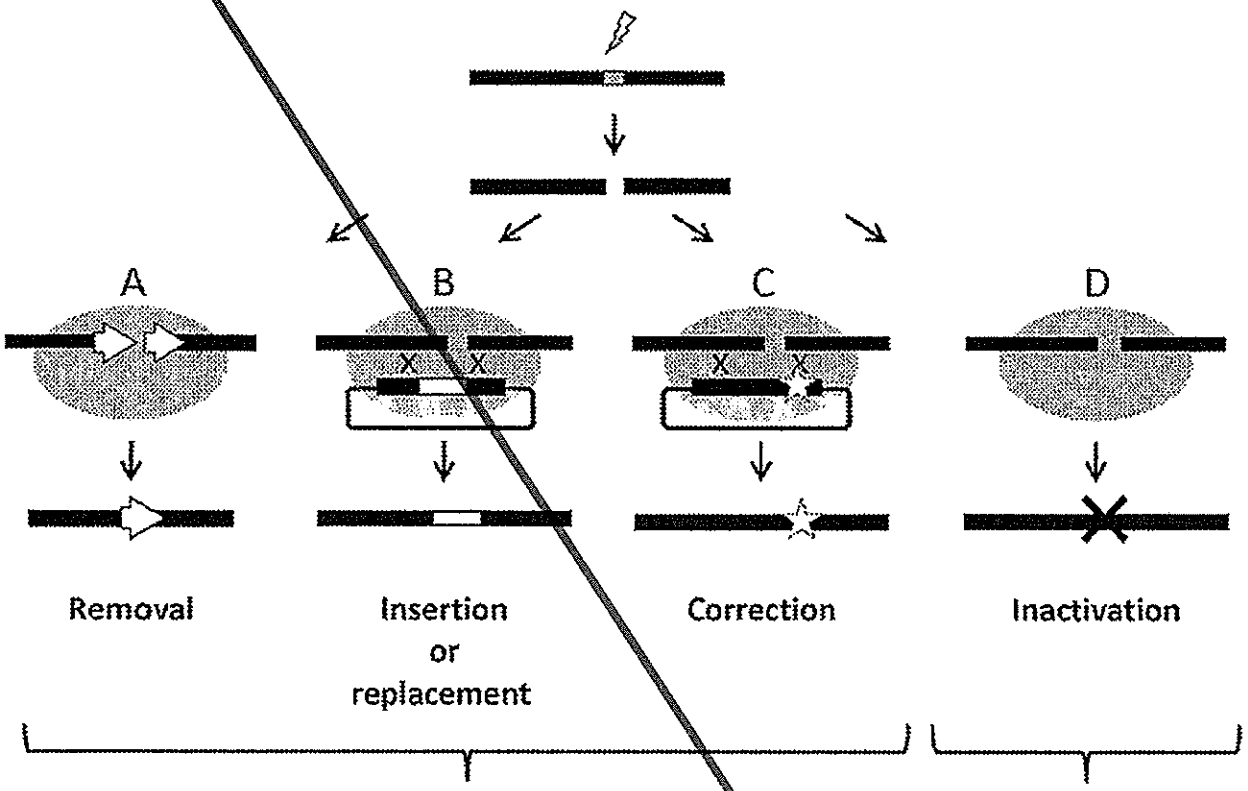

A
B
C
D
Removal
Insertion
or
replacement
Correction
Inactivation
Homologous Recombination (HR)
Non-Homologous
End Joining
(NHEJ)

Figure 1

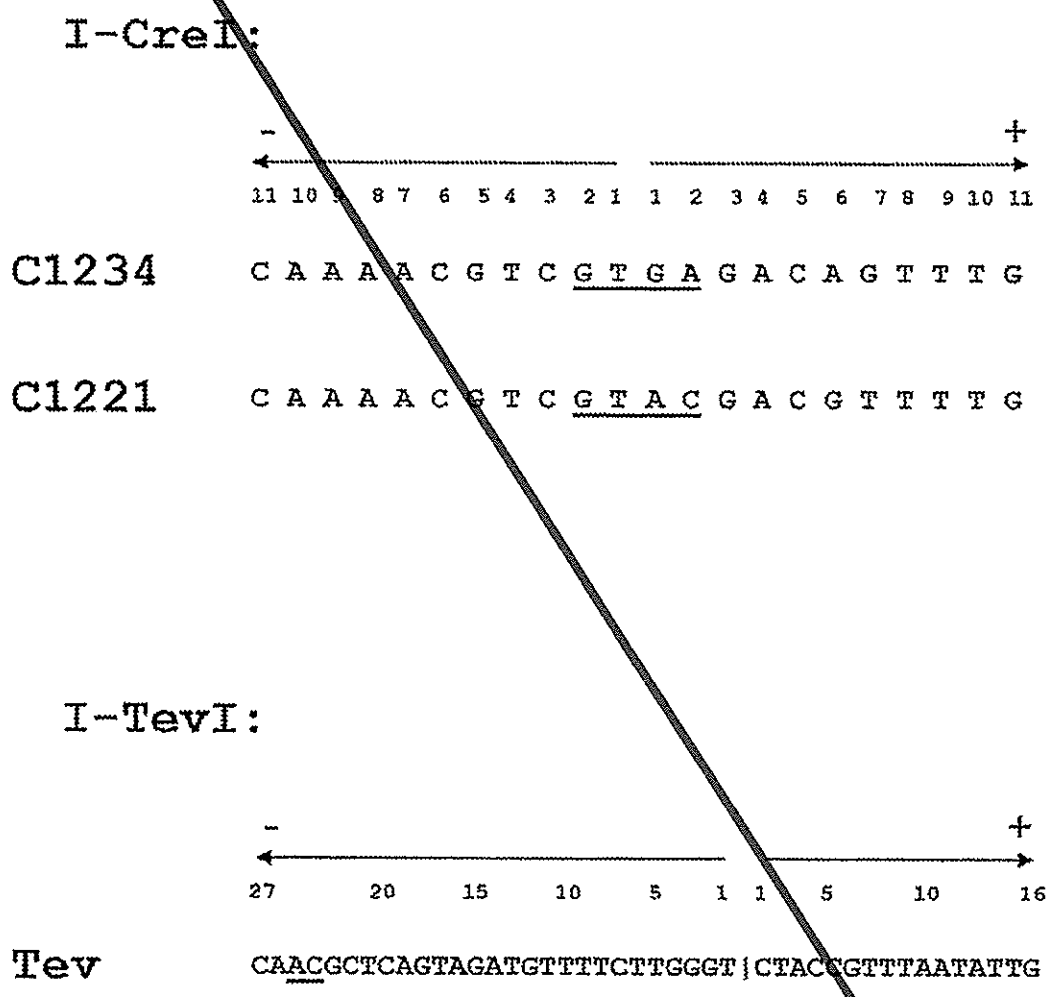

I-CreI:
-
+
11 10 9 8 7 6 5 4 3 2 1 1 2 3 4 5 6 7 8 9 10 11
C1234 C A A A A C G T C G T G A G A C A G T T T G
C1221 C A A A A C G T C G T A C G A C G T T T T G
I-TevI:
-
+
27 20 15 10 5 1 1 5 10 16
Tev CAACGCTCAGTAGATGTTTTCTTGGGT|CTACGGTTTAATATTG

Figure 2

Naturally derived RVDs

AvrBs3

Wild-type RVD:		NI	NG	NI	HD	NG	NI	HD	NG	NN	NG	NI	NG	HD	HD	HD	NG	NI	HD
Base:	T	A	T	A	T	A	A	A	C	C	T	A	A	C	C	C	T	C	T
Cipher RVD:		NI	NG	NI	HD	NG	NI	HD	NG	NN	NG	NI	NG	HD	HD	HD	NG	NI	HD
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18

PthXo1

Wild-type RVD:		NG	NG	NI	HD	NG	NG	NI	HD	NI	NG	NG	NG	NG	NG	NG	NI	HD	NI	NG	NI	NG	NI	NG
Base:	T	G	C	A	T	C	T	C	C	C	C	T	A	C	A	G	T	A	C	A	C	C	A	C
Cipher RVD:		NG	NG	NI	HD	NG	NG	NI	HD	NI	NG	NG	NG	NG	NG	NG	NI	HD	NI	NG	NI	NG	NI	NG
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24

Artificial RVDs

RagT2-R

Base:	T	G	T	T	T	A	C	G	G	T	T	A	C	T	T	A	T
Cipher RVD:		NG	NG	NI	HD	NG	NG	NG	NG	NI	HD	NI	NG	NG	NG	NI	NG
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

NptIIT5-L

Base:	T	C	C	T	T	G	C	G	C	A	G	C	T	G	T	G	C
Cipher RVD:		NG	NG	NI	HD	NG	NG	NG	NC	NI	NG	NG	NG	NG	NG	NG	NG
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

NptIIT5-R

Base:	T	A	G	C	A	G	C	C	A	G	T	C	C	C	T	T	C
Cipher RVD:		NI	NG	NG	NG	NG	NG	NG	NC	NG	NG	NG	NG	NG	NG	NG	NG
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

NptIIT6-L

Base:	T	G	A	A	G	C	G	G	G	A	A	G	G	G	A	G	T
Cipher RVD:		NG	NI	NG	NG	NG	NG	NG	NG	NI	NG	NG	NG	NG	NI	NG	NG
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

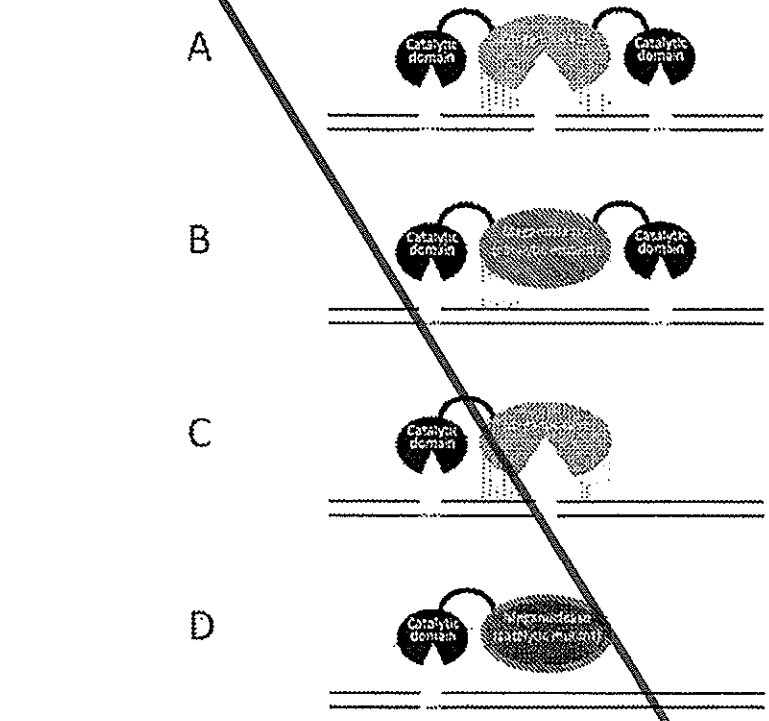
NptIIT6-R

Base:	T	G	A	C	A	G	G	A	G	A	T	C	C	T	G	C	C
Cipher RVD:		NG	NI	NC	NI	NG	NG	NI	NG	NI	NG	NG	NG	NG	NG	NG	NG
Position:	-1	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16

Generic Cipher RVDs

NI → A
HD → C
NN → G
NG → T

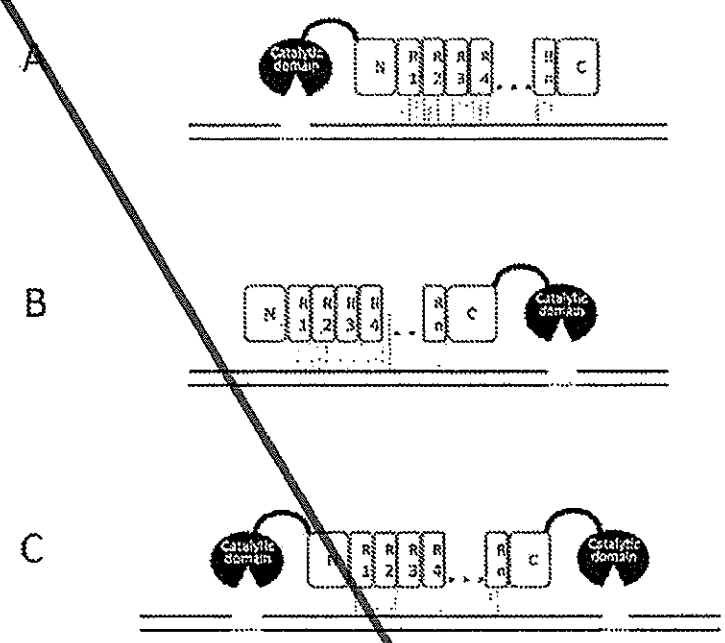
Figure 3



Legend

- Meganuclease (can be dimeric or monomeric)
- Catalytically inactive meganuclease; provides DNA binding specificity (can be dimeric or monomeric)
- Region contacting DNA
- Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

