.2	0.0	2.6	0.1	0.2	100	0.2	0.2	0.3	0.0	0.0	0.2	99.9	0.0	0.2	99.9	0.0	99.9	99.9	0.0	0.3	99.9	99.9

	A ₁	C ₂	A ₃	A ₄	A ₅	G ₆	A ₇	A ₈	A ₉	C ₁₀	C ₁₁	A ₁₂	G ₁₃	C ₁₄	A ₁₅	G ₁₆	T ₁₇	G ₁₈	G ₁₉	C ₂₀	A ₂₁	G ₂₂	G ₂₃
A	99.9	0.0	95.1	99.6	99.6	0.0	99.8	99.8	99.8	0.0	0.0	99.8	0.1	0.0	99.7	0.1	0.0	0.0	0.1	0.0	99.8	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	0.0	0.0	0.1	0.0	0.0	99.8	0.0	0.0	0.1	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	0.2	0.0	0.0	99.9	0.0	0.0	0.0
G	0.1	0.0	4.8	0.4	0.4	100	0.2	0.2	0.2	0.0	0.0	0.2	99.9	0.0	0.3	99.9	0.0	100	99.9	0.0	0.2	99.9	99.9

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

a

RPH3AL

dCas12f-ABE

Blank

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	99.9	0.0	99.9	99.9	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0
G	0.0	0.1	0.0	0.1	0.1	100	99.9	99.9	0.1	0.0	0.0	0.0	100	0.1	100	0.2	0.0	0.0	0.0	100	0.1	100	100

Normal

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	98.9	0.0	95.8	96.9	0.0	0.0	0.0	99.0	0.0	0.0	0.0	0.0	99.6	0.0	98.0	0.0	0.0	0.0	0.0	100	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.8	99.8	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	0.0	100	0.1	0.2	0.0	0.0	0.0	0.0
G	0.0	1.1	0.0	4.2	3.1	100	99.9	100	1.0	0.0	0.0	0.0	100	0.4	100	2.0	0.0	0.0	0.0	100	0.0	100	100

L-AC₅

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃	
A	0.0	99.6	0.0	98.8	99.3	0.0	0.0	0.0	99.8	0.0	0.0	0.0	0.0	99.8	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0
T	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	100	0.0	0.0	0.0	0.0	0.0
C	99.9	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0
G	0.0	0.4	0.0	1.2	0.7	100	100	100	0.2	0.0	0.0	0.0	100	0.2	100	0.2	0.0	0.0	0.0	100	0.1	100	100	0.0

L-AC₁₀

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃	
A	0.0	99.4	0.0	97.6	99.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	99.6	0.0	0.0	0.0	0.0	99.8	0.1	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.1	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	0.0	100	0.1	0.1	0.0	0.0	0.0	0.0	0.0
G	0.0	0.6	0.0	2.3	1.0	100	100	100	0.2	0.0	0.0	0.0	100	0.1	100	0.4	0.0	0.0	0.0	100	0.2	99.9	100	0.0

C-AC₅

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	97.5	0.0	89.9	97.0	0.1	0.1	0.0	99.9	0.0	0.0	0.1	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0
C	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.0	0.1	0.0	0.0	0.0	0.0
G	0.0	2.5	0.0	10.1	2.9	99.9	99.9	100	0.1	0.0	0.0	0.0	100	0.1	100	0.2	0.0	0.0	0.0	100	0.1	100	100

C-AC₁₀

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	97.9	0.0	87.7	95.0	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	100	99.9	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.2	100	0.1	0.0	0.0	0.0	0.0	100	0.0	0.1	0.0	0.0	0.0	0.0
G	0.0	2.1	0.0	12.3	5.0	100	100	99.9	0.1	0.0	0.0	0.0	100	0.1	100	0.1	0.0	0.0	0.0	100	0.1	100	100

Cas12f-ABE

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	99.9	0.0	99.9	99.9	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.1	0.1	0.0	0.0	0.0	0.0
G	0.0	0.1	0.0	0.1	0.1	99.9	100	99.9	0.1	0.0	0.0	0.0	100	0.1	100	0.2	0.0	0.0	0.0	100	0.1	100	100

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	99.8	0.0	98.3	99.0	0.0	0.0	0.0	99.7	0.0	0.0	0.0	0.0	99.9	0.0	99.7	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.1	0.1	0.0	0.0	0.0	0.0
G	0.0	0.2	0.0	1.7	1.0	99.9	100	99.9	0.3	0.0	0.0	0.0	100	0.1	100	0.3	0.0	0.0	0.0	100	0.1	99.9	100

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	99.8	0.0	98.9	99.6	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0
C	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	0.0	0.0
G	0.0	0.2	0.0	1.1	0.3	100	100	100	0.1	0.0	0.0	0.0	100	0.1	100	0.2	0.0	0.0	0.0	100	0.0	99.9	100

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	99.8	0.0	99.2	99.7	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.0	0.1	0.0	0.0	0.0	0.0
G	0.0	0.2	0.0	0.8	0.3	100	100	100	0.1	0.0	0.0	0.0	100	0.1	100	0.2	0.0	0.0	0.0	100	0.1	100	100

