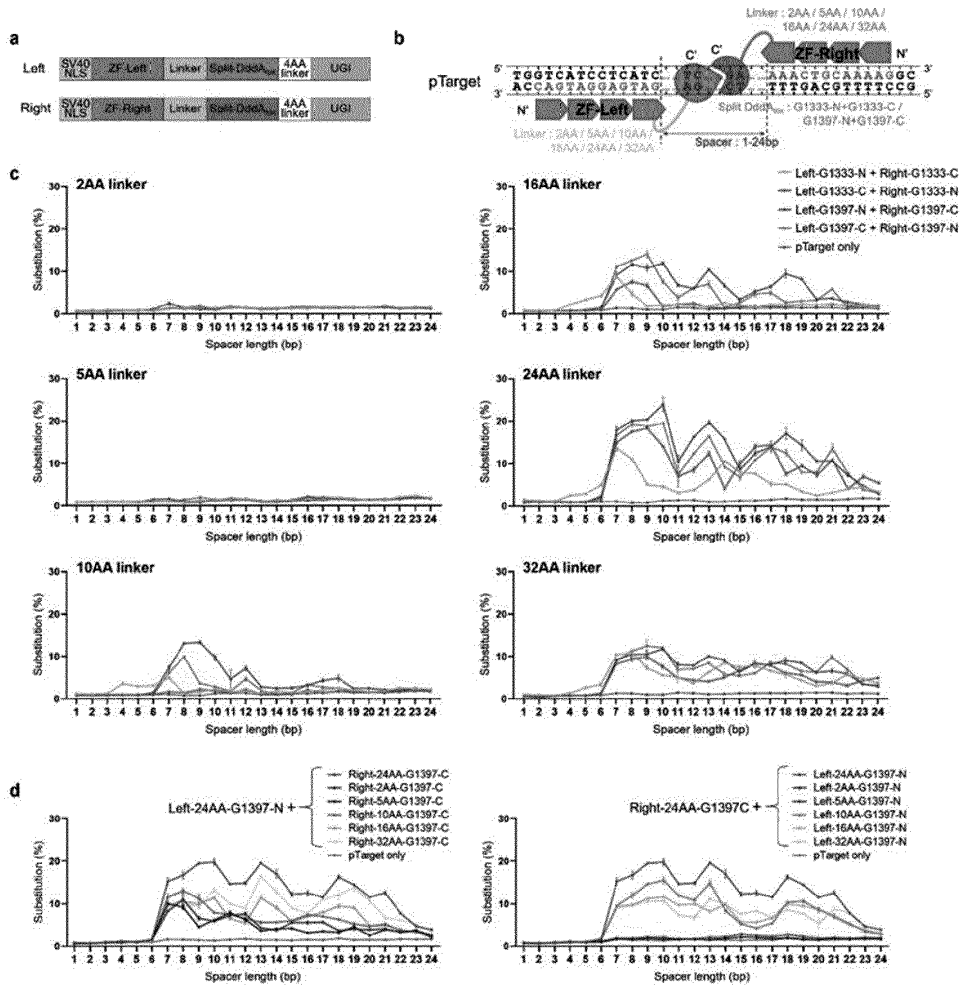
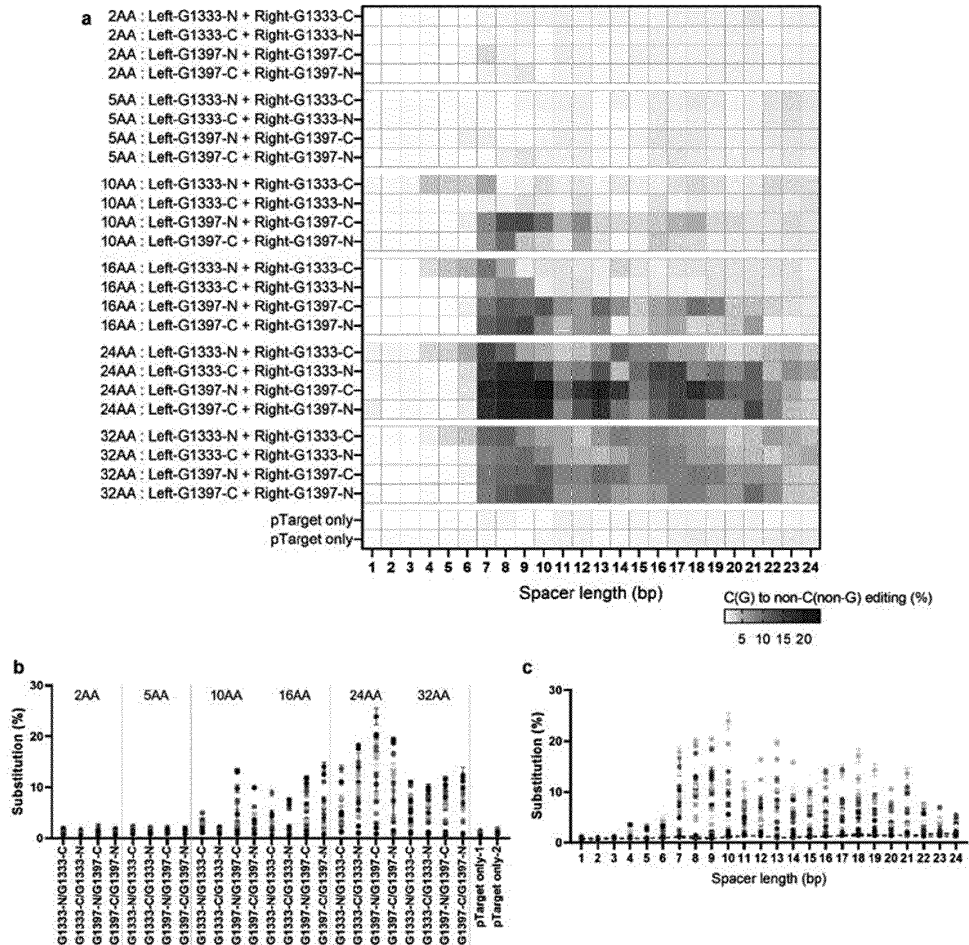


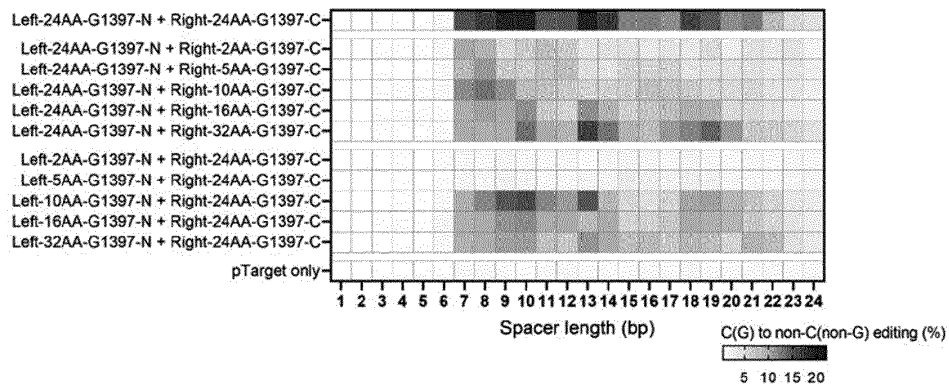
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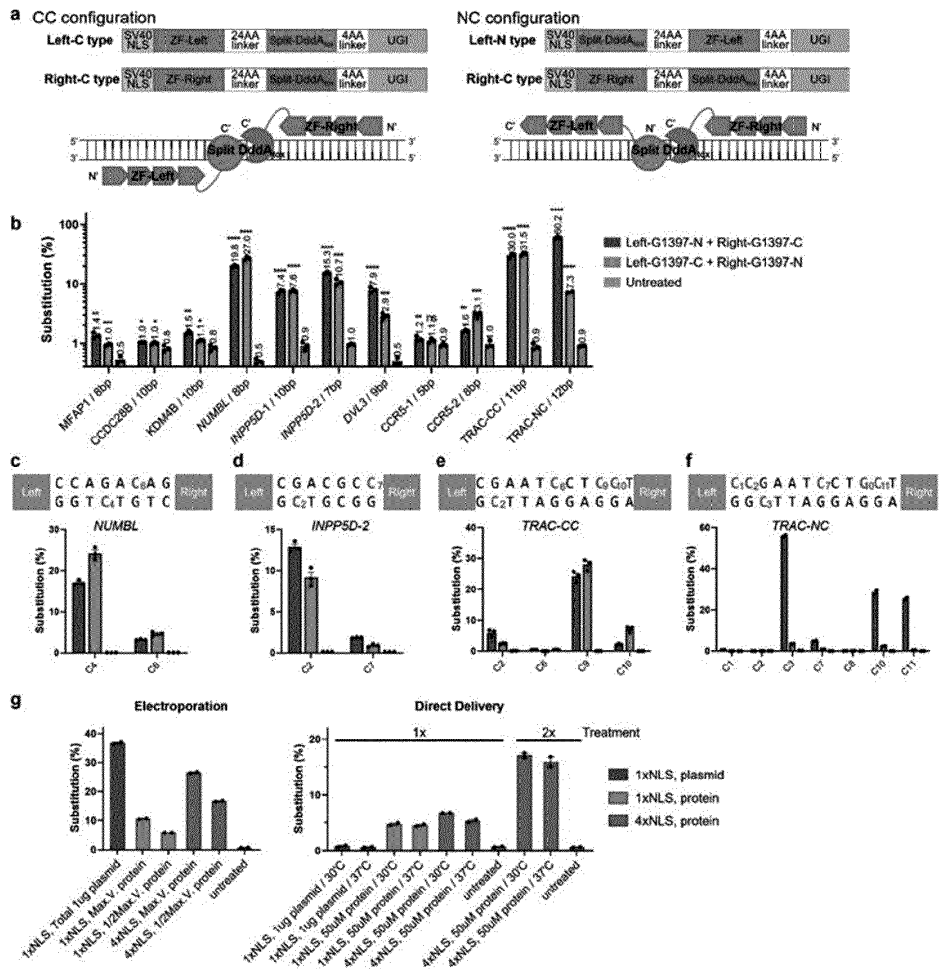
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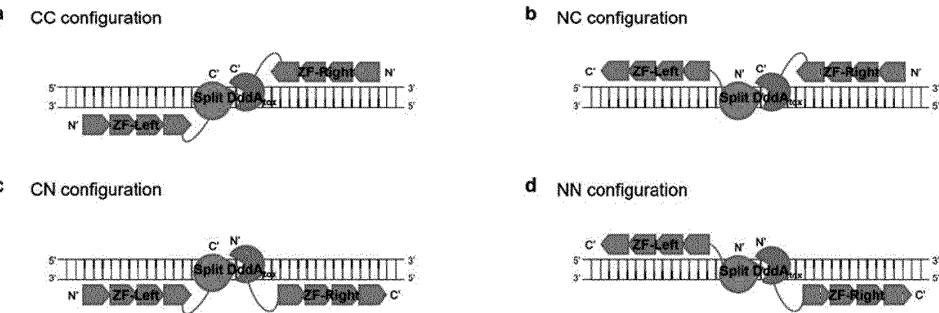
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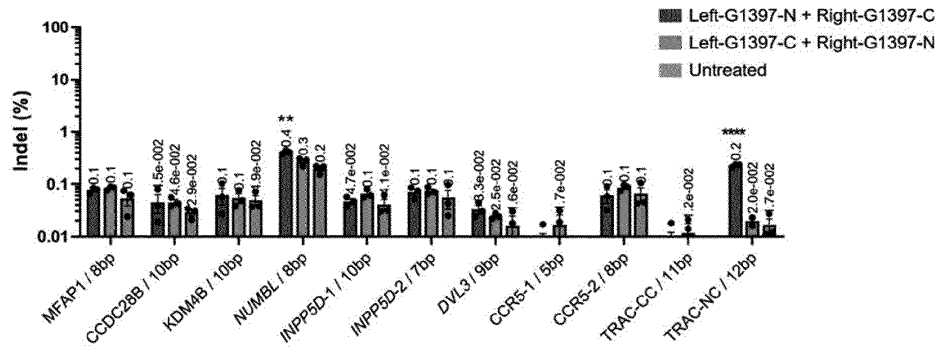
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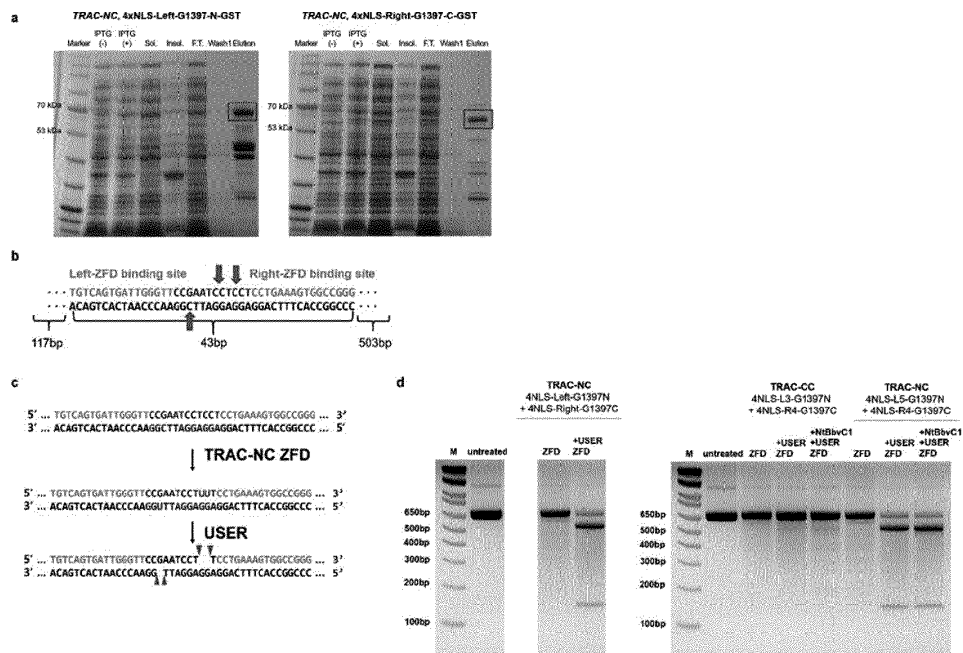
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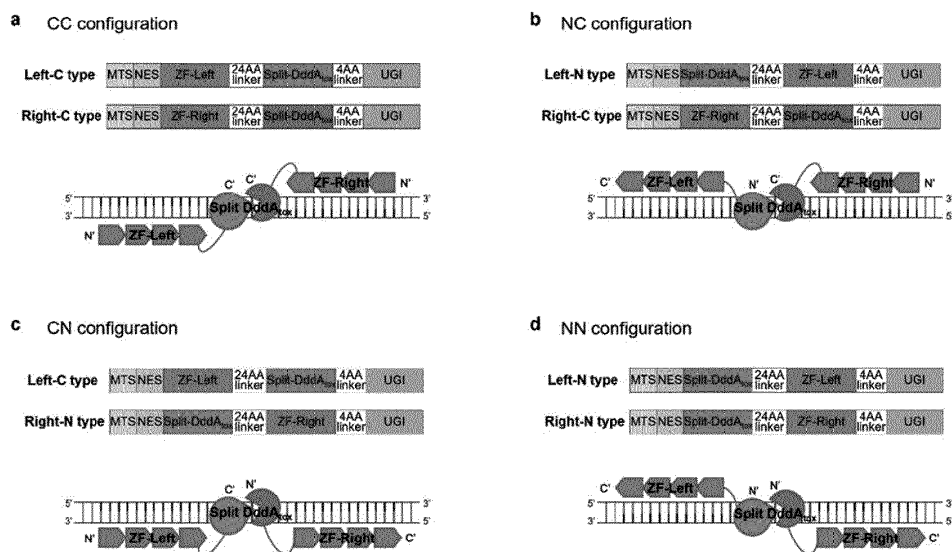
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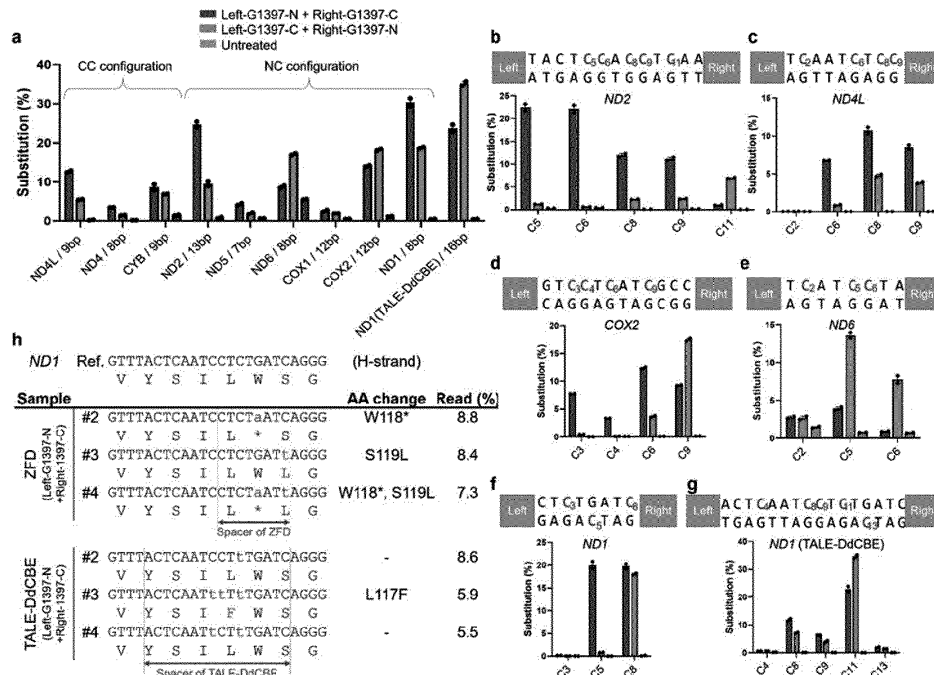
[도7]



[도8]



[도9]



[도10]

a

MT-ND1

GTTTACTCAATC CYCTGATC₅ AGGGTGAAGCATC
CAAAATGAGTATAG GAGAC₇TAG TCCCACTCTGATAG

	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

CTACGCCTAATC TACTC₅ A C₆ T C A A T C A C T A C T C C
GATGCGGATTA₆ ATGAGGTGGAGTT AGTGATGATGAGG

	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

[도 11]

Human MT-ND1	Ref.	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:143)	(H-strand)	
Sample			AA change	Read (%)
Clone 3 : 34 %	Allele-1	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:143) V Y S I L W S G W A S (SEQ ID NO:144) GTTTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:145) V Y S I L W L G W A S (SEQ ID NO:146)	-	62
	Allele-2	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:145) V Y S I L W L G W A S (SEQ ID NO:146)	S119L	21
	Allele-3	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:147) V Y S I L * S G W A S (SEQ ID NO:148)	W118*	13
	Allele-4	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA (SEQ ID NO:148) V Y S I L * S G W A S (SEQ ID NO:149)		
Clone 10 : 92 %	Allele-1	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W L G W A S	S119L	40
	Allele-2	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	32
	Allele-3	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * L G W A S	W118*, S119L	20
	Allele-4	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	2
Clone 16 : 80 %	Allele-1	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W L G W A S	S119L	40
	Allele-2	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	35
	Allele-3	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	16
	Allele-4	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * L G W A S	W118*, S119L	5
Clone 27 : 45 %	Allele-1	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	50
	Allele-2	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W L G W A S	S119L	26
	Allele-3	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	19
	Allele-4	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * L G W A S		
Clone 30 : 90 %	Allele-1	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W L G W A S	S119L	40
	Allele-2	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * S G W A S	W118*	35
	Allele-3	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L * L G W A S	W118*, S119L	15
	Allele-4	GTTTACTCAATCCTCTGATCAGGGTGAGCATCA V Y S I L W S G W A S	-	5