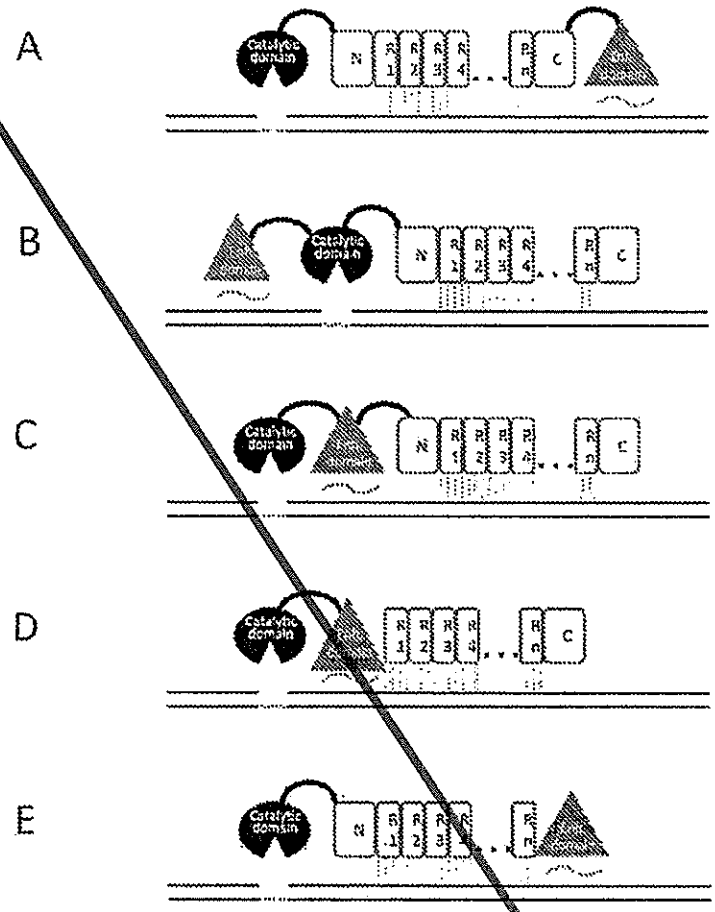
Figure 4



Legend

- TALE protein N-terminal region (including truncations thereof)
- TALE protein C-terminal region (including truncations thereof)
- TALE protein repeat region (n = final repeat; depends on construct)
- Additional TALE repeat regions (for brevity, not shown)
- TALE repeat region contacting DNA
- Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

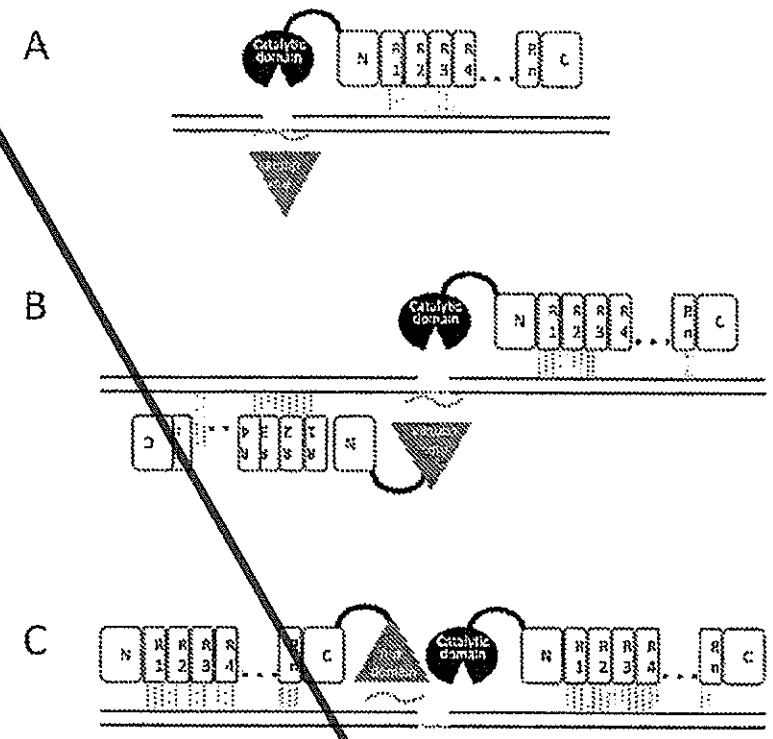
Figure 5



Legend

- N - TALE protein N-terminal region (including truncations thereof)
- C - TALE protein C-terminal region (including truncations thereof)
- R 1 - TALE protein repeat region (n = final repeat; depends on construct)
- ... - Additional TALE repeat regions (for brevity, not shown)
- TALE repeat region contacting DNA
- Enhancer domain; provides functional and/or structural support to scaffold
- Catalytic domain - Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

Figure 6



Legend

- TALE protein N-terminal region (including truncations thereof)
- TALE protein C-terminal region (including truncations thereof)
- TALE protein repeat region (n = final repeat; depends on construct)
- Additional TALE repeat regions (for brevity, not shown)
- TALE repeat region contacting DNA
- Auxiliary domain; provides optional external functional and/or structural support to scaffold
- Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

Figure 7

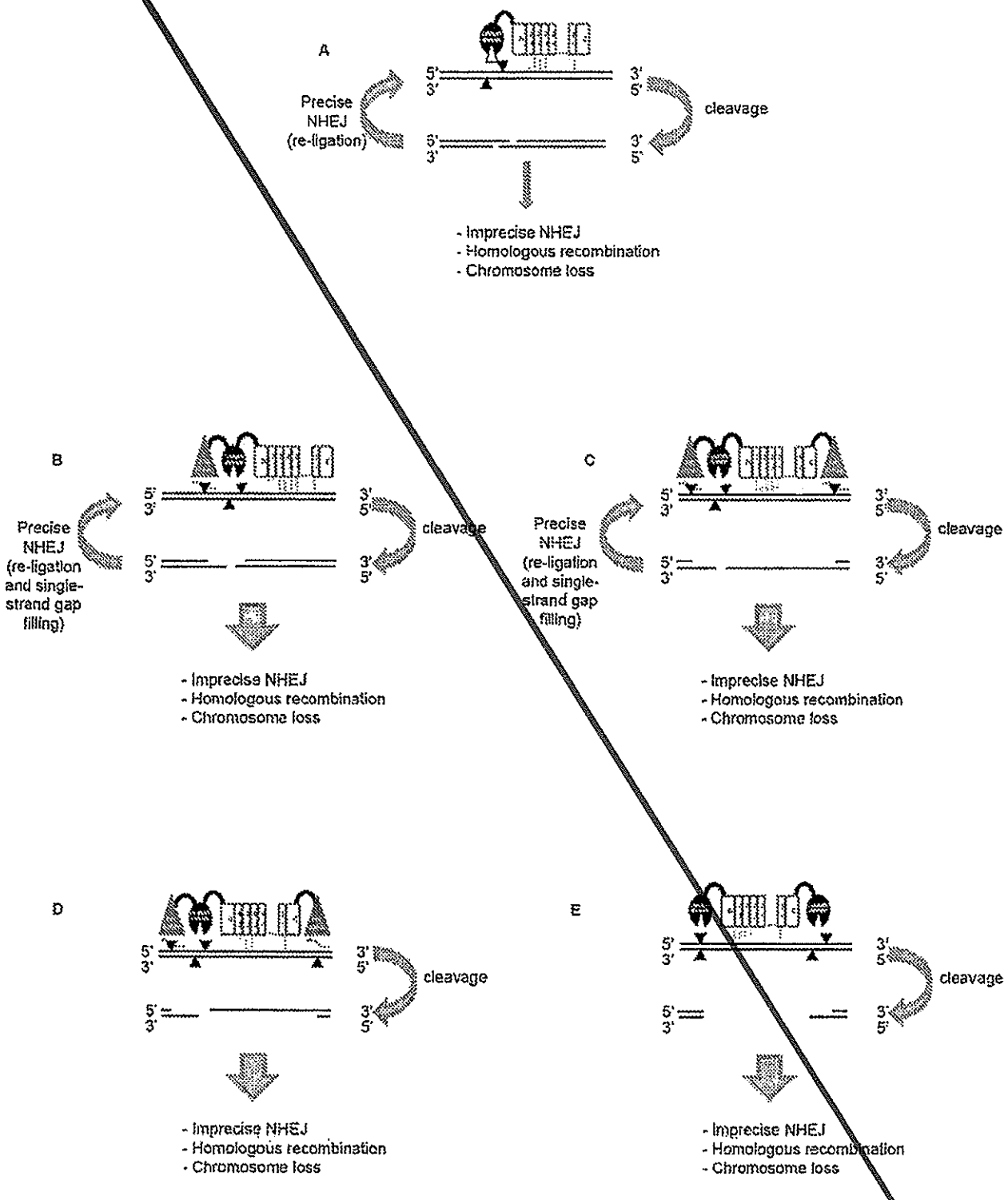

A
Precise NHEJ (re-ligation)
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
B
Precise NHEJ (re-ligation and single-strand gap filling)
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
C
Precise NHEJ (re-ligation and single-strand gap filling)
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
D
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
E
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss

Figure 8

Spacer length [bp]	Neg. Control	cT11Avr_TevD01	cT11Avr_TevD02	cT11Avr_TevD05
5	n.d.	n.d.	n.d.	n.d.
6	n.d.	n.d.	n.d.	n.d.
7	n.d.	n.d.	n.d.	n.d.
8	n.d.	n.d.	n.d.	n.d.
9	n.d.	n.d.	n.d.	n.d.
10	n.d.	+	+	n.d.
11	n.d.	+++	+	n.d.
12	n.d.	+	+	n.d.
13	n.d.	+	+	n.d.
14	n.d.	n.d.	n.d.	n.d.
15	n.d.	+++	+++	+++
16	n.d.	+	+	+
17	n.d.	n.d.	n.d.	n.d.
18	n.d.	n.d.	n.d.	n.d.
19	n.d.	+	n.d.	n.d.
20	n.d.	n.d.	n.d.	n.d.
21	n.d.		+	+
22	n.d.	+++	+++	+++
23	n.d.	+++	+++	+++
24	n.d.	+++	+++	+++
25	n.d.	+++	+++	+++
26	n.d.	+++	+++	+++
27	n.d.	+++	+++	+++
28	n.d.	+	+	n.d.
29	n.d.	n.d.	n.d.	n.d.
30	n.d.	n.d.	n.d.	n.d.

Figure 9

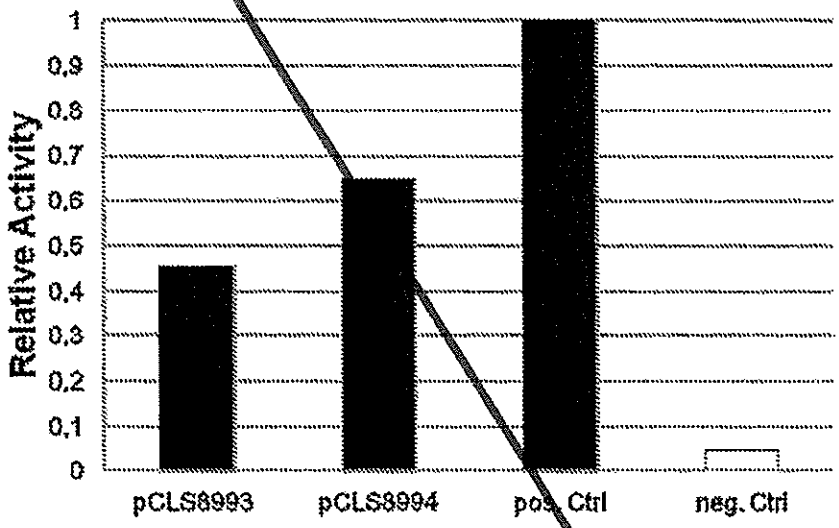

Relative Activity
1
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
pCLS8993
pCLS8994
pos. Ctrl
neg. Ctrl

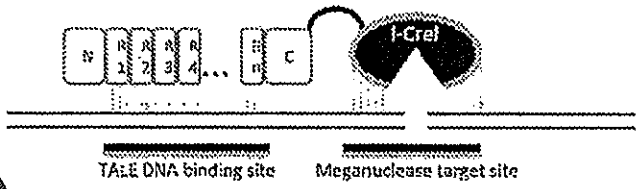
Figure 10

Spacer length [bp]	pCLS9596	pCLS9597	pCLS9599
5	+++	+++	+++
6	+++	+++	+++
7	+++	+++	+++
8	+++	+++	+++
9	+++	+++	+++
10	+++	+++	+++
11	+++	+++	+++
12	+++	+++	+++
13	+++	+++	+++
14	+++	+++	+++
15	+++	+++	+++
16	+++	+++	+++
17	+++	+++	+++
18	+++	+++	+++
19	+++	+++	+++
20	+++	+++	+++
21	+++	+++	+++
22	+++	+++	+++
23	+++	+++	+++
24	+++	+++	+++
25	+++	+++	+++
26	+++	+++	+++
27	+++	+++	+++
28	+++	+++	+++
29	+++	+++	+++
30	+++	+++	+++
31	+++	+++	+++
32	+++	+++	+++
33	+++	+++	+++
34	+++	+++	+++
35	+++	+++	+++
36	+++	+++	+++
37	+++	+++	+++
38	+++	+++	+++
39	+++	+++	+++
40	++	++	+++
compact	+++	+++	+++
neg ctrl	n.d.	n.d.	n.d.