	C ₁	A ₂	C ₃	A ₄	A ₅	G ₆	G ₇	G ₈	A ₉	T ₁₀	C ₁₁	T ₁₂	G ₁₃	A ₁₄	G ₁₅	A ₁₆	C ₁₇	T ₁₈	T ₁₉	G ₂₀	A ₂₁	G ₂₂	G ₂₃
A	0.0	99.1	0.0	94.0	99.2	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.9	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0
C	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	0.1	0.0	0.0	0.0	0.0	100	0.1	0.1	0.0	0.0	0.0	0.0
G	0.0	0.9	0.0	6.0	0.7	100	100	100	0.1	0.0	0.0	0.0	100	0.1	100	0.2	0.0	0.0	0.0	100	0.1	100	100

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		dCas12f-ABE																						
		C ₁	T ₂	T ₃	A ₄	G ₅	T ₆	A ₇	G ₈	T ₉	C ₁₀	T ₁₁	C ₁₂	A ₁₃	G ₁₄	A ₁₅	A ₁₆	C ₁₇	C ₁₈	A ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
Blank	A	0.0	0.0	0.0	99.9	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.8	0.0	99.8	99.8	0.0	0.0	99.9	99.9	0.1	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	99.9	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	0.1	100	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.2	0.2	0.0	0.0	0.1	0.1	99.9	100	99.9
Normal	A	0.0	0.0	0.0	97.6	0.0	0.0	98.4	0.1	0.0	0.0	0.0	0.0	99.7	0.0	99.7	99.3	0.0	0.0	99.6	99.9	0.0	0.1	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	99.9	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	2.4	100	0.0	1.6	99.9	0.0	0.0	0.0	0.0	0.3	100	0.3	0.7	0.0	0.0	0.4	0.1	100	99.9	99.9
L-AC ₅	A	0.0	0.0	0.0	97.6	0.0	0.0	99.1	0.1	0.0	0.0	0.0	0.0	99.9	0.0	99.8	99.7	0.0	0.0	99.9	99.9	0.0	0.0	0.0
	T	0.0	99.8	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.8	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	99.9	99.9	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	2.4	99.9	0.0	0.9	99.9	0.0	0.0	0.0	0.0	0.1	100	0.2	0.3	0.0	0.0	0.1	0.1	99.9	100	100
L-AC ₁₀	A	0.0	0.0	0.0	98.3	0.0	0.0	99.3	0.0	0.0	0.0	0.0	0.0	99.8	0.0	99.9	99.7	0.0	0.0	99.9	100	0.1	0.0	0.1
	T	0.0	99.9	100	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.0	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	1.7	99.9	0.0	0.7	100	0.0	0.0	0.0	0.0	0.2	100	0.1	0.3	0.0	0.0	0.1	0.0	99.9	100	99.9
C-AC ₅	A	0.0	0.0	0.0	96.0	0.1	0.0	99.5	0.0	0.0	0.0	0.0	0.0	99.8	0.0	99.9	99.9	0.0	0.0	99.9	99.9	0.0	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	4.0	99.9	0.0	0.5	99.9	0.0	0.0	0.0	0.0	0.2	100	0.1	0.1	0.0	0.0	0.1	0.1	99.9	100	99.9
C-AC ₁₀	A	0.0	0.0	0.0	94.1	0.1	0.0	99.1	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	99.8	0.0	0.0	99.9	99.9	0.1	0.0	0.0
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	99.9	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	5.9	99.9	0.0	0.9	100	0.0	0.0	0.0	0.0	0.1	100	0.1	0.2	0.0	0.0	0.1	0.1	99.9	99.9	100

		Cas12f-ABE																						
		C ₁	T ₂	T ₃	A ₄	G ₅	T ₆	A ₇	G ₈	T ₉	C ₁₀	T ₁₁	C ₁₂	A ₁₃	G ₁₄	A ₁₅	A ₁₆	C ₁₇	C ₁₈	A ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
Blank	A	0.0	0.0	0.0	99.9	0.1	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.8	0.0	99.8	99.8	0.0	0.0	99.9	99.9	0.1	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.8	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.2	100	0.0	0.0	0.0	0.0	99.9	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	0.1	99.9	0.0	0.1	99.9	0.0	0.0	0.0	0.0	0.1	100	0.2	0.2	0.0	0.0	0.1	0.1	99.9	99.9	99.9
Normal	A	0.0	0.0	0.0	99.0	0.0	0.0	99.7	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.8	99.9	0.0	0.0	99.9	99.9	0.0	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.1	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	0.9	100	0.0	0.3	100	0.0	0.0	0.0	0.0	0.1	100	0.1	0.1	0.0	0.0	0.1	0.1	99.9	100	99.9
L-AC ₅	A	0.0	0.0	0.0	99.6	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	99.9	0.0	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	0.4	100	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.1	0.1	0.0	0.0	0.1	0.0	100	100	99.9
L-AC ₁₀	A	0.0	0.0	0.0	99.5	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	99.9	0.0	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	100	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	0.5	100	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.1	0.1	0.0	0.0	0.1	0.1	100	100	99.9
C-AC ₅	A	0.0	0.0	0.0	98.1	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	99.9	0.0	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	1.9	99.9	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.1	0.1	0.0	0.0	0.1	0.1	99.9	99.9	99.9
C-AC ₁₀	A	0.0	0.0	0.0	98.1	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	99.9	0.0	0.0	0.1
	T	0.0	99.9	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	C	100	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.2	100	0.1	100	0.0	0.0	0.0	0.0	99.9	100	0.0	0.0	0.0	0.0	0.0
	G	0.0	0.0	0.0	1.9	100	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.1	0.1	0.0	0.0	0.0	0.1	100	100	99.9

