**FIG S1** Presence of *E. typhina × festucae* isolate Lp1 cloA constructs in genomic DNA preparations of *N. fumigata* transformants as detected by PCR with primer combination 1 (Table 2). Sizes in kb of relevant fragments of *BstE*II-digested bacteriophage lambda DNA are indicated to the left of the photo.

```
atgatattaccatggttatcccagcttcaatcggtctcactagggacgattttcctcacg
 M  I  L  P  W  L  S  Q  L  Q  S  V  S  L  G  T  I  F  L  T
ctattcctcgttatattgactcctttggttttcacaagcgtttaccgtctgtattttcat
 L  F  L  V  I  L  T  P  L  V  F  T  S  V  Y  R  L  Y  F  H
cctcttcgcaaaattcctggaccacgaaccggggtttgacaagtttctatgggttctat
 P  L  R  K  I  P  G  P  R  T  G  G  L  T  S  F  Y  G  F  Y
tggaactggatacgagatgaaggatactctaagctcttcaatccctgcataaacaatat
 W  N  W  I  R  D  E  G  Y  S  K  L  F  N  P  L  H  K  Q  Y
aattcccatatcatacgtatcggcccaaaccatgttcacatcaaccaaccgcaagctttt
 N  S  H  I  I  R  I  G  P  N  H  V  H  I  N  Q  P  Q  A  F
gatgagatattcaaagttggaacaacatggcgcaaagacagctcattttacaagtatttt
 D  E  I  F  K  V  G  T  T  W  R  K  D  S  S  F  Y  K  Y  F
aacggcttggacgccatgattgagccgacgcaatatcgcacctaccgaactcacttggcc
 N  G  L  D  A  M  I  E  P  T  Q  Y  R  T  Y  R  T  H  L  A
cctttatacgcacaacgctccattgatggcttaacaccaaagctccatgacgacctcgtg
 P  L  Y  A  Q  R  S  I  D  G  L  T  P  K  L  H  D  D  L  V
gtaactgccgaaaggatggccaagagcatcgaaaatggtgaacctgtgaacatggtgaag
 V  T  A  E  R  M  A  K  S  I  E  N  G  E  P  V  N  M  V  K
atattgcggacattgagtacctcaatgatgctttatactttgtattcgcaggacatcccg
 I  L  R  T  L  S  T  S  M  M  L  Y  T  L  Y  S  Q  D  I  P
ctctctcaatatgatgggtatcacccgtttctagaagctttttgagctgctcatgacccaa
 L  S  Q  Y  D  G  Y  H  P  F  L  E  A  F  E  L  L  M  T  Q
agttggctaatgatcaattatcccatgatgggtatgatccttggcctaattcccggcacg
 S  W  L  M  I  N  Y  P  M  M  G  M  I  L  G  L  I  P  G  T
agctttgcgaaattcaatgccgctttcggaaccttcttgaagtactgtaaagagtggaac
 S  F  A  K  F  N  A  A  F  G  T  F  L  K  Y  C  K  E  W  N
gacgaggatgaacgcattcaaaagcttgaaactgctgaatcactgcgggactcccacatg
 D  E  D  R  I  Q  K  L  E  T  A  E  S  L  R  D  S  H  M
aaacgataccttgccattgacccaaataacgagatcaaaaagaaggtcgtgccgcatccc