Figure 11

Spacer length [bp]	pCLS8589
5	+++
6	+++
7	+++
8	+++
9	+++
10	++
11	+++
12	+++
13	+++
14	++
15	++
16	+++
17	+++
18	+++
19	+++
20	+++
21	++
22	+++
23	+++
24	+++
25	+++
26	+++
27	+++
28	+++
29	+++
30	+++
31	+++
32	+++
33	+++
34	+++
35	+++
36	+++
37	++
38	++
39	++
40	++
compact	++
neg ctrl	n.d.

Figure 12



TALE::CreI prototype

TCRB02-A meganuclease target: GATGGCCATGGTAAGCAGGAGGGC

RVD name	Target sequence	Distance from the TCRB02-A site	RVD motif
TCRB2A1	TGCTGGTCAGCGGCCC	7 bp	NN-HD-NG-NN-NN-NG-HD-NI-NN-HD-NN-HD-HD-NG
TCRB2A2	TGCTGTGCTGGTCAG	12bp	NN-HD-NG-NN-NG-NN-HD-NG-NN-NN-NG-HD-NI-NG
TCRB2A3	TGTATGCTGTGCTGG	16 bp	NN-NG-NI-NG-NN-HD-NG-NN-NG-NN-HD-NG-NN-NG

TCRB02 gene region*	GCCAACAGTGTCCTACCAGCAAGGGGTCCTGTCTGCCACCATCCTCT ATGAGATCCTGCTAGGGAAGGCCACCCTGTATGCTGTGCTGGTCAGC GCCCTTGTGTTGATGGCCATGGTAAGCAGGAGGGCAGGATGGGGCCA GCAGGCTGGAGGTGACACACTGACACCAAGCACCCAGAAGTATAGAG TCCCTGCCAGGATTGGAGCTGGGCAGTAGGGA

*TCRB2A1 and TCRB02-A target sequences underlined for reference

Figure 13

Targets	Sequence
TCRB02.1	GATGGCCATGGTAAGCAGGAGGGC
TCRB02Tsp07	TGCTGGTCAGCGCCCttgtgttGATGGCCATGGTAAGCAGGAGGGC
TCRB02Tsp12	TGCTGTGCTGGTCAGcgcccttgtgttGATGGCCATGGTAAGCAGGAGGGC
TCRB02Tsp16	TGTATGCTGTGCTGGTcagcgcccttgtgttGATGGCCATGGTAAGCAGGAGGGC

Target	pCLS7185	pCLS13450	pCLS15148
TCRB02.1	+++	+	n.d.
TCRB02Tsp07	+++	+	+++
TCRB02Tsp12	+++	++	+++
TCRB02Tsp16	+++	+++	+++

Figure 14

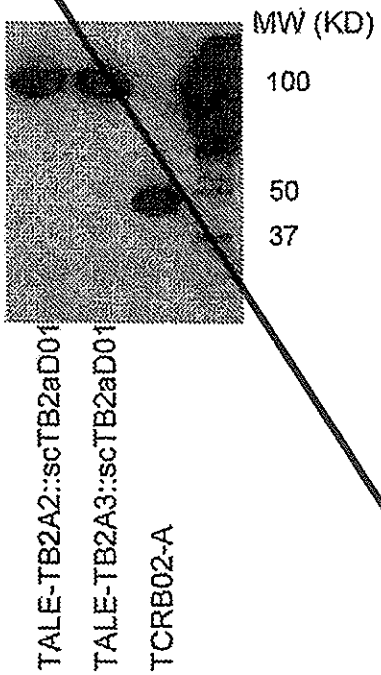

MW (KD)
100
50
37
TALE-TB2A2::scTB2aD01
TALE-TB2A3::scTB2aD01
TCRB02-A

Figure 15

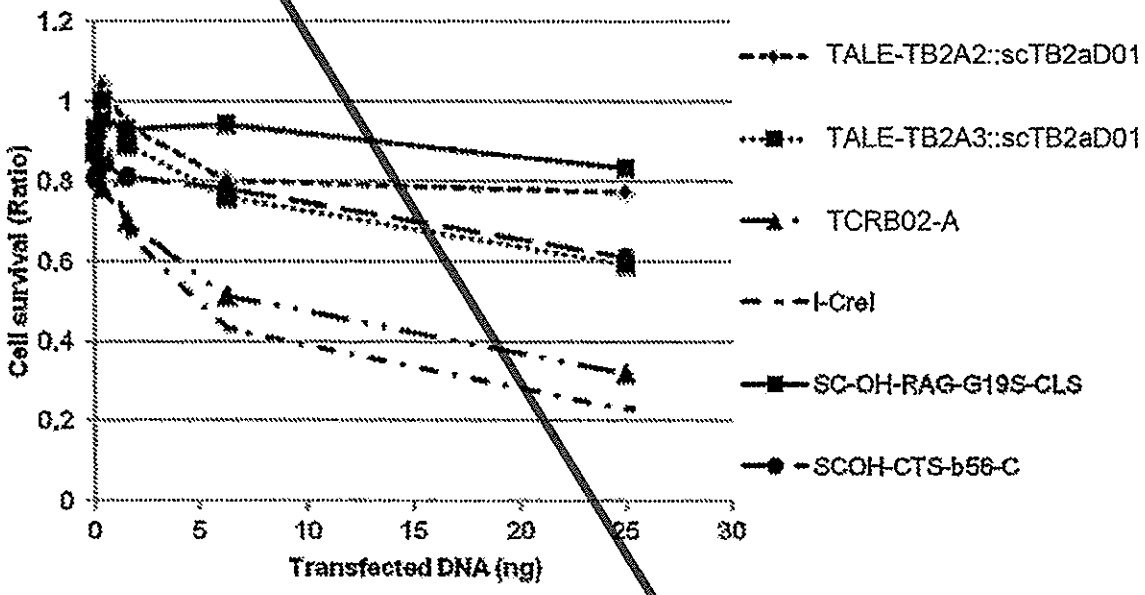

1.2
1
0.8
0.6
0.4
0.2
0
Cell survival (Ratio)
0
5
10
15
20
25
30
Transfected DNA (ng)
TALE-TB2A2::scTB2aD01
TALE-TB2A3::scTB2aD01
TCRB02-A
I-CreI
SC-OH-RAG-G19S-CLS
SCOH-CTS-b56-C

Figure 16

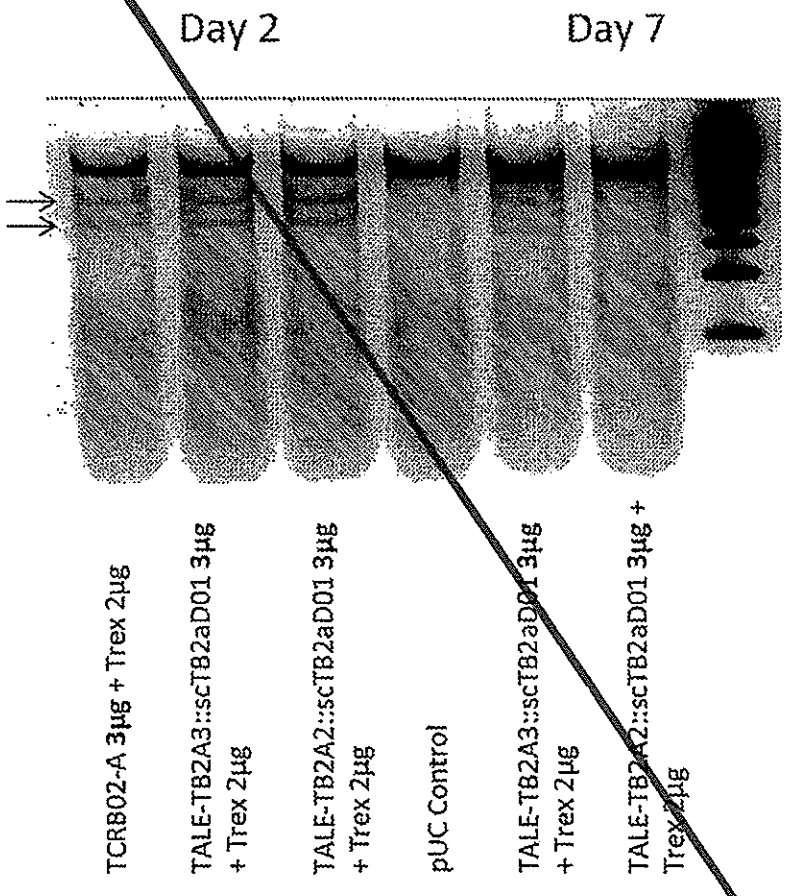

Day 2
Day 7
TCRB02-A 3µg + Trex 2µg
TALE-TB2A3::scTB2aD01 3µg + Trex 2µg
TALE-TB2A2::scTB2aD01 3µg + Trex 2µg
pUC Control
TALE-TB2A3::scTB2aD01 3µg + Trex 2µg
TALE-TB2A2::scTB2aD01 3µg + Trex 2µg

Figure 17

Target	pCLS8522+pCLS7763	pCLS8522+pCLS8990
C_N_RAGAvr05	+++	++
C_N_RAGAvr06	+++	+
C_N_RAGAvr07	++	+
C_N_RAGAvr08	+	n.d.
C_N_RAGAvr09	+	+
C_N_RAGAvr10	+	n.d.
C_N_RAGAvr11	+	n.d.
C_N_RAGAvr12	+	+
C_N_RAGAvr13	+	n.d.
C_N_RAGAvr14	+	+
C_N_RAGAvr15	+	++
C_N_RAGAvr16	n.d.	n.d.
C_N_RAGAvr17	n.d.	+
C_N_RAGAvr18	n.d.	++
C_N_RAGAvr19	n.d.	++
C_N_RAGAvr20	n.d.	++
C_N_RAGAvr21	n.d.	++
C_N_RAGAvr22	+	+++
C_N_RAGAvr23	+	+++
C_N_RAGAvr24	++	+++
C_N_RAGAvr25	+	+++
C_N_RAGAvr26	+	+++
C_N_RAGAvr27	+	+++
C_N_RAGAvr28	+	++
C_N_RAGAvr29	+	++
C_N_RAGAvr30	+++	++
C_N_RAGAvr31	+++	+++
C_N_RAGAvr32	++	+++
C_N_RAGAvr33	++	++
C_N_RAGAvr34	+++	+++
C_N_RAGAvr35	+++	+++
C_N_RAGAvr36	+++	+++
C_N_RAGAvr37	+++	+++
C_N_RAGAvr38	+	++
C_N_RAGAvr39	+	+
C_N_RAGAvr40	n.d.	n.d.
neg ctrl	n.d.	n.d.

Figure 18

spacer length [bp]	pCLS9081	pCLS9082
40	+	+
39	+	+
38	+	n.d.
37	+	n.d.
36	+	+/-
35	+	+
34	+	+
33	+	+
32	+	+
31	+	+
30	+	+
29	+	+
28	+	+/-
27	+	+
26	+	+
25	+	+
24	+	+
23	+	+
22	+	+
21	+	+
20	+	+
19	+	+
18	+	+
17	+	+
16	+	+
15	+	+
14	n.d.	+/-
13	+	+
12	+	+/-
11	+	+/-
10	+	n.d.
09	+	n.d.
08	+	+/-
07	+	+
06	+	+
05	+	+
Compact	+	+/-

Figure 19

		Spacer length [bp]				
Catalytic head SeqID	polypeptide linker SeqID	15	18	21	24	Compact
11	385	++	++	+++	+++	++
11	388	+++	+++	++	+++	++
11	394	++	+++	++	+++	++
11	400	+++	+++	+++	+++	++

