```
                                                                  10        20        30        40        50        60        70        80
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  GTTAGAACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAGAACGCGGCCGCCAG
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       GTTAGAACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTATAGAACGCGGCCGCCAG

                                                                  90       100       110       120       130       140       150       160
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  CTGAAGCTTCGTACGCTGCAGGTCGACGGATCCCCGGGTTAATTAACAGATCCATCGCCACCATGGTGAGCAAGGGCGAGGAG
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       CTGAAGCTTCGTACGCTGCAGGTCGACGGATCCCCGGGTTAATTAACAGATCCATCGCCACCATGGTGAGCAAGGGCGAGGAG
G0264774-1.seq(1>789)                                     →                                       TTAATTAACAGATCCATCGCCACCATGGTGAGCAAGGGCGAGGAG

                                                                 170       180       190       200       210       220       230       240
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  CTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       CTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA
G0264774-1.seq(1>789)                                     →       CTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←                       GGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA

                                                                 250       260       270       280       290       300       310       320       330
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGA
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGA
G0264774-1.seq(1>789)                                     →       GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGA
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGA

                                                                 340       350       360       370       380       390       400       410
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  CCACCCTGGGCTACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       CCACCCTGGGCTACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
G0264774-1.seq(1>789)                                     →       CCACCCTGGGCTACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       CCACCCTGGGCTACGGCCTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC

                                                                 420       430       440       450       460       470       480       490
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGA
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACaAGACCCGCGCCGAGGTGAAGTTCGAGGGCGA
G0264774-1.seq(1>789)                                     →       GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGA
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGA

                                                                 500       510       520       530       540       550       560       570       580
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  CACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACT
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       CACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACT
G0264774-1.seq(1>789)                                     →       CACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACT
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       CACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACT

                                                                 590       600       610       620       630       640       650       660
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  ACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAG
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       ACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAG
G0264774-1.seq(1>789)                                     →       ACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAG
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       ACAACAGCCACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAG

                                                                 670       680       690       700       710       720       730       740
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  TAGGGCGCGCCACTTCTAAATAAGCGAATTTCTTATGATTTATGATTTTTATTATTAAATAAGTTATAAAAAAAATAAGTGTA
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       TAGGGCGCGCCACTTCTAAATAAGCGAATTTCTTATGATTTATGATTTTTATTATTAAATAAGTTATAAAAAAAATAAGTGTA
G0264774-1.seq(1>789)                                     →       TAGGGCGCGCCACTTCTAAATAAGCGAATTTCTTATGATTTATGATTTTTATTATTAAATAAGTTATAAAAAAAATAAGTGTA
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       TAGGGCGCGCCACTTCTAAATAAGCGAATTTCTTATGATTTATGATTTTTATTATTAAATAAGTTATAAAAAAAATAAGTGTA

                                                                 750       760       770       780       790       800       810       820       830
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  TACAAATTTTAAAGTGACTCTTAGGTTTTAAAACGAAAATTCTTATTCTTGAGTAACTCTTTCCTGTAGGTCAGGTTGCTTTC
ZG01-V44171-G0264774-1_G0264774-1V-SEQF.ab1(1>798)        →       TACaAATTTTAAAGTGACTCTtAGGTTTTAAAACGAAaATTCTTATTCTTG
G0264774-1.seq(1>789)                                     →       TACAAATTTTAAAGTGACTCTTAGGTTTTAAAACGAAAATTCTTATTCTTGAGTAACTCTTTCCTGTAGGTCAGGTTGCTTTC
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       TACAAATTTTAAAGTGACTCTTAGGTTTTAAAACGAAAATTCTTATTCTTGAGTAACTCTTTCCTGTAGGTCAGGTTGCTTTC

                                                                 840       850       860       870       880       890       900       910
                                                                  ..........|.........|.........|.........|.........|.........|.........|
                                                                  TCAGGTATAGTATGAGGTCGCTCTTATTGACCACACCTCTACCGGCAGATCCGCTAGGGATAACAGGGTAATATAGATCTGTT
G0264774-1.seq(1>789)                                     →       TCAGGTATAGTATGAGGTCGCTCTTATTGACCACACCTCTACCGGCAGATCCGCTAGGGATAACAGGGTAATATAGATCT
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       TCAGGTATAGTATGAGGTCGCTCTTATTGACCACACCTCTACCGGCAGATCCGCTAGGGATAACAGGGTAATATAGATCTGTT

                                                                 920       930       940       950       960       970
                                                                  ..........|.........|.........|.........|.........|.
                                                                  TAGCTTGCCTCGTCCCCGCCGGGTCACCCGGCCAGCGACATGGAGGCCCAGAATACCCTCC
ZG02-V44171-G0264774-1_G0264774-1V-SEQR.ab1(1>794)        ←       TAGCTTGCCTCGTCCCCGCCGGGTCACCCGGCCAGCGACATGGAGGCCCAGAATACCCTCC
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