 K  R  Y  L  A  I  D  P  N  N  E  I  K  K  K  V  V  P  H  P
ctggaggatatatttaactttatcgcaggcggtagtgacactacttcatatacagctgca
 L  E  D  I  F  N  F  I  A  G  G  S  D  T  T  S  Y  T  A  A
tgtgcattcttccatgttctctcgtcgtctgaggtgcactctaagctcgtggcggagctc
 C  A  F  F  H  V  L  S  S  S  E  V  H  S  K  L  V  A  E  L
gatcaagcttcttcagtgatcagggataccttttgattacaataagattcaaaacttgcca
 D  Q  A  S  S  V  I  R  D  T  F  D  Y  N  K  I  Q  N  L  P
tatctgaatgccgtgatcaaggagacgcttcgtatctcttgtccggtaccagggtgtctt
 Y  L  N  A  V  I  K  E  T  L  R  I  S  C  P  V  P  G  C  L
ccccgagtcgtccctgagggggggaatgaatctgggttcagtaaatcttccagccggtaca
 P  R  V  V  P  E  G  G  M  N  L  G  S  V  N  L  P  A  G  T
gtggtgtcaatctcccagctagccatccactttaatgagacgattttctcgtcacctgac
 V  V  S  I  S  Q  L  A  I  H  F  N  E  T  I  F  S  S  P  D
aagttcatccccgaaagatggcttggggacgatagaaaatcgattgagaagtggaatatc
 K  F  I  P  E  R  W  L  G  D  D  R  K  S  I  E  K  W  N  I
gctttttagcagaggacctcgacagtgcattgggacaactctcgcttatatggaactacgc
 A  F  S  R  G  P  R  Q  C  I  G  T  T  L  A  Y  M  E  L  R
tgcgtcctcgcttatttcttctcccgctttgaatttaagttaacgggtagctgtggagat
 C  V  L  A  Y  F  F  S  R  F  E  F  K  L  T  G  S  C  G  D
aagttgcgctgggttgatcgatttgtctcagtcaacttggacgatgtcgaggtcactatc
 K  L  R  W  V  D  R  F  V  S  V  N  L  D  D  V  E  V  T  I
gtgaaggaccgatgggcgtaa
 V  K  D  R  W  A  *
```

**FIG S2** Sequence of cDNA derived from *E. typhina × festucae* isolate Lp1 allele of *cloA* expressed in *N. fumigata*. Deduced amino acid sequence is indicated below.

ATGTCGCAACTATGGCTATACAAGGCTCCAAGTCCCGGGCTTCTGATCACGGCATGTTTCTTCATTGTCTTGCCATGGCTCGTCA
AAGGCATCTACAATCTGTACTTCCACCCTCTTCGAAACATTCCTGGGCCCAAACTTGGCGCCTTGACCAGCTTTTACGCCTTCTA
CTGGAATTGGATTCGGGAGGGAGGATACTGTAAGAAATTCGCGCAATATCACAAGGACTACAGTACGAATCTCCAGTCAAAGACT
TTCTTTTTCTCACGGGACCTGCGCTAACTTGCAGACAAGACTCTCCCGTCGTTCGCATCGGCCCAAACGCTGTTCATACCAACCA
GGTGGAACTCTACGACGTGTAAGCACGGGGTCCTTGATCATAATGTCAGAAATGCTTTCTAACTCGAGACGCAAAAAAAAAAAAA
AAAAAAAAAAAAGAATATTCAAAGGTGGCTCGGCATGGCTGAAGGACTCGCAATTCTACCAACACTTCAATGGCGTGGATGCCAT
GATTGGACCGAAGCATTTCCGTACCTATCGCAACCACCTGGCCCCTTTGTATGCGCAGCGGGCGGTGGACGGCCTCACGCCCAAG