Figure 20

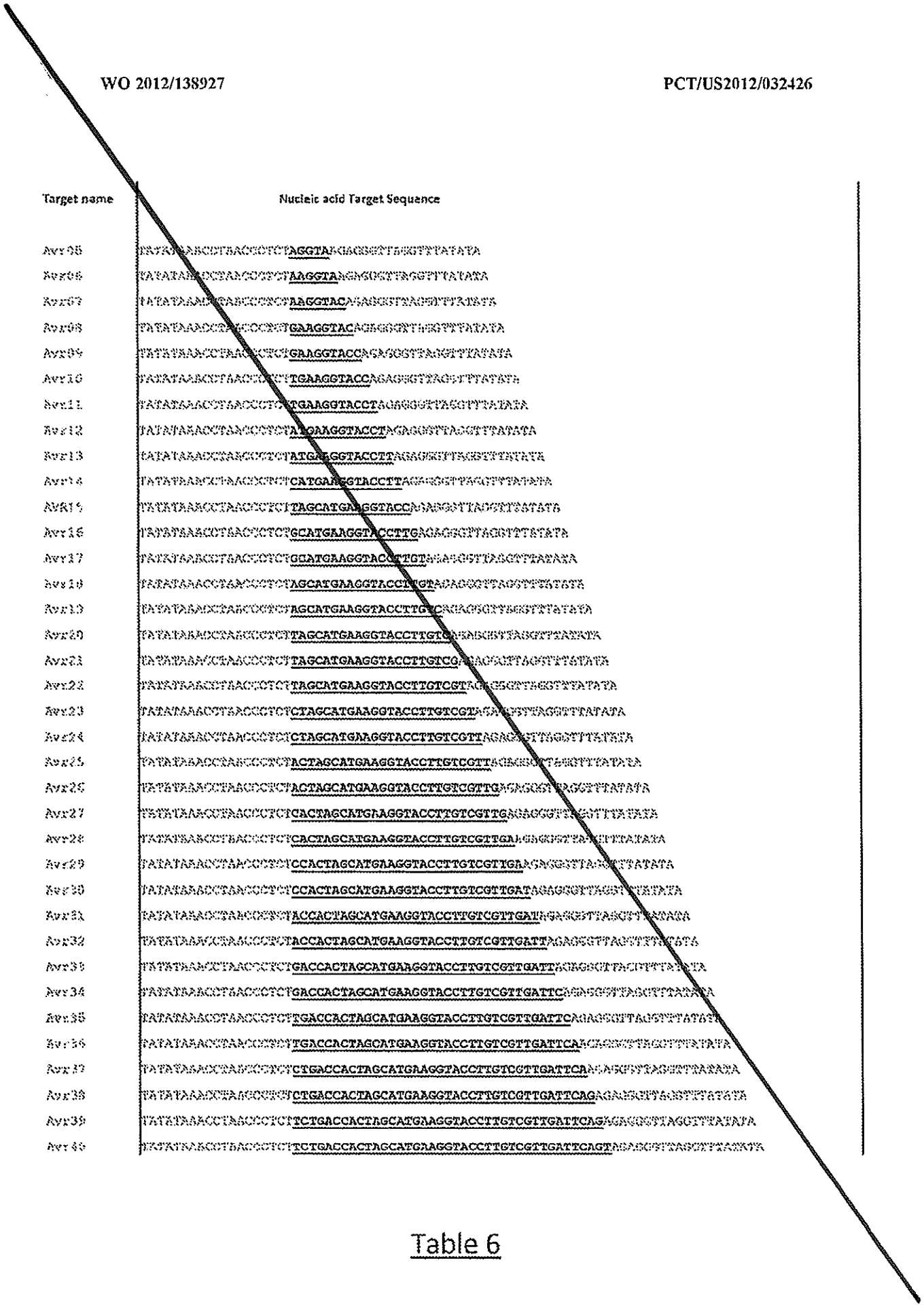


Table 6

Target name	Nucleic acid Target Sequence
Avr05	TATATAAACCTAACCCTCTAGGTAAGAGGGTTAGGTTTATATA
Avr06	TATATAAACCTAACCCTCTAAGGTAAGAGGGTTAGGTTTATATA
Avr07	TATATAAACCTAACCCTCTAAGGTACAGAGGGTTAGGTTTATATA
Avr08	TATATAAACCTAACCCTCTGAAGGTACAGAGGGTTAGGTTTATATA
Avr09	TATATAAACCTAACCCTCTGAAGGTACCAGAGGGTTAGGTTTATATA
Avr10	TATATAAACCTAACCCTCTTGAAGGTACCAGAGGGTTAGGTTTATATA
Avr11	TATATAAACCTAACCCTCTTGAAGGTACCTAGAGGGTTAGGTTTATATA
Avr12	TATATAAACCTAACCCTCTATGAAGGTACCTAGAGGGTTAGGTTTATATA
Avr13	TATATAAACCTAACCCTCTATGAAGGTACCTTAGAGGGTTAGGTTTATATA
Avr14	TATATAAACCTAACCCTCTCATGAAGGTACCTTAGAGGGTTAGGTTTATATA
AVR15	TATATAAACCTAACCCTCTTAGCATGAAGGTACCAGAGGGTTAGGTTTATATA
Avr16	TATATAAACCTAACCCTCTGCATGAAGGTACCTTGAGAGGGTTAGGTTTATATA
Avr17	TATATAAACCTAACCCTCTGCATGAAGGTACCTTGTAGAGGGTTAGGTTTATATA
Avr18	TATATAAACCTAACCCTCTAGCATGAAGGTACCTTGTAGAGGGTTAGGTTTATATA
Avr19	TATATAAACCTAACCCTCTAGCATGAAGGTACCTTGTCAGAGGGTTAGGTTTATATA
Avr20	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGAGAGGGTTAGGTTTATATA
Avr21	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGAGAGGGTTAGGTTTATATA
Avr22	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGTAGAGGGTTAGGTTTATATA
Avr23	TATATAAACCTAACCCTCTCTAGCATGAAGGTACCTTGTCGTAGAGGGTTAGGTTTATATA
Avr24	TATATAAACCTAACCCTCTCTAGCATGAAGGTACCTTGTCGTTAGAGGGTTAGGTTTATATA
Avr25	TATATAAACCTAACCCTCTACTAGCATGAAGGTACCTTGTCGTTAGAGGGTTAGGTTTATATA
Avr26	TATATAAACCTAACCCTCTACTAGCATGAAGGTACCTTGTCGTTGAGAGGGTTAGGTTTATATA
Avr27	TATATAAACCTAACCCTCTCACTAGCATGAAGGTACCTTGTCGTTGAGAGGGTTAGGTTTATATA
Avr28	TATATAAACCTAACCCTCTCACTAGCATGAAGGTACCTTGTCGTTGAAGAGGGTTAGGTTTATATA
Avr29	TATATAAACCTAACCCTCTCCACTAGCATGAAGGTACCTTGTCGTTGAAGAGGGTTAGGTTTATATA
Avr30	TATATAAACCTAACCCTCTCCACTAGCATGAAGGTACCTTGTCGTTGATAGAGGGTTAGGTTTATATA
Avr31	TATATAAACCTAACCCTCTACCACTAGCATGAAGGTACCTTGTCGTTGATAGAGGGTTAGGTTTATATA
Avr32	TATATAAACCTAACCCTCTACCACTAGCATGAAGGTACCTTGTCGTTGATTAGAGGGTTAGGTTTATATA
Avr33	TATATAAACCTAACCCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTAGAGGGTTAGGTTTATATA
Avr34	TATATAAACCTAACCCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGGGTTAGGTTTATATA
Avr35	TATATAAACCTAACCCTCTTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGGGTTAGGTTTATATA
Avr36	TATATAAACCTAACCCTCTTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAGAGGGTTAGGTTTATATA
Avr37	TATATAAACCTAACCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAGAGGGTTAGGTTTATATA
Avr38	TATATAAACCTAACCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGAGGGTTAGGTTTATATA
Avr39	TATATAAACCTAACCCTCTTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGAGGGTTAGGTTTATATA
Avr40	TATATAAACCTAACCCTCTTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGTAGAGGGTTAGGTTTATATA
compact	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGATGGTGTACAGTAGGGGGAGATGCA
neg. Ctrl.	TTGTTCTCAGGTACCTCAGCCAGA

Table 7

Target name	Nucleic acid Target Sequence
C_N_RAGAvr06	TGTTTATGGTTACTTATaggtaTATATAAACCTAACCCTCT
C_N_RAGAvr06	TGTTTATGGTTACTTATaaggtaTATATAAACCTAACCCTCT
C_N_RAGAvr07	TGTTTATGGTTACTTATaaggtacTATATAAACCTAACCCTCT
C_N_RAGAvr08	TGTTTATGGTTACTTATgaaggtacTATATAAACCTAACCCTCT
C_N_RAGAvr09	TGTTTATGGTTACTTATgaaggtaccTATATAAACCTAACCCTCT
C_N_RAGAvr10	TGTTTATGGTTACTTATtgaaggtaccTATATAAACCTAACCCTCT
C_N_RAGAvr11	TGTTTATGGTTACTTATtgaaggtacctTATATAAACCTAACCCTCT
C_N_RAGAvr12	TGTTTATGGTTACTTATatgaaggtacctTATATAAACCTAACCCTCT
C_N_RAGAvr13	TGTTTATGGTTACTTATatgaaggtaccttTATATAAACCTAACCCTCT
C_N_RAGAvr14	TGTTTATGGTTACTTATcatgaaggtaccttTATATAAACCTAACCCTCT
C_N_RAGAvr15	TGTTTATGGTTACTTATtagcatgaaggtaccTATATAAACCTAACCCTCT
C_N_RAGAvr16	TGTTTATGGTTACTTATgcatgaaggtaccttgTATATAAACCTAACCCTCT
C_N_RAGAvr17	TGTTTATGGTTACTTATgcatgaaggtaccttgtTATATAAACCTAACCCTCT
C_N_RAGAvr18	TGTTTATGGTTACTTATagcatgaaggtaccttgtTATATAAACCTAACCCTCT
C_N_RAGAvr19	TGTTTATGGTTACTTATagcatgaaggtaccttgtcTATATAAACCTAACCCTCT
C_N_RAGAvr20	TGTTTATGGTTACTTATtagcatgaaggtaccttgtcTATATAAACCTAACCCTCT
C_N_RAGAvr21	TGTTTATGGTTACTTATtagcatgaaggtaccttgtcgTATATAAACCTAACCCTCT
C_N_RAGAvr22	TGTTTATGGTTACTTATtagcatgaaggtaccttgtcgtTATATAAACCTAACCCTCT
C_N_RAGAvr23	TGTTTATGGTTACTTATctagcatgaaggtaccttgtcgtTATATAAACCTAACCCTCT
C_N_RAGAvr24	TGTTTATGGTTACTTATctagcatgaaggtaccttgtcgttTATATAAACCTAACCCTCT
C_N_RAGAvr25	TGTTTATGGTTACTTATactagcatgaaggtaccttgtcgttTATATAAACCTAACCCTCT
C_N_RAGAvr26	TGTTTATGGTTACTTATactagcatgaaggtaccttgtcgttgTATATAAACCTAACCCTCT
C_N_RAGAvr27	TGTTTATGGTTACTTATcactagcatgaaggtaccttgtcgttgTATATAAACCTAACCCTCT
C_N_RAGAvr28	TGTTTATGGTTACTTATcactagcatgaaggtaccttgtcgttgaTATATAAACCTAACCCTCT
C_N_RAGAvr29	TGTTTATGGTTACTTATccactagcatgaaggtaccttgtcgttgaTATATAAACCTAACCCTCT
C_N_RAGAvr30	TGTTTATGGTTACTTATccactagcatgaaggtaccttgtcgttgatTATATAAACCTAACCCTCT
C_N_RAGAvr31	TGTTTATGGTTACTTATaccactagcatgaaggtaccttgtcgttgatTATATAAACCTAACCCTCT
C_N_RAGAvr32	TGTTTATGGTTACTTATaccactagcatgaaggtaccttgtcgttgattTATATAAACCTAACCCTCT
C_N_RAGAvr33	TGTTTATGGTTACTTATgaccactagcatgaaggtaccttgtcgttgattTATATAAACCTAACCCTCT
C_N_RAGAvr34	TGTTTATGGTTACTTATgaccactagcatgaaggtaccttgtcgttgattcTATATAAACCTAACCCTCT
C_N_RAGAvr35	TGTTTATGGTTACTTATtgaccactagcatgaaggtaccttgtcgttgattcTATATAAACCTAACCCTCT
C_N_RAGAvr36	TGTTTATGGTTACTTATtgaccactagcatgaaggtaccttgtcgttgattcaTATATAAACCTAACCCTCT
C_N_RAGAvr37	TGTTTATGGTTACTTATctgaccactagcatgaaggtaccttgtcgttgattcaTATATAAACCTAACCCTCT
C_N_RAGAvr38	TGTTTATGGTTACTTATctgaccactagcatgaaggtaccttgtcgttgattcagTATATAAACCTAACCCTCT
C_N_RAGAvr39	TGTTTATGGTTACTTATtctgaccactagcatgaaggtaccttgtcgttgattcagTATATAAACCTAACCCTCT
C_N_RAGAvr40	TGTTTATGGTTACTTATtctgaccactagcatgaaggtaccttgtcgttgattcagtTATATAAACCTAACCCTCT