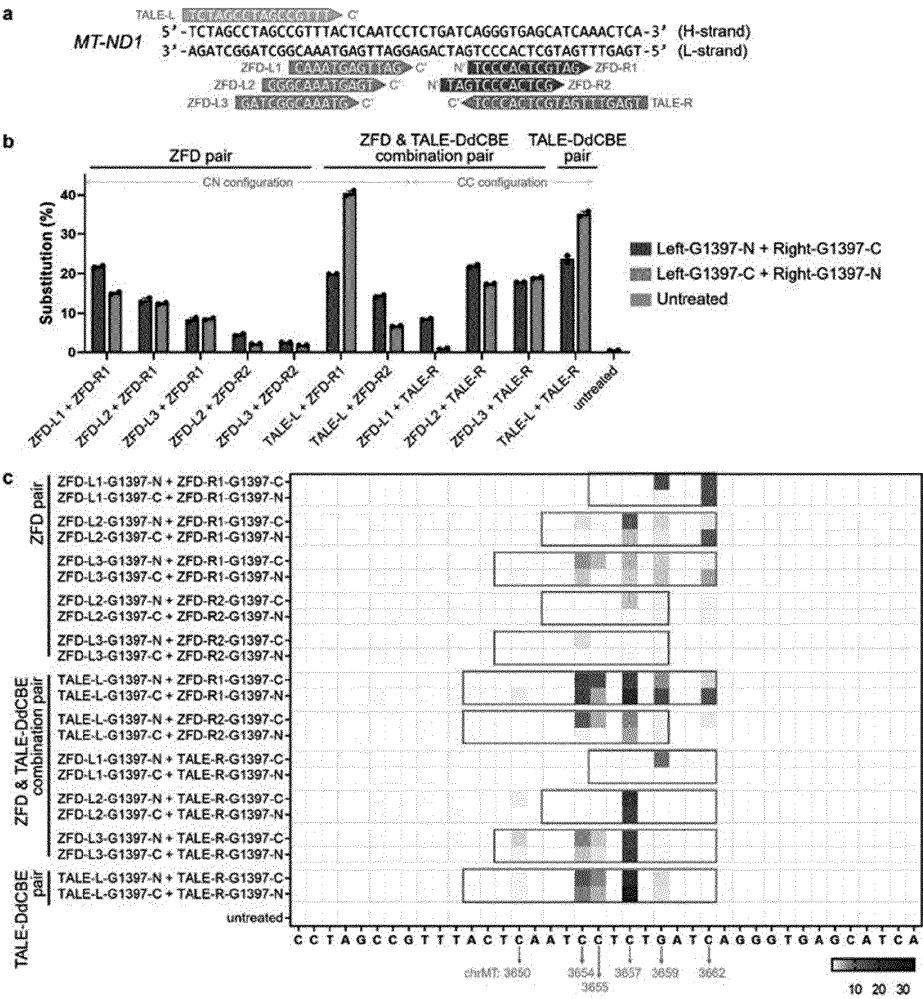
[E12a]

Human MT-ND2	Ref.	CTACGCCTAATCTACTCCACCTCAATCACA	(H-strand)	Read (%)
Sample		CTACGCCTAATCTACTCCACCTCAATCACA	AA change	
Clone 21	Allele-1	(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	(SEQ ID NO:152) L R L I Y S T S I T L L P (SEQ ID NO:153)	-	31
	Allele-3	(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	(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	(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	(SEQ ID NO:160) L R L I Y F T L I T L L P (SEQ ID NO:161)	S299F, S301L	1
Clone 23	Allele-1	CTACGCCTAATCTACTCCACCTCAATCACA	S299F	43
	Allele-2	CTACGCCTAATCTACTCCACCTCAATCACA	-	27
	Allele-3	CTACGCCTAATCTACTCCACCTCAATCACA	S299F, T300I	16
	Allele-4	CTACGCCTAATCTACTCCACCTCAATCACA	S299F, T300I	6
	Allele-5	CTACGCCTAATCTACTCCACCTCAATCACA	S299F, S301L	1
Clone 24	Allele-1	CTACGCCTAATCTACTCCACCTCAATCACA	S299F	34
	Allele-2	CTACGCCTAATCTACTCCACCTCAATCACA	S299F, T300I	30
	Allele-3	CTACGCCTAATCTACTCCACCTCAATCACA	-	23
	Allele-4	CTACGCCTAATCTACTCCACCTCAATCACA	S299F, T300I	3
	Allele-5	CTACGCCTAATCTACTCCACCTCAATCACA	S299F, T300I, S301L	1
	Allele-6	CTACGCCTAATCTACTCCACCTCAATCACA	S299F	1

[도 12b]

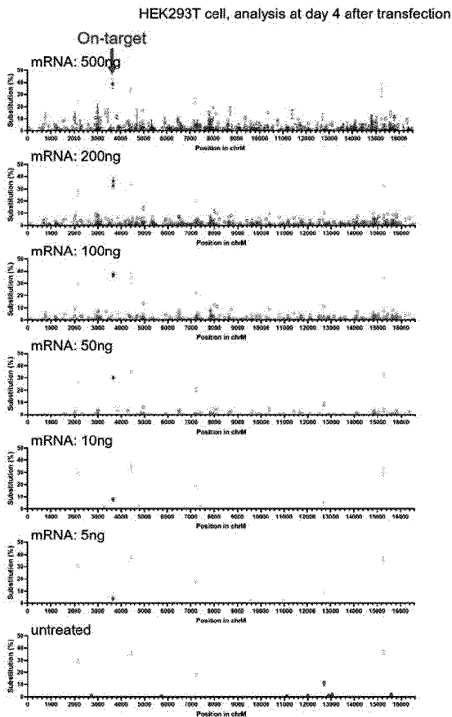
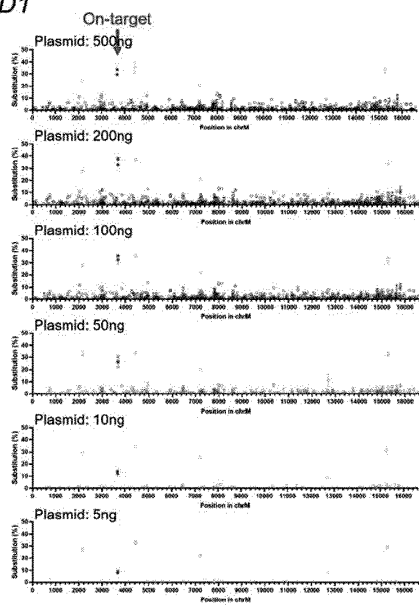
Human MT-ND2	Ref.	CTACGCCTAATCTACTCCACCTCAATCAGACTACTCCCC	(H-strand)	Read (%)
Sample			AA change	
Clone 31	Allele-1	CTACGCCTAATCTACTCCACCTCAATCAGACTACTCCCC L R L I Y S T S I T L L P	-	53
	Allele-2	CTACGCCTAATCTACTttACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	28
	Allele-3	CTACGCCTAATCTACTttAttTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	9
	Allele-4	CTACGCCTAATCTACTttAtCTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	2
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	2
Clone 32	Allele-1	CTACGCCTAATCTACTCCACCTCAATCAGACTACTCCCC L R L I Y S T S I T L L P	-	40
	Allele-2	CTACGCCTAATCTACTttACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	37
	Allele-3	CTACGCCTAATCTACTttAttTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	11
	Allele-4	CTACGCCTAATCTACTttAtCTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	3
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	2
Clone 33	Allele-1	CTACGCCTAATCTACTCCACCTCAATCAGACTACTCCCC L R L I Y S T S I T L L P	-	46
	Allele-2	CTACGCCTAATCTACTttACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	34
	Allele-3	CTACGCCTAATCTACTttAttTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	12
	Allele-4	CTACGCCTAATCTACTttAtCTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	2
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	1
Clone 34	Allele-1	CTACGCCTAATCTACTCCACCTCAATCAGACTACTCCCC L R L I Y S T S I T L L P	-	72
	Allele-2	CTACGCCTAATCTACTttACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	18
	Allele-3	CTACGCCTAATCTACTttAttTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	3
	Allele-4	CTACGCCTAATCTACTttAtCTCAATCAGACTACTCCCC L R L I Y F I S I T L L P	S299F, T300I	1
	Allele-5	CTACGCCTAATCTACTtCACCTCAATCAGACTACTCCCC L R L I Y F T S I T L L P	S299F	0.4

[513]



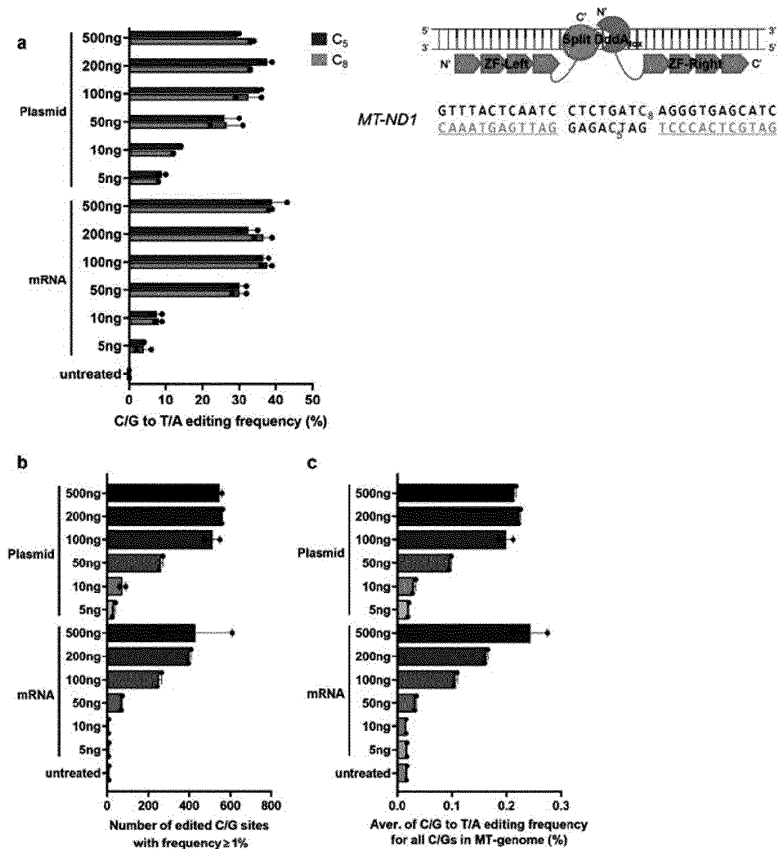
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ND1



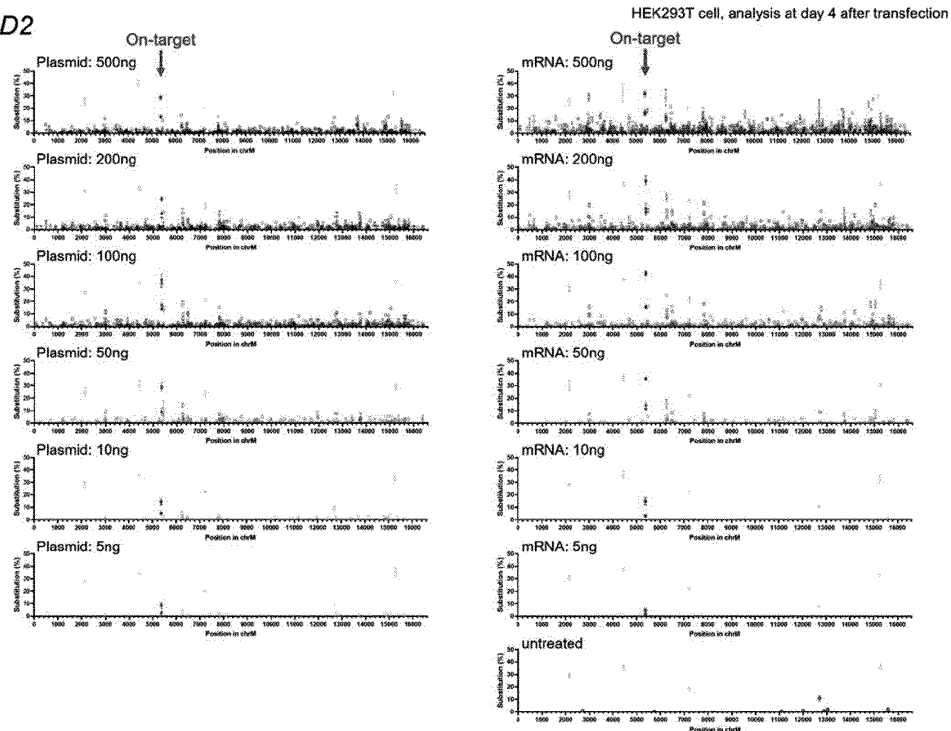
[515]

HEK293T cell, analysis at day 4 after transfection

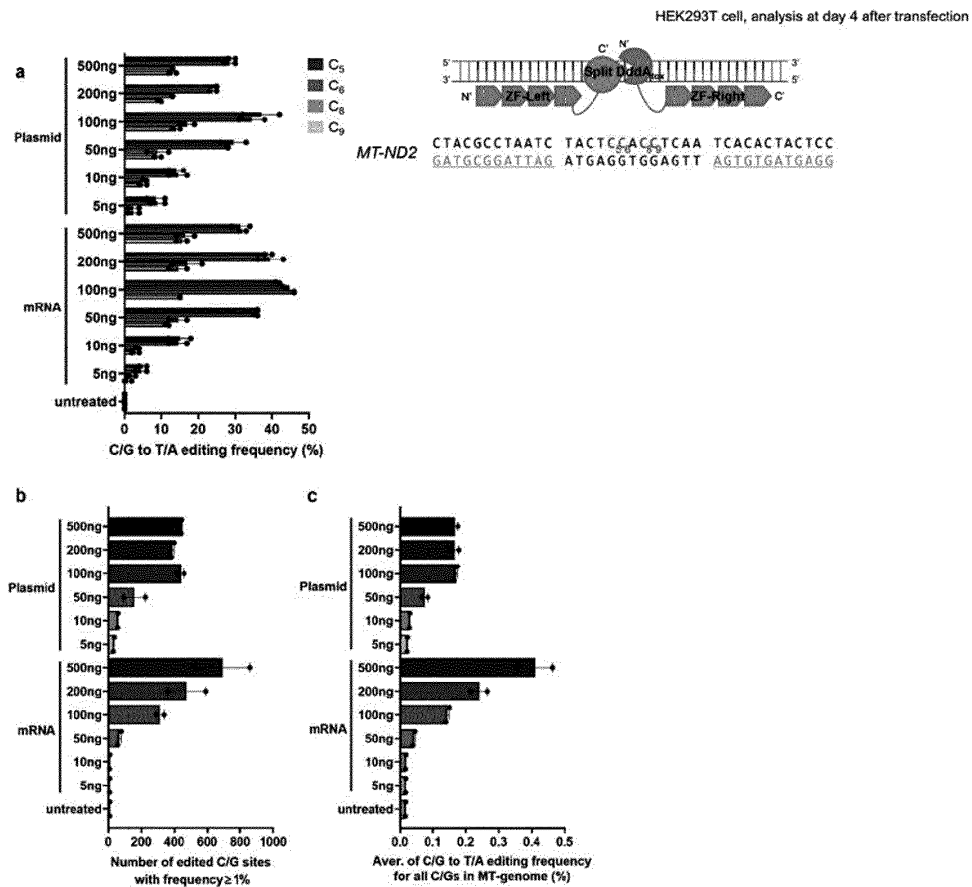


[도16]