ATTCATAACGACCTCGAACGCTGTGCTGCCAAAATCCACAAGACGGCCGGAACCGGCAAACCGGTGAACATGGCAAAGATGTTAC
GACTGTTGAGTGTGAGTATCCATGCATCGATGCTGCTCCGATACAAGGAGGCTGGGGGCTGAAAGAAAGAGGAGCTTAGAGCTCC
ATGATTCTCTACAACATTTTTTCGCTCGAAATCTCGCTCTTTGAGCACGACGGGTACCATCCGTTCCTCGCAGCGTTTGAACACG
TCATGACACAAAGCTGGCTGTGTGAGTTCCCTCGGTCCCTGGCCGCCTCGCATCCTCGCGCGAGGGATTAGAAATAGGGGGAACT
CTGCTGATCAAGGTTCTCGGTAACCTGGTTGCGCAAAAAAAAATGCCTAGTTGTGACGTATCCGCTGGTACCCGCGTGGCTGGGC
CTCATTCCGGGAACGATCTTCTCGCAGTTCAACTCATCTTGGAACACATTCATGAAGTACTGCACGGCTTGGAACGAGGAAGACA
TGCGCAGGCAGCACGCGAGCGACGAGCAGTCGATTCGCGATTCCCATTCCAAGCGGTACCTTGCCATGAAGAACGAGGGCGACGA
GGAGAAGAAGAGCATCATCCCCGACCCGATAGATGATGTTTTCAATTTCATTGCGGGGGGTAGCGACACCACGGCCTACACCACT
TCGGCCGCCTTCTTCTACATCCTCTCGTCGCCATCCGTGTGTACAAAGCTGGTGGAGGAACTCGACGAGAATCGCTCCGTCATCC
GCGATGCAATGGACTATCACAAGATTACAAGTCTACCTTATCTCGTACGTGCTAGAAACGACCGGCATCCTTCGCGCTCTGTTAT
CCGGAGAAAAAAGGAAAAAGAAAAAAAAAGGGAAAGAAAAAAAGGAAAGAAAGAAAAATGCCCTGTCACTACTGACTCCTGACTC
CTGCCTCCCCCACCTCTAGAACGCCGTGATCAAGGAGACGCTACGAATCTCCGTTCCACTTCCTGGCTGCCTGCCACGTGTCGTG
CCTGAAGGTGGCATCACCGTGGGGTCGTTCCATCTCCCAGCTGGGGTGAGTTCATGTCGTGCCCCCATGACCCTATTTCGAGAGC
CTCCTGACCGTGCGGCTGACTGATGAACTACAAATCGATCCACACAGACGTCTGTGTCTCTTACGCACCAAGTGATTAGCTTCAA
TGAAGAAATTTTCCCCTCGTCAAAGACGTTTCTTCCCGAAAGATGGCTGGGTCCGGAAGCGGTCGGGCTTGATAAGTGGAATGTG
GCGTTTAGCCGAGGCCCTCGCCAATGCCTTGGGACAACGTAAGTCGCAAAAAAAGAAAAAGAAAAAGAAAACAAAAAAAAAAGA
AAGAAAAAAAAAGGAAAAAAAAAAAAGAAAAGCACGAGTTTAAATCTACACATTATCTCTACGCCGTGAGCCCCCCAAGAGCTGC
AGTTAACCCTTTTGACACAGTCTGGCGTACTTGGAGCTTCGCTGCGTCCTCGCTTACTTCTTCTCTCGGTTCCAGATGGTCCTGA
CGGGAAACTGCGGGGATCGACTCCGCTGGGTTGACCGATTTGTTGCTGCAAACGTTGACGACGTGGAGGTGCGAGTAGTAGCTGA
TCGATGGACAGGAGATACGTTCTGA

**FIG S3** Sequence of *C. africana cloA* allele to demonstrate issues with intron processing in *N. fumigata*. Initiation and termination codons are highlighted with green and red, respectively. Intronic sequences processed from the mRNA are highlighted in blue. Retained introns are highlighted in gray. Yellow highlight indicates exonic sequences that were erroneously processed from the mRNA. Putative branch site sequences (consensus CTRAC) are underlined.

