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                                                  10        20        30        40        50        60
                                                  GCGCTaCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGG
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          GCGCTaCCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGG

                                                  70        80        90       100       110       120       130
                                                  ATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCT
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          ATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCT
G0151514-1.seq(1>737)                  →              ACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCT

                                                 140       150       160       170       180       190       200
                                                  GTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTAC
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          GTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTAC
G0151514-1.seq(1>737)                  →          GTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTAC

                                                 210       220       230       240       250       260
                                                  GAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCC
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          GAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCC
G0151514-1.seq(1>737)                  →          GAGGGCACCCAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCC

                                                 270       280       290       300       310       320       330
                                                  TGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTT
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          TGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTT
G0151514-1.seq(1>737)                  →          TGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTT

                                                 340       350       360       370       380       390       400
                                                  TAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTG
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          TAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTG
G0151514-1.seq(1>737)                  →          TAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTG

                                                 410       420       430       440       450       460
                                                  ACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGA
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          ACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGA
G0151514-1.seq(1>737)                  →          ACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGA

                                                 470       480       490       500       510       520       530
                                                  ACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCT
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          ACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCT
G0151514-1.seq(1>737)                  →          ACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCT

                                                 540       550       560       570       580       590       600
                                                  GTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCAC
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          GTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCAC
G0151514-1.seq(1>737)                  →          GTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCAC

                                                 610       620       630       640       650       660       670
                                                  CTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCG
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          CTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCG
G0151514-1.seq(1>737)                  →          CTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCG

                                                 680       690       700       710       720       730
                                                  TCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCA
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          TCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCA
G0151514-1.seq(1>737)                  →          TCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCA

                                                 740       750       760       770       780       790       800
                                                  CGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAACTTAATTGAGCGGCC
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →          CGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAACTTAATTGAGCGGCC
G0151514-1.seq(1>737)                  →          CGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACTGGGGCACAAACTTAATTGAGCGGCC
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                                                      810       820       830
                                                      GCGACTCTAGATCATAATCAGCCATACCACA
ZE12-M83848-G0151514-1_N-5.ab1(1>835)  →              GCGACTCTAGATCATAATCAGCCATACCACA
G0151514-1.seq(1>737)                  →              GC
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