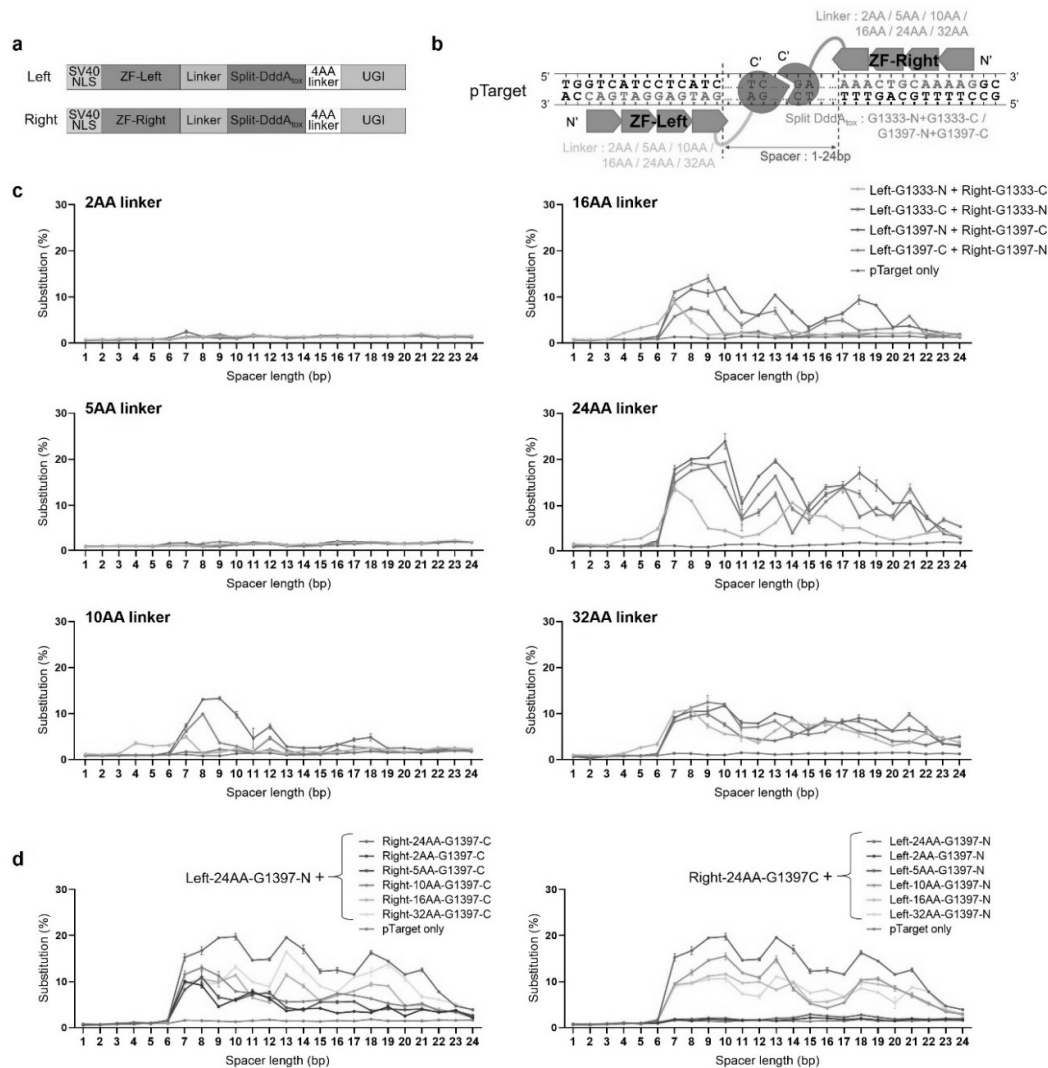
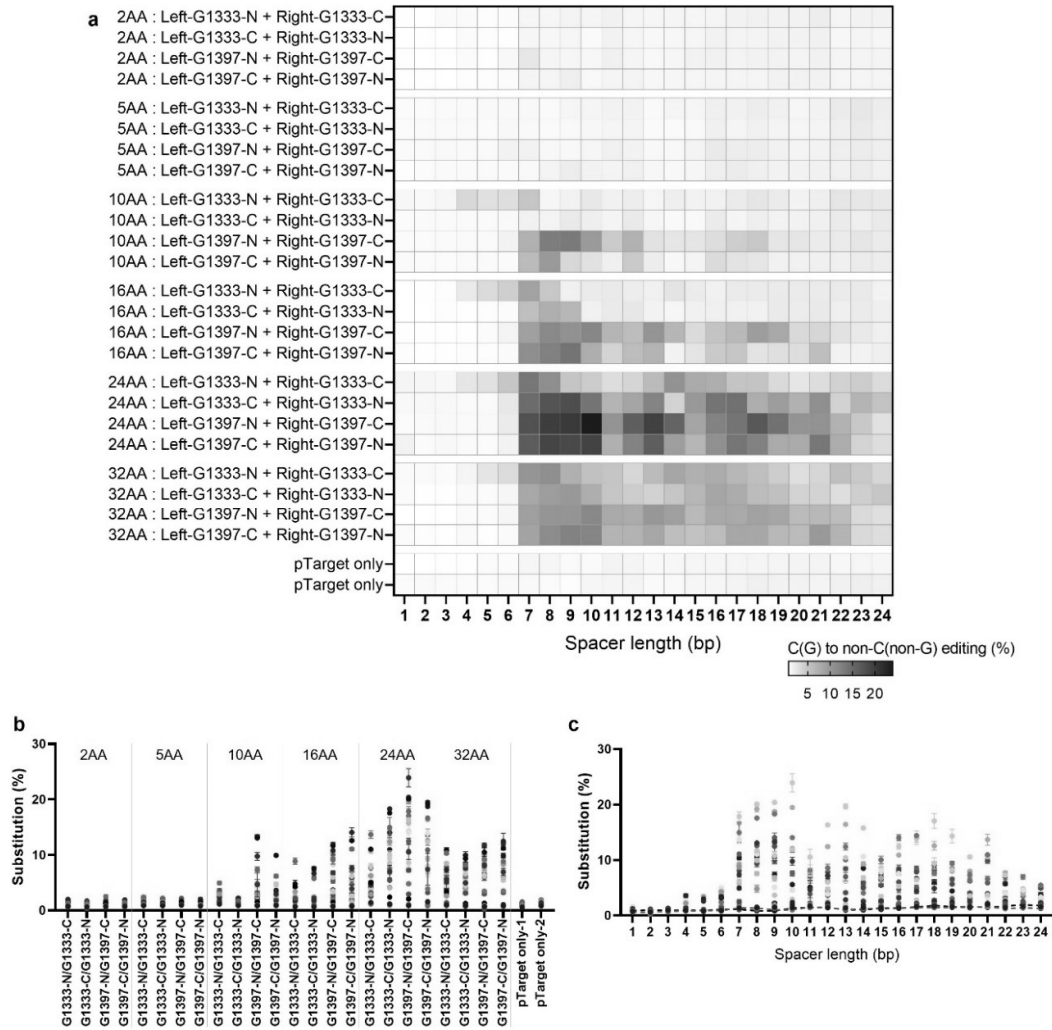


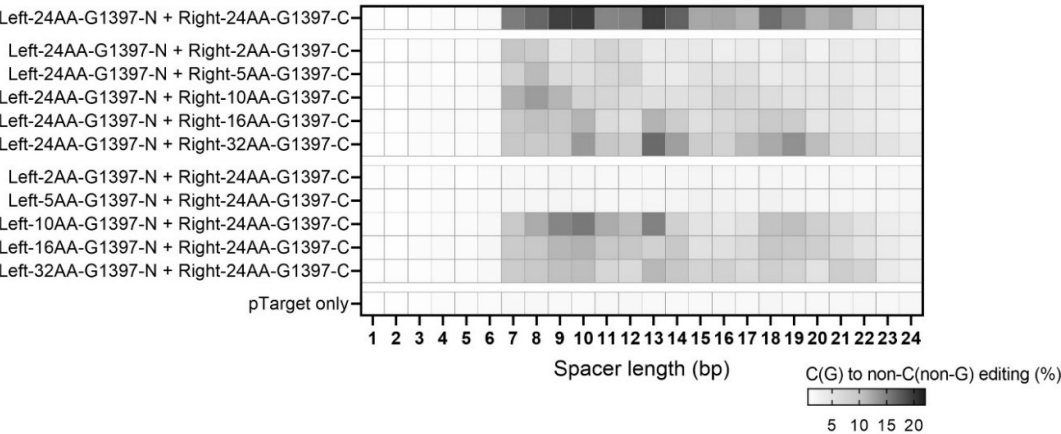
【Fig. 1】



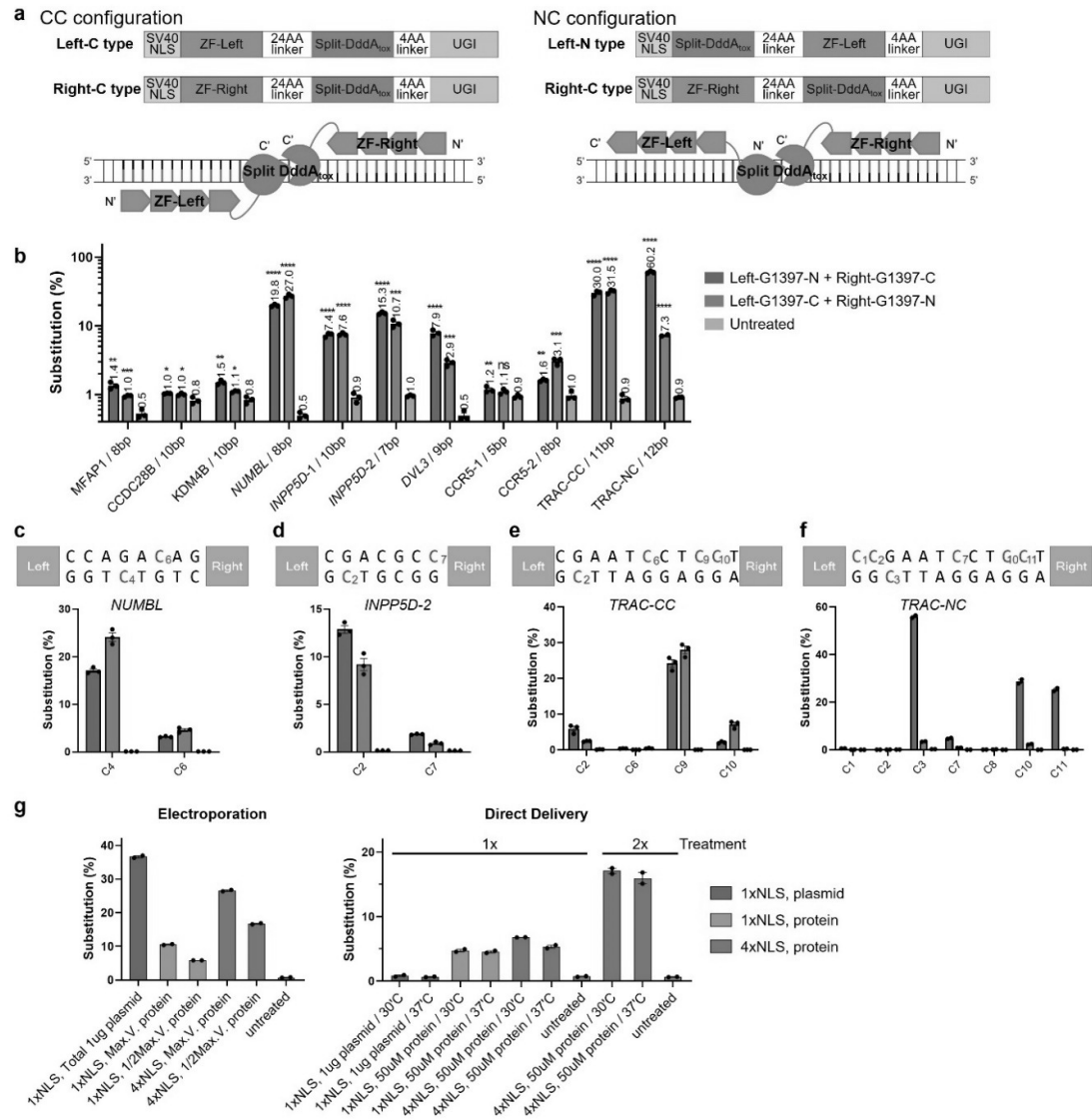
【Fig. 2】



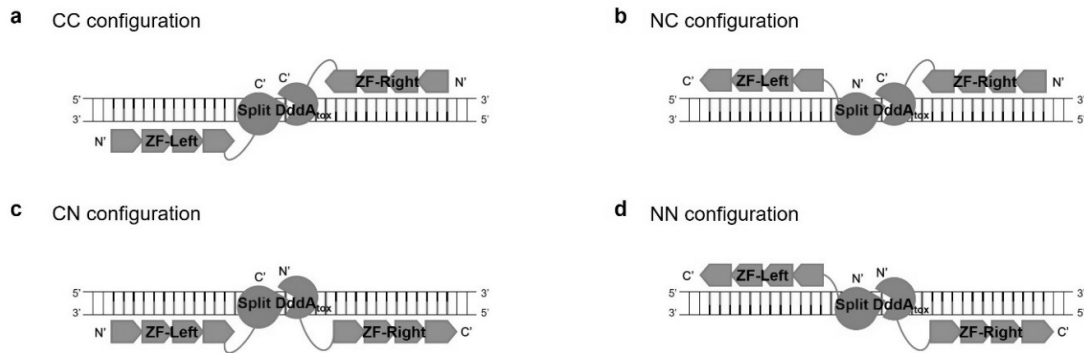
【Fig. 3】



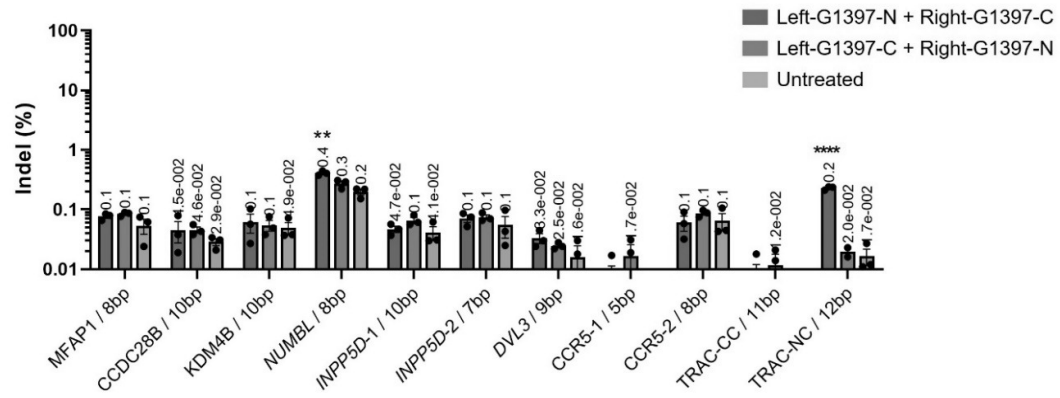
【Fig. 4】



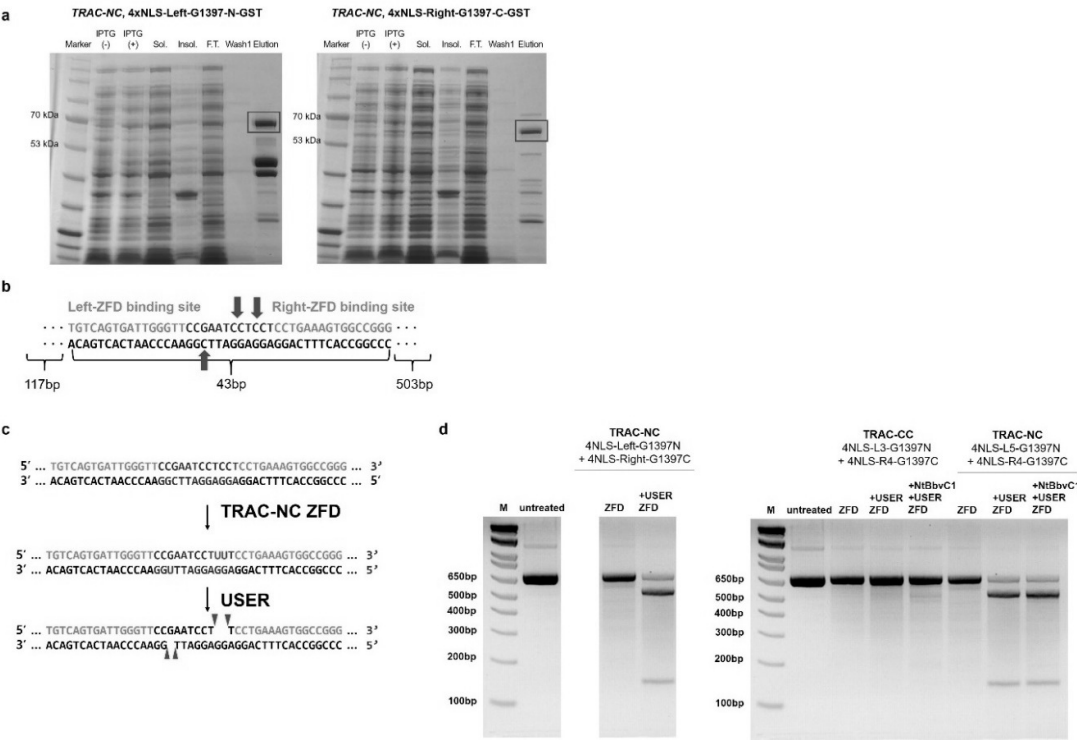
【Fig. 5】



【Fig. 6】

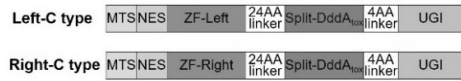


【Fig. 7】

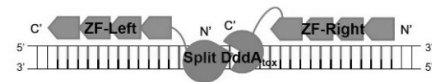


【Fig. 8】

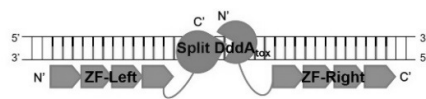
a CC configuration



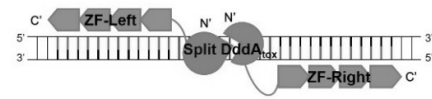
b NC configuration



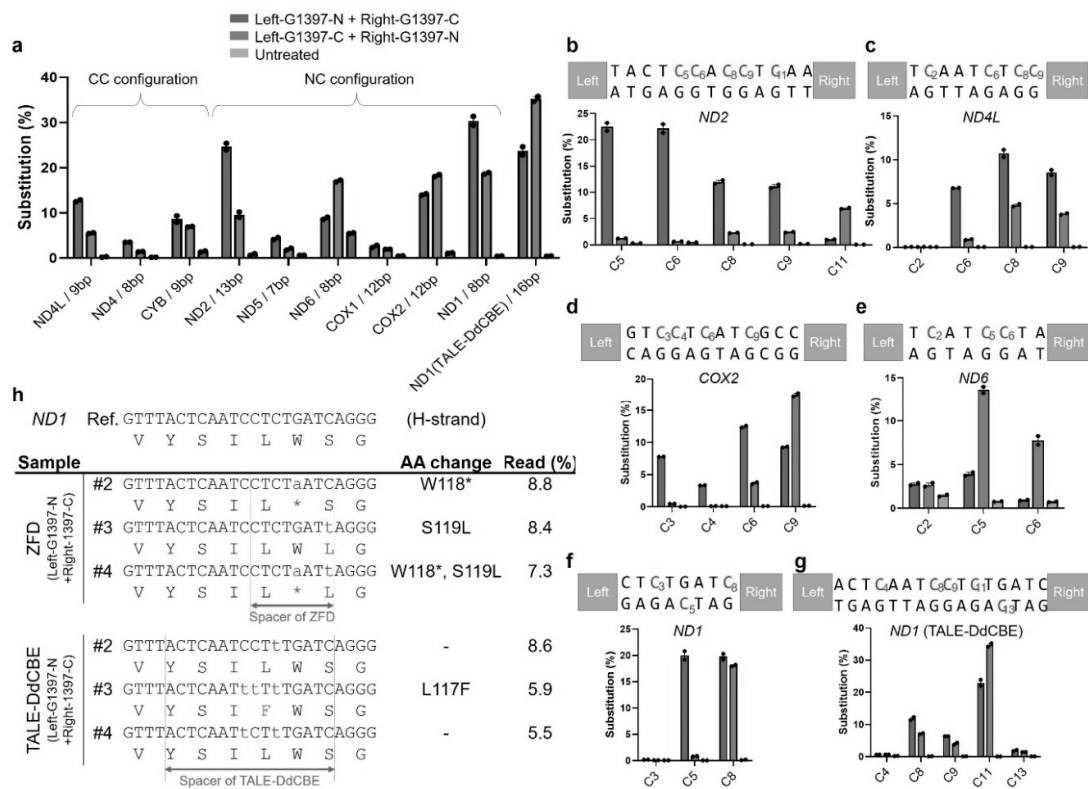
c CN configuration



d NN configuration



【Fig. 9】



【Fig. 10】

a

MT-ND1 G T T T A C T C A A T C C T C T G A T C ₈ A G G G T G A G C A T C
C A A A T G A G T T A G G A G A C T A G T C C C A C T C G T A G

	sub (%)		sub (%)
ND1-1	0.6	ND1-16	83.2
ND1-2	0.4	ND1-17	0.4
ND1-3	34.8	ND1-18	0.5
ND1-4	0.6	ND1-19	0.4
ND1-5	0.5	ND1-20	0.5
ND1-6	0.6	ND1-21	0.5
ND1-7	0.5	ND1-22	0.6
ND1-8	0.5	ND1-23	0.5
ND1-9	0.5	ND1-24	0.7
ND1-10	98.1	ND1-25	0.5
ND1-11	0.5	ND1-26	0.5
ND1-12	0.5	ND1-27	47.7
ND1-13	0.5	ND1-28	0.6
ND1-14	0.6	ND1-29	0.6
ND1-15	0.6	ND1-30	94.7

b

MT-ND2 C T A C G C C T A A T C T A C T C C A C C T C A A T C A C A C T A C T C C
G A T G C G G A T T A G A T G A G G T G G A G T T A G T G T G A T G A G G

	sub (%)		sub (%)
ND2-1	0.6	ND2-19	0.9
ND2-2	0.7	ND2-20	0.7
ND2-3	0.7	ND2-21	67.5
ND2-4	0.6	ND2-22	1.0
ND2-5	0.6	ND2-23	71.3
ND2-6	0.7	ND2-24	75.7
ND2-7	0.6	ND2-25	0.6
ND2-8	0.6	ND2-26	0.7
ND2-9	0.7	ND2-27	0.7
ND2-10	0.9	ND2-28	0.8
ND2-11	0.7	ND2-29	0.7
ND2-12	0.8	ND2-30	0.6
ND2-13	0.6	ND2-31	45.1
ND2-14	0.7	ND2-32	57.9
ND2-15	0.6	ND2-33	52.6
ND2-16	0.7	ND2-34	25.5
ND2-17	0.7	ND2-35	0.9
ND2-18	0.6	ND2-36	0.8

c

	ND1 region sub (%)	ND2 region sub (%)
untreated-1	0.5	0.8
untreated-2	0.6	0.7
untreated-3	0.6	0.7
untreated-4	1.1	0.8
untreated-5	0.5	0.7
untreated-6	0.5	0.7
untreated-7	0.6	0.9
untreated-8	0.5	0.8
untreated-9	0.5	0.9
untreated-10	0.6	0.8
untreated-11	0.5	0.9
untreated-12	0.6	0.7
untreated-13	0.5	0.7
untreated-14	0.6	0.7
untreated-15	0.5	0.7
untreated-16	0.5	0.8
untreated-17	0.5	0.9
untreated-18	0.4	0.6

【Fig. 11】

Human MT-ND1	Ref.	GTCTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:143)	(H-strand)	
Sample			AA change	Read (%)
Clone 3 : 34 %	Allele-1	GTCTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:143) V Y S I L W S G W A S (SEQ ID NO:144)	-	62
	Allele-2	GTCTACTCAATCCTCTGATtAGGGTGAGCATCA (SEQ ID NO:145) V Y S I L W L G W A S (SEQ ID NO:146)	S119L	21
	Allele-3	GTCTACTCAATCCTCTaATCAGGGTGAGCATCA (SEQ ID NO:147) V Y S I L * S G W A S (SEQ ID NO:148)	W118*	13
Clone 10 : 92%	Allele-1	GTCTACTCAATCCTCTGATtAGGGTGAGCATCA V Y S I L W L G W A S	S119L	40
	Allele-2	GTCTACTCAATCCTCTaATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	32
	Allele-3	GTCTACTCAATCCTCTaATtAGGGTGAGCATCA V Y S I L * L G W A S	W118*, S119L	20
	Allele-4	GTCTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	2
Clone 16 : 80%	Allele-1	GTCTACTCAATCCTCTGATtAGGGTGAGCATCA V Y S I L W L G W A S	S119L	40
	Allele-2	GTCTACTCAATCCTCTaATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	35
	Allele-3	GTCTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	16
	Allele-4	GTCTACTCAATCCTCTaATtAGGGTGAGCATCA V Y S I L * L G W A S	W118*, S119L	5
Clone 27 : 45%	Allele-1	GTCTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	50
	Allele-2	GTCTACTCAATCCTCTGATtAGGGTGAGCATCA V Y S I L W L G W A S	S119L	26
	Allele-3	GTCTACTCAATCCTCTaATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	19
Clone 30 : 90%	Allele-1	GTCTACTCAATCCTCTGATtAGGGTGAGCATCA V Y S I L W L G W A S	S119L	40
	Allele-2	GTCTACTCAATCCTCTaATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	35
	Allele-3	GTCTACTCAATCCTCTaATtAGGGTGAGCATCA V Y S I L * L G W A S	W118*, S119L	15
	Allele-4	GTCTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	5