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

a

LOC105370393

dCas12f-ABE

Blank

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.1	0.0	99.9	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.8	99.9	0.0	99.9	0.1	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	100	0.0	99.9	99.9	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	99.9	0.0	0.1	99.9	0.0	0.1	0.0	0.2	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.1	0.0	0.1	99.9	100	100

Normal

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	94.1	0.0	0.0	95.2	0.0	95.7	0.0	0.0	0.0	0.1	97.7	0.0	0.0	0.0	98.6	99.1	0.0	99.3	0.1	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	99.9	0.0	100	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	100	0.0	5.9	100	0.0	4.8	0.0	4.3	0.0	0.0	0.0	99.9	2.3	100	100	100	1.4	0.9	0.0	0.7	99.9	100	100

L-AC₅

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.1	0.0	96.7	0.0	0.0	97.8	0.0	97.9	0.0	0.0	0.0	0.0	99.0	0.0	0.0	0.0	99.3	99.6	0.0	99.7	0.1	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.0	0.0	100	0.0	100	99.9	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	99.9	0.0	3.3	100	0.0	2.2	0.0	2.1	0.0	0.0	0.0	100	1.0	100	100	100	0.7	0.4	0.0	0.3	99.9	100	99.9

L-AC₁₀

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	94.2	0.1	0.0	95.7	0.0	96.5	0.0	0.0	0.0	0.0	98.1	0.0	0.0	0.0	99.0	99.4	0.0	99.7	0.0	0.0	0.0
T	0.0	0.1	0.0	0.0	100	0.0	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.0	0.0	99.9	0.0	100	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	100	0.0	5.8	99.9	0.0	4.3	0.0	3.5	0.0	0.0	0.0	99.9	1.9	100	100	100	1.0	0.6	0.0	0.3	100	100	100

C-AC₅

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	89.8	0.1	0.0	98.6	0.0	99.6	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.8	99.8	0.0	99.9	0.0	0.0	0.1
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	100	0.0	99.9	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	100	0.0	10.2	99.9	0.0	1.4	0.0	0.4	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.2	0.0	0.1	100	100	99.9

C-AC₁₀

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	86.6	0.0	0.0	95.5	0.0	98.6	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.8	99.9	0.0	99.9	0.0	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.1	0.0	0.1	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	99.9	0.0	99.9	99.9	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0
G	100	0.0	13.4	100	0.0	4.5	0.0	1.4	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.1	0.0	0.1	100	100	100

Cas12f-ABE

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.1	0.0	99.9	0.0	0.0	99.9	0.0	99.8	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.8	99.8	0.0	99.9	0.0	0.0	0.1
T	0.0	0.1	0.0	0.0	99.9	0.0	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	99.9	0.0	99.9	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	99.9	0.0	0.1	100	0.0	0.1	0.0	0.2	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.2	0.0	0.1	99.9	100	99.9

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	96.0	0.1	0.0	98.2	0.0	98.9	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.7	99.8	0.0	99.9	0.0	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	100	0.0	100	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	100	0.0	4.0	99.9	0.0	1.8	0.0	1.1	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.2	0.0	0.1	99.9	99.9	99.9

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	98.2	0.1	0.0	99.4	0.0	99.4	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.8	99.8	0.0	99.9	0.0	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	100	0.0	100	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	99.9	0.0	1.7	99.9	0.0	0.6	0.0	0.6	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.1	0.0	0.1	99.9	100	100

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.1	0.0	97.3	0.0	0.0	99.0	0.0	99.2	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.8	99.8	0.0	99.9	0.0	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	100	0.0	99.9	100	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	99.9	0.0	2.7	100	0.0	1.0	0.0	0.8	0.0	0.0	0.0	100	0.2	100	100	100	0.2	0.1	0.0	0.1	99.9	99.9	99.9

	G ₁	C ₂	A ₃	G ₄	T ₅	A ₆	C ₇	A ₈	C ₉	C ₁₀	T ₁₁	G ₁₂	A ₁₃	G ₁₄	G ₁₅	G ₁₆	A ₁₇	A ₁₈	C ₁₉	A ₂₀	G ₂₁	G ₂₂	G ₂₃
A	0.0	0.0	91.2	0.0	0.0	98.9	0.0	99.6	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.9	99.9	0.0	99.9	0.1	0.0	0.0
T	0.0	0.1	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0
C	0.0	99.9	0.0	0.0	0.1	0.0	100	0.0	100	99.9	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0
G	100	0.0	8.8	100	0.0	1.1	0.0	0.4	0.0	0.0	0.0	100	0.1	100	100	100	0.1	0.1	0.0	0.1	99.9	100	100

