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                                                  10        20        30        40        50        60
                                                  CATCACCATCACCATCACGGATCCATGCTGATTGCCAAAGATCTGATGCAGAAAGGTGCAGAT
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      CATCACCATCACCATCACGGATCCATGCTGATTGCCAAAGATCTGATGCAGAAAGGTGCAGAT
725029-1.seq(1>471)                        →                         GGATCCATGCTGATTGCCAAAGATCTGATGCAGAAAGGTGCAGAT

                                                      70        80        90       100       110       120
                                                  AATAAGACCTATTGCATTAGCATTAACCTGGCAGTGCTGAAATTTGCAACCAATACCGGTAGC
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      AATAAGACCTATTGCATTAGCATTAACCTGGCAGTGCTGAAATTTGCAACCAATACCGGTAGC
725029-1.seq(1>471)                        →      AATAAGACCTATTGCATTAGCATTAACCTGGCAGTGCTGAAATTTGCAACCAATACCGGTAGC

                                                     130       140       150       160       170       180
                                                  CTGAGTCTGAGTAATGGTAGTCATTGCGATAGCGAAGATGAAGTTGCATATAGCGAAGTGTGC
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      CTGAGTCTGAGTAATGGTAGTCATTGCGATAGCGAAGATGAAGTTGCATATAGCGAAGTGTGC
725029-1.seq(1>471)                        →      CTGAGTCTGAGTAATGGTAGTCATTGCGATAGCGAAGATGAAGTTGCATATAGCGAAGTGTGC

                                                 190       200       210       220       230       240       250
                                                  CAGATGAGCAATGCCGTGCCGGTTTATGATATGAATTGGATGACCGCCAGTCTGAAAGCCAGT
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      CAGATGAGCAATGCCGTGCCGGTTTATGATATGAATTGGATGACCGCCAGTCTGAAAGCCAGT
725029-1.seq(1>471)                        →      CAGATGAGCAATGCCGTGCCGGTTTATGATATGAATTGGATGACCGCCAGTCTGAAAGCCAGT

                                                      260       270       280       290       300       310
                                                  CGCAAACTGTATACCTTTGAAAAAGCCGAAATGCTGCTGAGCAAAGTTCTGTTTCTGAAAGCA
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      CGCAAACTGTATACCTTTGAAAAAGCCGAAATGCTGCTGAGCAAAGTTCTGTTTCTGAAAGCA
725029-1.seq(1>471)                        →      CGCAAACTGTATACCTTTGAAAAAGCCGAAATGCTGCTGAGCAAAGTTCTGTTTCTGAAAGCA

                                                     320       330       340       350       360       370
                                                  TGGTTTCCGAGCCTGTGTGTGGCAGCCTTTCATGCCGAACTGGATACCGTGGATCGCGAAGCC
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      TGGTTTCCGAGCCTGTGTGTGGCAGCCTTTCATGCCGAACTGGATACCGTGGATCGCGAAGCC
725029-1.seq(1>471)                        →      TGGTTTCCGAGCCTGTGTGTGGCAGCCTTTCATGCCGAACTGGATACCGTGGATCGCGAAGCC

                                                 380       390       400       410       420       430       440
                                                  TGTCCGCAGAGCGAACAGTATGCCCGTCTGCTGAGTGTTCGTCGTGGCCTGGATAGTGCAGTT
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      TGTCCGCAGAGCGAACAGTATGCCCGTCTGCTGAGTGTTCGTCGTGGCCTGGATAGTGCAGTT
725029-1.seq(1>471)                        →      TGTCCGCAGAGCGAACAGTATGCCCGTCTGCTGAGTGTTCGTCGTGGCCTGGATAGTGCAGTT

                                                      450       460       470       480       490       500
                                                  CATGGTGAAAGTCATTGGCGTAAAGATGCCACCGATGGCGCCAAGCTTAATTAGCTGAGCTTG
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      CATGGTGAAAGTCATTGGCGTAAAGATGCCACCGATGGCGCCAAGCTTAATTAGCTGAGCTTG
725029-1.seq(1>471)                        →      CATGGTGAAAGTCATTGGCGTAAAGATGCCACCGATGGCGCCAAGCTT

                                                     510       520       530       540       550       560
                                                  GACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTCAGAACGCTCG
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      GACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTCAGAACGCTCG

                                                 570       580       590       600       610       620       630
                                                  GTTGCCGCCGGGCGTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCT
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      GTTGCCGCCGGGCGTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCT

                                                      640       650       660       670       680       690
                                                  AAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCAT
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      AAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCAT

                                                     700       710
                                                  CGTAAAGAACATTTTGA
B07-M87789-725029-1_PQE30-seqF.ab1(1>710)  →      CGTAAAGAACATTTTGA
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