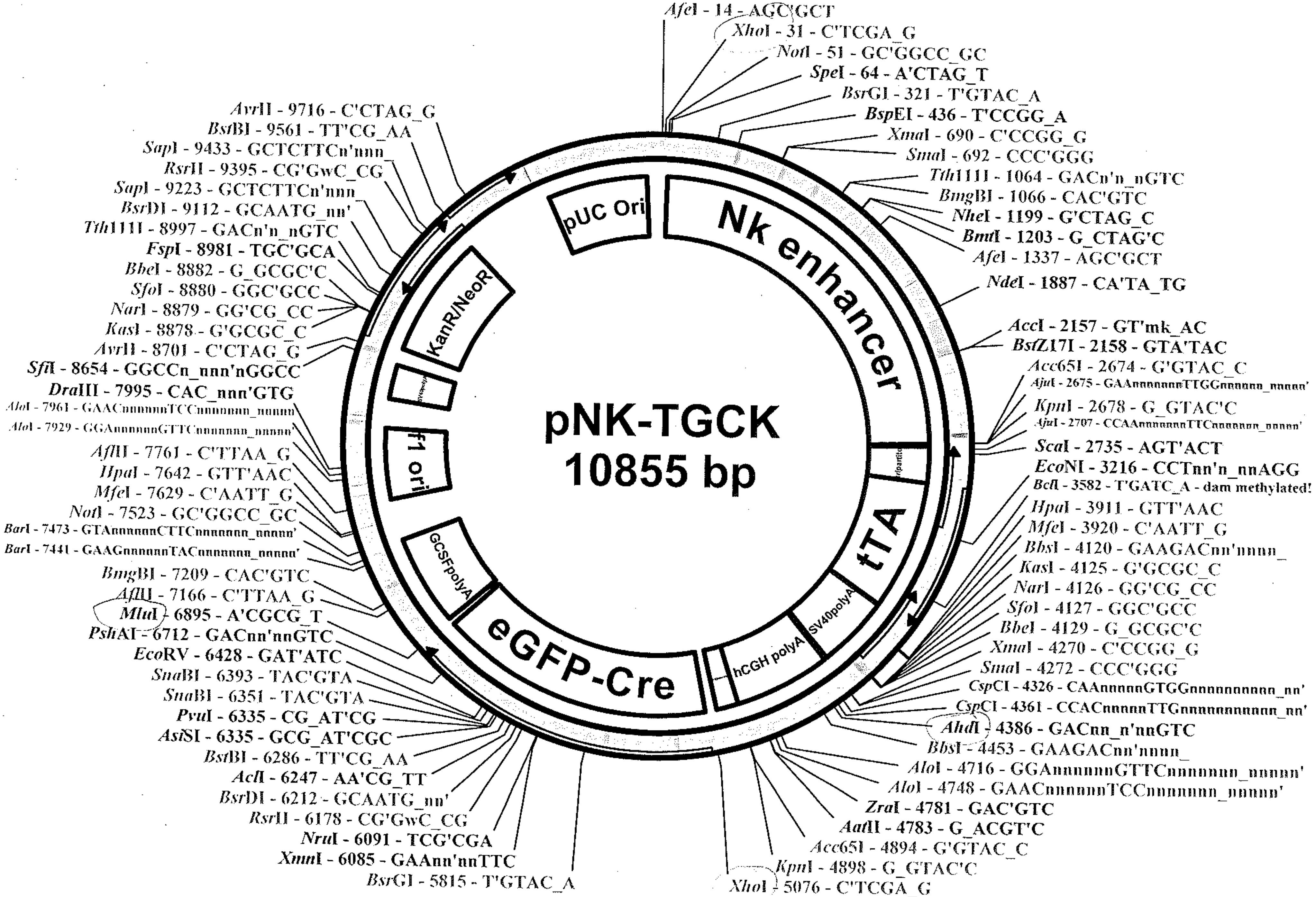
pNK-TGCK
10855 bp
Nk enhancer
ripartito
tTA
SV40polyA
hCGH polyA
eGFP-Cre
GCSFpolyA
f1 ori
SV40polyA
KanR/NeoR
pUC Ori
AfeI - 14 - AGC'GCT
XhoI - 31 - C'TCGA_G
NotI - 51 - GC'GGCC_GC
SpeI - 64 - A'CTAG_T
BsrGI - 321 - T'GTAC_A
BspEI - 436 - T'CCGG_A
XmaI - 690 - C'CCGG_G
SmaI - 692 - CCC'GGG
Tth111I - 1064 - GACn'n_nGTC
BmgBI - 1066 - CAC'GTC
NheI - 1199 - G'CTAG_C
BmtI - 1203 - G_CTAG'C
AfeI - 1337 - AGC'GCT
NdeI - 1887 - CA'TA_TG
AccI - 2157 - GT'mk_AC
BstZ17I - 2158 - GTA'TAC
Acc65I - 2674 - G'GTAC_C
AjuI - 2675 - GAAnnnnnnnTTGGnnnnnn_nnnnn'
KpnI - 2678 - G_GTAC'C
AjuI - 2707 - CCAAnnnnnnnTTCnnnnnn_nnnnn'
ScaI - 2735 - AGT'ACT
EcoNI - 3216 - CCTnn'n_nnAGG
BclI - 3582 - T'GATC_A - dam methylated!
HpaI - 3911 - GTT'AAC
MfeI - 3920 - C'AATT_G
BbsI - 4120 - GAAGACnn'nnnn_
KasI - 4125 - G'GCGC_C
NarI - 4126 - GG'CG_CC
SfoI - 4127 - GGC'GCC
BbeI - 4129 - G_GCGC'C
XmaI - 4270 - C'CCGG_G
SmaI - 4272 - CCC'GGG
CspCI - 4326 - CAAnnnnnGTGGnnnnnnnnnn_nn'
CspCI - 4361 - CCACnnnnnTTGnnnnnnnnnn_nn'
AhdI - 4386 - GACnn_n'nnGTC
BbsI - 4453 - GAAGACnn'nnnn_
AloI - 4716 - GGAnnnnnnGTTCnnnnnnn_nnnnn'
AloI - 4748 - GAACnnnnnnTCCnnnnnnn_nnnnn'
