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                                   10        20        30        40        50        60
                           TGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAG
G0241993-1.seq(1>5312)  →  TGGCGAATGGGACGCGCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGGTTACGCGCAG

                                70        80        90       100       110       120
                           CGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCT
G0241993-1.seq(1>5312)  →  CGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCTTCCCTTCCTTTCT

                            130       140       150       160       170       180
                           CGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATT
G0241993-1.seq(1>5312)  →  CGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCCCTTTAGGGTTCCGATT

                         190       200       210       220       230       240       250
                           TAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCC
G0241993-1.seq(1>5312)  →  TAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTGATGGTTCACGTAGTGGGCC

                                260       270       280       290       300       310
                           ATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACT
G0241993-1.seq(1>5312)  →  ATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGGACT

                             320       330       340       350       360       370
                           CTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGAT
G0241993-1.seq(1>5312)  →  CTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGGTCTATTCTTTTGATTTATAAGGGAT

                          380       390       400       410       420       430       440
                           TTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTT
G0241993-1.seq(1>5312)  →  TTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGCTGATTTAACAAAAATTTAACGCGAATTT

                                 450       460       470       480       490       500
                           TAACAAAATATTAACGTTTACAATTTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCC
G0241993-1.seq(1>5312)  →  TAACAAAATATTAACGTTTACAATTTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCC

                              510       520       530       540       550       560
                           TATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAATTAATTCTTAGAAAA
G0241993-1.seq(1>5312)  →  TATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAATTAATTCTTAGAAAA

                           570       580       590       600       610       620       630
                           ACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTT
G0241993-1.seq(1>5312)  →  ACTCATCGAGCATCAAATGAAACTGCAATTTATTCATATCAGGATTATCAATACCATATTTTT

                                  640       650       660       670       680       690
                           GAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGAT
G0241993-1.seq(1>5312)  →  GAAAAAGCCGTTTCTGTAATGAAGGAGAAAACTCACCGAGGCAGTTCCATAGGATGGCAAGAT

                               700       710       720       730       740       750
                           CCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGT
G0241993-1.seq(1>5312)  →  CCTGGTATCGGTCTGCGATTCCGACTCGTCCAACATCAATACAACCTATTAATTTCCCCTCGT

                            760       770       780       790       800       810
                           CAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCA
G0241993-1.seq(1>5312)  →  CAAAAATAAGGTTATCAAGTGAGAAATCACCATGAGTGACGACTGAATCCGGTGAGAATGGCA

                         820       830       840       850       860       870       880
                           AAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAAT
G0241993-1.seq(1>5312)  →  AAAGTTTATGCATTTCTTTCCAGACTTGTTCAACAGGCCAGCCATTACGCTCGTCATCAAAAT

                                890       900       910       920       930       940
                           CACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGAT
G0241993-1.seq(1>5312)  →  CACTCGCATCAACCAAACCGTTATTCATTCGTGATTGCGCCTGAGCGAGACGAAATACGCGAT
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                                            950       960       970       980       990       1000
                                          CGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCG
G0241993-1.seq(1>5312)                 →  CGCTGTTAAAAGGACAATTACAAACAGGAATCGAATGCAACCGGCGCAGGAACACTGCCAGCG

                                         1010      1020      1030      1040      1050      1060      1070
                                          CATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGG
G0241993-1.seq(1>5312)                 →  CATCAACAATATTTTCACCTGAATCAGGATATTCTTCTAATACCTGGAATGCTGTTTTCCCGG

                                                1080      1090      1100      1110      1120      1130
                                          GGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAA
G0241993-1.seq(1>5312)                 →  GGATCGCAGTGGTGAGTAACCATGCATCATCAGGAGTACGGATAAAATGCTTGATGGTCGGAA

                                             1140      1150      1160      1170      1180      1190
                                          GAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGC
G0241993-1.seq(1>5312)                 →  GAGGCATAAATTCCGTCAGCCAGTTTAGTCTGACCATCTCATCTGTAACATCATTGGCAACGC

                                          1200      1210      1220      1230      1240      1250      1260
                                          TACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTG
G0241993-1.seq(1>5312)                 →  TACCTTTGCCATGTTTCAGAAACAACTCTGGCGCATCGGGCTTCCCATACAATCGATAGATTG

