Figure 1

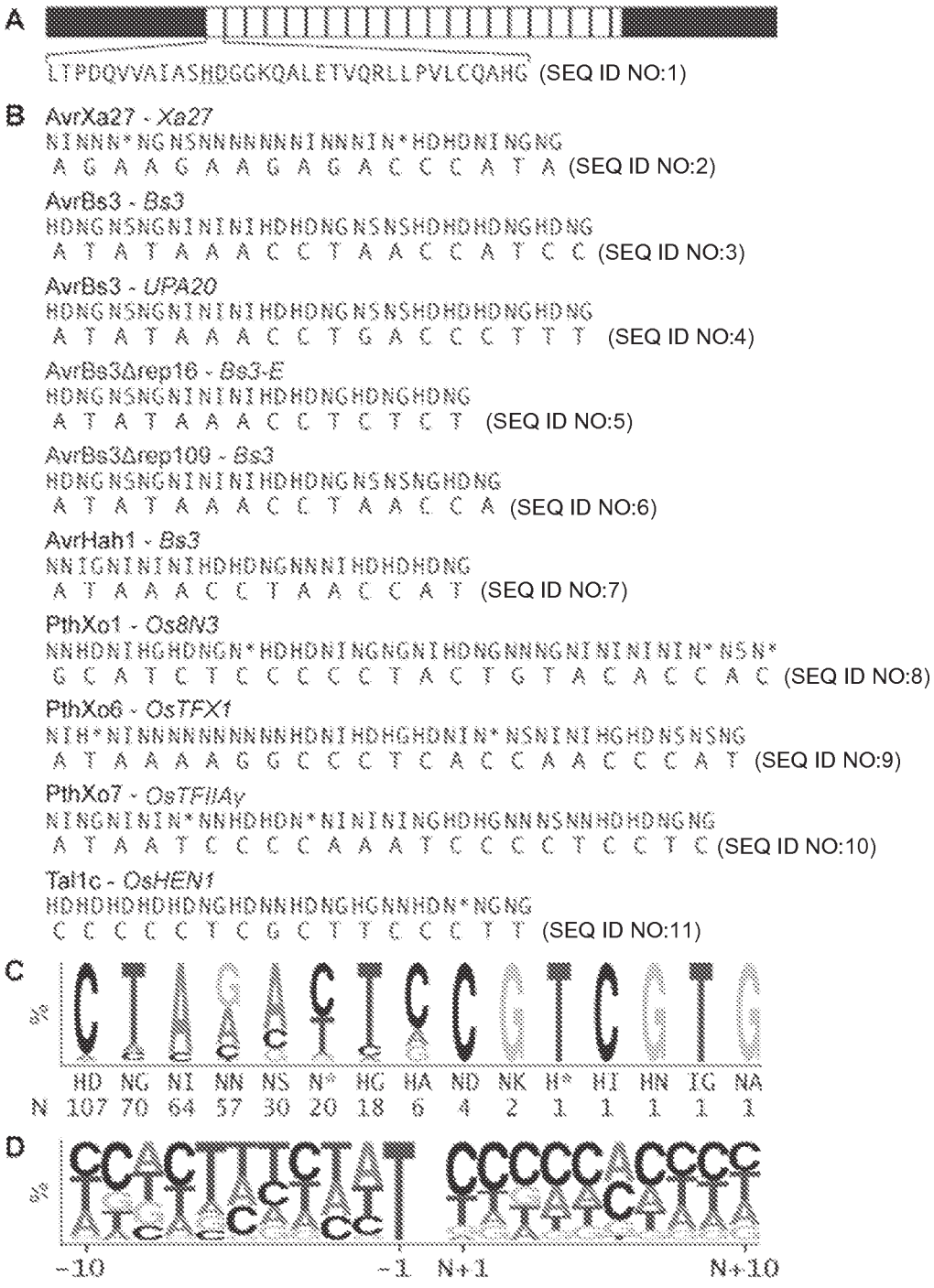

A
LTPDQVVAIASHDGGKQALETVQRLLPVLCQAHG (SEQ ID NO:1)
B
AvrXa27 - Xa27
NINNN*NGNSNNNNNNNINNNIN*HDHDNINGNG
A G A A G A A G A G A C C C A T A (SEQ ID NO:2)
AvrBs3 - Bs3
HDNGNSNGNININIHDHDNGNSNSHDHDHDNGHDNG
A T A T A A A C C T A A C C A T C C (SEQ ID NO:3)
AvrBs3 - UPA20
HDNGNSNGNININIHDHDNGNSNSHDHDHDNGHDNG
A T A T A A A C C T G A C C C T T T (SEQ ID NO:4)
AvrBs3Δrep16 - Bs3-E
HDNGNSNGNININIHDHDNGHDNGHDNG
A T A T A A A C C T C T C T (SEQ ID NO:5)
AvrBs3Δrep109 - Bs3
HDNGNSNGNININIHDHDNGNSNSNGHDNG
A T A T A A A C C T A A C C A (SEQ ID NO:6)
AvrHah1 - Bs3
NNIGNININIHDHDNGNNNIHDHDHDNG
A T A A A C C T A A C C A T (SEQ ID NO:7)
PthXo1 - Os8N3
NNHDNIHGHDNGN*HDHDNINGNGNIHDNGNNNGNINININ*N5N*
G C A T C T C C C C C T A C T G T A C A C C A C (SEQ ID NO:8)
PthXo6 - OsTFX1
NIH*NINNNNNNNNNNHDNIHDHGHDNIN*NSNINIHGHDNSNSNG
A T A A A A G G C C C T C A C C A A C C C A T (SEQ ID NO:9)
PthXo7 - OsTFIIAγ
NINGNININ*NNHDHDN*NINININGHDHGNNNSNNHDHDNGNG
A T A A T C C C C A A A T C C C C T C C T C (SEQ ID NO:10)
Tal1c - OsHEN1
HDHDHDHDHDNGHDNNHDNGHGNNHDN*NGNG
C C C C C T C G C T T C C C T T (SEQ ID NO:11)
C
bits
HD NG NI NN NS N* HG HA ND NK H* HI HN IG NA
N 107 70 64 57 30 20 18 6 4 2 1 1 1 1 1
D
bits
-10 -1 N+1 N+10

Figure 2

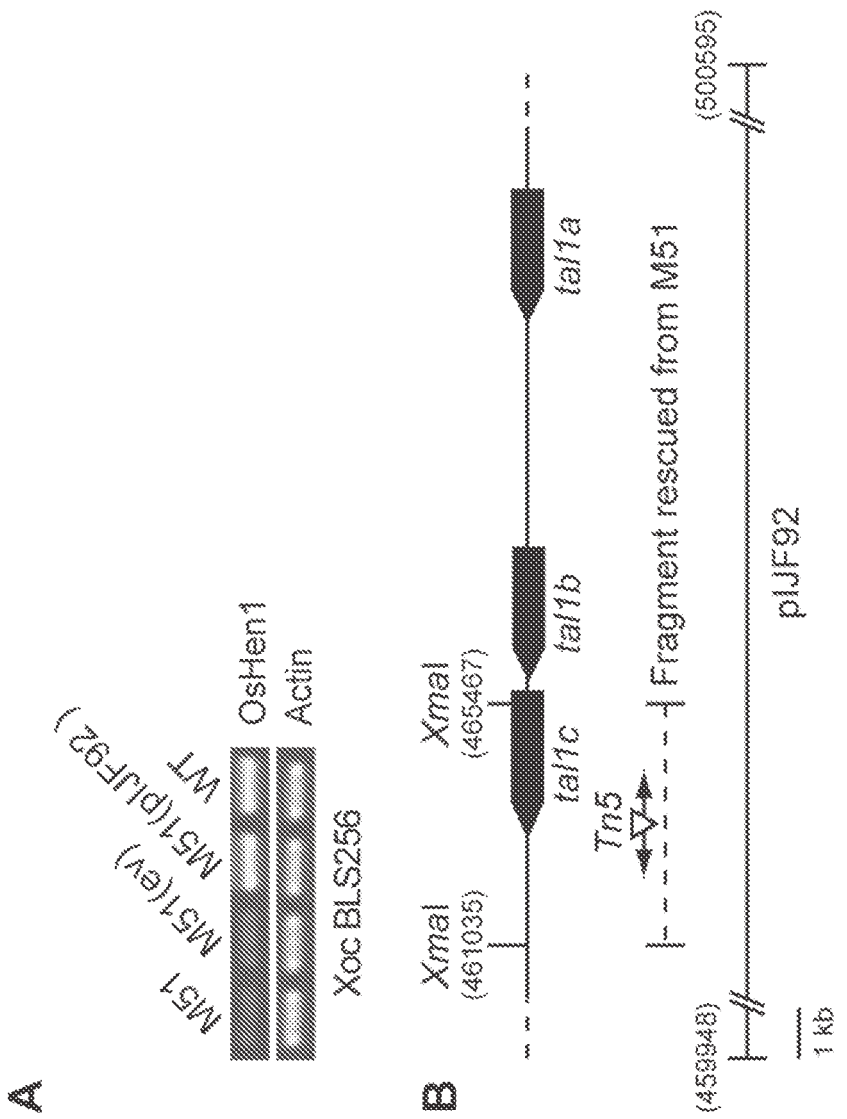

A
M51
M51(ev)
M51(pIJF92)
WT
Xoc BLS256
Actin
OsHen1
B
XmaI
(461035)
XmaI
(465467)
tal1c
tal1b
tal1a
Tn5
Fragment rescued from M51
(459948)
(500595)
pIJF92
1 kb

Figure 3

MDPIRSRTPSPARELLPGPQPDGVQPTADRGVSPPAGGPLDGLPARRTMSRTRLPSPPAPSPAFSAGSFSDLLRQFDPSLFNTSL
FDSLPPFGAHHTEAATGEWDEVQSGLRAADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTLGYSQQQQEKI
KPKVRSTVAQHHEALVGHGFTHAHIVALSQHPAALGTVAVKYQDMIAALPEATHEAIVGVGKQWSGARALEALLTVAGELRGPPL
QLDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLNLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGK
QALETVQRLLPVLCQAHGLTPQQVVAIASNSGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNGGGKQALETVQRLLPVLCQAH
GLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASNIGGKQALETVQALLPVLCQAHGLTPEQVVAIASNIGGKQA
LETVQALLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLT
PQQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPEQVVAIASNSGGKQALETVQALLPVLCQAHGLTPEQVVAIASNSGGKQAL
ETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQALETVQRLLPVLCQAHGLT
PEQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPQQVVAIASNGGGRPALETVQRLLPVLCQAHGLTPEQVVAIASHDGGKQAL
ETVQRLLPVLCQAHGLTPQQVVAIASNGGGRPALESIVAQLSRPDPALAALTNDHLVALACLGGRPALDAVKKGLPHAPALIKRTN
RRIPERTSHRVADHAQVVRVLGFFQCHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTELEARSGTLPPASQRWDRILQASGM
KRAKPSPTSTQTPDQASLHAFADSLERDLDAPSPMHEGDQTRASSRKRSRSDRAVTGPSAQQSFEVRVPEQRDALHLPLSWRV
KRPRTSIGGGLPDPGTPTAADLAASSTVMREQDEDPFAGAADDFPAFNEEELAWLMELLPQ (SEQ ID NO:12)

Figure 4

gaattcaaggtgtcaaaaagcgataggcggaattatagatgtactttagtgaacgggttcgacaaagcgaaaccaacacccaggcgcgaaagccttgcgccg
caatgctttccggcaatgtgacccagggcattgaccgaaacgggcgtaggaatttcggaacacgacggtagggaatgctctaccgcccggctacgcaaaagcactctcgcctgccagacgcgcc
actgcgtggaattggccgttatgtccgctggcggcctcgccgtagtgcttgcagcgcagccttgaatgatcgaacatcaaacatcactgtttgataggtcgatcatgacatcgcccatttcgagggt
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ttcgcgcacaccaagtcctgcccgcgagcttctgcccggaccccaacccgatgggttcagccgactgcagatcgtgggtgtctccgcctgccggcgggcccccttggatggcttgcccgctcggcg
gacgatgtcccggacccggctgccatctcccccctgcccctcacctgcgttctcggcgggcagcttcagtgaccttgttacgtcagttcgatccgtcactttttaatacatcgctttttgattcattgcctccctt
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ccaagccggcgccgcgacgacgtgctgccgcaacctccgacgcttgccggccgcgcaggtggatctacgcacgctcggctacagccagcagcaacaggagaagatcaaaccgaaggttcg
ttcgacagtggccgcagcaccacgaggcactggtcggccatgggtttacacacgcgcacatcgttgccgctcagccaacacccggcagcgttagggaccgtcgctgtcaagtatcaggacatgatcg
cagcgttgccagaggcgacacacgaagcgatcgttggcgtcggcgcacgcgctctggaggccttgctcacggtggcgggagagttgagaggtccaccgttacagttgga
cacaggccaacttctcaagattgcaaaacgtggcggcgtgaccgcagtggaggcagtgcatgcatggcgcaatgcactgaccgcgagcaggtggtggccat
cgccagccacgatggcggcaagcaggcgctggagacggtgcagcgtgctgttgccggtgctgtgccaggcccatgtgccgtgtcgccagcaatggcggtgtggca
agcaggcgctggagacggtgcagcggctgttgccaggcccatggcctgacccgcagcaggtggtggccatcgccaggcaggcgctggagacggtg
cagcggctgttgccggtgctgtgccaggcccatggcctgacccggagcaggtggtggccatcgccaggcgctgttgccggtgctgt
gccaggcccatggcctgacccggagcaggtggtggccatcgccaggcgctggagacggtgcaggcccatggcctgaccc
cggagcaggtggtggccatcgccagcaatattggtggcaagcaggcgctggagacggtgcaggcccatggcctgacccgcagccaggtggtggccatcg
ccagcaatattggtggccaagcaggcgctggagacggtgcaggcgctgttgccaggcccatggcctgacccggagcaggtggtggccaagc
aggcgctggagacggtgcagcggctgttgccaggcccatggcctgacccgcagcaatggcggctgttgccaggcccatggcctgacccgcaagc
cggctgttgccggtgctgtgccaggcccatggcctgacccgcagcaatggcggctgttgccaggcccatggcctgacccgcagc
agccacgatggcggcaagcaggcgctggagacggtgcagcggctgttgccaggcccatggcctgacccggagcaggtggtggccatcgccaggc
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cggctgttgccggtgctgtgccaggcccatggcctgacccgcagccaggcaggcggctgttgccggtgctgtgccaggcccatggcctgacccgcagc
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cagcaggtggtggccatcgccagcaatggcggcggcgctggagagcattgttgcccagttatctcgccctgatccggccgcgttggccgccgttggcc
tgcctcggcggacgtcctgcgctggatgcagtgaaaaaggattgccgcacgcgccggccttgatcaaaagaaccaatcgccgttattccgcgaacgcacatcccatcgcgttgccgaccacgcgc
aagtggttcgcgtgctgggttttttcagtgccactcccaccagccgcaagcatttgatgacgccatgacgcagttcgggatgagcaggcacgggttgttacagctctttcgcagagtgggcgtcaccg
aactcgaagcccgcagtggaacgctcccccagcctcgcagcgttgggaccgtatcctccaggcatcagggatgaaaagggccaaaccgtccctacttcaactcaaacgccggatcaggcgt
ctttgcatgcattcgccgattcgctggagcgtgacctttgatgcgcctagcccaatgcacgagggagatcagacgcgggcaagcagccgtaaacggtcccgatcggatcgtgctgtcaccggtccct
ccgcacagcaatcgttcgaggtgcgcgttcccgaacagcgcgatgcgctgcatttgccctcagttggagggtaaaacgcccgcgtaccagtatcgggggcggcctcccggatcctggtacgcccc
acggctgccgacctggcagcgtccagcaccgtgatgcgggaacaagatgaggaccccttcgcagggcagcggatgatttcccggcattcaacgaagaggagctcgcatggttgatggagctat
tgcctcagtgaggctcagtcggtgactacctgagcgtcggcagggattggtgtaagtaaccttactgacagcgagttagcccacttttggctgttttttacacaaatcctcgcctccccctctggttgcacca
cacccgtacaccaagcgcggcggcgaagcaggcaccgagtggttccgctcgcggtgttgcgttcctaaccaggcggtggctatacgctcaagctgcgcaccgtcccggtggcgatcgacgacg
aaatg (SEQ ID NO:13)

