Sequence: LSL-TOPO Range: 1 to 9267

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                10         20         30         40         50
          AGCGCCCAAT ACGCAAACCG CCTCTCCCCG CGCGTTGGCC GATTCATTAA
          TCGCGGGTTA TGCGTTTGGC GGAGAGGGGC GCGCAACCGG CTAAGTAATT

                60         70         80         90        100
          TGCAGCTGGC ACGACAGGTT TCCCGACTGG AAAGCGGGCA GTGAGCGCAA
          ACGTCGACCG TGCTGTCCAA AGGGCTGACC TTTCGCCCGT CACTCGCGTT

               110        120        130        140        150
          CGCAATTAAT GTGAGTTAGC TCACTCATTA GGCACCCCAG GCTTTACACT
          GCGTTAATTA CACTCAATCG AGTGAGTAAT CCGTGGGGTC CGAAATGTGA

               160        170        180        190        200
          TTATGCTTCC GGCTCGTATG TTGTGTGGAA TTGTGAGCGG ATAACAATTT
          AATACGAAGG CCGAGCATAC AACACACCTT AACACTCGCC TATTGTTAAA

               210        220        230        240        250
          CACACAGGAA ACAGCTATGA CCATGATTAC GCCAAGCTAT TTAGGTGACA
          GTGTGTCCTT TGTCGATACT GGTACTAATG CGGTTCGATA AATCCACTGT

               260        270        280        290        300
          CTATAGAATA CTCAAGCTAT GCATCAAGCT TGGTACCAAT CTCGAGCCTT
          GATATCTTAT GAGTTCGATA CGTAGTTCGA ACCATGGTTA GAGCTCGGAA

               310        320        330        340        350
          AATTAACCAC GCGTGGCGCG CCTTGAGCTC GGATCCGGGC CCCCCCTCGA
          TTAATTGGTG CGCACCGCGC GGAACTCGAG CCTAGGCCCG GGGGGGAGCT

                     >LoxP
                       |
               360     |  370        380        390        400
          TCGAGGTCGA CATAACTTCG TATAATGTAT GCTATACGAA GTTATTAGGT
          AGCTCCAGCT GTATTGAAGC ATATTACATA CGATATGCTT CAATAATCCA

>SV40_PA_#4   >Kozak-TGA-SD                    <SD5'
          |      |                               |
          |    410        420        430        440        450
          CCCTCGACCT GCAGACTTAC TCAAGCCATG GTGGCTAGCT TGCGGAATTC
          GGGAGCTGGA CGTCTGAATG AGTTCGGTAC CACCGATCGA ACGCCTTAAG

               460        470        480        490        500
          CAGACATGAT AAGATACATT GATGAGTTTG GACAAACCAC AACTAGAATG
          GTCTGTACTA TTCTATGTAA CTACTCAAAC CTGTTTGGTG TTGATCTTAC

               510        520        530        540        550
          CAGTGAAAAA AATGCTTTAT TTGTGAAATT TGTGATGCTA TTGCTTTATT
          GTCACTTTTT TTACGAAATA AACACTTTAA ACACTACGAT AACGAAATAA

               560        570        580        590        600
          TGTAACCATT ATAAGCTGCA ATAAACAAGT TAACAACAAC AATTGCATTC
          ACATTGGTAA TATTCGACGT TATTTGTTCA ATTGTTGTTG TTAACGTAAG

               610        620        630        640        650
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ATTTTATGTT TCAGGTTCAG GGGGAGGTGT GGGAGGTTTT TTAAAGCAAG
TAAAATACAA AGTCCAAGTC CCCCTCCACA CCCTCCAAAA AATTTCGTTC

       660        670        680        690        700
TAAAACCTCT ACAAATGTGG TATGGCTGAT TATGATCTCT AGTCAAGGCA
ATTTTGGAGA TGTTTACACC ATACCGACTA ATACTAGAGA TCAGTTCCGT

       710        720        730        740        750
CTATACATCA AATATTCCTT ATTAACCCCT TTACAAATTA AAAAGCTAAA
GATATGTAGT TTATAAGGAA TAATTGGGGA AATGTTTAAT TTTTCGATTT

       760        770        780        790        800
GGTACACAAT TTTTGAGCAT AGTTATTAAT AGCAGACACT CTATGCCTGT
CCATGTGTTA AAAACTCGTA TCAATAATTA TCGTCTGTGA GATACGGACA

       810        820        830        840        850
GTGGAGTAAG AAAAAACAGT ATGTTATGAT TATAACTGTT ATGCCTACTT
CACCTCATTC TTTTTTGTCA TACAATACTA ATATTGACAA TACGGATGAA

       860        870        880        890        900
ATAAAGGTTA CAGAATATTT TTCCATAATT TTCTTGTATA GCAGTGCAGC
TATTTCCAAT GTCTTATAAA AAGGTATTAA AAGAACATAT CGTCACGTCG

       910        920        930        940        950
TTTTTCCTTT GTGGTGTAAA TAGCAAAGCA AGCAAGAGTT CTATTACTAA
AAAAAGGAAA CACCACATTT ATCGTTTCGT TCGTTCTCAA GATAATGATT

       960        970        980        990       1000
ACACAGCATG ACTCAAAAAA CTTAGCAATT CTGAAGGAAA GTCCTTGGGG
TGTGTCGTAC TGAGTTTTTT GAATCGTTAA GACTTCCTTT CAGGAACCCC

      1010       1020       1030       1040       1050
TCTTCTACCT TTCTCTTCTT TTTTGGAGGA GTAGAATGTT GAGAGTCAGC
AGAAGATGGA AAGAGAAGAA AAAACCTCCT CATCTTACAA CTCTCAGTCG

      1060       1070       1080       1090       1100
AGTAGCCTCA TCATCACTAG ATGGCATTTC TTCTGAGCAA AACAGGTTTT
TCATCGGAGT AGTAGTGATC TACCGTAAAG AAGACTCGTT TTGTCCAAAA

      1110       1120       1130       1140       1150
CCTCATTAAA GGCATTCCAC CACTGCTCCC ATTCATCAGT TCCATAGGTT
GGAGTAATTT CCGTAAGGTG GTGACGAGGG TAAGTAGTCA AGGTATCCAA

      1160       1170       1180       1190       1200
GGAATCTAAA ATACACAAAC AATTAGAATC AGTAGTTTAA CACATTATAC
CCTTAGATTT TATGTGTTTG TTAATCTTAG TCATCAAATT GTGTAATATG

