



## Table

Table S1. Primers for construction of pCAGO

Name	Sequence
(pkd46)_forward	CCAGGTCTCACCATGGATATTAATACTGAAACTGAGATCAAGC
(pkd46)_reverse	CCAGGTCTCAATTTTTTATAACCTCCTTAGAGCTCGAATCCC
(cas9)_forward	CCAGGTCTCAAAATGGATAAGAAATACTCAATAGGCTTAGATATCGGC
(cas9)_N20A_reverse	CCAGGTCTCATTTCGGTTCGATGGACTAGCTAAGATCTGACTCCATAACAGAGTACTCGCC
(N20B)_gRNA_forward	CCAGGTCTCACGAAGTAGTTTTAGAGCTAGAAAATAGCAAGTTAAAATAAGGC
(gRNA)_reverse	CCAGGTCTCAGGAGAGAACATACTGGCTAAATACGGAAGG
(ptrc)_forward	CCAGGTCTCACTCCATACGATATAAGTTGTAATTCTCATGTTG
(ptrc)_reverse	CCAGGTCTCAATGGTATATCTCCTTGAATTCCATGGTC

Table S2. Primers used for analysis of chromosomal areas most similar to the selected N20PAM<sup>a</sup>

Primer Name	Sequence
N1G_F	GATTGCGCTGTCAAAC
N1G_R	ATCACCGCAAAGTGAAG
N2G_F	GGCGGCATTTCGTATCGAAGAC
N2G_R	TGGCCGATGGCATCAAAGG
N3G_F	CACCAGCATTGTCGGTTAC
N3G_R	AAGCCGTGAAGGAGTGAAAG
N4G_F	CGCGTTAATCACGTCTCTATCG
N4G_R	TTTGATCTGGAGGCGCTAAAGG
N5G_F	TTCACGGAATGCGGCAACC
N5G_R	AGCGAACGAAGCGGAACTG
N6G_F	GGAACACCAGGCGATGATGTC
N6G_R	GCACCACCTGCTGTATGATCC
N7G_F	ATGGCAGGCCAGAATGAC
N7G_R	CTGCTGCTGCAACTCAC
N8G_F	AAACCCGTCTGGTTCATACCC
N8G_R	GCCCTTCAACCAGAATATAAGC
N9G_F	GGATGATGTTGGCTTCAG
N9G_R	TACGGCTTCGATATCACC

<sup>a</sup> : Chromosomal areas most similar to selected N20PAM were predicted by Cas-OFFinder

Table S3. N20PAM similar areas<sup>a</sup> sequences and analysis result after Cas9/gRNA expression

number	similar DNA sequences	Positions <sup>b</sup>	Mismatches	Positive colonies <sup>c</sup> /Tested	
				pCAGO exp <sup>d</sup>	Pm4 exp <sup>e</sup>
1	cAGaCCAcCaAACCcAAGTgCGG	29456	6	10/10	10/10
2	TAGTtCtgCaAAaCGAAGTgGGG	608522	6	10/10	10/10
3	TgGcCaATCaAACaGAAaTATGG	507357	6	10/10	10/10

4	TAAAACCATCtAcCgGAAtTACGG	1067543	6	10/10	10/10
5	TtcgCCATtGAAcTGAACtAAAGG	1398303	6	10/10	10/10
6	TgGTtCATCaAACCGcgGaAGGG	1580707	6	10/10	10/10
7	TAtTaCAcCGAtCCGAAGaATGG	2247074	5	10/10	10/10
8	gAGTctATCtAtCtGAACtATGG	3700191	6	10/10	10/10
9	TAtgtaATCaAACCGAAaTACGG	4619275	6	10/10	10/10

<sup>a</sup> : Chromosomal areas most similar to selected N20PAM were predicted by Cas-OFFinder

<sup>b</sup> : Genome positions of *Escherichia coli* (K-12, MG1655) predicted by Cas-OFFinder

<sup>c</sup> : Strains with wild type *E. coli* MG1655 sequeunce identified with PCR amplified and DNA sequencing

<sup>d</sup> : N20PAM Similar areas were PCR amplified and sequenced to check off-target possibility after expression pCAGO

<sup>e</sup> : N20PAM Similar areas were PCR amplified and sequenced to check off-target possibility after editing editing experiment

pm4

Table S4 Primers for construction of editing cassettes and colony PCR identification