Figure 5

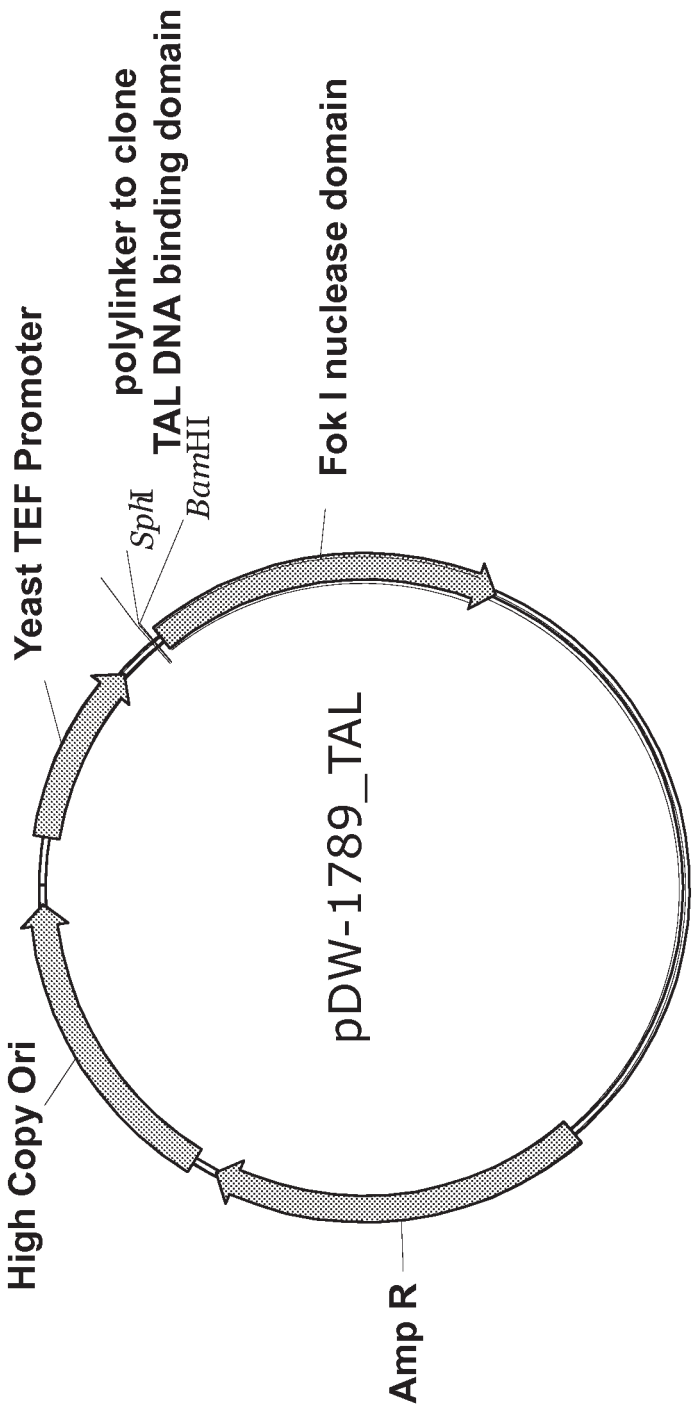

Yeast TEF Promoter
polylinker to clone
TAL DNA binding domain
SphI
BamHI
Fok I nuclease domain
pDW-1789_TAL
High Copy Ori
Amp R

Figure 6

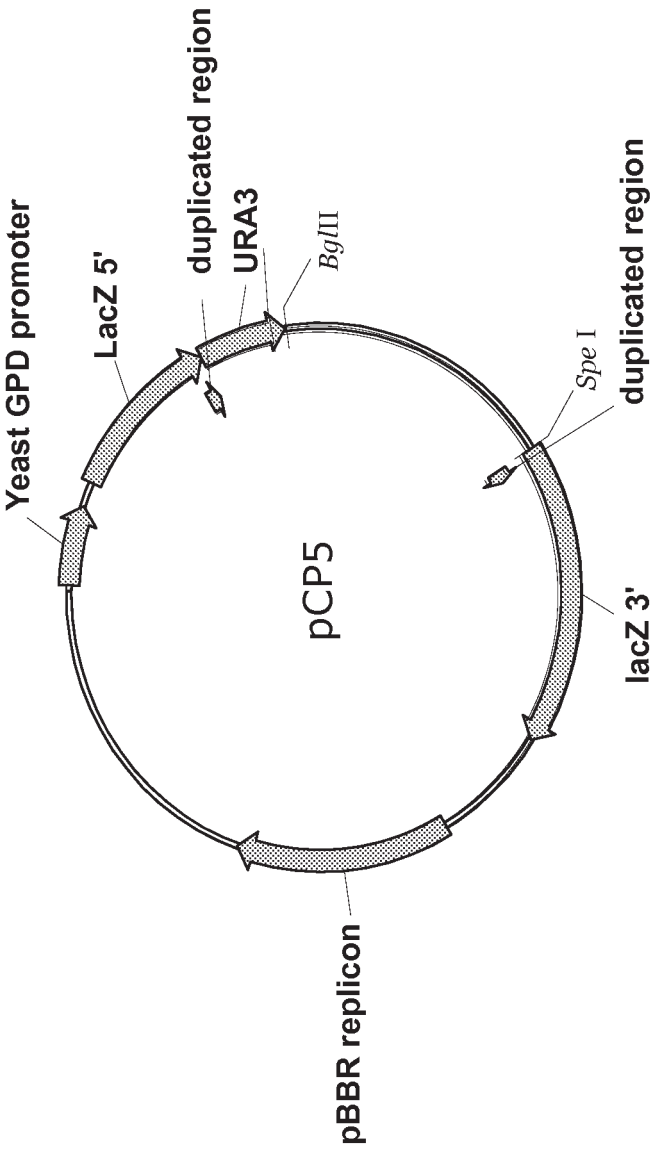

Yeast GPD promoter
LacZ 5'
duplicated region
URA3
BglII
SpeI
duplicated region
pCP5
lacZ 3'
pBBR replicon

Figure 7

TAL DNA Binding Repeats
FokI Nuclease
FokI Nuclease
TAL DNA Binding Repeats
5′-TATATAAACCTAACCATCCtcacaacttcaagttatcGGATGGTTAGGTTTATATA-3′ (SEQ ID NO:14)
3′-ATATATTTGGATTGGTAGGagtgttgaagttcaatagCCTACCAATCCAAATATAT-5′ (SEQ ID NO:15)

Figure 8

LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHG
LTPQQVVAIASNSGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASNGGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASNIGGKQALETVQALLPVLCQAHG
LTPEQVVAIASNIGGKQALETVQALLPVLCQAHG
LTPEQVVAIASNIGGKQALETVQALLPVLCQAHG
LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPQQVVAIASNGGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASNSGGKQALETVQALLPVLCQAHG
LTPEQVVAIASNSGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPQQVVAIASNGGGRPALETVQRLLPVLCQAHG
LTPEQVVAIASHDGGKQALETVQRLLPVLCQAHG
LTPQQVVAIASNGGGRPALE (SEQ ID NO:16)

Figure 9

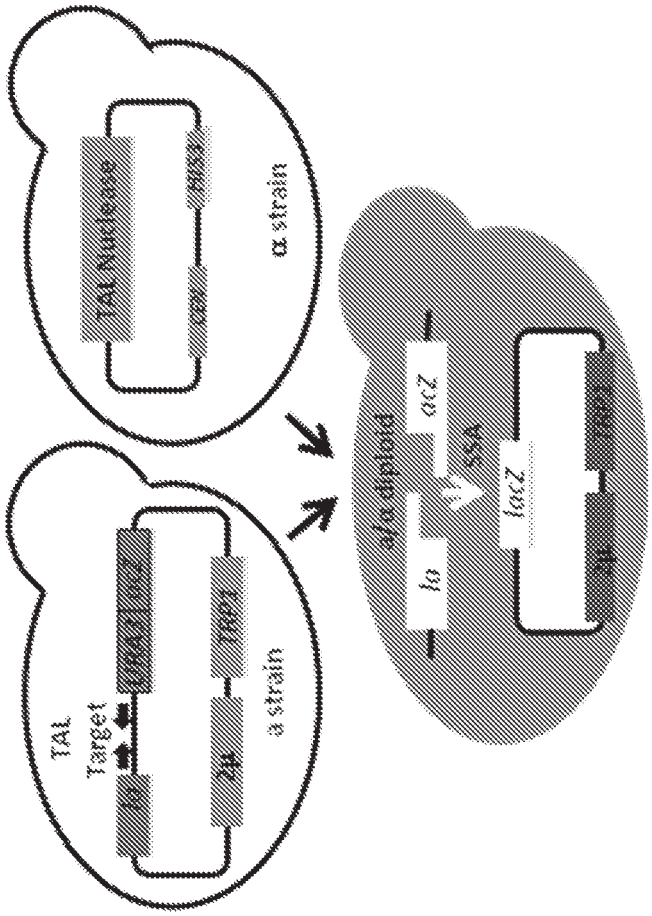

TAL Nuclease
α strain
TAL Target
a strain
a/α diploid
SSA
lacZ

Figure 10

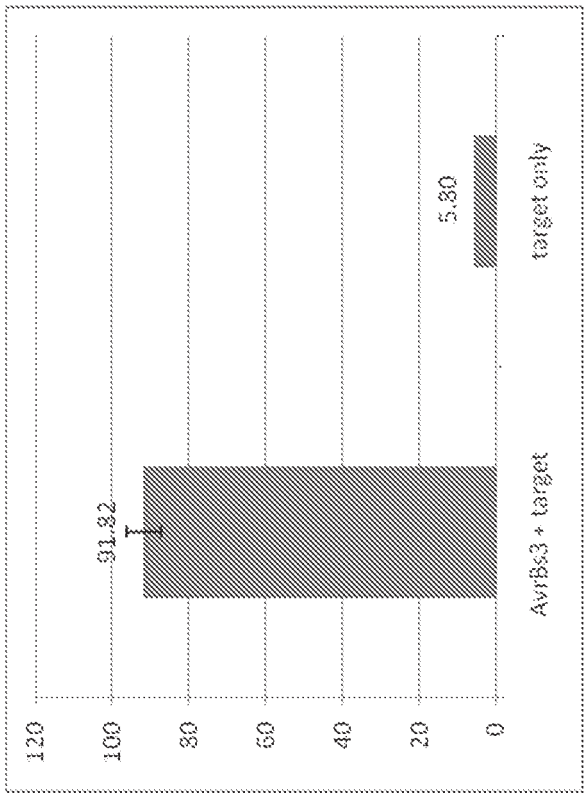


Figure 11

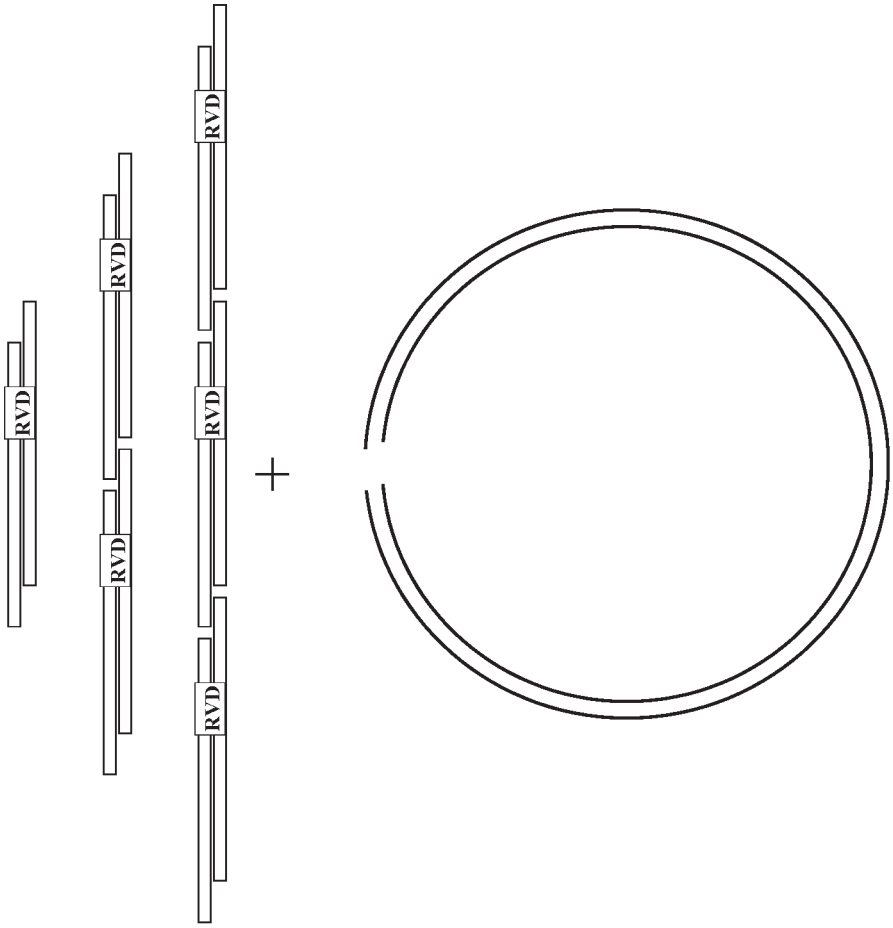


Figure 12

A

MscI

CTGACCCCGGCACAGGTGGTGGCCATCGCCAGCNNNNNNGGCGGCAAGCAGGCGCTGGAGACGGTGCAGCGGCTGTTGCCGGTGCTGTGCCAGGACCATGGC (SEQ ID NO:17)

L T P A Q V V A I A S X X G G K Q A L E T V Q R L L P V L C Q D H G (SEQ ID NO:18)

1 2 3 4 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

B

MscI

CTGACCCCGGCACAGGTGGTGGCCATCGCCAGCNNNNNNGGCGGCAAGCAGGCGCTCGAGAGC (SEQ ID NO:19)

L T P A Q V V A I A S X X G G K Q A L E S (SEQ ID NO:20)