                                                 1270      1280      1290      1300      1310      1320
                                          TCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGT
G0241993-1.seq(1>5312)                 →  TCGCACCTGATTGCCCGACATTATCGCGAGCCCATTTATACCCATATAAATCAGCATCCATGT

                                              1330      1340      1350      1360      1370      1380
                                          TGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTG
G0241993-1.seq(1>5312)                 →  TGGAATTTAATCGCGGCCTAGAGCAAGACGTTTCCCGTTGAATATGGCTCATAACACCCCTTG

                                           1390      1400      1410      1420      1430      1440
                                          TATTACTGTTTATGTAAGCAGACAGTTTTATTGTTCATGACCAAAATCCCTTAACGTGAGTTT
G0241993-1.seq(1>5312)                 →  TATTACTGTTTATGTAAGCAGACAGTTTTATTGTTCATGACCAAAATCCCTTAACGTGAGTTT

                                        1450      1460      1470      1480      1490      1500      1510
                                          TCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT
G0241993-1.seq(1>5312)                 →  TCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTT

                                               1520      1530      1540      1550      1560      1570
                                          CTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCG
G0241993-1.seq(1>5312)                 →  CTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCG

                                            1580      1590      1600      1610      1620      1630
                                          GATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAAT
G0241993-1.seq(1>5312)                 →  GATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAAT

                                         1640      1650      1660      1670      1680      1690      1700
                                          ACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACA
G0241993-1.seq(1>5312)                 →  ACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACA

                                                1710      1720      1730      1740      1750      1760
                                          TACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACC
G0241993-1.seq(1>5312)                 →  TACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACC

                                             1770      1780      1790      1800      1810      1820
                                          GGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCG
G0241993-1.seq(1>5312)                 →  GGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCG

                                          1830      1840      1850      1860      1870      1880      1890
                                          TGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTA
G0241993-1.seq(1>5312)                 →  TGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTA
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                                     1900      1910      1920      1930      1940      1950
                              TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTC
G0241993-1.seq(1>5312)     →  TGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTC

                                  1960      1970      1980      1990      2000      2010
                              GGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTC
G0241993-1.seq(1>5312)     →  GGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTC

                               2020      2030      2040      2050      2060      2070
                              GGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTA
G0241993-1.seq(1>5312)     →  GGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTA

                            2080      2090      2100      2110      2120      2130      2140
                              TGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCAC
G0241993-1.seq(1>5312)     →  TGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCAC

                                   2150      2160      2170      2180      2190      2200
                              ATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCT
G0241993-1.seq(1>5312)     →  ATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTGAGCT

                                2210      2220      2230      2240      2250      2260
                              GATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG
G0241993-1.seq(1>5312)     →  GATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCGAGTCAGTGAGCGAGGAAGCGGAAGAG

                             2270      2280      2290      2300      2310      2320      2330
                              CGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATATGGTGCA
G0241993-1.seq(1>5312)     →  CGCCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTCACACCGCATATATGGTGCA

                                    2340      2350      2360      2370      2380      2390
                              CTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGCTACG
G0241993-1.seq(1>5312)     →  CTCTCAGTACAATCTGCTCTGATGCCGCATAGTTAAGCCAGTATACACTCCGCTATCGCTACG

                                 2400      2410      2420      2430      2440      2450
                              TGACTGGGTCATGGCTGCGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTG
G0241993-1.seq(1>5312)     →  TGACTGGGTCATGGCTGCGCCCCGACACCCGCCAACACCCGCTGACGCGCCCTGACGGGCTTG

                              2460      2470      2480      2490      2500      2510      2520
                              TCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAG
G0241993-1.seq(1>5312)     →  TCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCTGCATGTGTCAGAG

                                     2530      2540      2550      2560      2570      2580
                              GTTTTCACCGTCATCACCGAAACGCGCGAGGCAGCTGCGGTAAAGCTCATCAGCGTGGTCGTG
G0241993-1.seq(1>5312)     →  GTTTTCACCGTCATCACCGAAACGCGCGAGGCAGCTGCGGTAAAGCTCATCAGCGTGGTCGTG