Primers	Sequence	Characteristics
N20PAM_Cm_F	<u>TTCATGTGCAGTCCATC</u> ACTGGAGCACCTCAAAAACACCA	
N20PAM_Cm_R	CAACGTCATCTCGTTCTCCGTTATTTGTTAACTGTAAATTGTCCTTACTTCGGTTCGATGGACTATTACGCCCGC CCTGCCA	Selection marker - N20PAM part amplification
Large_L500F	CCACGGCTGTGATTAGAAC	
Large_ReN20PAM2_L500R	CCAGGTCTCetggTACCCGCCGAAGAAATTC	
ReN20PAM2BsaI_F	CCAGGTCTCAaccgTTCATGTGCAGTCCATC	
ReN20PAM2_large_BsaI_R	CCAGGTCTCAaggeCAACGTCATCTCGTTCTC	
large_L10K_BSAI_R500F	CCAGGTCTCAgect acacgccggtgaacggcgtagatctcagaaaacgctcGCGATTTCGTTGAGTACAG	
large_L30K_BSAI_R500F	CCAGGTCTCAgect tatatgctgtgatcgaagaacagtttgctggcgctgaGCGATTTCGTTGAGTACAG	
large_L70K_BSAI_R500F	CCAGGTCTCAgect ttacgatgaagcaccgctccggcagtggtgatggcctcaGCGATTTCGTTGAGTACAG	
large_L100K_BSAI_R500F	CCAGGTCTCAgect ccaaagcagaatccaagctaatcctgatgctggcagGCGATTTCGTTGAGTACAG	Large genome deletion
large_R500R	TGCGCTATCGAAAGTGAG	
Large_genome_R	TAGATGCGCCAGGATGCAG	
Large_genome_10k_F	ACCACCGAAGGGTATACG	
Large_genome_30k_F	CGCGCCGATTCTGTTTAGTTTC	
Large_genome_70kA_F	GAAGAGAACGTCGATCTAC	
Large_genome_70kA_R	CGAAGATATTGCCCTCTCAC	
Large_genome_100kA_F	GCGGTCAGCTGTATCAAC	
Large_genome_100kA_R	TGCCCTCTCACTTTCATCGG	
Poxb_L500F	CCCTCCGTCAGATGAACTAAAC	
Poxb_L500BSAI_R	CCAGGTCTCACTGGTAACACGACAACCGAAAC	
ReN20PAM2BSAI_F	CCAGGTCTCAccAGTTCATGTGCAGTCCATC	
ReN20PAM2_poxb_BSAI_R	CCAGGTCTCAgeCTGACAACCGAAACGCCACGGTTAAGCACCGCTTTGCGCATGCAACGTCATCTCGTTCTC	
Poxb_R500BSAI_F	CCAGGTCTCAaGGCACTGGTTCGGGATATCAAG	Poxb editing
Poxb_R500R	CGACCACCACATCCACCAACAC	
kan_re_poxbfullF	CCAGGTCTCAaggeCGTCGGAATTGCCAGCTGGG	
kan_re_fullR	CCAGGTCTCAagteTCAGAAGAAGTCTGCAAGAAGGC	
poxb_kan_R500BSAI_F	CCAGGTCTCAgaetACTGGTTCGGGATATCAAG	