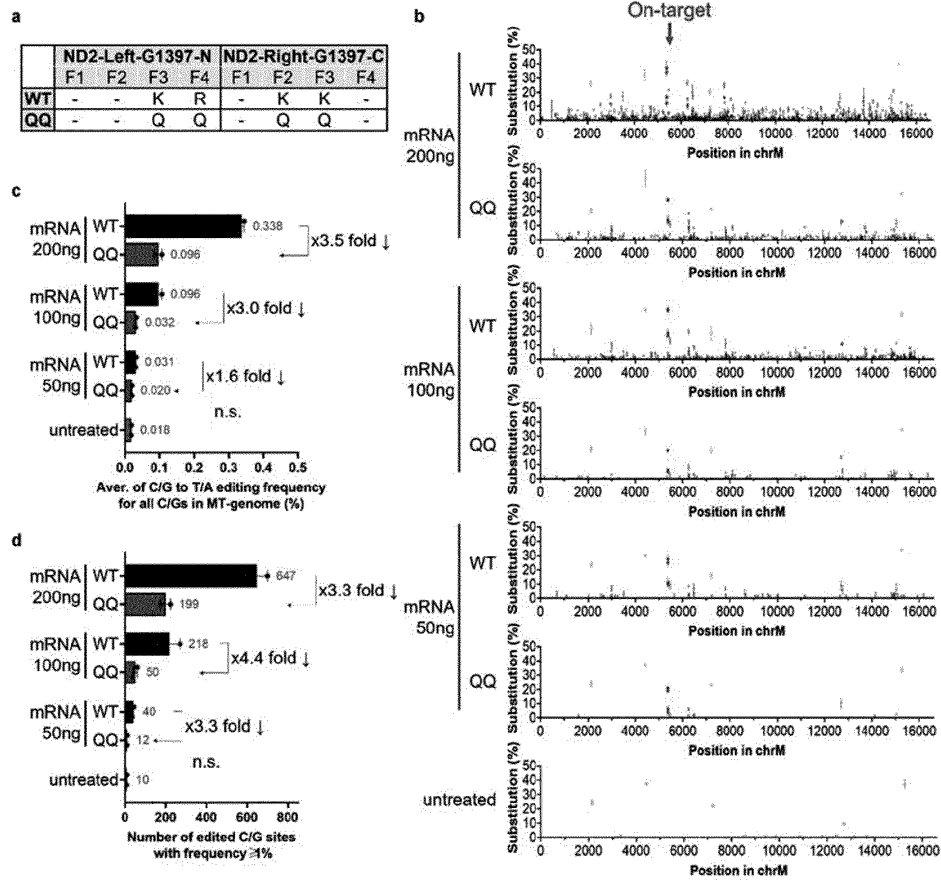
ND2



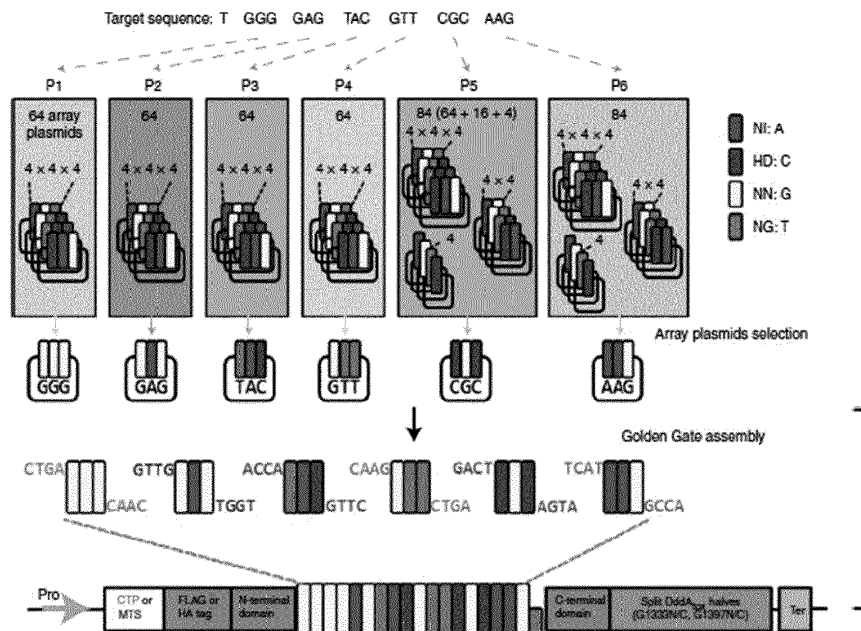
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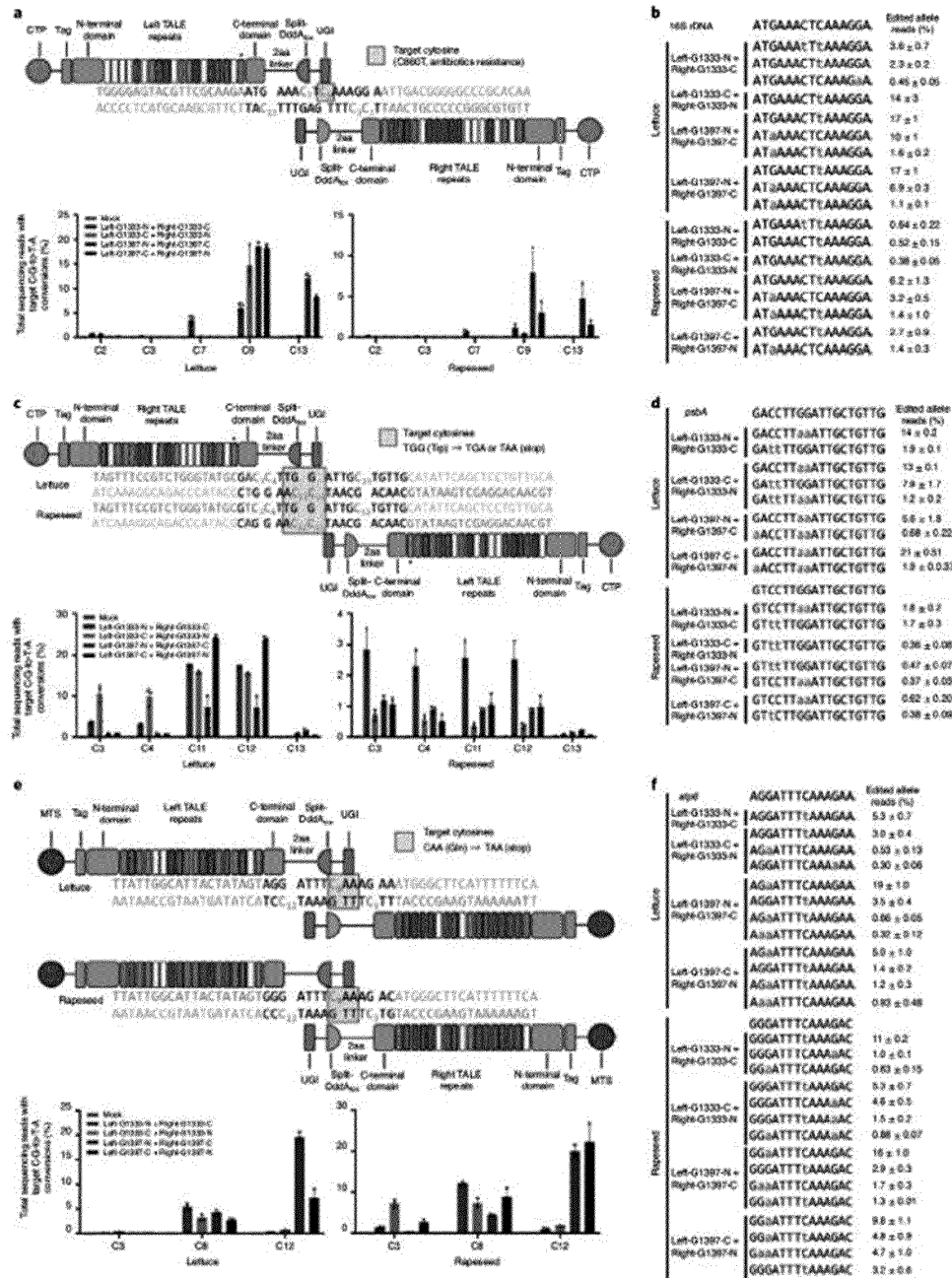
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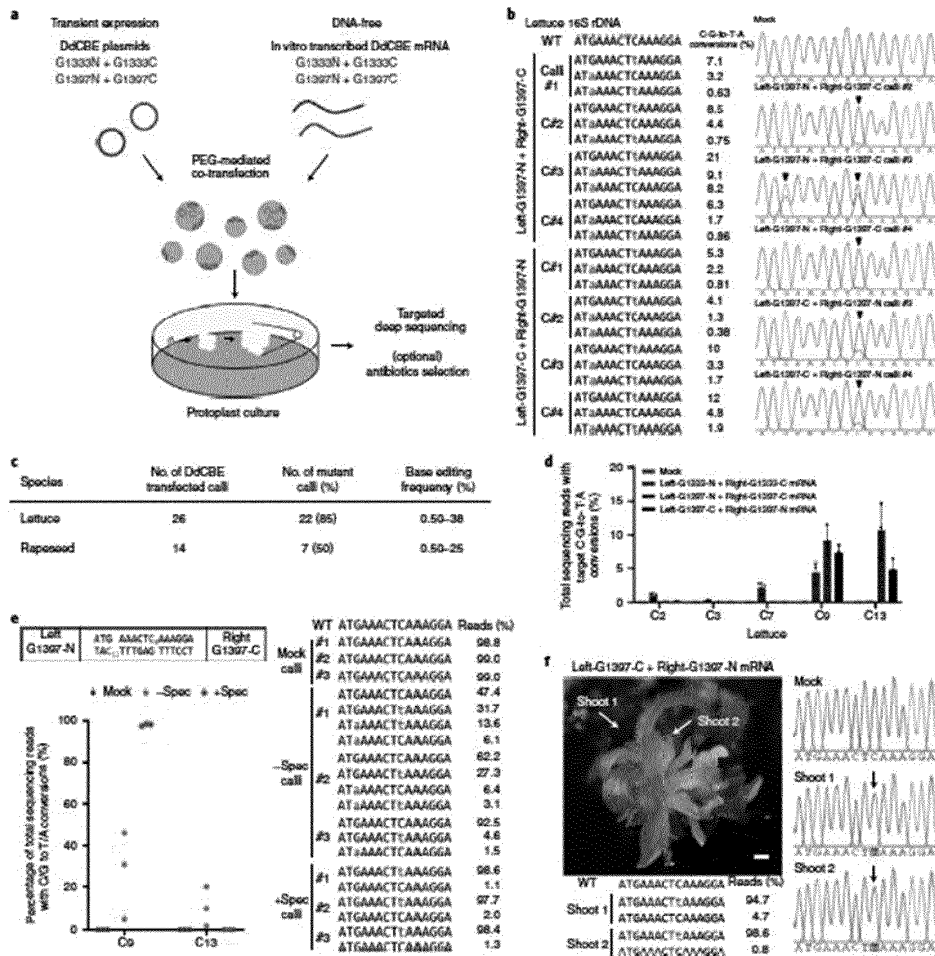
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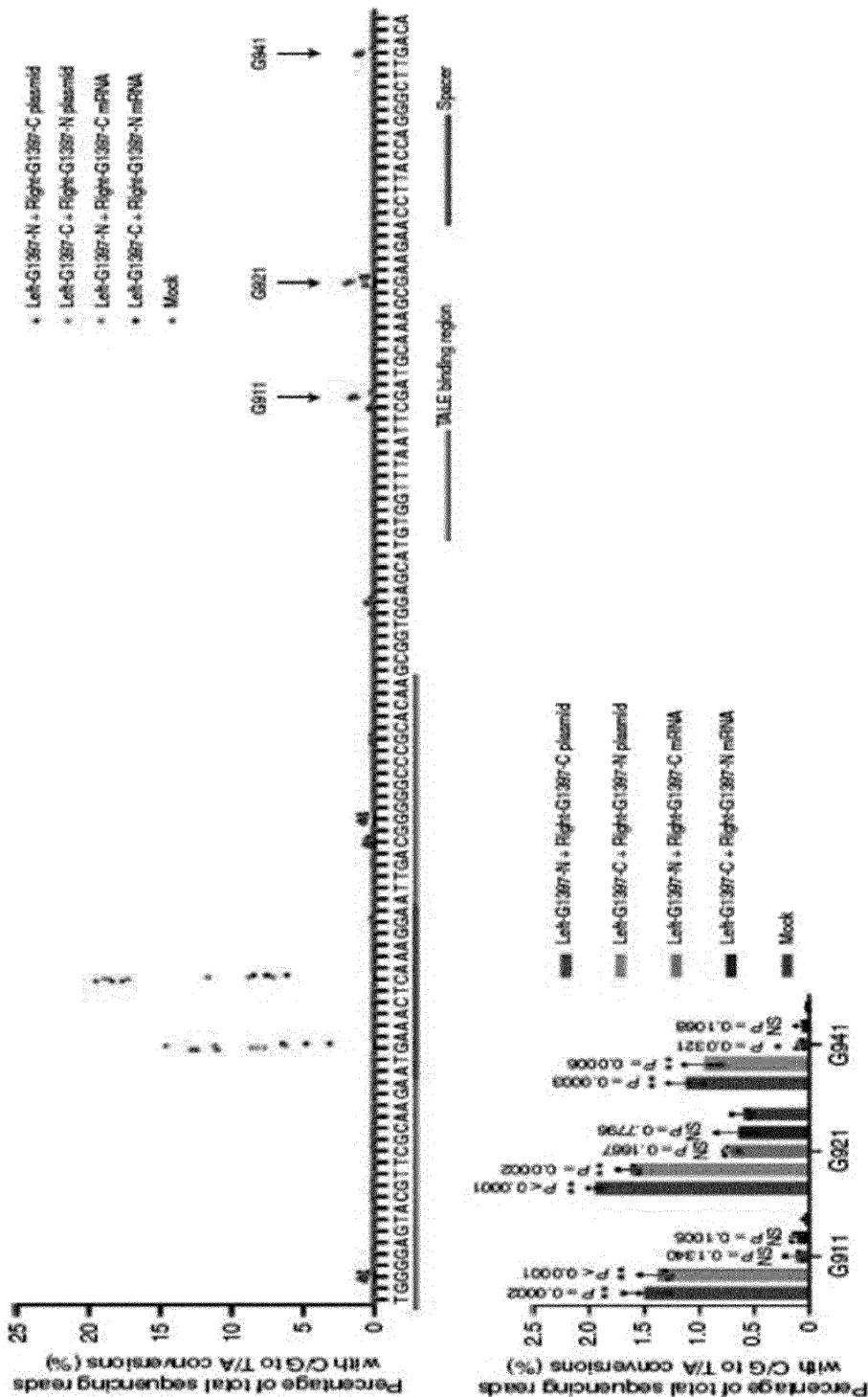
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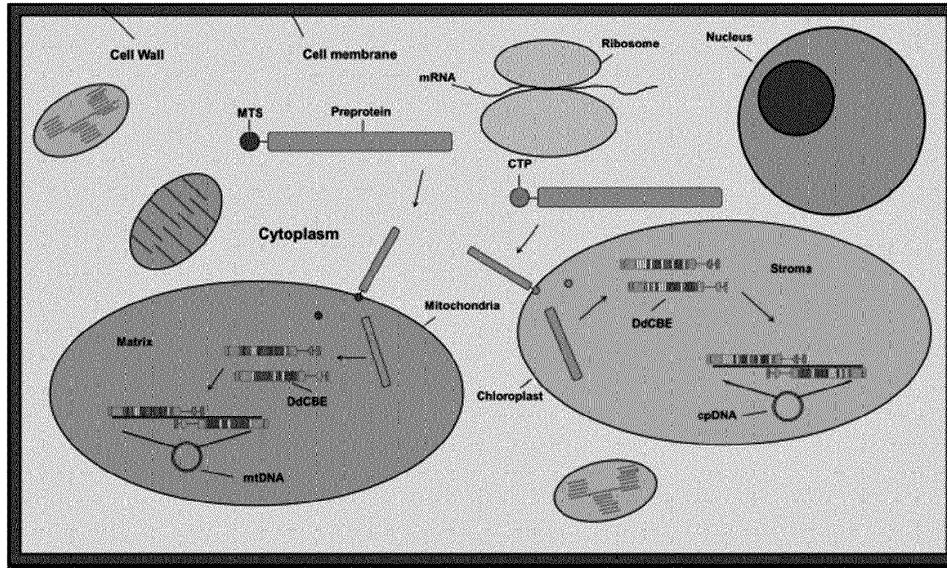
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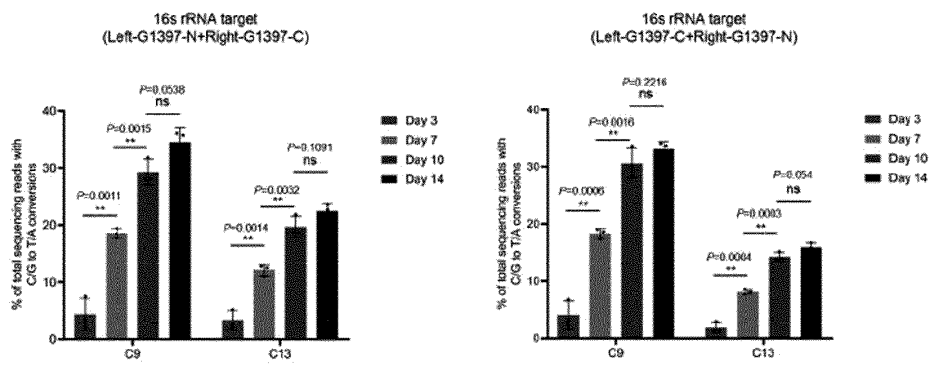
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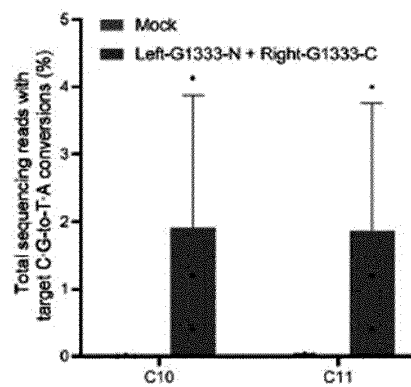
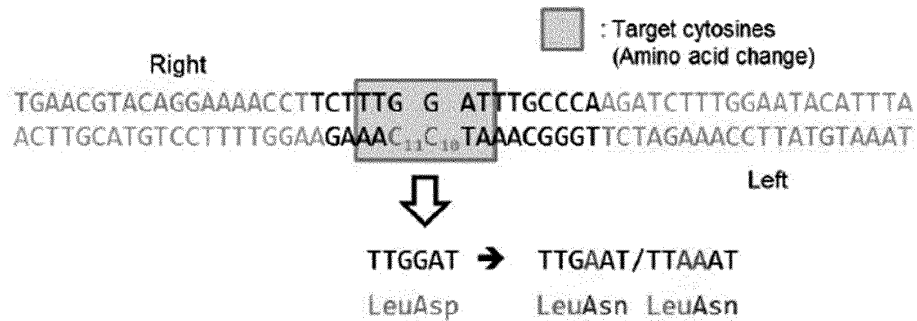
[도 23]



[도 24]

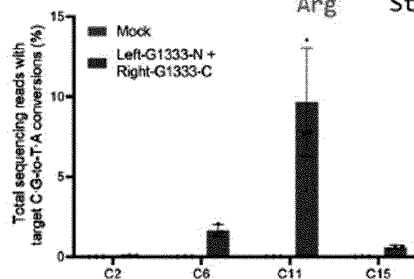
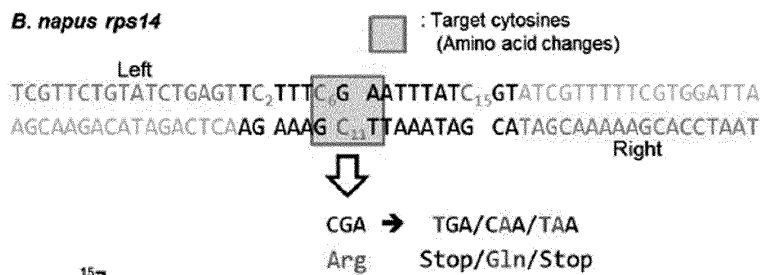


[525]

B. napus psbB

WT	TCTTTGGATTGCCCCA	Edited allele reads (%)
G1333N left - G1333C right	TCTTTaaATTGCCCCA	1.6±1.4

[526]

B. napus rps14

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

[도27]

(a)

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

Lettuce psbA		
	WT	GACCTTGGATTGCTGTTG C-G-to-T-A conversions (%)
G1333N-Left + G1333C-Right	C#1	GACCTTaaATTGCTGTTG 2.91 %
		GAttTTGGATTGCTGTTG 0.26 %
		GAttTTaaATTGCTGTTG 0.22 %
		GACCTTaaATTGCTGTTG 3.11 %
	C#2	GAttTTaaATTGCTGTTG 0.51 %
		aACCTTaaATTGCTGTTG 0.29 %
		GACCTTaaATTGCTGTTG 1.36 %
	C#3	GAtCTTGGATTGCTGTTG 0.45 %
		GACCTTGGATTaCTGTTG 0.25 %
		GACCTTaaATTGCTGTTG 2.31 %
	C#4	GACCTTGaATTGCTGTTG 0.27 %
		GAttTTGGATTGCTGTTG 0.24 %

(b)

Rapeseed atp6		
	WT	GGGATTTCAAAGAC C-G-to-T-A conversions (%)
G1333N-Left + G1333C-Right	C#1	GGGATTtTAAAGAC 24.92 %
		GGGATTtTAAAGAC 0.41 %
	C#2	GGGATTtTAAaAC 0.13 %

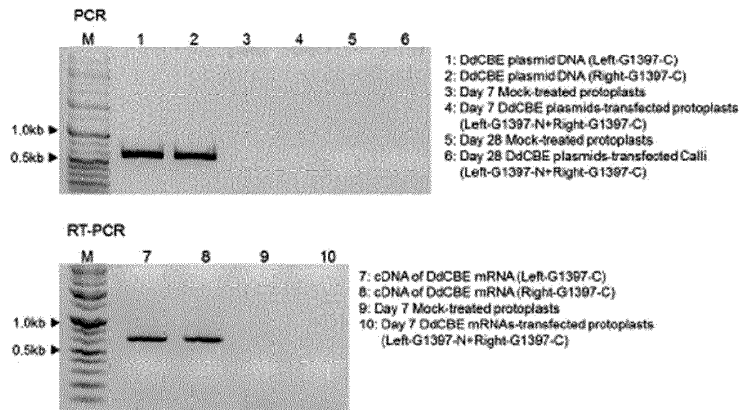
Rapeseed rps14		
	WT	TCTTTCGAATTATCGT
G1333N-Left + G1333C-Right	C#1	TCTTTCaAATTATCGT 0.52 %
		TCTTtTGAATTATCGT 0.30 %
		TCTTTCaAATTATCaT 1.00 %
	C#2	TCTTTCaAATTATCGT 0.53 %
		TCTTTCGAATTATCaT 0.37 %

[도28]

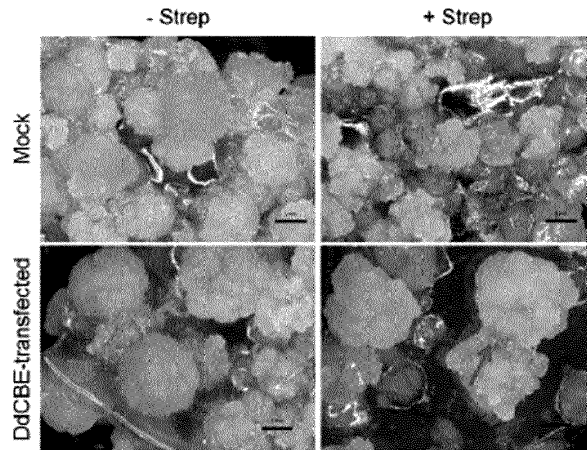
Lettuce 16s rDNA

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

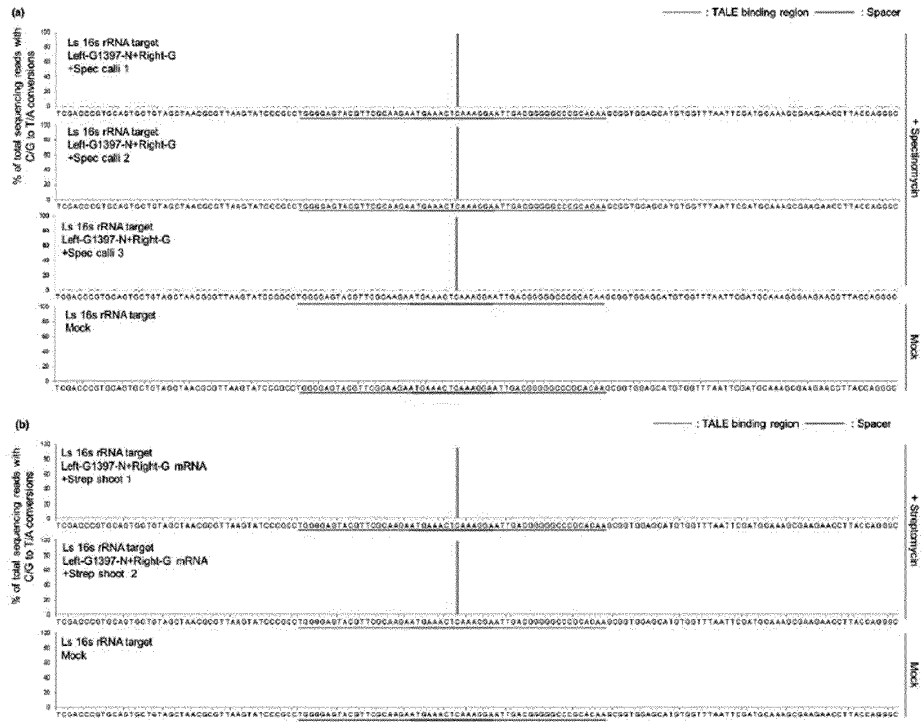
[도29]