                                  2590      2600      2610      2620      2630      2640
                              AAGCGATTCACAGATGTCTGCCTGTTCATCCGCGTCCAGCTCGTTGAGTTTCTCCAGAAGCGT
G0241993-1.seq(1>5312)     →  AAGCGATTCACAGATGTCTGCCTGTTCATCCGCGTCCAGCTCGTTGAGTTTCTCCAGAAGCGT

                               2650      2660      2670      2680      2690      2700
                              TAATGTCTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTTCCTGTTTGGTCACTGA
G0241993-1.seq(1>5312)     →  TAATGTCTGGCTTCTGATAAAGCGGGCCATGTTAAGGGCGGTTTTTTCCTGTTTGGTCACTGA

                            2710      2720      2730      2740      2750      2760      2770
                              TGCCTCCGTGTAAGGGGGATTTCTGTTCATGGGGGTAATGATACCGATGAAACGAGAGAGGAT
G0241993-1.seq(1>5312)     →  TGCCTCCGTGTAAGGGGGATTTCTGTTCATGGGGGTAATGATACCGATGAAACGAGAGAGGAT

                                   2780      2790      2800      2810      2820      2830
                              GCTCACGATACGGGTTACTGATGATGAACATGCCCGGTTACTGGAACGTTGTGAGGGTAAACA
G0241993-1.seq(1>5312)     →  GCTCACGATACGGGTTACTGATGATGAACATGCCCGGTTACTGGAACGTTGTGAGGGTAAACA
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                                          2840      2850      2860      2870      2880      2890
                                       ACTGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTCAGGGTCAATGCCAGCGCTTCGT
G0241993-1.seq(1>5312)              →  ACTGGCGGTATGGATGCGGCGGGACCAGAGAAAAATCACTCAGGGTCAATGCCAGCGCTTCGT

                                      2900      2910      2920      2930      2940      2950      2960
                                       TAATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCGATGCAGATCCGGAACAT
G0241993-1.seq(1>5312)              →  TAATACAGATGTAGGTGTTCCACAGGGTAGCCAGCAGCATCCTGCGATGCAGATCCGGAACAT

                                              2970      2980      2990      3000      3010      3020
                                       AATGGTGCAGGGCGCTGACTTCCGCGTTTCCAGACTTTACGAAACACGGAAACCGAAGACCAT
G0241993-1.seq(1>5312)              →  AATGGTGCAGGGCGCTGACTTCCGCGTTTCCAGACTTTACGAAACACGGAAACCGAAGACCAT

                                           3030      3040      3050      3060      3070      3080
                                       TCATGTTGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCACGTTCGCTCGCGTAT
G0241993-1.seq(1>5312)              →  TCATGTTGTTGCTCAGGTCGCAGACGTTTTGCAGCAGCAGTCGCTTCACGTTCGCTCGCGTAT

                                       3090      3100      3110      3120      3130      3140      3150
                                       CGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGCCAGCCTAGCCGGGTCCTCAACGACAG
G0241993-1.seq(1>5312)              →  CGGTGATTCATTCTGCTAACCAGTAAGGCAACCCCGCCAGCCTAGCCGGGTCCTCAACGACAG

                                               3160      3170      3180      3190      3200      3210
                                       GAGCACGATCATGCGCACCCGTGGGGCCGCCATGCCGGCGATAATGGCCTGCTTCTCGCCGAA
G0241993-1.seq(1>5312)              →  GAGCACGATCATGCGCACCCGTGGGGCCGCCATGCCGGCGATAATGGCCTGCTTCTCGCCGAA

                                          3220      3230      3240      3250      3260      3270
                                       ACGTTTGGTGGCGGGACCAGTGACGAAGGCTTGAGCGAGGGCGTGCAAGATTCCGAATACCGC
G0241993-1.seq(1>5312)              →  ACGTTTGGTGGCGGGACCAGTGACGAAGGCTTGAGCGAGGGCGTGCAAGATTCCGAATACCGC

