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                                                  10        20        30        40        50        60        70        80        90       100
                                                  ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                  GAGAcCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCGCCACCATGTCCGACAACGGCCCCCAAAATCAGAGGAACGCCCCTAGAATCACC
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GAGAcCCAAGCTGGCTAGCGTTTAAACTTAAGCTTGGTACCGAGCTCGGATCCGCCACCATGTCCGACAACGGCCCCCAAAATCAGAGGAACGCCCCTAGAATCACC
U194RFE240-8.seq(1>1280)                        →                                                   GGATCCgccaccATGTCCGACAACGGCCCCCAAAATCAGAGGAACGCCCCTAGAATCACC

                                                 110       120       130       140       150       160       170       180       190       200       210
                                                 ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                 TTCGGCGGCCCCAGCGACAGCACAGGCTCCAACCAGAACGGCGAGAGAAGCGGCGCCAGATCCAAGCAGCGGAGACCTCAGGGACTGCCTAACAACACAGCCTCCTG
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  TTCGGCGGCCCCAGCGACAGCACAGGCTCCAACCAGAACGGCGAGAGAAGCGGCGCCAGATCCAAGCAGCGGAGACCTCAGGGACTGCCTAACAACACAGCCTCCTG
U194RFE240-8.seq(1>1280)                        →  TTCGGCGGCCCCAGCGACAGCACAGGCTCCAACCAGAACGGCGAGAGAAGCGGCGCCAGATCCAAGCAGCGGAGACCTCAGGGACTGCCTAACAACACAGCCTCCTG

                                                    220       230       240       250       260       270       280       290       300       310       320
                                                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                    GTTCACCGCCCTCACCCAGCACGGCAAGGAAGATCTGAAGTTCCCCAGAGGACAGGGCGTGCCCATCAACACCAACAGCAGCCCTGATGACCAGATCGGCTACTATA
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GTTCACCGCCCTCACCCAGCACGGCAAGGAAGATCTGAAGTTCCCCAGAGGACAGGGCGTGCCCATCAACACCAACAGCAGCCCTGATGACCAGATCGGCTACTATA
U194RFE240-8.seq(1>1280)                        →  GTTCACCGCCCTCACCCAGCACGGCAAGGAAGATCTGAAGTTCCCCAGAGGACAGGGCGTGCCCATCAACACCAACAGCAGCCCTGATGACCAGATCGGCTACTATA

                                                        330       340       350       360       370       380       390       400       410       420
                                                        ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                        GACGGGCCACCAGAAGAATCAGAGGCGGCGACGGCAAGATGAAGGACCTGAGCCCCCGGTGGTACTTCTACTACCTGGGCACAGGACCTGAGGCTGGCCTGCCCTAC
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GACGGGCCACCAGAAGAATCAGAGGCGGCGACGGCAAGATGAAGGACCTGAGCCCCCGGTGGTACTTCTACTACCTGGGCACAGGACCTGAGGCTGGCCTGCCCTAC
U194RFE240-8.seq(1>1280)                        →  GACGGGCCACCAGAAGAATCAGAGGCGGCGACGGCAAGATGAAGGACCTGAGCCCCCGGTGGTACTTCTACTACCTGGGCACAGGACCTGAGGCTGGCCTGCCCTAC

                                                    430       440       450       460       470       480       490       500       510       520       530
                                                    ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                    GGCGCTAACAAGGACGGCATCATCTGGGTCGCCACAGAGGGCGCTCTGAATACACCTAAGGACCACATTGGAACAAGAAACCCCGCAAATAACGCCGCTATCGTGCT
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GGCGCTAACAAGGACGGCATCATCTGGGTCGCCACAGAGGGCGCTCTGAATACACCTAAGGACCACATTGGAACAAGAAACCCCGCAAATAACGCCGCTATCGTGCT
U194RFE240-8.seq(1>1280)                        →  GGCGCTAACAAGGACGGCATCATCTGGGTCGCCACAGAGGGCGCTCTGAATACACCTAAGGACCACATTGGAACAAGAAACCCCGCAAATAACGCCGCTATCGTGCT

                                                     540       550       560       570       580       590       600       610       620       630       640
                                                     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                     GCAGCTGCCACAGGGAACCACCCTGCCGAAGGGCTTCTACGCCGAGGGCAGTCGCGGAGGCTCTCAGGCCTCTAGCCGGAGCTCTAGCCGGAGCAGAAATAGCAGCA
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GCAGCTGCCACAGGGAACCACCcTGCCGAAGGGCTTCTACGCCGAGGGCAGTCGCGGAGGCTCTCAGGCCTCTAGCCGGAGCTCTAGCCGGAGCAGAAATAGCAGCA
U194RFE240-8.seq(1>1280)                        →  GCAGCTGCCACAGGGAACCACCCTGCCGAAGGGCTTCTACGCCGAGGGCAGTCGCGGAGGCTCTCAGGCCTCTAGCCGGAGCTCTAGCCGGAGCAGAAATAGCAGCA
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←                                                                                                   GAGCAGAAATAGCAGCA

                                                         650       660       670       680       690       700       710       720       730       740
                                                         ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                         GAAACAGCACCCCAGGCAGCTCTAGAGGCACCAGCCCCGCCCGGATGGCCGGCAACGGCGGAGATGCCGCCCTGGCCCTCCTGCTGCTGGATAGACTGAACCAACTG
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GAAACAGCACCCCAGGCAGCTCTAGAGGCACCAGCCCCGCCCGGATGGCCGGCAACGGCGGAGATGCCGCCCTGGCCCTCCTGCTGCTGGATAGACTGAACCAACTG
U194RFE240-8.seq(1>1280)                        →  GAAACAGCACCCCAGGCAGCTCTAGAGGCACCAGCCCCGCCCGGATGGCCGGCAACGGCGGAGATGCCGCCCTGGCCCTCCTGCTGCTGGATAGACTGAACCAACTG
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←  GAAACAGCACCCCAGGCAGCTCTAGAGGCACCAGCCCCGCCCGGATGGCCGGCAACggCgGAGATgCCGCCCTgGCCCTCCTGCTgCTgGATAGACTGAACCAACTG