Table 13

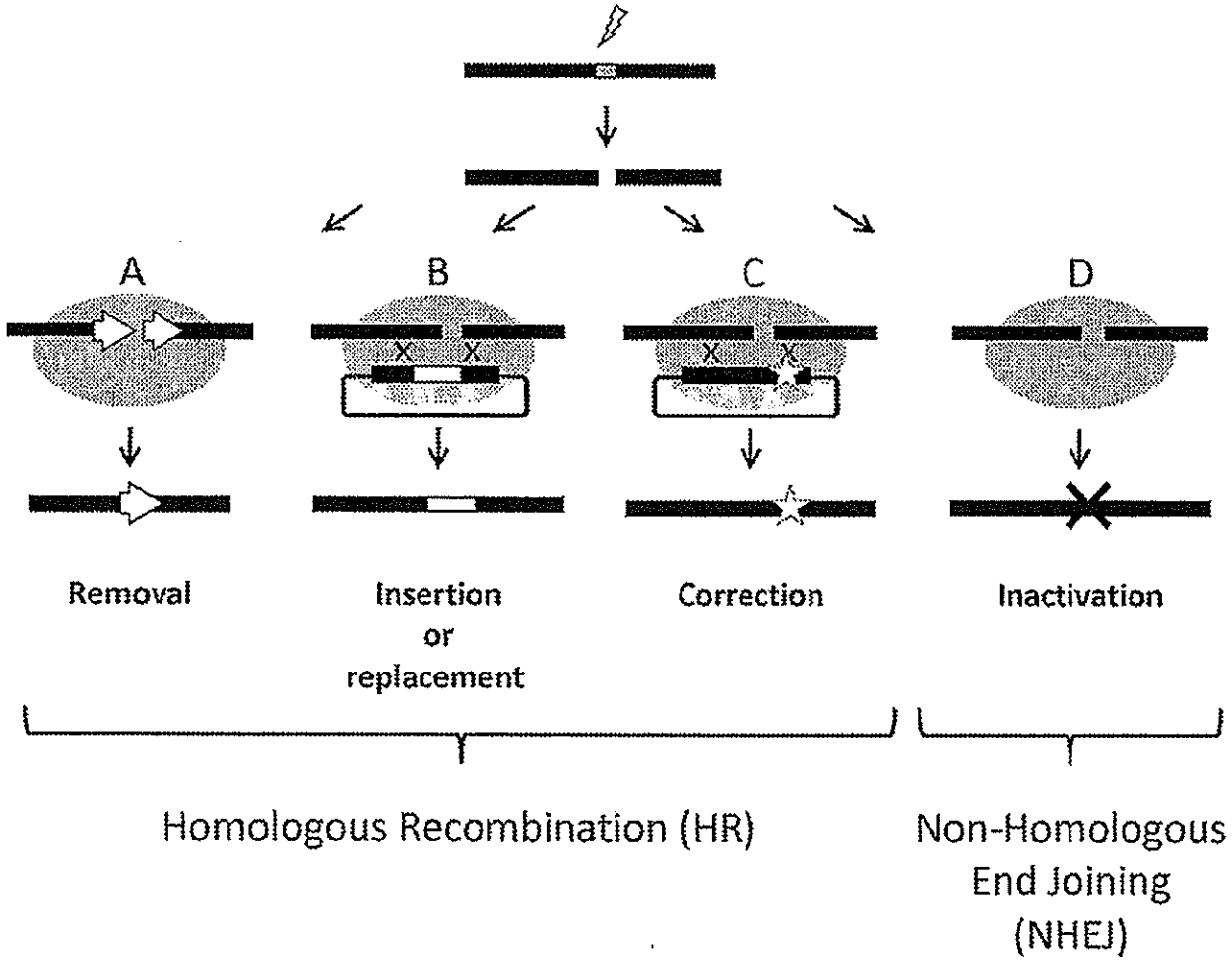
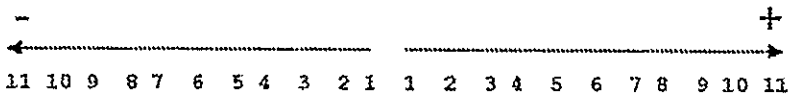

A
B
C
D
Removal
Insertion
or
replacement
Correction
Inactivation
Homologous Recombination (HR)
Non-Homologous
End Joining
(NHEJ)

Figure 1

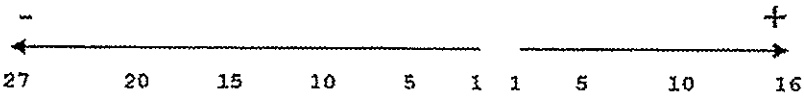
I-CreI:



C1234 C A A A A C G T C G T G A G A C A G T T T G

C1221 C A A A A C G T C G T A C G A C G T T T T G

I-TevI:



Tev CAACGCTCAGTAGATGTTTTCTTGGGT|CTACCGTTTAATATTG

Figure 2

Naturally derived RVDs

AvrBs3

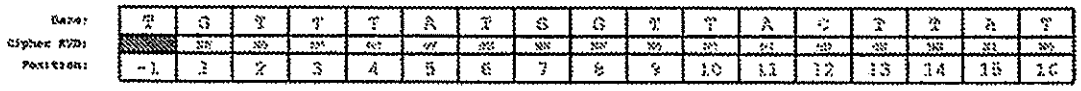


PthXo1

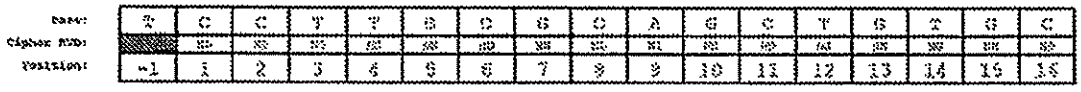


Artificial RVDs

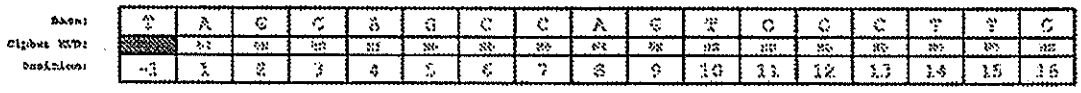
RagT2-R



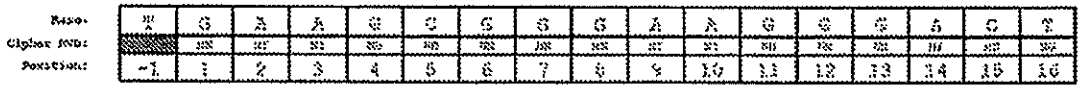
NptIIT5-L



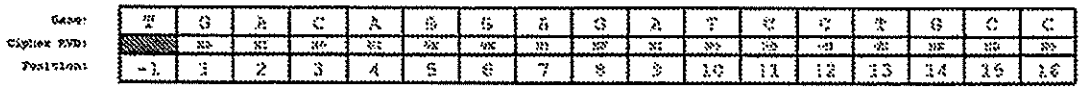
NptIIT5-R



NptIIT6-L



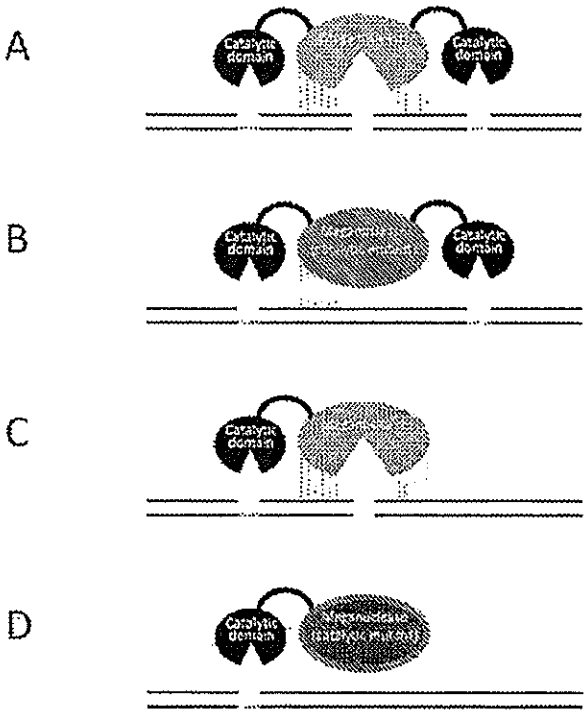
NptIIT6-R



Generic Cipher RVDs

NI → A
HD → C
NN → G
NG → T

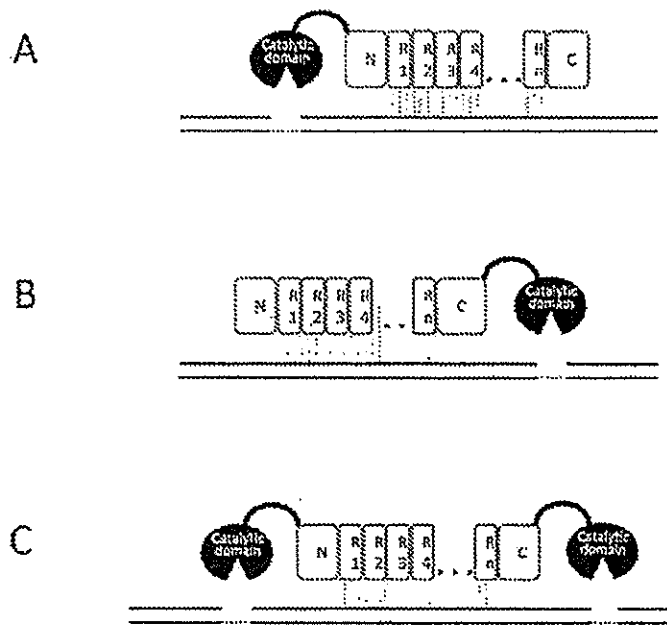
Figure 3



Legend

- Meganuclease (can be dimeric or monomeric)
- Catalytically inactive meganuclease; provides DNA binding specificity (can be dimeric or monomeric)
- Region contacting DNA
- Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

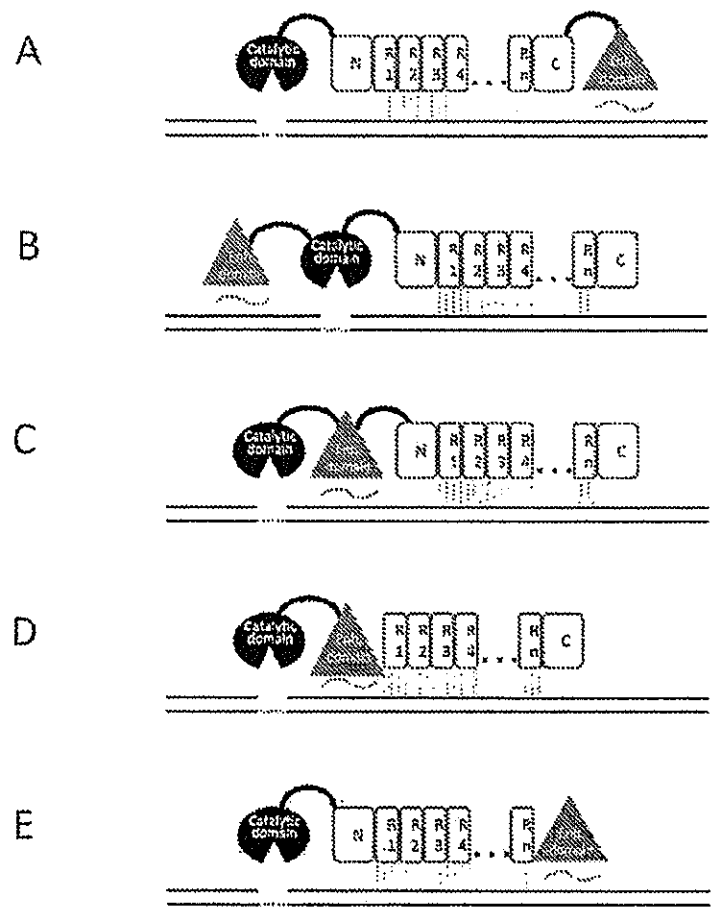
Figure 4



Legend

- N - TALE protein N-terminal region (including truncations thereof)
- C - TALE protein C-terminal region (including truncations thereof)
- R 1 - TALE protein repeat region (n = final repeat; depends on construct)
- * * * - Additional TALE repeat regions (for brevity, not shown)
- TALE repeat region contacting DNA
- Catalytic domain - Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

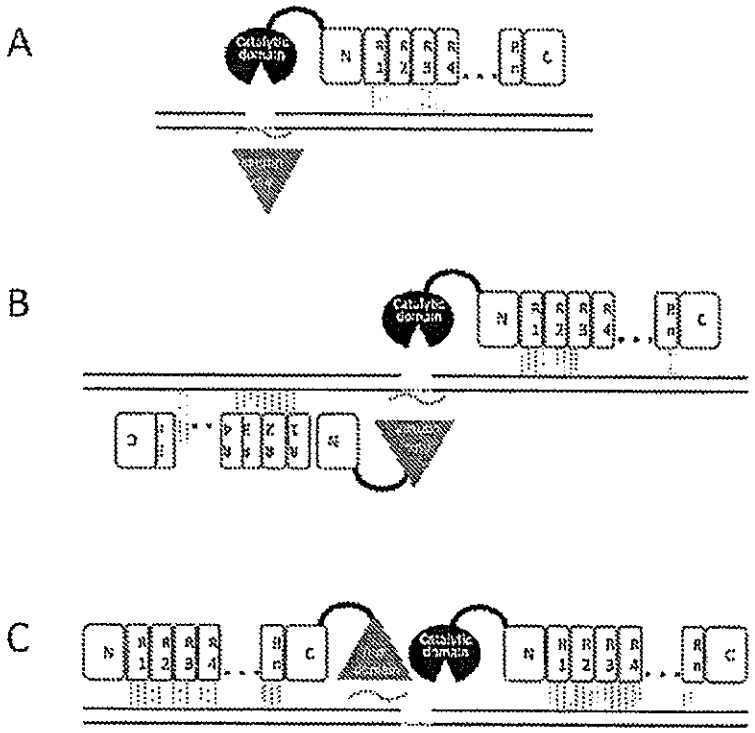
Figure 5



Legend

- N - TALE protein N-terminal region (including truncations thereof)
- C - TALE protein C-terminal region (including truncations thereof)
- R 1 - TALE protein repeat region (n = final repeat; depends on construct)
- ... - Additional TALE repeat regions (for brevity, not shown)
- TALE repeat region contacting DNA
- Enhancer domain; provides functional and/or structural support to scaffold
- Catalytic domain - Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