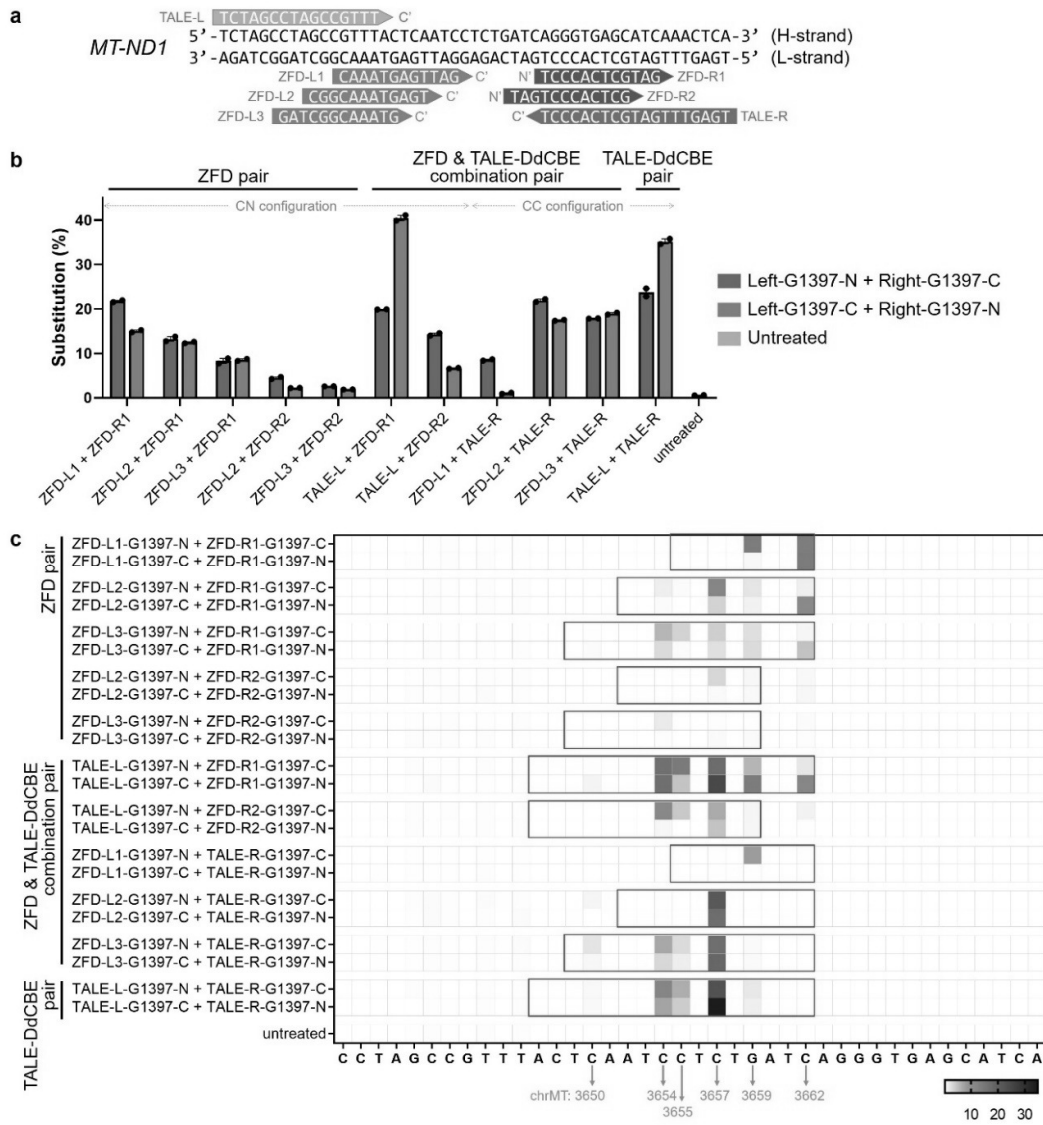
【Fig. 12a】

Human <i>MT-ND2</i>	Ref.	CTACGCCTAATCTACTCCACCTCAATCACACTACTCCCC (SEQ ID NO:149)	(H-strand)	
Sample			AA change	Read (%)
Clone 21	Allele-1	CTACGCCTAATCTACTttACCTCAATCACACTACTCCCC (SEQ ID NO:150) L R L I Y F T S I T L L P (SEQ ID NO:151)	S299F	45
	Allele-2	CTACGCCTAATCTACTCCACCTCAATCACACTACTCCCC (SEQ ID NO:152) L R L I Y S T S I T L L P (SEQ ID NO:153)	-	31
	Allele-3	CTACGCCTAATCTACTttAtttCAATCACACTACTCCCC (SEQ ID NO:154) L R L I Y F I S I T L L P (SEQ ID NO:155)	S299F, T300I	10
	Allele-4	CTACGCCTAATCTACTtCACCTCAATCACACTACTCCCC (SEQ ID NO:156) L R L I Y F T S I T L L P (SEQ ID NO:157)	S299F	4
	Allele-5	CTACGCCTAATCTACTttAtCTCAATCACACTACTCCCC (SEQ ID NO:158) L R L I Y F I S I T L L P (SEQ ID NO:159)	S299F, T300I	3
	Allele-6	CTACGCCTAATCTACTttACCTtAATCACACTACTCCCC (SEQ ID NO:160) L R L I Y F T L I T L L P (SEQ ID NO:161)	S299F, S301L	1
	Allele-1	CTACGCCTAATCTACTttACCTCAATCACACTACTCCCC L R L I Y F T S I T L L P	S299F	43
	Allele-2	CTACGCCTAATCTACTCCACCTCAATCACACTACTCCCC L R L I Y S T S I T L L P	-	27
	Allele-3	CTACGCCTAATCTACTttAtttCAATCACACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	16
	Allele-4	CTACGCCTAATCTACTttAtCTCAATCACACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	6
	Allele-5	CTACGCCTAATCTACTttACCTtAATCACACTACTCCCC L R L I Y F T L I T L L P	S299F, S301L	1
Clone 24	Allele-1	CTACGCCTAATCTACTttACCTCAATCACACTACTCCCC L R L I Y F T S I T L L P	S299F	34
	Allele-2	CTACGCCTAATCTACTttAtttCAATCACACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	30
	Allele-3	CTACGCCTAATCTACTCCACCTCAATCACACTACTCCCC L R L I Y S T S I T L L P	-	23
	Allele-4	CTACGCCTAATCTACTttAtCTCAATCACACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	3
	Allele-5	CTACGCCTAATCTACTttAtttAATCACACTACTCCCC L R L I Y F I L I T L L P	S299F, T300I, S301L	1
	Allele-6	CTACGCCTAATCTACTtCACCTCAATCACACTACTCCCC L R L I Y F T S I T L L P	S299F	1

【Fig. 12b】

Human <i>MT-ND2</i>		Ref.	CTACGCCTAATCTACTCCACCTCAATCACA	CTACTCCCC	(H-strand)	Read (%)
Sample					AA change	
Clone 31	Allele-1	CTACGCCTAATCTACTCCACCTCAATCACA	CTACTCCCC		-	53
		L R L I Y S T S I T L L P				
	Allele-2	CTACGCCTAATCTACTTtACCTCAATCACA	CTACTCCCC		S299F	28
		L R L I Y F T S I T L L P				
	Allele-3	CTACGCCTAATCTACTTtAttTCAATCACA	CTACTCCCC		S299F, T300I	9
Clone 32		L R L I Y F I S I T L L P				
	Allele-4	CTACGCCTAATCTACTTtAtCTCAATCACA	CTACTCCCC		S299F, T300I	2
		L R L I Y F I S I T L L P				
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCACA	CTACTCCCC		S299F	2
		L R L I Y F T S I T L L P				
Clone 33	Allele-1	CTACGCCTAATCTACTCCACCTCAATCACA	CTACTCCCC		-	40
		L R L I Y S T S I T L L P				
	Allele-2	CTACGCCTAATCTACTTtACCTCAATCACA	CTACTCCCC		S299F	37
		L R L I Y F T S I T L L P				
	Allele-3	CTACGCCTAATCTACTTtAttTCAATCACA	CTACTCCCC		S299F, T300I	11
Clone 34		L R L I Y F I S I T L L P				
	Allele-4	CTACGCCTAATCTACTTtAtCTCAATCACA	CTACTCCCC		S299F, T300I	3
		L R L I Y F I S I T L L P				
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCACA	CTACTCCCC		S299F	2
		L R L I Y F T S I T L L P				
Clone 35	Allele-1	CTACGCCTAATCTACTCCACCTCAATCACA	CTACTCCCC		-	46
		L R L I Y S T S I T L L P				
	Allele-2	CTACGCCTAATCTACTTtACCTCAATCACA	CTACTCCCC		S299F	34
		L R L I Y F T S I T L L P				
	Allele-3	CTACGCCTAATCTACTTtAttTCAATCACA	CTACTCCCC		S299F, T300I	12
Clone 36		L R L I Y F I S I T L L P				
	Allele-4	CTACGCCTAATCTACTTtAtCTCAATCACA	CTACTCCCC		S299F, T300I	2
		L R L I Y F I S I T L L P				
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCACA	CTACTCCCC		S299F	1
		L R L I Y F T S I T L L P				
Clone 37	Allele-1	CTACGCCTAATCTACTCCACCTCAATCACA	CTACTCCCC		-	72
		L R L I Y S T S I T L L P				
	Allele-2	CTACGCCTAATCTACTTtACCTCAATCACA	CTACTCCCC		S299F	18
		L R L I Y F T S I T L L P				
	Allele-3	CTACGCCTAATCTACTTtAttTCAATCACA	CTACTCCCC		S299F, T300I	3
Clone 38		L R L I Y F I S I T L L P				
	Allele-4	CTACGCCTAATCTACTTtAtCTCAATCACA	CTACTCCCC		S299F, T300I	1
		L R L I Y F I S I T L L P				
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCACA	CTACTCCCC		S299F	0.4
		L R L I Y F T S I T L L P				