a

DNMT1

dCas12f-ABE

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃	
Blank	A	0.1	0.0	99.8	0.0	100	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.8	99.9	0.0	0.0	0.0	99.8	0.1	0.0	0.0	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
	C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	99.9	99.9	0.1	0.1
	G	99.9	100	0.2	0.0	0.0	0.0	0.0	0.1	100	100	0.2	100	0.2	0.1	0.0	0.0	100	0.2	99.9	0.0	0.0	0.0	0.0
Normal	A	0.1	0.0	94.9	0.0	98.8	0.0	0.0	99.1	0.0	0.0	99.8	0.0	99.8	99.9	0.0	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	99.9	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
	C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
	G	99.9	100	5.1	0.0	1.2	0.0	0.0	0.9	100	100	0.2	100	0.2	0.1	0.0	0.0	100	0.2	100	0.0	0.0	0.0	0.0
L-AC ₅	A	0.0	0.0	96.1	0.0	99.4	0.0	0.0	99.7	0.0	0.0	99.8	0.0	99.9	99.9	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
	C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
	G	99.9	100	3.9	0.0	0.6	0.0	0.0	0.3	100	100	0.1	100	0.1	0.1	0.0	0.0	100	0.1	100	0.0	0.0	0.0	0.0
L-AC ₁₀	A	0.0	0.0	95.4	0.0	99.2	0.0	0.0	99.5	0.0	0.0	99.8	0.0	99.8	99.9	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
	C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
	G	100	100	4.6	0.0	0.8	0.0	0.0	0.5	100	100	0.1	100	0.2	0.1	0.0	0.0	100	0.1	99.9	0.0	0.0	0.0	0.0
C-AC ₅	A	0.1	0.0	87.9	0.0	98.9	0.0	0.0	99.8	0.0	0.0	99.8	0.0	99.9	99.9	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
	C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
	G	99.9	100	12.0	0.0	1.1	0.0	0.0	0.2	100	100	0.1	100	0.1	0.1	0.0	0.0	100	0.1	100	0.0	0.0	0.0	0.0
C-AC ₁₀	A	0.0	0.0	86.3	0.0	97.9	0.0	0.0	99.7	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0
	T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
	C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
	G	100	100	13.7	0.0	2.1	0.0	0.0	0.3	100	100	0.1	100	0.1	0.1	0.0	0.0	100	0.1	100	0.0	0.0	0.0	0.0

Cas12f-ABE

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃
A	0.1	0.0	99.7	0.0	99.9	0.0	0.0	99.9	0.0	0.0	99.8	0.0	99.8	99.9	0.0	0.0	0.0	99.8	0.1	0.0	0.0	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.1	0.0	99.8	99.9
C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
G	99.9	100	0.3	0.0	0.1	0.0	0.0	0.1	100	100	0.2	100	0.2	0.1	0.0	0.0	100	0.2	99.9	0.0	0.0	0.0	0.0

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃
A	0.1	0.0	99.5	0.0	99.9	0.0	0.0	99.8	0.0	0.0	99.7	0.0	99.7	99.8	0.0	0.0	0.1	99.7	0.1	0.0	0.0	0.0	0.0
T	0.0	0.0	0.0	0.1	0.0	99.9	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.1	0.0	99.8	99.8
C	0.0	0.0	0.0	99.9	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	99.8	99.9	0.2	0.2
G	99.9	99.9	0.5	0.0	0.1	0.0	0.0	0.2	99.9	99.9	0.3	99.9	0.3	0.2	0.0	0.0	99.9	0.2	99.9	0.0	0.0	0.0	0.0

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃
A	0.1	0.0	99.6	0.0	99.9	0.0	0.0	99.8	0.0	0.0	99.7	0.0	99.7	99.8	0.0	0.0	0.1	99.7	0.1	0.0	0.0	0.0	0.0
T	0.0	0.0	0.0	0.1	0.0	99.9	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.8	0.0	0.0	0.0	0.2	0.1	99.8	99.8
C	0.0	0.0	0.0	99.9	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	99.8	99.9	0.2	0.2
G	99.9	99.9	0.4	0.0	0.1	0.0	0.0	0.2	99.9	99.9	0.3	99.9	0.3	0.2	0.0	0.0	99.9	0.2	99.9	0.0	0.0	0.0	0.0

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃
A	0.1	0.0	99.6	0.0	99.9	0.0	0.0	99.8	0.0	0.0	99.7	0.0	99.7	99.8	0.0	0.0	0.1	99.8	0.1	0.0	0.0	0.0	0.0
T	0.0	0.0	0.0	0.1	0.0	99.9	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.1	99.9	0.0	0.0	0.0	0.1	0.0	99.8	99.8
C	0.0	0.0	0.0	99.9	0.0	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.1	0.0	0.0	0.0	99.8	99.9	0.2	0.2
G	99.9	99.9	0.4	0.0	0.1	0.0	0.0	0.2	99.9	99.9	0.3	99.9	0.3	0.2	0.0	0.0	99.9	0.2	99.9	0.0	0.0	0.0	0.0

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃
A	0.0	0.0	95.2	0.0	99.2	0.0	0.0	99.8	0.0	0.0	99.8	0.0	99.9	99.9	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
G	99.9	100	4.8	0.0	0.8	0.0	0.0	0.2	100	100	0.1	100	0.1	0.1	0.0	0.0	100	0.1	100	0.0	0.0	0.0	0.0