      1210       1220       1230       1240       1250
ACTTAAAAAT TTTATATTTA CCTTAGAGCT TTAAATCTCT GTAGGTAGTT
TGAATTTTTA AAATATAAAT GGAATCTCGA AATTTAGAGA CATCCATCAA

                                                >SV40_PA_#3
                                                     |
      1260       1270       1280       1290       1300
TGTCCAATTA TGTCACACCA CAGAAGTAAG GTTCCTTCAC AAAGATCCCT
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ACAGGTTAAT ACAGTGTGGT GTCTTCATTC CAAGGAAGTG TTTCTAGGGA

      1310       1320       1330       1340       1350
CGACCAGACA TGATAAGATA CATTGATGAG TTTGGACAAA CCACAACTAG
GCTGGTCTGT ACTATTCTAT GTAACTACTC AAACCTGTTT GGTGTTGATC

      1360       1370       1380       1390       1400
AATGCAGTGA AAAAAATGCT TTATTTGTGA AATTTGTGAT GCTATTGCTT
TTACGTCACT TTTTTTACGA AATAAACACT TTAAACACTA CGATAACGAA

      1410       1420       1430       1440       1450
TATTTGTAAC CATTATAAGC TGCAATAAAC AAGTTAACAA CAACAATTGC
ATAAACATTG GTAATATTCG ACGTTATTTG TTCAATTGTT GTTGTTAACG

      1460       1470       1480       1490       1500
ATTCATTTTA TGTTTCAGGT TCAGGGGGAG GTGTGGGAGG TTTTTTAAAG
TAAGTAAAAT ACAAAGTCCA AGTCCCCCTC CACACCCTCC AAAAAATTTC

      1510       1520       1530       1540       1550
CAAGTAAAAC CTCTACAAAT GTGGTATGGC TGATTATGAT CTCTAGTCAA
GTTCATTTTG GAGATGTTTA CACCATACCG ACTAATACTA GAGATCAGTT

      1560       1570       1580       1590       1600
GGCACTATAC ATCAAATATT CCTTATTAAC CCCTTTACAA ATTAAAAAGC
CCGTGATATG TAGTTTATAA GGAATAATTG GGGAAATGTT TAATTTTTCG

      1610       1620       1630       1640       1650
TAAAGGTACA CAATTTTTGA GCATAGTTAT TAATAGCAGA CACTCTATGC
ATTTCCATGT GTTAAAAACT CGTATCAATA ATTATCGTCT GTGAGATACG

      1660       1670       1680       1690       1700
CTGTGTGGAG TAAGAAAAAA CAGTATGTTA TGATTATAAC TGTTATGCCT
GACACACCTC ATTCTTTTTT GTCATACAAT ACTAATATTG ACAATACGGA

      1710       1720       1730       1740       1750
ACTTATAAAG GTTACAGAAT ATTTTTCCAT AATTTTCTTG TATAGCAGTG
TGAATATTTC CAATGTCTTA TAAAAAGGTA TTAAAAGAAC ATATCGTCAC

      1760       1770       1780       1790       1800
CAGCTTTTTC CTTTGTGGTG TAAATAGCAA AGCAAGCAAG AGTTCTATTA
GTCGAAAAAG GAAACACCAC ATTTATCGTT TCGTTCGTTC TCAAGATAAT

      1810       1820       1830       1840       1850
CTAAACACAG CATGACTCAA AAAACTTAGC AATTCTGAAG GAAAGTCCTT
GATTTGTGTC GTACTGAGTT TTTTGAATCG TTAAGACTTC CTTTCAGGAA

      1860       1870       1880       1890       1900
GGGGTCTTCT ACCTTTCTCT TCTTTTTTGG AGGAGTAGAA TGTTGAGAGT
CCCCAGAAGA TGGAAAGAGA AGAAAAAACC TCCTCATCTT ACAACTCTCA

      1910       1920       1930       1940       1950
CAGCAGTAGC CTCATCATCA CTAGATGGCA TTTCTTCTGA GCAAAACAGG
GTCGTCATCG GAGTAGTAGT GATCTACCGT AAAGAAGACT CGTTTTGTCC

      1960       1970       1980       1990       2000
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   TTTTCCTCAT TAAAGGCATT CCACCACTGC TCCCATTCAT CAGTTCCATA
   AAAAGGAGTA ATTTCCGTAA GGTGGTGACG AGGGTAAGTA GTCAAGGTAT

         2010       2020       2030       2040       2050
   GGTTGGAATC TAAAATACAC AAACAATTAG AATCAGTAGT TTAACACATT
   CCAACCTTAG ATTTTATGTG TTTGTTAATC TTAGTCATCA AATTGTGTAA

         2060       2070       2080       2090       2100
   ATACACTTAA AAATTTTATA TTTACCTTAG AGCTTTAAAT CTCTGTAGGT
   TATGTGAATT TTTAAAATAT AAATGGAATC TCGAAATTTA GAGACATCCA

         2110       2120       2130       2140       2150
   AGTTTGTCCA ATTATGTCAC ACCACAGAAG TAAGGTTCCT TCACAAAGAT
   TCAAACAGGT TAATACAGTG TGGTGTCTTC ATTCCAAGGA AGTGTTTCTA

>SV40_PA_#2
      |
      |    2160       2170       2180       2190       2200
   CCCTCGACCA GACATGATAA GATACATTGA TGAGTTTGGA CAAACCACAA
   GGGAGCTGGT CTGTACTATT CTATGTAACT ACTCAAACCT GTTTGGTGTT

         2210       2220       2230       2240       2250
   CTAGAATGCA GTGAAAAAAA TGCTTTATTT GTGAAATTTG TGATGCTATT
   GATCTTACGT CACTTTTTTT ACGAAATAAA CACTTTAAAC ACTACGATAA

         2260       2270       2280       2290       2300
   GCTTTATTTG TAACCATTAT AAGCTGCAAT AAACAAGTTA ACAACAACAA
   CGAAATAAAC ATTGGTAATA TTCGACGTTA TTTGTTCAAT TGTTGTTGTT

         2310       2320       2330       2340       2350
   TTGCATTCAT TTTATGTTTC AGGTTCAGGG GGAGGTGTGG GAGGTTTTTT
   AACGTAAGTA AAATACAAAG TCCAAGTCCC CCTCCACACC CTCCAAAAAA

         2360       2370       2380       2390       2400
   AAAGCAAGTA AAACCTCTAC AAATGTGGTA TGGCTGATTA TGATCTCTAG
   TTTCGTTCAT TTTGGAGATG TTTACACCAT ACCGACTAAT ACTAGAGATC