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

Figure 13

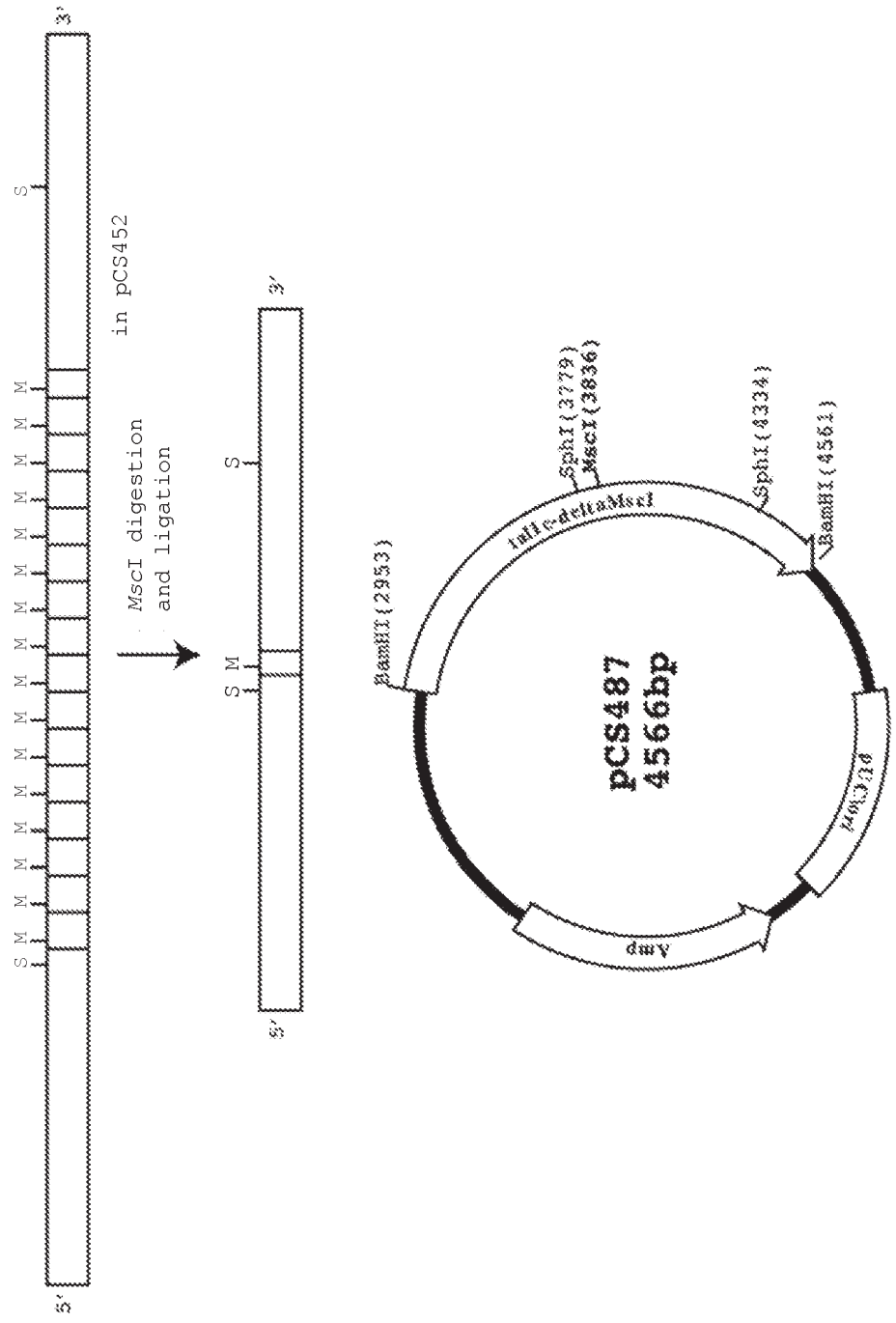

3'
S
M
5'
MscI digestion
and ligation
in pCS452
S
M
3'
5'
pCS487
4566bp
BamHI(2953)
tufA-deltaMscI
SphI(3779)
MscI(3836)
SphI(4334)
BamHI(4561)
pUC ori
Amp

Figure 14

XhoI (CTCGAG)
PspXI (A/C/GCTCGAGC/G/T)
(SEQ ID NO:21) GCG CTG GAG AGC
(SEQ ID NO:22) A L E S
18 19 20
pCS487
GCG CTC GAG TCC (SEQ ID NO:23)
A L E S (SEQ ID NO:22)
18 19 20
pCS489

Figure 15

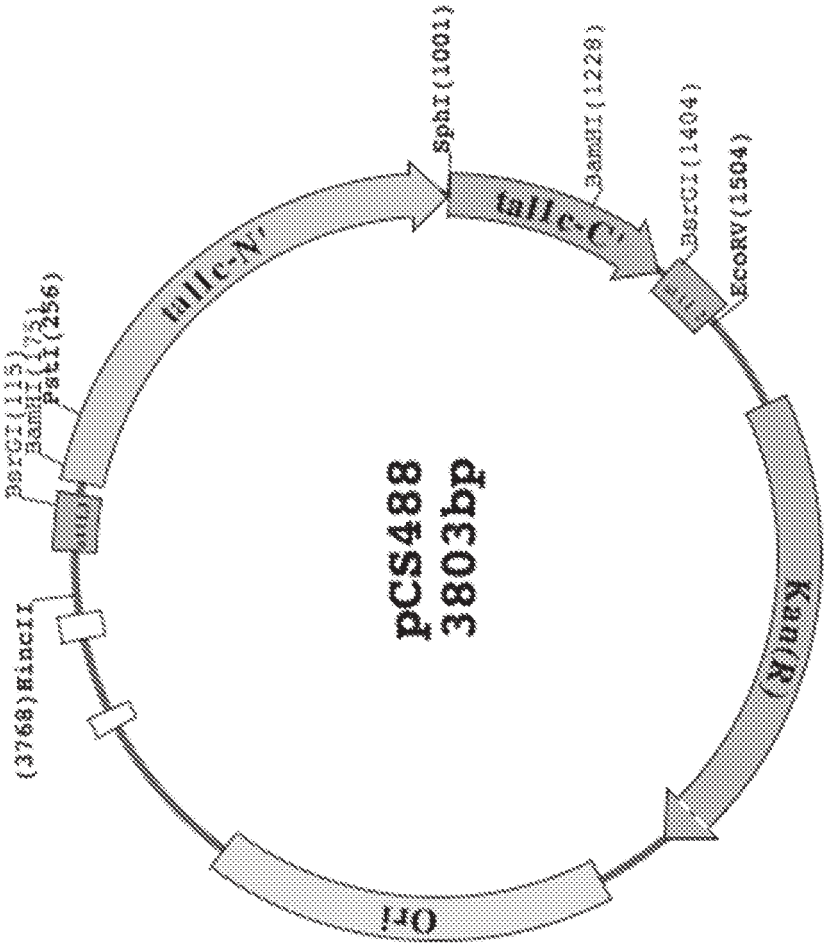

pCS488
3803bp
SpaI(1001)
SamHI(1220)
BsrGI(1404)
EcoRV(1504)
Kan(R)
Ori
(3768)HindIII
BsrGI(115)
SamHI(?)
PstI(256)
hIL-6-N'
hIL-6-C'

Figure 16

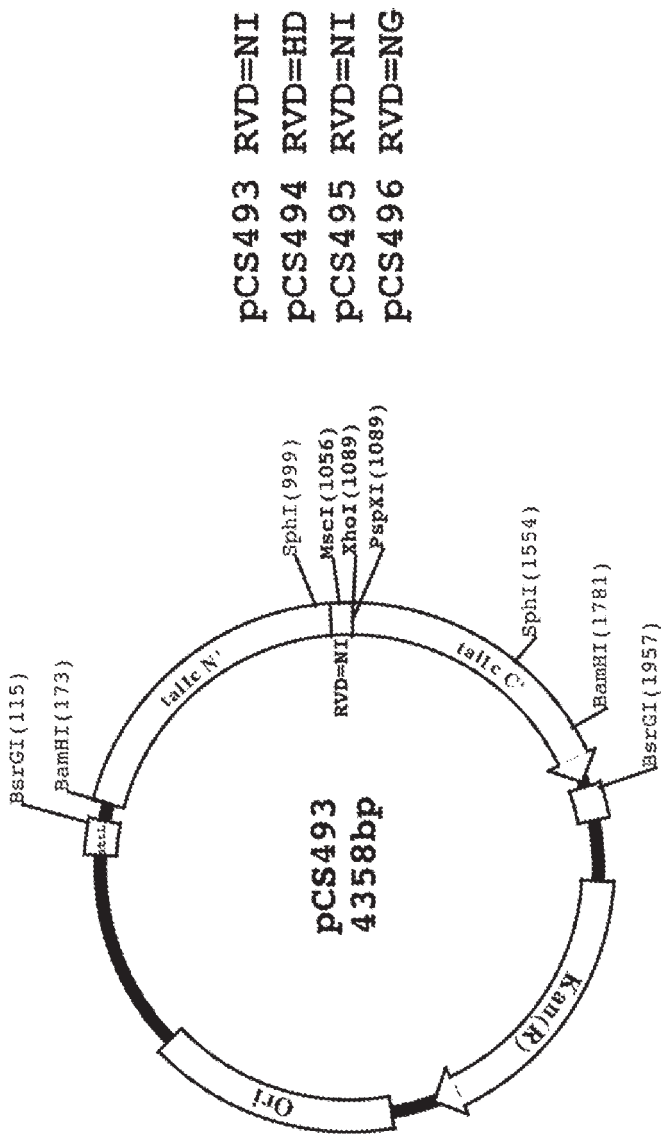

pCS493 RVD=NI
pCS494 RVD=HD
pCS495 RVD=NI
pCS496 RVD=NG
BsrGI(115)
BamHI(173)
SphI(999)
MscI(1056)
XhoI(1089)
PspXI(1089)
SphI(1554)
BamHI(1781)
BsrGI(1957)
talTc N'
RVD=NI
talTc C'
pCS493
4358bp
Ori
KanR

Figure 17

A

*Xho*I *Msc*I

5′-TCGAGACGGTGCAGCGGCTGTTGCCGGTGCTGTGCCAGGACCATGGCCTGACCCCGGACCAAGTGGTGGCCATCGCCAGC**AACATT**GGCGGCAAGCAAGCGC-3′ (SEQ ID NO:24)

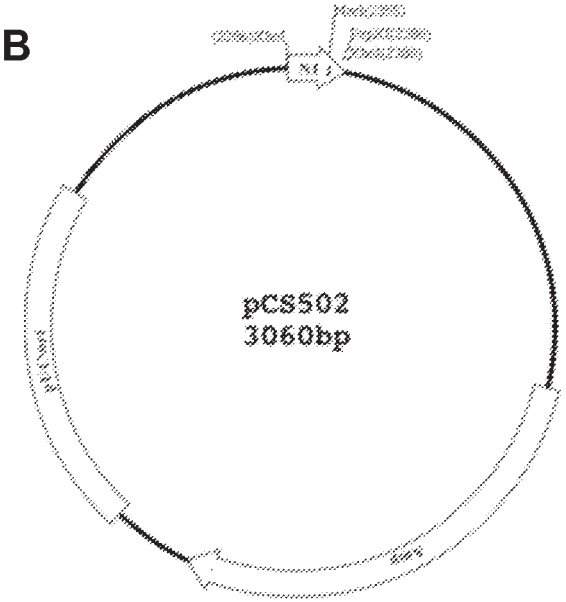
3′-CTGCCACGTCGCCGACAACGGCCACGACACGGTCCTGGTACCGGACTGGGGCCTGGTTCACCACCGGTAGCGGTCGTTGTAACCGCCGTTCGTTCGCGAGCT-5′ (SEQ ID NO:25)

*Psp*XI/*Xho*I

E T V Q R L L P V L C Q D H G L T P D Q V V A I A S **N** **I** G G K Q A L E (SEQ ID NO:26)

21 22 23 24 25 26 27 28 29 30 31 32 33 34 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

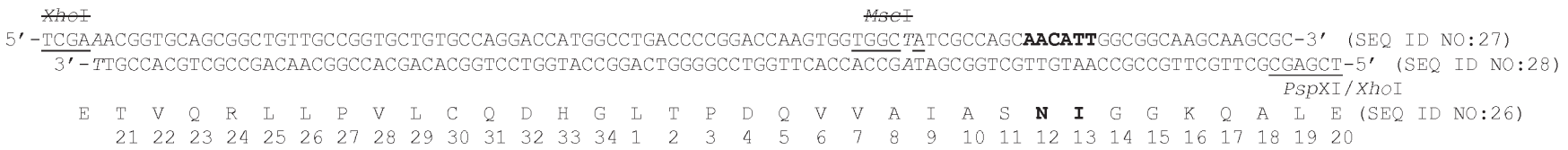
B



pCS502 RVD=NI
pCS503 RVD=HD
pCS504 RVD=NI
pCS505 RVD=NG

Figure 18

A


XhoI
MscI
5′-TCGAACGGTGCAGCGGCTGTTGCCGGTGCTGTGCCAGGACCATGGCCTGACCCCGGACCAAGTGGTGGCTATCGCCAGCAACATTGGCGGCAAGCAAGCGC-3′ (SEQ ID NO:27)
3′-TTGCCACGTCGCCGACAACGGCCACGACACGGTCCTGGTACCGGACTGGGGCCTGGTTCACCACCGATAGCGGTCGTTGTAACCGCCGTTCGTTCGCGAGCT-5′ (SEQ ID NO:28)
PspXI/XhoI
E T V Q R L L P V L C Q D H G L T P D Q V V A I A S N I G G K Q A L E (SEQ ID NO:26)
21 22 23 24 25 26 27 28 29 30 31 32 33 34 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20

B

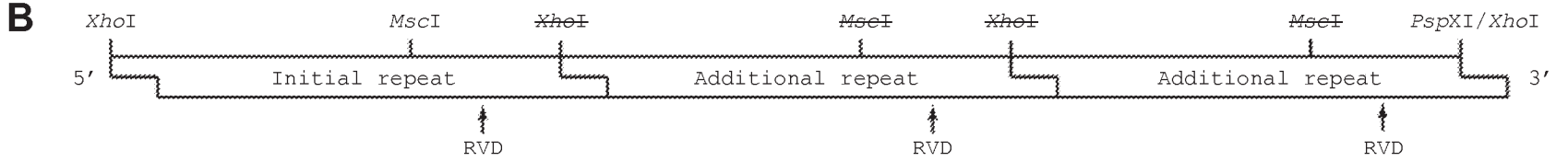

XhoI
MscI
XhoI
MscI
XhoI
MscI
PspXI/XhoI
5′
Initial repeat
Additional repeat
Additional repeat
3′
RVD
RVD
RVD

Figure 19

Plasmid	Description
pCS602	NI
pCS603	HD
pCS604	NN
pCS605	NG

Plasmid	Description
pCS606	NI-NI
pCS607	NI-HD
pCS608	NI-NN
pCS609	NI-NG
pCS610	HD-NI
pCS611	HD-HD
pCS612	HD-NN
pCS613	HD-NG
pCS614	NN-NI
pCS615	NN-HD
pCS616	NN-NN
pCS617	NN-NG
pCS618	NG-NI
pCS619	NG-HD
pCS620	NG-NN
pCS621	NG-NG

Plasmid	Description
pCS622	NI-NI-NI
pCS623	NI-NI-HD
pCS624	NI-NI-NN
pCS625	NI-NI-NG
pCS626	NI-HD-NI
pCS627	NI-HD-HD
pCS628	NI-HD-NN
pCS629	NI-HD-NG
pCS630	NI-NN-NI
pCS631	NI-NN-HD
pCS632	NI-NN-NN
pCS633	NI-NN-NG
pCS634	NI-NG-NI
pCS635	NI-NG-HD
pCS636	NI-NG-NN
pCS637	NI-NG-NG

Plasmid	Description
pCS638	HD-NI-NI
pCS639	HD-NI-HD
pCS640	HD-NI-NN
pCS641	HD-NI-NG
pCS642	HD-HD-NI
pCS643	HD-HD-HD
pCS644	HD-HD-NN
pCS645	HD-HD-NG
pCS646	HD-NN-NI
pCS647	HD-NN-HD
pCS648	HD-NN-NN
pCS649	HD-NN-NG
pCS650	HD-NG-NI
pCS651	HD-NG-HD
pCS652	HD-NG-NN
pCS653	HD-NG-NG

Plasmid	Description
pCS654	NN-NI-NI
pCS655	NN-NI-HD
pCS656	NN-NI-NN
pCS657	NN-NI-NG
pCS658	NN-HD-NI
pCS659	NN-HD-HD
pCS660	NN-HD-NN
pCS661	NN-HD-NG
pCS662	NN-NN-NI
pCS663	NN-NN-HD
pCS664	NN-NN-NN
pCS665	NN-NN-NG
pCS666	NN-NG-NI
pCS667	NN-NG-HD
pCS668	NN-NG-NN
pCS669	NN-NG-NG