	G ₁	G ₂	A ₃	C ₄	A ₅	T ₆	T ₇	A ₈	G ₉	G ₁₀	A ₁₁	G ₁₂	A ₁₃	A ₁₄	C ₁₅	T ₁₆	G ₁₇	A ₁₈	G ₁₉	C ₂₀	C ₂₁	T ₂₂	T ₂₃
A	0.0	0.0	95.2	0.0	98.9	0.0	0.0	99.7	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0
T	0.0	0.0	0.0	0.0	0.0	100	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	99.9	99.9
C	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	0.1	0.0	0.0	0.0	99.9	100	0.1	0.1
G	100	100	4.8	0.0	1.1	0.0	0.0	0.3	100	100	0.1	100	0.1	0.1	0.0	0.0	100	0.1	100	0.0	0.0	0.0	0.0

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

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HEK3		dCas12f-ABE																						
		A ₁	G ₂	T ₃	A ₄	T ₅	T ₆	A ₇	G ₈	T ₉	C ₁₀	T ₁₁	C ₁₂	A ₁₃	G ₁₄	C ₁₅	G ₁₆	A ₁₇	A ₁₈	A ₁₉	T ₂₀	G ₂₁	G ₂₂	A ₂₃
Blank	A	100	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.1	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.8	99.9	0.0	0.0	99.8	0.0	99.8	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.2	100	0.2	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	0.1	0.0	0.0	0.0	100	0.0	0.0	0.0	0.1	100	0.0	99.9	0.1	0.1	0.1	0.0	100	100	0.2	
Normal	A	100	0.0	0.0	94.6	0.0	0.0	99.4	0.1	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.9	99.8	99.8	0.0	0.1	0.0	99.9
	T	0.0	0.0	99.9	0.0	99.9	100	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	5.4	0.0	0.0	0.6	99.9	0.0	0.0	0.1	0.0	0.2	100	0.0	100	0.1	0.2	0.2	0.0	99.9	100	0.1
L-AC ₅	A	100	0.0	0.0	97.6	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	2.4	0.0	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.1	0.1	0.1	0.0	100	100	0.1
L-AC ₁₀	A	100	0.0	0.0	94.3	0.0	0.0	99.7	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	5.7	0.0	0.0	0.3	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.1	0.1	0.1	0.0	100	100	0.1
C-AC ₅	A	100	0.0	0.0	93.2	0.0	0.0	99.8	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	6.8	0.0	0.0	0.2	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.1	0.1	0.1	0.0	100	100	0.1
C-AC ₁₀	A	100	0.0	0.0	91.7	0.0	0.0	99.7	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.9
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	8.3	0.0	0.0	0.3	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.0	0.1	0.1	0.0	100	100	0.1

		Cas12f-ABE																						
		A ₁	G ₂	T ₃	A ₄	T ₅	T ₆	A ₇	G ₈	T ₉	C ₁₀	T ₁₁	C ₁₂	A ₁₃	G ₁₄	C ₁₅	G ₁₆	A ₁₇	A ₁₈	A ₁₉	T ₂₀	G ₂₁	G ₂₂	A ₂₃
Blank	A	100	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.8	100	0.0	0.0	99.8	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.2	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	0.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.1	99.9	0.0	100	0.1	0.1	0.1	0.0	100	100	0.2
Normal	A	100	0.0	0.0	98.8	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.9
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	1.2	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.1	0.1	0.1	0.0	100	100	0.1
L-AC ₅	A	100	0.0	0.0	99.5	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	0.5	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.0	0.1	0.1	0.0	100	100	0.1
L-AC ₁₀	A	100	0.0	0.0	99.5	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	0.5	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.1	99.9	0.0	100	0.1	0.1	0.1	0.0	100	100	0.2
C-AC ₅	A	100	0.0	0.0	97.3	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.1	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	2.7	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.1	0.1	0.1	0.0	100	100	0.2
C-AC ₁₀	A	100	0.0	0.0	98.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	99.9	99.9	99.9	0.0	0.0	0.0	99.8
	T	0.0	0.0	99.9	0.0	99.9	99.9	0.0	0.0	99.9	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.1	0.0	0.1	0.0	0.0	0.0	0.1	100	0.1	100	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.0	100	0.0	2.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.1	100	0.0	100	0.0	0.1	0.1	0.0	100	100	0.1

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

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		dCas12f-ABE																			
		A ₁	G ₂	A ₃	G ₄	C ₅	A ₆	G ₇	C ₈	G ₉	A ₁₀	T ₁₁	T ₁₂	G ₁₃	T ₁₄	A ₁₅	A ₁₆	G ₁₇	G ₁₈	A ₁₉	G ₂₀
Blank	A	99.9	0.0	99.8	0.1	0.0	99.8	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	100	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	0.2	99.9	0.0	0.2	99.9	0.0	100	0.0	0.0	0.0	100	0.0	0.0	0.2	100	100	0.1	100
Normal	A	99.9	0.0	94.7	0.0	0.0	99.2	0.0	0.0	0.0	99.7	0.0	0.0	0.0	0.0	98.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	99.9	0.0	99.3	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.1	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	5.2	100	0.0	0.8	100	0.0	100	0.3	0.0	0.0	100	0.0	1.1	0.2	100	100	0.1	100
L-AC ₅	A	99.9	0.0	97.1	0.0	0.0	99.6	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.7	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.5	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	2.9	100	0.0	0.4	100	0.0	100	0.1	0.0	0.0	100	0.0	0.3	0.1	100	100	0.1	100
L-AC ₁₀	A	99.9	0.0	97.2	0.0	0.0	99.6	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.7	99.9	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.5	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	2.8	100	0.0	0.4	100	0.0	100	0.1	0.0	0.0	100	0.0	0.3	0.1	100	100	0.1	100
C-AC ₅	A	99.9	0.0	91.2	0.0	0.0	99.5	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	8.8	100	0.0	0.5	100	0.0	100	0.1	0.0	0.0	100	0.0	0.1	0.1	100	100	0.1	100
C-AC ₁₀	A	99.9	0.0	87.6	0.0	0.0	99.5	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	12.4	100	0.0	0.5	100	0.0	100	0.0	0.0	0.0	100	0.0	0.1	0.1	100	100	0.1	100