         2410       2420       2430       2440       2450
   TCAAGGCACT ATACATCAAA TATTCCTTAT TAACCCCTTT ACAAATTAAA
   AGTTCCGTGA TATGTAGTTT ATAAGGAATA ATTGGGGAAA TGTTTAATTT

         2460       2470       2480       2490       2500
   AAGCTAAAGG TACACAATTT TTGAGCATAG TTATTAATAG CAGACACTCT
   TTCGATTTCC ATGTGTTAAA AACTCGTATC AATAATTATC GTCTGTGAGA

         2510       2520       2530       2540       2550
   ATGCCTGTGT GGAGTAAGAA AAAACAGTAT GTTATGATTA TAACTGTTAT
   TACGGACACA CCTCATTCTT TTTTGTCATA CAATACTAAT ATTGACAATA

         2560       2570       2580       2590       2600
   GCCTACTTAT AAAGGTTACA GAATATTTTT CCATAATTTT CTTGTATAGC
   CGGATGAATA TTTCCAATGT CTTATAAAAA GGTATTAAAA GAACATATCG

         2610       2620       2630       2640       2650
   AGTGCAGCTT TTTCCTTTGT GGTGTAAATA GCAAAGCAAG CAAGAGTTCT
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TCACGTCGAA AAAGGAAACA CCACATTTAT CGTTTCGTTC GTTCTCAAGA

      2660        2670        2680        2690        2700
ATTACTAAAC ACAGCATGAC TCAAAAAACT TAGCAATTCT GAAGGAAAGT
TAATGATTTG TGTCGTACTG AGTTTTTTGA ATCGTTAAGA CTTCCTTTCA

      2710        2720        2730        2740        2750
CCTTGGGGTC TTCTACCTTT CTCTTCTTTT TTGGAGGAGT AGAATGTTGA
GGAACCCCAG AAGATGGAAA GAGAAGAAAA AACCTCCTCA TCTTACAACT

      2760        2770        2780        2790        2800
GAGTCAGCAG TAGCCTCATC ATCACTAGAT GGCATTTCTT CTGAGCAAAA
CTCAGTCGTC ATCGGAGTAG TAGTGATCTA CCGTAAAGAA GACTCGTTTT

      2810        2820        2830        2840        2850
CAGGTTTTCC TCATTAAAGG CATTCCACCA CTGCTCCCAT TCATCAGTTC
GTCCAAAAGG AGTAATTTCC GTAAGGTGGT GACGAGGGTA AGTAGTCAAG

      2860        2870        2880        2890        2900
CATAGGTTGG AATCTAAAAT ACACAAACAA TTAGAATCAG TAGTTTAACA
GTATCCAACC TTAGATTTTA TGTGTTTGTT AATCTTAGTC ATCAAATTGT

      2910        2920        2930        2940        2950
CATTATACAC TTAAAAATTT TATATTTACC TTAGAGCTTT AAATCTCTGT
GTAATATGTG AATTTTTAAA ATATAAATGG AATCTCGAAA TTTAGAGACA

      2960        2970        2980        2990        3000
AGGTAGTTTG TCCAATTATG TCACACCACA GAAGTAAGGT TCCTTCACAA
TCCATCAAAC AGGTTAATAC AGTGTGGTGT CTTCATTCCA AGGAAGTGTT

 >SV40_PA_#1
      |
      3010        3020        3030        3040        3050
AGATCCCTCG ACCAGACATG ATAAGATACA TTGATGAGTT TGGACAAACC
TCTAGGGAGC TGGTCTGTAC TATTCTATGT AACTACTCAA ACCTGTTTGG

      3060        3070        3080        3090        3100
ACAACTAGAA TGCAGTGAAA AAAATGCTTT ATTTGTGAAA TTTGTGATGC
TGTTGATCTT ACGTCACTTT TTTTACGAAA TAAACACTTT AAACACTACG

      3110        3120        3130        3140        3150
TATTGCTTTA TTTGTAACCA TTATAAGCTG CAATAAACAA GTTAACAACA
ATAACGAAAT AAACATTGGT AATATTCGAC GTTATTTGTT CAATTGTTGT

      3160        3170        3180        3190        3200
ACAATTGCAT TCATTTTATG TTTCAGGTTC AGGGGGAGGT GTGGGAGGTT
TGTTAACGTA AGTAAAATAC AAAGTCCAAG TCCCCCTCCA CACCCTCCAA

      3210        3220        3230        3240        3250
TTTTAAAGCA AGTAAAACCT CTACAAATGT GGTATGGCTG ATTATGATCT
AAAATTTCGT TCATTTTGGA GATGTTTACA CCATACCGAC TAATACTAGA

      3260        3270        3280        3290        3300
CTAGTCAAGG CACTATACAT CAAATATTCC TTATTAACCC CTTTACAAAT
GATCAGTTCC GTGATATGTA GTTTATAAGG AATAATTGGG GAAATGTTTA
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      3310        3320        3330        3340        3350
TAAAAAGCTA AAGGTACACA ATTTTTGAGC ATAGTTATTA ATAGCAGACA
ATTTTTCGAT TTCCATGTGT TAAAAACTCG TATCAATAAT TATCGTCTGT

      3360        3370        3380        3390        3400
CTCTATGCCT GTGTGGAGTA AGAAAAAACA GTATGTTATG ATTATAACTG
GAGATACGGA CACACCTCAT TCTTTTTTGT CATACAATAC TAATATTGAC

      3410        3420        3430        3440        3450
TTATGCCTAC TTATAAAGGT TACAGAATAT TTTTCCATAA TTTTCTTGTA
AATACGGATG AATATTTCCA ATGTCTTATA AAAAGGTATT AAAAGAACAT

      3460        3470        3480        3490        3500
TAGCAGTGCA GCTTTTTCCT TTGTGGTGTA AATAGCAAAG CAAGCAAGAG
ATCGTCACGT CGAAAAAGGA AACACCACAT TTATCGTTTC GTTCGTTCTC

      3510        3520        3530        3540        3550
TTCTATTACT AAACACAGCA TGACTCAAAA AACTTAGCAA TTCTGAAGGA
AAGATAATGA TTTGTGTCGT ACTGAGTTTT TTGAATCGTT AAGACTTCCT

      3560        3570        3580        3590        3600
AAGTCCTTGG GGTCTTCTAC CTTTCTCTTC TTTTTTGGAG GAGTAGAATG
TTCAGGAACC CCAGAAGATG GAAAGAGAAG AAAAAACCTC CTCATCTTAC

      3610        3620        3630        3640        3650
TTGAGAGTCA GCAGTAGCCT CATCATCACT AGATGGCATT TCTTCTGAGC
AACTCTCAGT CGTCATCGGA GTAGTAGTGA TCTACCGTAA AGAAGACTCG