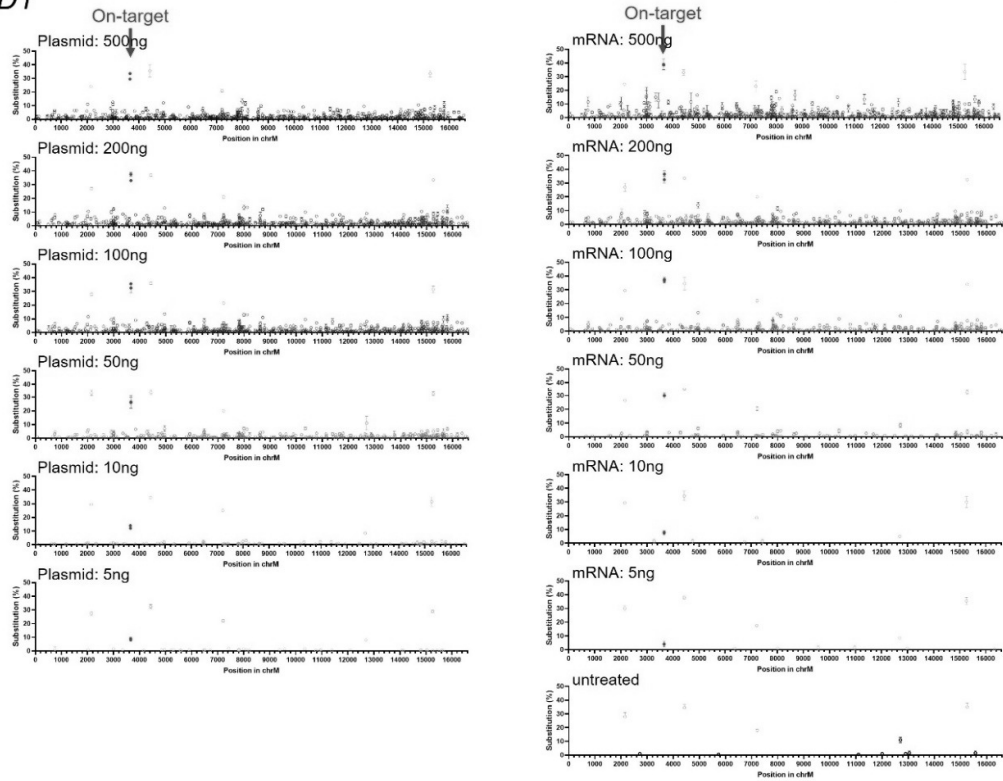
【Fig. 13】



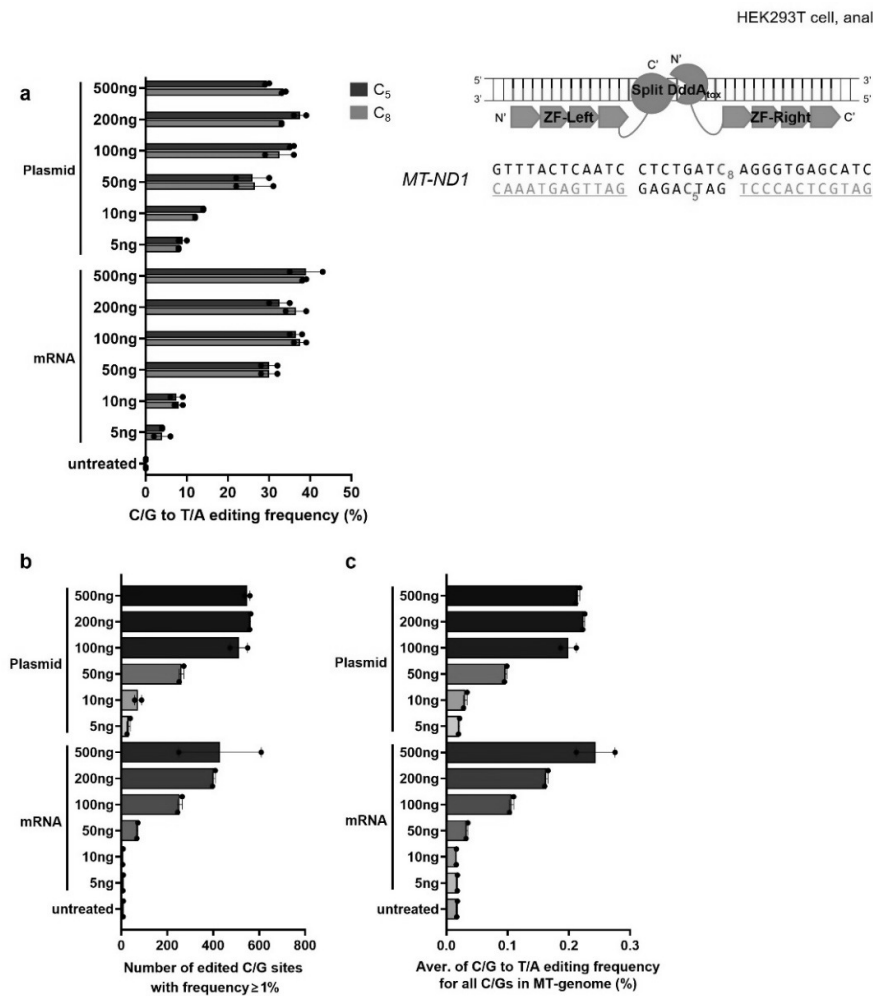
【Fig. 14】

ND1

HEK293T cell, analysis at day 4 after transfection

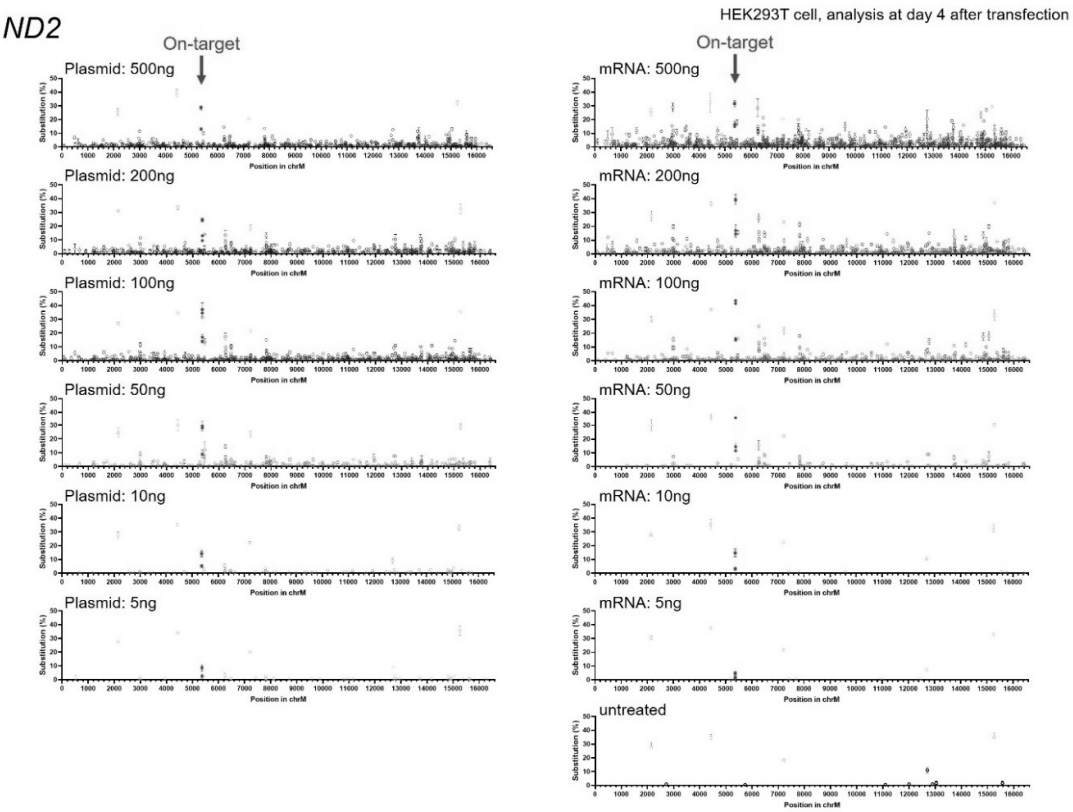


【Fig. 15】

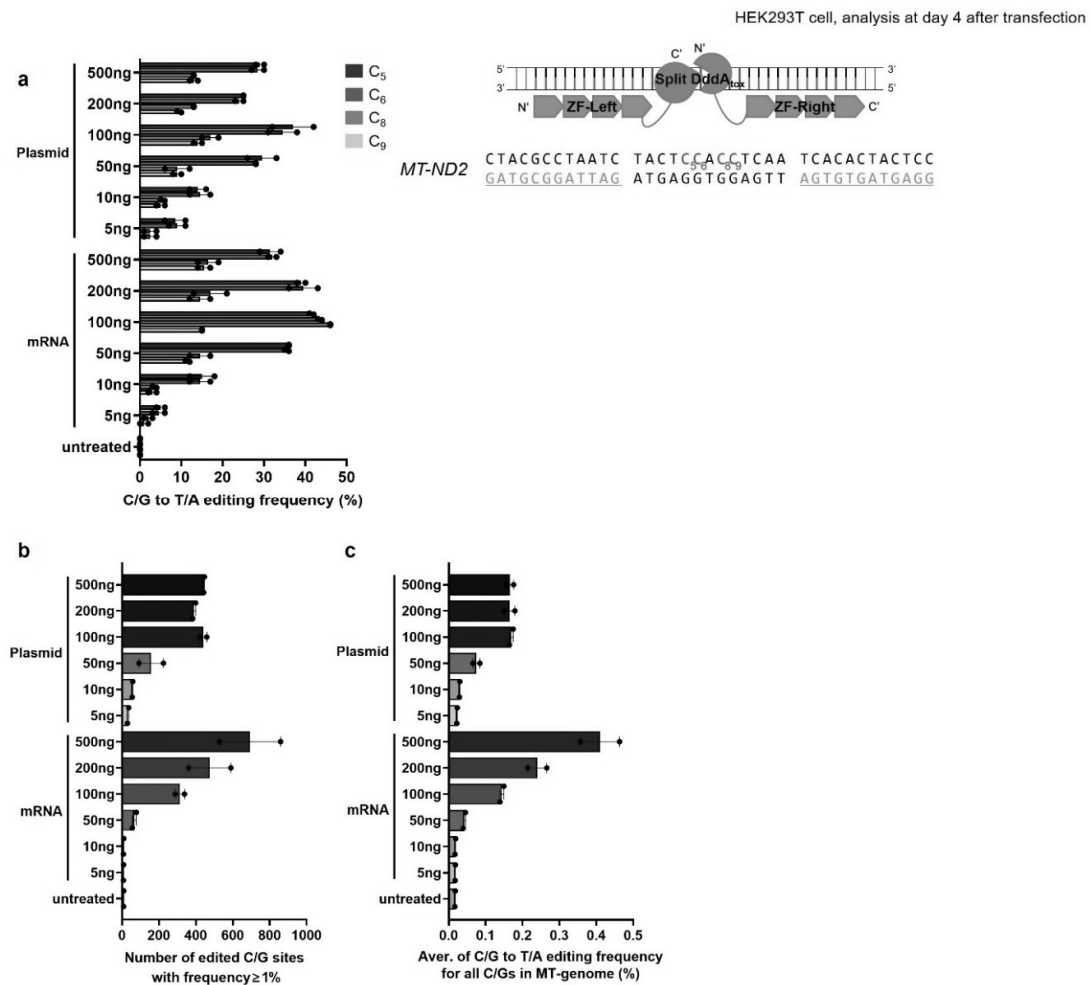


【Fig. 16】

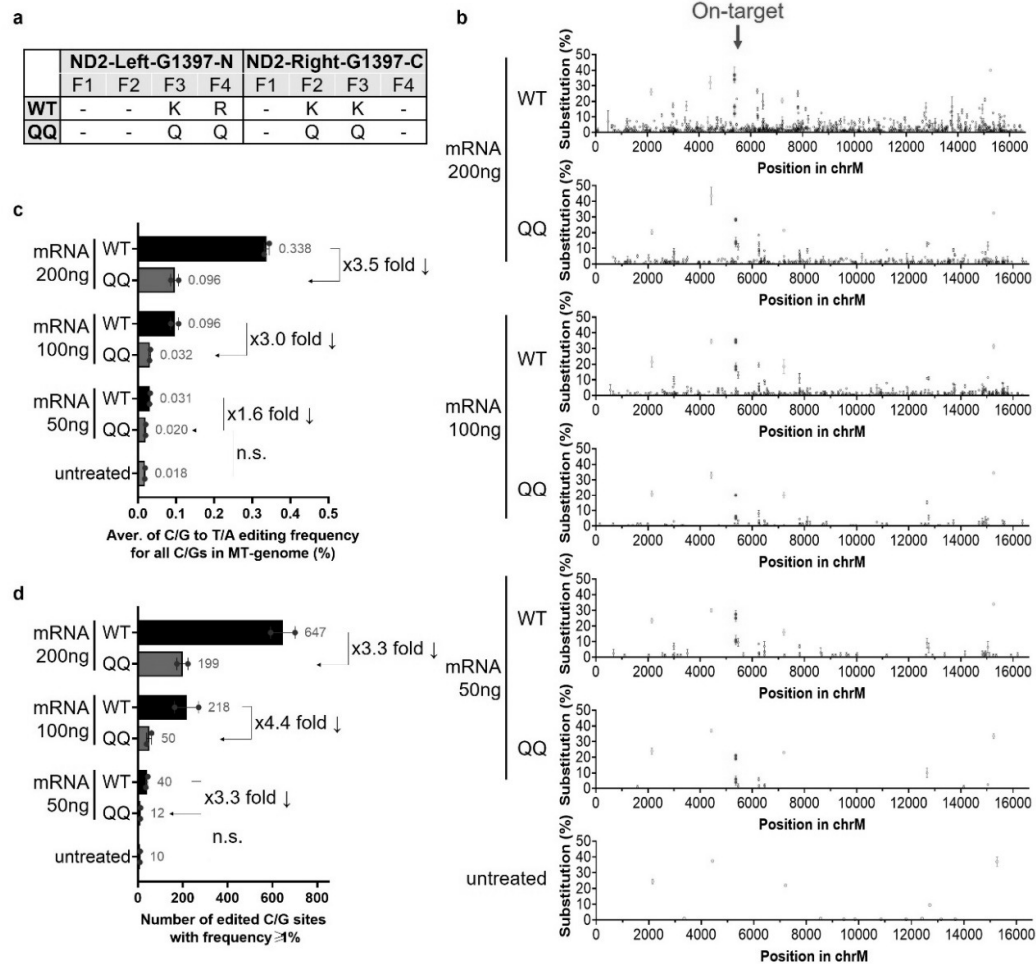
ND2



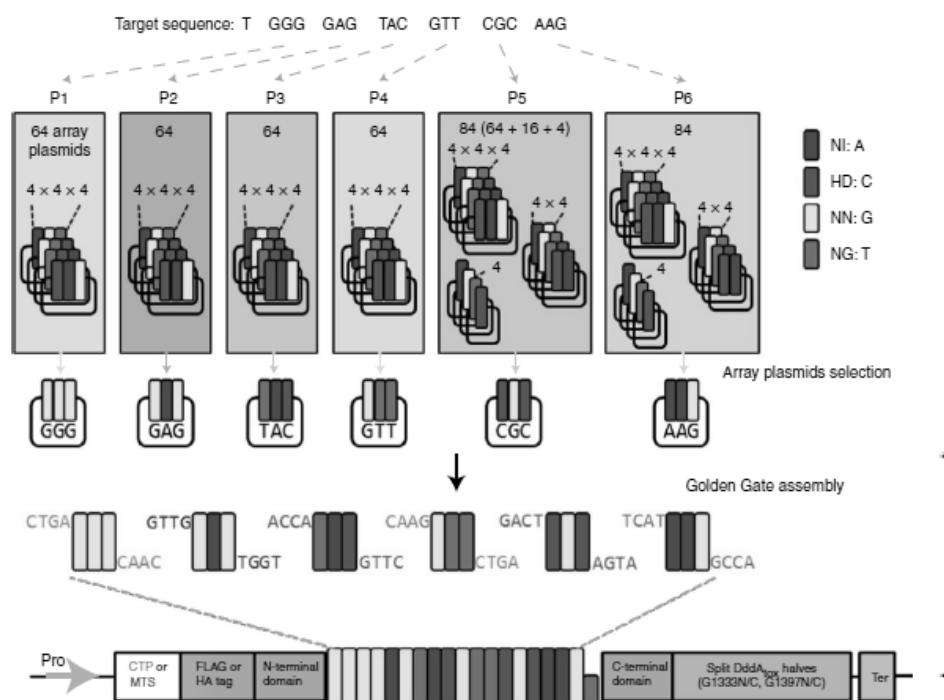
【Fig. 17】



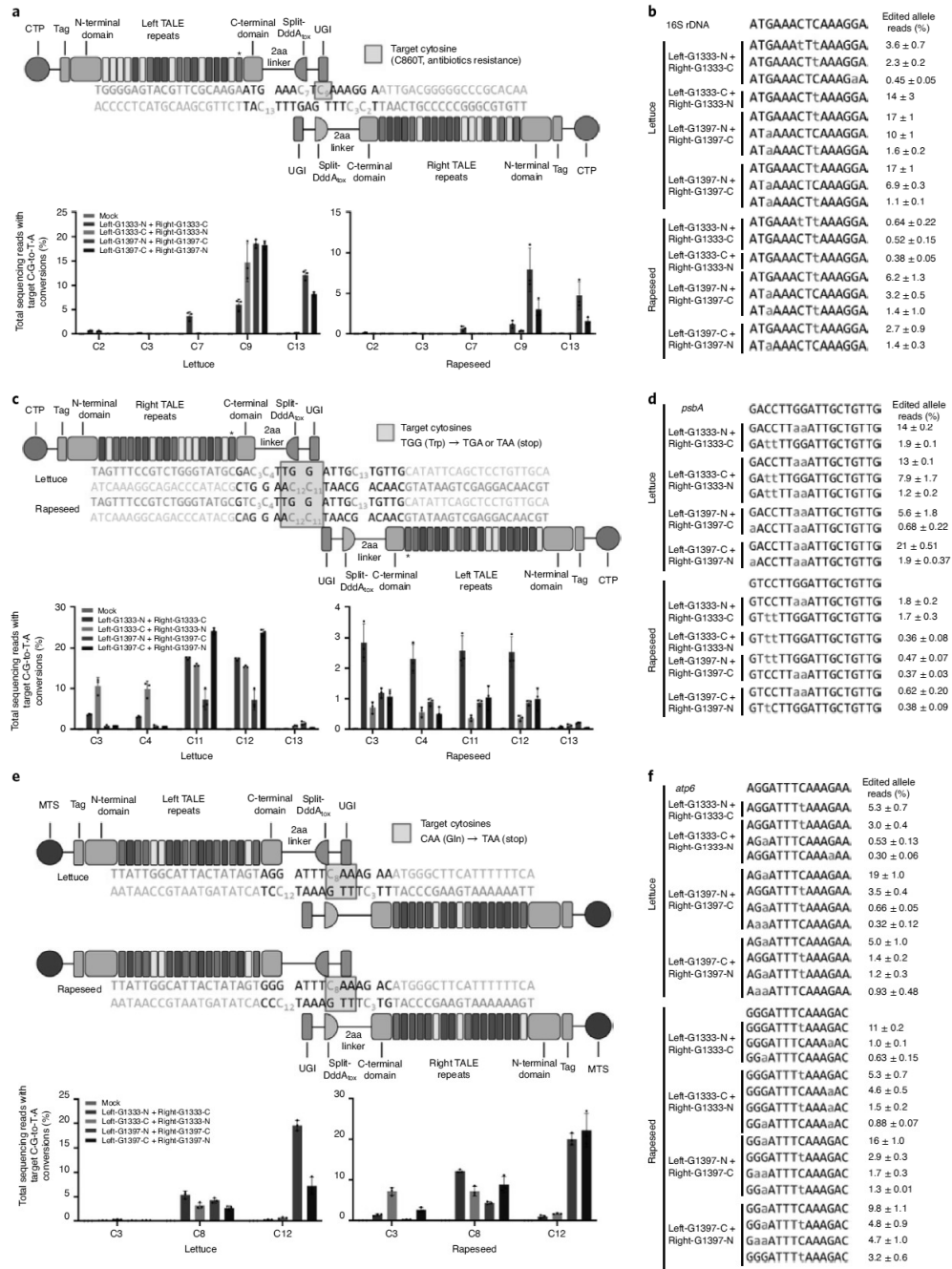
【Fig. 18】



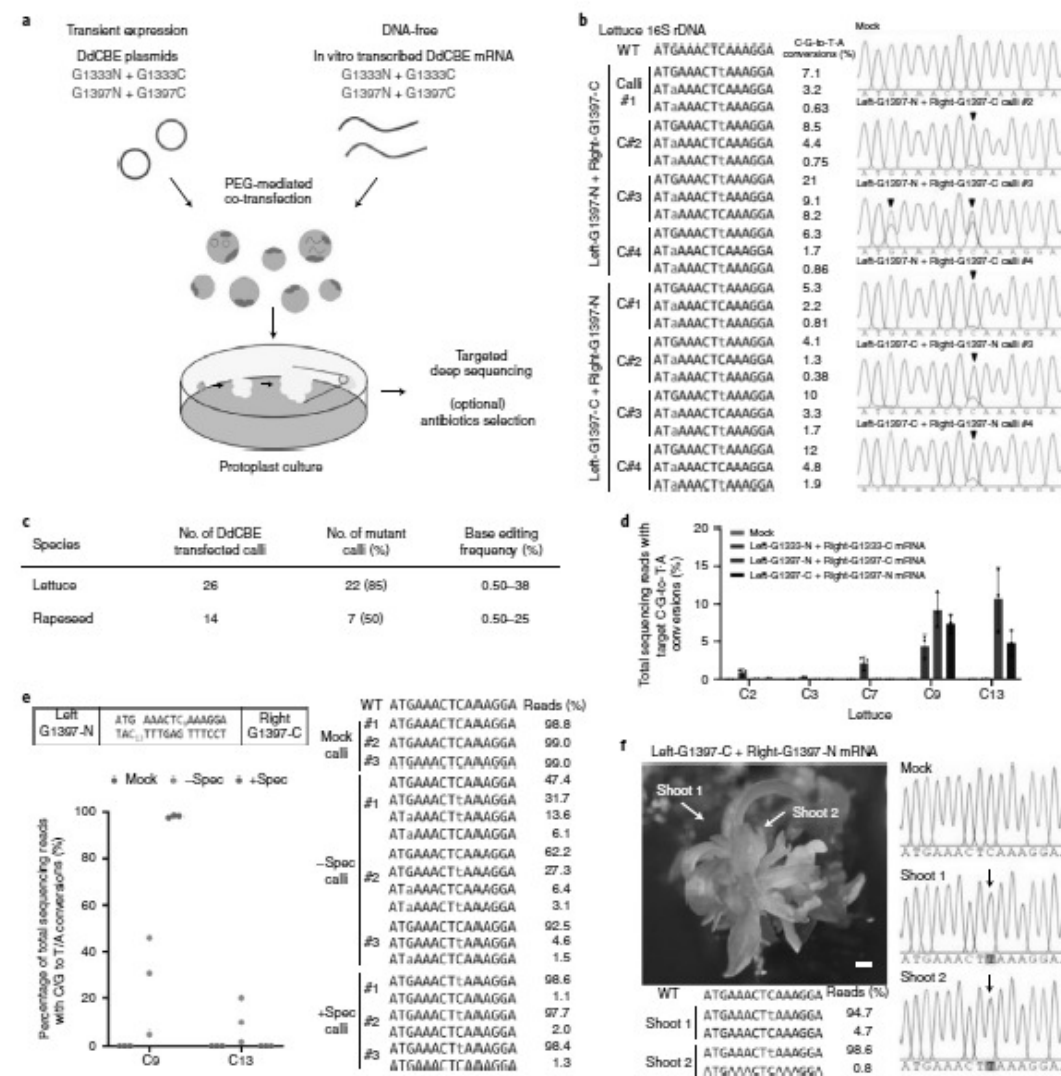
【Fig. 19】



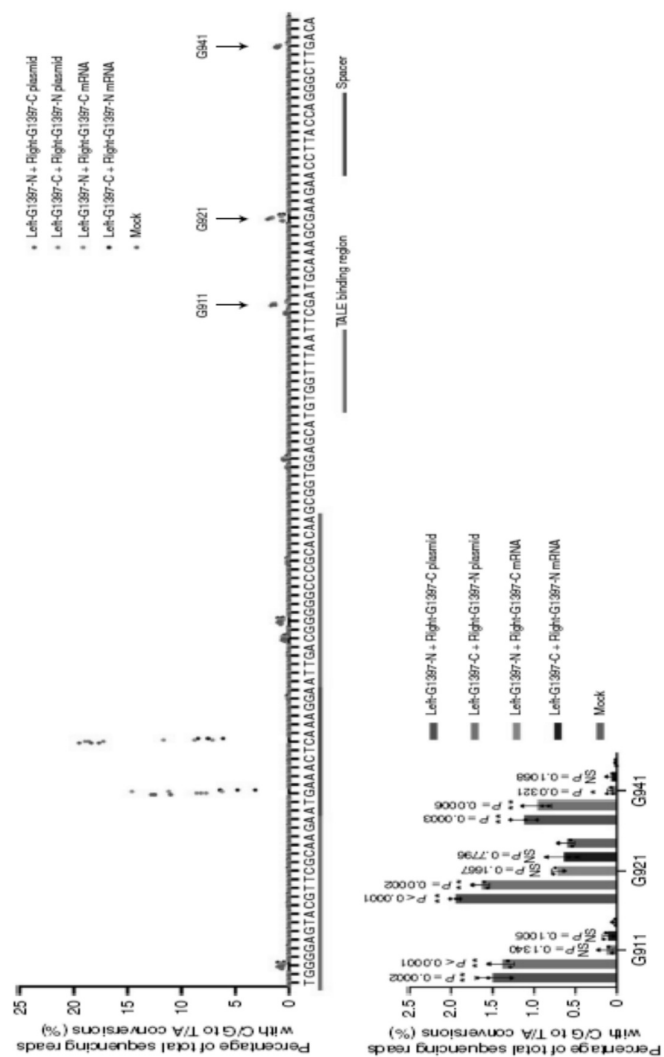
[Fig. 20]



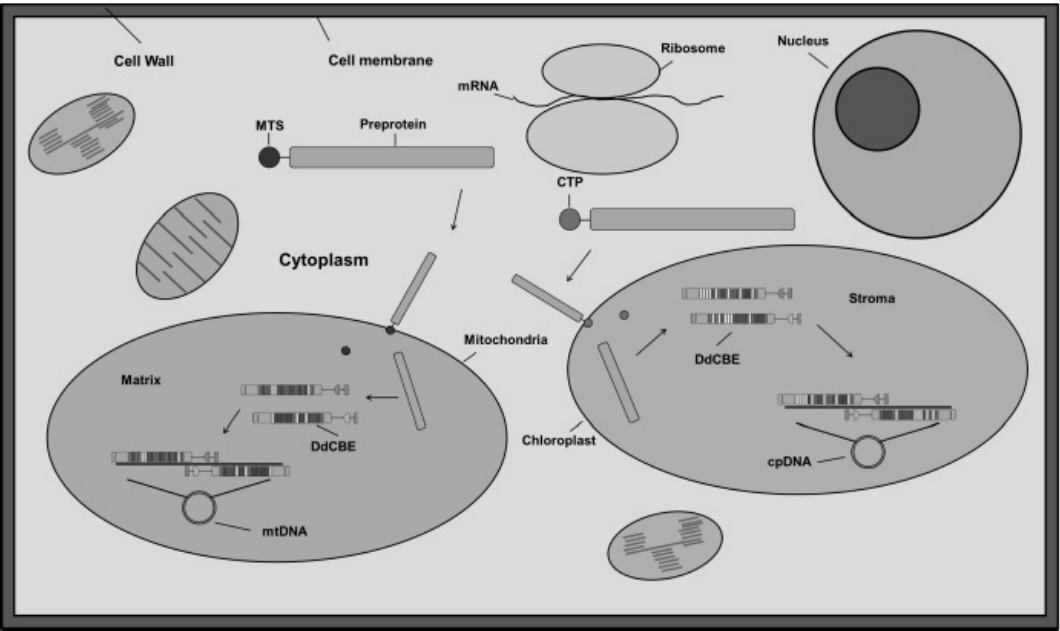
【Fig. 21】



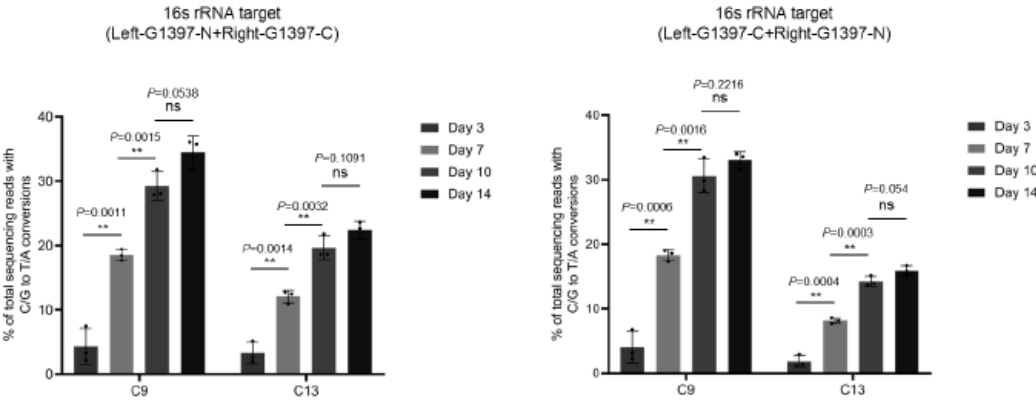
【Fig. 22】



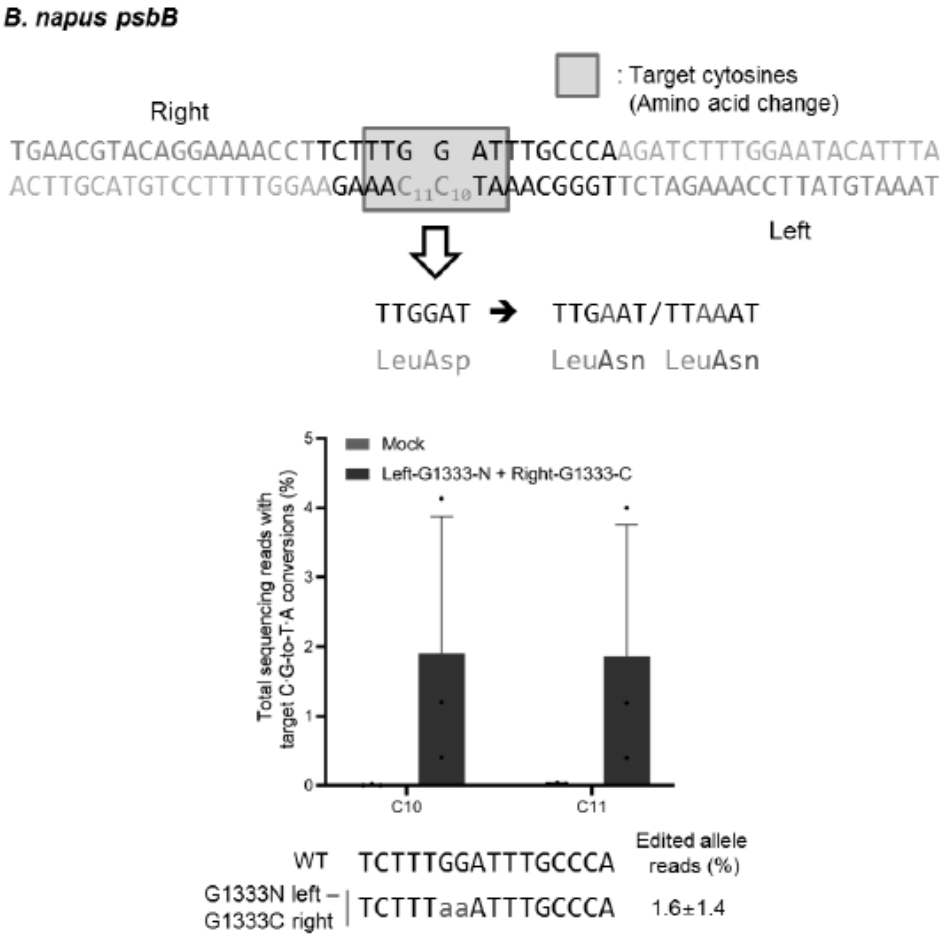
【Fig. 23】



【Fig. 24】



【Fig. 25】



【Fig. 26】

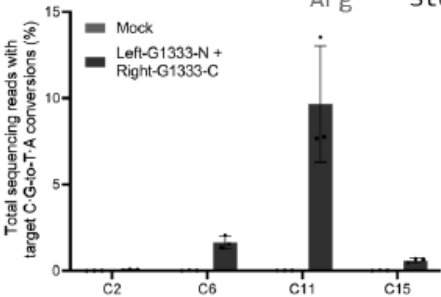
B. napus rps14

□ : Target cytosines
(Amino acid changes)

Left
TCGTTCTGTATCTGAGTTC₂TTTC₆G AATTATC₁₅GTATCGTTTTTCGTGGATTA
AGCAAGACATAGACTCAAG AAAG C₁₁TTAAATAG CATAGCAAAAAGCACCTAAT
Right



CGA → TGA/CAA/TAA
Arg Stop/Gln/Stop



WT	TCTTTCGAATTTATCGT	Edited allele reads (%)
G1333N left -	TCTTTCaAATTTATCGT	9.3±2.7
G1333C right	TCTTTtGAATTTATCGT	1.4±0.25
	TCTTTCGAATTTATtGT	0.39±0.094

【Fig. 27】

(a)

Lettuce 16s rDNA				Rapeseed 16s rDNA			
G1333N-Left + G1333C-Right	WT	ATGAAACTCAAAGGA	C-G-to-T-A conversions (%)	WT	ATGAAACTCAAAGGA	C-G-to-T-A conversions (%)	
	Callus #1	ATGAAACTtAAAGGA	0.82 %	G1333N-Left + G1333C-Right	ATGAAAtTtAAAGGA	0.32 %	
		ATGAAAtTtAAAGGA	0.67 %		ATGAAACTCAAAAaA	0.25 %	
		ATGAAACTCAAAGaA	0.33 %		ATaAAAtTtAAAAaA	0.11 %	
		ATGAAACTCAAAGGA	1.02 %		ATGAAAtTtAAAGaA	0.10 %	
	C#2	ATGAAAtTtAAAGGA	0.62 %		ATGAAAtTtAAAGGA	0.84 %	
		ATGAAACTtAAAGGA	0.66 %	C#2	ATGAAACTCAAAAaA	0.28 %	
	C#3	ATGAAAtTtAAAGGA	0.33 %		ATGAAACTtAAAaA	0.10 %	
		ATGAAACTtAAAGGA	0.35 %				
	C#4	ATGAAAtTtAAAGGA	0.19 %				
		ATGAAAtTtAAAGGA					

Lettuce <i>psbA</i>			
G1333N-Left + G1333C-Right	WT	GACCTTGGATTGCTGTTG	C-G-to-T-A conversions (%)
	C#1	GACCTTaaATTGCTGTTG	2.91 %
		GAAttTGGATTGCTGTTG	0.26 %
		GAAttTaaATTGCTGTTG	0.22 %
		GACCTTaaATTGCTGTTG	3.11 %
	C#2	GAAttTaaATTGCTGTTG	0.51 %
		aACCTTaaATTGCTGTTG	0.29 %
		GACCTTaaATTGCTGTTG	1.36 %
		GAAttTGGATTGCTGTTG	0.45 %
	C#3	GACCTTGGATTaCTGTTG	0.25 %
		GACCTTaaATTGCTGTTG	2.31 %
		GACCTTGaATTGCTGTTG	0.27 %
		GAAttTGGATTGCTGTTG	0.24 %

(b)

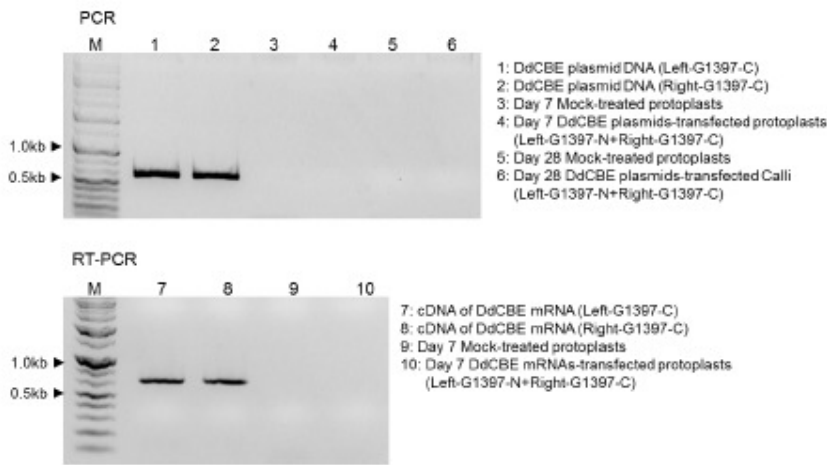
Rapeseed <i>atp6</i>			
G1333N-Left + G1333C-Right	WT	GGGATTTCAAAGAC	C-G-to-T-A conversions (%)
	C#1	GGGATTTtAAAGAC	24.92 %
	C#2	GGGATTTtAAAGAC	0.41 %
		GGGATTTtAAAaAC	0.13 %

Rapeseed <i>rps14</i>			
G1333N-Left + G1333C-Right	WT	TCITTCGAATTTATCGT	
	C#1	TCITTCaAATTTATCGT	0.52 %
		TCITTTtGAATTTATCGT	0.30 %
		TCITTCaAATTTATCaT	1.00 %
	C#2	TCITTCaAATTTATCGT	0.53 %
		TCITTCGAATTTATCaT	0.37 %

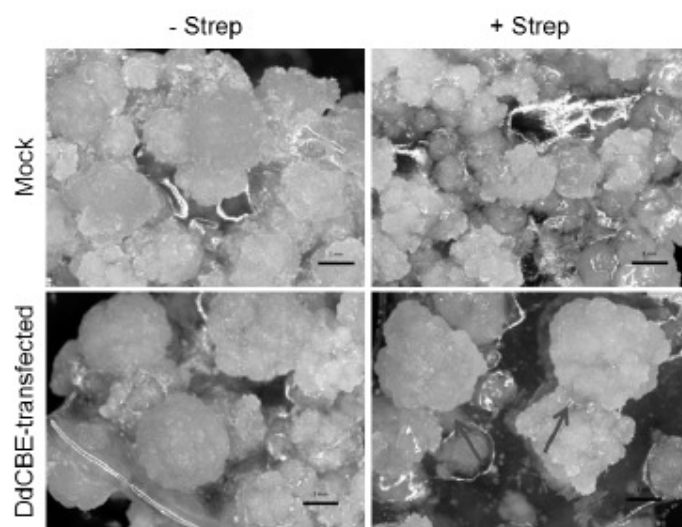
【Fig. 28】

Lettuce 16s rDNA		
	WT	Edited allele reads (%)
Left-G1333-N + Right- G1333-C mRNA	ATGAAACTCAAAGGA	
	ATGAAACTtAAAGGA	2.1±0.51
	ATGAAAtTtAAAGGA	2.09±0.70
Left-G1397-N + Right- G1397-C mRNA	ATGAAACTCAAAGaA	0.69±0.25
	ATaAAACTCAAAGGA	9.8±3.2
	ATGAAACTtAAAGGA	8.3±1.8
Left-G1397-C + Right- G1397-N mRNA	ATaAAACTtAAAGGA	0.75±0.13
	ATGAAACTtAAAGGA	6.9±0.88
	ATaAAACTCAAAGGA	4.4±1.3
	ATaAAACTtAAAGGA	0.34±0.089