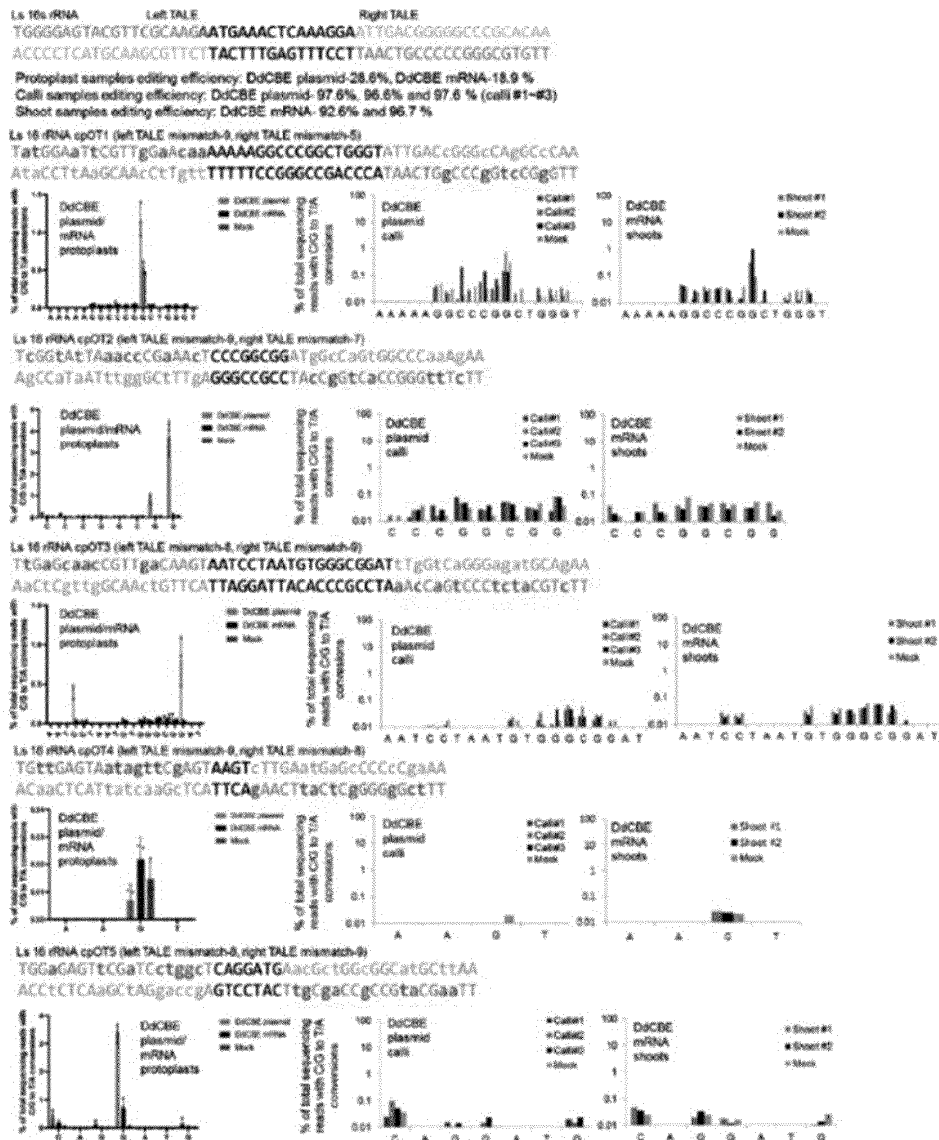
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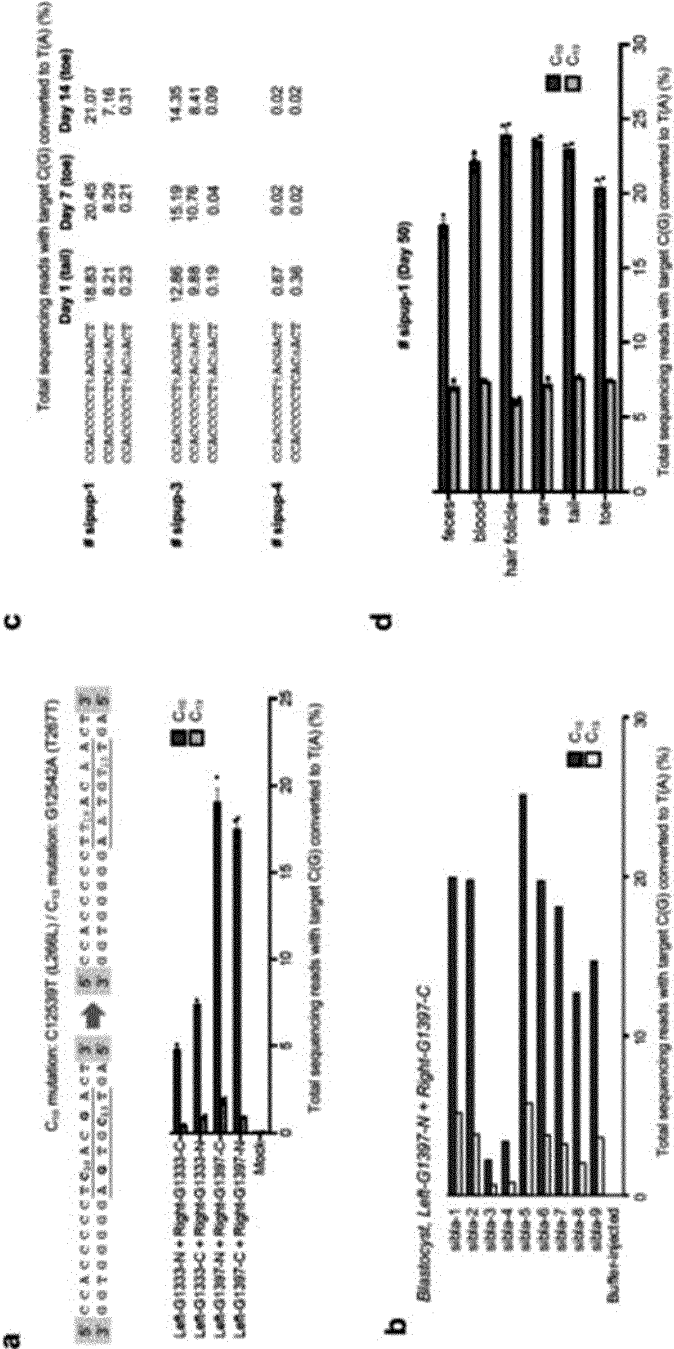
[도 31]



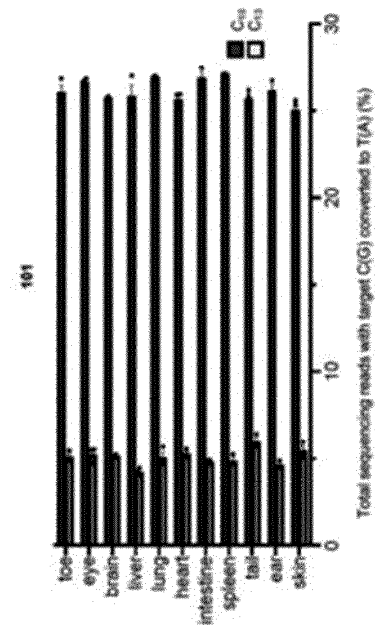
[도32]



[도34]



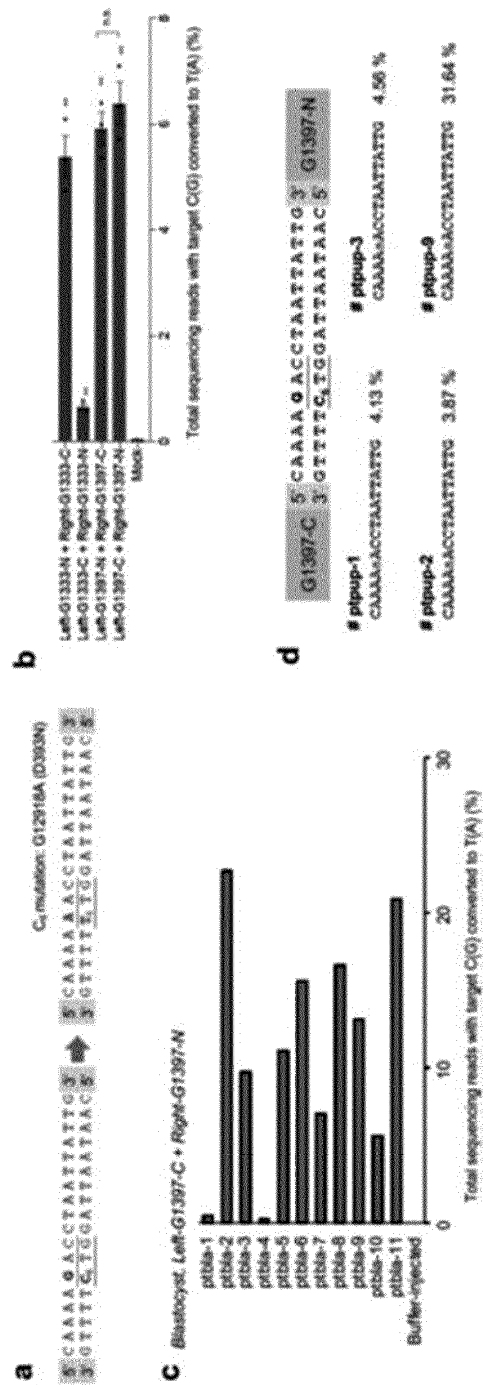
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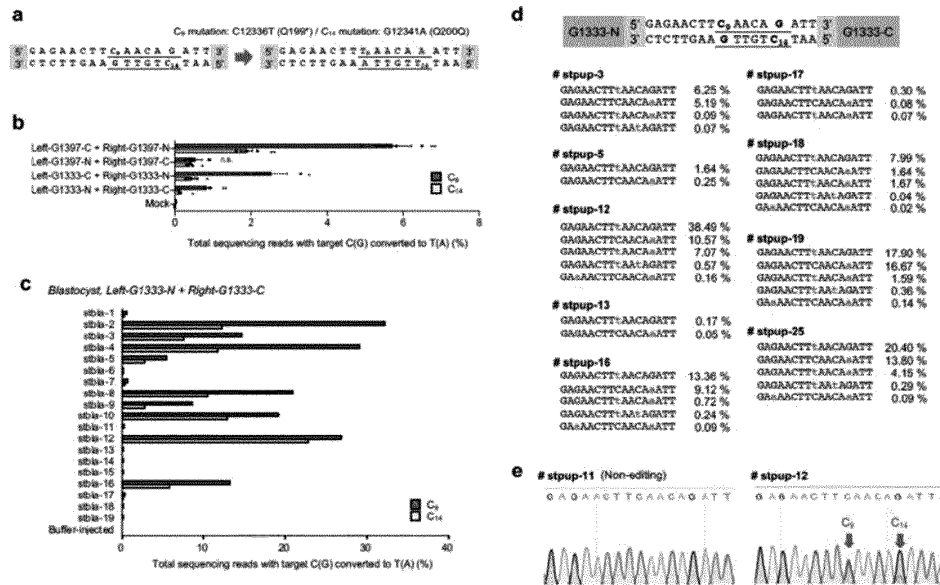
a

		Total sequencing reads with target C(G) converted to T(A) (%)	
F0	WT	CCCCCCCCCCCC	
	# slipup-3 (Day 50)	CCCCCCCCCCCC CCCCCCCCCCCC CCCCCCCCCCCC	13.28 11.64 0.14
F1	101	CCCCCCCCCCCC CCCCCCCCCCCC	25.55 5.66
	102	CCCCCCCCCCCC CCCCCCCCCCCC	25.76 7.11

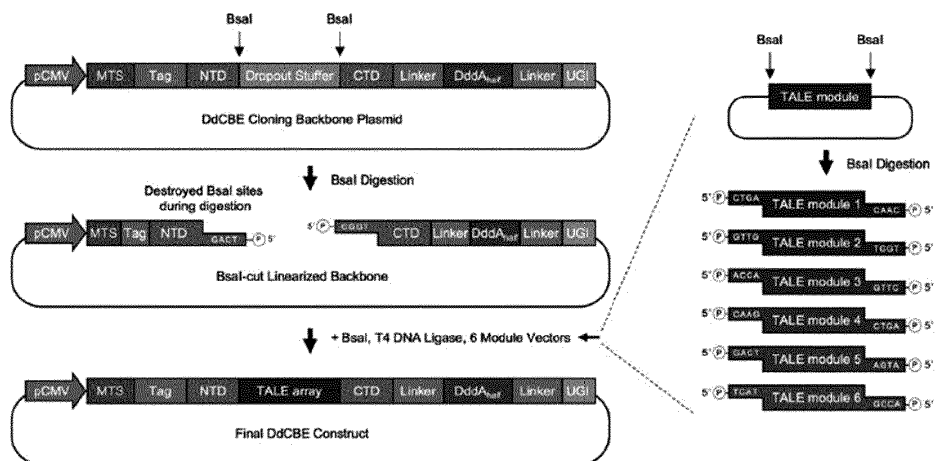
[도36]



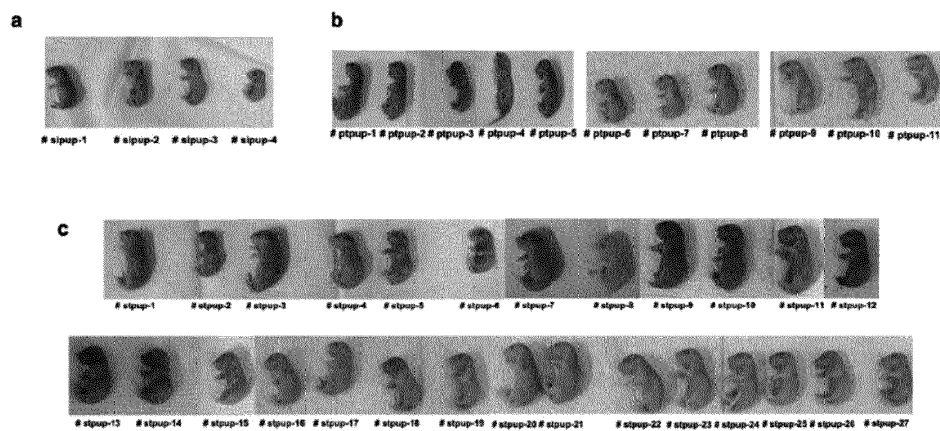
[도37]



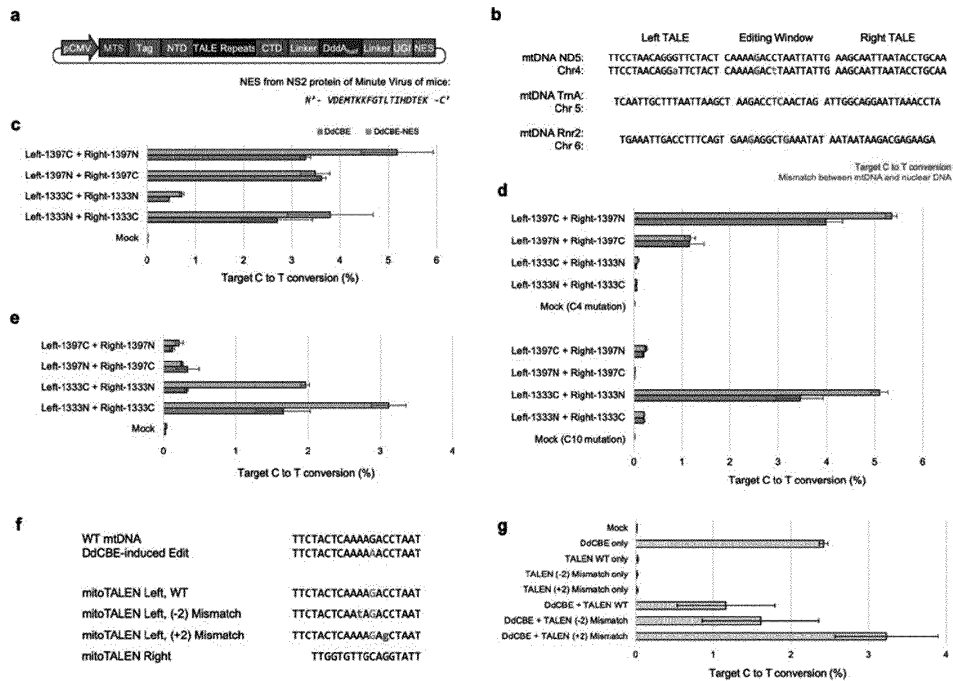
[도38]



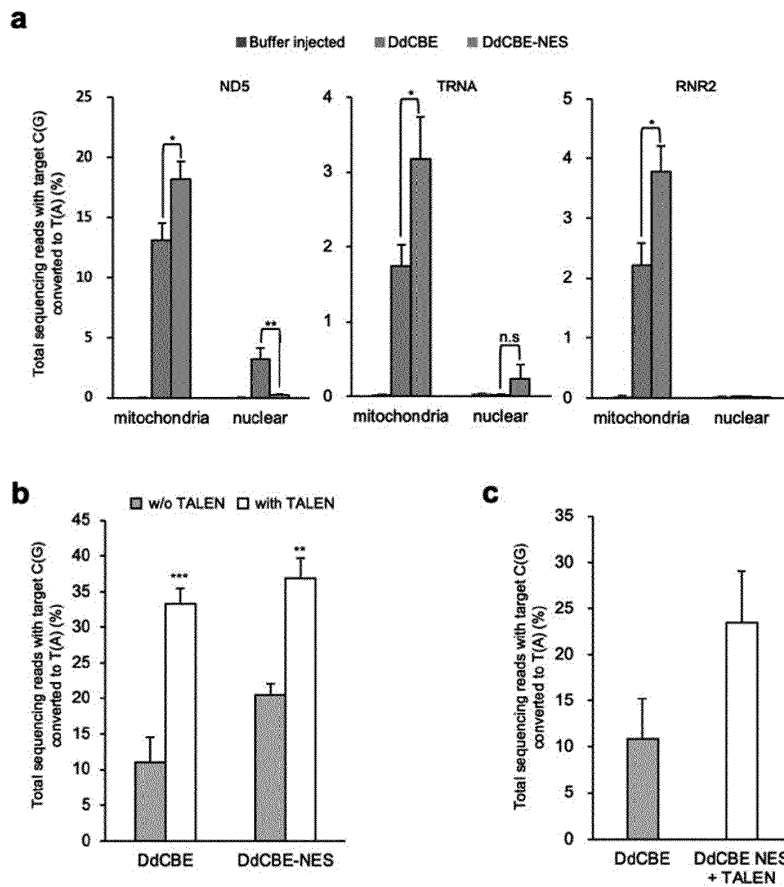
[도39]



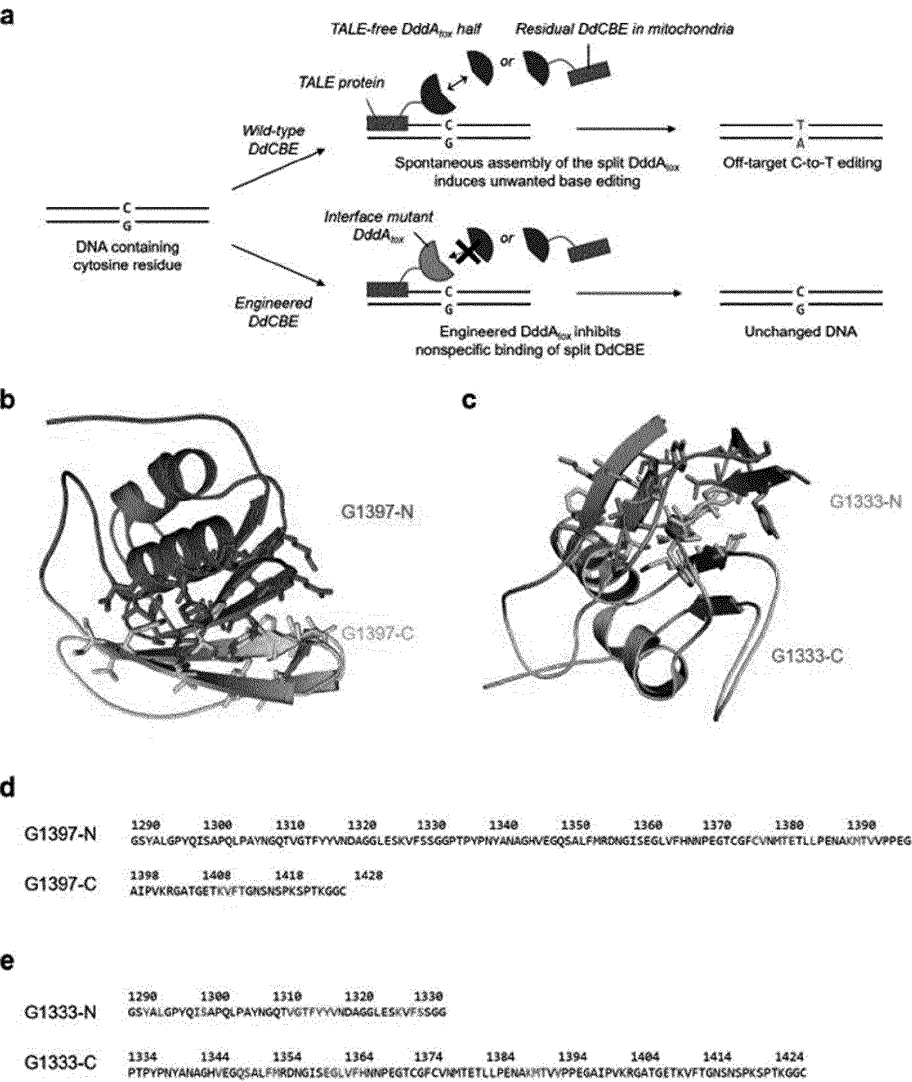
[540]