poxb_genome_F	CGCCTTATGCCCGATGATAATTC	
poxb_genome_R	CCAGCACGCTGTTGTTAAAGAC	
lacZ_L500F	CTTCCGGCTCGTATGTTG	
lacZ_L500BSAI_R	CCAGGTCTCACTGGGATAACTGCCGTCCTCC	
ReN20PAM2BSAI_F	CCAGGTCTCACAGTTCATGTGCAGCTCCATC	
ReN20PAM2_lacZ_BSAI_R	CCAGGTCTCAGCCTCCGGCGCTAAAAATGCGCTCAGGTCAAATTCAGACGGCACAACGTCATCTCGTTCTC	
lacZ_R500BSAI_F	CCAGGTCTCAAGGCTGGCTTTCGCTACCTGGAGAG	
lacZ_R500R	TCGCGTTCCGGTTCCTACTAC	<i>LacZ</i> editing
kan_re_lacZfullF	CCAGGTCTCAagctCGTCGGAATTGCCAGCTGGG	
kan_re_fullR	CCAGGTCTCAagtcTCAGAAGAAGCTCGTCAAGAAGGC	
lacZ_kan_R500BSAI_F	CCAGGTCTCAgactGGCTTTCGCTACCTGGAGAG	
lacZ_genome_F	AAAACCCCTGGCGTTACCCA	
lacZ_genome_R	CAGGCAGTCAATCAACTGTTTACC	
ldhApm_L500F	TACTTACACATCCCGCCATCAGCAGG	
ldhApm_L500BSAI_R	CCAGGTCTCACTGGTCCGATCCAAGTGCAGCGGCG	
ReN20PAM2BSAI_F	CCAGGTCTCACAGTTCATGTGCAGCTCCATC	
ReN20PAM2_ldhA_BSAI_R	CCAGGTCTCATCCGATCCAAGTGCAGCGGCTGGAACCTCGGTGTGGAGCAACGTCATCTCGTTCTC	
ReN20PAM2_ldhAS_BSAI_R	CCAGGTCTCATCCGCAACGTCATCTCGTTCTC	
ldhApm1_R500BSAI_F	CCAGGTCTCACGGA <sup>Ceg aacg</sup> CCAGCAGACGCATACCAAAAACC	CRISPR-tolerant and PAM-free
ldhApm2_R500BSAI_F	CCAGGTCTCACGGA <sup>AtcA aacg</sup> CCAGCAGACGCATACCAAAAACC	regions editing
ldhApm3_R500BSAI_F	CCAGGTCTCACGGA <sup>Atcg Gacg</sup> CCAGCAGACGCATACCAAAAACC	
ldhApm4_R500BSAI_F	CCAGGTCTCACGGA <sup>Atcg</sup> CCAGCAGACGCATACCAAAAACC	
ldhApm_R500R	CAACAGGTGAACGAGTCCTTTGGC	
ldhA_genome_F	TTAGCGCACATACCGGTC	
ldhA_genome_R	GCGCCTACACTAAGCATAGTTG	
Poxb_L65F	ccgcaagtgtactactattgcagctggtttccagccggagcagatcccacaagtactggcgaTTCATGTGCAGCTCCATC	<i>Poxb</i> deletion using simple
Poxb_R40L40QR	CTTTTTCTCCACCAATGGAAGCAATGCACGCAGAGTCGAAATAGCTCTTGTTGGGTGGGTTTCCTGAAATA	editing cassette construction
	<u>GCCGCTGCAACGTCATCTCGTTCTC</u>	strage

## CAGO technique protocol

### Step1: Editing cassette construction

#### (1) Amplification of modularized parts

The selection marker part with CRISPR/Cas9 recognition region (N20PAM) are PCR-amplified from plasmid pACYC184-M-crt with N20PAM sequence embedded in reverse primer, which is used as template for PCR amplification to add type IIS linkers. Primer pairs are designed as:

5'..TTCATGTGCAGCTCCATCACTGGAGCACCTCAAAAACACCA..3' and  
 5'..CAACGTCATCTCGTTCTCCGCTTATTTGTTAACTGTTAATTGTCCTTACTTTCGGTTCGATGGACTATTACGCCCCGCCCTGCCA..3'.

For genome deletion, three modularized parts are used for editing cassette construction. The primers used for amplification of each part are in the following table.

Table S5. Primers designed for modularized parts amplification in genome deletion experiment

modularized parts	Primers design
left homology arm (L)	5'.. 18~22nt forward primer..3'
	5'..CCAGGTCTCACTGG-18~22nt reverse primer..3'
marker with N20PAM	5'..CCAGGTCTCACCAGTTCATGTGCAGCTCCATC..3'
	5'..CCAGGTCTCANNNN-40nt L_short-CAACGTCATCTCGTTTCTC..3 <sup>a</sup>
right homology arm (R)	5'..CCAGGTCTCANNNN-18~22nt reverse primer..3'
	5'.. 18~22nt reverse primer ..3'

<sup>a</sup> :The 40nt L\_short could be any DNA fragment upstream of L homologous arm as necessary.

<sup>b</sup> : “NNNN” was the 4 nt linkers between L\_short and R, was alterable as needed.

For genome insertion and replacement, four modularized parts are used for editing cassette construction, the primers used for amplification of each part are in the following table.