Figure 6



Legend

- TALE protein N-terminal region (including truncations thereof)
- TALE protein C-terminal region (including truncations thereof)
- TALE protein repeat region (n = final repeat; depends on construct)
- Additional TALE repeat regions (for brevity, not shown)
- TALE repeat region contacting DNA
- Auxiliary domain; provides optional external functional and/or structural support to scaffold
- Catalytic domain for DNA strand cleavage (can be cleavase or nickase domain)
- Protein linker region
- Double-strand DNA
- Single-strand of DNA optionally cleaved depending on the catalytic domain attached

Figure 7

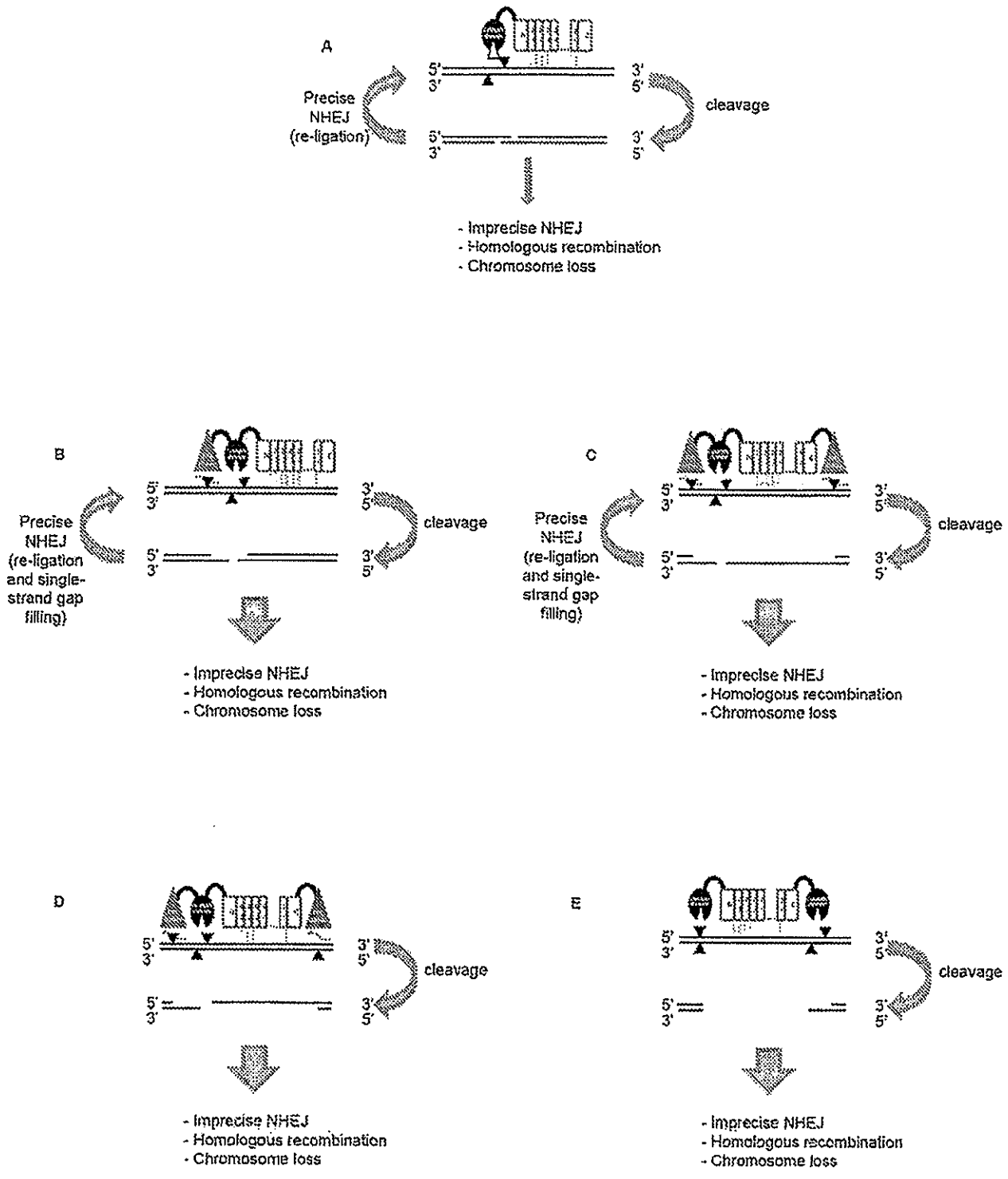

A
Precise NHEJ (re-ligation)
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
B
Precise NHEJ (re-ligation and single-strand gap filling)
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
C
Precise NHEJ (re-ligation and single-strand gap filling)
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
D
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss
E
cleavage
- Imprecise NHEJ
- Homologous recombination
- Chromosome loss

Figure 8

Spacer length [bp]	Neg. Control	cT11Avr_TevD01	cT11Avr_TevD02	cT11Avr_TevD05
5	n.d.	n.d.	n.d.	n.d.
6	n.d.	n.d.	n.d.	n.d.
7	n.d.	n.d.	n.d.	n.d.
8	n.d.	n.d.	n.d.	n.d.
9	n.d.	n.d.	n.d.	n.d.
10	n.d.	+	+	n.d.
11	n.d.	+++	+	n.d.
12	n.d.	+	+	n.d.
13	n.d.	+	+	n.d.
14	n.d.	n.d.	n.d.	n.d.
15	n.d.	+++	+++	+++
16	n.d.	+	+	+
17	n.d.	n.d.	n.d.	n.d.
18	n.d.	n.d.	n.d.	n.d.
19	n.d.	+	n.d.	n.d.
20	n.d.	n.d.	n.d.	n.d.
21	n.d.	+	+	+
22	n.d.	+++	+++	+++
23	n.d.	+++	+++	+++
24	n.d.	+++	+++	+++
25	n.d.	+++	+++	+++
26	n.d.	+++	+++	+++
27	n.d.	+++	+++	+++
28	n.d.	+	+	n.d.
29	n.d.	n.d.	n.d.	n.d.
30	n.d.	n.d.	n.d.	n.d.

Figure 9

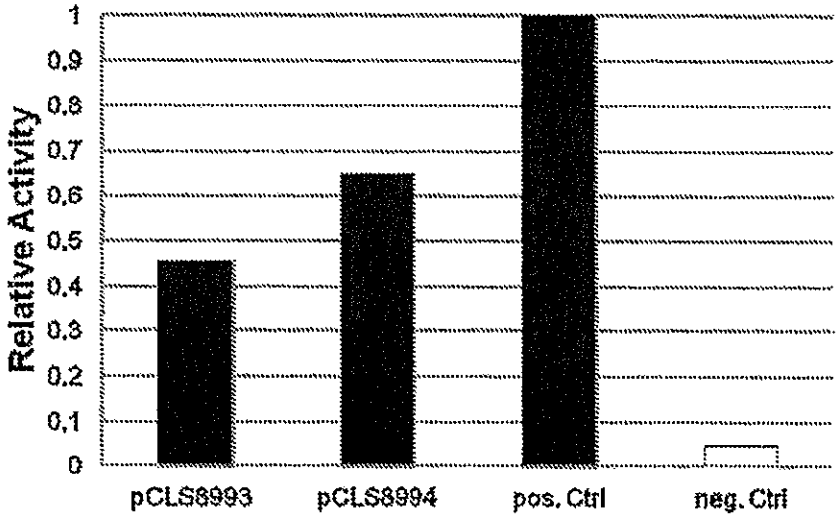

Relative Activity
1
0,9
0,8
0,7
0,6
0,5
0,4
0,3
0,2
0,1
0
pCLS8993
pCLS8994
pos. Ctrl
neg. Ctrl

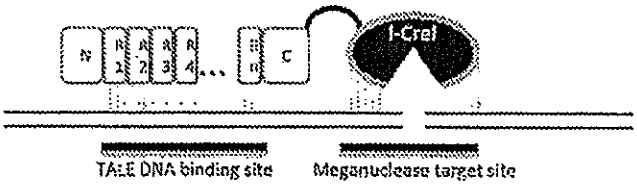
Figure 10

Spacer length [bp]	pCLS9596	pCLS9597	pCLS9599
5	+++	+++	+++
6	+++	+++	+++
7	+++	+++	+++
8	+++	+++	+++
9	+++	+++	+++
10	+++	+++	+++
11	+++	+++	+++
12	+++	+++	+++
13	+++	+++	+++
14	+++	+++	+++
15	+++	+++	+++
16	+++	+++	+++
17	+++	+++	+++
18	+++	+++	+++
19	+++	+++	+++
20	+++	+++	+++
21	+++	+++	+++
22	+++	+++	+++
23	+++	+++	+++
24	+++	+++	+++
25	+++	+++	+++
26	+++	+++	+++
27	+++	+++	+++
28	+++	+++	+++
29	+++	+++	+++
30	+++	+++	+++
31	+++	+++	+++
32	+++	+++	+++
33	+++	+++	+++
34	+++	+++	+++
35	+++	+++	+++
36	+++	+++	+++
37	+++	+++	+++
38	+++	+++	+++
39	+++	+++	+++
40	++	++	+++
compact	+++	+++	+++
neg ctrl	n.d.	n.d.	n.d.

Figure 11

Spacer length [bp]	pCL58589
5	+++
6	+++
7	+++
8	+++
9	+++
10	++
11	+++
12	+++
13	+++
14	++
15	++
16	+++
17	+++
18	+++
19	+++
20	+++
21	++
22	+++
23	+++
24	+++
25	+++
26	+++
27	+++
28	+++
29	+++
30	+++
31	+++
32	+++
33	+++
34	+++
35	+++
36	+++
37	++
38	++
39	++
40	++
compact	++
neg ctrl	n.d.

Figure 12



TALE::CreI prototype

TCRB02-A meganuclease target: GATGGCCATGGTAAGCAGGAGGGC

RVD name	Target sequence	Distance from the TCRB02-A site	RVD motif
TCRB2A1	TGCTGGTCAGCGCCC	7 bp	NN-HD-NG-NN-NN-NG-HD-NI-NN-HD-NN-HD-HD-NG
TCRB2A2	TGCTGTGCTGGTCAG	12bp	NN-HD-NG-NN-NG-NN-HD-NG-NN-NN-NG-HD-NI-NG
TCRB2A3	TGTATGCTGTGCTGG	16 bp	NN-NG-NI-NG-NN-HD-NG-NN-NG-NN-HD-NG-NN-NG

TCRB02 gene region*	GCCAACAGTGTCCTACCAGCAAGGGGTCCTGTCTGCCACCATCCTCT ATGAGATCCTGCTAGGGAAGGCCACCCTGTATGCTGTGCTGGTCAGC GCCCTTGTGTTGATGGCCATGGTAAGCAGGAGGGCAGGATGGGGCCA GCAGGCTGGAGGTGACACACTGACACCAAGCACCCAGAAGTATAGAG TCCCTGCCAGGATTGGAGCTGGGCAGTAGGGA

*TCRB2A1 and TCRB02-A target sequences underlined for reference

Figure 13

Targets	Sequence
TCRB02.1	GATGGCCATGGTAAGCAGGAGGGC
TCRB02Tsp07	TGCTGGTCAGCGCCCttgtgttGATGGCCATGGTAAGCAGGAGGGC
TCRB02Tsp12	TGCTGTGCTGGTCAGcgcccttgtgttGATGGCCATGGTAAGCAGGAGGGC
TCRB02Tsp16	TGTATGCTGTGCTGGtcagcgcccttgtgttGATGGCCATGGTAAGCAGGAGGGC

Target	pCLS7185	pCLS13450	pCLS15148
TCRB02.1	+++	+	n.d.
TCRB02Tsp07	+++	+	+++
TCRB02Tsp12	+++	++	+++
TCRB02Tsp16	+++	+++	+++