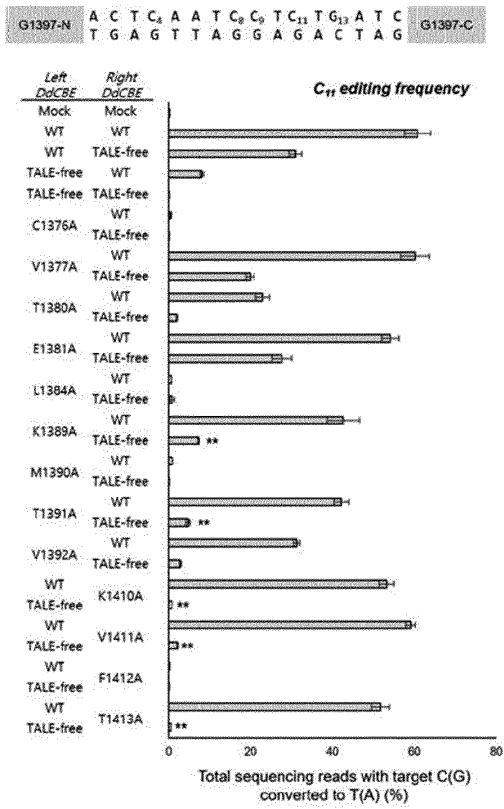
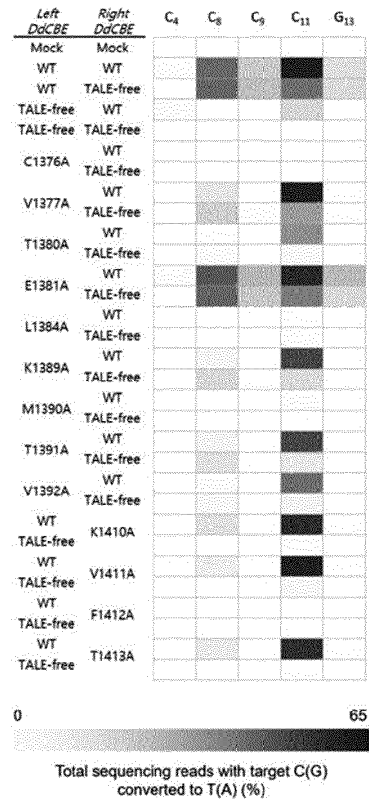
[541]



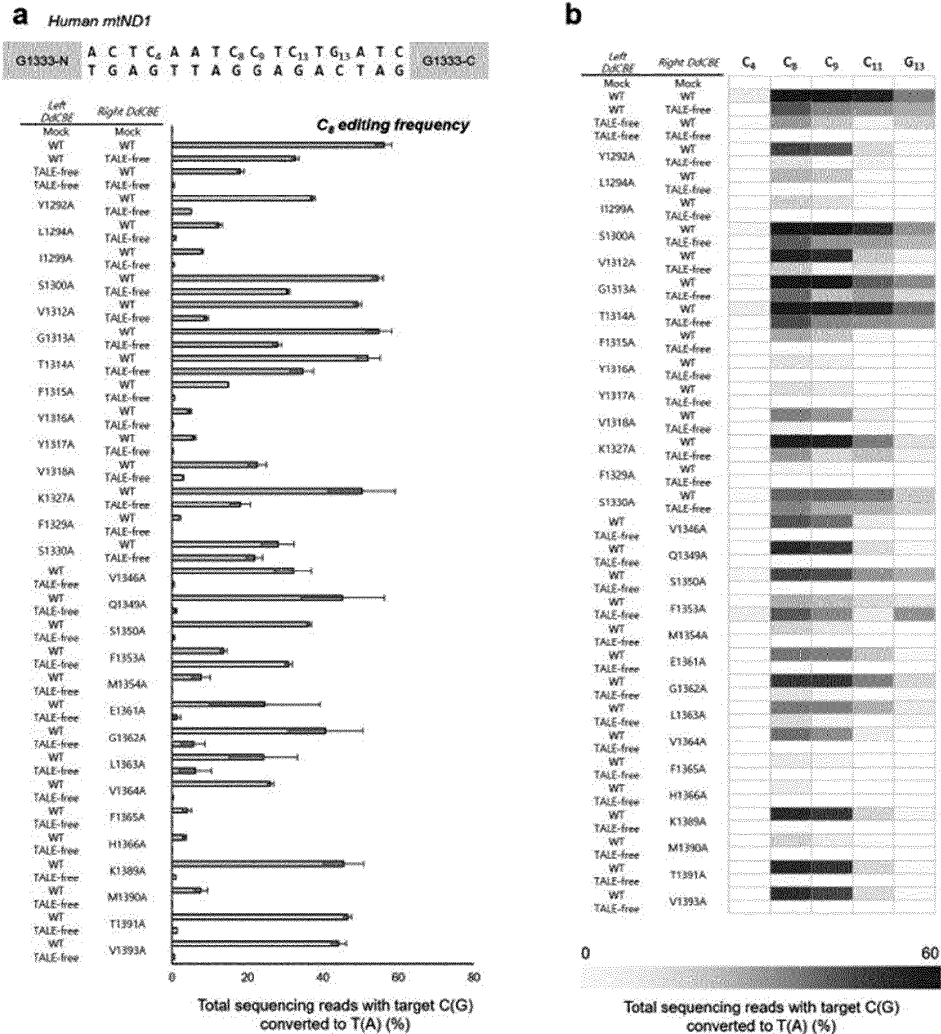
[542]



[도43]

a Human mtND1**b**

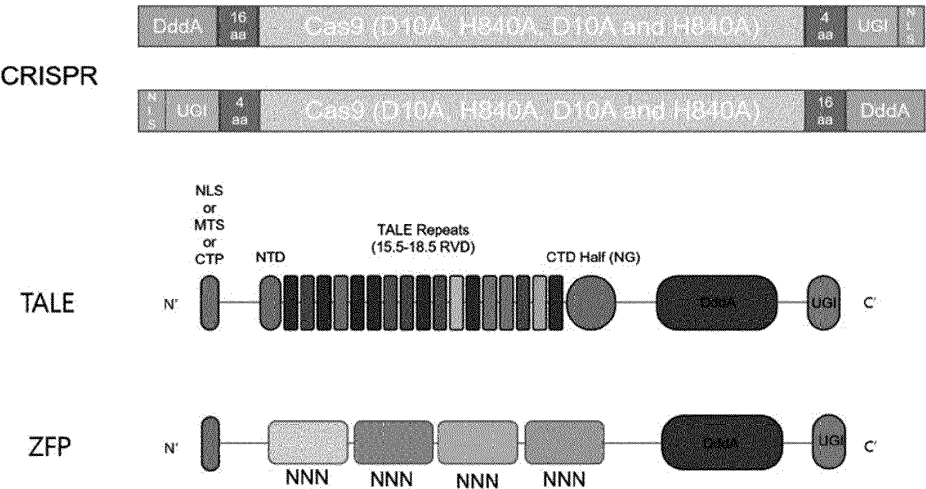
[544]



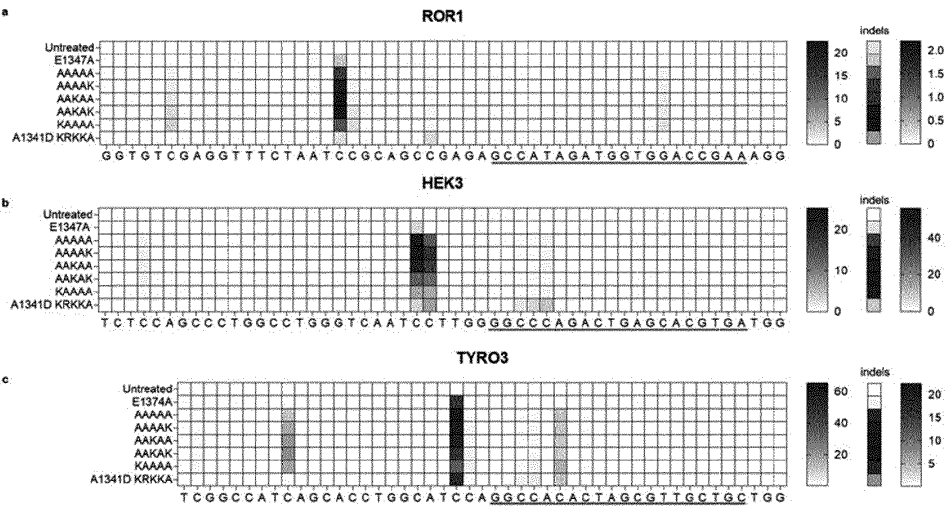
[도45]

Wild Type	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
AAKAK	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
AAKAA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
AAAAA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
AAAAK	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
KAAAA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
A1341D_KRKKA	GSYALGPYQISAPQLPAYNGQTVGTFYYVNDAGGLESKFSSGGPTTPYPNYANAGHVEGQ	60
Wild Type	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVKRGATGET	120
AAKAK	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVAGATGET	120
AAKAA	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVAGATGET	120
AAAAA	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVAGATGET	120
AAAAK	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVAGATGET	120
KAAAA	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVAGATGET	120
A1341D_KRKKA	SALFMRDNGISEGLVFHNNPEGTGCFVNMTEITLLPENAKMTVVPPEGAIPVKRGATGET	120
Wild Type	KVFTGNSNSPKSP TK GGC	138
AAKAK	KVFTGNSNSPKSP TK GGC	138
AAKAA	KVFTGNSNSPKSP TK GGC	138
AAAAA	KVFTGNSNSPKSP TK GGC	138
AAAAK	KVFTGNSNSPKSP TK GGC	138
KAAAA	KVFTGNSNSPKSP TK GGC	138
A1341D_KRKKA	KVFTGNSNSPKSP TK GGC	138

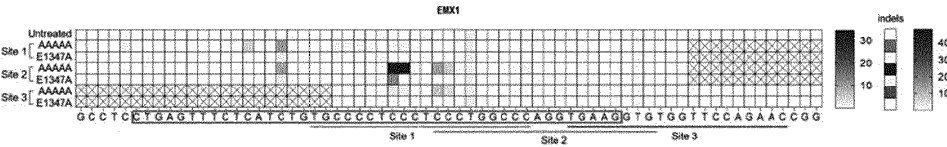
[546]



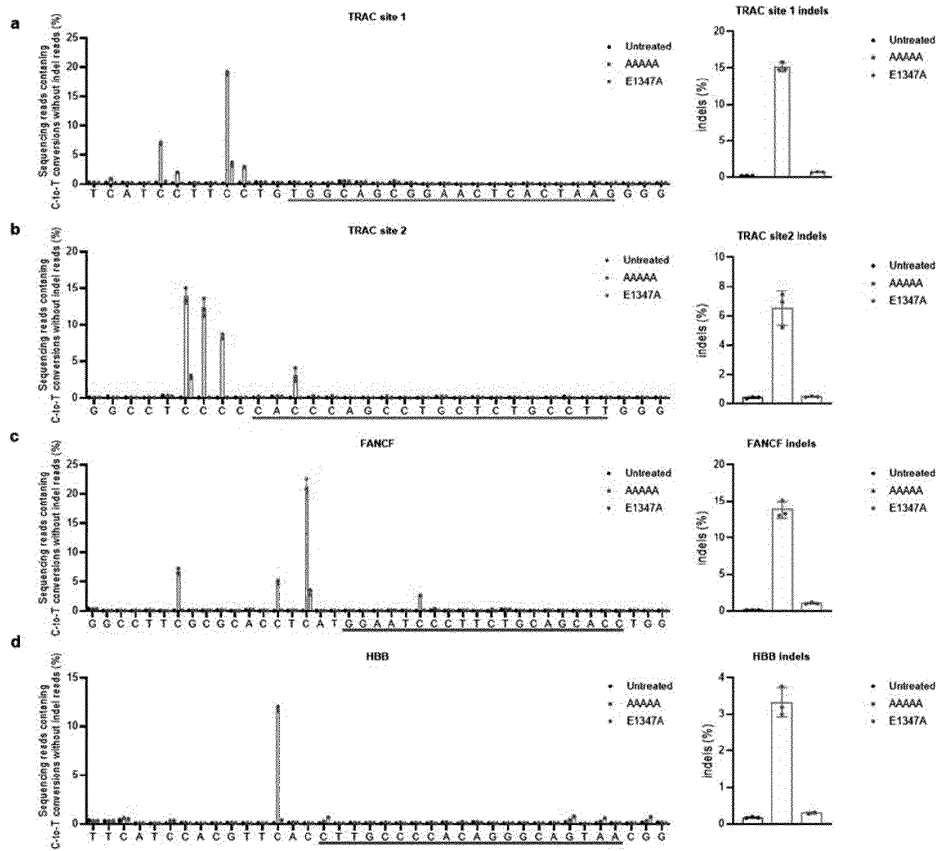
[547]



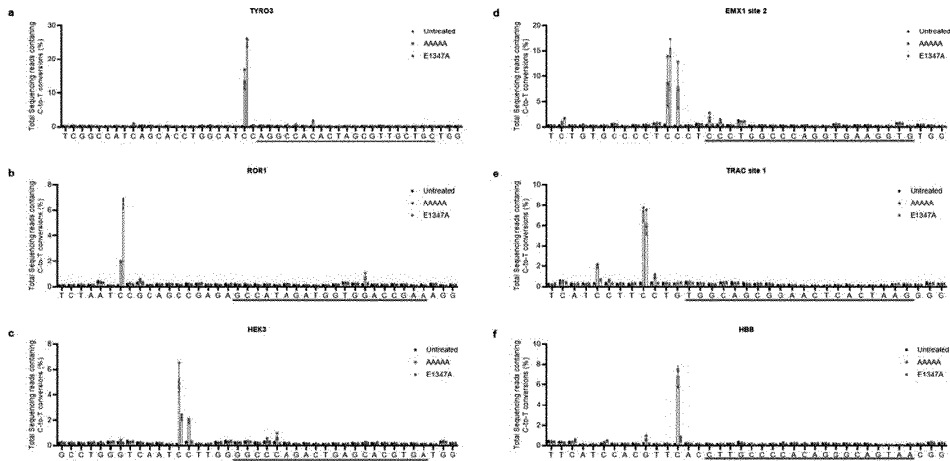
[548]



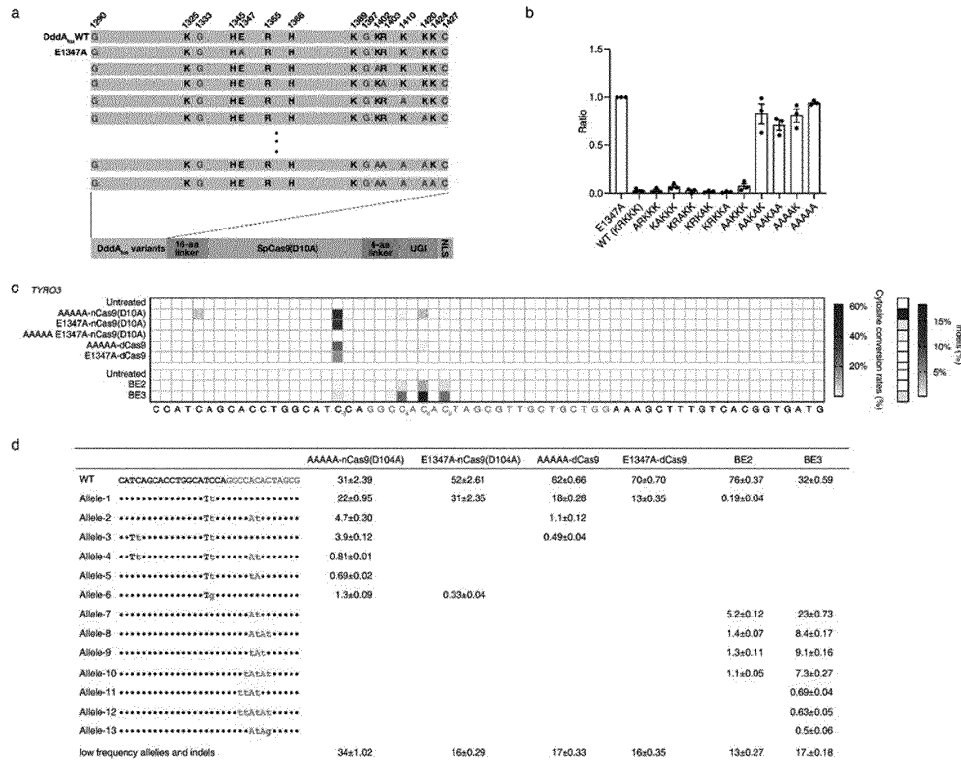
[도49]



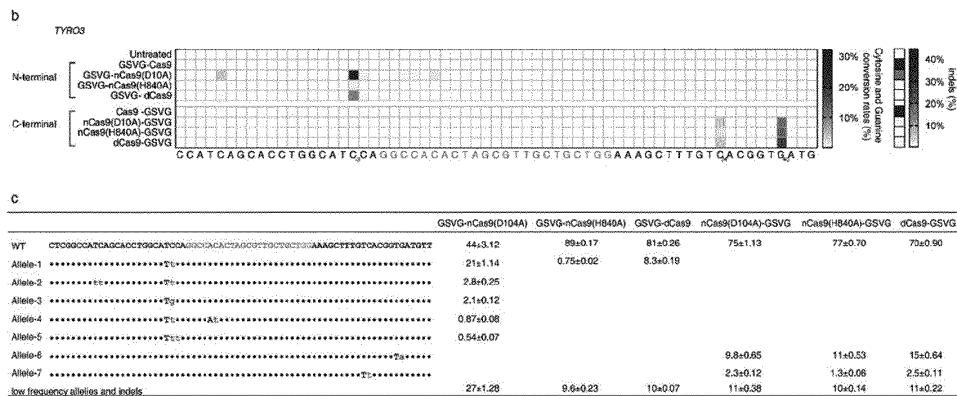
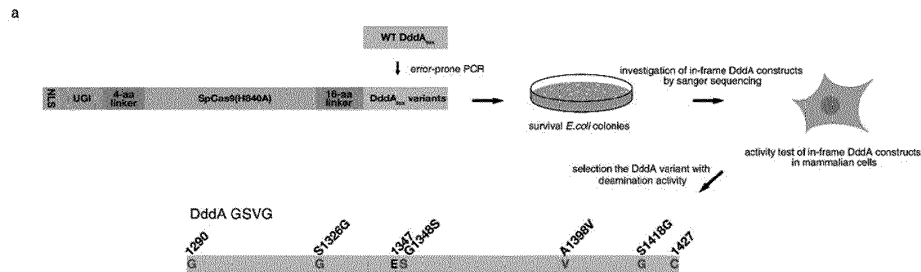
[도50]



[도51]



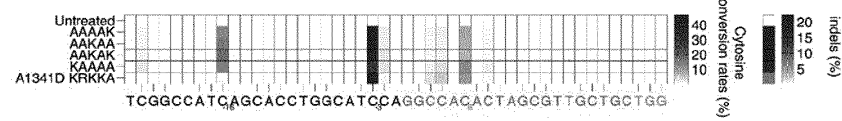
[도52]



[53]

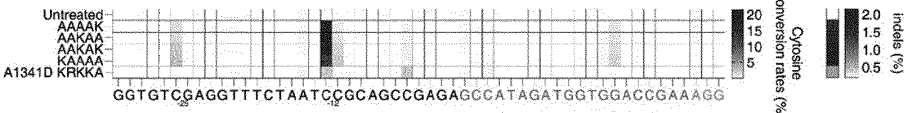
a

TYRO3



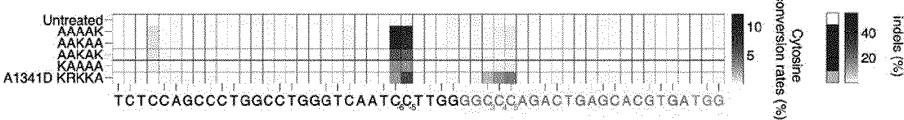
b

ROR1 site 1



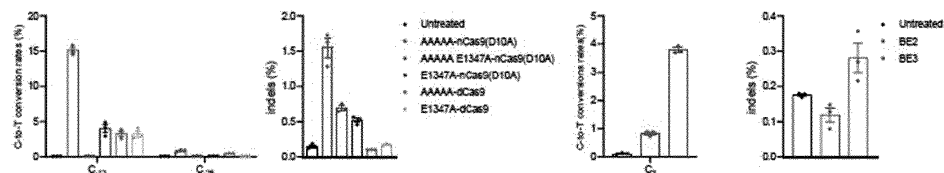
c

HEK3



[54a]