Cas12f-ABE

		A ₁	G ₂	A ₃	G ₄	C ₅	A ₆	G ₇	C ₈	G ₉	A ₁₀	T ₁₁	T ₁₂	G ₁₃	T ₁₄	A ₁₅	A ₁₆	G ₁₇	G ₁₈	A ₁₉	G ₂₀
Blank	A	99.9	0.0	99.8	0.0	0.0	99.8	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	0.2	99.9	0.0	0.1	99.9	0.0	100	0.0	0.0	0.0	100	0.0	0.0	0.2	100	100	0.1	100
Normal	A	99.9	0.0	96.9	0.0	0.0	99.7	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.7	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	3.1	100	0.0	0.3	100	0.0	100	0.1	0.0	0.0	100	0.0	0.1	0.1	100	100	0.1	100
L-AC ₅	A	99.9	0.0	98.4	0.0	0.0	99.8	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	99.9	100	0.0	99.7	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	1.5	100	0.0	0.2	100	0.0	100	0.1	0.0	0.0	100	0.0	0.1	0.1	100	100	0.1	100
L-AC ₁₀	A	99.9	0.0	98.3	0.0	0.0	99.8	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.7	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.3	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	1.7	100	0.0	0.2	100	0.0	100	0.1	0.0	0.0	100	0.0	0.1	0.1	100	100	0.1	100
C-AC ₅	A	99.9	0.0	93.6	0.0	0.0	99.7	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	6.4	100	0.0	0.2	100	0.0	100	0.1	0.0	0.0	100	0.0	0.1	0.1	100	100	0.1	100
C-AC ₁₀	A	99.9	0.0	91.7	0.0	0.0	99.8	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	99.9	99.8	0.0	0.0	99.9	0.0
	T	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.1	0.0	0.0	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	99.9	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	0.0	0.0	0.0
	G	0.1	100	8.2	100	0.0	0.2	100	0.0	100	0.0	0.0	0.0	100	0.0	0.0	0.1	100	100	0.1	100

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

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		dCas12f-ABE																						
		G ₁	G ₂	A ₃	G ₄	G ₅	T ₆	C ₇	A ₈	G ₉	A ₁₀	A ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	G ₁₆	G ₁₇	G ₁₈	G ₁₉	T ₂₀	C ₂₁	C ₂₂	A ₂₃
Blank	A	0.0	0.0	99.9	0.0	0.0	0.0	0.1	99.9	0.0	99.8	99.3	99.7	0.0	99.1	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	99.9
	T	0.3	0.1	0.1	0.4	0.2	99.9	0.0	0.1	0.2	0.1	0.2	0.1	98.5	0.2	0.2	0.3	0.2	0.3	0.1	99.9	0.0	0.0	0.1
	C	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.1	0.4	0.2	0.0	0.8	0.0	0.0	0.0	0.0	0.0	0.0	99.8	99.8	0.0
	G	99.6	99.9	0.0	99.6	99.8	0.0	0.1	0.0	99.8	0.0	0.0	0.0	1.5	0.0	99.7	99.7	99.8	99.7	99.8	0.1	0.0	0.1	0.0
Normal	A	0.0	0.0	94.1	0.0	0.0	0.0	0.0	96.5	0.0	97.9	99.6	99.5	0.0	97.3	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9
	T	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	98.5	0.0	0.5	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	1.5	0.0	0.0	0.0	0.0	0.0	0.1	0.1	100	100	0.0
	G	100	100	5.9	100	100	0.0	0.0	3.4	100	2.1	0.4	0.5	0.0	2.7	99.4	99.9	100	100	99.9	0.0	0.0	0.0	0.1
L-AC ₅	A	0.0	0.0	95.7	0.0	0.0	0.0	0.0	98.0	0.0	98.6	99.6	99.7	0.0	98.9	0.1	0.1	0.0	0.0	0.0	0.0	0.0	0.0	99.9
	T	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	99.5	0.0	0.4	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	0.5	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	100	0.0
	G	100	100	4.3	100	100	0.0	0.0	2.0	100	1.4	0.4	0.3	0.0	1.1	99.5	99.9	100	100	99.9	0.0	0.0	0.0	0.1
L-AC ₁₀	A	0.0	0.0	97.1	0.0	0.0	0.0	0.0	98.7	0.0	99.2	99.8	99.8	0.0	99.2	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9
	T	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	99.6	0.0	0.4	0.1	0.0	0.0	0.0	99.9	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	0.4	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	100	0.0
	G	99.9	100	2.9	100	100	0.0	0.0	1.3	100	0.8	0.2	0.2	0.0	0.8	99.5	99.9	100	100	99.9	0.0	0.0	0.0	0.1
C-AC ₅	A	0.0	0.0	87.7	0.0	0.0	0.0	0.0	98.9	0.0	99.8	99.9	99.9	0.0	99.9	0.1	0.0	0.0	0.0	0.0	0.0	0.0	0.0	99.9
	T	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.3	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	100	100	0.0
	G	100	100	12.3	100	100	0.0	0.0	1.1	100	0.2	0.1	0.1	0.0	0.1	99.7	99.9	99.9	100	99.9	0.0	0.0	0.0	0.1
C-AC ₁₀	A	0.0	0.0	92.2	0.0	0.0	0.0	0.0	99.4	0.0	99.8	99.9	99.9	0.0	99.9	0.0	0.0	0.0	0.0	0.1	0.0	0.0	0.0	99.9
	T	0.0	0.0	0.0	0.0	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.3	0.1	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.1	100	0.0	0.0	0.0	0.0	0.0	0.2	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0
	G	100	100	7.8	100	100	0.0	0.0	0.6	100	0.2	0.0	0.1	0.0	0.1	99.7	99.9	100	100	99.9	0.0	0.0	0.0	0.1