      3660        3670        3680        3690        3700
AAAACAGGTT TTCCTCATTA AAGGCATTCC ACCACTGCTC CCATTCATCA
TTTTGTCCAA AAGGAGTAAT TTCCGTAAGG TGGTGACGAG GGTAAGTAGT

      3710        3720        3730        3740        3750
GTTCCATAGG TTGGAATCTA AAATACACAA ACAATTAGAA TCAGTAGTTT
CAAGGTATCC AACCTTAGAT TTTATGTGTT TGTTAATCTT AGTCATCAAA

      3760        3770        3780        3790        3800
AACACATTAT ACACTTAAAA ATTTTATATT TACCTTAGAG CTTTAAATCT
TTGTGTAATA TGTGAATTTT TAAAATATAA ATGGAATCTC GAAATTTAGA

      3810        3820        3830        3840        3850
CTGTAGGTAG TTTGTCCAAT TATGTCACAC CACAGAAGTA AGGTTCCTTC
GACATCCATC AAACAGGTTA ATACAGTGTG GTGTCTTCAT TCCAAGGAAG

      3860        3870        3880        3890        3900
ACAAAGATCC CTCGATCGAG AAAAAAAATA TAAAAGAGAT GGAGGAACGG
TGTTTCTAGG GAGCTAGCTC TTTTTTTTAT ATTTTCTCTA CCTCCTTGCC

      3910        3920        3930        3940        3950
GAAAAAGTTA GTTGTGGTGA TAGGTGGCAA GTGGTATTCC GTAAGAACAA
CTTTTTCAAT CAACACCACT ATCCACCGTT CACCATAAGG CATTCTTGTT

      3960        3970        3980        3990        4000
CAAGAAAAGC ATTTCATATT ATGGCTGAAC TGAGCGAACA AGTGCAAAAT
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  GTTCTTTTCG TAAAGTATAA TACCGACTTG ACTCGCTTGT TCACGTTTTA

        4010        4020        4030        4040        4050
  TTAAGCATCA ACGACAACAA CGAGAATGGT TATGTTCCTC CTCACTTAAG
  AATTCGTAGT TGCTGTTGTT GCTCTTACCA ATACAAGGAG GAGTGAATTC

        4060        4070        4080        4090        4100
  AGGAAAACCA AGAAGTGCCA GAAATAACAT GAGCAACTAC AATAACAACA
  TCCTTTTGGT TCTTCACGGT CTTTATTGTA CTCGTTGATG TTATTGTTGT

        4110        4120        4130        4140        4150
  ACGGCGGCTA CAACGGTGGC CGTGGCGGTG GCAGCTTCTT TAGCAACAAC
  TGCCGCCGAT GTTGCCACCG GCACCGCCAC CGTCGAAGAA ATCGTTGTTG

        4160        4170        4180        4190        4200
  CGTCGTGGTG GTTACGGCAA CGGTGGTTTC TTCGGTGGAA ACAACGGTGG
  GCAGCACCAC CAATGCCGTT GCCACCAAAG AAGCCACCTT TGTTGCCACC

        4210        4220        4230        4240        4250
  CAGCAGATCT AACGGCCGTT CTGGTGGTAG ATGGATCGAT GGCAAACATG
  GTCGTCTAGA TTGCCGGCAA GACCACCATC TACCTAGCTA CCGTTTGTAC

        4260        4270        4280        4290        4300
  TCCCAGCTCC AAGAAACGAA AAGGCCGAGA TCGCCATATT TGGTGTCCCC
  AGGGTCGAGG TTCTTTGCTT TTCCGGCTCT AGCGGTATAA ACCACAGGGG

>Adeno_SA
    |
    |   4310        4320        4330        4340        4350
  GAGGATCCCT GTGGAAAAAA AAGGGACAGG ATAAGTATGA CATCATCAAG
  CTCCTAGGGA CACCTTTTTT TTCCCTGTCC TATTCATACT GTAGTAGTTC

                          >pgk
                            |
        4360        4370        |4380        4390        4400
  GAAACCCTGG ACTACTGCGC CCTTCGACCT CGAAATTCTA CCGGGTAGGG
  CTTTGGGACC TGATGACGCG GGAAGCTGGA GCTTTAAGAT GGCCCATCCC

        4410        4420        4430        4440        4450
  GAGGCGCTTT TCCCAAGGCA GTCTGGAGCA TGCGCTTTAG CAGCCCCGCT
  CTCCGCGAAA AGGGTTCCGT CAGACCTCGT ACGCGAAATC GTCGGGGCGA

        4460        4470        4480        4490        4500
  GGGCACTTGG CGCTACACAA GTGGCCTCTG GCCTCGCACA CATTCCACAT
  CCCGTGAACC GCGATGTGTT CACCGGAGAC CGGAGCGTGT GTAAGGTGTA

        4510        4520        4530        4540        4550
  CCACCGGTAG GCGCCAACCG GCTCCGTTCT TTGGTGGCCC CTTCGCGCCA
  GGTGGCCATC CGCGGTTGGC CGAGGCAAGA AACCACCGGG GAAGCGCGGT

        4560        4570        4580        4590        4600
  CCTTCTACTC CTCCCCTAGT CAGGAAGTTC CCCCCCGCCC CGCAGCTCGC
  GGAAGATGAG GAGGGGATCA GTCCTTCAAG GGGGGGCGGG GCGTCGAGCG

        4610        4620        4630        4640        4650
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GTCGTGCAGG ACGTGACAAA TGGAAGTAGC ACGTCTCACT AGTCTCGTGC
CAGCACGTCC TGCACTGTTT ACCTTCATCG TGCAGAGTGA TCAGAGCACG

          >Forward_Primer
                  |
      4660        4670        4680        4690        4700
AGATGGACAG CACCGCTGAG CAATGGAAGC GGGTAGGCCT TTGGGGCAGC
TCTACCTGTC GTGGCGACTC GTTACCTTCG CCCATCCGGA AACCCCGTCG

      4710        4720        4730        4740        4750
GGCCAATAGC AGCTTTGCTC CTTCGCTTTC TGGGCTCAGA GGCTGGGAAG
CCGGTTATCG TCGAAACGAG GAAGCGAAAG ACCCGAGTCT CCGACCCTTC

      4760        4770        4780        4790        4800
GGGTGGGTCC GGGGGCGGGC TCAGGGGCGG GCTCAGGGGC GGGGCGGGCG
CCCACCCAGG CCCCCGCCCG AGTCCCCGCC CGAGTCCCCG CCCCGCCCGC