Plasmid	Description
pCS670	NG-NI-NI
pCS671	NG-NI-HD
pCS672	NG-NI-NN
pCS673	NG-NI-NG
pCS674	NG-HD-NI
pCS675	NG-HD-HD
pCS676	NG-HD-NN
pCS677	NG-HD-NG
pCS678	NG-NN-NI
pCS679	NG-NN-HD
pCS680	NG-NN-NN
pCS681	NG-NN-NG
pCS682	NG-NG-NI
pCS683	NG-NG-HD
pCS684	NG-NG-NN
pCS685	NG-NG-NG

Figure 20

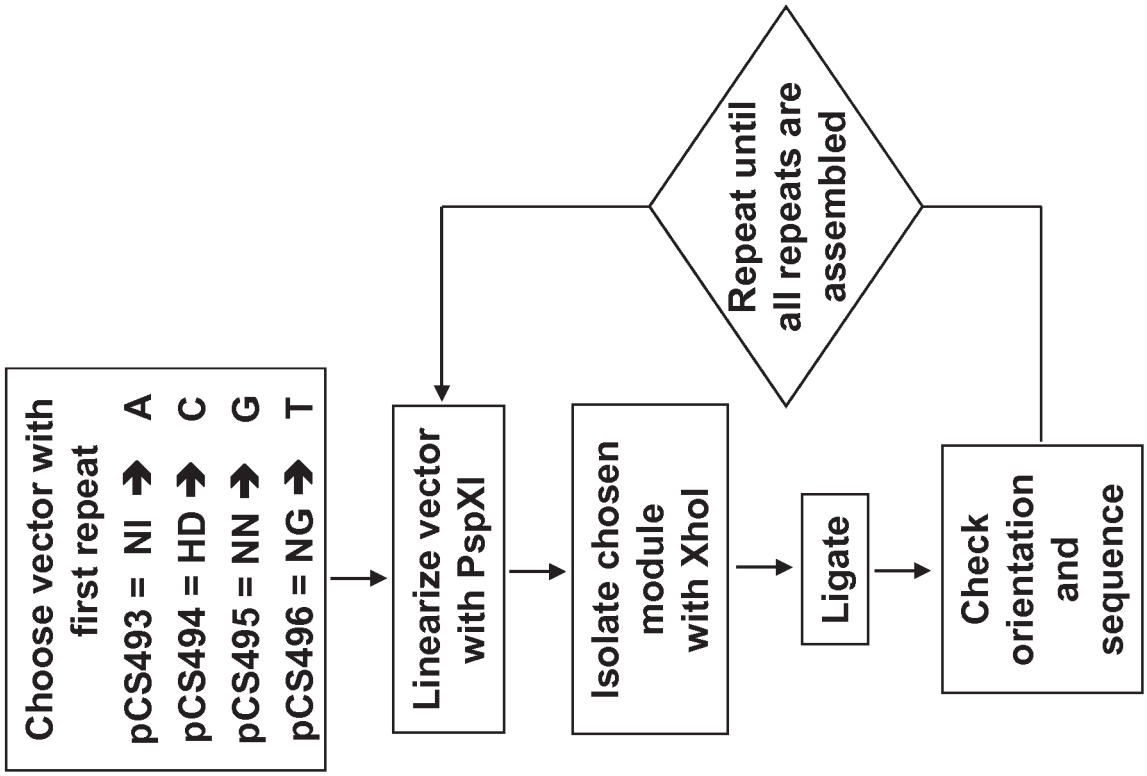

Choose vector with first repeat
pCS493 = NI → A
pCS494 = HD → C
pCS495 = NN → G
pCS496 = NG → T
Linearize vector with PspXI
Isolate chosen module with XhoI
Ligate
Check orientation and sequence
Repeat until all repeats are assembled

Figure 21A

Adh Target DNA	A	T	C	A	A	G	A	T	T	C	T	C	T	T	C	A	C	T (SEQ ID NO:29)
Adh RVDs	NI	NG	HD	NI	NI	NN	NI	NG	NG	HD	NG	HD	NG	NG	HD	NI	HD	NG

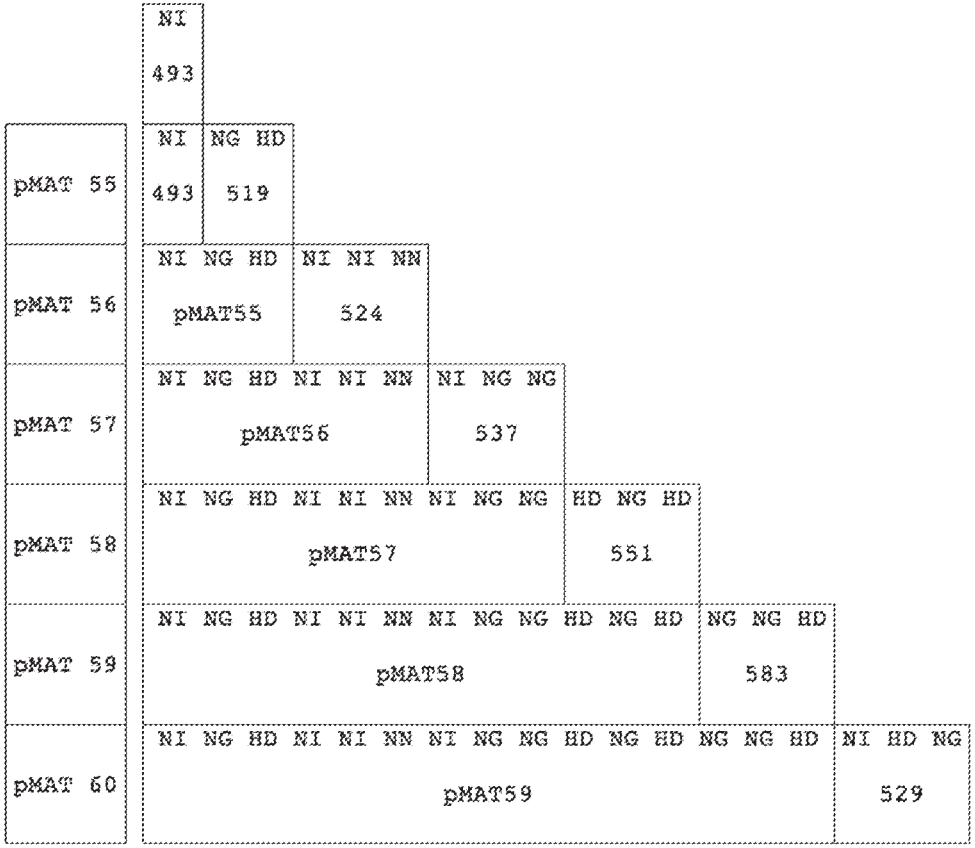


Figure 21B

Adh Target DNA C C C A G A A G T A A A C A T (SEQ ID NO:30)
Adh RVDs HD HD HD HI NN NI NI NN NG NI NI NI HD NI NG

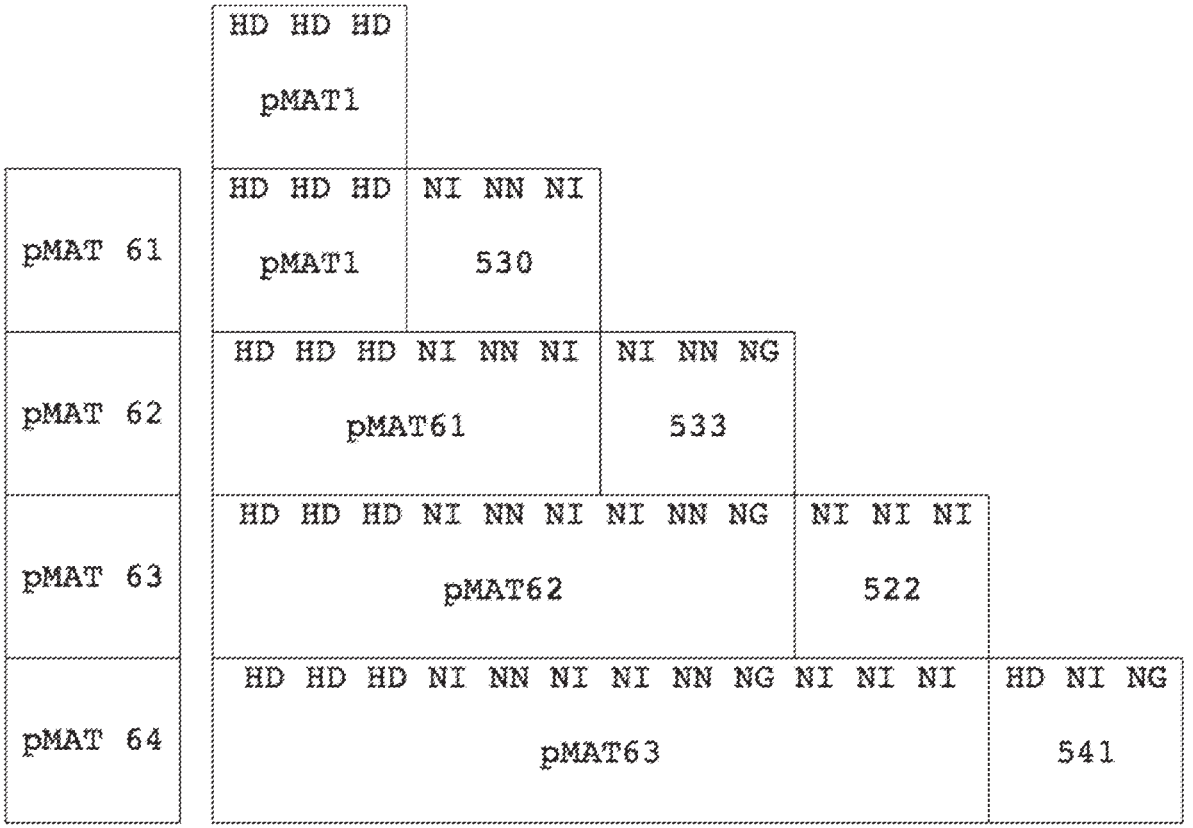


Figure 22

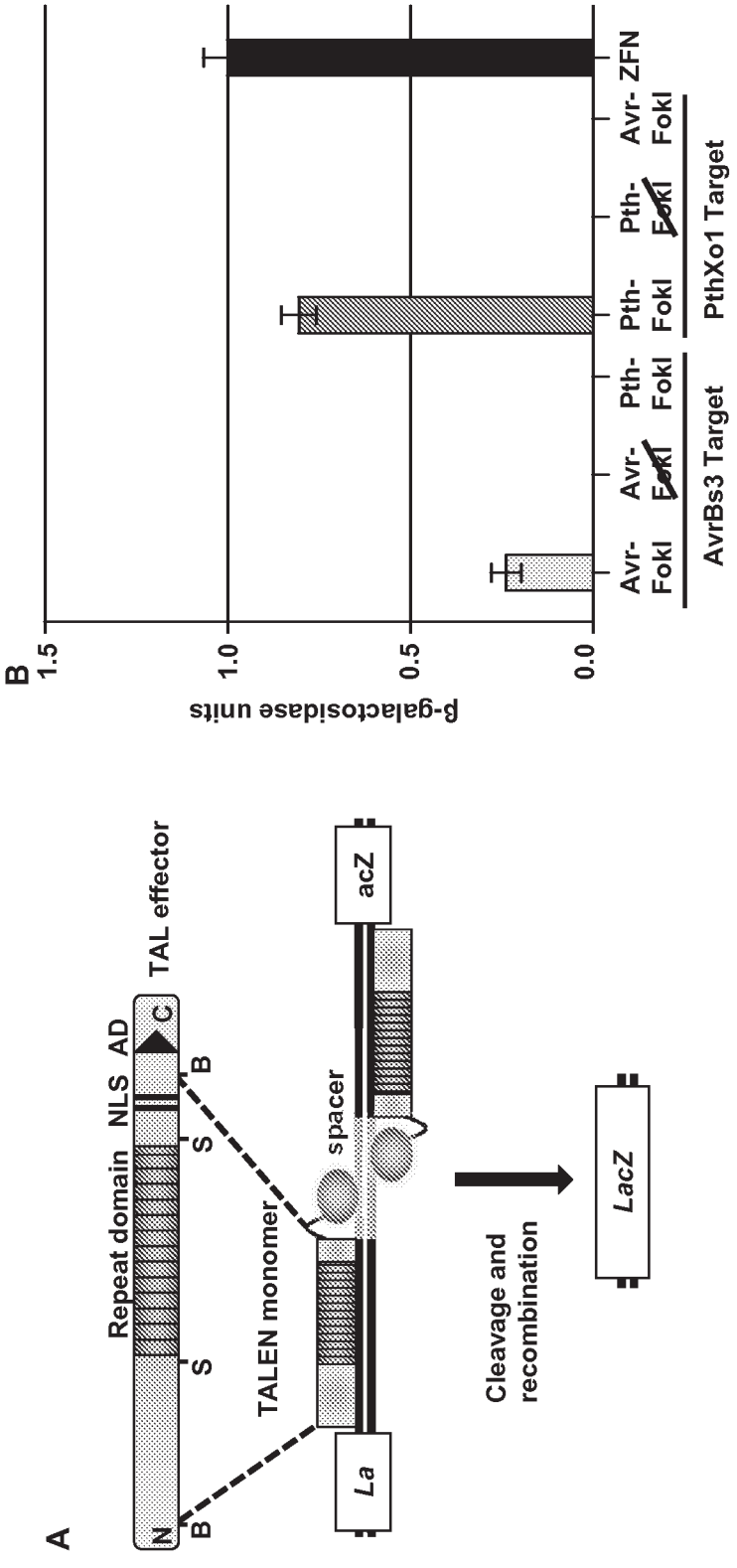

A
TAL effector
Repeat domain
NLS
AD
C
N
B
S
TALEN monomer
spacer
La
acZ
Cleavage and recombination
LacZ
B
β-galactosidase units
1.5
1.0
0.5
0.0
Avr-FokI
Avr-FokI
Pth-FokI
Pth-FokI
Pth-FokI
Avr- ZFN FokI
AvrBs3 Target
PthXo1 Target

Figure 23

MDPIRSRTPSPARELLPGPQPDRVQPTADRGGAPPAGGPLDGLPARRTMSRTRLPSPPAPSPAFSAGSFSDLLRQFDPS
LLDTSLLDSMPAVGTPHTAAAPAECDEVQSGLRAADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSDASPAAQVDLRTL
GYSQQQQEKIKPKVGSTVAQHHEALVGHGFTHAHIVALSRHPAALGTVAVKYQDMIAALPEATHEDIVGVGKQWSGARA
LEALLTVAGELRGPPLQLDTGQLVKIAKRGGVTAVEAVHASRNALTGAPLNLTPAQVVAIASNNGGKQALETVQRLLPVLC
QAHGLTPAQVVAIASHDGGKQALETMQRLLPVLCQAHGLPPDQVVAIASNIGGKQALETVQRLLPVLCQAHGLTPDQVVA
IASHGGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALE
TVQRLLPVLCQAHGLTPDQVVAIASNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASHDGGKQALETVQRLLPVLCQTH
GLTPAQVVAIASHDGGKQALETVQQLLPVLCQAHGLTPDQVVAIASNIGGKQALATVQRLLPVLCQAHGLTPDQVVAIASN
GGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTQVQVVAIASNIGGKQALETVQR
LLPVLCQAHGLTPAQVVAIASHDGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLT
QEQVVAIASNNGGKQALETVQRLLPVLCQAHGLTPDQVVAIASNGGGKQALETVQRLLPVLCQAHGLTPAQVVAIASNIG
GKQALETVQRLLPVLCQDHGLTLAQVVAIASNIGGKQALETVQRLLPVLCQAHGLTQDQVVAIASNIGGKQALETVQRLLP
VLCQDHGLTPDQVVAIASNIGGKQALETVQRLLPVLCQDHGLTLDQVVAIASNGGKQALETVQRLLPVLCQDHGLTPDQV
VAIASNSGGKQALETVQRLLPVLCQDHGLTPNQVVAIASNGGKQALESIVAQLSRPDPALAALTNDHLVALACLGGRPAM
DAVKKGLPHAPELIRRVNRRIGERTSHRVADYAQVVRVLEFFQCHSHPAYAFDEAMTQFGMSRNGLVQLFRRVGVTELE
ARGGTLPPASQRWDRILQASGMKRAKPSPTSAQTPDQASLHAFADSLERDLDAPSPMHEGDQTGASSRKRSRSDRAVT
GPSAQHSFEVRVPEQRDALHLPLSWRVKRPRTRIGGGLPDPGTPIAADLAASSTVMWEQDAAPFAGAADDFPAFNEEEL
AWLMELLPQSGSVGGTI (SEQ ID NO:31)