		Cas12f-ABE																						
		G ₁	G ₂	A ₃	G ₄	G ₅	T ₆	C ₇	A ₈	G ₉	A ₁₀	A ₁₁	A ₁₂	T ₁₃	A ₁₄	G ₁₅	G ₁₆	G ₁₇	G ₁₈	G ₁₉	T ₂₀	C ₂₁	C ₂₂	A ₂₃
Blank	A	0.0	0.0	99.8	0.0	0.0	0.0	0.1	99.9	0.0	99.8	99.4	99.7	0.0	99.2	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.1	99.9
	T	0.4	0.2	0.1	0.4	0.2	99.9	0.0	0.1	0.2	0.2	0.3	0.1	98.6	0.2	0.2	0.3	0.2	0.3	0.1	99.9	0.0	0.0	0.1
	C	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.1	0.4	0.2	0.0	0.6	0.0	0.0	0.0	0.0	0.0	0.0	99.8	99.8	0.0
	G	99.6	99.8	0.0	99.5	99.8	0.0	0.1	0.0	99.7	0.0	0.0	0.0	1.4	0.0	99.7	99.7	99.7	99.6	99.8	0.1	0.1	0.1	0.0
Normal	A	0.0	0.0	96.6	0.0	0.0	0.0	0.1	99.3	0.0	99.6	99.3	99.6	0.0	98.9	0.0	0.0	0.0	0.0	0.0	0.0	0.2	0.1	99.9
	T	0.4	0.2	0.1	0.5	0.2	99.9	0.0	0.1	0.3	0.2	0.3	0.1	98.4	0.2	0.3	0.3	0.3	0.4	0.2	99.9	0.0	0.0	0.1
	C	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.1	0.4	0.2	0.0	0.8	0.1	0.0	0.0	0.0	0.0	0.0	99.7	99.8	0.0
	G	99.6	99.8	3.3	99.5	99.8	0.0	0.1	0.6	99.7	0.1	0.0	0.0	1.6	0.1	99.7	99.7	99.7	99.6	99.8	0.1	0.1	0.1	0.0
L-AC ₅	A	0.0	0.0	98.5	0.0	0.0	0.0	0.0	99.8	0.0	99.9	100	100	0.0	99.9	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100
	T	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.2	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0
	G	100	100	1.5	100	100	0.0	0.0	0.2	100	0.1	0.0	0.0	0.0	0.0	99.8	100	100	100	100	0.0	0.0	0.0	0.0
L-AC ₁₀	A	0.0	0.0	97.9	0.0	0.0	0.0	0.0	99.8	0.0	99.9	100	100	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100
	T	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.3	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0
	C	0.0	0.0	0.0	0.0	0.0	0.0	100	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	0.0	100	100	0.0
	G	100	100	2.1	100	100	0.0	0.0	0.2	100	0.1	0.0	0.0	0.0	0.0	99.7	99.9	100	100	100	0.0	0.0	0.0	0.0
C-AC ₅	A	0.0	0.0	93.8	0.0	0.0	0.0	0.1	99.8	0.0	99.7	99.4	99.7	0.0	99.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	99.9
	T	0.4	0.2	0.1	0.4	0.2	99.9	0.0	0.1	0.3	0.2	0.2	0.1	98.5	0.2	0.2	0.3	0.2	0.3	0.2	99.9	0.0	0.0	0.1
	C	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.1	0.4	0.2	0.0	0.6	0.0	0.0	0.0	0.0	0.0	0.0	99.8	99.8	0.0
	G	99.6	99.8	6.0	99.5	99.8	0.0	0.1	0.1	99.7	0.0	0.0	0.0	1.4	0.0	99.7	99.7	99.7	99.7	99.8	0.1	0.0	0.1	0.0
C-AC ₁₀	A	0.0	0.0	97.0	0.0	0.0	0.0	0.1	99.9	0.0	99.8	99.4	99.7	0.0	99.2	0.0	0.0	0.0	0.0	0.0	0.0	0.1	0.1	99.9
	T	0.4	0.2	0.1	0.4	0.2	99.9	0.0	0.1	0.2	0.2	0.2	0.1	98.5	0.2	0.2	0.3	0.2	0.4	0.1	99.9	0.0	0.0	0.1
	C	0.0	0.0	0.0	0.0	0.0	0.0	99.8	0.0	0.0	0.1	0.4	0.2	0.0	0.7	0.0	0.0	0.0	0.0	0.0	0.0	99.8	99.8	0.0
	G	99.6	99.8	2.9	99.5	99.8	0.0	0.1	0.0	99.7	0.0	0.0	0.0	1.5	0.0	99.7	99.7	99.7	99.6	99.8	0.1	0.1	0.1	0.0