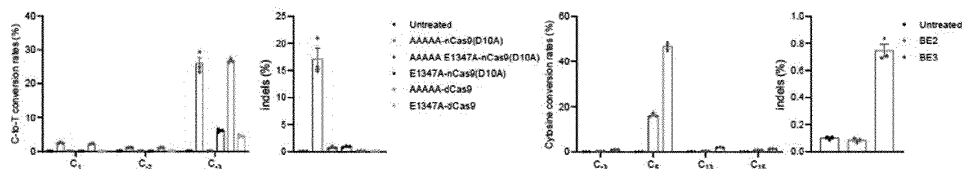
a

ROR1 site 1 GGTGTC₋₂₃GAGGTTTCTAATC₋₁₂CGCAGCCGAGAGCC₃ATAGATGGTGGACCGAAAGG

	AAAAA-nCas9(D10A)	E1347A-nCas9(D10A)	AAAAA-dCas9	E1347-dCas9	BE2	BE3
WT	TGTCGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACCGAAAGG	74±0.39	87±0.50	86±0.33	87±0.52	
Allele-1	TGTCGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACCGAAAGG	13±0.34	3.6±0.51	2.8±0.34	90±0.21	87±0.16
Allele-2	TGTCGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACCGAAAGG	0.47±0.02				
Allele-3	TGTCGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACCGAAAGG				0.58±0.04	3.2±0.04

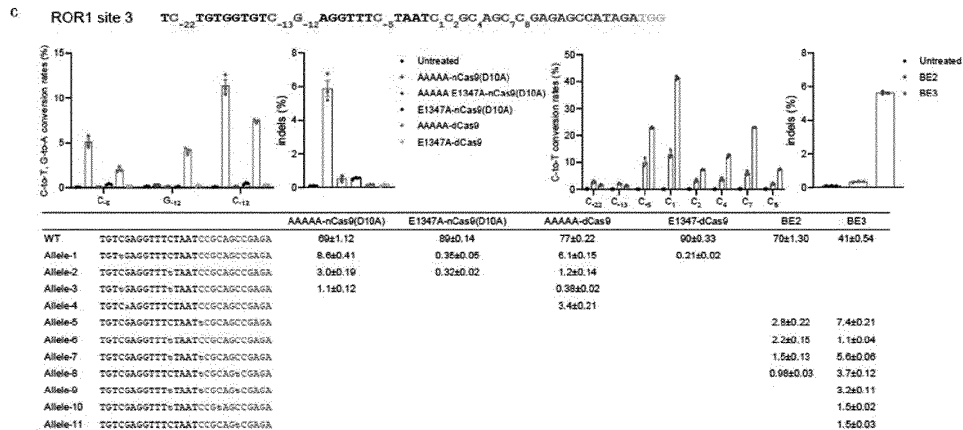
[54b]

b

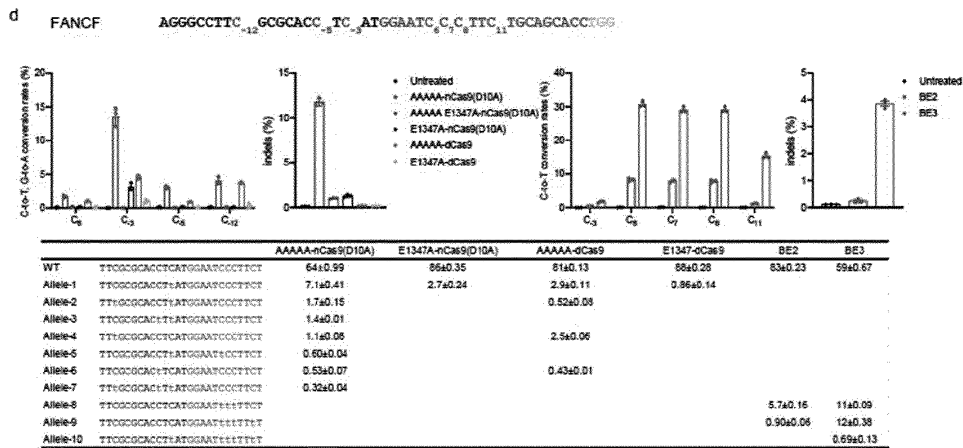
ROR1 site 2 TTGGGTC₋₃C₋₂AC₋₁CATC₅TATGGGTC₁₃TC₁₅GGCTGCGG

	AAAAA-nCas9(D10A)	E1347A-nCas9(D10A)	AAAAA-dCas9	E1347-dCas9	BE2	BE3
Allele-1	TTGGGTCACCATCTATGGGCTCTGGG	61±3.50	84±0.30	66±0.26	86±0.34	75±0.36
Allele-2	TTGGGTCACCATCTATGGGCTCTGGG	18±1.12	5.4±0.25	20±0.35	3.0±0.20	47±0.07
Allele-3	TTGGGTCACCATCTATGGGCTCTGGG	1.6±0.08		1.5±0.07		
Allele-4	TTGGGTCACCATCTATGGGCTCTGGG	0.81±0.1		0.80±0.06		
Allele-5	TTGGGTCACCATCTATGGGCTCTGGG				13±0.53	36±0.92
Allele-6	TTGGGTCACCATCTATGGGCTCTGGG					2.6±0.10
Allele-7	TTGGGTCACCATCTATGGGCTCTGGG					1.1±0.12

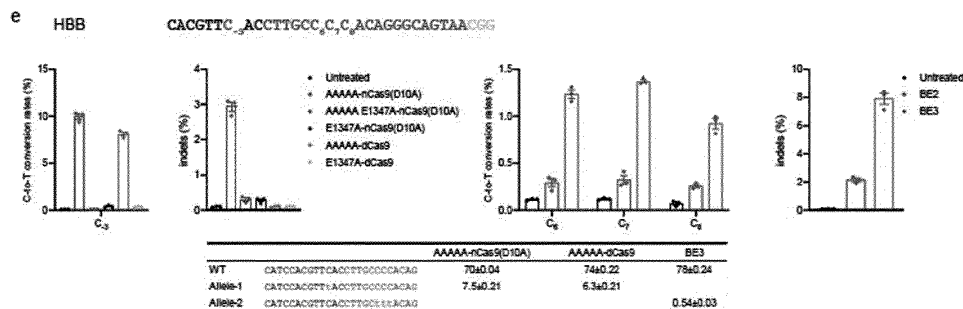
[54c]



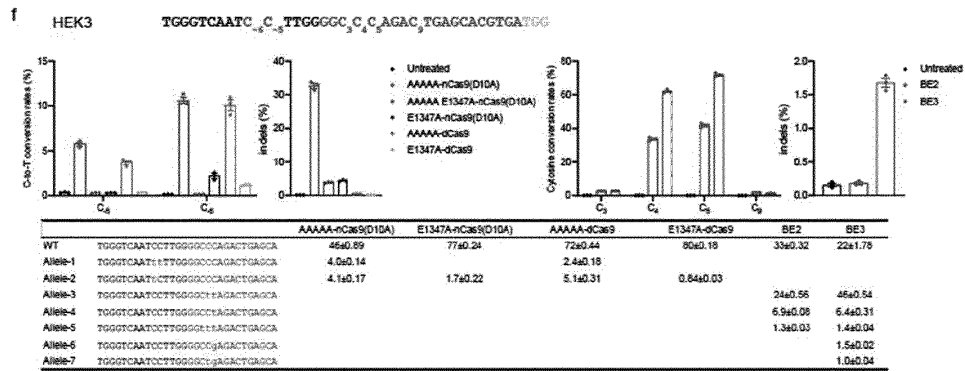
[54d]



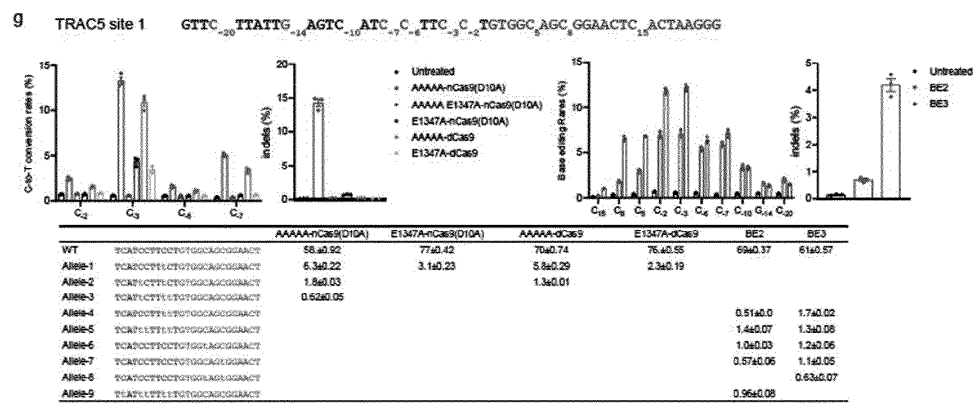
[54e]



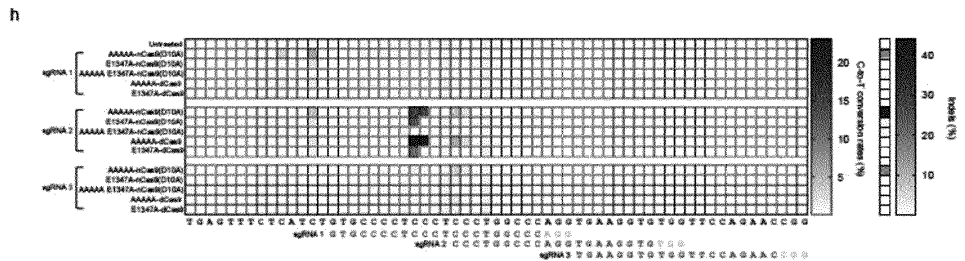
[554f]



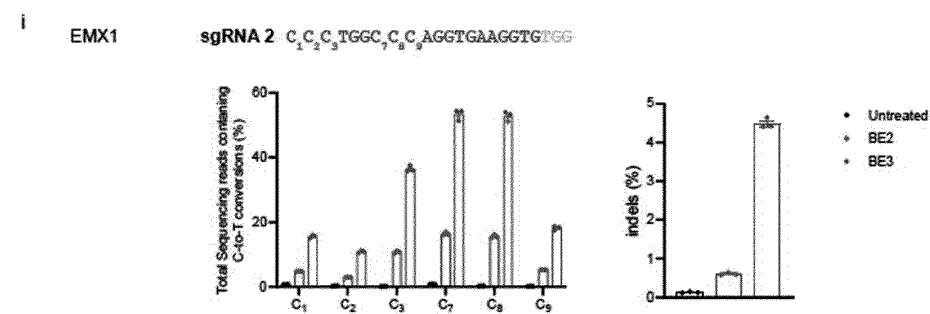
[554g]



[554h]



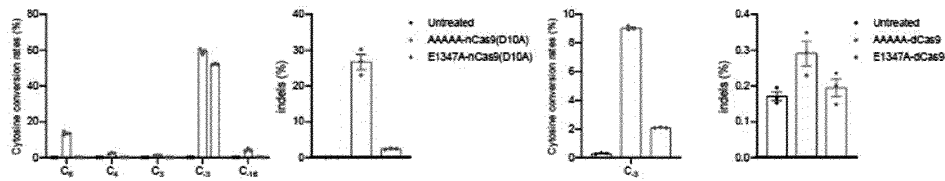
[554i]



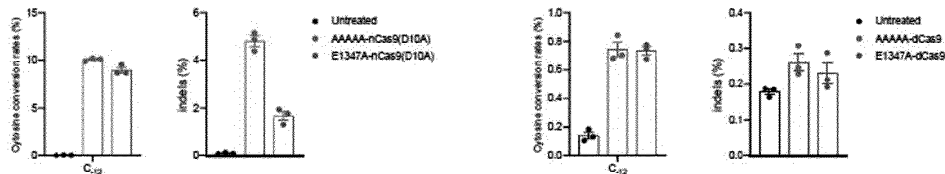
[도54]

		AAAAA-nCas9(D10A)	E1347A-nCas9(D10A)	AAAAA-dCas9	E1347A-dCas9	BE2	BE3
WT	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG	34±1.32	69±0.44	62±0.30	73±1.02	55±0.38	22±0.60
Allele-1	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG	5.7±0.15		12±0.55			
Allele-2	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG	1.7±0.11		0.78±0.02			
Allele-3	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG	1.0±0.05		1.8±0.02			
Allele-4	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG	0.87±0.06		1.4±0.03			
Allele-5	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG		10±0.56	1.4±0.05	7.6±0.71		
Allele-6	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG		0.95±0.02		0.50±0.01		
Allele-7	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG					3.2±0.14	10±0.09
Allele-8	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG					2.6±0.14	8.2±0.17
Allele-9	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG					1.3±0.06	2.6±0.11
Allele-10	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG					1.1±0.06	3.7±0.10
Allele-11	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG						3.5±0.14
Allele-12	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG						2.4±0.15
Allele-13	TCTCATCTGTGCCCTCCCTCCCTGGCCAGGTG						2.3±0.18

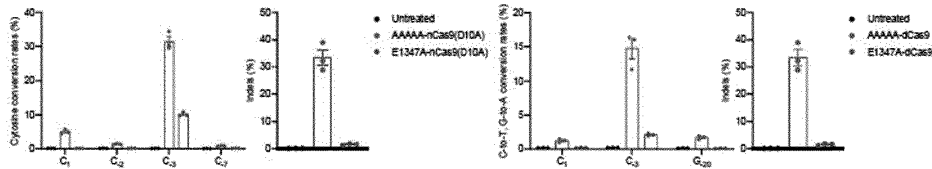
[도55a]

a TYRO3 CATC₋₁₃AGCACCTGGCATC₋₃CAGGC₋₃C₄AC₂ACTAGCGTTGCTGCTGG

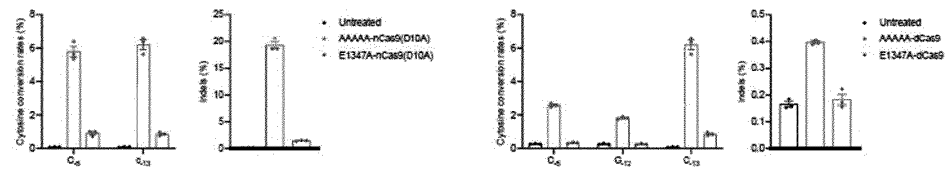
[도55b]

b ROR1 site 1 AGGTTTCTAATC₋₁₂CGCAGCCGAGAGCC₋₃ATAGATGGTGGACCGAAAGG

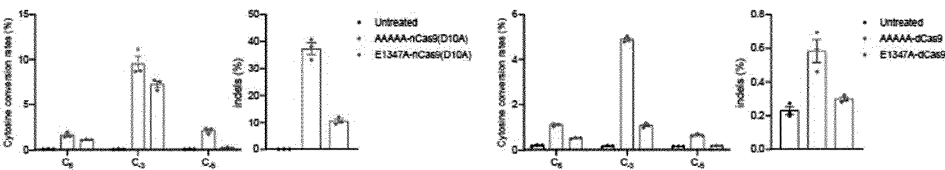
[도55c]

c ROR1 site 2 GCTCTCCTTTC₋₇GGTC₋₃C₂AC₂CATCTATGGCTCTGGGCTGCGG

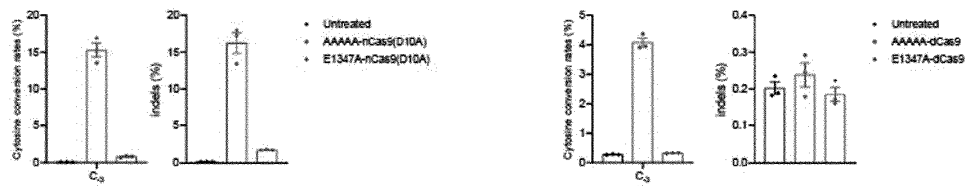
[도55d]

d ROR1 site 3 TGTGGTGTG₋₁₃G₋₁₂AGGTTTC₋₅TAATCCGAGCCGAGAGCCATAGATGG

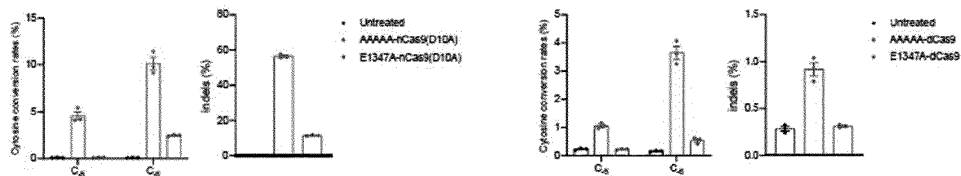
[도55e]

e FANCF GCGCAC₋₅TC₋₃ATGGAATC₋₆CCTTCGAGCAGCCTGG

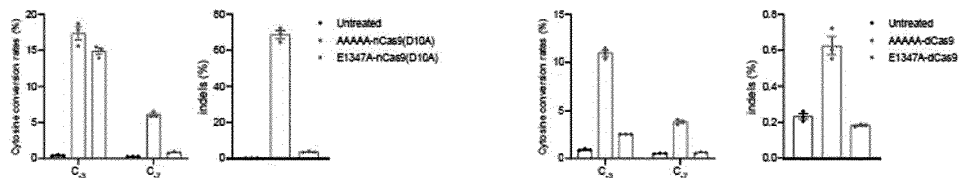
[55f]

f HBB CACGTTTC₃ACCTTGCCCCACAGGGCAGTAA_{CGG}

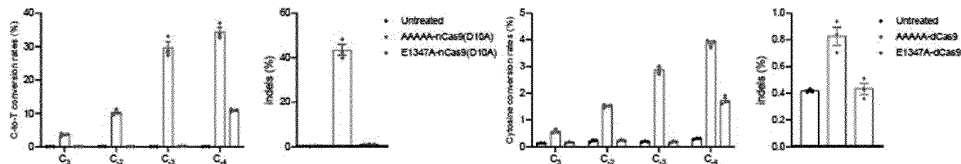
[55g]

g HEK3 TGGGTCAATC₆C₃TGGGGCCAGACTGAGCACGTGATGG

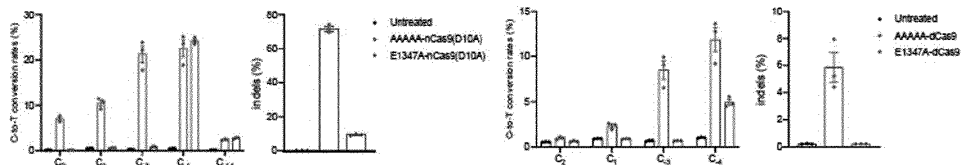
[55h]

h TRAC5 site 1 ATC₃CTTC₃CTGTGGTAGCGGAATCACTAA_{GGG}

[55i]

i TRAC5 site 2 CAGGCCTC₄C₃C₂CCAC₃CCAGCCTGCTCTGCCTT_{GGG}

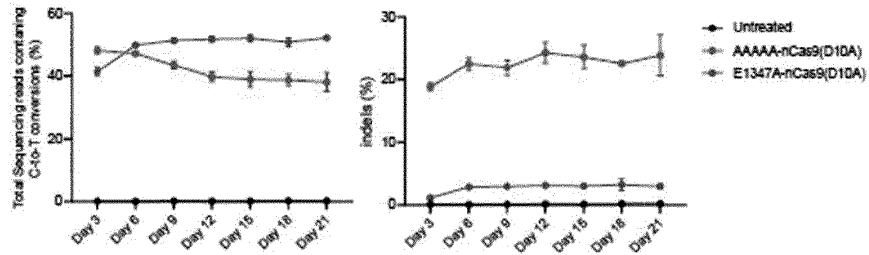
[55j]

j EMX1 site 2 TC₁₄TGTGCCCTC₄C₃CTC₄C₂TGGCCAGGTGAAGGTG_{TGG}

[556]