      4810        4820        4830        4840        4850
CCCGAAGGTC CTCCGGAGGC CCGGCATTCT GCACGCTTCA AAAGCGCACG
GGGCTTCCAG GAGGCCTCCG GGCCGTAAGA CGTGCGAAGT TTTCGCGTGC

  >Reverse_Primer
          |
      4860        4870        4880        4890        4900
TCTGCCGCGC TGTTCTCCTC TTCCTCATCT CCGGGCCTTT CGACCTGCAT
AGACGGCGCG ACAAGAGGAG AAGGAGTAGA GGCCCGGAAA GCTGGACGTA

      4910        4920        4930        4940        4950
CCATCTAGAT CTCGATCGAG CAGCTGAAGC TTACCATGAC CGAGTACAAG
GGTAGATCTA GAGCTAGCTC GTCGACTTCG AATGGTACTG GCTCATGTTC
                                          _____PURO_____>

      4960        4970        4980        4990        5000
CCCACGGTGC GCCTCGCCAC CCGCGACGAC GTCCCCAGGG CCGTACGCAC
GGGTGCCACG CGGAGCGGTG GGCGCTGCTG CAGGGGTCCC GGCATGCGTG
__________a__________a__PURO____a__________a__________>

      5010        5020        5030        5040        5050
CCTCGCCGCC GCGTTCGCCG ACTACCCCGC CACGCGCCAC ACCGTCGATC
GGAGCGGCGG CGCAAGCGGC TGATGGGGCG GTGCGCGGTG TGGCAGCTAG
__________a__________a__PURO____a__________a__________>

      5060        5070        5080        5090        5100
CGGACCGCCA CATCGAGCGG GTCACCGAGC TGCAAGAACT CTTCCTCACG
GCCTGGCGGT GTAGCTCGCC CAGTGGCTCG ACGTTCTTGA GAAGGAGTGC
__________a__________a__PURO____a__________a__________>

      5110        5120        5130        5140        5150
CGCGTCGGGC TCGACATCGG CAAGGTGTGG GTCGCGGACG ACGGCGCCGC
GCGCAGCCCG AGCTGTAGCC GTTCCACACC CAGCGCCTGC TGCCGCGGCG
__________a__________a__PURO____a__________a__________>

      5160        5170        5180        5190        5200
GGTGGCGGTC TGGACCACGC CGGAGAGCGT CGAAGCGGGG GCGGTGTTCG
CCACCGCCAG ACCTGGTGCG GCCTCTCGCA GCTTCGCCCC CGCCACAAGC
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__________a__________a__PURO____a__________a__________>

      5210       5220       5230       5240       5250
CCGAGATCGG CCCGCGCATG GCCGAGTTGA GCGGTTCCCG GCTGGCCGCG
GGCTCTAGCC GGGCGCGTAC CGGCTCAACT CGCCAAGGGC CGACCGGCGC
__________a__________a__PURO____a__________a__________>

      5260       5270       5280       5290       5300
CAGCAACAGA TGGAAGGCCT CCTGGCGCCG CACCGGCCCA AGGAGCCCGC
GTCGTTGTCT ACCTTCCGGA GGACCGCGGC GTGGCCGGGT TCCTCGGGCG
__________a__________a__PURO____a__________a__________>

      5310       5320       5330       5340       5350
GTGGTTCCTG GCCACCGTCG GCGTCTCGCC CGACCACCAG GGCAAGGGTC
CACCAAGGAC CGGTGGCAGC CGCAGAGCGG GCTGGTGGTC CCGTTCCCAG
__________a__________a__PURO____a__________a__________>

      5360       5370       5380       5390       5400
TGGGCAGCGC CGTCGTGCTC CCCGGAGTGG AGGCGGCCGA GCGCGCCGGG
ACCCGTCGCG GCAGCACGAG GGGCCTCACC TCCGCCGGCT CGCGCGGCCC
__________a__________a__PURO____a__________a__________>

      5410       5420       5430       5440       5450
GTGCCCGCCT TCCTGGAGAC CTCCGCGCCC CGCAACCTCC CCTTCTACGA
CACGGGCGGA AGGACCTCTG GAGGCGCGGG GCGTTGGAGG GGAAGATGCT
__________a__________a__PURO____a__________a__________>

      5460       5470       5480       5490       5500
GCGGCTCGGC TTCACCGTCA CCGCCGACGT CGAGGTGCCC GAAGGACCGC
CGCCGAGCCG AAGTGGCAGT GGCGGCTGCA GCTCCACGGG CTTCCTGGCG
__________a__________a__PURO____a__________a__________>

                                  >pgk.PA
                                     |
      5510       5520       5530       |5540       5550
GCACCTGGTG CATGACCCGC AAGCCCGGTG CCTGACGCCC GCCCCACGAC
CGTGGACCAC GTACTGGGCG TTCGGGCCAC GGACTGCGGG CGGGGTGCTG
__________a_____PURO_a__________a_____>

      5560       5570       5580       5590       5600
CCGCAGCGCC CGACCGAAAG GAGCGCACGA CCCCATGCAT CGATGATATC
GGCGTCGCGG GCTGGCTTTC CTCGCGTGCT GGGGTACGTA GCTACTATAG

      5610       5620       5630       5640       5650
AGATCCCCGG GATGCAGAAA TTGATGATCT ATTAAACAAT AAAGATGTCC
TCTAGGGGCC CTACGTCTTT AACTACTAGA TAATTTGTTA TTTCTACAGG

      5660       5670       5680       5690       5700
ACTAAAATGG AAGTTTTTCC TGTCATACTT TGTTAAGAAG GGTGAGAACA
TGATTTTACC TTCAAAAAGG ACAGTATGAA ACAATTCTTC CCACTCTTGT

      5710       5720       5730       5740       5750
GAGTACCTAC ATTTTGAATG GAAGGATTGG AGCTACGGGG GTGGGGGTGG
CTCATGGATG TAAAACTTAC CTTCCTAACC TCGATGCCCC CACCCCCACC
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      5760        5770        5780        5790        5800
GGTGGGATTA GATAAATGCC TGCTCTTTAC TGAAGGCTCT TTACTATTGC
CCACCCTAAT CTATTTACGG ACGAGAAATG ACTTCCGAGA AATGATAACG

      5810        5820        5830        5840        5850
TTTATGATAA TGTTTCATAG TTGGATATCA TAATTTAAAC AAGCAAAACC
AAATACTATT ACAAAGTATC AACCTATAGT ATTAAATTTG TTCGTTTTGG