Table S6. Primers designed for modularized parts amplification in genome insertion and replacement experiment

modularized parts	Primers design
left homology arm (L)	5'.. 18~22nt forward primer..3'
	5'..CCAGGTCTCACTGG-18~22nt reverse primer..3'
marker with N20PAM	5'..CCAGGTCTCACCAGTTCATGTGCAGCTCCATC..3'
	5'..CCAGGTCTCAGCCT-40nt L_short-CAACGTCATCTCGTTTCTC..3 <sup>a</sup>
insertion	5'..CCAGGTCTCAAGGC-18~22nt forward primer..3'
	5'..CCAGGTCTCANNNN-18~22nt reverse primer..3' <sup>b</sup>
right homology arm (R)	5'..CCAGGTCTCANNNN-18~22nt reverse primer..3'
	5'.. 18~22nt reverse primer ..3'

<sup>a</sup> :The 40nt L\_short could be any DNA frsgmmt upstream of L homologous arm as necessary.

<sup>b</sup> : “NNNN” was the 4 nt linkers between insertion part and R, was alterable as needed.

## (2) Modular parts assembly

Add around 100 ng of marker N20PAM part and equal molar amounts of the other assembly parts into a 15 µl total volume assembly reaction mixture:

marker N20PAM part (100 ng)  
+ each additional assembly parts (to equal molar with marker with N20PAM part)  
+ 1.5 µl 10X NEB T4 Buffer  
+ 0.15 µl 100X BSA  
+ 1 µl BsaI  
+ 1 µl NEB T4 Ligase, 2 million cohesive end units / mL  
+ dH2O to 15 µl

Perform the assembly reaction in a thermocycler with following condition:

3 min @ 37 C }  
4 min @ 16 C } 25 cycles  
5 min @ 50 C }  
5 min @ 80 C } 1 cycle

Forward primer of L and reverse primer of R are used for the amplification from the assembly reaction to get large number of editing cassette.

For genome deletion, the editing cassette could also be constructed by PCR amplification without assembly. The left homology arm (L) is embedded in the forward primer with a length of about 65bp, the right homology arm (R) and L\_short are embedded in the reverse primer with the length of 40bp for each. Two primers are designed as followed:

5'..65nt left homology arm-TTCATGTGCAGCTCCATC..3' and

5'..40nt reverse right homology arm-40nt reverse L\_short-CAACGTCATCTCGTTCTC..3'. The PCR product is the editing cassette for genome editing.

## **Step2: Procedure for genome editing**

MG1655 competent cells harboring pCAGO are prepared with IPTG induced λ-RED proteins. 50 µL competent cells are mixed with 400 ng editing cassette in a 2-mm Gene Pulser cuvette (Bio-Rad). After electroporation at 2.5 kV and suspended immediately in 1 ml of ice cold medium, cells are incubated for 2 hours at 30°C, and then plated on solid LB medium with ampicillin, chloramphenicol and 1% glucose.

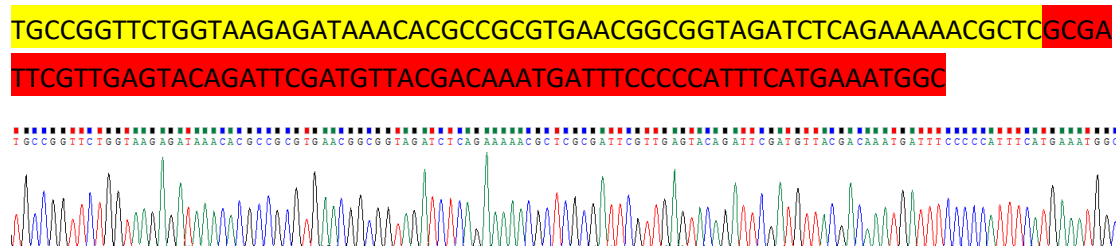
For each editing experiment, five transformants are analyzed by colony PCR. A correct clone with inserted editing cassette is inoculated into LB media with ampicillin, IPTG, and L-arabinose for CRISPR/Cas9 system and λ-RED protein expression. After culturing for more than 6 hours, cells are plated on LB agar plates with ampicillin. Colonies are identified by colony PCR and the correct colonies are used for further verification by DNA sequencing.