Figure 14

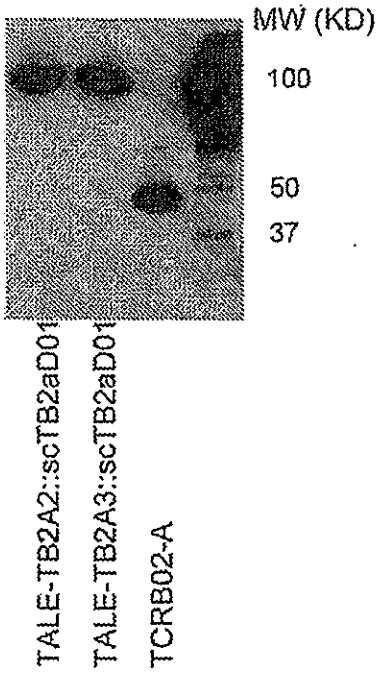

MW (KD)
100
50
37
TALE-TB2A2::scTB2aD01
TALE-TB2A3::scTB2aD01
TCRB02-A

Figure 15

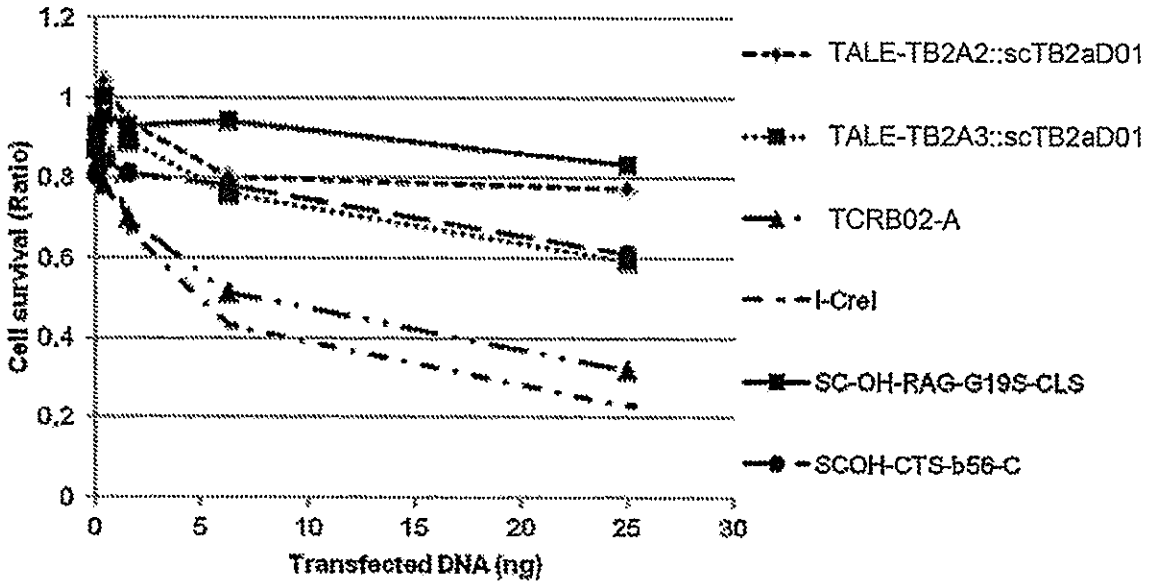

1.2
1
0.8
0.6
0.4
0.2
0
Cell survival (Ratio)
0
5
10
15
20
25
30
Transfected DNA (ng)
TALE-TB2A2::scTB2aD01
TALE-TB2A3::scTB2aD01
TCRB02-A
I-CreI
SC-OH-RAG-G19S-CLS
SCOH-CTS-b56-C

Figure 16

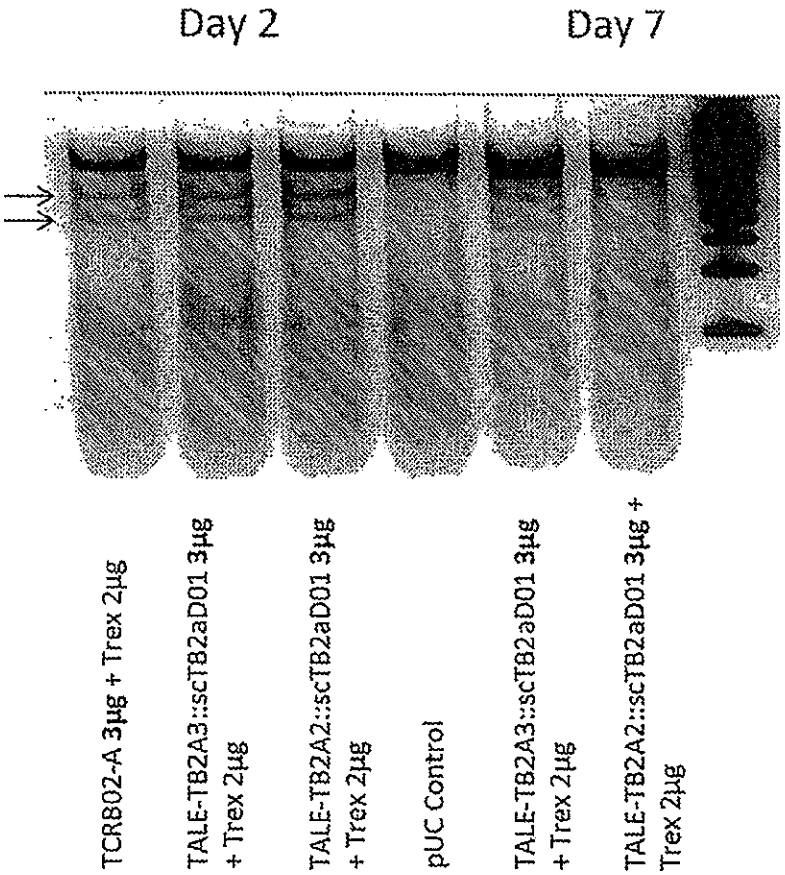

Day 2
Day 7
TCRB02-A 3µg + Trex 2µg
TALE-TB2A3::scTB2aD01 3µg + Trex 2µg
TALE-TB2A2::scTB2aD01 3µg + Trex 2µg
pUC Control
TALE-TB2A3::scTB2aD01 3µg + Trex 2µg
TALE-TB2A2::scTB2aD01 3µg + Trex 2µg

Figure 17

Target	pCLS8522+pCLS7763	pCLS8522+pCLS8990
C_N_RAGAvr05	+++	++
C_N_RAGAvr06	+++	+
C_N_RAGAvr07	++	+
C_N_RAGAvr08	+	n.d.
C_N_RAGAvr09	+	+
C_N_RAGAvr10	+	n.d.
C_N_RAGAvr11	+	n.d.
C_N_RAGAvr12	+	+
C_N_RAGAvr13	+	n.d.
C_N_RAGAvr14	+	+
C_N_RAGAvr15	+	++
C_N_RAGAvr16	n.d.	n.d.
C_N_RAGAvr17	n.d.	+
C_N_RAGAvr18	n.d.	++
C_N_RAGAvr19	n.d.	++
C_N_RAGAvr20	n.d.	++
C_N_RAGAvr21	n.d.	++
C_N_RAGAvr22	+	+++
C_N_RAGAvr23	+	+++
C_N_RAGAvr24	++	+++
C_N_RAGAvr25	+	+++
C_N_RAGAvr26	+	+++
C_N_RAGAvr27	+	+++
C_N_RAGAvr28	+	++
C_N_RAGAvr29	+	++
C_N_RAGAvr30	+++	++
C_N_RAGAvr31	+++	+++
C_N_RAGAvr32	++	+++
C_N_RAGAvr33	++	++
C_N_RAGAvr34	+++	+++
C_N_RAGAvr35	+++	+++
C_N_RAGAvr36	+++	+++
C_N_RAGAvr37	+++	+++
C_N_RAGAvr38	+	++
C_N_RAGAvr39	+	+
C_N_RAGAvr40	n.d.	n.d.
neg ctrl	n.d.	n.d.

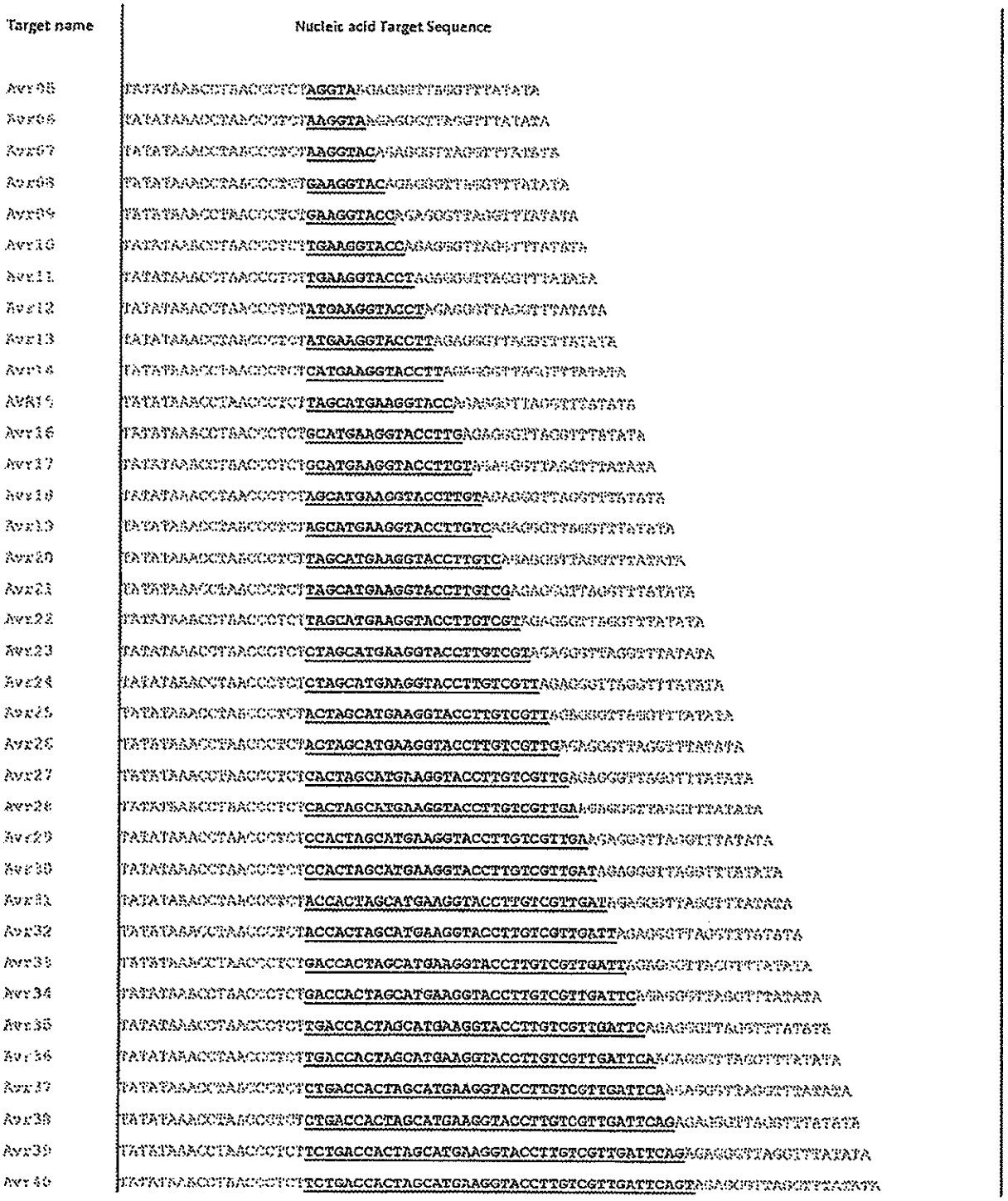
Figure 18

spacer length [bp]	pCLS9081	pCLS9082
40	+	+
39	+	+
38	+	n.d.
37	+	n.d.
36	+	+/-
35	+	+
34	+	+
33	+	+
32	+	+
31	+	+
30	+	+
29	+	+
28	+	+/-
27	+	+
26	+	+
25	+	+
24	+	+
23	+	+
22	+	+
21	+	+
20	+	+
19	+	+
18	+	+
17	+	+
16	+	+
15	+	+
14	n.d.	+/-
13	+	+
12	+	+/-
11	+	+/-
10	+	n.d.
09	+	n.d.
08	+	+/-
07	+	+
06	+	+
05	+	+
Compact	+	+/-

Figure 19

		Spacer length [bp]				
Catalytic head SeqID	polypeptide linker SeqID	15	18	21	24	Compact
11	385	++	++	+++	+++	++
11	388	+++	+++	++	+++	++
11	394	++	+++	++	+++	++
11	400	+++	+++	+++	+++	++