```
CLUSTAL O(1.2.4) multiple sequence alignment


Epichloe_typhina_x_festucae      MILPWLSQLQSVSLGTIFLTLFLVILTPLVFTSVYRLYFHPLRKIPGPRTGGLTSFYGFY
Claviceps_africana               MSQLWLYKAPS--P-GLLITACFFIVLPWLVKGIYNLYFHPLRNIPGPKLGALTSFYAFY
C_africana_synthetic             MSQLWLYKAPS--P-GLLITACFFIVLPWLVKGIYNLYFHPLRNIPGPKLGALTSFYAFY
                                 *   ** : *     :::*  :.*: * :....:*.*******:****: *.*****.**


Epichloe_typhina_x_festucae      WNWIRDEGYSKLFNPLHKQYNSHIIRIGPNHVHINQPQAFDEIFKVGTTWRKDSSFYKYF
Claviceps_africana               WNWIREGGYCKKFAQYHKDYNSPVVRIGPNAVHTNQVELYDVIFKGGSAWLKDSQFYQHF
C_africana_synthetic             WNWIREGGYCKKFAQYHKDYNSPVVRIGPNAVHTNQVELYDVIFKGGSAWLKDSQFYQHF
                                 *****: **.* *   **:*** ::***** ** ** : :* *** *::* ***.**::*


Epichloe_typhina_x_festucae      NGLDAMIEPTQYRTYRTHLAPLYAQRSIDGLTPKLHDDLVVTAERMAKSIENGEPVNMVK
Claviceps_africana               NGVDAMIGPKHFRTYRNHLAPLYAQRAVDGLTPKIHNDLERCAAKIHKTAGTGKPVNMAK
C_africana_synthetic             NGVDAMIGPKHFRTYRNHLAPLYAQRAVDGLTPKIHNDLERCAAKIHKTAGTGKPVNMAK
                                 **:**** *.::****.*********::******:*:**   * :: *:  .*:****.*


Epichloe_typhina_x_festucae      ILRTLSTSMMLYTLYSQDIPLSQYDGYHPFLEAFELLMTQSWLMINYPMMGMILGLIPGT
Claviceps_africana               MLRLLSSSMILYNIFSLEISLFEHDGYHPFLAAFEHVMTQSWLFVTYPLVPAWLGLIPGT
C_africana_synthetic             MLRLLSSSMILYNIFSLEISLFEHDGYHPFLAAFEHVMTQSWLFVTYPLVPAWLGLIPGT
                                 :** **:**:**.::* :* * :.******** *** :******::.**::   *******


Epichloe_typhina_x_festucae      SFAKFNAAFGTFLKYCKEWNDEDERIQKLETAESLRDSHMKRYLAIDPN-NEIKKKVVPH
Claviceps_africana               IFSQFNSSWNTFMKYCTAWNEEDMRRQHASDEQSIRDSHSKRYLAMKNEGDEEKKSIIPD
C_africana_synthetic             IFSQFNSSWNTFMKYCTAWNEEDMRRQHASDEQSIRDSHSKRYLAMKNEGDEEKKSIIPD
                                  *::**::.**:***. **:** * *: .  :*:**** *****:. : :* **.::*.


Epichloe_typhina_x_festucae      PLEDIFNFIAGGSDTTSYTAACAFFHVLSSSEVHSKLVAELDQASSVIRDTFDYNKIQNL
Claviceps_africana               PIDDVFNFIAGGSDTTAYTTSAAFFYILSSPSVCTKLVEELDENRSVIRDAMDYHKITSL
C_africana_synthetic             PIDDVFNFIAGGSDTTAYTTSAAFFYILSSPSVCTKLVEELDENRSVIRDAMDYHKITSL
                                 *:::*:************:**::.***::*** .* :*** ***:  *****::**:** .*


Epichloe_typhina_x_festucae      PYLNAVIKETLRISCPVPGCLPRVVPEGGMNLGSVNLPAGTVVSISQLAIHFNETIFSSP
Claviceps_africana               PYLNAVIKETLRISVPLPGCLPRVVPEGGITVGSFHLPAGTSVSLTHQVISFNEEIFPSS
C_africana_synthetic             PYLNAVIKETLRISVPLPGCLPRVVPEGGITVGSFHLPAGTSVSLTHQVISFNEEIFPSS
                                 ************** *:*************:.:**.:***** **:::  .* *** ** *


Epichloe_typhina_x_festucae      DKFIPERWLGDDRKSIEKWNIAFSRGPRQCIGTTLAYMELRCVLAYFFSRFEFKLTGSCG
Claviceps_africana               KTFLPERWLGPEAVGLDKWNVAFSRGPRQCLGTTLAYLELRCVLAYFFSRFQMVLTGNCG
C_africana_synthetic             KTFLPERWLGPEAVGLDKWNVAFSRGPRQCLGTTLAYLELRCVLAYFFSRFQMVLTGNCG
                                 ..*:****** :  .::***:*********:******:******:**************:: ***.**


Epichloe_typhina_x_festucae      DKLRWVDRFVSVNLDDVEVTIVKDRWA----
Claviceps_africana               DRLRWVDRFVAANVDDVEVRVVADRWTGDTF
C_africana_synthetic             DRLRWVDRFVAANVDDVEVRVVADRWTGDTF
                                 *:********:.*:***** :* ***:
```

**FIG S4** Alignment of CloA amino acid sequences deduced from the indicated alleles.  The red-highlighted valine residue represents the last amino acid in the version of CloA that would be translated from the misprocessed *C. africana* genomic *cloA* allele expressed in *N. fumigata*. Alignment was produced with CLUSTAL Omega.