### Step3: Plasmid curing and multiple rounds of genome editing

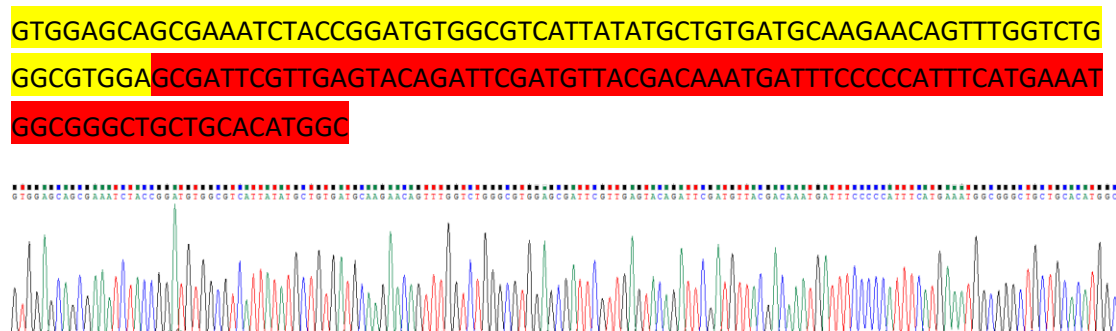
In edited strain, pCAGO is cured by growing overnight at 42°C. For consecutive editing, edited clone carrying pCAGO is used as parent strain for transformation of new editing DNA cassette.

### Sequencing data

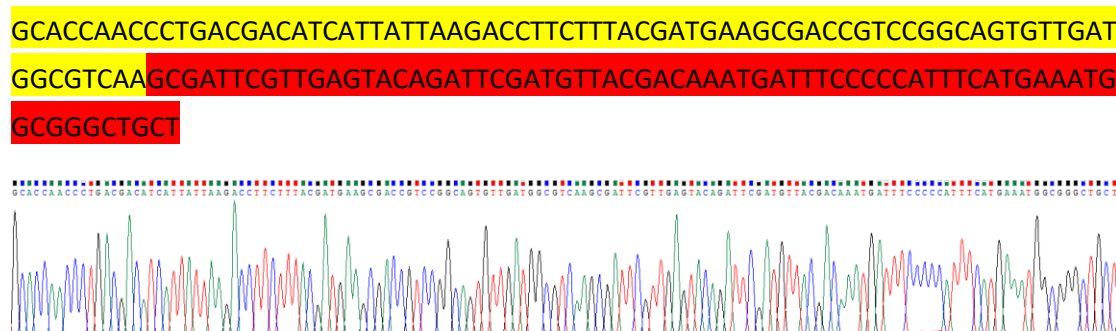
Deletion of 9.53kb:



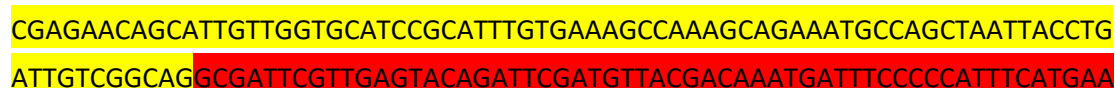
Deletion of 30.08kb:



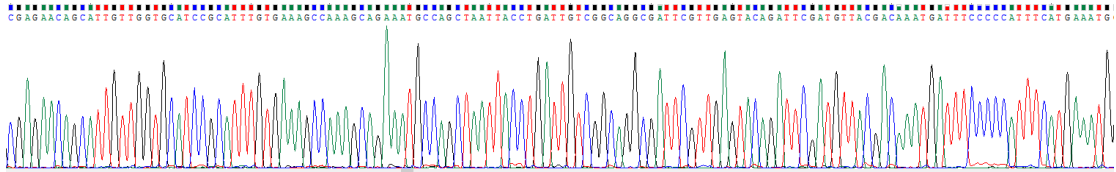
Deletion of 70.04kb:



Deletion of 99.99kb:

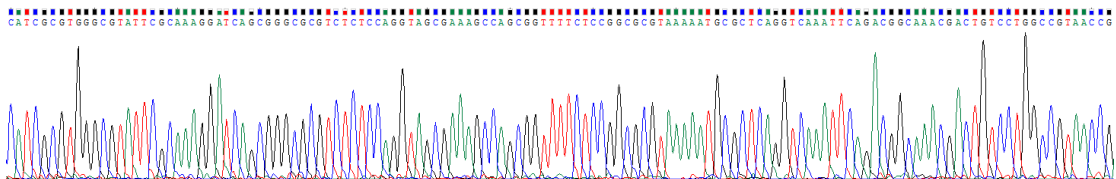


ATG



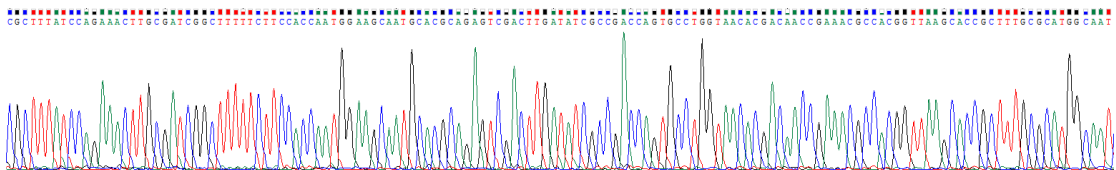
**LacZ deletion:** 1018bp was deleted from the *lacZ* gene

CATCGCGTGGGCGTATTCGCAAAGGATCAGCGGGCGGTCTCTCCAGGTAGCGAAAGCCA GCGGTT  
TTCTCCGGCGCGTAAAAATGCGCTCAGGTCAAATTCAGACGGCAAACGACTGTCCTGGCCGTAACCG



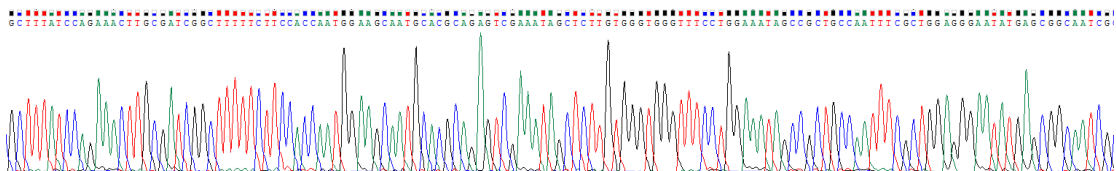
**Poxb deletion:** 443 bp was deleted from the *poxb* gene

CGCTTTATCCAGAACTTGCATCGGCTTTTTCTTCCACCAATGGAAGCAATGCACGCAGAGTCGACT  
TGATATCGCCGACCAGTGCCTGGTAACACGACAACCGAAACGCCACGGTTAAGCACCGCTTTGCGCA  
TGGCAAT



**Poxb deletion using simple editing cassette construction strage:** 587bp was deleted from the *poxb* gene

GCTTTATCCAGAACTTGCATCGGCTTTTTCTTCCACCAATGGAAGCAATGCACGCAGAGTCGAAAT  
AGCTCTGTGGGTGGGTTTCTGGAAATAGCCGCTGCCAATTCGCTGGAGGGAATATGAGCGGCA  
ATCG

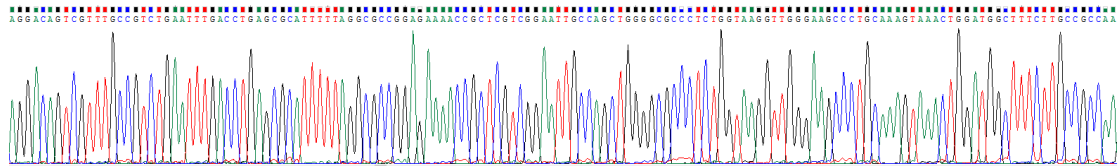


**LacZ replaced by kan:** 1018bp of *lacZ* was replaced by 915 bp fragment derived from the *kan* gene

Forward

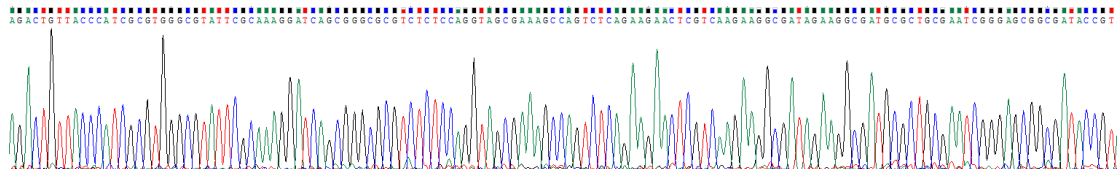


AGGACAGTCGTTGCCGTCTGAATTTGACCTGAGCGCATTTTTAGGCGCCGGAGAAAACCGCTCGTCT  
GGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGGGAAGCCCTGCAAAGTAAACTGGATGGCTTT  
CTTGCCGCCAA