ZraI - 4781 - GAC'GTC
AatII - 4783 - G_ACGT'C
Acc65I - 4894 - G'GTAC_C
KpnI - 4898 - G_GTAC'C
XhoI - 5076 - C'TCGA_G
BsrGI - 5815 - T'GTAC_A
XmnI - 6085 - GAAnn'nnTTC
NruI - 6091 - TCG'CGA
RsrII - 6178 - CG'GwC_CG
BsrDI - 6212 - GCAATG_nn'
AclI - 6247 - AA'CG_TT
BstBI - 6286 - TT'CG_AA
AsiSI - 6335 - GCG_AT'CGC
PvuI - 6335 - CG_AT'CG
SnaBI - 6351 - TAC'GTA
SnaBI - 6393 - TAC'GTA
EcoRV - 6428 - GAT'ATC
PshAI - 6712 - GACnn'nnGTC
MluI - 6895 - A'CGCG_T
AflII - 7166 - C'TTAA_G
BmgBI - 7209 - CAC'GTC
BarI - 7441 - GAAGnnnnnnTACnnnnnnn_nnnnn'
BarI - 7473 - GTAnnnnnnCTTCnnnnnnn_nnnnn'
NotI - 7523 - GC'GGCC_GC
MfeI - 7629 - C'AATT_G
HpaI - 7642 - GTT'AAC
AflII - 7761 - C'TTAA_G
AloI - 7929 - GGAnnnnnnGTTCnnnnnnn_nnnnn'
AloI - 7961 - GAACnnnnnnTCCnnnnnnn_nnnnn
DraIII - 7995 - CAC_nnn'GTG
SfiI - 8654 - GGCCn_nnn'nGGCC
AvrII - 8701 - C'CTAG_G
KasI - 8878 - G'GCGC_C
NarI - 8879 - GG'CG_CC
SfoI - 8880 - GGC'GCC
BbeI - 8882 - G_GCGC'C
FspI - 8981 - TGC'GCA
Tth111I - 8997 - GACn'n_nGTC
BsrDI - 9112 - GCAATG_nn'
SapI - 9223 - GCTCTTCn'nnn_
RsrII - 9395 - CG'GwC_CG
SapI - 9433 - GCTCTTCn'nnn_
BstBI - 9561 - TT'CG_AA
AvrII - 9716 - C'CTAG_G