Figure 24

at**<u>ggatcc</u>**cattcgttcgcgcacgccaagtcctgcccgcgagcttctgcccggaccccaaccggatagggttcagccgactgcagatcgggggggggctccgcctgctggcggcccctgga
tggcttgcccgctcggcggacgatgtcccggacccggctgccatctcccctgcgccctcgcctgcgttctcggcgggcagcttcagcgatctgctccgtcagttcgatccgtcgcttcttgatacat
cgcttcttgattcgatgcctgccgtcggcacgccgcatacagcggctgccccagcagagtgcgatgaggtgcaatcgggtctgcgtgcagccgatgacccgccacccaccgtgcgtgtcgctgt
cactgccgcgcggccgccgcgcgccaagccggccccgcgacggcgtgcggcgcaaccctccgacgcttcgccggccgcgcaggtggatctacgcacgctcggctacagtcagcagcagc
aagagaagatcaaaccgaaggtgggttcgacagtggcgcagcaccacgaggcactggtgggccatgggtttacacacgcgcacatcgttgcgctcagccgacacccggcagcgttaggga
ccgtcgctgtcaagtatcaggacatgatcgcggcgttaccagaggcgacacacgaagacatcgttggtgtcggcaaacagtggtccggcgcacgcgccctggaggccttgctcacggtggcg
ggagagttgagaggtccaccgttacagttggacacaggccaacttgtcaagattgcaaaacgtggcggcgtgaccgcagtggaggcagt**<u>gcatgc</u>**atcgcgcaatgcactgacgggtgccc
ccctgaacctgaccccggcacaggtggtggccatcgccagcaataacggtggcaagcaggcgctggagacggtgcagcggctgttgccggtgctgtgccaggcccatggcctgaccccggc
gcaggtggtggccatcgccagccacgatggcggcaagcaggcactggagacgatgcagcggctgttgccggtgctgtgccaggcccatggcctgcccccggaccaggtggtggccatcgc
cagcaatattggcggcaagcaggcgctggagacggtgcagcggctgttgccggtgctctgccaggcccatggcctgaccccggaccaggtggtggccatcgccagccatggcggcggcaa
gcaggcgctggagacggtgcagcggctgttgccggtgctctgccaggcccatggcctgaccccggaccaggtggtggccatcgccagccacgatggcggcaagcaggcgctggagacggt
gcagcggctgttgccggtgctgtgccaggcccatggcctgaccccggaccaggtggtggccatcgccagcaatggcggcggcaagcaggcgctggagacggtgcagcggctgttgccggtg
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cggcaagcaggcgctagcgacggtgcagcggctgttgccggtgctgtgccaagcccatggcctgaccccggaccaggtggtggccatcgccagcaatggcggcggcaagcaggcgctgg
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atcgccagcaatggcggcaagcaggcgctggagacggtgcagcggctgttgccggtgctgtgccaggaccatggactgaccccggaccaggtcgtggccatcgccagcaatagtggcggc
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gttgcccagttatctcgccctgatccggcgttggccgcgttgaccaacgaccacctcgtcgccttggcctgcctcggcggacgtcctgccatggatgcagtgaaaaagggattgccgcacgcgcc
ggaattgatcagaagagtcaatcgccgtattggcgaacgcacgtcccatcgcgttgccgactacgcgcaagtggttcgcgtgctggagtttttccagtgccactcccacccagcgtacgcatttgat
gaggccatgacgcagttcgggatgagcaggaacgggttggtacagctctttcgcagagtgggcgtcaccgaactcgaagcccgcggtggaacgctcccccagcctcgcagcgttgggacc
gtatcctccaggcatcagggatgaaaagggccaaaccgtcccctacttcagctcaaacaccggatcaggcgtcttt**<u>gcatgc</u>**attcgccgattcgctggagcgtgaccttgatgcgcctagccc
aatgcacgagggagatcagacaggggcaagcagccgtaaacggtcccgatcggatcgtgctgtcaccggcccctccgcacagcactctttcgaggtgcgcgttcccgaacagcgcgatgcg
ctgcatttgcccctcagctggagggtaaaacgcccgcgtaccaggatcgggggcggcctccc**<u>ggatcc</u>**tggtacgcccatcgctgccgacctggcagcgtccagcaccgtgatgtgggaaca
agatgcggccccccttcgcaggggcagcggatgatttcccggcattcaacgaagaggagctcgcatggttgatggagctattgcctcagtcaggctcagtcggagggacgatctga (SEQ ID
NO:32)

Figure 25

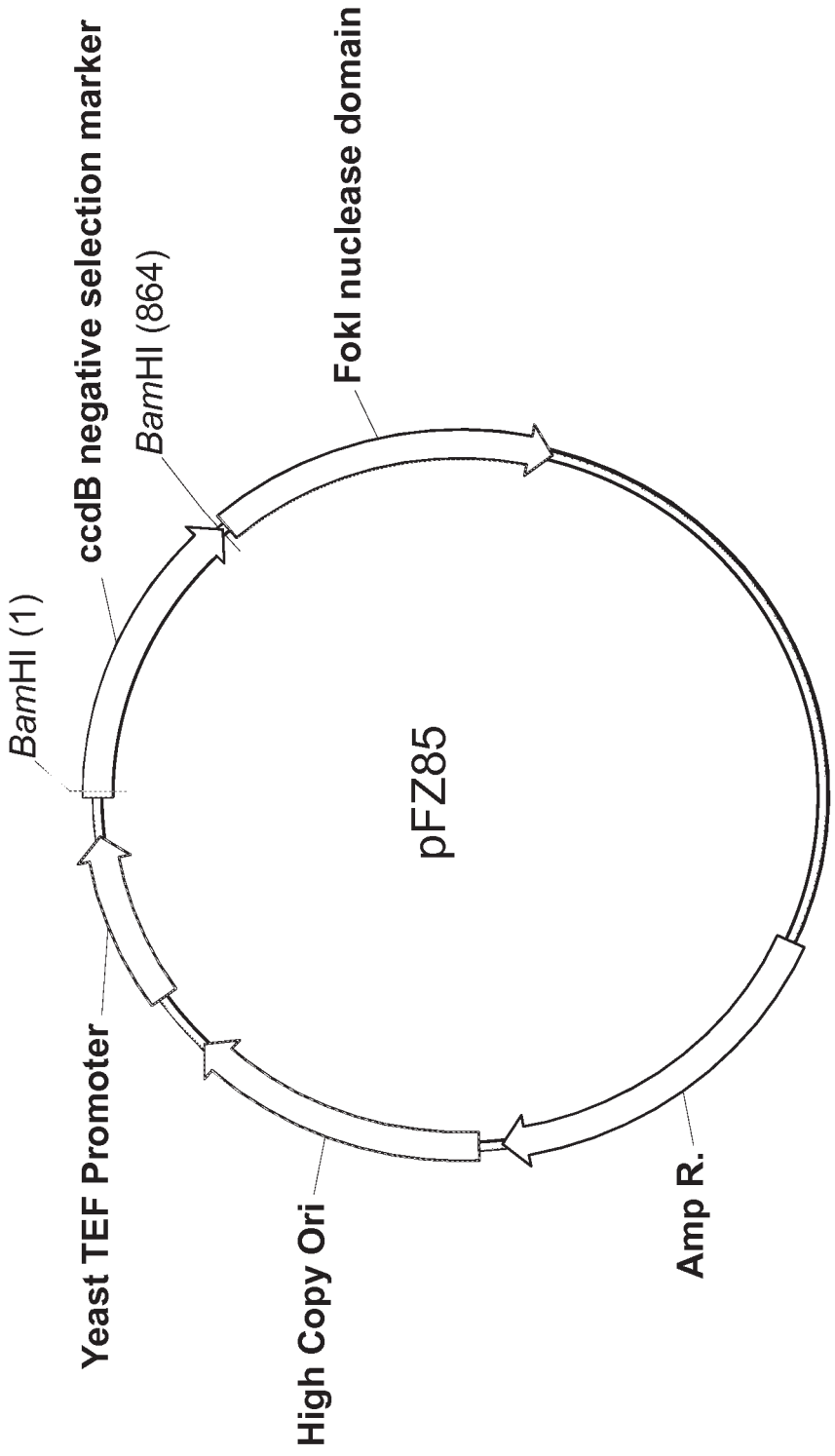

BamHI (1)
ccdB negative selection marker
BamHI (864)
FokI nuclease domain
pFZ85
Yeast TEF Promoter
High Copy Ori
Amp R.

Figure 26

avrBs3_TALEN
MASSPPKKKRKVSWKDASGWSRMHADPIRSRTPS
PARELLPGPQPDGVQPTADRGVSPPAGGPLDGLP
ARRTMSRTRLPSPPAPSPAFSAGSFSDLLRQFDP
SLFNTSLFDSLPPFGAHHTEAATGEWDEVQSGLR
AADAPPPTMRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVKYQDMI
AALPEATHEAIVGVGKQWSGARALEALLTVAGEL
RGPPLQLDTGQLLKIAKRGGVTAVEAVHAWRNAL
TGAPLNLTPEQVVAIASHDGGKQALETVQRLLPV
LCQAHGLTPQQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPQQVVAIASNSGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASNGGGKQALETVQRLLPV
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LCQAHGLTPEQVVAIASNIGGKQALETVQALLPV
LCQAHGLTPEQVVAIASNIGGKQALETVQALLPV
LCQAHGLTPEQVVAIASHDGGKQALETVQRLLPV
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LCQAHGLTPEQVVAIASHDGGKQALETVQRLLPV
LCQAHGLTPEQVVAIASHDGGKQALETVQRLLPV
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LCQAHGLTPQQVVAIASNGGGRPALETVQRLLPV
LCQAHGLTPEQVVAIASHDGGKQALETVQRLLPV
LCQAHGLTPQQVVAIASNGGGRPALESIVAQLSR
PDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APALIKRTNRRIPERTSHRVADHAQVVRVLGFFQ
CHSHPAQAFDDAMTQFGMSRHGLLQLFRRVGVTE
LEARSGTLPPASQRWDRILQASGMKRAKPSPTST
QTPDQASLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQSFEVRVPEQRDALHLP
LSWRVKRPRTSIGGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:33)

Figure 27

pthXo1_TALEN
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNNGGKQALETVQRLLPV
LCQAHGLTPAQVVAIASHDGGKQALETMQRLLPV
LCQAHGLPPDQVVAIASNIGGKQALETVQRLLPV
LCQAHGLTPDQVVAIASHGGGKQALETVQRLLPV
LCQAHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQAHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQAHGLTPDQVVAIASNGGKQALETVQRLLPVL
CQAHGLTPDQVVAIASHDGGKQALETVQRLLPVL
CQTHGLTPAQVVAIASHDGGKQALETVQQLLPVL
CQAHGLTPDQVVAIASNIGGKQALATVQRLLPVL
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CQAHGLTPDQVVAIASNGGGKQALETVQRLLPVL
CQAHGLTQVQVVAIASNIGGKQALETVQRLLPVL
CQAHGLTPAQVVAIASHDGGKQALETVQRLLPVL
CQAHGLTPDQVVAIASNGGGKQALETVQRLLPVL
CQAHGLTQEQVVAIASNNGGKQALETVQRLLPVL
CQAHGLTPDQVVAIASNGGGKQALETVQRLLPVL
CQAHGLTPAQVVAIASNIGGKQALETVQRLLPVL
CQDHGLTLAQVVAIASNIGGKQALETVQRLLPVL
CQAHGLTQDQVVAIASNIGGKQALETVQRLLPVL
CQDHGLTPDQVVAIASNIGGKQALETVQRLLPVL
CQDHGLTLDQVVAIASNGGKQALETVQRLLPVLC
QDHGLTPDQVVAIASNSGGKQALETVQRLLPVLC
QDHGLTPNQVVAIASNGGKQALESIVAQLSRPDP
ALAALTNDHLVALACLGGRPAMDAVKKGLPHAPE
LIRRVNRRIGERTSHRVADYAQVVRVLEFFQCHS
HPAYAFDEAMTQFGMSRNGLVQLFRRVGVTELEA
RGGTLPPASQRWDRILQASGMKRAKPSPTSAQTP
DQASLHAFADSLERDLDAPSPMHEGDQTRASSRK
RSRSDRAVTGPSAQQAVEVRVPEQRDALHLPLSW
RVKRPRTRIWGGLPDPISRSQLVKSELEEKKSEL
RHKLKYVPHEYIELIEIARNSTQDRILEMKVMEF
FMKVYGYRGKHLGGSRKPDGAIYTVGSPIDYGVI
VDTKAYSGGYNLPIGQADEMQRYVEENQTRNKHI
NPNEWWKVYPSSVTEFKFLFVSGHFKGNYKAQLT
RLNHITNCNGAVLSVEELLIGGEMIKAGTLTLEE
VRRKFNNGEINF (SEQ ID NO:34)