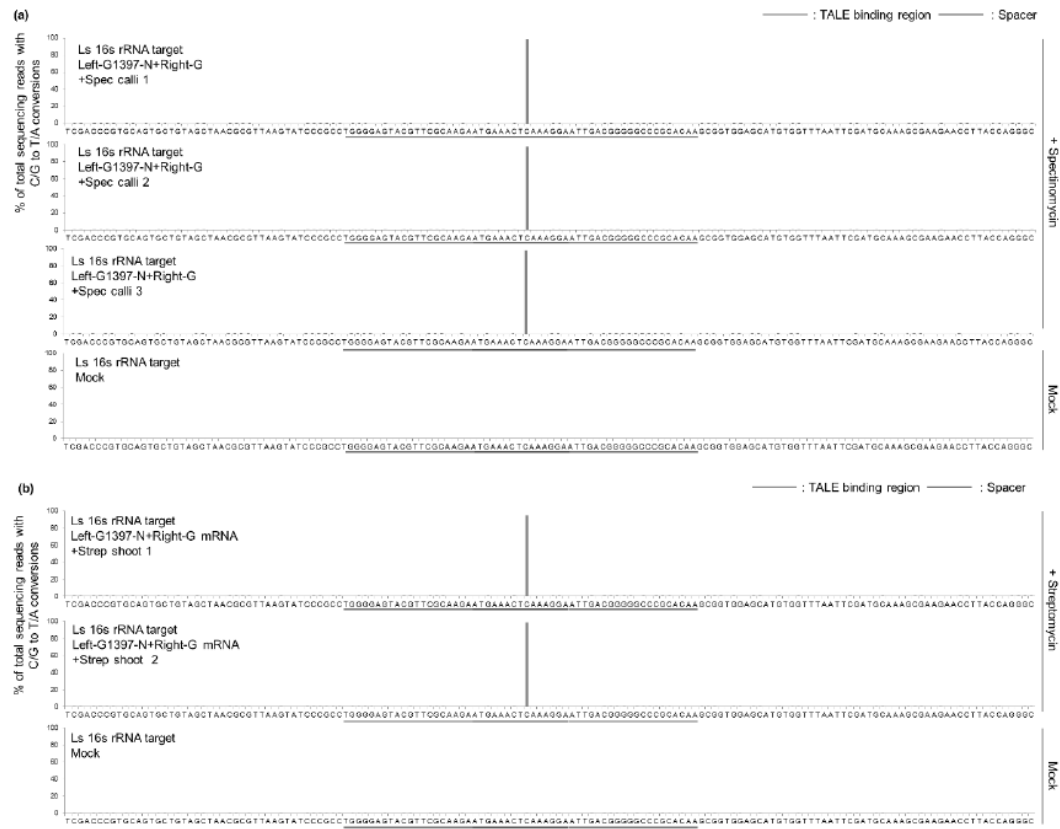
【Fig. 29】



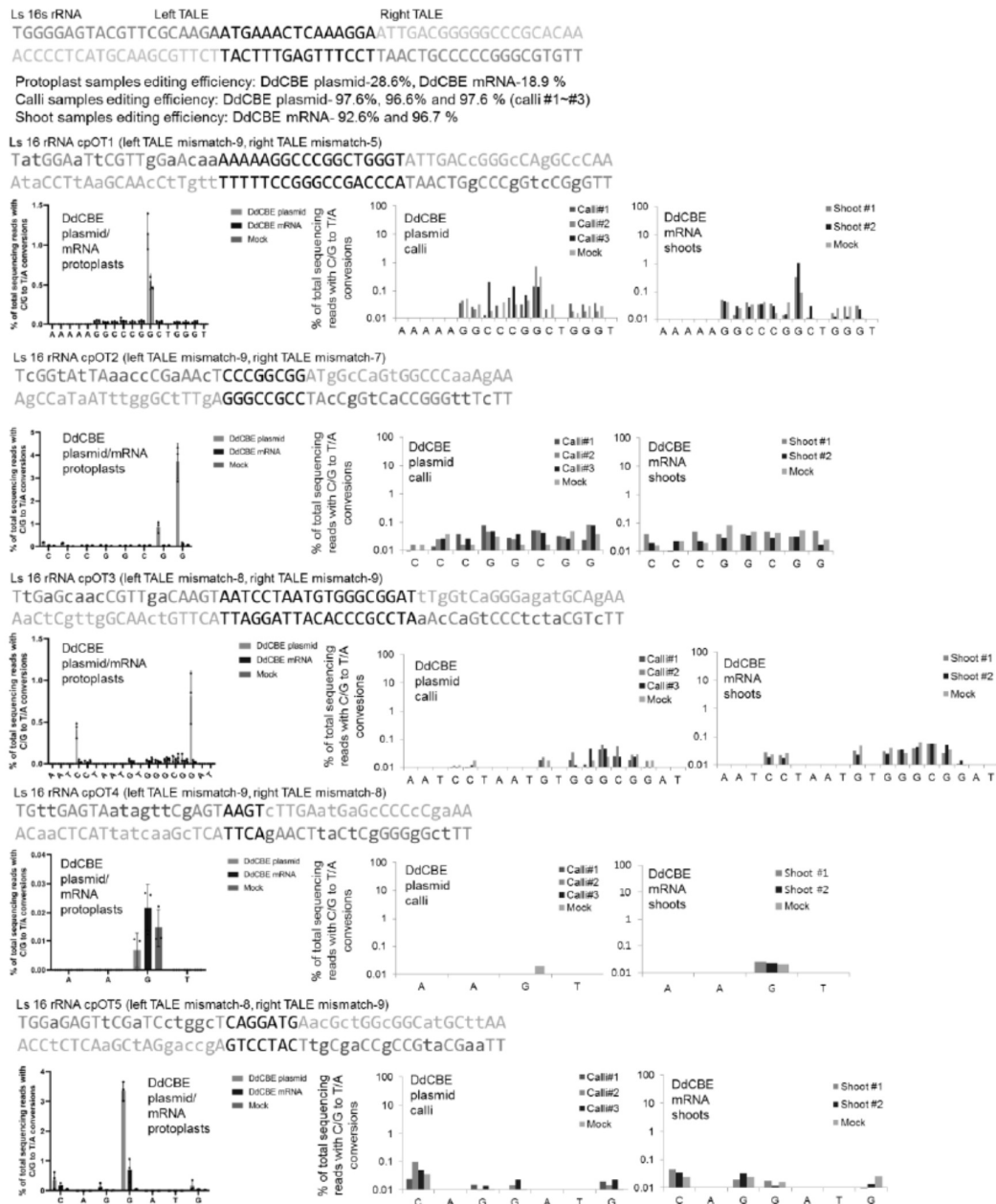
【Fig. 30】



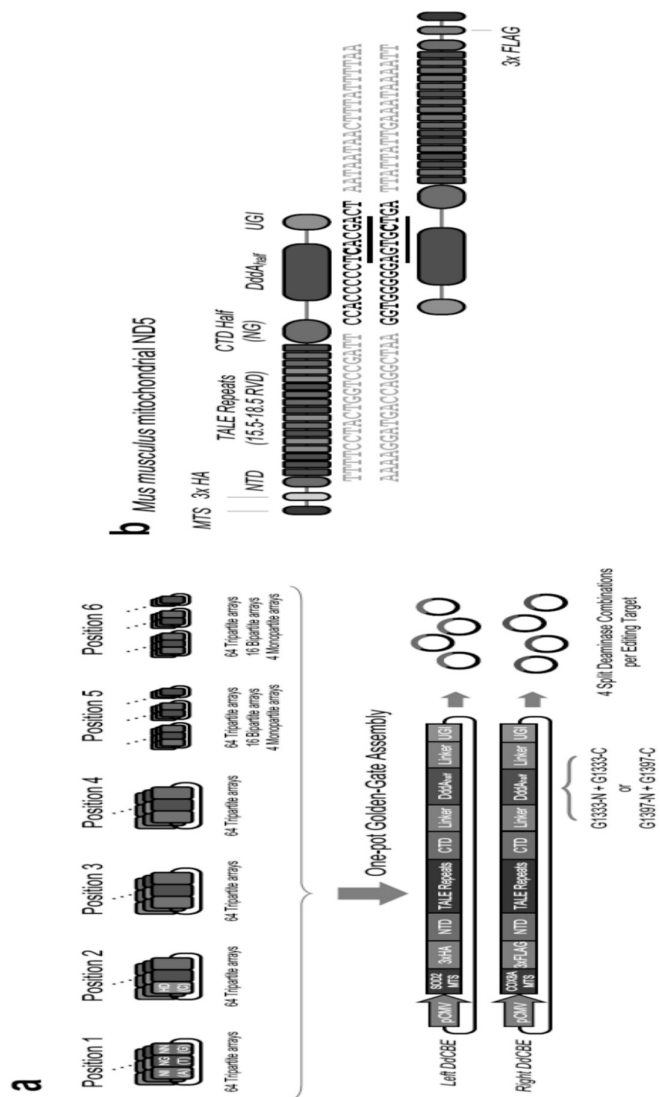
【Fig. 31】



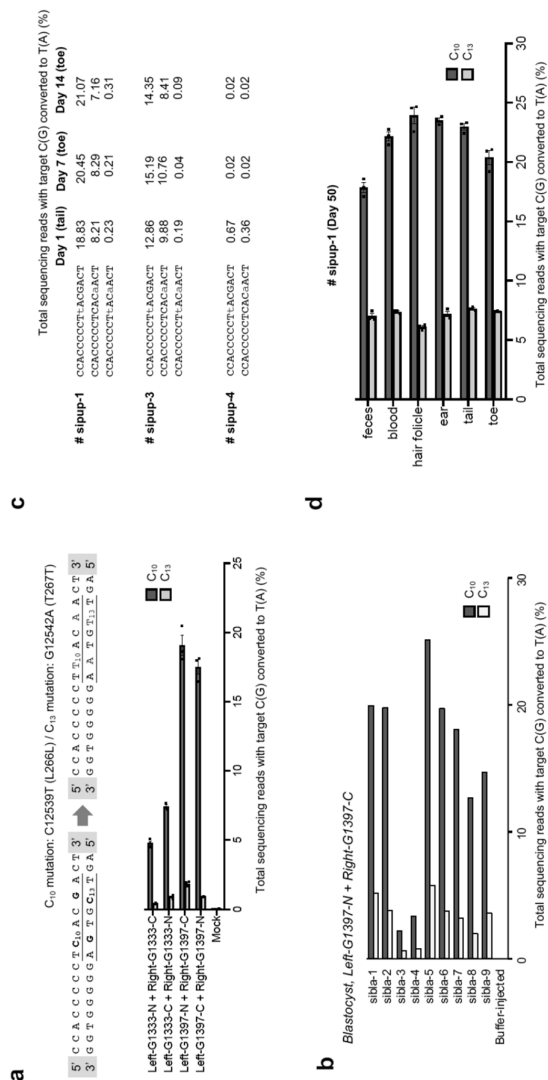
[Fig. 32]