                                        3280      3290      3300      3310      3320      3330
                                       AAGCGACAGGCCGATCATCGTCGCGCTCCAGCGAAAGCGGTCCTCGCCGAAAATGACCCAGAG
G0241993-1.seq(1>5312)              →  AAGCGACAGGCCGATCATCGTCGCGCTCCAGCGAAAGCGGTCCTCGCCGAAAATGACCCAGAG

                                     3340      3350      3360      3370      3380      3390      3400
                                       CGCTGCCGGCACCTGTCCTACGAGTTGCATGATAAAGAAGACAGTCATAAGTGCGGCGACGAT
G0241993-1.seq(1>5312)              →  CGCTGCCGGCACCTGTCCTACGAGTTGCATGATAAAGAAGACAGTCATAAGTGCGGCGACGAT

                                             3410      3420      3430      3440      3450      3460
                                       AGTCATGCCCCGCGCCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCG
G0241993-1.seq(1>5312)              →  AGTCATGCCCCGCGCCCACCGGAAGGAGCTGACTGGGTTGAAGGCTCTCAAGGGCATCGGTCG

                                          3470      3480      3490      3500      3510      3520
                                       AGATCCCGGTGCCTAATGAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTT
G0241993-1.seq(1>5312)              →  AGATCCCGGTGCCTAATGAGTGAGCTAACTTACATTAATTGCGTTGCGCTCACTGCCCGCTTT

                                      3530      3540      3550      3560      3570      3580      3590
                                       CCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGG
G0241993-1.seq(1>5312)              →  CCAGTCGGGAAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAACGCGCGGGGAGAGGCGG

                                              3600      3610      3620      3630      3640      3650
                                       TTTGCGTATTGGGCGCCAGGGTGGTTTTTCTTTTCACCAGTGAGACGGGCAACAGCTGATTGC
G0241993-1.seq(1>5312)              →  TTTGCGTATTGGGCGCCAGGGTGGTTTTTCTTTTCACCAGTGAGACGGGCAACAGCTGATTGC

                                           3660      3670      3680      3690      3700      3710
                                       CCTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTTGCCCCAGCAGGC
G0241993-1.seq(1>5312)              →  CCTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGCGGTCCACGCTGGTTTGCCCCAGCAGGC

                                       3720      3730      3740      3750      3760      3770      3780
                                       GAAAATCCTGTTTGATGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGGTATCGTCGT
G0241993-1.seq(1>5312)              →  GAAAATCCTGTTTGATGGTGGTTAACGGCGGGATATAACATGAGCTGTCTTCGGTATCGTCGT
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                                                              3790      3800      3810      3820      3830      3840
                                                          ATCCCACTACCGAGATATCCGCACCAACGCGCAGCCCGGACTCGGTAATGGCGCGCATTGCGC
G0241993-1.seq(1>5312)                               →    ATCCCACTACCGAGATATCCGCACCAACGCGCAGCCCGGACTCGGTAATGGCGCGCATTGCGC

                                                           3850      3860      3870      3880      3890      3900
                                                          CCAGCGCCATCTGATCGTTGGCAACCAGCATCGCAGTGGGAACGATGCCCTCATTCAGCATTT
G0241993-1.seq(1>5312)                               →    CCAGCGCCATCTGATCGTTGGCAACCAGCATCGCAGTGGGAACGATGCCCTCATTCAGCATTT

                                                        3910      3920      3930      3940      3950      3960
                                                          GCATGGTTTGTTGAAAACCGGACATGGCACTCCAGTCGCCTTCCCGTTCCGCTATCGGCTGAA
G0241993-1.seq(1>5312)                               →    GCATGGTTTGTTGAAAACCGGACATGGCACTCCAGTCGCCTTCCCGTTCCGCTATCGGCTGAA

                                                     3970      3980      3990      4000      4010      4020      4030
                                                          TTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGCAGACGCGCCGAGACAGAACTTA
G0241993-1.seq(1>5312)                               →    TTTGATTGCGAGTGAGATATTTATGCCAGCCAGCCAGACGCAGACGCGCCGAGACAGAACTTA