Figure 28

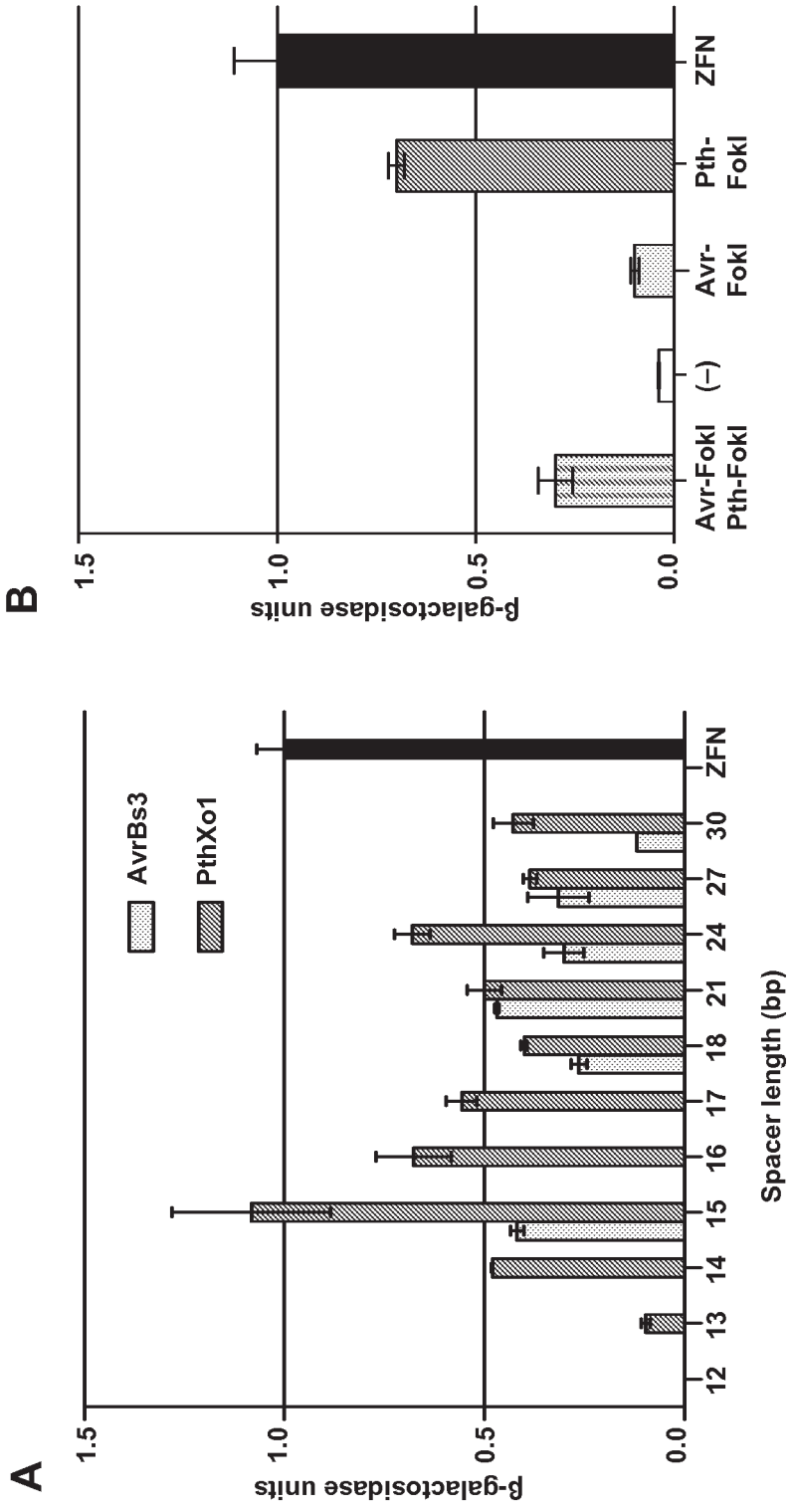

A
B
β-galactosidase units
1.5
1.0
0.5
0.0
AvrBs3
PthXo1
12
13
14
15
16
17
18
21
24
27
30
ZFN
Spacer length (bp)
Avr-FokI
Pth-FokI
(–)
Avr-FokI
Pth-FokI
ZFN

Figure 29A

Custom TALEN	1	2	3	4	5	6	7	8	9	10	11	12	13
***ADH*1-360-12**	NI A	NG T	HD C	NI A	NI A	NN G	NI A	NG T	NG T	HD C	NG T	HD C	
***ADH1*-408-12r**	HD C	HD C	HD C	NI A	NN G	NI A	NI A	NN G	NG T	NI A	NI A	NI A	
***ADH1*-928-12**	HD C	HD C	NN G	NN G	NI A	NG T	NN G	HD C	NG T	HD C	HD C	NG T	
***ADH1*-975-12r**	NI A	NN G	NI A	HD C	NI A	NI A	NI A	HD C	HD C	NI A	HD C	NI A	
***gridlock*-2356-13r**	NI A	HD C	HD C	HD C	HD C	NG T	HD C	NG T	HD C	HD C	NN G	HD C	NG T

NI = A HD = C NN = G NG = T

Figure 29B

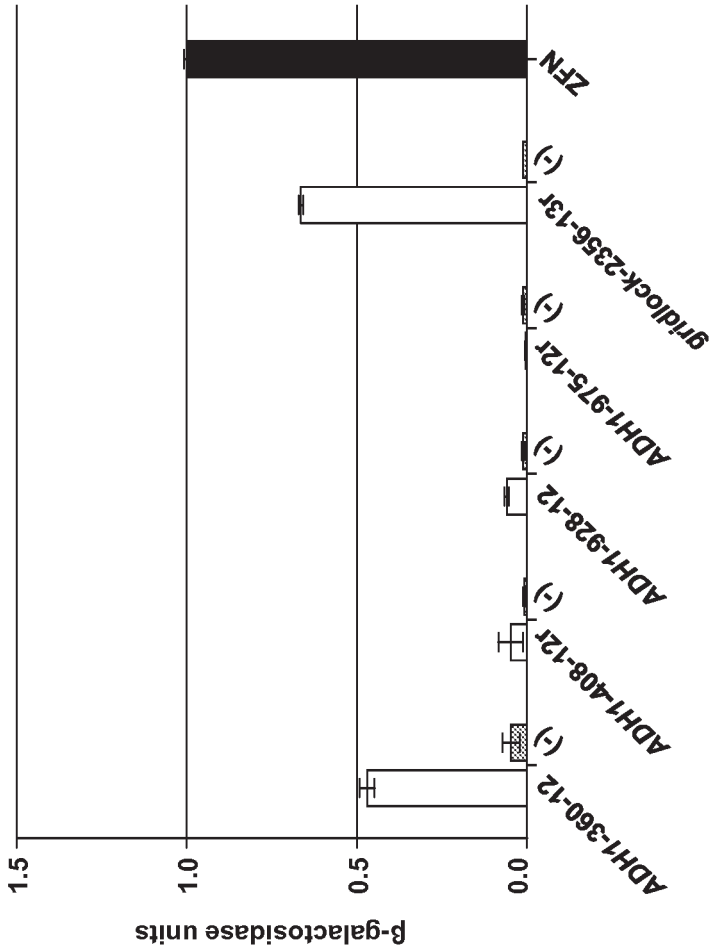
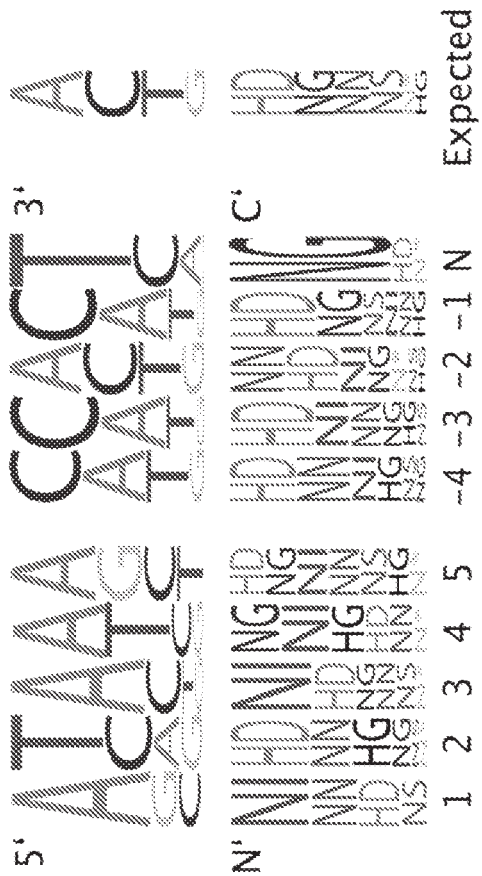

ZEN
(-)
gridlock-2356-13r
(-)
ADH1-975-12r
(-)
ADH1-928-12
(-)
ADH1-408-12r
(-)
ADH1-360-12
1.5
1.0
0.5
0.0
β-galactosidase units

Figure 30



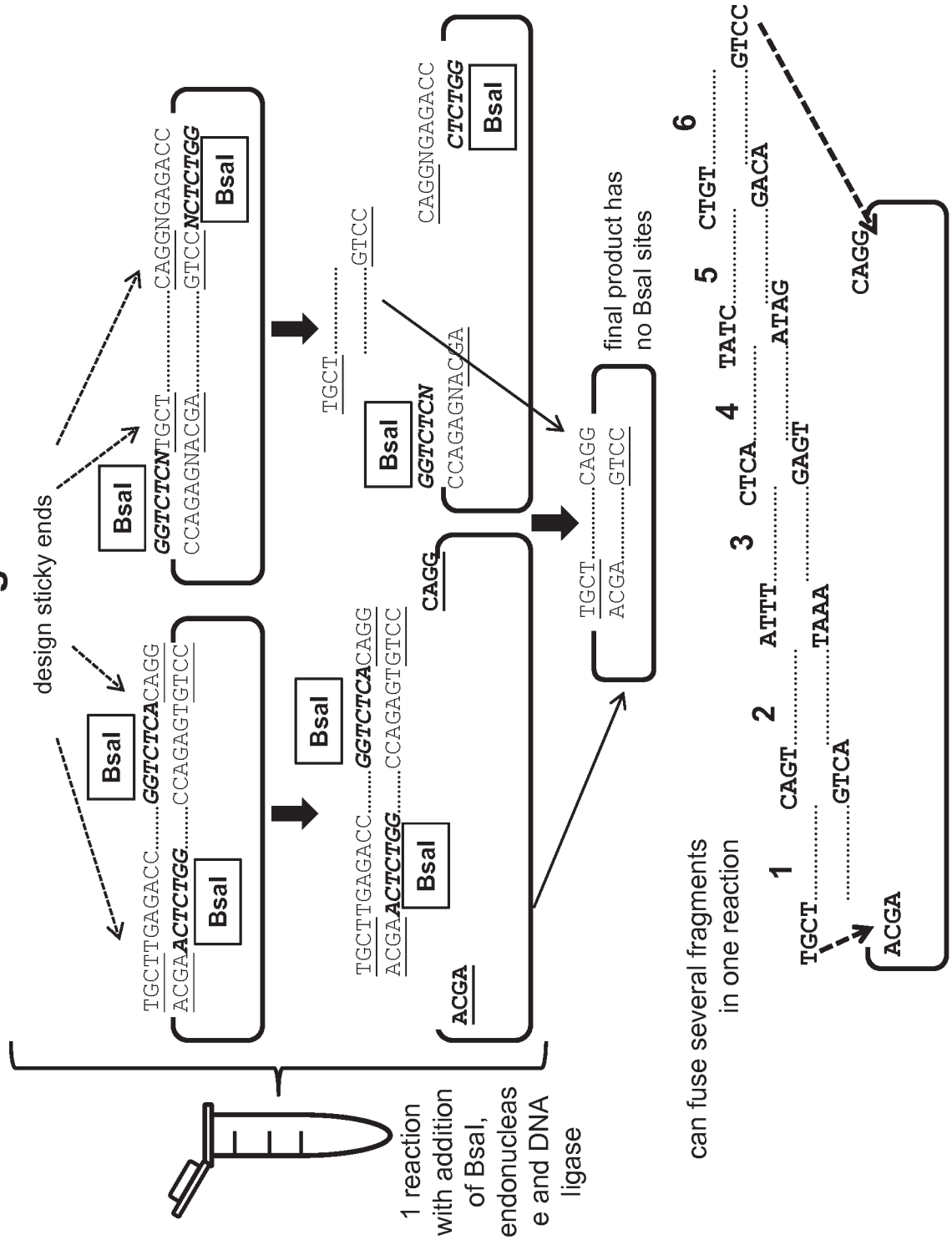

Figure 31
design sticky ends
BsaI
BsaI
BsaI
BsaI
BsaI
BsaI
TGCTTGAGACC.....GGTCTCACAGG
ACGAACTCTGG.....CCAGAGTGTCC
GGTCTCNTGCT.....CAGGNGAGACC
CCAGAGNACGA.....GTCCNCTCTGG
TGCTTGAGACC.....GGTCTCACAGG
ACGAACTCTGG.....CCAGAGTGTCC
TGCT.....GTCC
GGTCTCN
CCAGAGNACGA
CAGGNGAGACC
CTCTGG
CAGG
ACGA
TGCT.....CAGG
ACGA.....GTCC
final product has no BsaI sites
1 reaction with addition of BsaI, endonuclease and DNA ligase
can fuse several fragments in one reaction
1 TGCT.....
2 CAGT.....
3 ATTT.....
4 CTCA.....
5 TATC.....
6 CTGT.....
GTCA
TAAA
GAGT
ATAG
GACA
GTCC
ACGA
CAGG

Figure 32A

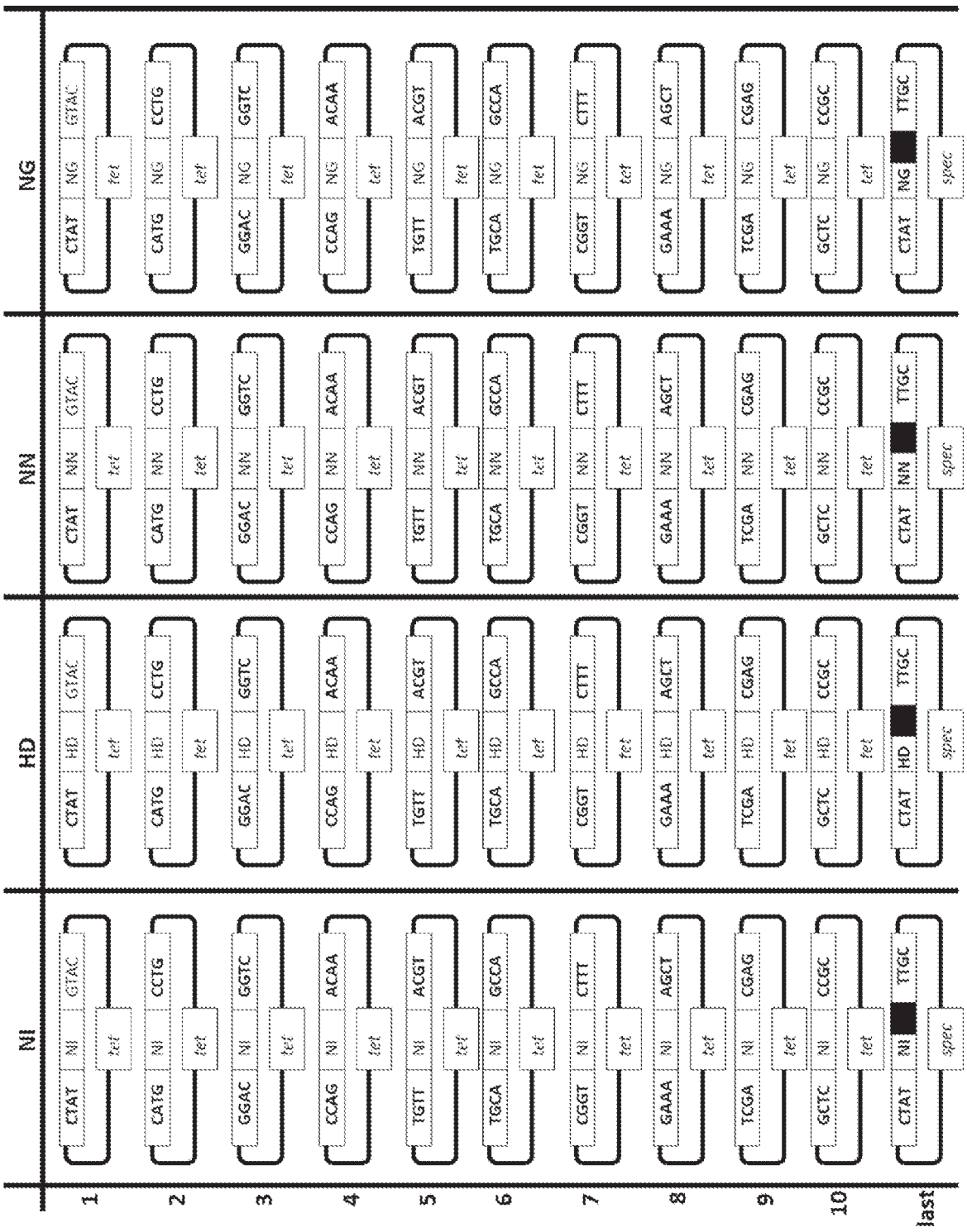

NI
HD
NN
NG
1
2
3
4
5
6
7
8
9
10
last
CTAT
CATG
GGAC
CCAG
TGTT
TGCA
CGGT
GAAA
TCGA
GCTC
NI
HD
NN
NG
GTAC
CCTG
GGTC
ACAA
ACGT
GCCA
CTTT
AGCT
CGAG
CCGC
TTGC
tet
spec