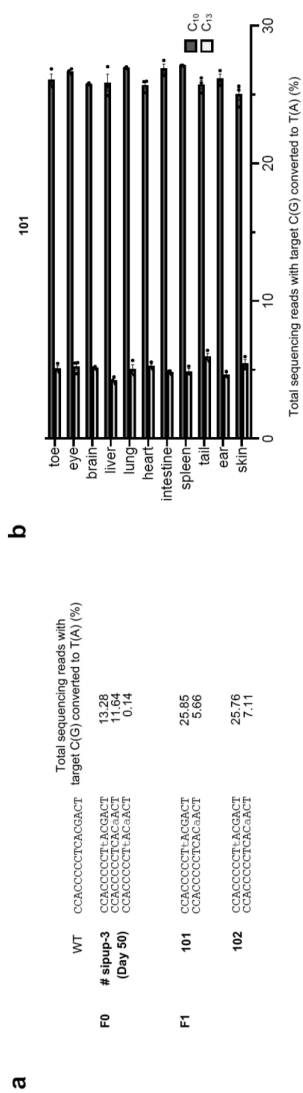
【Fig. 33】



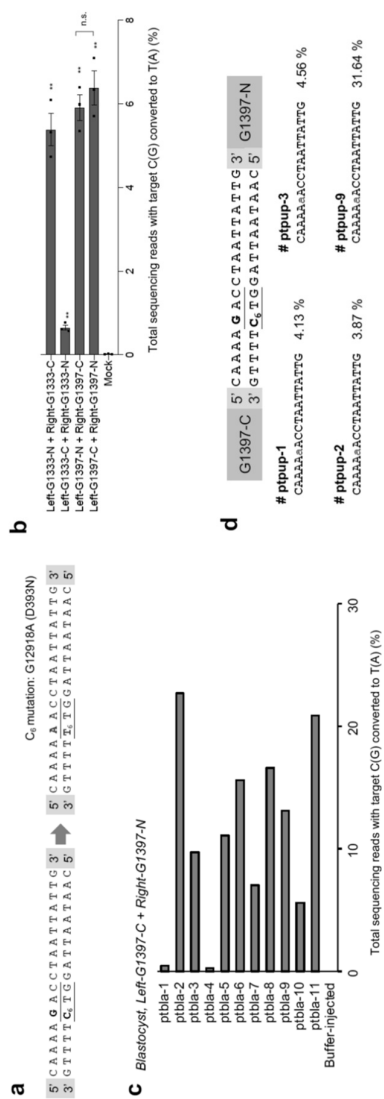
【Fig. 34】



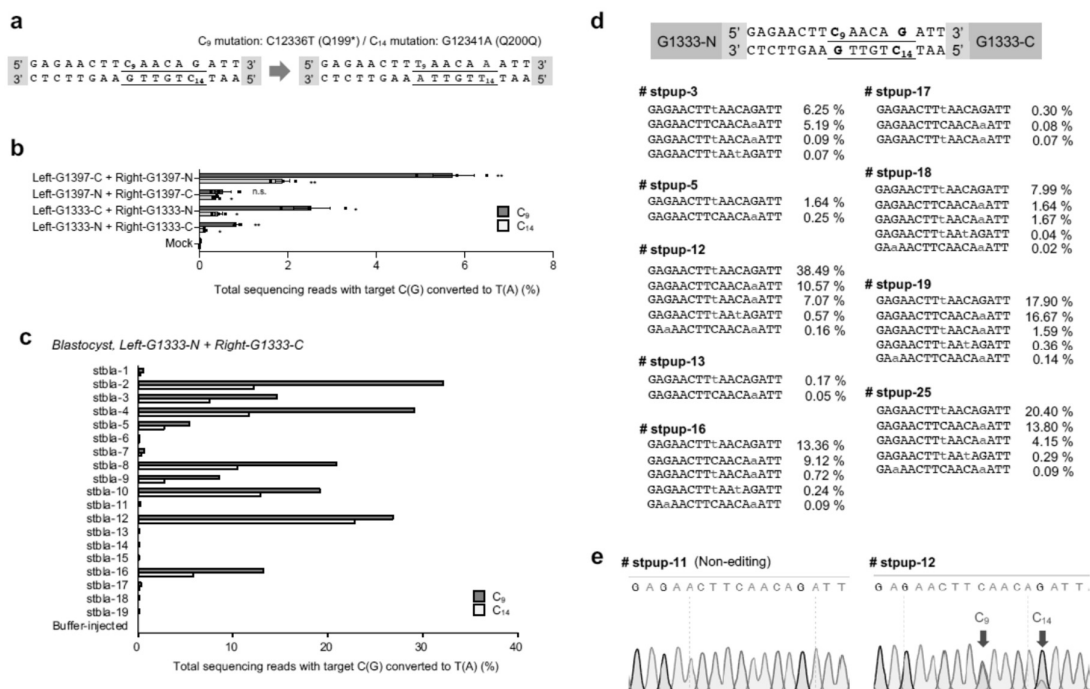
【Fig. 35】



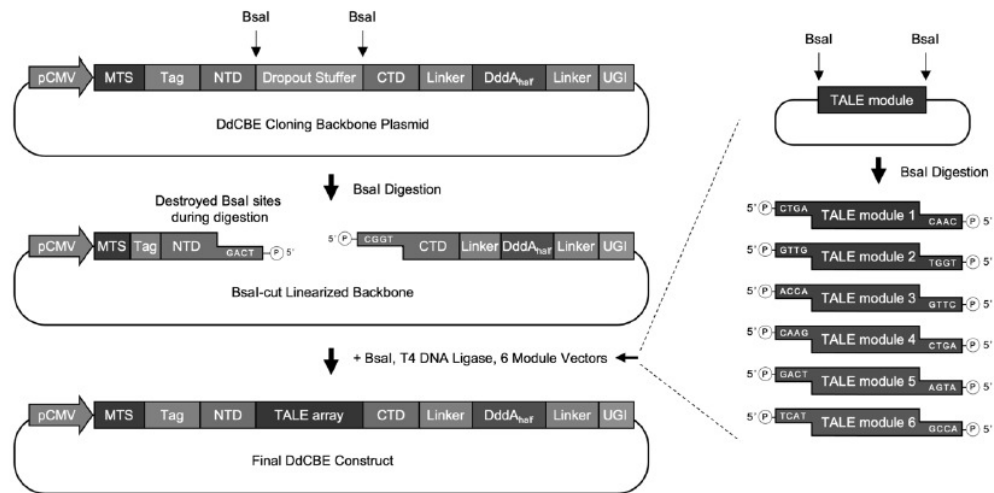
【Fig. 36】



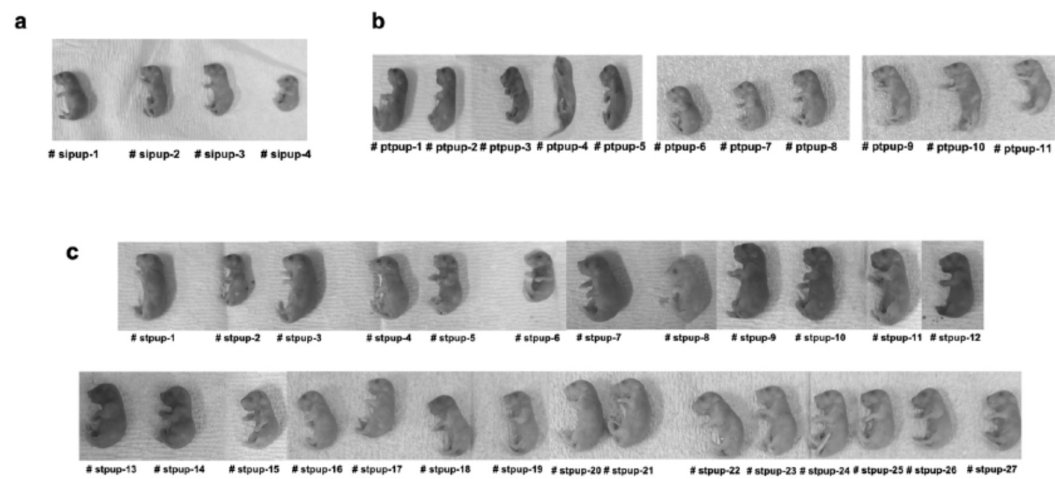
【Fig. 37】



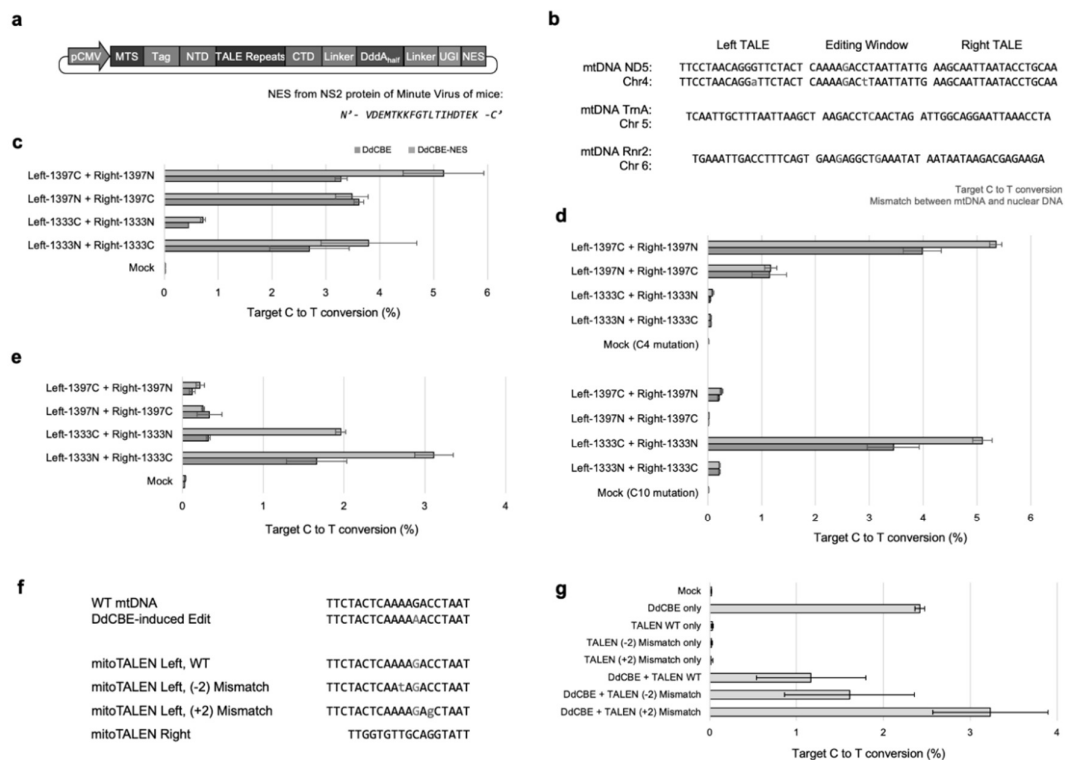
【Fig. 38】



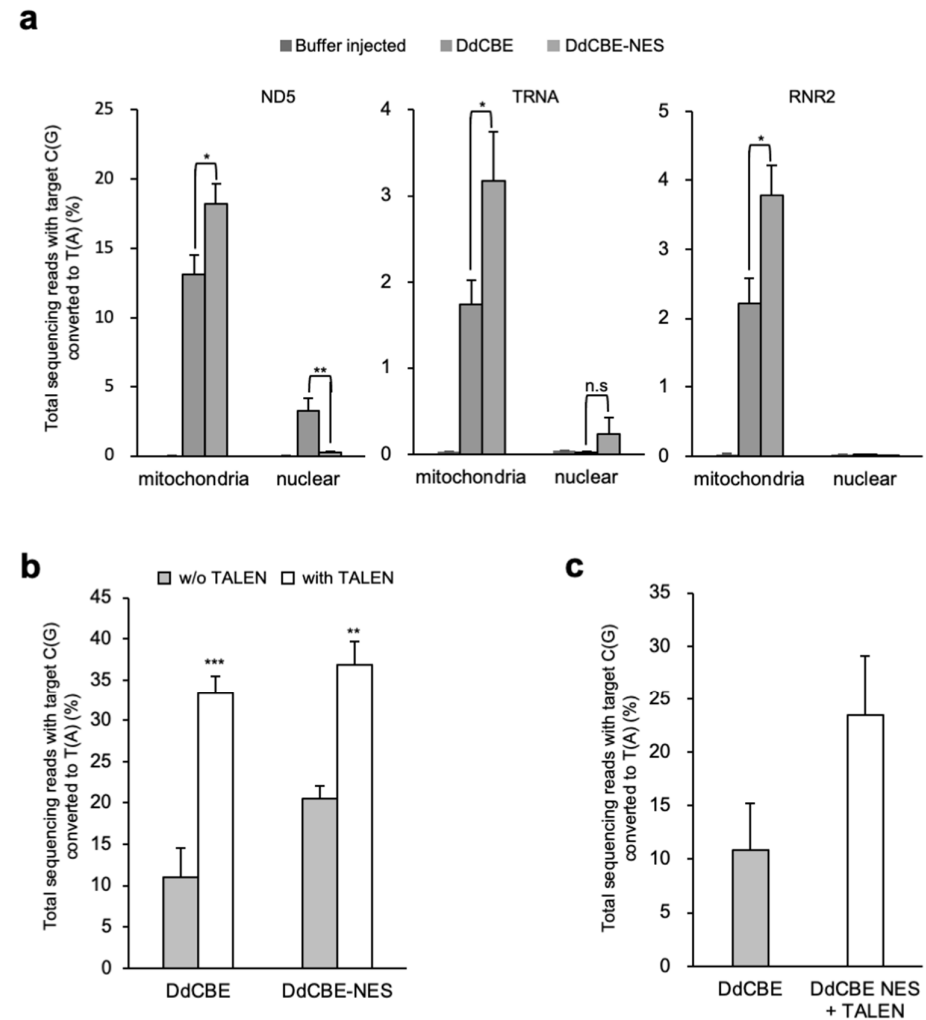
【Fig. 39】



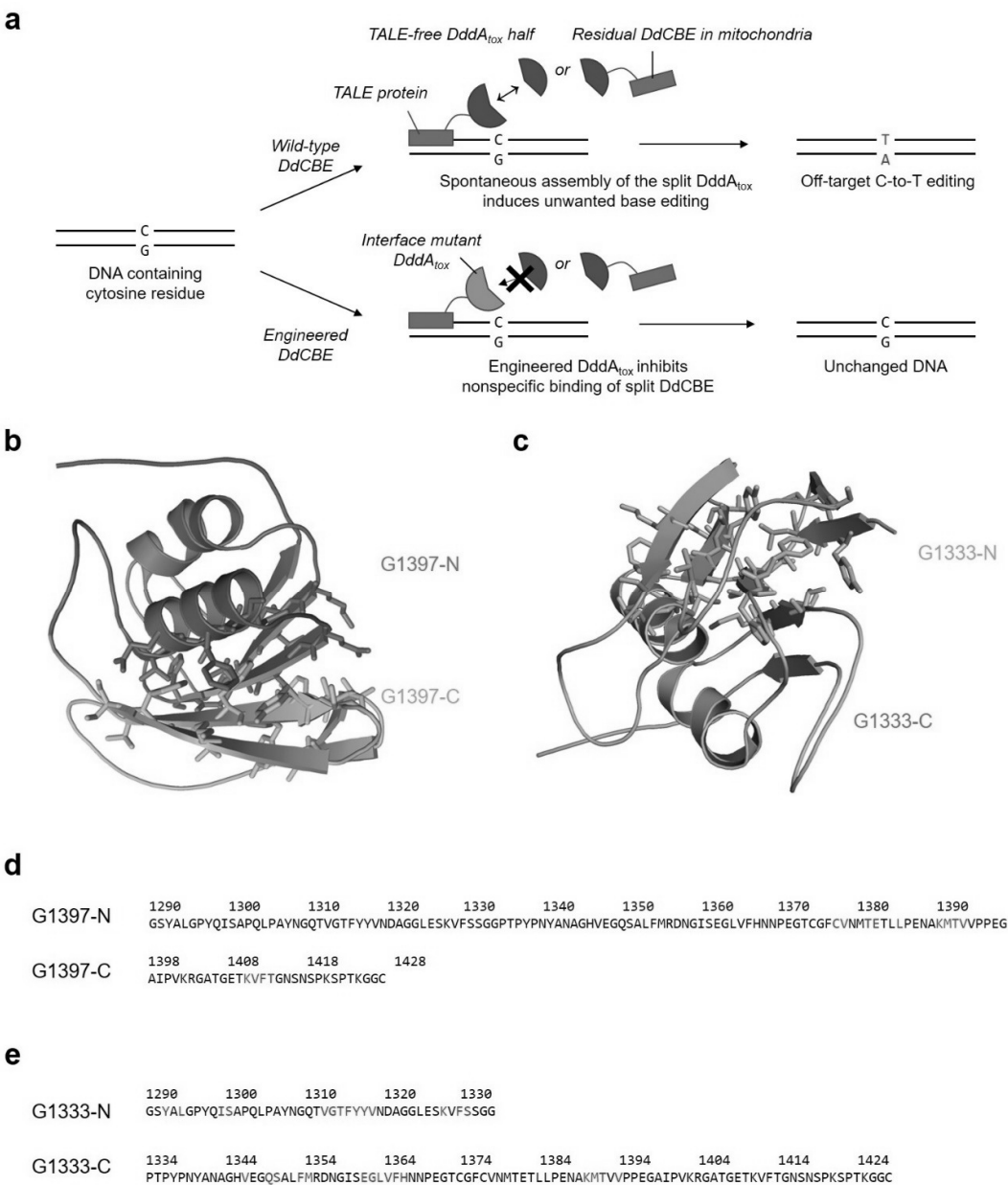
【Fig. 40】



【Fig. 41】

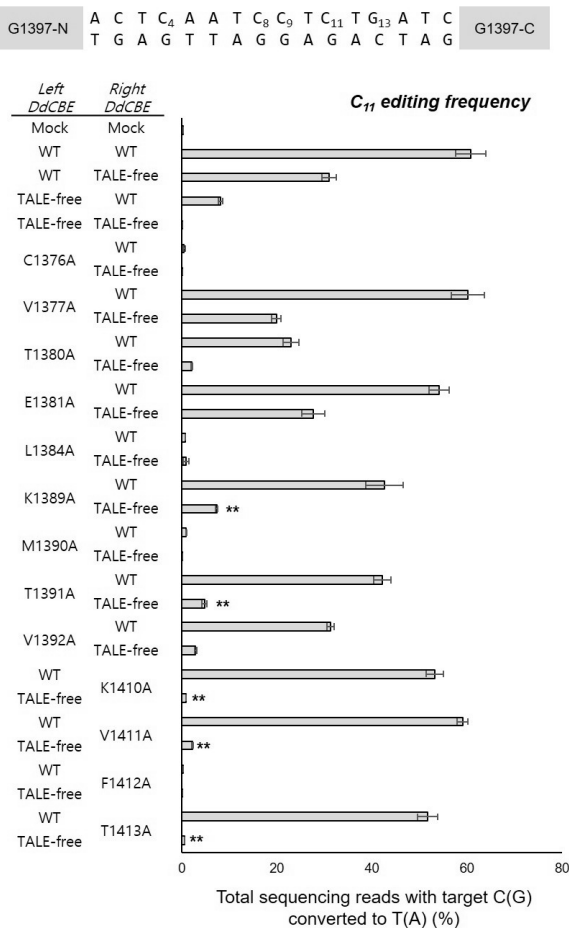


【Fig. 42】

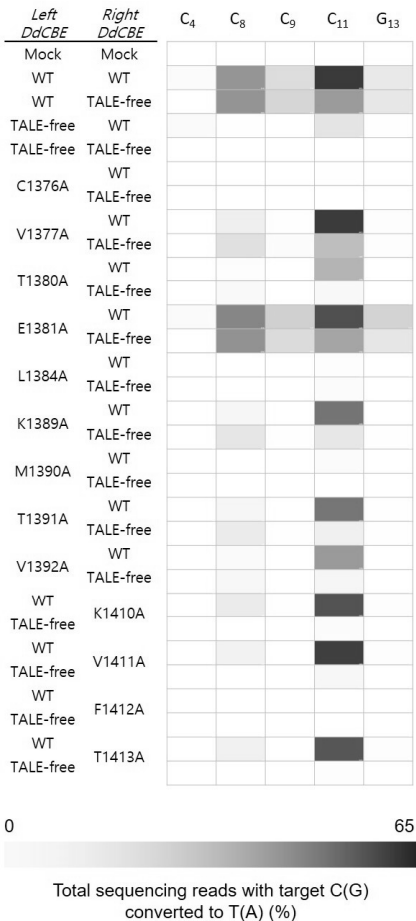


【Fig. 43】

a Human mtND1

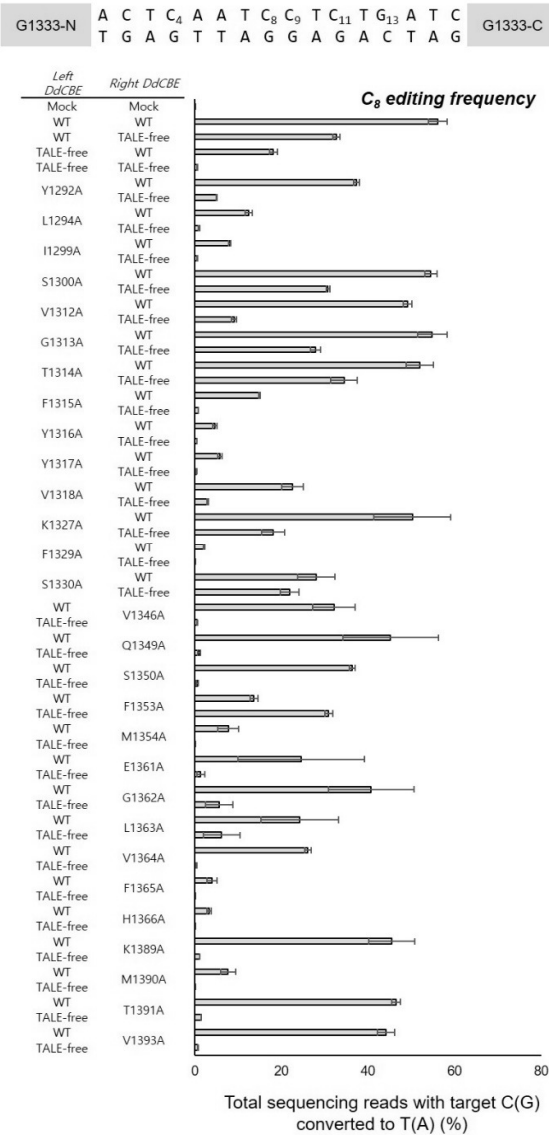


b

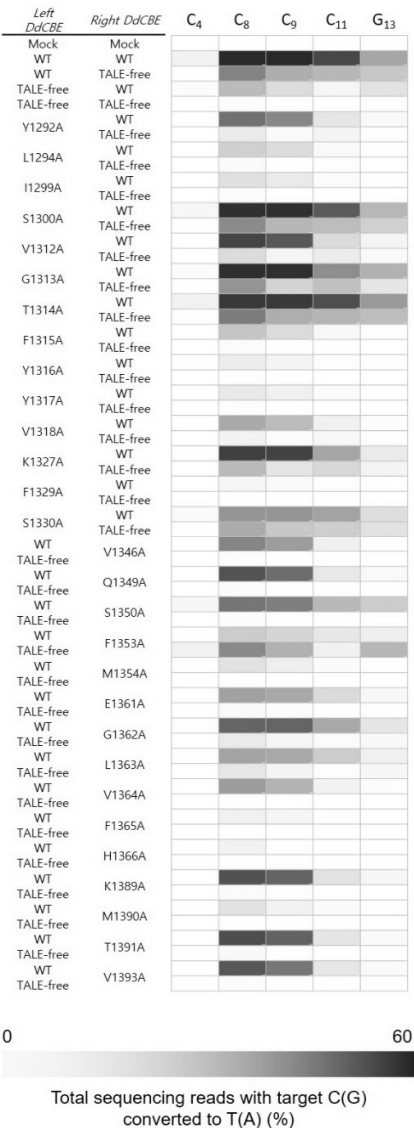


【Fig. 44】

a Human mtND1



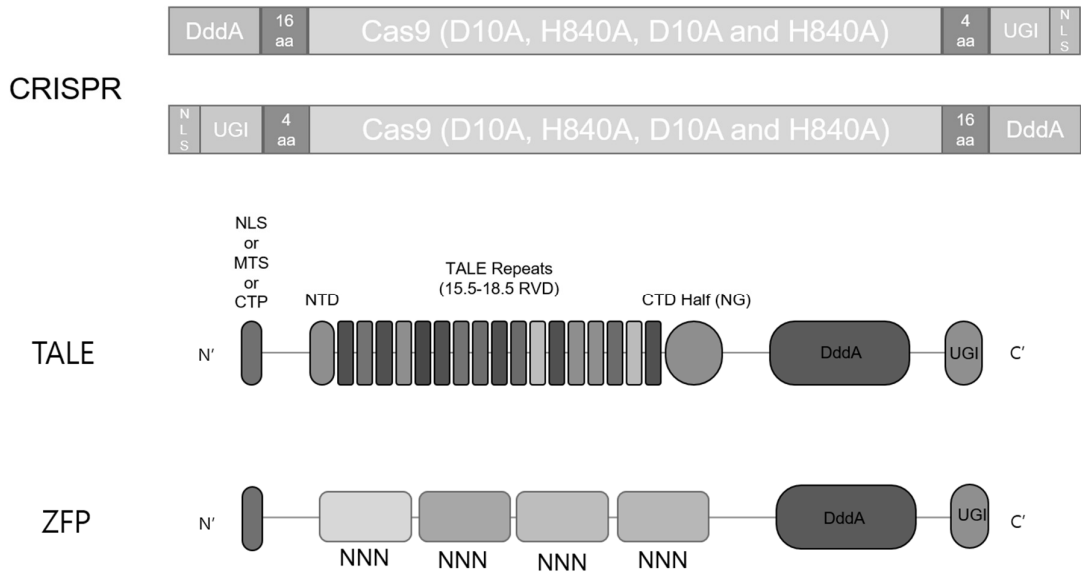
b



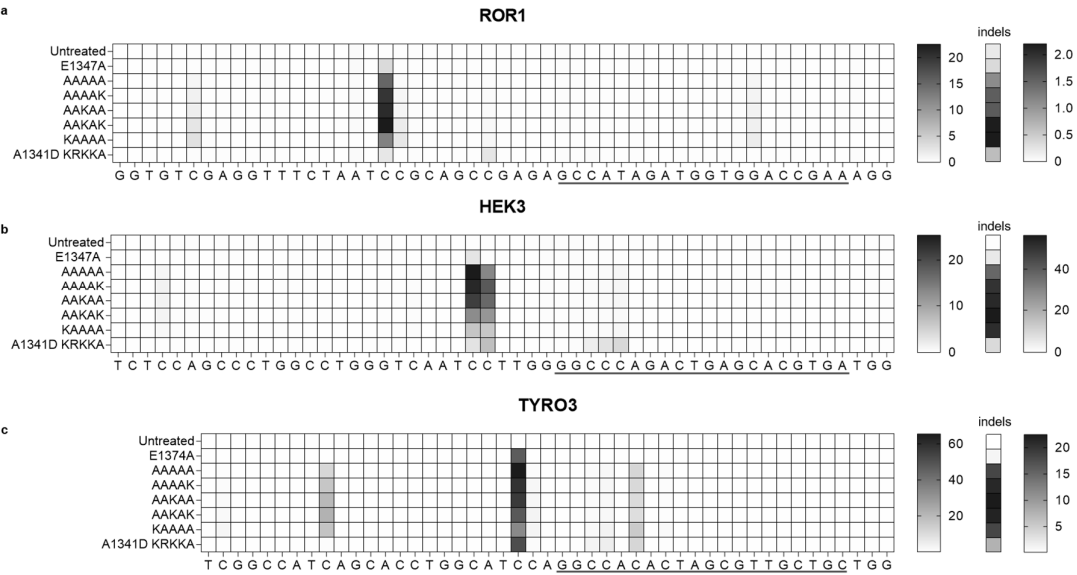
【Fig. 45】

Wild Type	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYANAGHVEGQ	60
AAKAK	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYANAGHVEGQ	60
AAKAA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYANAGHVEGQ	60
AAAAA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYANAGHVEGQ	60
AAAAK	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYANAGHVEGQ	60
KAAAA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYANAGHVEGQ	60
A1341D_KRKKA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTYPNYDNAGHVEGQ	60
Wild Type	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVKRGATGET	120
AAKAK	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVAAAGATGET	120
AAKAA	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVAAAGATGET	120
AAAAA	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVAAAGATGET	120
AAAAK	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVAAAGATGET	120
KAAAA	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVKAAGATGET	120
A1341D_KRKKA	SALFMRDNGISEGLVFHNNPEGTCGFCVNMTEPLLPEAKMTVVPPEGAIPVKRGATGET	120
Wild Type	KVFTGNSNSPKSPTKGGC	138
AAKAK	KVFTGNSNSPASPPTKGGC	138
AAKAA	KVFTGNSNSPASPPTAGGC	138
AAAAA	AVFTGNSNSPASPPTAGGC	138
AAAAK	AVFTGNSNSPASPPTKGGC	138
KAAAA	AVFTGNSNSPASPPTAGGC	138
A1341D_KRKKA	KVFTGNSNSPKSPTAGGC	138

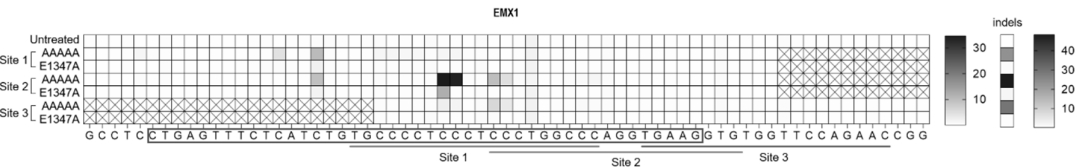
【Fig. 46】



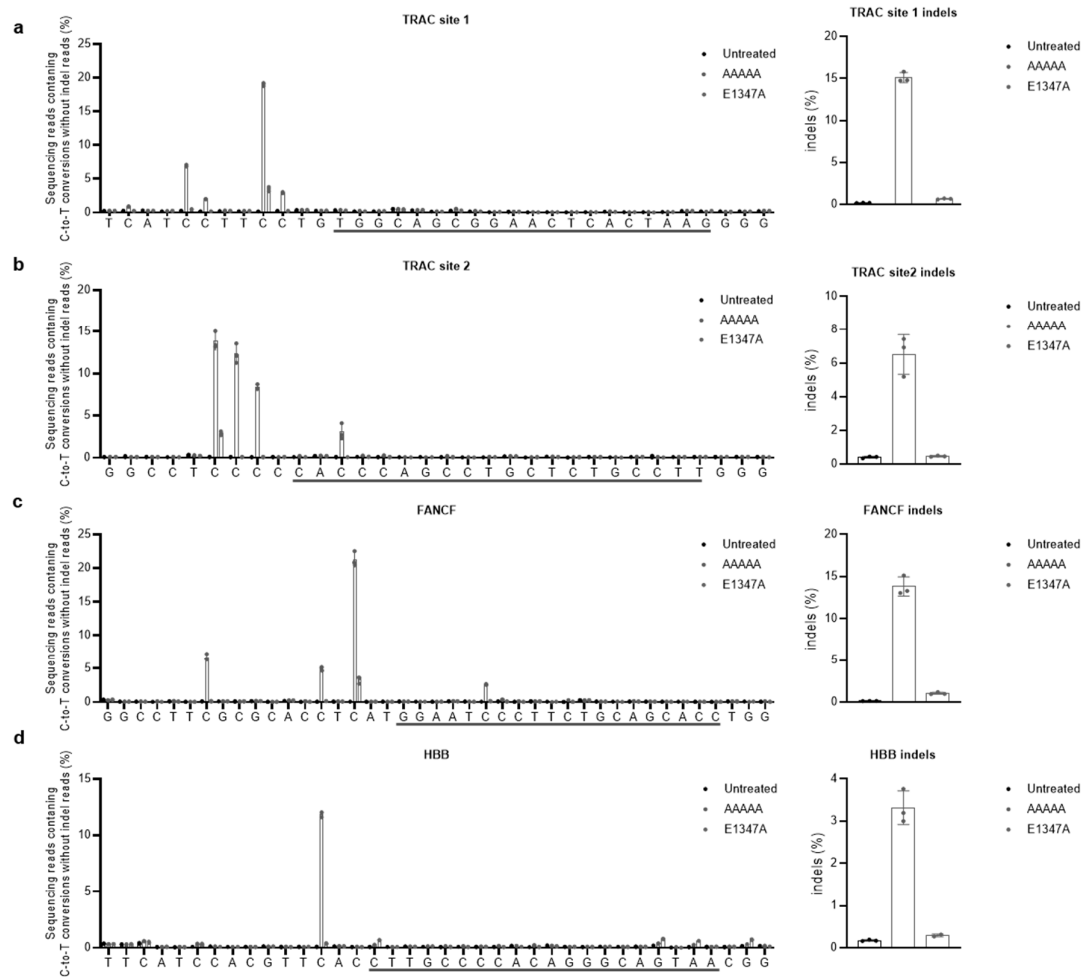
【Fig. 47】



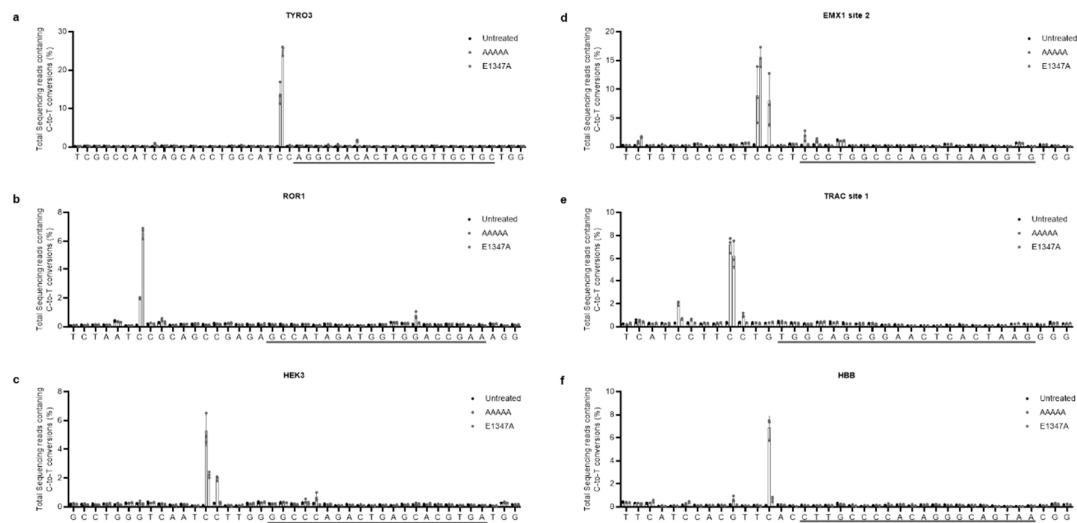
【Fig. 48】



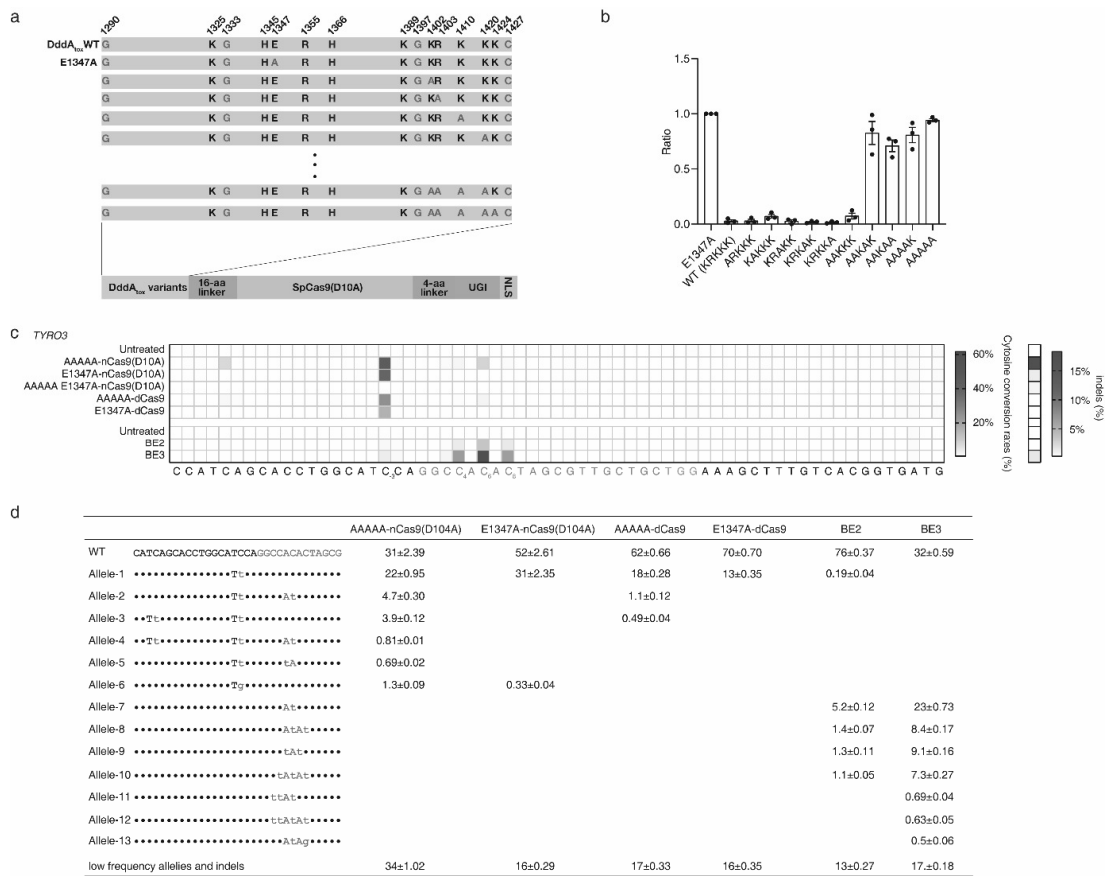
【Fig. 49】



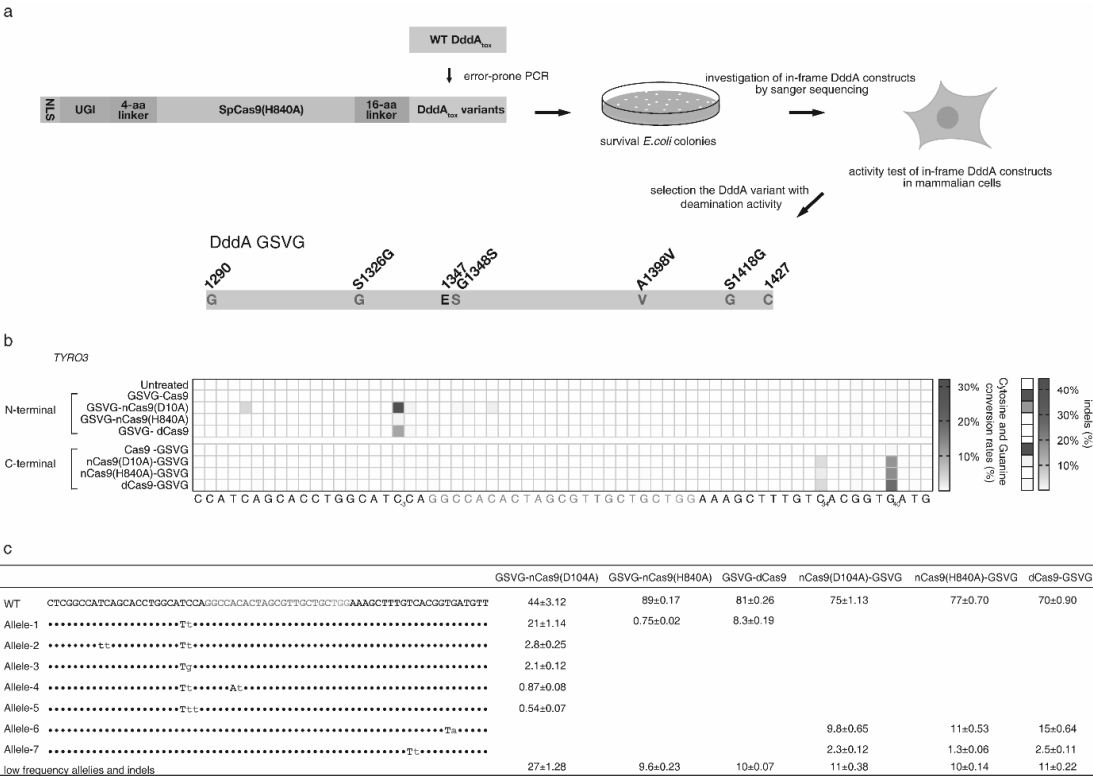
[Fig. 50]