```
C.afr   1    ATGTCGCAACTATGGCTATACAAGGCTCCAAGTCCCGGGCTTCTGATCACGGCATGTTTC   60
             ||||| || || ||||| ||||||||||| |||||||| |||||||||||||| || |||
Synth   1    ATGTCTCAGCTTTGGCTGTACAAGGCTCCTAGTCCCGGCCTTCTGATCACGGCTTGCTTC   60

C.afr   61   TTCATTGTCTTGCCATGGCTCGTCAAAGGCATCTACAATCTGTACTTCCACCCTCTTCGA   120
             ||||| ||||||||| ||||||||||| |||||||||||| ||||||||||||||||||
Synth   61   TTCATCGTCTTGCCTTGGCTCGTCAAGGGCATCTACAACCTGTACTTCCACCCTCTTCGT   120

C.afr   121  AACATTCCTGGGCCCAAACTTGGCGCCTTGACCAGCTTTTACGCCTTCTACTGGAATTGG   180
             |||||||||| ||||| |||||||||||||||||||||| |||||||||||||||| |||
Synth   121  AACATTCCTGGTCCCAAGCTTGGCGCCTTGACCAGCTTCTACGCCTTCTACTGGAACTGG   180

C.afr   181  ATTCGGGAGGGAGGATACTGTAAGAAATTCGCGCAATATCACAAGGACTACAACTCTCCC   240
             ||||| ||||||||||||||| |||||||||||| ||||| ||||||||||||||||||||
Synth   181  ATTCGCGAGGGAGGATACTGCAAGAAATTCGCTCAATACCACAAGGACTACAACTCTCCC   240

C.afr   241  GTCGTTCGCATCGGCCCAAACGCTGTTCATACCAACCAGGTGGAACTCTACGACGTAATA   300
             |||||||||||||||||| ||||||||||| |||||||||||| || |||||||||| ||
Synth   241  GTCGTTCGCATCGGCCCCTAACGCTGTTCACACCAACCAGGTTGAGCTCTACGACGTTATC   300

C.afr   301  TTCAAAGGTGGCTCGGCATGGCTGAAGGACTCGCAATTCTACCAACACTTCAATGGCGTG   360
             ||||| ||||||||| || |||||||||||| || ||||||||| ||||||| |||||
Synth   301  TTCAAGGGTGGCTCTGCTTGGCTGAAGGACTCTCAGTTCTACCAGCACTTCAACGGCGTT   360

C.afr   361  GATGCCATGATTGGACCGAAGCATTTCCGTACCTATCGCAACCACCTGGCCCCTTTGTAT   420
             || || ||||| || || ||||| |||||||| || |||||||||||||||| ||| ||||
Synth   361  GACGCTATGATCGGTCCTAAGCACTTCCGTACTTACCGCAACCACCTGGCTCCTCTGTAC   420

C.afr   421  GCGCAGCGGGCGGTGGACGGCCTCACGCCCAAGATTCATAACGACCTCGAACGCTGTGCT   480
             || ||||| || || ||||| ||||| || ||||| || ||||||||||||| |||| |||
Synth   421  GCTCAGCGCGCTGTTGACGGTCTCACTCCTAAGATCCACAACGACCTCGAGCGCTGCGCT   480

C.afr   481  GCCAAAATCCACAAGACGGCCGGAACCGGCAAACCGGTGAACATGGCAAAGATGTTACGA   540
             ||||| |||||||||| || || ||||||||| || || ||||||||| |||||| | ||
Synth   481  GCCAAGATCCACAAGACTGCTGGTACCGGCAAGCCTGTTAACATGGCTAAGATGCTCCGC   540

C.afr   541  CTGTTGAGTAGCTCCATGATTCTCTACAACATTTTTTCGCTCGAAATCTCGCTCTTTGAG   600