Reverse

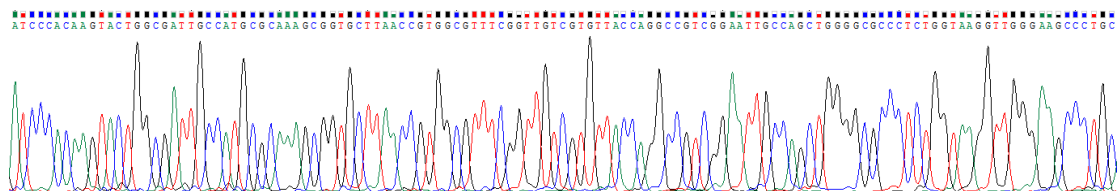
AGACTGTTACCCATCGCGTGGGCGTATTGCAAAGGATCAGCGGGCGCTCTCCAGGTAGCGAA  
AGCCAGTCTCAGAAGAAGTCTCAAGAAGGCGATAGAAGGCGATGCGCTGCGAATCGGGAGCGGC  
GATACCGT



*Poxb* replaced by *kan*: 443 bp of *poxb* was replaced by 915 bp fragment derived from the *kan* gene

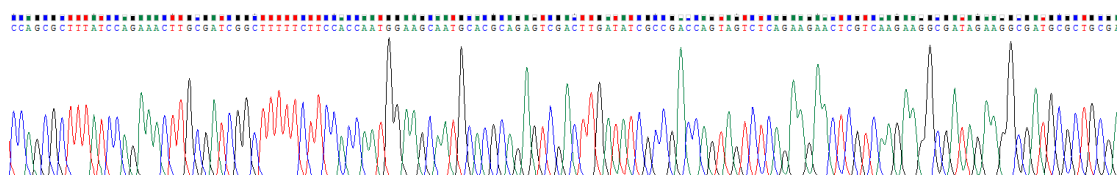
Forward

ATCCACAAGTACTGGCGATTGCCATGCGCAAAGCGGTGCTTAACCGTGGCGTTTCGGTTGTCGTGT  
TACCAGGCCGTCGGAATTGCCAGCTGGGGCGCCCTCTGGTAAGGTTGGGAAGCCCTGC



Reverse

CCAGCGCTTTATCCAGAAACTTGCATCGGCTTTTTCTCCACCAATGGAAGCAATGCACGCAGAGTC  
GACTTGATATCGCCGACCAGTAGTCTCAGAAGAAGTCTCAAGAAGGCGATAGAAGGCGATGCGCT  
GCG



## pCAGO Sequence

>

CACAACCGGCACGGAACCTCGCTCGGGCTGGCCCCGGTGCATTTTTTAAATACCCG  
CGAGAAATAGAGTTGATCGTCAAACCAACATTGCGACCGACGGTGGCGATAGG  
CATCCGGGTGGTGCTCAAAGCAGCTTCGCTGGCTGATACGTTGGTCCTCGCGC  
CAGCTTAAGACGCTAATCCCTAACTGCTGGCGGAAAAGATGTGACAGACGCGAC  
GGCGACAAGCAAACATGCTGTGCGACGCTGGCGATATCAAATTGCTGTCTGCCA  
GGTGATCGCTGATGTACTGACAAGCCTCGCGTACCCGATTATCCATCGGTGGATG  
GAGCGACTCGTTAATCGCTTCCATGCGCCGCAGTAACAATTGCTCAAGCAGATTT  
ATCGCCAGCAGCTCCGAATAGCGCCCTTCCCCTTGCCCGGCGTTAATGATTTGCC  
CAAACAGGTCGCTGAAATGCGGCTGGTGGCTTCATCCGGGCGAAAGAACCCCG  
TATTGGCAAATATTGACGGCCAGTTAAGCCATTCATGCCAGTAGGCGCGCGGACG  
AAAGTAAACCCACTGGTGATAACCATTGCGGAGCCTCCGGATGACGACCGTAGTG  
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CGTCCCTGATTTTTACCACCCCTGACCGCGAATGGTGAGATTGAGAATATAAC  
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CGGCGTTAAACCCGCCACCAGATGGGCATTAAACGAGTATCCCGGCAGCAGGGG  
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ATTGTCCATATTGCATCAGACATTGCCGTCACTGCGTCTTTTACTGGCTCTTCTCG  
CTAACCAAACCGGTAACCCCGCTTATTAAGCATTCTGTAACAAAGCGGGACCA  
AAGCCATGACAAAACGCGTAACAAAAGTGTCTATAATCACGGCAGAAAAGTCC  
ACATTGATTATTTGCACGGCGTCACACTTTGCTATGCCATAGCATTTTTATCCATA  
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ACGTCATCCTATTTTTGGAAATATAGTAGATGAAGTTGCTTATCATGAGAAATAT  
CCAATATCTATCATCTGCGAAAAAATTGGTAGATTCTACTGATAAAGCGGATT  
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TGGTACAAACCTACAATCAATTATTTGAAGAAAACCCTATTAACGCAAGTGGAGT  
AGATGCTAAAGCGATTCTTCTGCACGATTGAGTAAATCAAGACGATTAGAAAAT  
CTCATTGCTCAGCTCCCCGGTGAGAAGAAAAATGGCTTATTTGGGAATCTCATTG  
CTTTGTCATTGGGTTTGACCCCTAATTTTAAATCAAATTTTGATTTGGCAGAAGAT