nK- TGCK

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                AfeI                 XhoI                NotI
   1 TAGTTATTAC TAGCGCTACC GGACTCAGAT CTCGAGCTCC ACCGCGGTGG

                  SpeI
  51 CGGCCGCTCT AGAACTAGTC CAGTCTGGGT CCTAATGCGG GTGGCGTCTC

 101 TCTTGACAGG CAGCGTTTGG GGACAACAGC GGGGAAGGGA GATAAGATGA

 151 CATACCAGAG CAGATTTGGT GTGCGCGCTG ATACTCCTGG CCCGACAGGA

 201 AACTCGGAGC TATTTAAAAA GGCCCTATCG ATTACTTTAT CTTCCCCGGA

 251 GGAAAACTTC TTGCCGAGAG ACAAAAGATG TCCCCCTACC TAAAGATACA

                          BsrGI
 301 AGGCCACACA GCAGAGGGTT TGTACAGGCG ACGCGAGT AGATCCCTGG

 351 GAGCGCAGAG ACGCCTTTCT ACCGGCAGAG ACTGAAGTTT GACTGGAGCG

                                          BspEI
 401 AGGCGGGGCG GAGCCACCTC CCGGTCCCCG TGCACTCCGG AATTGTGAAC

 451 GCTCCCGCAA AGTCCCCGCG AGTGTTGTGT TCACACTAAT TGGTGTGCCT

 501 CTGAGTTCCA TCCGTACTCC CCCCCCCCCA AGTTTAAATG CTCCTTTTAA

 551 GGGCTTGAGT GTCTGCAGCC GTCATGTGCA CCTTGAAAGC TTGGCGTGTG

 601 ACATTGTGTT CCTCTAGCGT CTCCATCCCG CTTTTCACCA ATTCGTGCCC

                                             XmaI
                                             SmaI
 651 TGGCCGAATC CCGTGGGAGC AGAGGTGGCC CCTCGAAGTC CCGGGCCACC

 701 CAGGGAGGCT CCGGGTACAC CCAGATTCCC AGCAGTCCGT AGTCTGGGCT

 751 TTCCCCGTGT GACACTTTGC CGCCTACCGG TTCACAATCC TCTCGGCCCG

 801 CGTGAGAGAA GGCGGCATGT TCCGTGGGAC ACAGTTTATT TTATGCACAT

 851 TAAGGGCTGT AAAGCACGGT CTGAAAGAAA AAGATGGTGC GGCGGGGAGG

 901 AGCGGGAGAA GGGGCAGCGA TGATCCTGGG ACTGTGCAGC GACCACTTAC

 951 AACCTGATTC ATGCCCACCG GAGACCCCAG CGGTCCTGGA GGGAGGCGGA

1001 GGCTCCGAGG CTTCCGGTTG GGTTTCAGCC ACCAGGTTCG GGCAGTGACT

                   BmgBI
                Tth111I
1051 CTTGGACTCT GACCACGTCC CGCGGCACAC TCGGAGACCC GGCTCGTCCG

1101 CGAAGCTAGG AGCGAATGGC CCGCAGCTGC GCGTCGCTCA ATCTGAGCTC

                                                        NheI
                                                        BmtI
1151 TCAAGCCCAA AGCGTCTGCA GAGCCGCTTC CCAGAGCTCC AAGCCACCGC
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1201 TAGCAGAGCT CTGAAGGCAC CTTGAAGCCT CGACCCACTT CAATGTCACC