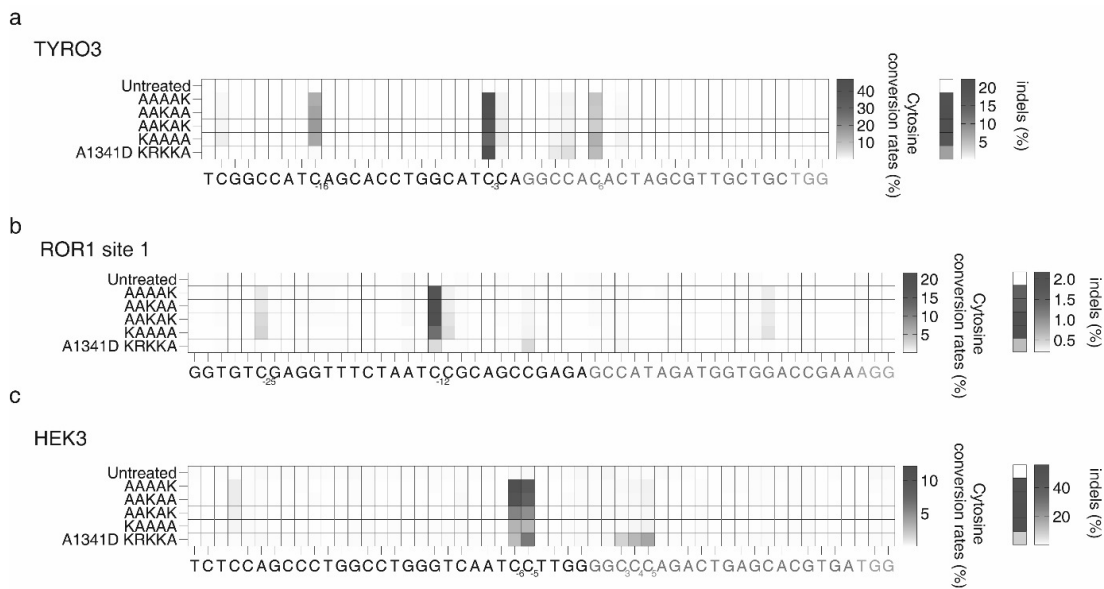
【Fig. 51】



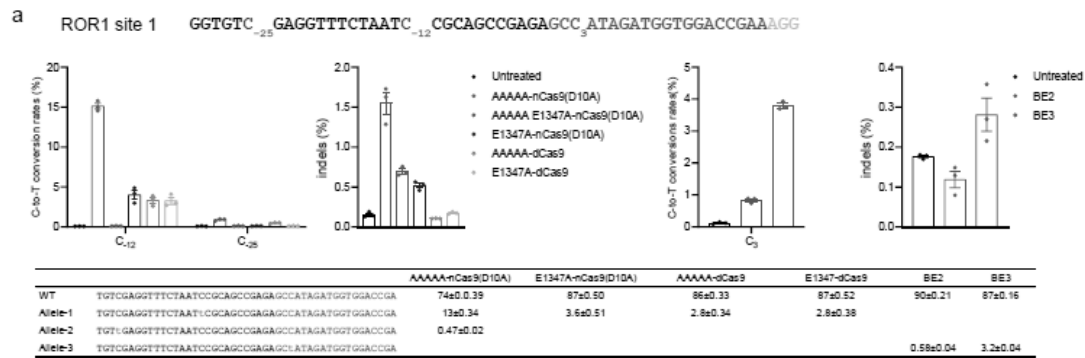
【Fig. 52】



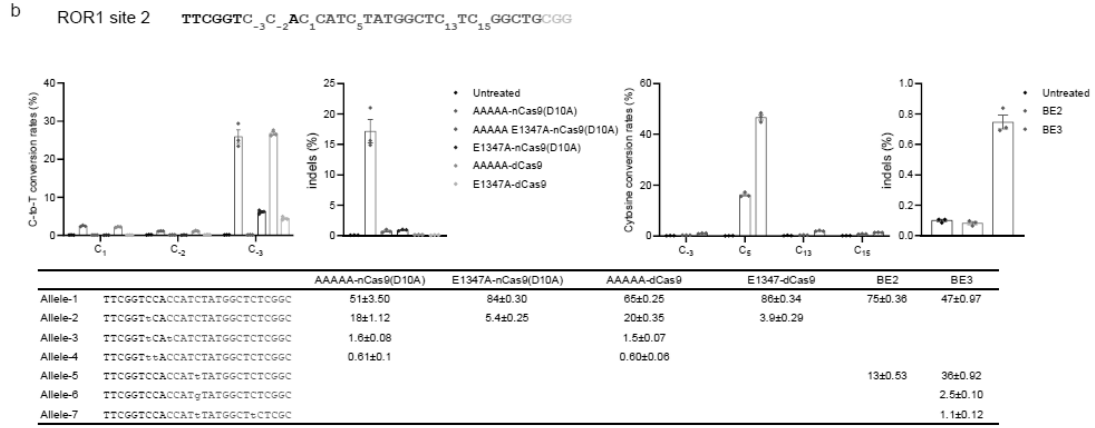
【Fig. 53】



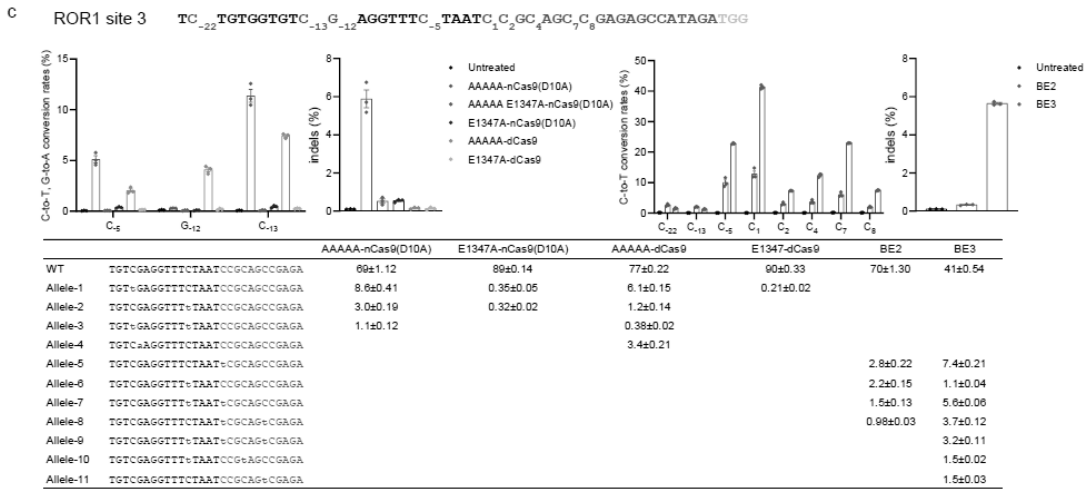
【Fig. 54a】



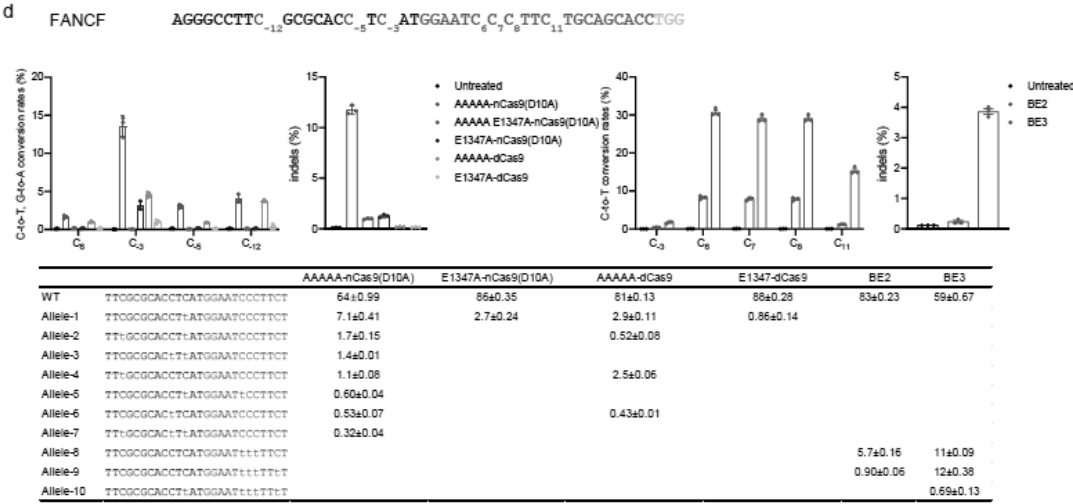
【Fig. 54b】



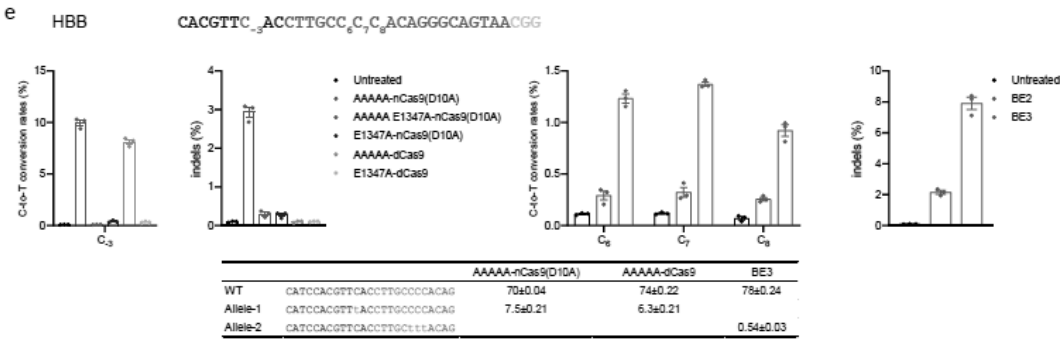
【Fig. 54c】



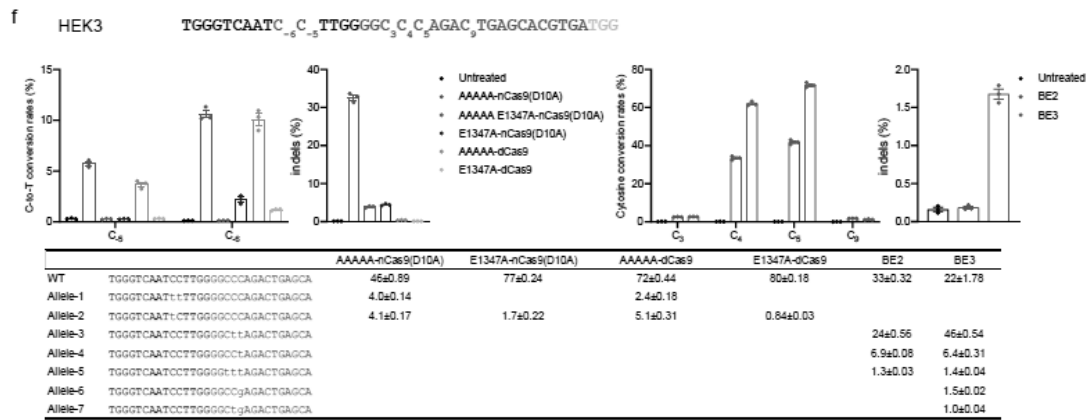
【Fig. 54d】



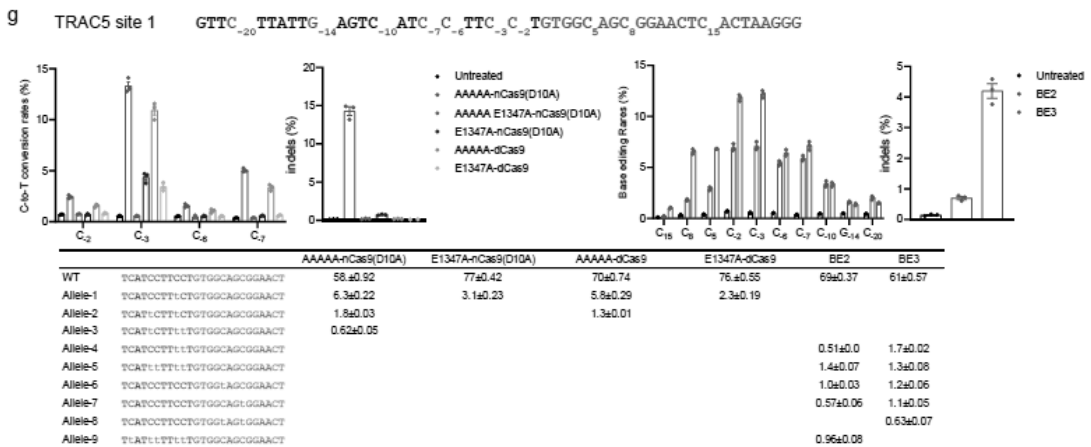
【Fig. 54e】



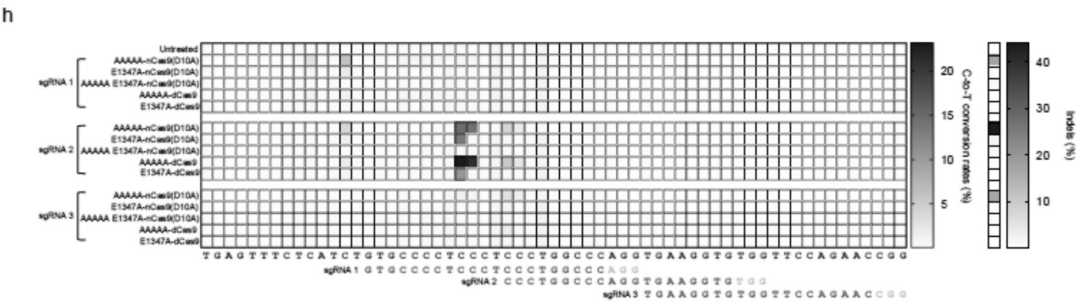
[Fig. 54f]



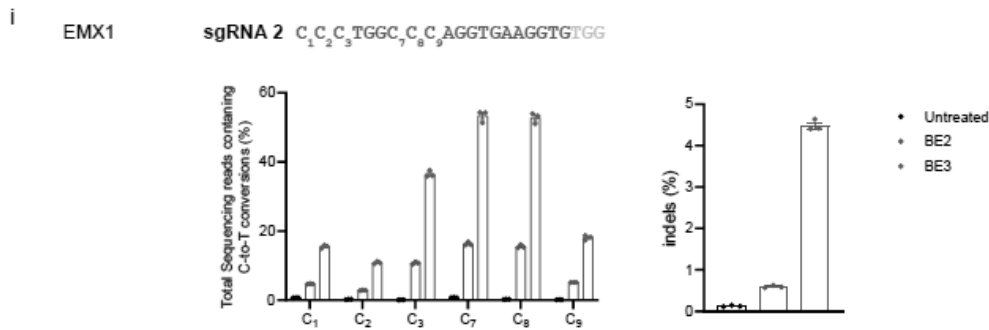
[Fig. 54g]



【Fig. 54h】



【Fig. 54i】

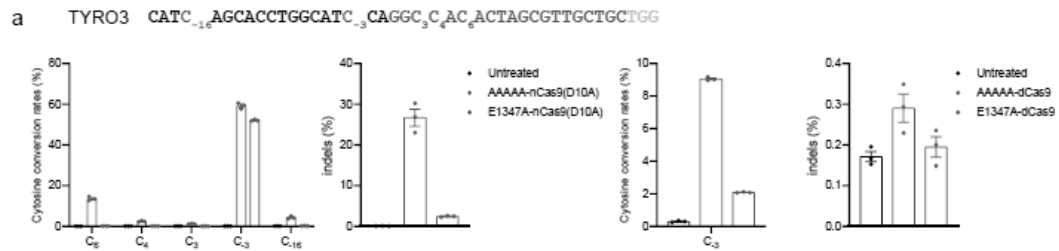


【Fig. 54j】

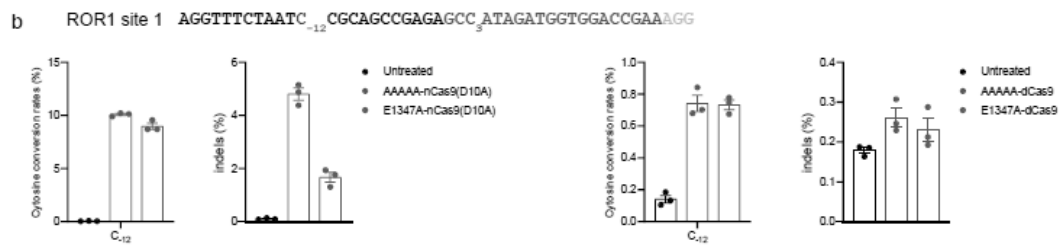
j

		AAAAA-nCas9(D10A)	E1347A-nCas9(D10A)	AAAAA-dCas9	E1347A-dCas9	BE2	BE3
WT	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG	34±1.32	69±0.44	62±0.38	73±1.02	55±0.38	22±0.60
Allele-1	TCTCATCTGTGCCCTTCTCCCTGGCCAGGTG	5.7±0.15		12±0.55			
Allele-2	TCTCATCTGTGCCCTTCTCCCTGGCCAGGTG	1.7±0.11		0.78±0.02			
Allele-3	TCTCATCTGTGCCCTTCTCCCTGGCCAGGTG	1.0±0.05		1.8±0.02			
Allele-4	TCTCATCTGTGCCCTTCTTCTGGCCAGGTG	0.87±0.06		1.4±0.03			
Allele-5	TCTCATCTGTGCCCTTCTCCCTGGCCAGGTG		10±0.55	1.4±0.05	7.8±0.71		
Allele-6	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG		0.95±0.02		0.50±0.01		
Allele-7	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG					3.2±0.14	10±0.09
Allele-8	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG					2.6±0.14	8.2±0.17
Allele-9	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG					1.3±0.06	2.6±0.11
Allele-10	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG					1.1±0.05	3.7±0.10
Allele-11	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG						3.5±0.14
Allele-12	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG						2.4±0.15
Allele-13	TCTCATCTGTGCCCTCCCTCCCTGGTTCAGGTG						2.3±0.18