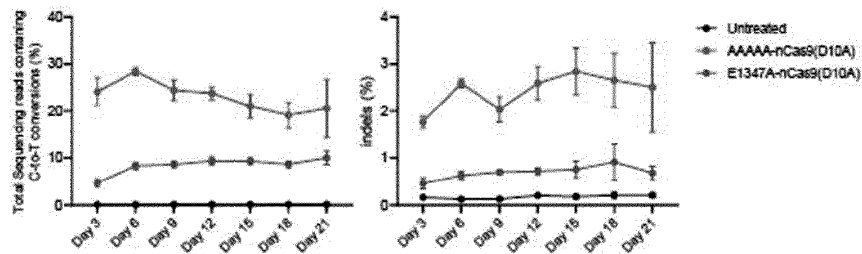
a

TYRO3

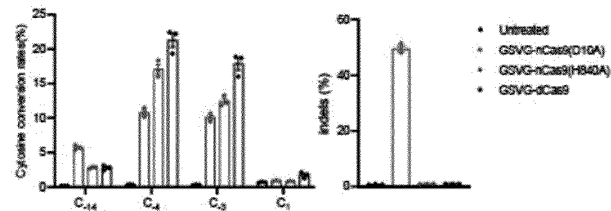


b

ROR1

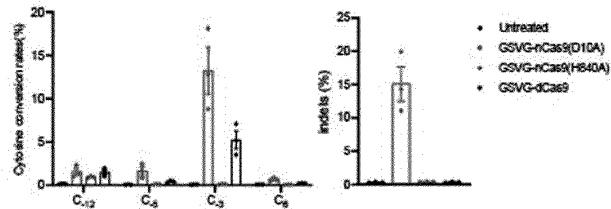


[557a]

a EMX1 site 2 GAGTTTCTCATC₋₁₄TGTGCCCTC₋₄C₋₂CTC₁CCTGGCCAGGTGAAGGTGTGGTTCCAG

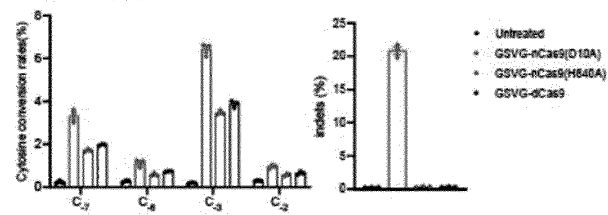
		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	TCTCATCTGTGCCCTTCCTCTCTGGCCAGGTG	33±1.3	87±1.2	83±1.5
Allele-1	TCTCATCTGTGCCCTTCCTCTCTGGCCAGGTG	3.9±0.13	1.1±0.09	1.5±0.28
Allele-2	TCTCATCTGTGCCCTTCCTCTCTGGCCAGGTG	3.5±0.31	8.5±0.59	12±0.77
Allele-3	TCTCATCTGTGCCCTTCCTCTCTGGCCAGGTG		3.8±0.36	2.6±0.16
Allele-4	TCTCATCTGTGCCCTTCCTCTCTGGCCAGGTG		0.66±0.02	
Allele-5	TCTCATCTGTGCCCTTCCTCTCTGGCCAGGTG			0.68±0.25

[557b]

b FANCF AGTAGGGCTTC₋₁₂GCGCACC₋₈TC₋₃ATGGAATC₆CCTTCTGCAGCACCCTGGATCGCT

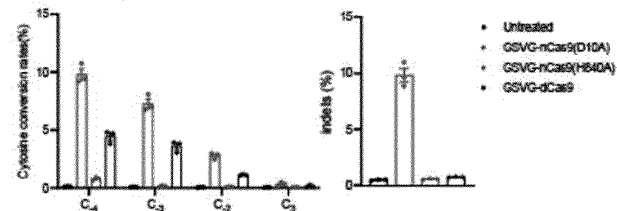
		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	TTTGGGCACTTCATGGAATCCTTCT	64±4.9	90±0.08	84±1.9
Allele-1	TTTGGGCACTTCATGGAATCCTTCT	8.9±1.7		4.0±1.4
Allele-2	TTTGGGCACTTCATGGAATCCTTCT	0.95±0.23		
Allele-3	TTTGGGCACTTCATGGAATCCTTCT	0.81±0.18	0.78±0.11	0.32±0.04
Allele-4	TTTGGGCACTTCATGGAATCCTTCT	0.47±0.17		
Allele-5	TTTGGGCACTTCATGGAATCCTTCT	0.38±0.11		0.90±0.33
Allele-6	TTTGGGCACTTCATGGAATCCTTCT	0.38±0.04		

[57c]

C TRAC5 site 1 TCTTATTGAGTCATC₋₇C₋₆TTC₋₃C₋₂TGTGGCAGCGGAACCTACTAAGGGCCCATC

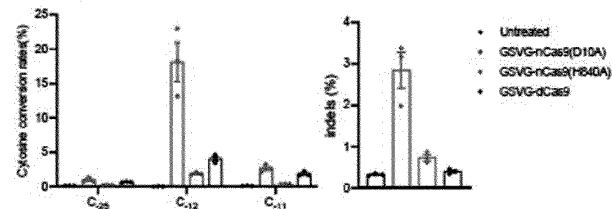
		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	GAGTCATCCTTCTGTGGCAGCGGAA	61±1.4	82±0.38	61±0.26
Allele-1	GAGTCATCCTTCTGTGGCAGCGGAA	2.9±0.18	2.1±0.08	2.0±0.21
Allele-2	GAGTCATCCTTCTGTGGCAGCGGAA	1.2±0.19		0.53±0.02
Allele-3	GAGTCATCCTTCTGTGGCAGCGGAA		0.53±0.06	0.43±0.11

[57d]

d TRAC5 site 2 CAGGAGCTGCAGGCCTC₋₄C₋₃CCACC₃CAGCCTGCTCTGCCTTGGGAAACCC

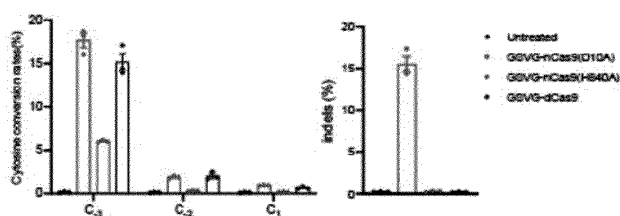
		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	GGCCTTCCGACCCAGCCTCTGTGCTTGGGAAACCTGGGTGTGT	68±1.0	84±0.23	80±0.83
Allele-1	GGCCTTCCGACCCAGCCTCTGTGCTTGGGAAACCTGGGTGTGT	3.74±0.44		2.04±0.33
Allele-2	GGCCTTCCGACCCAGCCTCTGTGCTTGGGAAACCTGGGTGTGT	2.34±0.15	0.56±0.08	0.714±0.03
Allele-3	GGCCTTCCGACCCAGCCTCTGTGCTTGGGAAACCTGGGTGTGT	1.94±0.22		0.834±0.08
Allele-4	GGCCTTCCGACCCAGCCTCTGTGCTTGGGAAACCTGGGTGTGT	0.82±0.12	0.83±0.05	0.87±0.03
Allele-5	GGCCTTCCGACCCAGCCTCTGTGCTTGGGAAACCTGGGTGTGT	0.59±0.09	0.71±0.05	0.73±0.07

[57e]

e ROR1 site 1 TC₋₂₅GAGGTTTCTAATC₋₁₂C₋₁₁GCAGCCGAGAGCCATAGATGGTGGACCGAAAGGAGAGCC

		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	TGTCGAGTTTCTAATCCGACCCAGAGCCATAGATGGTGGACCGAAAGGAGAGCC	69±5.5	67±0.16	64±0.44
Allele-1	TGTCGAGTTTCTAATCCGACCCAGAGCCATAGATGGTGGACCGAAAGGAGAGCC	14±4.1	1.6±0.16	3.1±0.45
Allele-2	TGTCGAGTTTCTAATCCGACCCAGAGCCATAGATGGTGGACCGAAAGGAGAGCC	1.34±0.20		1.4±0.23
Allele-3	TGTCGAGTTTCTAATCCGACCCAGAGCCATAGATGGTGGACCGAAAGGAGAGCC	0.95±0.26		

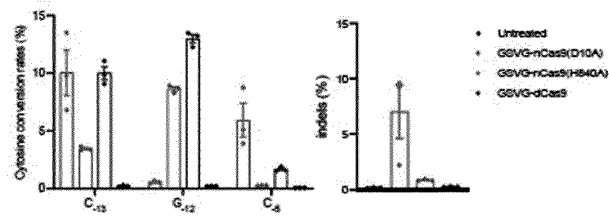
[57f]

f ROR1 site 2 GCTCTCCTTTTCGGTC₋₂C₋₁ACATCATATGGCTCTCGGCTCGGATTAGA

		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
Allele-1	TTCGGTCCACCATCTATGGCTCTCGGC	58±2.6	84±0.46	75±1.8
Allele-2	TTCGGTCCACCATCTATGGCTCTCGGC	12±1.1	5.0±0.08	11±1.1
Allele-3	TTCGGTCCACCATCTATGGCTCTCGGC	1.1±0.06		1.4±0.3

[57g]

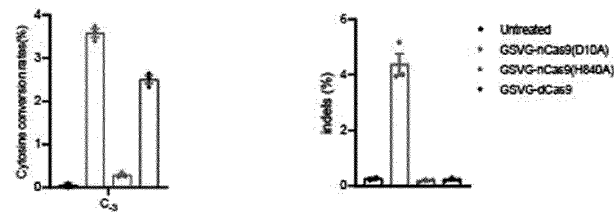
g ROR1 site 3 GGTGTC₋₁₃G₋₁₂AGGTTTC₋₅TAATCCGCAGCCGAGAGCCATAGATGGTGGACC



		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	TGTCGAGGTTCTTAATCCGCAGCCGAGAGCCATAGATGGTGGACC	70±8.0	78±0.59	68±1.6
Allele-1	TGTGAGGTTCTTAATCCGCAGCCGAGAGCCATAGATGGTGGACC	6.8±1.9	2.8±0.19	8.5±0.8
Allele-2	TGTCGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACC	2.7±1.0		0.81±0.07
Allele-3	TGTGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACC	1.8±0.95		
Allele-4	TGTCGAGGTTTCTAATCCGCAGCCGAGAGCCATAGATGGTGGACC	0.4±0.13		
Allele-5	TGTCAGGTTCTTAATCCGCAGCCGAGAGCCATAGATGGTGGACC		7.5±0.27	11±0.6

[57h]

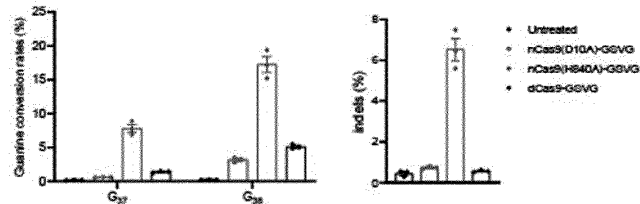
h HBB site TCACCACCAACTTCATCCACGTTTC₋₅ACCTTGCCCCACAGGGCAGTAAAGGCAGACT



		GSVG-nCas9(D10A)	GSVG-nCas9(H840A)	GSVG-dCas9
WT	ACCCACCAACTTCATCCACGTTTCACCTTGCCCCACAGGGCAGTAAAGGCAGACT	80±0.34	88±0.35	85±0.46
Allele-1	ACCCACCAACTTCATCCACGTTTCACCTTGCCCCACAGGGCAGTAAAGGCAGACT	2.9±0.17		2.2±0.13
Allele-2	ACCCACCAACTTCATCCACGTTTCACCTTGCCCCACAGGGCAGTAAAGGCAGACT		0.50±0.06	

[58a]

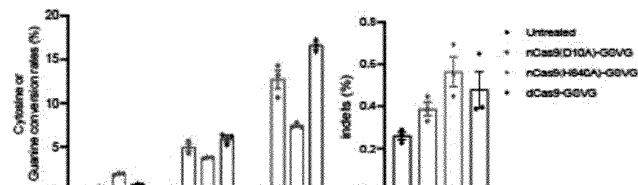
a EMX1 site 2 CTCCCTCCCTGGCCCAGGTGAAGGTGTGGTTCCAGAACCGGAG₃₇G₃₈ACAAAGT



		nCas9(D10A)-GSVG	nCas9(H840A)-GSVG	dCas9-GSVG
WT	CCCTGGCCCAGGTGAAGGTGTGGTTCCAGAACCGGAGGACAAAGT	84±0.35	67±1.6	63±0.21
Allele-1	CCCTGGCCCAGGTGAAGGTGTGGTTCCAGAACCGGAGGACAAAGT	2.1±0.15	8.0±0.45	3.1±0.07
Allele-2	CCCTGGCCCAGGTGAAGGTGTGGTTCCAGAACCGGAGGACAAAGT		6.5±0.49	1.1±0.08

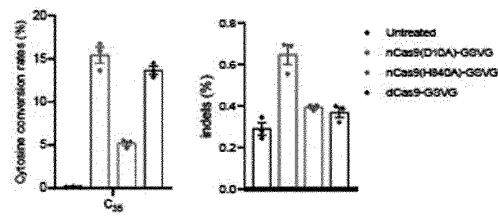
[58b]

b EMX1 site 4 GAGGACAAAGTACAAACGGCAGAAAGCTGGAGGAGG₂₇AAGGGCCTGAGTC₄₂C₄₃GAGCAGA



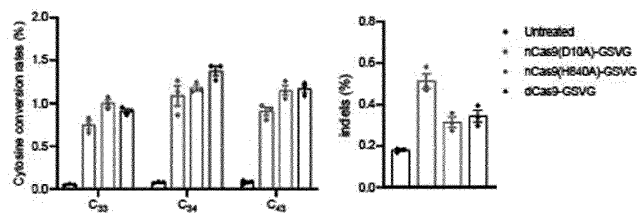
		nCas9(D10A)-GSVG	nCas9(H840A)-GSVG	dCas9-GSVG
WT	AAAGTCAAAAGTACAAACGGCAGAAAGCTGGAGGAGGAAAGGGCCTGAGTCGAGCAGA	74±1.2	78±0.13	70±0.47
Allele-1	AAAGTCAAAAGTACAAACGGCAGAAAGCTGGAGGAGGAAAGGGCCTGAGTCGAGCAGA	8.6±0.74	4.8±0.17	11±0.26
Allele-2	AAAGTCAAAAGTACAAACGGCAGAAAGCTGGAGGAGGAAAGGGCCTGAGTCGAGCAGA	2.1±0.17	1.2±0.03	2.8±0.11
Allele-3	AAAGTCAAAAGTACAAACGGCAGAAAGCTGGAGGAGGAAAGGGCCTGAGTCGAGCAGA	2.0±0.19	1.7±0.06	2.1±0.16
Allele-4	AAAGTCAAAAGTACAAACGGCAGAAAGCTGGAGGAGGAAAGGGCCTGAGTCGAGCAGA		0.87±0.08	

[58c]

c ROR1 site 2 GGTCCACCATCTATGGCTCTCGGCTG~~CGG~~ATTAGAAACCTC₃₅GACACCACA

		nCas9(D10A)-GSVG	nCas9(H840A)-GSVG	dCas9-GSVG
WT	CCATCTATGGCTCTCGGCTG CGG ATTAGAAACCTCGACACCACA	75±0.84	86±0.32	78±0.39
Allele-1	CCATCTATGGCTCTCGGCTG CGG ATTAGAAACCTCGACACCACA	14±0.84	4.6±0.24	12±0.41

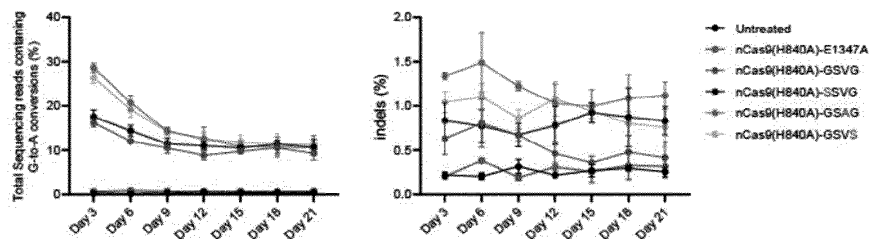
[58d]

d HBB site GTTCACCTTGCCCCACAGGGCAGTAA~~CGG~~CAGACTTCTC₃₄TCAGGAGTC₄₅AGGTGC

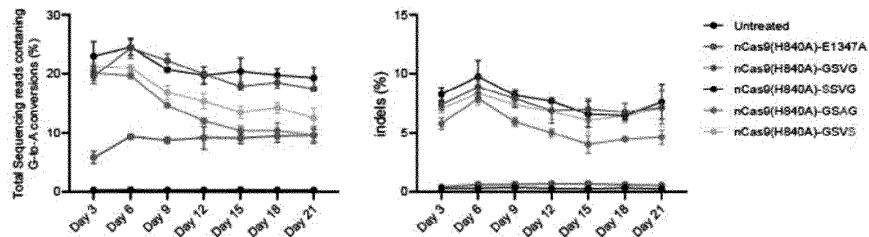
		nCas9(D10A)-GSVG	nCas9(H840A)-GSVG	dCas9-GSVG
WT	CTTGCCCCACAGGGCAGTAA CGG CAGACTTCTCTCAGGAGTCAGGTGC	88±0.25	88±0.06	87±0.17
Allele-1	CTTGCCCCACAGGGCAGTAA CGG CAGACTTCTCTCAGGAGTCAGGTGC	0.59±0.04	0.80±0.07	0.80±0.04
Allele-2	CTTGCCCCACAGGGCAGTAA CGG CAGACTTCTCTCTCAGGAGTCAGGTGC	0.42±0.05	0.53±0.03	0.52±0.03
Allele-3	CTTGCCCCACAGGGCAGTAA CGG CAGACTTCTCTCTCAGGAGTCAGGTGC			0.46±0.03

[59]