                                                            4040      4050      4060      4070      4080      4090
                                                          ATGGGCCCGCTAACAGCGCGATTTGCTGGTGACCCAATGCGACCAGATGCTCCACGCCCAGTC
G0241993-1.seq(1>5312)                               →    ATGGGCCCGCTAACAGCGCGATTTGCTGGTGACCCAATGCGACCAGATGCTCCACGCCCAGTC

                                                         4100      4110      4120      4130      4140      4150
                                                          GCGTACCGTCTTCATGGGAGAAAATAATACTGTTGATGGGTGTCTGGTCAGAGACATCAAGAA
G0241993-1.seq(1>5312)                               →    GCGTACCGTCTTCATGGGAGAAAATAATACTGTTGATGGGTGTCTGGTCAGAGACATCAAGAA

                                                      4160      4170      4180      4190      4200      4210      4220
                                                          ATAACGCCGGAACATTAGTGCAGGCAGCTTCCACAGCAATGGCATCCTGGTCATCCAGCGGAT
G0241993-1.seq(1>5312)                               →    ATAACGCCGGAACATTAGTGCAGGCAGCTTCCACAGCAATGGCATCCTGGTCATCCAGCGGAT

                                                             4230      4240      4250      4260      4270      4280
                                                          AGTTAATGATCAGCCCACTGACGCGTTGCGCGAGAAGATTGTGCACCGCCGCTTTACAGGCTT
G0241993-1.seq(1>5312)                               →    AGTTAATGATCAGCCCACTGACGCGTTGCGCGAGAAGATTGTGCACCGCCGCTTTACAGGCTT

                                                          4290      4300      4310      4320      4330      4340
                                                          CGACGCCGCTTCGTTCTACCATCGACACCACCACGCTGGCACCCAGTTGATCGGCGCGAGATT
G0241993-1.seq(1>5312)                               →    CGACGCCGCTTCGTTCTACCATCGACACCACCACGCTGGCACCCAGTTGATCGGCGCGAGATT

                                                       4350      4360      4370      4380      4390      4400      4410
                                                          TAATCGCCGCGACAATTTGCGACGGCGCGTGCAGGGCCAGACTGGAGGTGGCAACGCCAATCA
G0241993-1.seq(1>5312)                               →    TAATCGCCGCGACAATTTGCGACGGCGCGTGCAGGGCCAGACTGGAGGTGGCAACGCCAATCA

                                                              4420      4430      4440      4450      4460      4470
                                                          GCAACGACTGTTTGCCCGCCAGTTGTTGTGCCACGCGGTTGGGAATGTAATTCAGCTCCGCCA
G0241993-1.seq(1>5312)                               →    GCAACGACTGTTTGCCCGCCAGTTGTTGTGCCACGCGGTTGGGAATGTAATTCAGCTCCGCCA
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)            ←       ACGACTGTTTGCCCGCCAGTTGTTGTGCCACGCGGTTGGGAATGTAATTCAGCTCCGCCA

                                                           4480      4490      4500      4510      4520      4530
                                                          TCGCCGCTTCCACTTTTTCCCGCGTTTTCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGG
G0241993-1.seq(1>5312)                               →    TCGCCGCTTCCACTTTTTCCCGCGTTTTCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGG
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)            ←    TCGCCGCTTCCACTTTTTCCCGCGTTTTCGCAGAAACGTGGCTGGCCTGGTTCACCACGCGGG

                                                        4540      4550      4560      4570      4580      4590
                                                          AAACGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACAT
G0241993-1.seq(1>5312)                               →    AAACGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACAT
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)            ←    AAACGGTCTGATAAGAGACACCGGCATACTCTGCGACATCGTATAACGTTACTGGTTTCACAT