Figure 32B

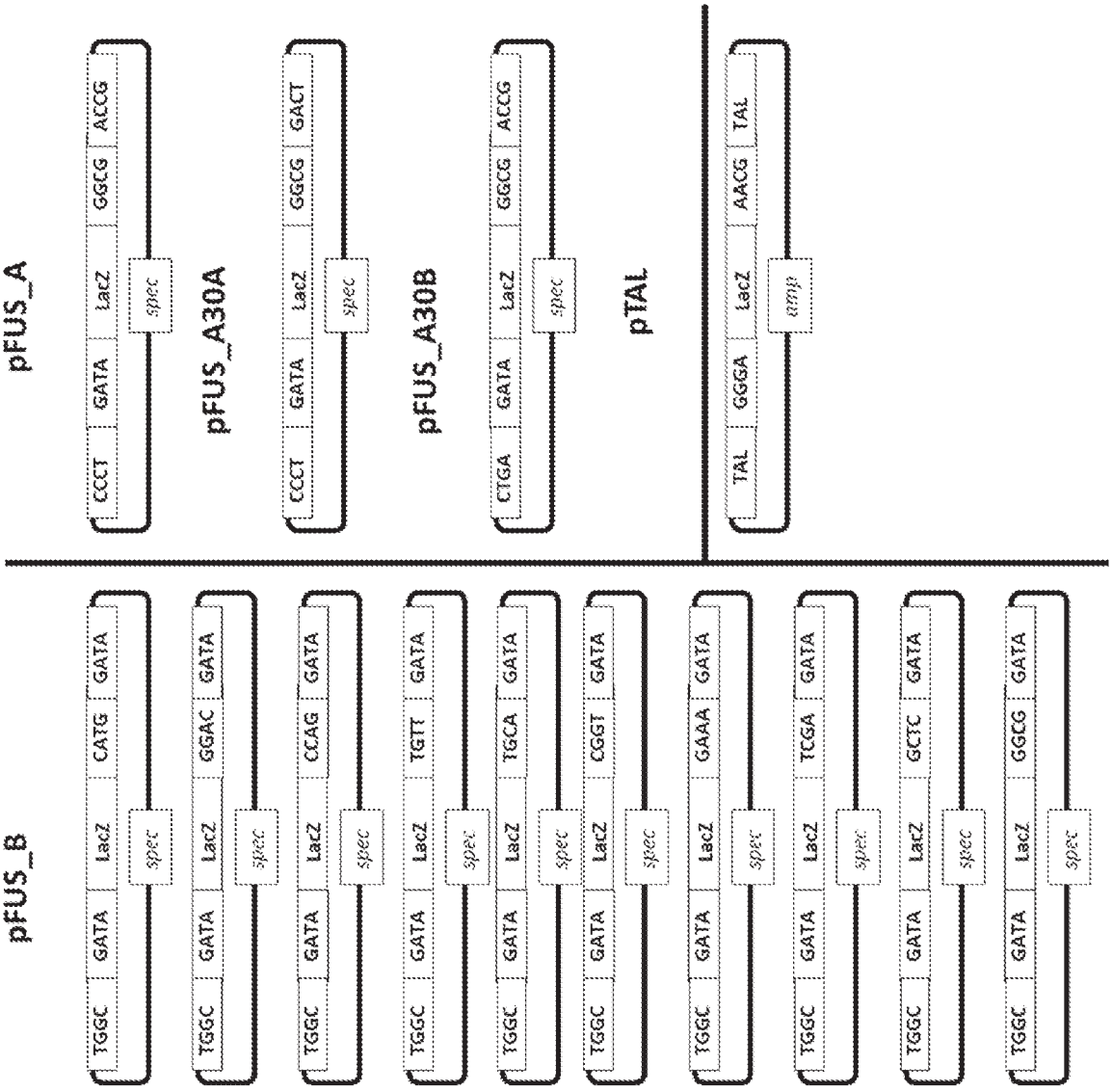

pFUS_A
pFUS_A30A
pFUS_A30B
pTAL
pFUS_B
TGGC GATA LacZ CATG GATA spec
TGGC GATA LacZ GGAC GATA spec
TGGC GATA LacZ CCAG GATA spec
TGGC GATA LacZ TGTT GATA spec
TGGC GATA LacZ TGCA GATA spec
TGGC GATA LacZ CGGT GATA spec
TGGC GATA LacZ GAAA GATA spec
TGGC GATA LacZ TCGA GATA spec
TGGC GATA LacZ GCTC GATA spec
TGGC GATA LacZ GGCG GATA spec
CCCT GATA LacZ GGCG ACCG spec
CCCT GATA LacZ GGCG GACT spec
CTGA GATA LacZ GGCG ACCG spec
TAL GGGA LacZ AACG TAL amp

Figure 33

TALEN sequence: NI NN HD HD HD NI NI NG HD NG HD NI NI NG HD NG

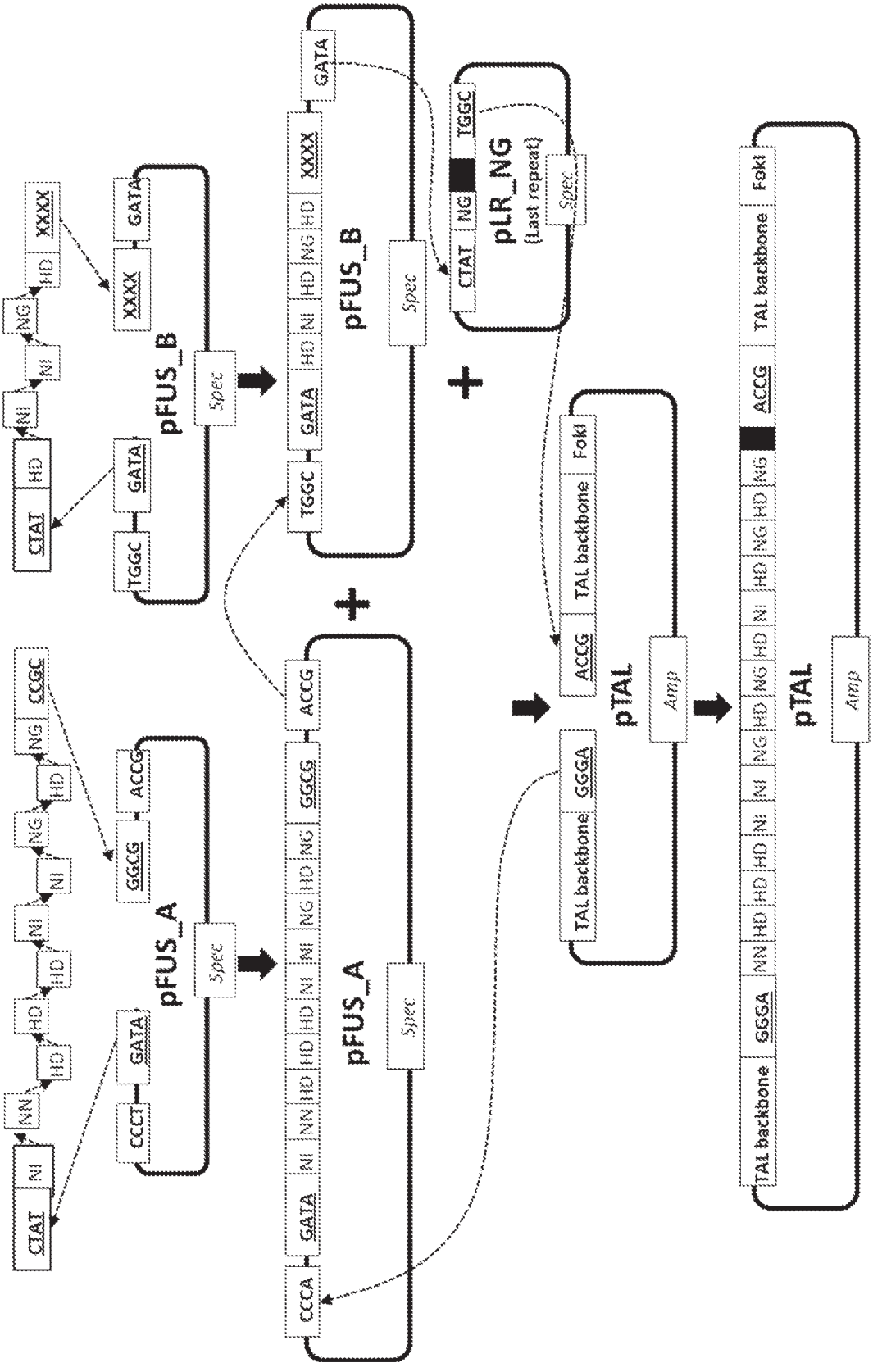


Figure 34A

telomerase-TALEN124_9RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:35)

Figure 34B

gridlock-TALEN105_10RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:36)

Figure 34C

adh1-TALEN58_12RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:37)

Figure 34D

adh1-TALEN63_12RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:38)

Figure 34E

adh1-TALEN68_12RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:39)

Figure 34F

adh1-TALEN73_12RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF(SEQ ID NO:40)

Figure 34G

adh1-TALEN89_12RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:41)

Figure 34H

gridlock-TALEN106_13RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:42)

Figure 34I

adh1-TALEN64_15RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
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LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:43)

Figure 34J

adh1-TALEN69_15RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
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LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:44)

Figure 34K

adh1-TALEN74_15RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:45)

Figure 34L

tt4-TALEN90_15RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:46)

Figure 34M

telomerase-TALEN121_15RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:47)

Figure 34N

telomerase-TALEN126_15RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:48)

Figure 34O

gridlock-TALEN107_16RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:49)

Figure 34P

gridlock-TALEN117_16RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
PDPALAALTNDHLVALACLGGRPAMDAVKKGLPH
APELIRRVNRRIGERTSHRVADYAQVVRVLEFFQ
CHSHPAYAFDEAMTQFGMSRNGLVQLFRRVGVTE
LEARGGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQASLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:50)

Figure 34Q

telomerase-TALEN131_16RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF(SEQ ID NO:51)

Figure 34R

telomerase-TALEN136_17RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NDO:52)

Figure 34S

adh1-TALEN60_18RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIANNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
RDPALAALTNDHLVALACLGGRPALDAVKKGLPH
APEFIRRVNRRIAERTSHRVADYAHVVRVLEFFQ
CHSHPAHAFDEAMTQFGMSRHGLVQLFRRVGVTE
FEARYGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQTSLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:53)

Figure 34T

tt4-TALEN85_18RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
PDPALAALTNDHLVALACLGGRPAMDAVKKGLPH
APELIRRVNRRIGERTSHRVADYAQVVRVLEFFQ
CHSHPAYAFDEAMTQFGMSRNGLVQLFRRVGVTE
LEARGGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQASLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:54)

Figure 34U

gridlock-TALEN102_18RVDs
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALESIVAQLSR
PDPALAALTNDHLVALACLGGRPAMDAVKKGLPH
APELIRRVNRRIGERTSHRVADYAQVVRVLEFFQ
CHSHPAYAFDEAMTQFGMSRNGLVQLFRRVGVTE
LEARGGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQASLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:55)

Figure 35

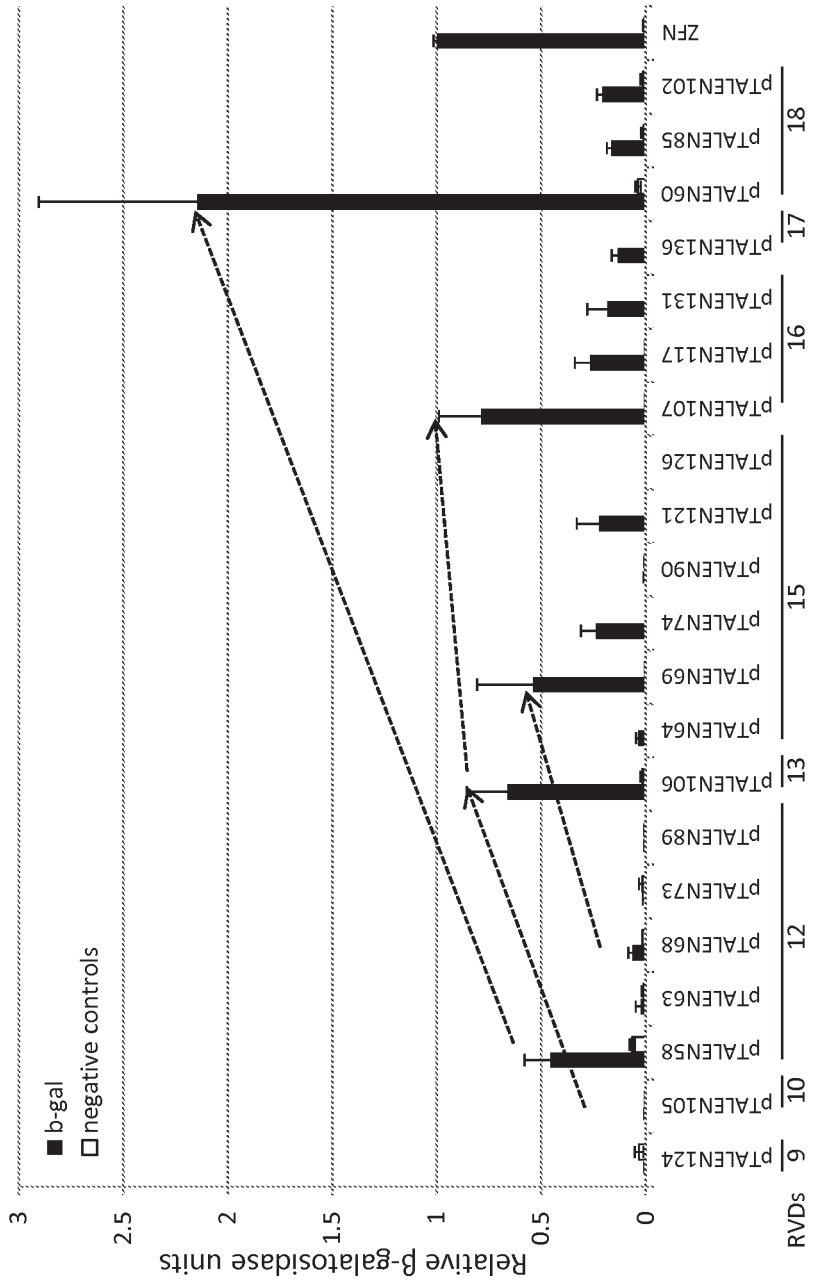

Relative β-galatosidase units
3
2.5
2
1.5
1
0.5
0
■ b-gal
□ negative controls
RVDs
9
10
12
13
15
16
17
18
pTALEN124
pTALEN105
pTALEN58
pTALEN63
pTALEN68
pTALEN73
pTALEN89
pTALEN106
pTALEN64
pTALEN69
pTALEN74
pTALEN90
pTALEN121
pTALEN126
pTALEN107
pTALEN117
pTALEN131
pTALEN136
pTALEN60
pTALEN85
pTALEN102
ZFN

Figure 36

A

pTALEN 60 target pTALEN 64 target

Adh1 target T**ATCAAGATTCTCTTCAC**TTCTCTCTGTCACACCG**ATGTTTACTTCTGGG**A (SEQ ID NO:56)

pTALEN 69 target pTALEN 74 target

Adh1 target T**CCGGATGCTCCTCTT**GACAAGGTCTGTATTGTC**AGTTGTGGTTTGTCT**A (SEQ ID NO:57)