                                                     750       760       770       780       790       800       810       820       830       840       850
                                                     ....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|....|
                                                     GAATCTAAGATGTCCGGCAAAGGCCAGCAGCAACAAGGCCAGACCGTGACAAAGAAAAGCGCCGCTGAAGCCAGCAAGAAACCTCGGCAGAAGCGGACCGCCACCAA
E10-TG176300-U194RFE240-8-PCDNA3.1F.ab1(1>789)  →  GAATCTAAGATGTCCGGCAAAGGCCAGCAGCAACAAGGCC
U194RFE240-8.seq(1>1280)                        →  GAATCTAAGATGTCCGGCAAAGGCCAGCAGCAACAAGGCCAGACCGTGACAAAGAAAAGCGCCGCTGAAGCCAGCAAGAAACCTCGGCAGAAGCGGACCGCCACCAA
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←  GAATCTAAGATGTCCGGCAAAGGCCAGCAGCAACAAGGCCAGACCGTGACAAAGAAAAGCGCCGCTGAAGCCAGCAAGAAACCTCGGCAGAAGCGGACCGCCACCAA
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                                                   860       870       880       890       900       910       920       930       940       950       960
                                                   GGCCTACAACGTGACACAGGCTTTTGGCAGACGGGGCCCTGAACAAACCCAGGGCAATTTCGGAGATCAGGAGCTGATCCGGCAGGGCACAGACTACAAGCACTGGC
U194RFE240-8.seq(1>1280)                   →       GGCCTACAACGTGACACAGGCTTTTGGCAGACGGGGCCCTGAACAAACCCAGGGCAATTTCGGAGATCAGGAGCTGATCCGGCAGGGCACAGACTACAAGCACTGGC
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←   GGCCTACAACGTGACACAGGCTTTTGGCAGACGGGGCCCTGAACAAACCCAGGGCAATTTCGGAGATCAGGAGCTGATCCGGCAGGGCACAGACTACAAGCACTGGC

                                                       970       980       990      1000      1010      1020      1030      1040      1050      1060      1070
                                                   CTCAGATCGCCCAGTTCGCCCCTAGCGCCAGCGCCTTTTTCGGCATGTCTAGAATCGGAATGGAAGTGACCCCTTCTGGGACCTGGCTGACCTACACCGGAGCCATC
U194RFE240-8.seq(1>1280)                   →       CTCAGATCGCCCAGTTCGCCCCTAGCGCCAGCGCCTTTTTCGGCATGTCTAGAATCGGAATGGAAGTGACCCCTTCTGGGACCTGGCTGACCTACACCGGAGCCATC
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←   CTCAGATCGCCCAGTTCGCCCCTAGCGCCAGCGCCTTTTTCGGCATGTCTAGAATCGGAATGGAAGTGACCCCTTCTGGGACCTGGCTGACCTACACCGGAGCCATC

                                                      1080      1090      1100      1110      1120      1130      1140      1150      1160      1170
                                                   AAGCTGGACGACAAGGACCCTAACTTCAAGGACCAGGTGATCCTGCTGAACAAGCATATCGACGCCTATAAGACCTTTCCACCTACCGAGCCTAAGAAAGATAAGAA
U194RFE240-8.seq(1>1280)                   →       AAGCTGGACGACAAGGACCCTAACTTCAAGGACCAGGTGATCCTGCTGAACAAGCATATCGACGCCTATAAGACCTTTCCACCTACCGAGCCTAAGAAAGATAAGAA
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←   AAGCTGGACGACAAGGACCCTAACTTCAAGGACCAGGTGATCCTGCTGAACAAGCATATCGACGCCTATAAGACCTTTCCACCTACCGAGCCTAAGAAAGATAAGAA

                                                   1180      1190      1200      1210      1220      1230      1240      1250      1260      1270      1280
                                                   GAAAAAAGCCGACGAGACACAGGCCCTGCCTCAGAGACAGAAAAAGCAGCAGACCGTGACACTGCTGCCTGCTGCTGATCTGGACGACTTCAGCAAGCAACTGCAGC
U194RFE240-8.seq(1>1280)                   →       GAAAAAAGCCGACGAGACACAGGCCCTGCCTCAGAGACAGAAAAAGCAGCAGACCGTGACACTGCTGCCTGCTGCTGATCTGGACGACTTCAGCAAGCAACTGCAGC
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←   GAAAAAAGCCGACGAGACACAGGCCCTGCCTCAGAGACAGAAAAAGCAGCAGACCGTGACACTGCTGCCTGCTGCTGATCTGGACGACTTCAGCAAGCAACTGCAGC

                                                      1290      1300      1310      1320      1330      1340      1350      1360      1370      1380      1390
                                                   AGAGCATGAGCAGCGCCGATAGCACCCAGGCCTGAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCC
U194RFE240-8.seq(1>1280)                   →       AGAGCATGAGCAGCGCCGATAGCACCCAGGCCTGAGCGGCCGC
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←   AGAGCATGAGCAGCGCCGATAGCACCCAGGCCTGAGCGGCCGCTCGAGTCTAGAGGGCCCGTTTAAACCCGCTGATCAGCCTCGACTGTGCCTTCTAGTTGCCAGCC

                                                      1400
                                                   ATCTGTTG
A11-TG176300-U194RFE240-8-CMVR-SeqR.ab1(1>774)  ←   ATCTGTTG
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