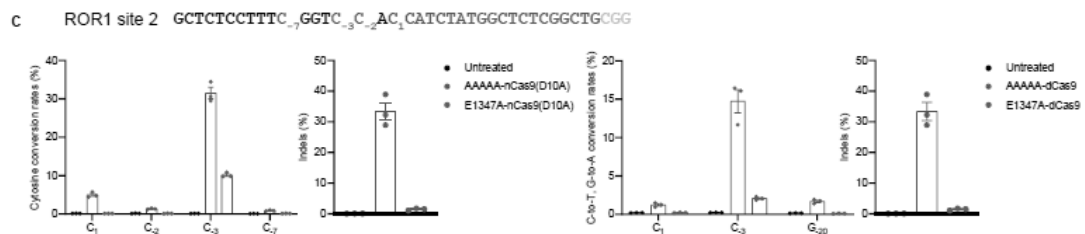
【Fig. 55a】



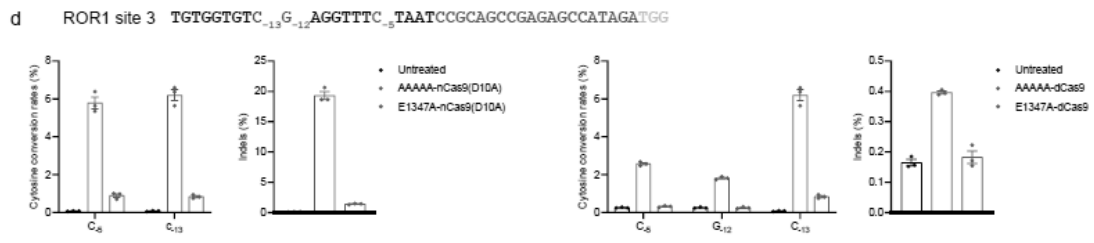
【Fig. 55b】



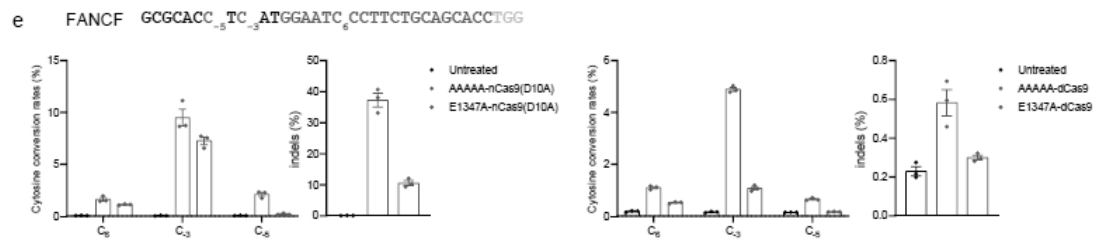
【Fig. 55c】



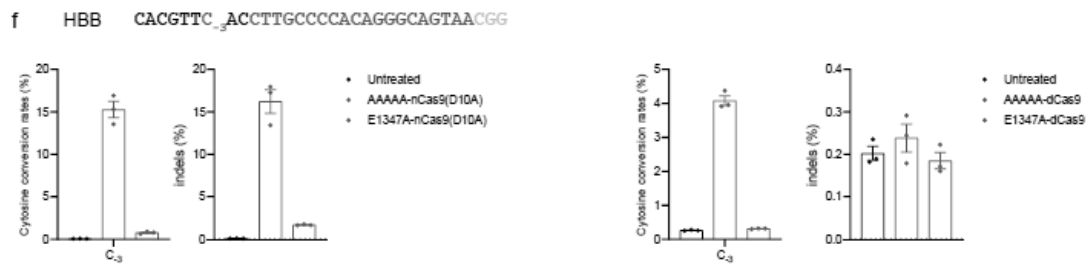
【Fig. 55d】



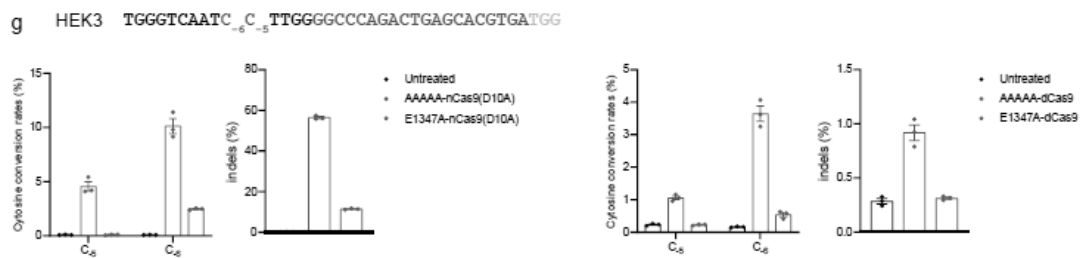
【Fig. 55e】



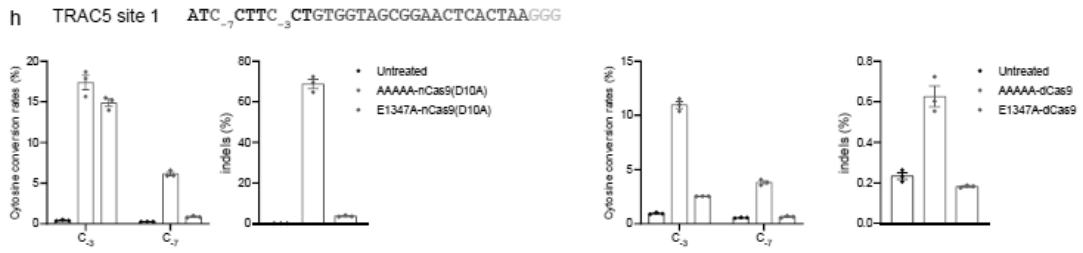
【Fig. 55f】



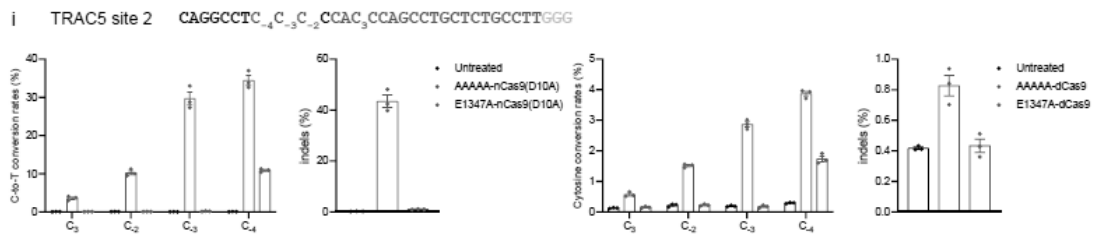
【Fig. 55g】



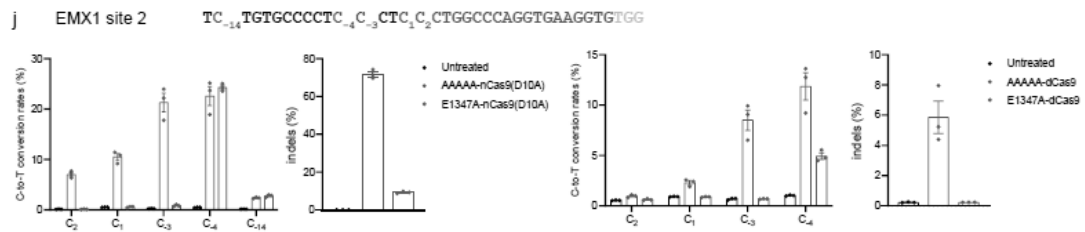
【Fig. 55h】



【Fig. 55i】



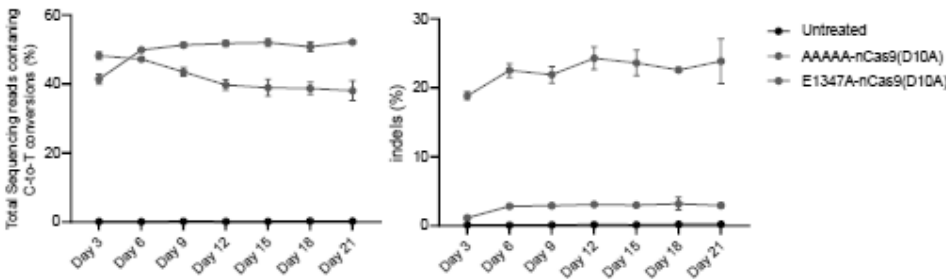
【Fig. 55j】



【Fig. 56】

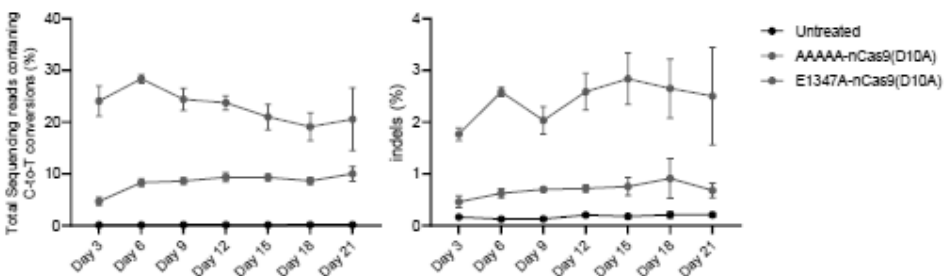
a

TYRO3



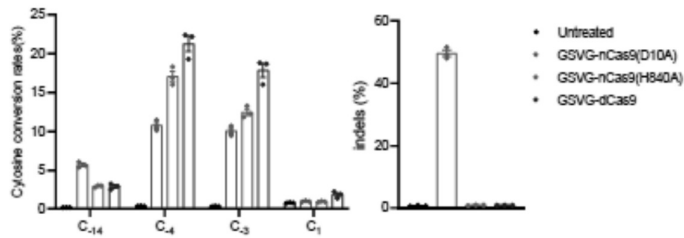
b

ROR1



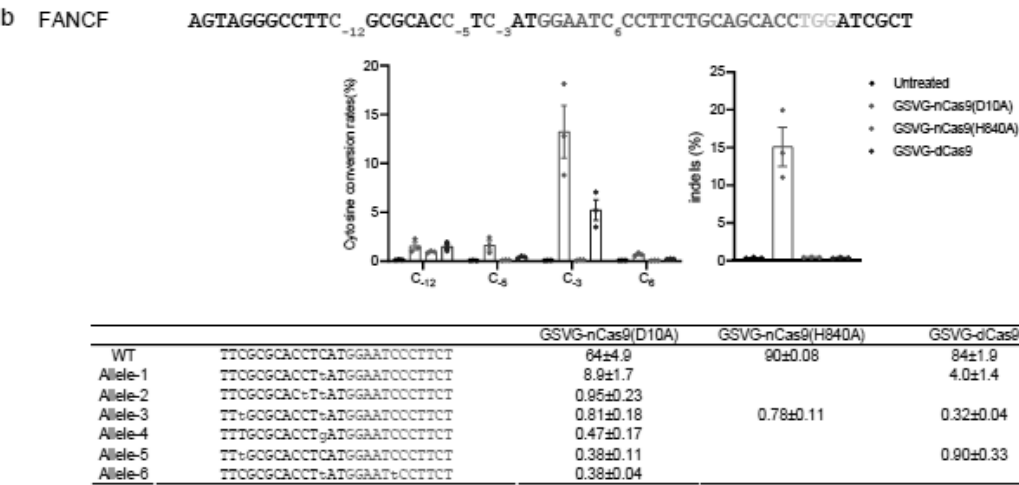
【Fig. 57a】

a EMX1 site 2 GAGTTTCTCATC₋₁₄TGTGCCCCCTC₋₄C₋₃CTC₁CCTGGCCCAGGTGAAGGTGTGGTTCCAG

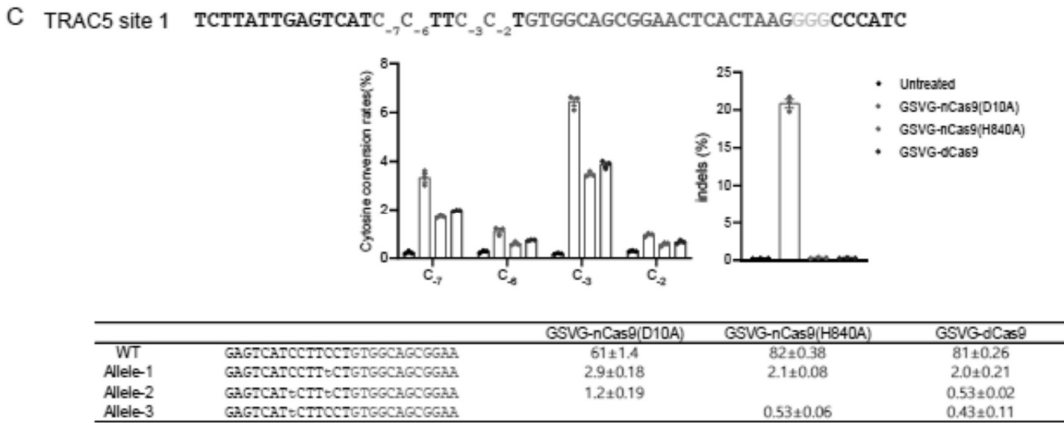


		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	TCTCATCTGTGCCCCCTCCTCCTGCCCCAGGTG	33±1.3	67±1.2	63±1.5
Allele-1	TCTCATCTGTGCCCCCTCTCCTGCCCCAGGTG	3.8±0.13	1.1±0.09	1.5±0.26
Allele-2	TCTCATCTGTGCCCCCTCTCCTGCCCCAGGTG	3.5±0.31	8.5±0.59	12±0.77
Allele-3	TCTCATCTGTGCCCCCTCCTCCTGCCCCAGGTG		3.6±0.36	2.6±0.16
Allele-4	TCTCATCTGTGCCCCCTCCTCCTGCCCCAGGTG		0.66±0.02	
Allele-5	TCTCATCTGTGCCCCCTCTCTCCTGCCCCAGGTG			0.68±0.25

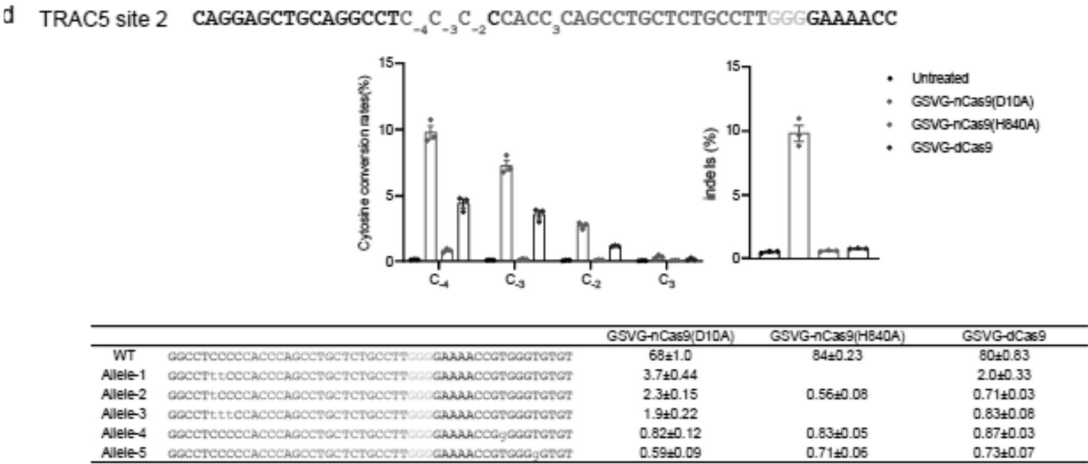
【Fig. 57b】



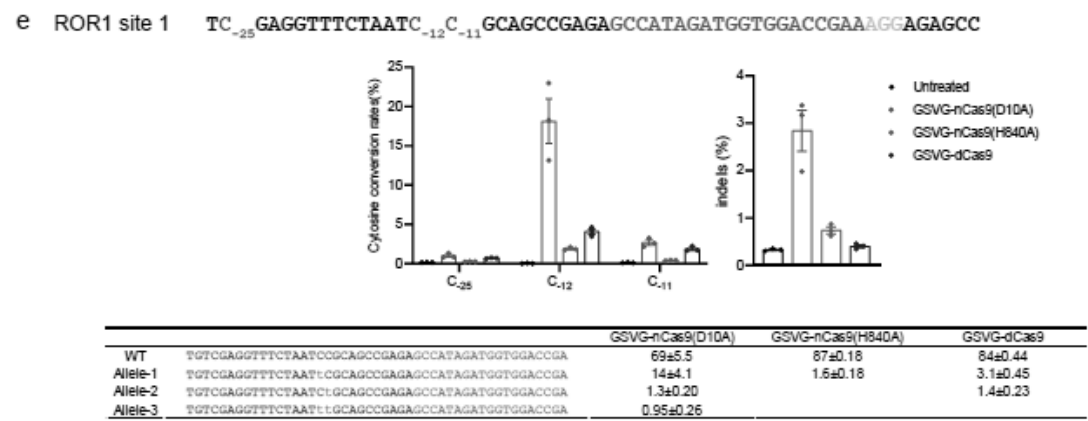
【Fig. 57c】



【Fig. 57d】

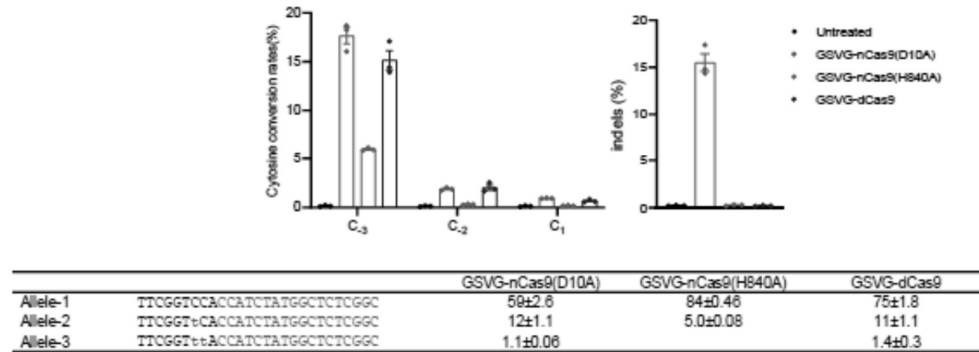


【Fig. 57e】



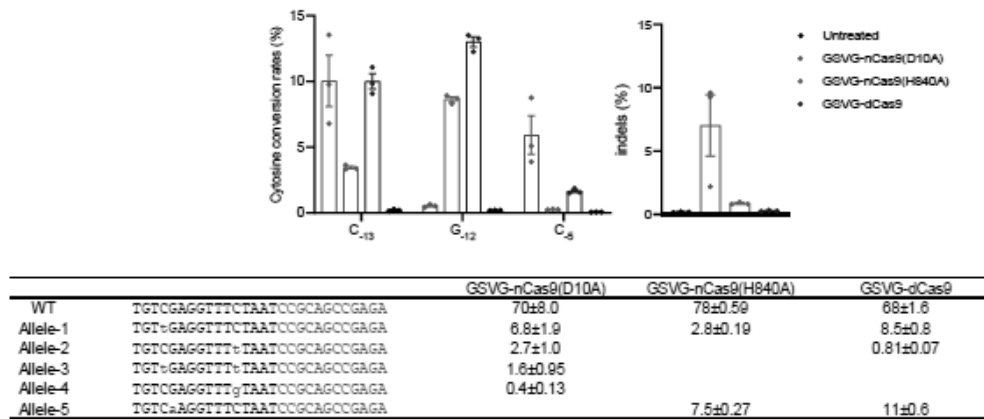
【Fig. 57f】

f ROR1 site 2 GCTCTCCTTTCGGTC₋₃C₋₂AC₁CATCTATGGCTCTCGGCTGCGGATTAGA

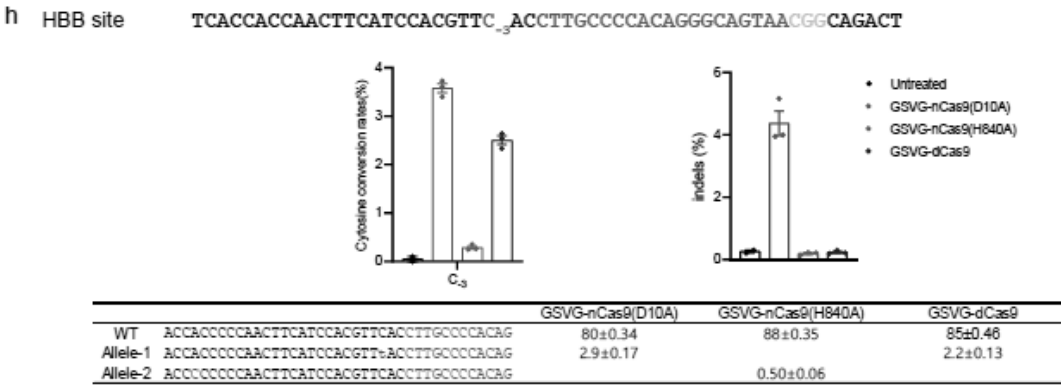


【Fig. 57g】

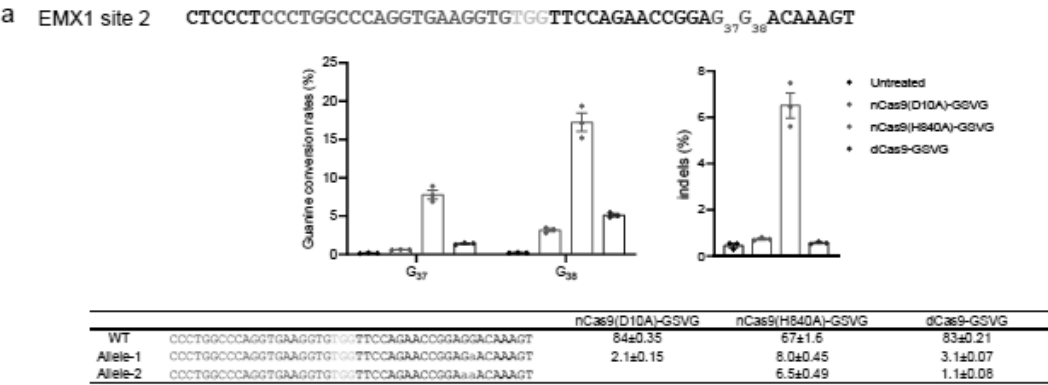
g ROR1 site 3 GGTGTC₋₁₃G₋₁₂AGGTTTC₋₅TAATCCGCAGCCGAGAGCCATAGATGGTGGACC