GCTAAATTACAGCTTTCAAAAGATACTTACGATGATGATTTAGATAAATTTATTGG  
CGCAAATTGGAGATCAATATGCTGATTTGTTTTTGGCAGCTAAGAATTTATCAGA  
TGCTATTTTACTTTCAGATATCCTAAGAGTAAATACTGAAATAACTAAGGCTCCC  
CTATCAGCTTCAATGATTAACGCTACGATGAACATCATCAAGACTTGACTCTTTT  
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CAATCAAAAAACGGATATGCAGGTTATATTGATGGGGGAGCTAGCCAAGAAGAA  
TTTTATAAATTTATCAAACCAATTTTAGAAAAAATGGATGGTACTGAGGAATTAT  
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GCTCTATTCCCATCAAATTCACTTGGGTGAGCTGCATGCTATTTTGAGAAGACA  
AGAAGACTTTTATCCATTTTTAAAAGACAATCGTGAGAAGATTGAAAAAATCTTG  
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TACGGTTTATAACGAATTGACAAAGGTCAAATATGTTACTGAAGGAATGCGAAA  
ACCAGCATTTCTTTCAGGTGAACAGAAGAAAGCCATTGTTGATTTACTCTTCAAA  
ACAAATCGAAAAGTAACCGTTAAGCAATTAAGAAGATTATTTCAAAAAAATA  
GAATGTTTTGATAGTGTGAAATTTCAGGAGTTGAAGATAGATTTAATGCTTCATT  
AGGTACCTACCATGATTTGCTAAAAATTATTAAGATAAAGATTTTTTGGATAAT  
GAAGAAAATGAAGATATCTTAGAGGATATTGTTTTAACATTGACCTTATTTGAAG  
ATAGGGAGATGATTGAGGAAAGACTTAAAACATATGCTCACCTCTTTGATGATAA  
GGTGATGAAACAGCTTAAACGTCGCCGTTATACTGGTTGGGGACGTTTGTCTCGA  
AAATTGATTAATGGTATTAGGGATAAGCAATCTGGCAAACAATATTAGATTTTT  
TGAAATCAGATGGTTTTGCCAATCGCAATTTTATGCAGCTGATCCATGATGATAG  
TTTGACATTTAAGAAGACATTCAAAAAGCACAAAGTGTCTGGACAAGGCGATAG  
TTTACATGAACATATTGCAAATTTAGCTGGTAGCCCTGCTATTA AAAAAGGTATT  
TTACAGACTGTAAAAGTTGTTGATGAATTGGTCAAAGTAATGGGGCGGCATAAGC  
CAGAAAATATCGTTATTGAAATGGCACGTGAAAATCAGACAACCTCAAAGGGCC  
AGAAAAATTCGCGAGAGCGTATGAAACGAATCGAAGAAGGTATCAAAGAATTAG  
GAAGTCAGATTCTTAAAGAGCATCCTGTTGAAAATACTCAATTGCAAAAATGAAAA  
GCTCTATCTCTATTATCTCCAAAATGGAAGAGACATGTATGTGGACCAAGAATTA  
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AAATCGGATAACGTTCCAAGTGAAGAAGTAGTCAAAAAGATGAAAACTATTGG  
AGACAACCTTCTAAACGCCAAGTTAATCACTCAACGTAAGTTTGATAATTTAACGA  
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