      5860        5870        5880        5890        5900
AAATTAAGGG CCAGCTCATT CCTCCCACTC ATGATCTATA GATCTATAGA
TTTAATTCCC GGTCGAGTAA GGAGGGTGAG TACTAGATAT CTAGATATCT

      5910        5920        5930        5940        5950
TCTCTCGTGG GATCATTGTT TTTCTCTTGA TTCCCACTTT GTGGTTCTAA
AGAGAGCACC CTAGTAACAA AAAGAGAACT AAGGGTGAAA CACCAAGATT

      5960        5970        5980        5990        6000
GTACTGTGGT TTCCAAATGT GTCAGTTTCA TAGCCTGAAG AACGAGATCA
CATGACACCA AAGGTTTACA CAGTCAAAGT ATCGGACTTC TTGCTCTAGT

      6010        6020        6030        6040        6050
GCAGCCTCTG TTCCACATAC ACTTCATTCT CAGTATTGTT TTGCCAAGTT
CGTCGGAGAC AAGGTGTATG TGAAGTAAGA GTCATAACAA AACGGTTCAA

                        >LoxP
                          |
      6060        6070        6080        6090        6100
CTAATTCCAT CAGAAGCTGG TCGAGATAAC TTCGTATAAT GTATGCTATA
GATTAAGGTA GTCTTCGACC AGCTCTATTG AAGCATATTA CATACGATAT

      6110        6120        6130        6140        6150
CGAAGTTATG TCGACAGCGG CCGCTCGAGC ATGCATCTAG AGGGCCCAAT
GCTTCAATAC AGCTGTCGCC GGCGAGCTCG TACGTAGATC TCCCGGGTTA

      6160        6170        6180        6190        6200
TCGCCCTATA GTGAGTCGTA TTACAATTCA CTGGCCGTCG TTTTACAACG
AGCGGGATAT CACTCAGCAT AATGTTAAGT GACCGGCAGC AAAATGTTGC

      6210        6220        6230        6240        6250
TCGTGACTGG GAAAACCCTG GCGTTACCCA ACTTAATCGC CTTGCAGCAC
AGCACTGACC CTTTTGGGAC CGCAATGGGT TGAATTAGCG GAACGTCGTG

      6260        6270        6280        6290        6300
ATCCCCCTTT CGCCAGCTGG CGTAATAGCG AAGAGGCCCG CACCGATCGC
TAGGGGGAAA GCGGTCGACC GCATTATCGC TTCTCCGGGC GTGGCTAGCG

      6310        6320        6330        6340        6350
CCTTCCCAAC AGTTGCGCAG CCTATACGTA CGGCAGTTTA AGGTTTACAC
GGAAGGGTTG TCAACGCGTC GGATATGCAT GCCGTCAAAT TCCAAATGTG

      6360        6370        6380        6390        6400
CTATAAAAGA GAGAGCCGTT ATCGTCTGTT TGTGGATGTA CAGAGTGATA
GATATTTTCT CTCTCGGCAA TAGCAGACAA ACACCTACAT GTCTCACTAT

      6410        6420        6430        6440        6450
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TTATTGACAC GCCGGGGCGA CGGATGGTGA TCCCCCTGGC CAGTGCACGT
AATAACTGTG CGGCCCCGCT GCCTACCACT AGGGGGACCG GTCACGTGCA

      6460       6470       6480       6490       6500
CTGCTGTCAG ATAAAGTCTC CCGTGAACTT TACCCGGTGG TGCATATCGG
GACGACAGTC TATTTCAGAG GGCACTTGAA ATGGGCCACC ACGTATAGCC

      6510       6520       6530       6540       6550
GGATGAAAGC TGGCGCATGA TGACCACCGA TATGGCCAGT GTGCCGGTCT
CCTACTTTCG ACCGCGTACT ACTGGTGGCT ATACCGGTCA CACGGCCAGA

      6560       6570       6580       6590       6600
CCGTTATCGG GGAAGAAGTG GCTGATCTCA GCCACCGCGA AAATGACATC
GGCAATAGCC CCTTCTTCAC CGACTAGAGT CGGTGGCGCT TTTACTGTAG

      6610       6620       6630       6640       6650
AAAAACGCCA TTAACCTGAT GTTCTGGGGA ATATAAATGT CAGGCATGAG
TTTTTGCGGT AATTGGACTA CAAGACCCCT TATATTTACA GTCCGTACTC

      6660       6670       6680       6690       6700
ATTATCAAAA AGGATCTTCA CCTAGATCCT TTTCACGTAG AAAGCCAGTC
TAATAGTTTT TCCTAGAAGT GGATCTAGGA AAAGTGCATC TTTCGGTCAG

      6710       6720       6730       6740       6750
CGCAGAAACG GTGCTGACCC CGGATGAATG TCAGCTACTG GGCTATCTGG
GCGTCTTTGC CACGACTGGG GCCTACTTAC AGTCGATGAC CCGATAGACC

      6760       6770       6780       6790       6800
ACAAGGGAAA ACGCAAGCGC AAAGAGAAAG CAGGTAGCTT GCAGTGGGCT
TGTTCCCTTT TGCGTTCGCG TTTCTCTTTC GTCCATCGAA CGTCACCCGA

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                                                   |
      6810       6820       6830       6840       6850
TACATGGCGA TAGCTAGACT GGGCGGTTTT ATGGACAGCA AGCGAACCGG
ATGTACCGCT ATCGATCTGA CCCGCCAAAA TACCTGTCGT TCGCTTGGCC

      6860       6870       6880       6890       6900
AATTGCCAGC TGGGGCGCCC TCTGGTAAGG TTGGGAAGCC CTGCAAAGTA
TTAACGGTCG ACCCCGCGGG AGACCATTCC AACCCTTCGG GACGTTTCAT

      6910       6920       6930       6940       6950
AACTGGATGG CTTTCTCGCC GCCAAGGATC TGATGGCGCA GGGGATCAAG
TTGACCTACC GAAAGAGCGG CGGTTCCTAG ACTACCGCGT CCCCTAGTTC

      6960       6970       6980       6990       7000
CTCTGATCAA GAGACAGGAT GAGGATCGTT TCGCATGATT GAACAAGATG
GAGACTAGTT CTCTGTCCTA CTCCTAGCAA AGCGTACTAA CTTGTTCTAC
                                        ______KAN_______>

      7010       7020       7030       7040       7050
GATTGCACGC AGGTTCTCCG GCCGCTTGGG TGGAGAGGCT ATTCGGCTAT
CTAACGTGCG TCCAAGAGGC CGGCGAACCC ACCTCTCCGA TAAGCCGATA
__________b__________b___KAN____b__________b__________>
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      7060       7070       7080       7090       7100
GACTGGGCAC AACAGACAAT CGGCTGCTCT GATGCCGCCG TGTTCCGGCT
CTGACCCGTG TTGTCTGTTA GCCGACGAGA CTACGGCGGC ACAAGGCCGA
__________b__________b___KAN____b__________b__________>