【Fig. 57h】

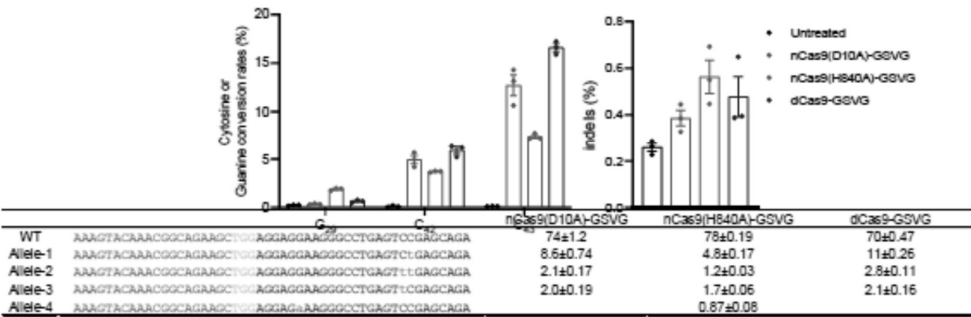


【Fig. 58a】



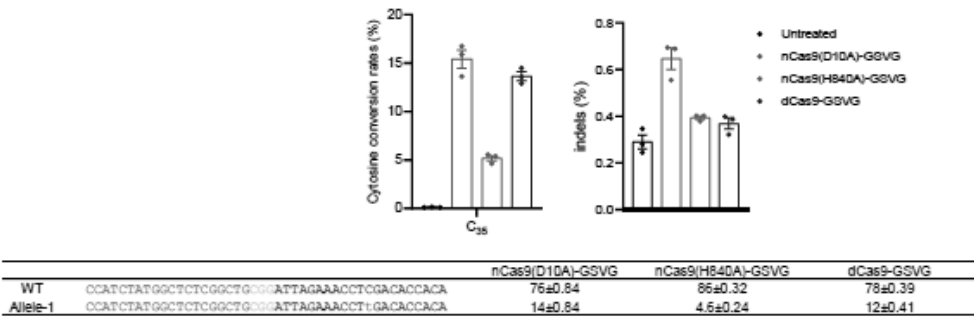
【Fig. 58b】

b EMX1 site 4 GAGGACAAAGTACAAACGGCAGAAGCTGGAGGAGG₂₉AAGGGCCTGAGTC₄₂C₄₃GAGCAGA



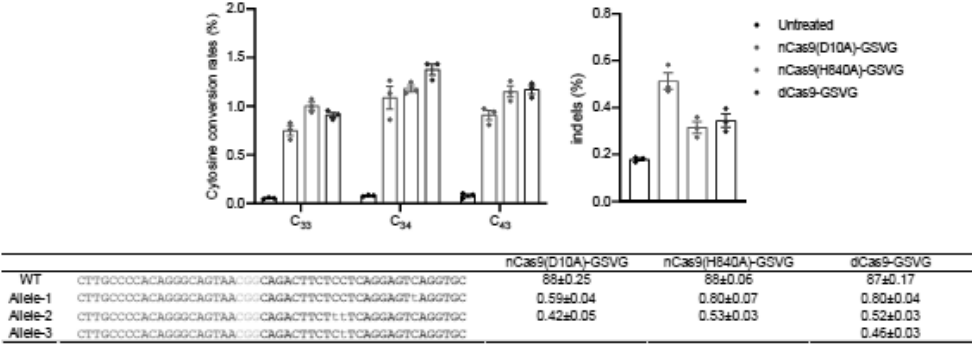
【Fig. 58c】

c ROR1 site 2 GGTCACCATCTATGGCTCTCGGCTGCGGATTAGAAACCTC₃₅GACACCACA

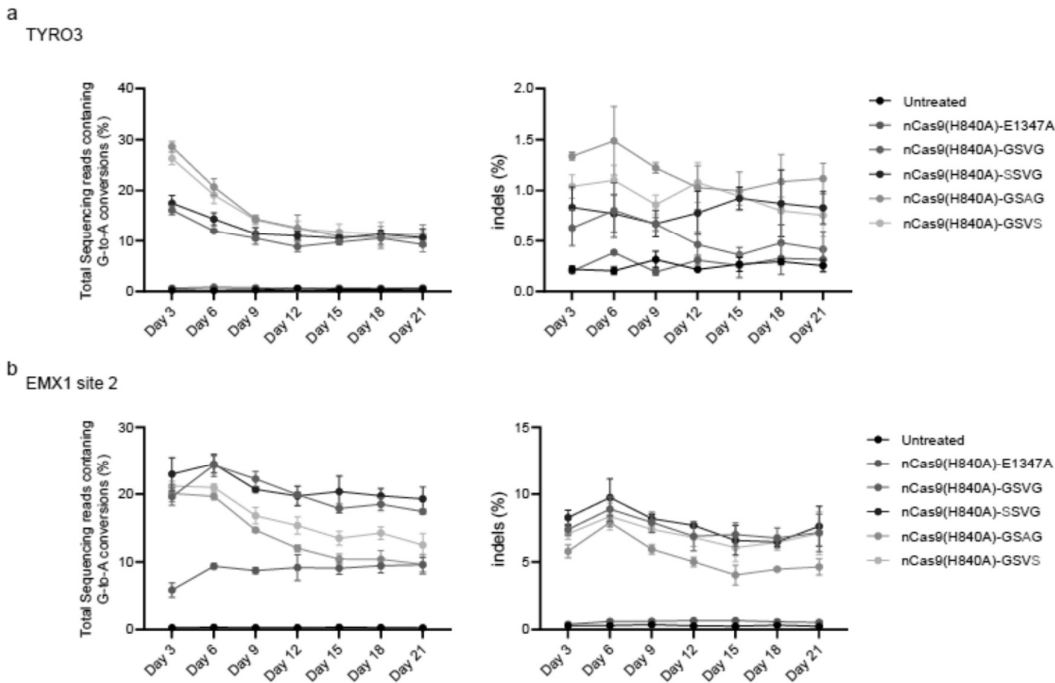


【Fig. 58d】

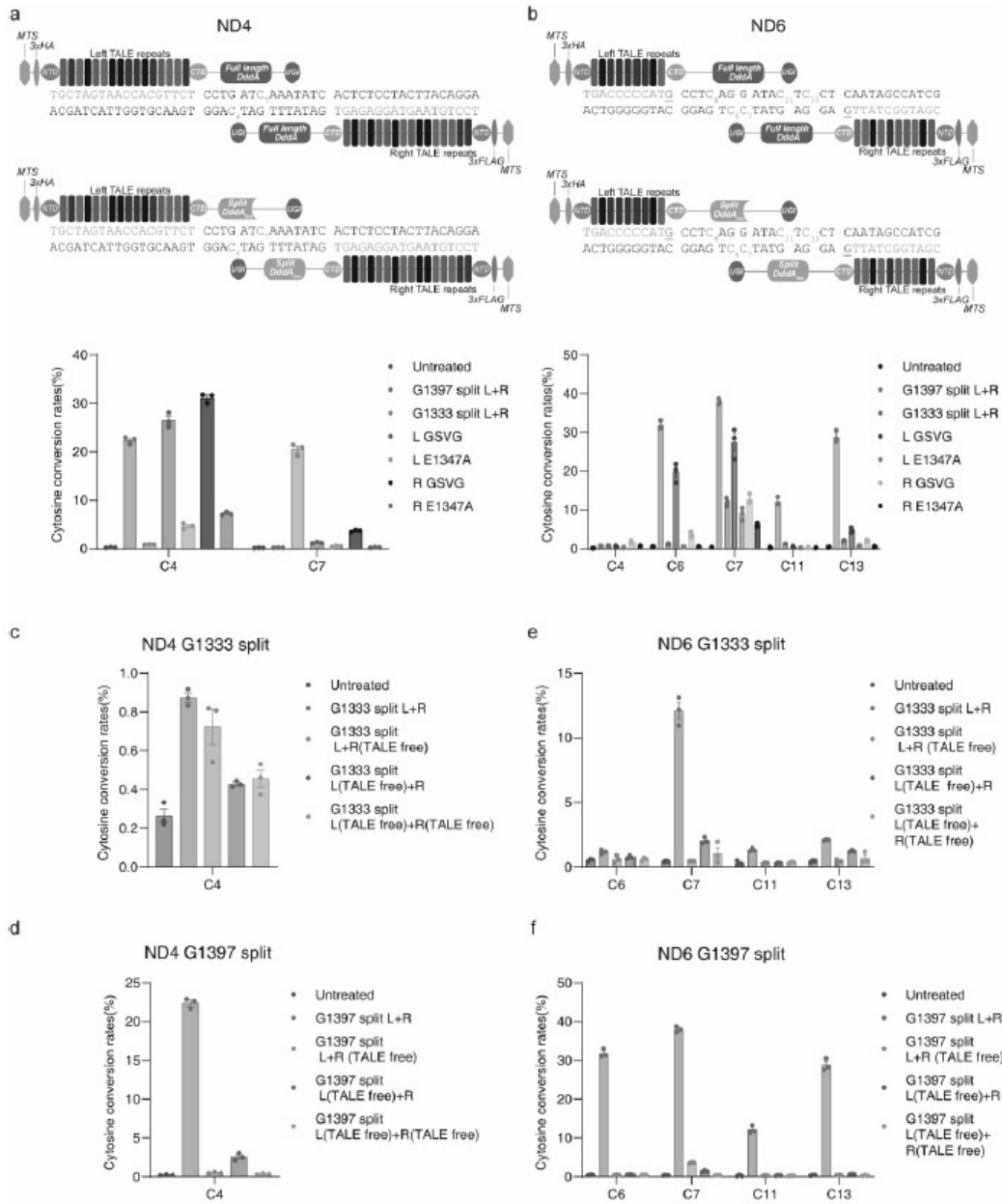
d HBB site GTTCACCTTGCCCCACAGGGCAGTAACGGCAGACTTCTC₃₄C₃₅TCAGGAGTC₄₃AGGTGC



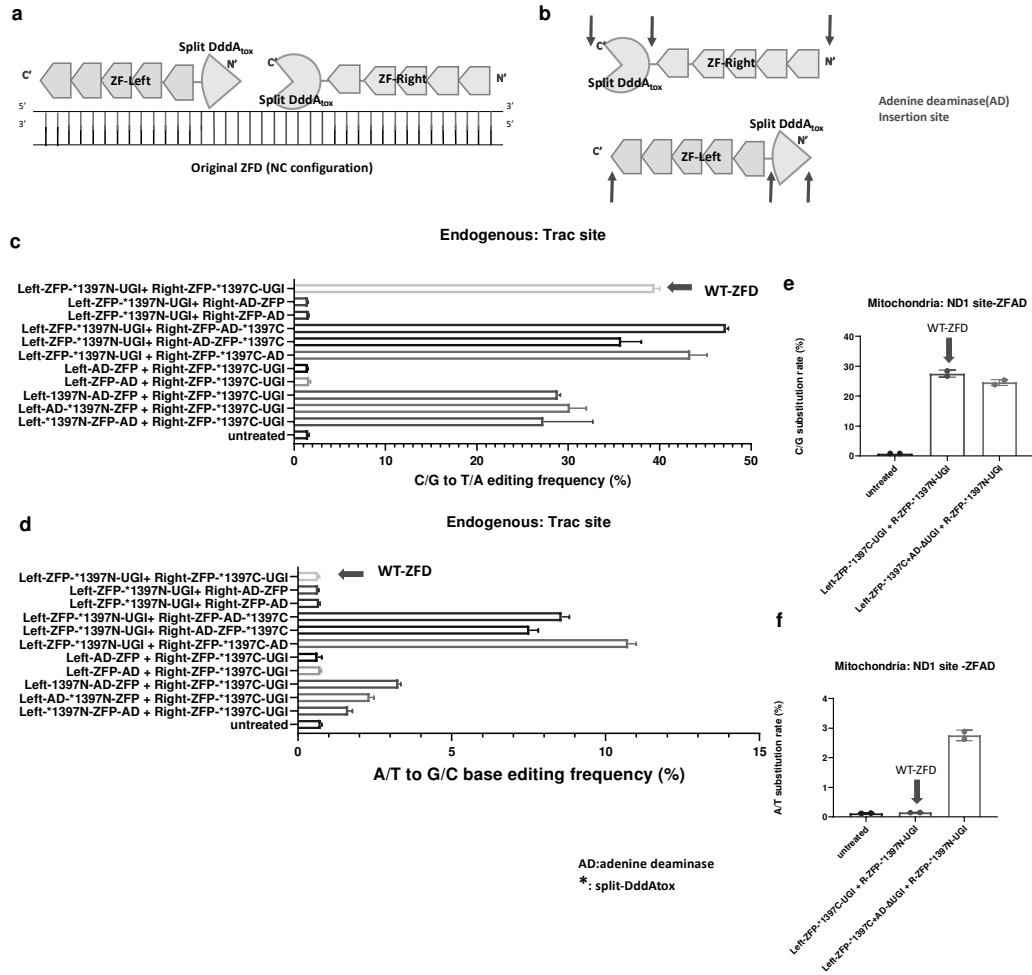
【Fig. 59】



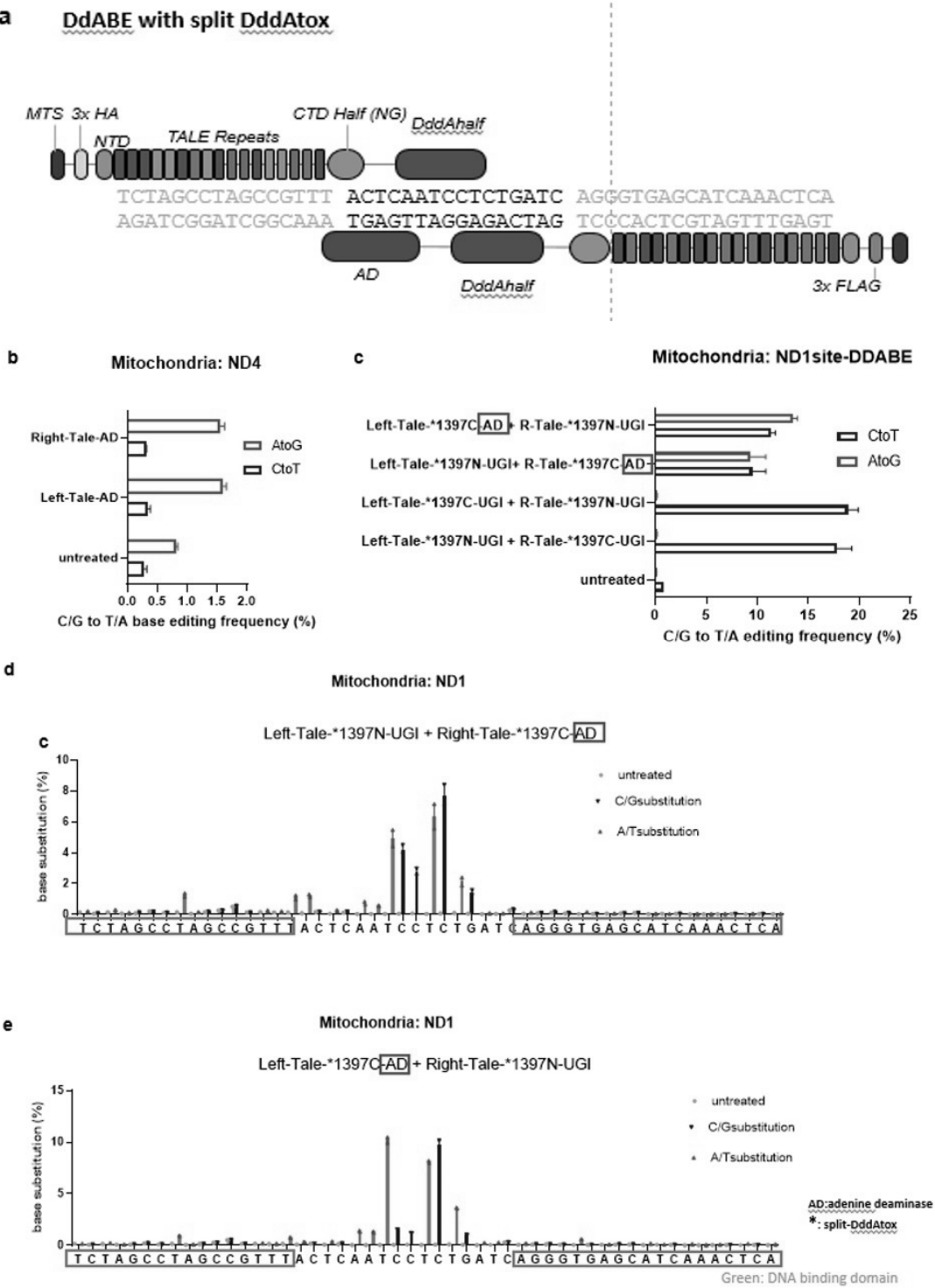
[Fig. 60]



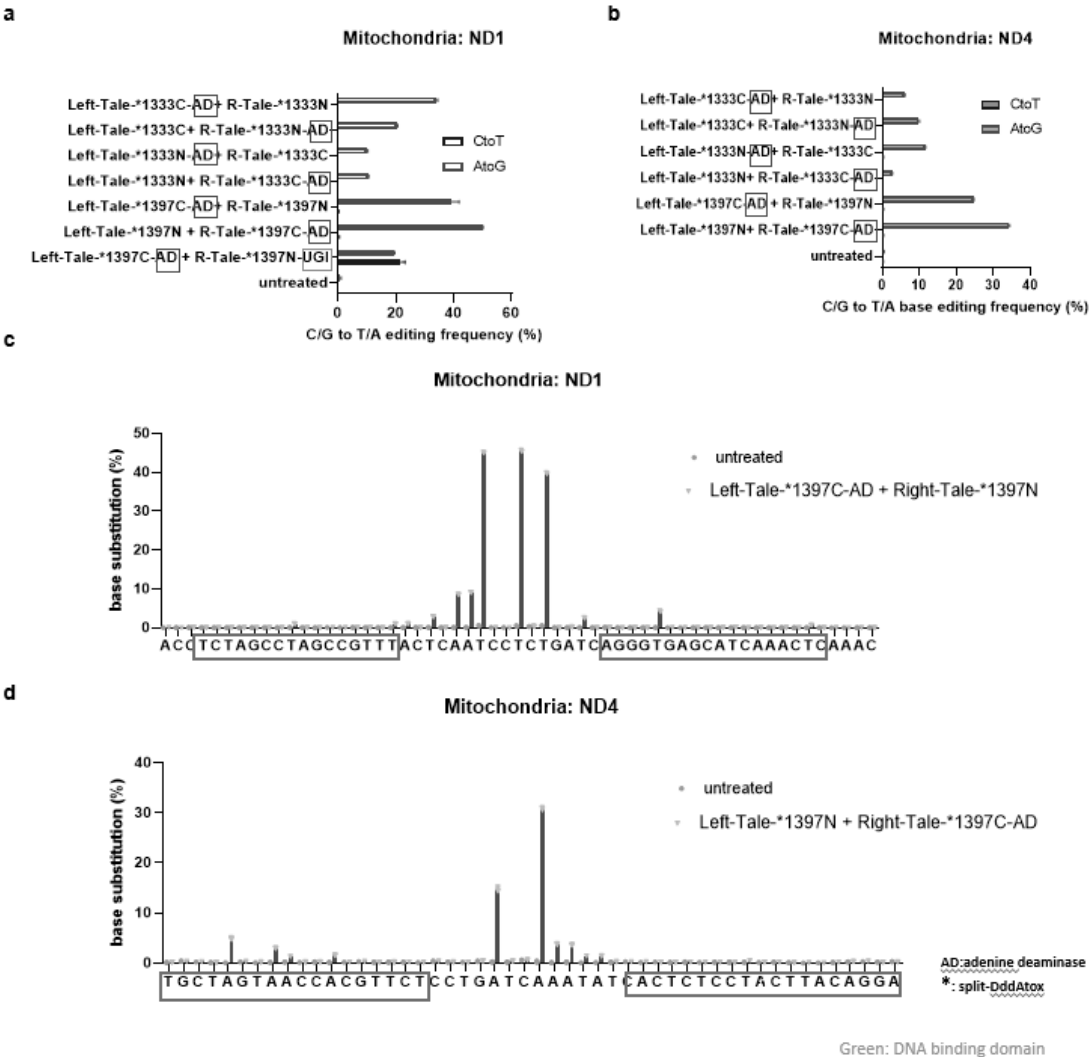
【Fig. 61】



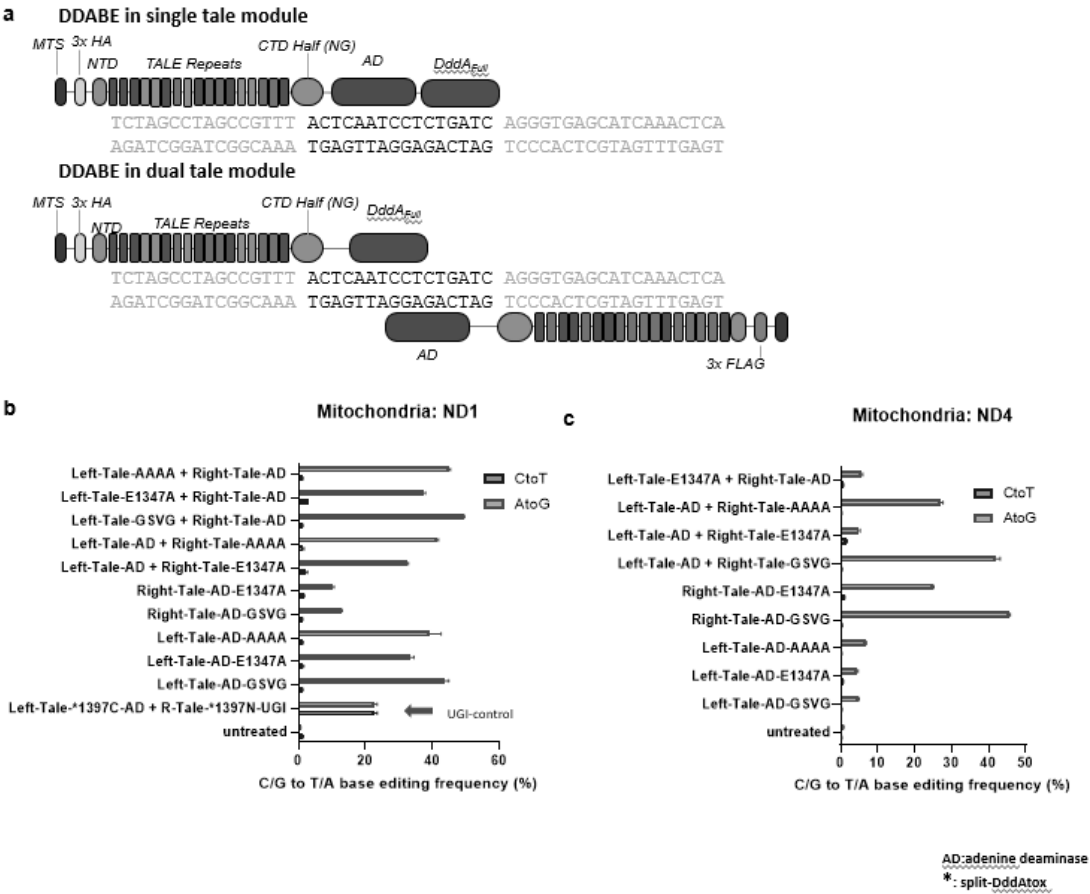
【Fig. 62】



【Fig. 63】

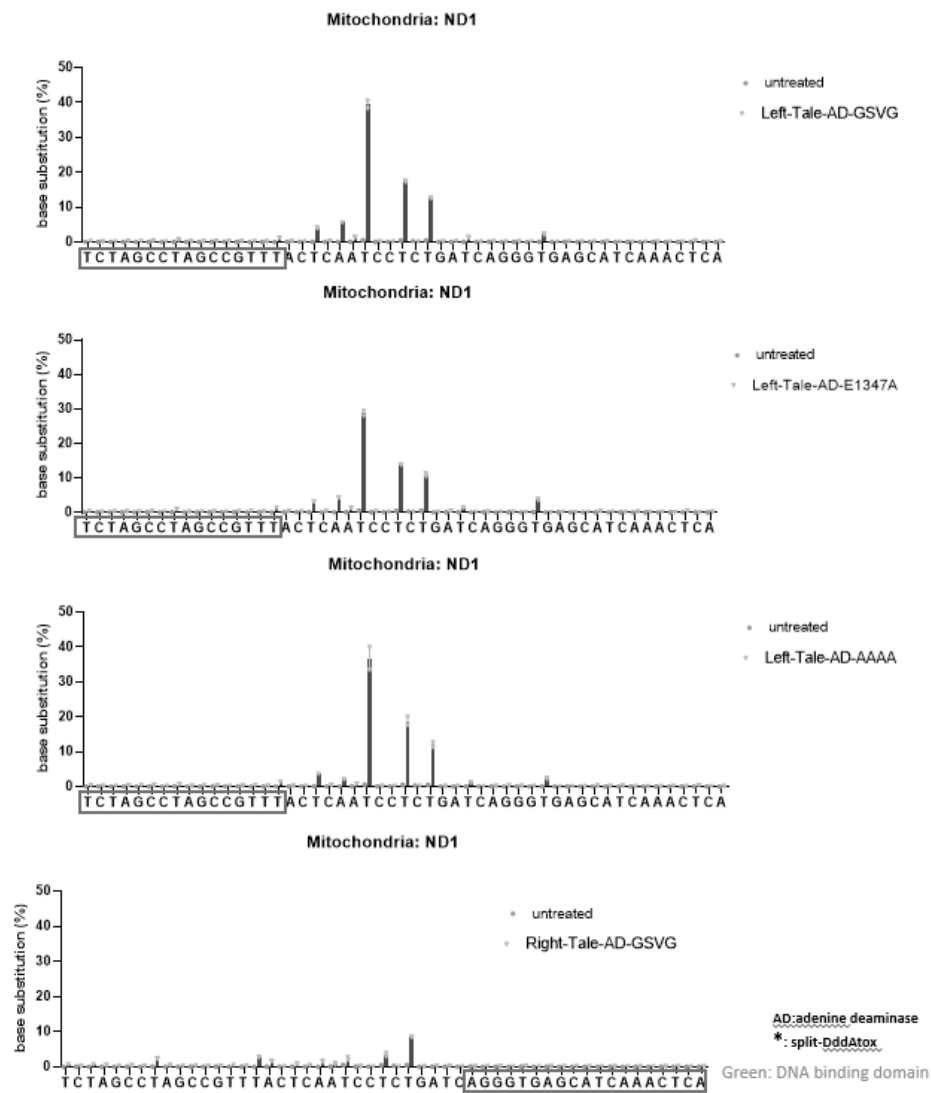


【Fig. 64】

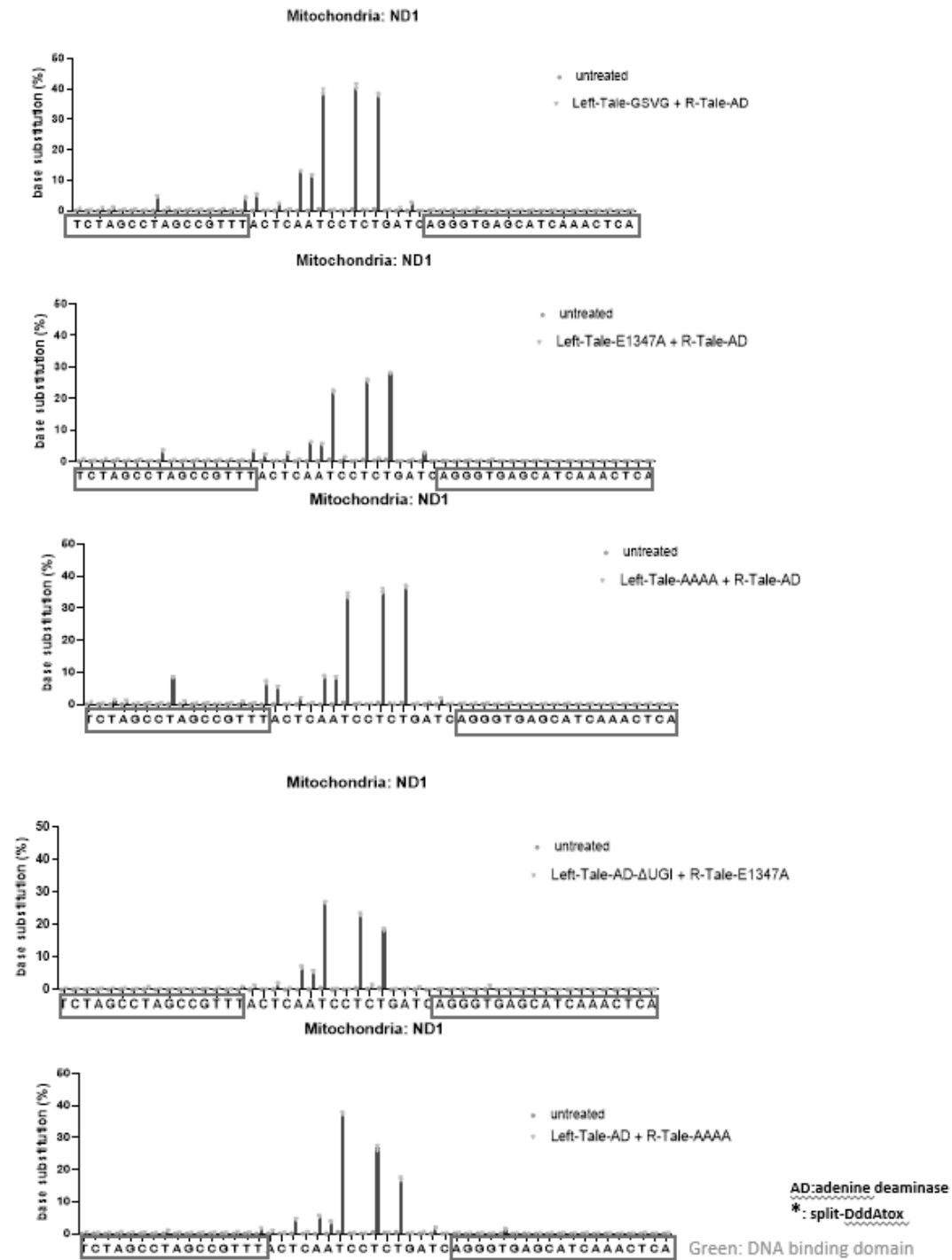


【Fig. 65】

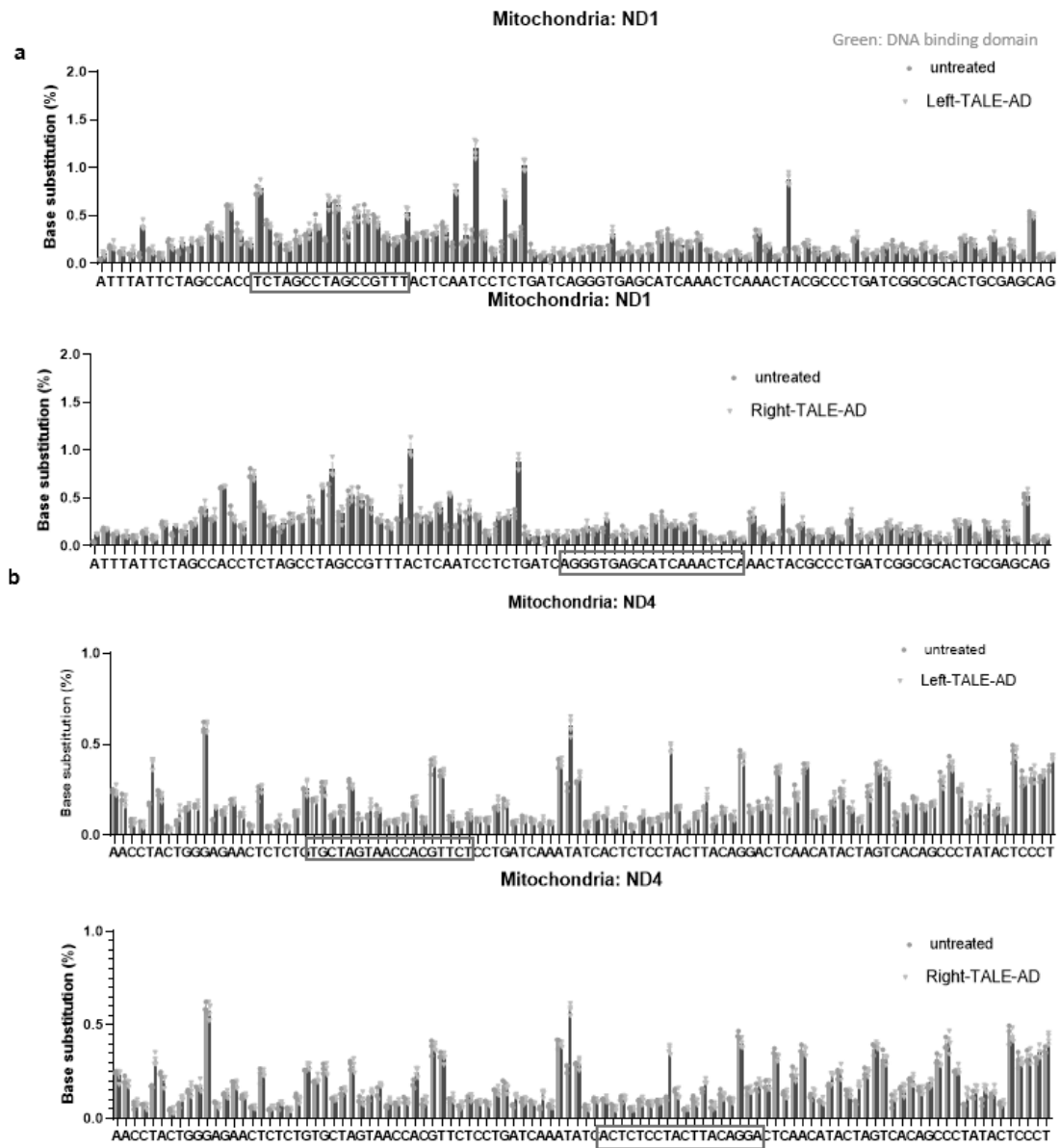
a



【Fig. 66】



【Fig. 67】



【Fig. 68】

