```
                                                  10        20        30        40        50        60        70        80
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGA
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     AACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGA

                                                  90       100       110       120       130       140       150       160       170
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  TCCGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     TCCGCTAGCGCTACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
G0221659-1.seq(1>764)                     →                ACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGC
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←                                                          GTGGTGCCCATCCTGGTCGAGCTGGACGGC

                                                 180       190       200       210       220       230       240       250       260
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA
G0221659-1.seq(1>764)                     →     GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  GACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCA

                                                 270       280       290       300       310       320       330       340       350
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAA
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAA
G0221659-1.seq(1>764)                     →     CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAA
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  CCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAA

                                                 360       370       380       390       400       410       420       430       440
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  GCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACC
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     GCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACC
G0221659-1.seq(1>764)                     →     GCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACC
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  GCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACC

                                                 450       460       470       480       490       500       510       520
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  CGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     CGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG
G0221659-1.seq(1>764)                     →     CGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  CGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG

                                                 530       540       550       560       570       580       590       600       610
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  GGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     GGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT
G0221659-1.seq(1>764)                     →     GGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  GGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGAT

                                                 620       630       640       650       660       670       680       690       700
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCC
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCC
G0221659-1.seq(1>764)                     →     CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCC
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCC

                                                 710       720       730       740       750       760       770       780       790
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  GACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCG
ZA03-K11696-g0221659-1_H1.3F.ab1(1>792)   →     GACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCG
G0221659-1.seq(1>764)                     →     GACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCG
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  GACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCG

                                                 800       810       820       830       840       850       860       870       880
                                                  ..........|.........|.........|.........|.........|.........|.........|.........|
                                                  CCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTCCGGCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACG
G0221659-1.seq(1>764)                     →     CCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTCCGGCCGGACTCAGATCTCGAGCTCAAGCTT
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  CCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGTCCGGCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACG

                                                 890       900       910       920       930
                                                  ..........|.........|.........|.........|.....
                                                  GTACCGCGGGCCCGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCAC
ZA04-K11696-g0221659-1_PFastBac1-R.ab1(1>792)  ←  GTACCGCGGGCCCGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATACCAC
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