      7110       7120       7130       7140       7150
GTCAGCGCAG GGGCGCCCGG TTCTTTTTGT CAAGACCGAC CTGTCCGGTG
CAGTCGCGTC CCCGCGGGCC AAGAAAAACA GTTCTGGCTG GACAGGCCAC
__________b__________b___KAN____b__________b__________>

      7160       7170       7180       7190       7200
CCCTGAATGA ACTGCAAGAC GAGGCAGCGC GGCTATCGTG GCTGGCCACG
GGGACTTACT TGACGTTCTG CTCCGTCGCG CCGATAGCAC CGACCGGTGC
__________b__________b___KAN____b__________b__________>

      7210       7220       7230       7240       7250
ACGGGCGTTC CTTGCGCAGC TGTGCTCGAC GTTGTCACTG AAGCGGGAAG
TGCCCGCAAG GAACGCGTCG ACACGAGCTG CAACAGTGAC TTCGCCCTTC
__________b__________b___KAN____b__________b__________>

      7260       7270       7280       7290       7300
GGACTGGCTG CTATTGGGCG AAGTGCCGGG GCAGGATCTC CTGTCATCTC
CCTGACCGAC GATAACCCGC TTCACGGCCC CGTCCTAGAG GACAGTAGAG
__________b__________b___KAN____b__________b__________>

      7310       7320       7330       7340       7350
ACCTTGCTCC TGCCGAGAAA GTATCCATCA TGGCTGATGC AATGCGGCGG
TGGAACGAGG ACGGCTCTTT CATAGGTAGT ACCGACTACG TTACGCCGCC
__________b__________b___KAN____b__________b__________>

      7360       7370       7380       7390       7400
CTGCATACGC TTGATCCGGC TACCTGCCCA TTCGACCACC AAGCGAAACA
GACGTATGCG AACTAGGCCG ATGGACGGGT AAGCTGGTGG TTCGCTTTGT
__________b__________b___KAN____b__________b__________>

      7410       7420       7430       7440       7450
TCGCATCGAG CGAGCACGTA CTCGGATGGA AGCCGGTCTT GTCGATCAGG
AGCGTAGCTC GCTCGTGCAT GAGCCTACCT TCGGCCAGAA CAGCTAGTCC
__________b__________b___KAN____b__________b__________>

      7460       7470       7480       7490       7500
ATGATCTGGA CGAAGAGCAT CAGGGGCTCG CGCCAGCCGA ACTGTTCGCC
TACTAGACCT GCTTCTCGTA GTCCCCGAGC GCGGTCGGCT TGACAAGCGG
__________b__________b___KAN____b__________b__________>

      7510       7520       7530       7540       7550
AGGCTCAAGG CGAGCATGCC CGACGGCGAG GATCTCGTCG TGACCCATGG
TCCGAGTTCC GCTCGTACGG GCTGCCGCTC CTAGAGCAGC ACTGGGTACC
__________b__________b___KAN____b__________b__________>

      7560       7570       7580       7590       7600
CGATGCCTGC TTGCCGAATA TCATGGTGGA AAATGGCCGC TTTTCTGGAT
GCTACGGACG AACGGCTTAT AGTACCACCT TTTACCGGCG AAAAGACCTA
__________b__________b___KAN____b__________b__________>
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      7610       7620       7630       7640       7650
TCATCGACTG TGGCCGGCTG GGTGTGGCGG ACCGCTATCA GGACATAGCG
AGTAGCTGAC ACCGGCCGAC CCACACCGCC TGGCGATAGT CCTGTATCGC
__________b__________b___KAN____b__________b__________>

      7660       7670       7680       7690       7700
TTGGCTACCC GTGATATTGC TGAAGAGCTT GGCGGCGAAT GGGCTGACCG
AACCGATGGG CACTATAACG ACTTCTCGAA CCGCCGCTTA CCCGACTGGC
__________b__________b___KAN____b__________b__________>

      7710       7720       7730       7740       7750
CTTCCTCGTG CTTTACGGTA TCGCCGCTCC CGATTCGCAG CGCATCGCCT
GAAGGAGCAC GAAATGCCAT AGCGGCGAGG GCTAAGCGTC GCGTAGCGGA
__________b__________b___KAN____b__________b__________>

      7760       7770       7780       7790       7800
TCTATCGCCT TCTTGACGAG TTCTTCTGAA TTATTAACGC TTACAATTTC
AGATAGCGGA AGAACTGCTC AAGAAGACTT AATAATTGCG AATGTTAAAG
__________b__KAN_____b_________>

      7810       7820       7830       7840       7850
CTGATGCGGT ATTTTCTCCT TACGCATCTG TGCGGTATTT CACACCGCAT
GACTACGCCA TAAAAGAGGA ATGCGTAGAC ACGCCATAAA GTGTGGCGTA

      7860       7870       7880       7890       7900
ACAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT
TGTCCACCGT GAAAAGCCCC TTTACACGCG CCTTGGGGAT AAACAAATAA

      7910       7920       7930       7940       7950
TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT
AAAGATTTAT GTAAGTTTAT ACATAGGCGA GTACTCTGTT ATTGGGACTA

      7960       7970       7980       7990       8000
AAATGCTTCA ATAATAGCAC GTGAGGAGGG CCACCATGGC CAAGTTGACC
TTTACGAAGT TATTATCGTG CACTCCTCCC GGTGGTACCG GTTCAACTGG
                                      ___ZEOCIN RE____>

      8010       8020       8030       8040       8050
AGTGCCGTTC CGGTGCTCAC CGCGCGCGAC GTCGCCGGAG CGGTCGAGTT
TCACGGCAAG GCCACGAGTG GCGCGCGCTG CAGCGGCCTC GCCAGCTCAA
__________c__________ZEOCIN RES_c__________c__________>

      8060       8070       8080       8090       8100
CTGGACCGAC CGGCTCGGGT TCTCCCGGGA CTTCGTGGAG GACGACTTCG
GACCTGGCTG GCCGAGCCCA AGAGGGCCCT GAAGCACCTC CTGCTGAAGC
__________c__________ZEOCIN RES_c__________c__________>

      8110       8120       8130       8140       8150
CCGGTGTGGT CCGGGACGAC GTGACCCTGT TCATCAGCGC GGTCCAGGAC
GGCCACACCA GGCCCTGCTG CACTGGGACA AGTAGTCGCG CCAGGTCCTG
__________c__________ZEOCIN RES_c__________c__________>