                                                     4600      4610      4620      4630      4640      4650      4660
                                                          TCACCACCCTGAATTGACTCTCTTCCGGGCGCTATCATGCCATACCGCGAAAGGTTTTGCGCC
G0241993-1.seq(1>5312)                               →    TCACCACCCTGAATTGACTCTCTTCCGGGCGCTATCATGCCATACCGCGAAAGGTTTTGCGCC
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)            ←    TCACCACCCTGAATTGACTCTCTTCCGGGCGCTATCATGCCATACCGCGAAAGGTTTTGCGCC
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                                                           4670      4680      4690      4700      4710      4720
                                                        ATTCGATGGTGTCCGGGATCTCGACGCTCTCCCTTATGCGACTCCTGCATTAGGAAGCAGCCC
G0241993-1.seq(1>5312)                           →      ATTCGATGGTGTCCGGGATCTCGACGCTCTCCCTTATGCGACTCCTGCATTAGGAAGCAGCCC
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      ATTCGATGGTGTCCGGGATCTCGACGCTCTCCCTTATGCGACTCCTGCATTAGGAAGCAGCCC

                                                        4730      4740      4750      4760      4770      4780
                                                        AGTAGTAGGTTGAGGCCGTTGAGCACCGCCGCCGCAAGGAATGGTGCATGCAAGGAGATGGCG
G0241993-1.seq(1>5312)                           →      AGTAGTAGGTTGAGGCCGTTGAGCACCGCCGCCGCAAGGAATGGTGCATGCAAGGAGATGGCG
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      AGTAGTAGGTTGAGGCCGTTGAGCACCGCCGCCGCAAGGAATGGTGCATGCAAGGAGATGGCG

                                                     4790      4800      4810      4820      4830      4840      4850
                                                        CCCAACAGTCCCCCGGCCACGGGGCCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGC
G0241993-1.seq(1>5312)                           →      CCCAACAGTCCCCCGGCCACGGGGCCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGC
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      CCCAACAGTCCCCCGGCCACGGGGCCTGCCACCATACCCACGCCGAAACAAGCGCTCATGAGC

                                                            4860      4870      4880      4890      4900      4910
                                                        CCGAAGTGGCGAGCCCGATCTTCCCCATCGGTGATGTCGGCGATATAGGCGCCAGCAACCGCA
G0241993-1.seq(1>5312)                           →      CCGAAGTGGCGAGCCCGATCTTCCCCATCGGTGATGTCGGCGATATAGGCGCCAGCAACCGCA
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      CCGAAGTGGCGAGCCCGATCTTCCCCATCGGTGATGTCGGCGATATAGGCGCCAGCAACCGCA

                                                         4920      4930      4940      4950      4960      4970
                                                        CCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGATCTCGATCCCG
G0241993-1.seq(1>5312)                           →      CCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGATCTCGATCCCG
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      CCTGTGGCGCCGGTGATGCCGGCCACGATGCGTCCGGCGTAGAGGATCGAGATCTCGATCCCG

                                                       4980      4990      5000      5010      5020      5030      5040
                                                        CGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAA
G0241993-1.seq(1>5312)                           →      CGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAA
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      CGAAATTAATACGACTCACTATAGGGGAATTGTGAGCGGATAACAATTCCCCTCTAGAAATAA

                                                             5050      5060      5070      5080      5090      5100
                                                        TTTTGTTTAACTTTAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGG
G0241993-1.seq(1>5312)                           →      TTTTGTTTAACTTTAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGG
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      TTTTGTTTAACTTTAAGAAGGAGATATACATATGGCTAGCATGACTGGTGGACAGCAAATGGG

                                                          5110      5120      5130      5140      5150      5160
                                                        TCGCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCACCACC
G0241993-1.seq(1>5312)                           →      TCGCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGCACTCGAGCACCACCACCACC
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      TCGCGGATCCGAATTCGAGCTCCGTCGACAAGCTTGCGGCCGCACTCGAGCaCCACCACCACC

                                                       5170      5180      5190      5200      5210      5220
                                                        ACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTG
G0241993-1.seq(1>5312)                           →      ACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGCTGAGTTGGCTGCTGCCACCGCTG
C11-E35899-G0241993-1_PET-SEQF.ab1(1>793)        ←      ACCACTGAGATCCGGCTGCTAACAAAGCCCGAAAGGAAGC

                                                    5230      5240      5250      5260      5270      5280      5290
                                                        AGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAG
G0241993-1.seq(1>5312)                           →      AGCAATAACTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTGCTGAAAG

                                                           5300      5310
                                                        GAGGAACTATATCCGGAT
G0241993-1.seq(1>5312)                           →      GAGGAACTATATCCGGAT
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