             ||| || |||||||||||||| ||||||||||| || || ||||| ||||| ||||| |||
Synth   541  CTGCTGTCTAGCTCCATGATCCTCTACAACATCTTCTCTCTCGAGATCTCTCTCTTCGAG   600

C.afr   601  CACGACGGGTACCATCCGTTCCTCGCAGCGTTTGAACACGTCATGACACAAAGCTGGCTG   660
             |||||||| ||||| ||||| || || ||||| | || ||||||||||| || |||||||
Synth   601  CACGACGGTTACCACCCTTTCCTCGCTGCTTTCGAGCACGTCATGACTCAGAGCTGGCTG   660

C.afr   661  TTTGTGACGTATCCGCTGGTACCCGCGTGGCTGGGCCTCATTCCGGGAACGATCTTCTCG   720
             || || || || || || ||||| ||||| || || ||||| || || || |||||||
Synth   661  TTCGTTACTTACCCTCTGGTTCCCGCTTGGCTCGGTCTCATCCCTGGTACTATCTTCTCT   720

C.afr   721  CAGTTCAACTCATCTTGGAACACATTCATGAAGTACTGCACGGCTTGGAACGAGGAAGAC   780
             ||||||||||| ||||||||||| ||||||||||||||||| ||||||||||||| |||
Synth   721  CAGTTCAACTCTTCTTGGAACACTTTCATGAAGTACTGCACTGCTTGGAACGAGGAGGAC   780

C.afr   781  ATGCGCAGGCAGCACGCGAGCGACGAGCAGTCGATTCGCGATTCCCATTCCAAGCGGTAC   840
             |||||| | |||||||||| ||||||||||| || ||||| ||||| |||||||| |||
Synth   781  ATGCGCCGCCAGCACGCTAGCGACGAGCAGTCTATCCGCGACTCCCACTCCAAGCGTTAC   840

C.afr   841  CTTGCCATGAAGAACGAGGGCGACGAGGAGAAGAAGAGCATCATCCCCGACCCGATAGAT   900
             || |||||||||||||||||||||||||||||||||||||||||||||| ||||| || ||
Synth   841  CTGGCCATGAAGAACGAGGGCGACGAGGAGAAGAAGAGCATCATCCCTGACCCTATCGAC   900

C.afr   901  GATGTTTTCAATTTCATTGCGGGGGGGTAGCGACACCACGGCCTACACCCACTTCGGCCGCC   960
             || |||||||| ||||| || ||||||| |||||||||||||| ||||||||||| ||||||
Synth   901  GACGTTTTCAACTTCATCGCCGGTGGTAGCGACACCACTGCCTACACCACTTCCGCCGCC   960
```

```
C.afr   961   TTCTTCTACATCCTCTCGTCGCCATCCGTGTGTACAAAGCTGGTGGAGGAACTCGACGAG   1020
              ||||||||||||||||||      ||  ||||||  ||  ||  ||||||||  |||||  ||  ||||||
Synth   961   TTCTTCTACATCCTCTCTAGCCCTTCCGTTTGCACTAAGCTGGTTGAGGAGCTGGACGAG   1020

C.afr  1021   AATCGCTCCGTCATCCGCGATGCAATGGACTATCACAAGATTACAAGTCTACCTTATCTC   1080
              ||  ||||||||||||||||||  ||  ||||||||  ||||||||  ||  |||||  |||||  |||
Synth  1021   AACCGCTCCGTCATCCGCGACGCTATGGACTACCACAAGATCACTAGTCTGCCTTACCTC   1080

C.afr  1081   AACGCCGTGATCAAGGAGACGCTACGAATCTCCGTTCCACTTCCTGGCTGCCTGCCACGT   1140