      8160       8170       8180       8190       8200
CAGGTGGTGC CGGACAACAC CCTGGCCTGG GTGTGGGTGC GCGGCCTGGA
GTCCACCACG GCCTGTTGTG GGACCGGACC CACACCCACG CGCCGGACCT
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__________c__________ZEOCIN RES_c__________c__________>

      8210       8220       8230       8240       8250
CGAGCTGTAC GCCGAGTGGT CGGAGGTCGT GTCCACGAAC TTCCGGGACG
GCTCGACATG CGGCTCACCA GCCTCCAGCA CAGGTGCTTG AAGGCCCTGC
__________c__________ZEOCIN RES_c__________c__________>

      8260       8270       8280       8290       8300
CCTCCGGGCC GGCCATGACC GAGATCGGCG AGCAGCCGTG GGGGCGGGAG
GGAGGCCCGG CCGGTACTGG CTCTAGCCGC TCGTCGGCAC CCCCGCCCTC
__________c__________ZEOCIN RES_c__________c__________>

      8310       8320       8330       8340       8350
TTCGCCCTGC GCGACCCGGC CGGCAACTGC GTGCACTTCG TGGCCGAGGA
AAGCGGGACG CGCTGGGCCG GCCGTTGACG CACGTGAAGC ACCGGCTCCT
__________c__________ZEOCIN RES_c__________c__________>

      8360       8370       8380       8390       8400
GCAGGACTGA CACGTGCTAA AACTTCATTT TTAATTTAAA AGGATCTAGG
CGTCCTGACT GTGCACGATT TTGAAGTAAA AATTAAATTT TCCTAGATCC
__________>

      8410       8420       8430       8440       8450
TGAAGATCCT TTTTGATAAT CTCATGACCA AAATCCCTTA ACGTGAGTTT
ACTTCTAGGA AAAACTATTA GAGTACTGGT TTTAGGGAAT TGCACTCAAA

                >pUC_origin
                     |
      8460       8470  |    8480       8490       8500
TCGTTCCACT GAGCGTCAGA CCCCGTAGAA AAGATCAAAG GATCTTCTTG
AGCAAGGTGA CTCGCAGTCT GGGGCATCTT TTCTAGTTTC CTAGAAGAAC

      8510       8520       8530       8540       8550
AGATCCTTTT TTTCTGCGCG TAATCTGCTG CTTGCAAACA AAAAAACCAC
TCTAGGAAAA AAAGACGCGC ATTAGACGAC GAACGTTTGT TTTTTTGGTG

      8560       8570       8580       8590       8600
CGCTACCAGC GGTGGTTTGT TTGCCGGATC AAGAGCTACC AACTCTTTTT
GCGATGGTCG CCACCAAACA AACGGCCTAG TTCTCGATGG TTGAGAAAAA

      8610       8620       8630       8640       8650
CCGAAGGTAA CTGGCTTCAG CAGAGCGCAG ATACCAAATA CTGTCCTTCT
GGCTTCCATT GACCGAAGTC GTCTCGCGTC TATGGTTTAT GACAGGAAGA

      8660       8670       8680       8690       8700
AGTGTAGCCG TAGTTAGGCC ACCACTTCAA GAACTCTGTA GCACCGCCTA
TCACATCGGC ATCAATCCGG TGGTGAAGTT CTTGAGACAT CGTGGCGGAT

      8710       8720       8730       8740       8750
CATACCTCGC TCTGCTAATC CTGTTACCAG TGGCTGCTGC CAGTGGCGAT
GTATGGAGCG AGACGATTAG GACAATGGTC ACCGACGACG GTCACCGCTA

      8760       8770       8780       8790       8800
AAGTCGTGTC TTACCGGGTT GGACTCAAGA CGATAGTTAC CGGATAAGGC
TTCAGCACAG AATGGCCCAA CCTGAGTTCT GCTATCAATG GCCTATTCCG
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      8810        8820        8830        8840        8850
GCAGCGGTCG GGCTGAACGG GGGGTTCGTG CACACAGCCC AGCTTGGAGC
CGTCGCCAGC CCGACTTGCC CCCCAAGCAC GTGTGTCGGG TCGAACCTCG

      8860        8870        8880        8890        8900
GAACGACCTA CACCGAACTG AGATACCTAC AGCGTGAGCT ATGAGAAAGC
CTTGCTGGAT GTGGCTTGAC TCTATGGATG TCGCACTCGA TACTCTTTCG

      8910        8920        8930        8940        8950
GCCACGCTTC CCGAAGGGAG AAAGGCGGAC AGGTATCCGG TAAGCGGCAG
CGGTGCGAAG GGCTTCCCTC TTTCCGCCTG TCCATAGGCC ATTCGCCGTC

      8960        8970        8980        8990        9000
GGTCGGAACA GGAGAGCGCA CGAGGGAGCT TCCAGGGGGA AACGCCTGGT
CCAGCCTTGT CCTCTCGCGT GCTCCCTCGA AGGTCCCCCT TTGCGGACCA

      9010        9020        9030        9040        9050
ATCTTTATAG TCCTGTCGGG TTTCGCCACC TCTGACTTGA GCGTCGATTT
TAGAAATATC AGGACAGCCC AAAGCGGTGG AGACTGAACT CGCAGCTAAA

      9060        9070        9080        9090        9100
TTGTGATGCT CGTCAGGGGG GCGGAGCCTA TGGAAAAACG CCAGCAACGC
AACACTACGA GCAGTCCCCC CGCCTCGGAT ACCTTTTTGC GGTCGTTGCG

      9110        9120        9130        9140        9150
GGCCTTTTTA CGGTTCCTGG GCTTTTGCTG GCCTTTTGCT CACATGTTCT
CCGGAAAAAT GCCAAGGACC CGAAAACGAC CGGAAAACGA GTGTACAAGA

      9160        9170        9180        9190        9200
TTCCTGCGTT ATCCCCTGAT TCTGTGGATA ACCGTATTAC CGCCTTTGAG
AAGGACGCAA TAGGGGACTA AGACACCTAT TGGCATAATG GCGGAAACTC

      9210        9220        9230        9240        9250
TGAGCTGATA CCGCTCGCCG CAGCCGAACG ACCGAGCGCA GCGAGTCAGT
ACTCGACTAT GGCGAGCGGC GTCGGCTTGC TGGCTCGCGT CGCTCAGTCA

      9260
GAGCGAGGAA GCGGAAG
CTCGCTCCTT CGCCTTC
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