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

b

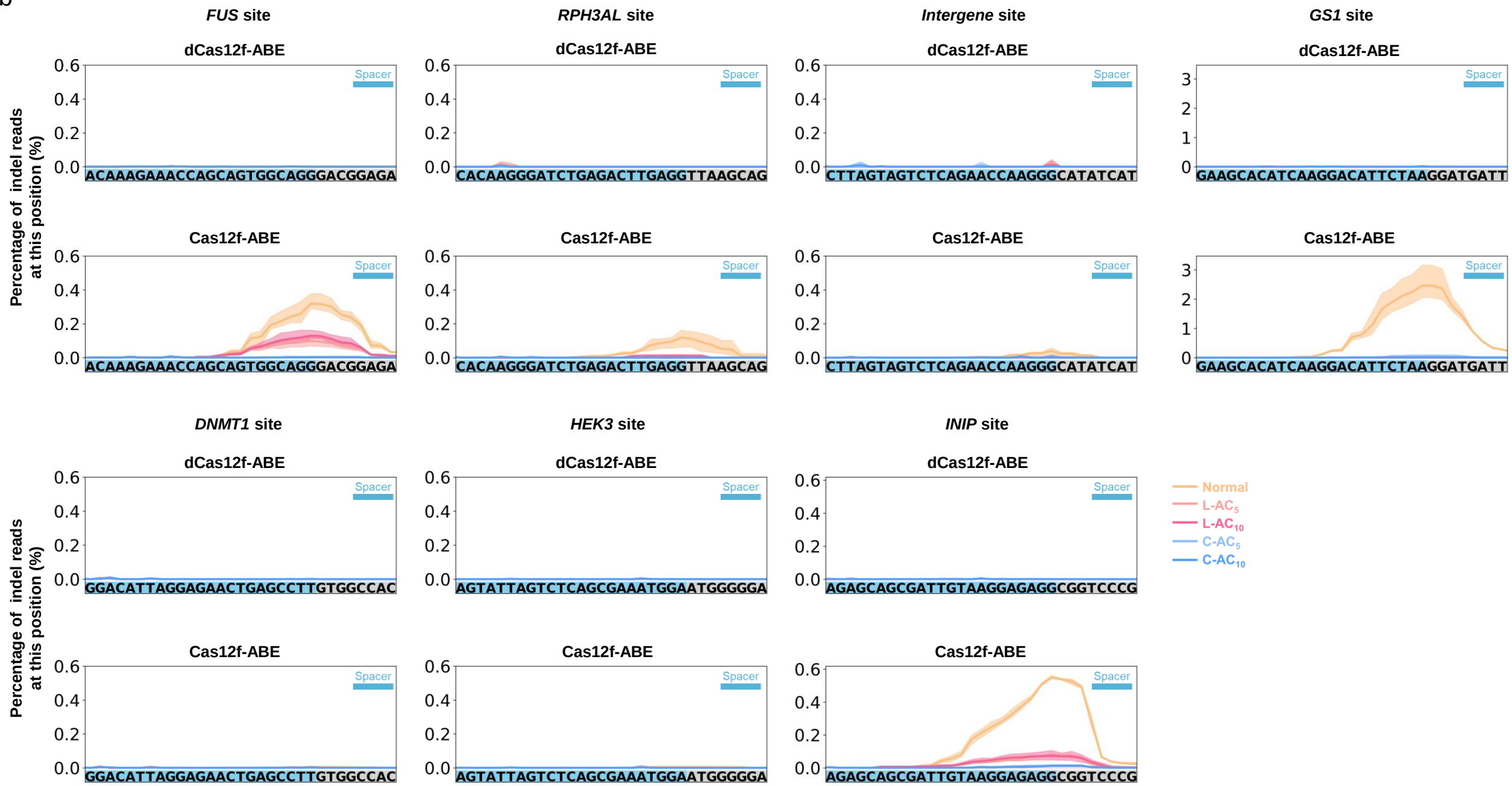


Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing

Fig. S15: Product purity of the Cas12f/cgRNA system-induced adenine base editing. **a**, Product distributions at the indicated nine human genomic DNA sites in the HEK293T cells treated with dCas12f-ABE or Cas12f-ABE and the corresponding sgRNAs, or in untreated HEK293T cells (Blank). **b**, The indel distribution induced by dCas12f-ABE design or Cas12f-ABE design at the indicated seven target sites. For **a-b**, n = 3 independent experiments.