              ||||||||| ||||||||||||  ||  ||  |||||||||||  ||  |||||  |||||||||  |||
Synth  1081   AACGCCGTTATCAAGGAGACTCTGCGCATCTCCGTTCCTCTGCCTGGTTGCCTGCCTCGT   1140

C.afr  1141   GTCGTGCCTGAAGGTGGCATCACCGTGGGGTCGTTCCATCTCCCAGCTGGGACGTCTGTG   1200
              ||||| ||||| ||||| ||||||||  ||  ||||| ||||| ||||| ||  |||||
Synth  1141   GTCGTTCCTGAGGGTGGTATCACCGTTGGCTCTTTCCACCTCCCTGCTGGCACTTCTGTT   1200

C.afr  1201   TCTCTTACGCACCAAGTGATTAGCTTCAATGAAGAAATTTTCCCCTCGTCAAAGACGTTT   1260
              ||||| || ||||| ||  |||||||||||| ||  ||  ||  |||||||  ||  |||||  ||
Synth  1201   TCTCTGACTCACCAGGTTATTAGCTTCAACGAGGAGATCTTCCCCTCTTCTAAGACTTTC   1260

C.afr  1261   CTTCCCGAAAGATGGCTGGGTCCGGAAGCGGTCGGGCTTGATAAGTGGAATGTGGCGTTT   1320
              ||  |||||    |  ||||||||||| ||  ||  ||||| ||  ||  |||||||||  ||  ||  ||
Synth  1261   CTGCCCGAGCGCTGGCTGGGTCCTGAGGCTGTCGGTCTCGACAAGTGGAACGTTGCCTTC   1320

C.afr  1321   AGCCGAGGCCCTCGCCAATGCCTTGGGACAACTCTGGCGTACTTGGAGCTTCGCTGCGTC   1380
              |||||||||||||||||||||||||||||  ||  |||||||||  |||  ||||||||  ||||||||||
Synth  1321   AGCCGAGGCCCTCGCCAATGCCTCGGTACTACTCTGGCTTACCTGGAGCTCCGCTGCGTC   1380

C.afr  1381   CTCGCTTACTTCTTCTCGGTTCCAGATGGTCCTGACGGGAAACTGCGGGGATCGACTC   1440
              ||  ||||||||||||||||||| ||||||||||||||||||  ||  ||||||||  ||  |||||
Synth  1381   CTGGCTTACTTCTTCTCGTTTCCAGATGGTCCTGACTGGCAACTGCGGTGACCGACTG   1440

C.afr  1441   CGCTGGGTTGACCGATTTGTTGCTGCAAACGTTGACGACGTGGAGGTGCGAGTAGTAGCT   1500
              |||||||||||||||  ||  ||||||||| |||||||||||||| ||||| ||||| ||  |||
Synth  1441   CGCTGGGTTGACCGTTTCGTTGCTGCTAACGTTGACGACGTTGAGGTTCGAGTTGTTGCT   1500

C.afr  1501   GATCGATGGACAGGAGATACGTTCTGA   1527
              ||  ||  ||||| ||  ||  ||  ||||||
Synth  1501   GACCGCTGGACTGGTGACACTTTCTGA   1527
```

**FIG S5** Alignment showing changes in coding sequences to optimize codon usage in the synthetic allele derived from *C. africana cloA* (lower sequence) as compared to the coding sequences from the genomic sequence of *C. africana cloA* (upper sequence). Changes in nucleotide sequence did not change amino acid sequence (Fig S3).