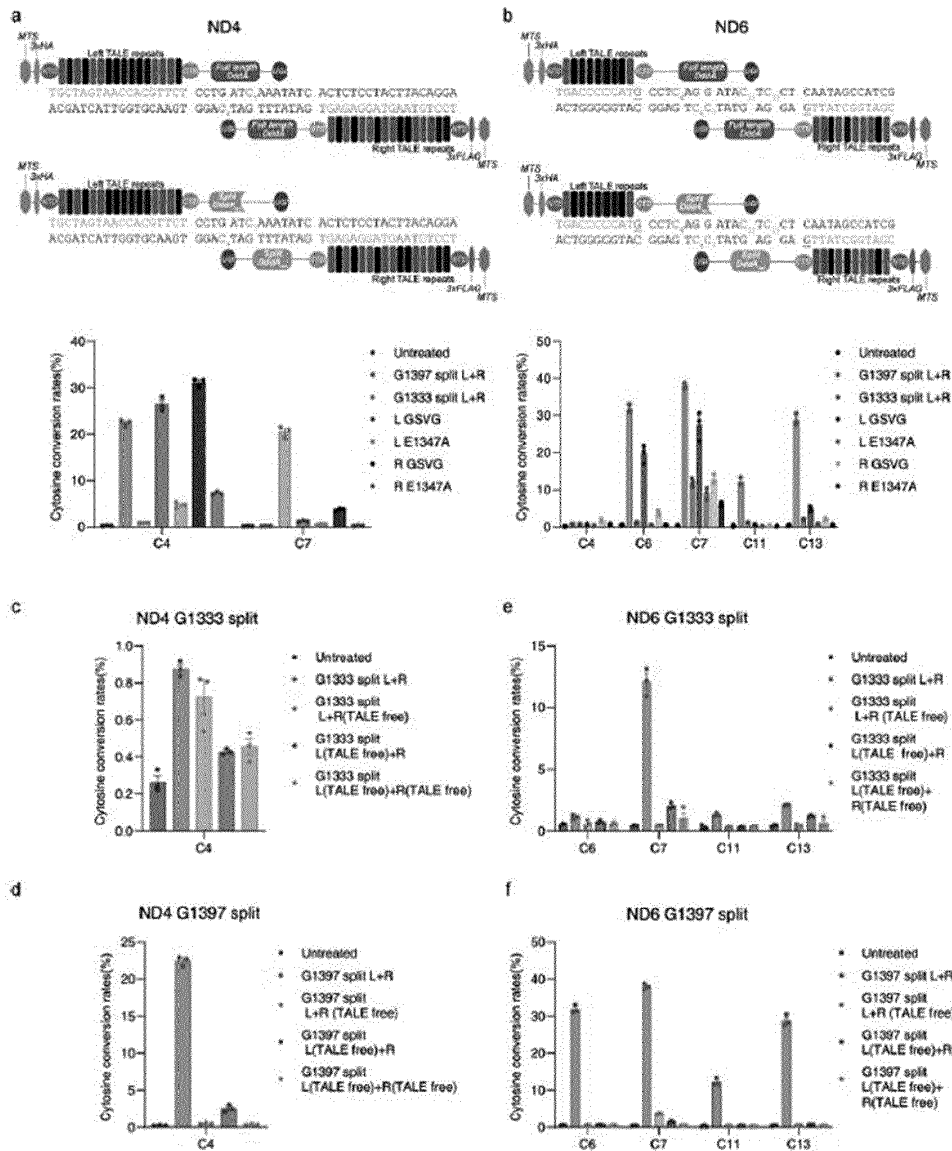
a TYRO3



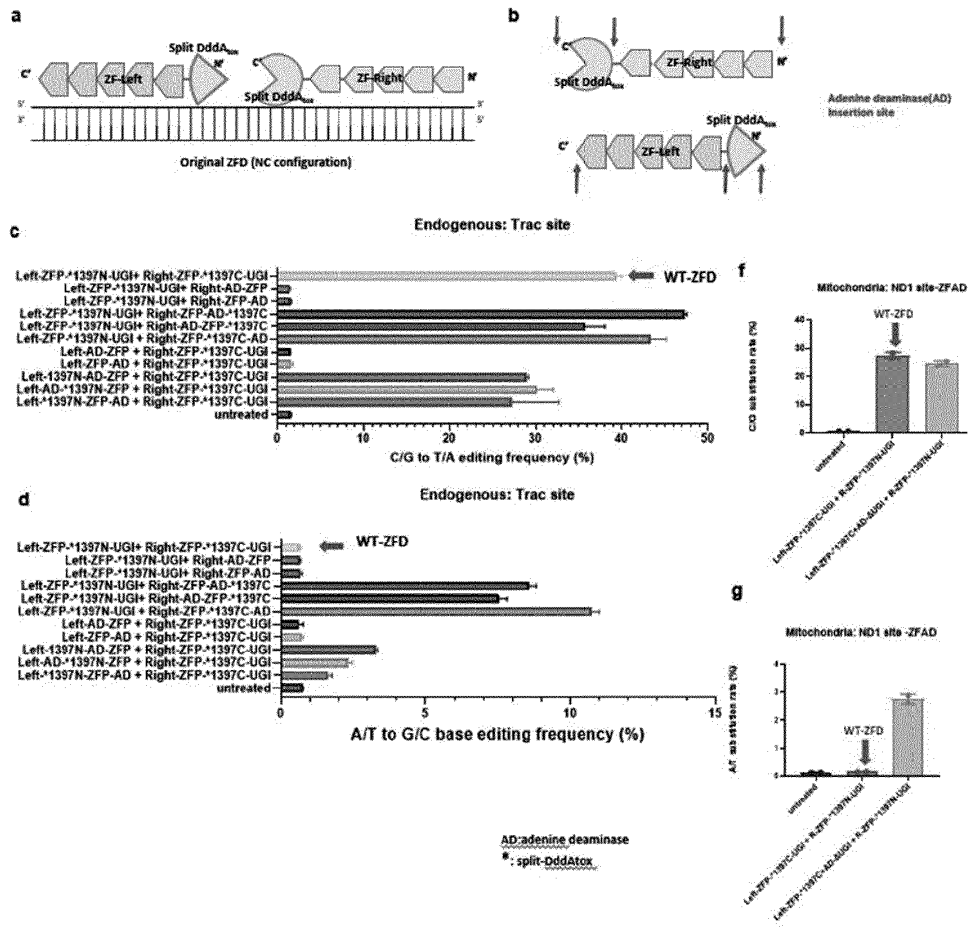
b EMX1 site 2



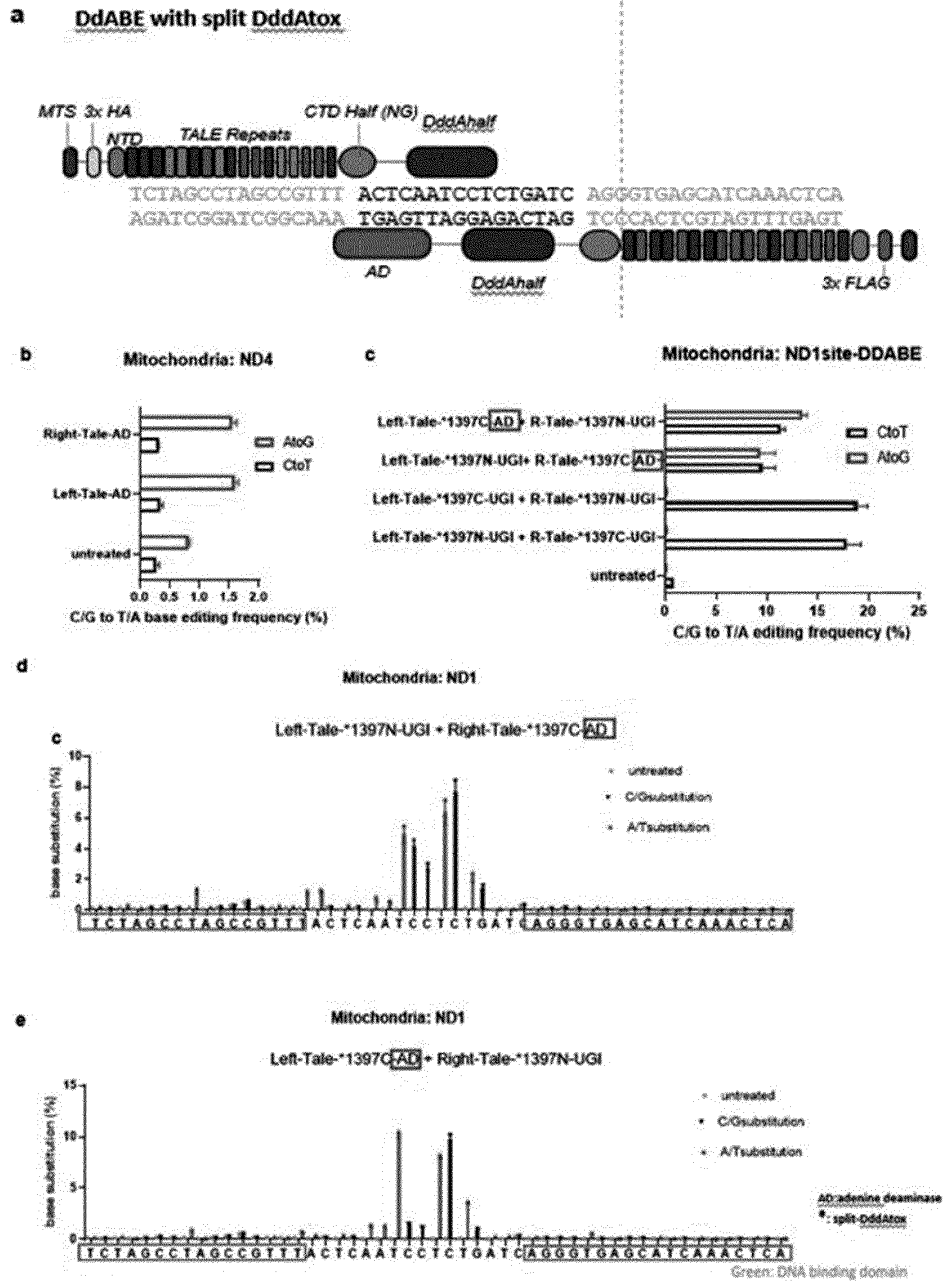
[도 60]



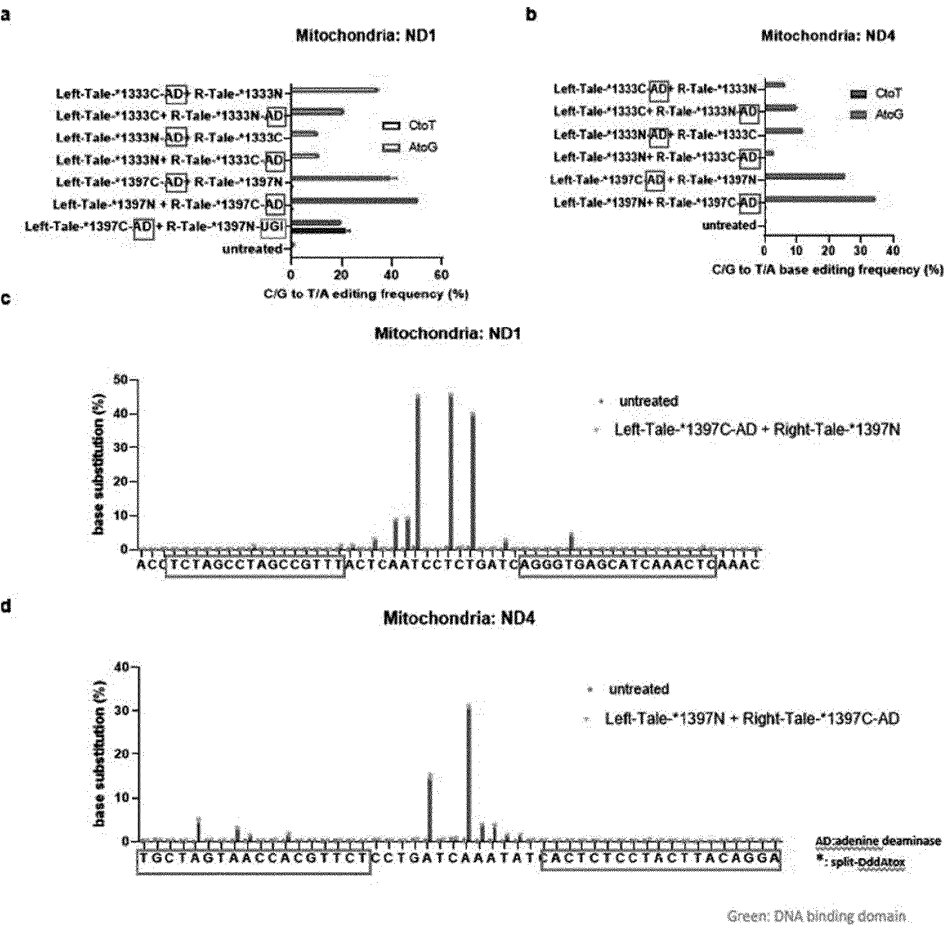
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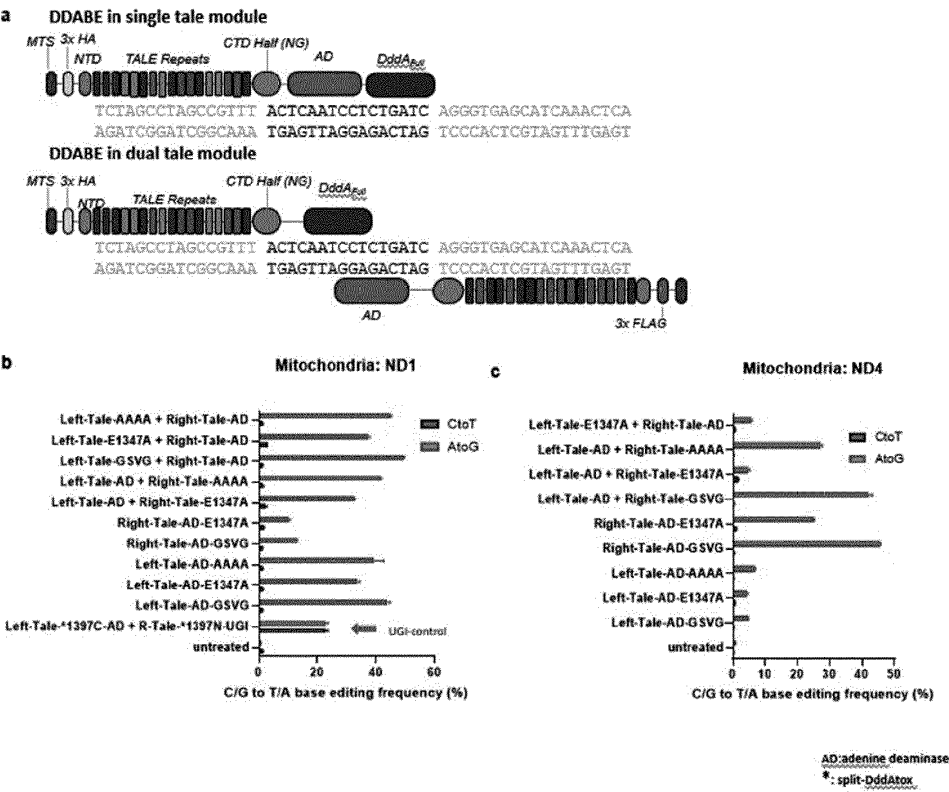
[562]



[563]

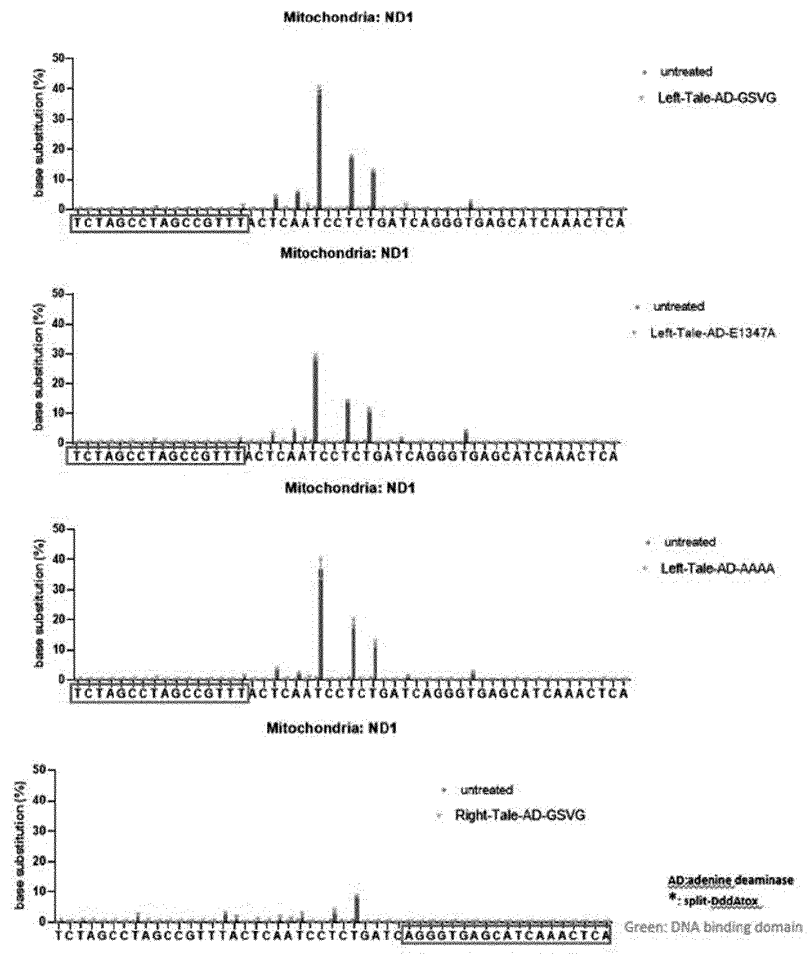


[도 64]

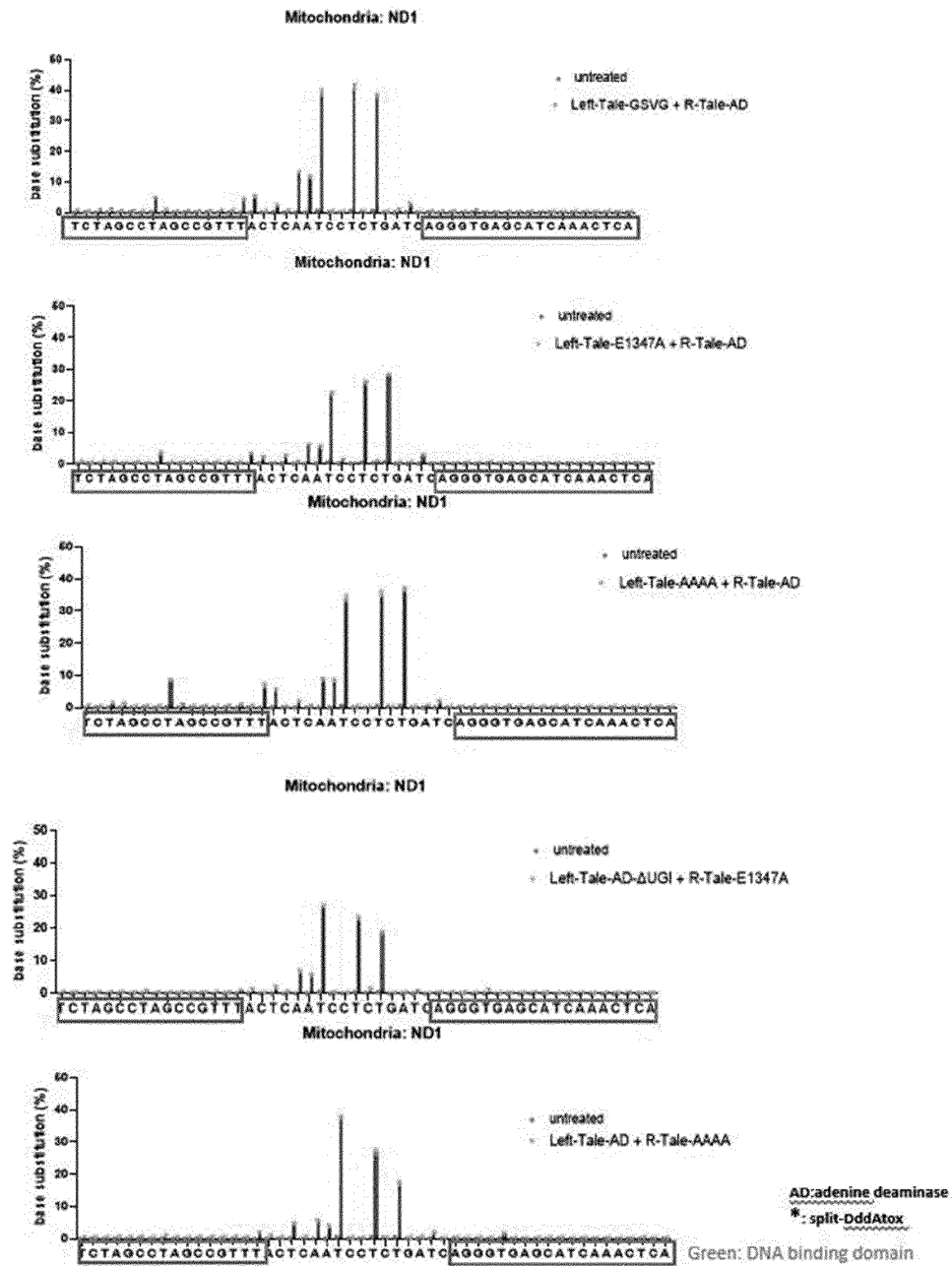


[도 65]

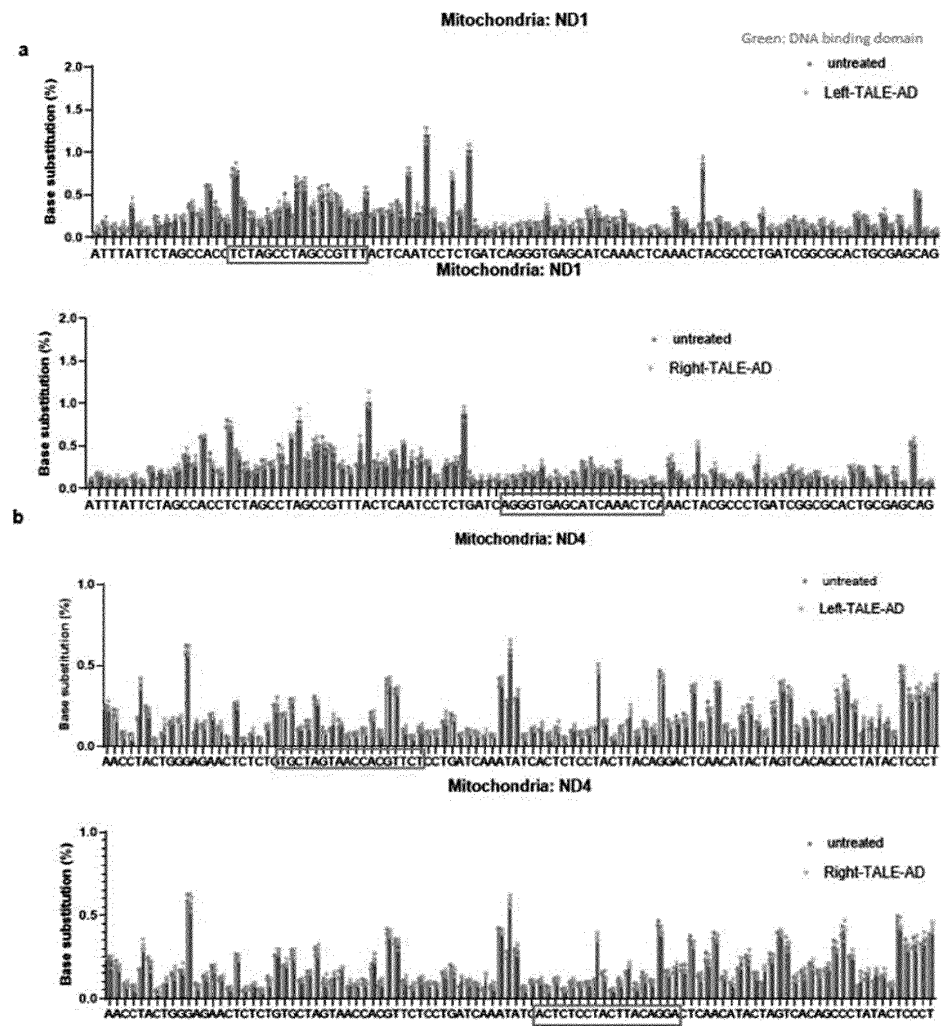
a



[66]



[567]



[568]