B

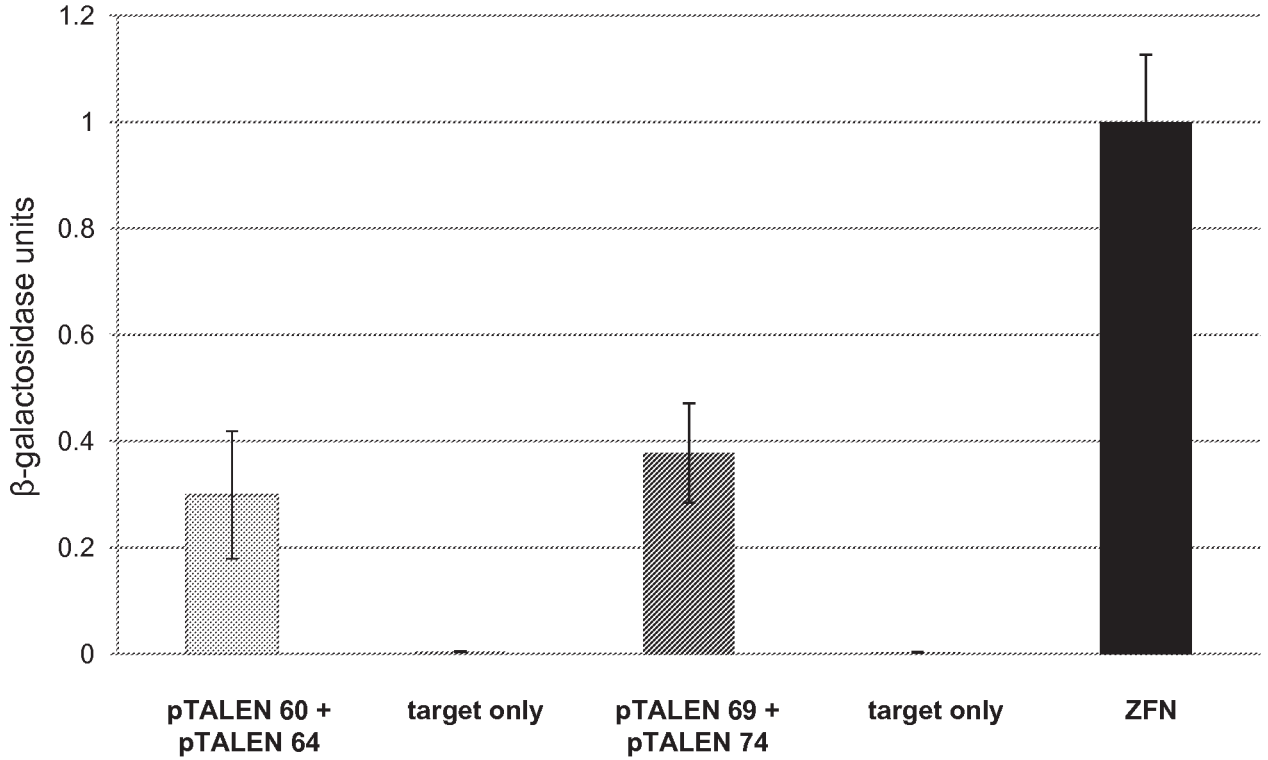


Figure 37

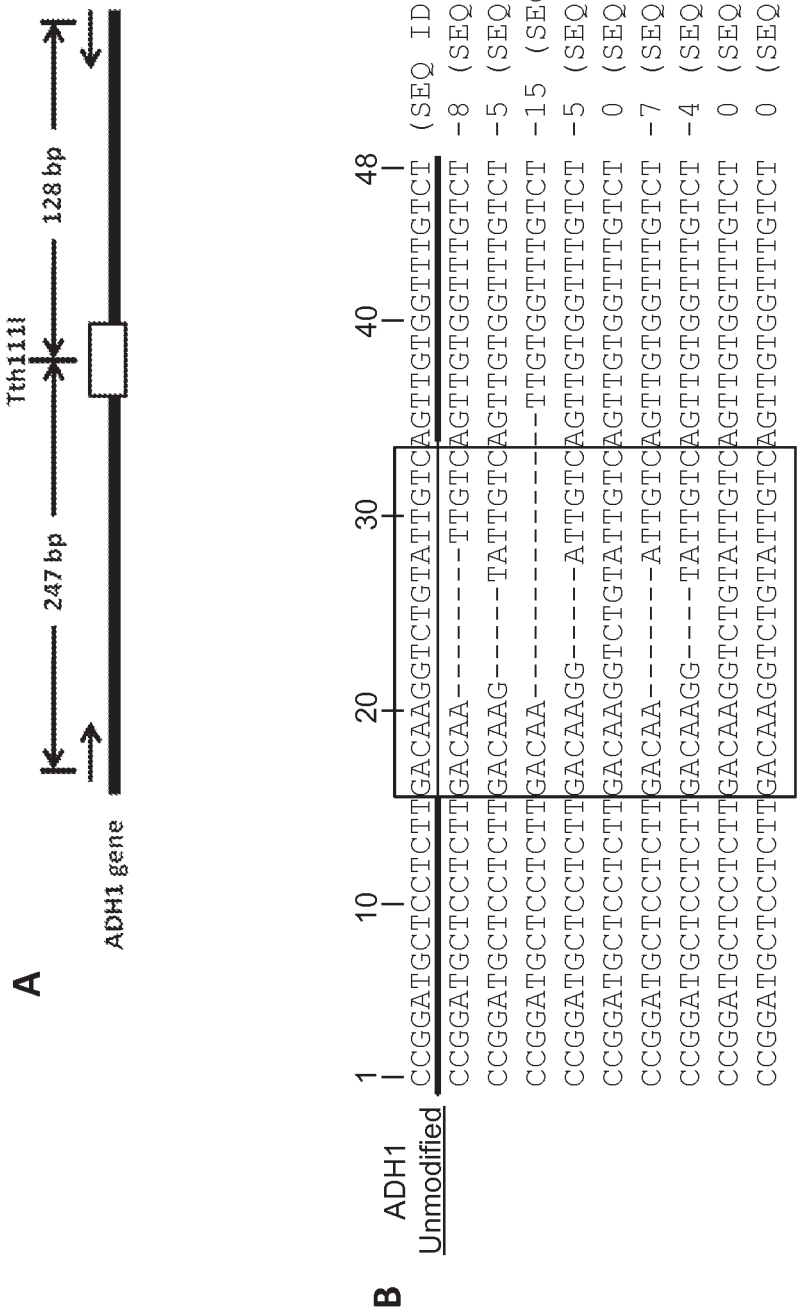

A
Tth111I
247 bp
128 bp
ADH1 gene
B
ADH1
Unmodified
1
10
20
30
40
48
CCGGATGCTCCTCTTGACAAGGTCTGTATTGTCAGTTGTGGTTTGTCT (SEQ ID NO:58)
CCGGATGCTCCTCTTGACAA----------TTGTCAGTTGTGGTTTGTCT -8 (SEQ ID NO:59
CCGGATGCTCCTCTTGACAAG----------TATTGTCAGTTGTGGTTTGTCT -5 (SEQ ID NO:60)
CCGGATGCTCCTCTTGACAA----------TTGTGGTTTGTCT -15 (SEQ ID NO:61)
CCGGATGCTCCTCTTGACAAGG---------ATTGTCAGTTGTGGTTTGTCT -5 (SEQ ID NO:62)
CCGGATGCTCCTCTTGACAAGGTCTGTATTGTCAGTTGTGGTTTGTCT 0 (SEQ ID NO:58)
CCGGATGCTCCTCTTGACAA----------ATTGTCAGTTGTGGTTTGTCT -7 (SEQ ID NO:63)
CCGGATGCTCCTCTTGACAAGG---------TATTGTCAGTTGTGGTTTGTCT -4 (SEQ ID NO:64)
CCGGATGCTCCTCTTGACAAGGTCTGTATTGTCAGTTGTGGTTTGTCT 0 (SEQ ID NO:58)
CCGGATGCTCCTCTTGACAAGGTCTGTATTGTCAGTTGTGGTTTGTCT 0 (SEQ ID NO:58)

Figure 38

A

```
AvrHah1   LDTGQLFKIAKRGGVTAVEAVHAWRNALTGAPLN (SEQ ID NO:65)
AvrBs3    LDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLN (SEQ ID NO:66)
PthXo1    LDTGQLVKIAKRGGVTAVEAVHASRNALTGAPLN (SEQ ID NO:67)
PthA      LDTGQLLKIAKRGGVTAVEAVHAWRNALTGAPLN (SEQ ID NO:68)
Tal1C     LDTGQLVKIAKRGGVTAMEAVHASRNALTGAPLN (SEQ ID NO:69)
```

B

```
                HHHHHHHHH      HHHHHHHHHHHHHH
"0th" repeat    LDTGQLVKIA*KRGGVTAMEAVHASRNALTGAPLN (SEQ ID NO:70)
                |    | | ||    ||   | | |       |   |
1st repeat      LTPAQVVAIASNNGGKQALETVQRLLPVLCQAHG (SEQ ID NO:71)
                   HEEEEEE      HHHHHHHHHHHHHHH
```

Figure 39

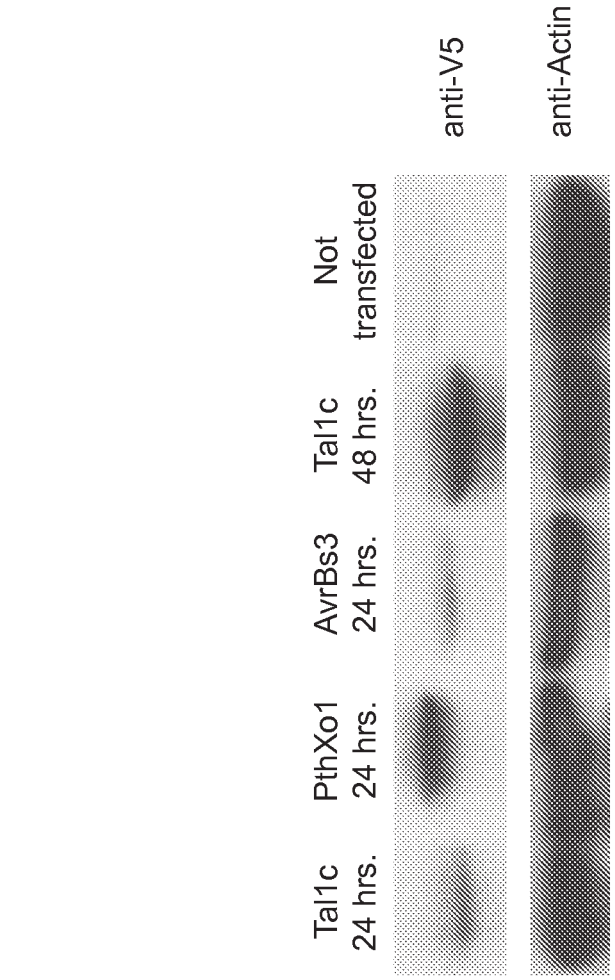

Tal1c 24 hrs.
PthXo1 24 hrs.
AvrBs3 24 hrs.
Tal1c 48 hrs.
Not transfected
anti-V5
anti-Actin

Figure 40A

HPRT-3254-17
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASNNGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
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LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
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LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
PDPALAALTNDHLVALACLGGRPAMDAVKKGLPH
APELIRRVNRRIGERTSHRVADYAQVVRVLEFFQ
CHSHPAYAFDEAMTQFGMSRNGLVQLFRRVGVTE
LEARGGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQASLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:72)

Figure 40B

HPRT-3286-20r
MASSPPKKKRKVSWKDASGWSRMHADPIRPRRPS
PARELLPGPQPDRVQPTADRGVSAPAGSPLDGLP
ARRTVSRTRLPSPPAPSPAFSAGSFSDLLRPFDP
SLLDTSLLDSMPAVGTPHTAAAPAEWDEAQSALR
AADDPPPTVRVAVTAARPPRAKPAPRRRAAQPSD
ASPAAQVDLRTLGYSQQQQEKIKPKVRSTVAQHH
EALVGHGFTHAHIVALSQHPAALGTVAVTYQHII
TALPEATHEDIVGVGKQWSGARALEALLTDAGEL
RGPPLQLDTGQLVKIAKRGGVTAMEAVHASRNAL
TGAPLNLTPAQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASHDGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNIGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNGGGKQALETVQRLLPV
LCQDHGLTPDQVVAIASNNGGKQALETVQRLLPV
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LCQDHGLTPDQVVAIASNGGGKQALESIVAQLSR
PDPALAALTNDHLVALACLGGRPAMDAVKKGLPH
APELIRRVNRRIGERTSHRVADYAQVVRVLEFFQ
CHSHPAYAFDEAMTQFGMSRNGLVQLFRRVGVTE
LEARGGTLPPASQRWDRILQASGMKRAKPSPTSA
QTPDQASLHAFADSLERDLDAPSPMHEGDQTRAS
SRKRSRSDRAVTGPSAQQAVEVRVPEQRDALHLP
LSWRVKRPRTRIWGGLPDPISRSQLVKSELEEKK
SELRHKLKYVPHEYIELIEIARNSTQDRILEMKV
MEFFMKVYGYRGKHLGGSRKPDGAIYTVGSPIDY
GVIVDTKAYSGGYNLPIGQADEMQRYVEENQTRN
KHINPNEWWKVYPSSVTEFKFLFVSGHFKGNYKA
QLTRLNHITNCNGAVLSVEELLIGGEMIKAGTLT
LEEVRRKFNNGEINF (SEQ ID NO:73)

Figure 41A

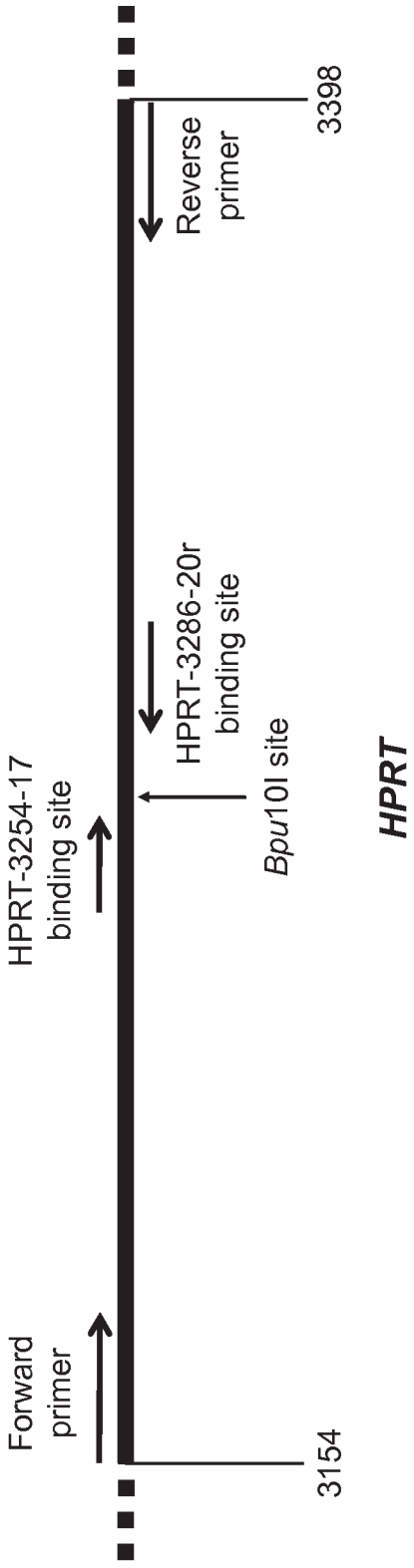

Forward primer
HPRT-3254-17 binding site
Bpu10I site
HPRT-3286-20r binding site
Reverse primer
3154
3398
HPRT

Figure 41B