Figure 20



Target name	Nucleic acid Target Sequence
Avr05	TATATAAAGCTAAGCCTCTAGGTAAGAGGTTAGGTTTATATA
Avr06	TATATAAAGCTAAGCCTCTAAGGTAAGAGGTTAGGTTTATATA
Avr07	TATATAAAGCTAAGCCTCTAAGGTACAAGAGTTAGGTTTATATA
Avr08	TATATAAAGCTAAGCCTCTGAAGGTACAGAGGTTAGGTTTATATA
Avr09	TATATAAAGCTAAGCCTCTGAAGGTACCAAGAGGTTAGGTTTATATA
Avr10	TATATAAAGCTAAGCCTCTTGAAGGTACCAAGAGGTTAGGTTTATATA
Avr11	TATATAAAGCTAAGCCTCTTGAAGGTACCTAGAGGTTAGGTTTATATA
Avr12	TATATAAAGCTAAGCCTCTATGAAGGTACCTAGAGGTTAGGTTTATATA
Avr13	TATATAAAGCTAAGCCTCTATGAAGGTACCTTAGAGGTTAGGTTTATATA
Avr14	TATATAAAGCTAAGCCTCTCATGAAGGTACCTTAGAGGTTAGGTTTATATA
Avr15	TATATAAAGCTAAGCCTCTTAGCATGAAGGTACCAAGAGGTTAGGTTTATATA
Avr16	TATATAAAGCTAAGCCTCTGCATGAAGGTACCTTGAGAGGTTAGGTTTATATA
Avr17	TATATAAAGCTAAGCCTCTGCATGAAGGTACCTTGTAAAGGTTAGGTTTATATA
Avr18	TATATAAAGCTAAGCCTCTAGCATGAAGGTACCTTGTAGAGGTTAGGTTTATATA
Avr19	TATATAAAGCTAAGCCTCTAGCATGAAGGTACCTTGTCAGAGGTTAGGTTTATATA
Avr20	TATATAAAGCTAAGCCTCTTAGCATGAAGGTACCTTGTCAAAGGTTAGGTTTATATA
Avr21	TATATAAAGCTAAGCCTCTTAGCATGAAGGTACCTTGTCGAGAGGTTAGGTTTATATA
Avr22	TATATAAAGCTAAGCCTCTTAGCATGAAGGTACCTTGTCGTAGAGGTTAGGTTTATATA
Avr23	TATATAAAGCTAAGCCTCTCTAGCATGAAGGTACCTTGTCGTAGAGGTTAGGTTTATATA
Avr24	TATATAAAGCTAAGCCTCTCTAGCATGAAGGTACCTTGTCGTTAGAGGTTAGGTTTATATA
Avr25	TATATAAAGCTAAGCCTCTACTAGCATGAAGGTACCTTGTCGTTAGAGGTTAGGTTTATATA
Avr26	TATATAAAGCTAAGCCTCTACTAGCATGAAGGTACCTTGTCGTTGAGAGGTTAGGTTTATATA
Avr27	TATATAAAGCTAAGCCTCTCACTAGCATGAAGGTACCTTGTCGTTGAGAGGTTAGGTTTATATA
Avr28	TATATAAAGCTAAGCCTCTCACTAGCATGAAGGTACCTTGTCGTTGAAAGGTTAGGTTTATATA
Avr29	TATATAAAGCTAAGCCTCTCCACTAGCATGAAGGTACCTTGTCGTTGAAGAGGTTAGGTTTATATA
Avr30	TATATAAAGCTAAGCCTCTCCACTAGCATGAAGGTACCTTGTCGTTGATAGAGGTTAGGTTTATATA
Avr31	TATATAAAGCTAAGCCTCTACCACTAGCATGAAGGTACCTTGTCGTTGATAGAGGTTAGGTTTATATA
Avr32	TATATAAAGCTAAGCCTCTACCACTAGCATGAAGGTACCTTGTCGTTGATTAGAGGTTAGGTTTATATA
Avr33	TATATAAAGCTAAGCCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTAGAGGTTAGGTTTATATA
Avr34	TATATAAAGCTAAGCCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAGAGGTTAGGTTTATATA
Avr35	TATATAAAGCTAAGCCTCTTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGGTTAGGTTTATATA
Avr36	TATATAAAGCTAAGCCTCTTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAAGAGGTTAGGTTTATATA
Avr37	TATATAAAGCTAAGCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAAGAGGTTAGGTTTATATA
Avr38	TATATAAAGCTAAGCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGAGGTTAGGTTTATATA
Avr39	TATATAAAGCTAAGCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAAGAGGTTAGGTTTATATA
Avr40	TATATAAAGCTAAGCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGTAAAGGTTAGGTTTATATA

Table 6

Target name	Nucleic acid Target Sequence
Avr05	TATATAAACCTAACCCTCTAGGTAAGAGGGTTAGGTTTATATA
Avr06	TATATAAACCTAACCCTCTAAGGTAAGAGGGTTAGGTTTATATA
Avr07	TATATAAACCTAACCCTCTAAGGTACAGAGGGTTAGGTTTATATA
Avr08	TATATAAACCTAACCCTCTGAAGGTACAGAGGGTTAGGTTTATATA
Avr09	TATATAAACCTAACCCTCTGAAGGTACCAGAGGGTTAGGTTTATATA
Avr10	TATATAAACCTAACCCTCTTGAAGGTACCAGAGGGTTAGGTTTATATA
Avr11	TATATAAACCTAACCCTCTTGAAGGTACCTAGAGGGTTAGGTTTATATA
Avr12	TATATAAACCTAACCCTCTATGAAGGTACCTAGAGGGTTAGGTTTATATA
Avr13	TATATAAACCTAACCCTCTATGAAGGTACCTTAGAGGGTTAGGTTTATATA
Avr14	TATATAAACCTAACCCTCTCATGAAGGTACCTTAGAGGGTTAGGTTTATATA
AVR15	TATATAAACCTAACCCTCTTAGCATGAAGGTACCAGAGGGTTAGGTTTATATA
Avr16	TATATAAACCTAACCCTCTGCATGAAGGTACCTTGAGAGGGTTAGGTTTATATA
Avr17	TATATAAACCTAACCCTCTGCATGAAGGTACCTTGTAGAGGGTTAGGTTTATATA
Avr18	TATATAAACCTAACCCTCTAGCATGAAGGTACCTTGTAGAGGGTTAGGTTTATATA
Avr19	TATATAAACCTAACCCTCTAGCATGAAGGTACCTTGTCAGAGGGTTAGGTTTATATA
Avr20	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCAGAGGGTTAGGTTTATATA
Avr21	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGAGAGGGTTAGGTTTATATA
Avr22	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGTAGAGGGTTAGGTTTATATA
Avr23	TATATAAACCTAACCCTCTCTAGCATGAAGGTACCTTGTCGTAGAGGGTTAGGTTTATATA
Avr24	TATATAAACCTAACCCTCTCTAGCATGAAGGTACCTTGTCGTTAGAGGGTTAGGTTTATATA
Avr25	TATATAAACCTAACCCTCTACTAGCATGAAGGTACCTTGTCGTTAGAGGGTTAGGTTTATATA
Avr26	TATATAAACCTAACCCTCTACTAGCATGAAGGTACCTTGTCGTTGAGAGGGTTAGGTTTATATA
Avr27	TATATAAACCTAACCCTCTCACTAGCATGAAGGTACCTTGTCGTTGAGAGGGTTAGGTTTATATA
Avr28	TATATAAACCTAACCCTCTCACTAGCATGAAGGTACCTTGTCGTTGAAGAGGGTTAGGTTTATATA
Avr29	TATATAAACCTAACCCTCTCCACTAGCATGAAGGTACCTTGTCGTTGAAGAGGGTTAGGTTTATATA
Avr30	TATATAAACCTAACCCTCTCCACTAGCATGAAGGTACCTTGTCGTTGATAGAGGGTTAGGTTTATATA
Avr31	TATATAAACCTAACCCTCTACCACTAGCATGAAGGTACCTTGTCGTTGATAGAGGGTTAGGTTTATATA
Avr32	TATATAAACCTAACCCTCTACCACTAGCATGAAGGTACCTTGTCGTTGATTAGAGGGTTAGGTTTATATA
Avr33	TATATAAACCTAACCCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTAGAGGGTTAGGTTTATATA
Avr34	TATATAAACCTAACCCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGGGTTAGGTTTATATA
Avr35	TATATAAACCTAACCCTCTTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGGGTTAGGTTTATATA
Avr36	TATATAAACCTAACCCTCTTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAGAGGGTTAGGTTTATATA
Avr37	TATATAAACCTAACCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAAGAGGGTTAGGTTTATATA
Avr38	TATATAAACCTAACCCTCTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGAGGGTTAGGTTTATATA
Avr39	TATATAAACCTAACCCTCTTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGAGAGGGTTAGGTTTATATA
Avr40	TATATAAACCTAACCCTCTTCTGACCACTAGCATGAAGGTACCTTGTCGTTGATTCAGTAGAGGGTTAGGTTTATATA
compact	TATATAAACCTAACCCTCTTAGCATGAAGGTACCTTGTCGATGGTGTACAGTAGGGGGAGATGCA
neg. Ctrl.	TTGTTCTCAGGTACCTCAGCCAGA

Table 7

Target name	Nucleic acid Target Sequence
C_N_RAGAvr05	TGTTTATGGTTACTTATaggtaTATATAAACCTAACCCTCT
C_N_RAGAvr06	TGTTTATGGTTACTTATaaggtaTATATAAACCTAACCCTCT
C_N_RAGAvr07	TGTTTATGGTTACTTATaaggtacTATATAAACCTAACCCTCT
C_N_RAGAvr08	TGTTTATGGTTACTTATgaaggtacTATATAAACCTAACCCTCT
C_N_RAGAvr09	TGTTTATGGTTACTTATgaaggtaccTATATAAACCTAACCCTCT
C_N_RAGAvr10	TGTTTATGGTTACTTATtgaaggtaccTATATAAACCTAACCCTCT
C_N_RAGAvr11	TGTTTATGGTTACTTATtgaaggtacctTATATAAACCTAACCCTCT
C_N_RAGAvr12	TGTTTATGGTTACTTATatgaaggtacctTATATAAACCTAACCCTCT
C_N_RAGAvr13	TGTTTATGGTTACTTATatgaaggtaccttTATATAAACCTAACCCTCT
C_N_RAGAvr14	TGTTTATGGTTACTTATcatgaaggtaccttTATATAAACCTAACCCTCT
C_N_RAGAvr15	TGTTTATGGTTACTTATtagcatgaaggtaccTATATAAACCTAACCCTCT
C_N_RAGAvr16	TGTTTATGGTTACTTATgcatgaaggtaccttgTATATAAACCTAACCCTCT
C_N_RAGAvr17	TGTTTATGGTTACTTATgcatgaaggtaccttgtTATATAAACCTAACCCTCT
C_N_RAGAvr18	TGTTTATGGTTACTTATagcatgaaggtaccttgtTATATAAACCTAACCCTCT
C_N_RAGAvr19	TGTTTATGGTTACTTATagcatgaaggtaccttgtcTATATAAACCTAACCCTCT
C_N_RAGAvr20	TGTTTATGGTTACTTATtagcatgaaggtaccttgtcTATATAAACCTAACCCTCT
C_N_RAGAvr21	TGTTTATGGTTACTTATtagcatgaaggtaccttgtcgTATATAAACCTAACCCTCT
C_N_RAGAvr22	TGTTTATGGTTACTTATtagcatgaaggtaccttgtcgtTATATAAACCTAACCCTCT
C_N_RAGAvr23	TGTTTATGGTTACTTATctagcatgaaggtaccttgtcgtTATATAAACCTAACCCTCT
C_N_RAGAvr24	TGTTTATGGTTACTTATctagcatgaaggtaccttgtcgttTATATAAACCTAACCCTCT
C_N_RAGAvr25	TGTTTATGGTTACTTATactagcatgaaggtaccttgtcgttTATATAAACCTAACCCTCT
C_N_RAGAvr26	TGTTTATGGTTACTTATactagcatgaaggtaccttgtcgttgTATATAAACCTAACCCTCT
C_N_RAGAvr27	TGTTTATGGTTACTTATcactagcatgaaggtaccttgtcgttgTATATAAACCTAACCCTCT
C_N_RAGAvr28	TGTTTATGGTTACTTATcactagcatgaaggtaccttgtcgttgaTATATAAACCTAACCCTCT
C_N_RAGAvr29	TGTTTATGGTTACTTATccactagcatgaaggtaccttgtcgttgaTATATAAACCTAACCCTCT
C_N_RAGAvr30	TGTTTATGGTTACTTATccactagcatgaaggtaccttgtcgttgatTATATAAACCTAACCCTCT
C_N_RAGAvr31	TGTTTATGGTTACTTATaccactagcatgaaggtaccttgtcgttgatTATATAAACCTAACCCTCT
C_N_RAGAvr32	TGTTTATGGTTACTTATaccactagcatgaaggtaccttgtcgttgattTATATAAACCTAACCCTCT
C_N_RAGAvr33	TGTTTATGGTTACTTATgaccactagcatgaaggtaccttgtcgttgattTATATAAACCTAACCCTCT
C_N_RAGAvr34	TGTTTATGGTTACTTATgaccactagcatgaaggtaccttgtcgttgattcTATATAAACCTAACCCTCT
C_N_RAGAvr35	TGTTTATGGTTACTTATtgaccactagcatgaaggtaccttgtcgttgattcTATATAAACCTAACCCTCT
C_N_RAGAvr36	TGTTTATGGTTACTTATtgaccactagcatgaaggtaccttgtcgttgattcaTATATAAACCTAACCCTCT
C_N_RAGAvr37	TGTTTATGGTTACTTATctgaccactagcatgaaggtaccttgtcgttgattcaTATATAAACCTAACCCTCT
C_N_RAGAvr38	TGTTTATGGTTACTTATctgaccactagcatgaaggtaccttgtcgttgattcagTATATAAACCTAACCCTCT
C_N_RAGAvr39	TGTTTATGGTTACTTATtctgaccactagcatgaaggtaccttgtcgttgattcagTATATAAACCTAACCCTCT
C_N_RAGAvr40	TGTTTATGGTTACTTATtctgaccactagcatgaaggtaccttgtcgttgattcagtTATATAAACCTAACCCTCT

Table 13