1251 TGATTTTTCA AATTATCACC TTCTGAGACG CGATCCTTCG GAACCGGCAG

                                          AfeI
1301 AGCCCCCACC TTTGAGCGCC GCCGTTTATG CTGTAGCGCT GTAGCGGTTT

1351 GCAGCAGTCA GGGCAGGTGG AGGACCTTGT TACTGGCACT GCGGAGCCCG

1401 GAGCTGAGGG GAAAGAAAAC GGAGATAAGG AAAAGGGCTG CAGAGGTCGG

1451 AAAGCAGCTC CCATCGGATC CATCAAATCA ATCACAGCCC CAAGTGACCA

1501 AAGAGAAATT TTGCGTTTTG GAAATATCCC CACCACCAAA AGCACGAGGA

1551 AAGTGTGAGC AGCAAGAAAC TAACAATAAA TTTTAGGTGC AAAAATATAA

1601 AGAAGCACAC AGAATTTGAA AAAAAAAACC CGCACATTCT GCTATTTGAG

1651 TTTTCCATAA ACATACAAAT AAAACCTGCG GAAGATGTAC TTCTTCAAGT

1701 CTGTGACAGA CCCTGGACTG ACTAACGGGG ACGCGCTCAT TTAAAATGTC

1751 AGCGGTTCCT ATATTTCACC GAACTTTCAA CGAGCTTTTC CACATGTCCA

1801 GACTCATGGG ACAGTATGCT TATGACCCTG TTAATTGTAG TTCAGACTTA

                                           NdeI
1851 CTATGTCTCA ATAAAGTGAC TCAGCACTTG ACCAGCATAT GAGGCTCCCC

1901 GAGTCCAGTC CCCAGAAACA AGTAGAATAT ACATATATAT ATAATTCTAT

1951 ATATCTATCT ATATATTATT CTATATATAT ATTCTACTTG TATATATATG

2001 TATTACATAA TATATATACA AGTAGAATAT ATATAATATA ATTTATATTA

2051 TATATAGAAT ATATATAGAA ACAAGTAGAT TATATATATA TATATATATA

2101 GTATATATAT ATATATATAT ATATATATAT ATAGTATTGT ATTACATACA

         BstZ17I
         AccI
2151 TGTGGGTATA CATCATACAC ATGGCTTTCA ATCCATCCTC ACCAGCCCAT

2201 TTAGTGATAC AGGACACAGT GCAAAGAATA TTTATTCAAA TCCTCGACCC

2251 ACCCCCAACC CTGCGTTTAG ACTCAGCATA ACAGAATCAG GTATTTTCTT

2301 TGAGTGTGTT GGCTGGGATT TTCAGGCTAA CGAGGAGCAA TCTCCTTGCA

2351 GGAGTGGGAG ACTATCCCAA ATGTGTCGCG GCCCCTTTAA AAAAAGCTGA

2401 GCAGGATTTT TTTTTCCCAT CCCTATGTCT ATATTAGGTG ACGCAGAACT

2451 GCCCGTCGCT CCTGTCATCC AGGCCCCTGG CCCAATGGCA GGCTGAATCC

2501 CCCCTACTCC AGCCTGCTCC CGCCTCTTCT GCCCCTGGTG CTCCGCGCTA
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2551 CCTGCTGCCG CGCACCACAT CCAGGACAGA GAGGCGGGTG CGCGGGCGGG

2601 CGGCGGCACC ATGCGGGGAG GCTGTCCCCA GGGGTGGCAG CACCACTCTC

                              KpnI     AjuI
                              Acc65I   AjuI
2651 TGCTACCCAC CTGGCCCAAG CTGGGTACCT GCCAAGCTCT AGTTCTAGAA
                                                       *  F    Frame 4

                                        ScaI
2701 TTCGCTGTCT GCGAGGGCCA GCTGTTGGGG TGAGTACTCC CTCTCAAAAG
       E  S  D   A  L  A   L  Q  Q  P   S  Y  E   R  E  F      Frame 4

2751 CGGGCATGAC TTCTGCGCTA AGATTGTCAG TTTCCAAAAA CGAGGAGGAT
     A  P  M  V   E  A  S   L  N  D   T  E  L  F   S  S  S     Frame 4

2801 TTGATATTCA CCTGGCCCGC GGTGATGCCT TTGAGGGTGG CCGCGTCCAT
      K  I  N   V  Q  G  A   T  I  G   K  L  T   A  A  D  M    Frame 4

2851 CTGGTCAGAA AAGACAATCT TTTTGTTGTC AAGCTTGAGG TGTGGCAGGC
       Q  D  S   F  V  I   K  K  N  D   L  K  L   H  P  L      Frame 4

2901 TTGAGATCTG GCCATACACT TGAGTGACAA TGACATCCAC TTTGCCTTTC
                                    M   T  S  T   L  P  F      Frame 2
     S  S  I  Q   S  Y  V   Q  T  V   I  V  D  V   K  G  K     Frame 4

2951 TCTCCACAGG TGTCCACTCC CAGGTCCAAC TGCAGCCCAA GCGGATCCGA
     S  P  Q  V   S  T  P   R  S  N   C  S  P  S   G  S  E     Frame 2
      E  G  C   T  D  V  G   L  D  L   Q  L  G   L  P  D  S    Frame 4

3001 ATTCACCATG TCCAGACTGG ACAAGAGCAA AGTCATCAAC TCTGCCTTGG
      F  T  M   S  R  L  D   K  S  K   V  I  N   S  A  L  E    Frame 2
       N  V  M   D  L  S   S  L  L  L   T  M  L   E  A  K      Frame 4

3051 AGCTCGTGAA TGAAGTTGGC ATTGAGGGCT TGACCACCAG GAAGCTGGCC
       L  V  N   E  V  G   I  E  G  L   T  T  R   K  L  A      Frame 2
     S  S  T  F   S  T  P   M  S  P   K  V  V  L   F  S  A     Frame 4

3101 CAGAAGCTGG GTGTGGAGCA GCCTACCCTG TACTGGCATG TGAAGAACAA
     Q  K  L  G   V  E  Q   P  T  L   Y  W  H  V   K  N  K     Frame 2
      W  F  S   P  T  S  C   G  V  R   Y  Q  C   T  F  F  L    Frame 4

3151 GAGGGCTCTG CTTGATGCCC TGGCCATTGA GATGTTGGAC AGGCACCACA
      R  A  L   L  D  A  L   A  I  E   M  L  D   R  H  H  T    Frame 2
       L  A  R   S  S  A   R  A  M   Frame 4

                EcoNI
3201 CCCACTTCTG CCCTCTGGAA GGGGAGTCCT GGCAGGACTT CCTGAGGAAC
       H  F  C   P  L  E   G  E  S  W   Q  D  F   L  R  N      Frame 2

3251 AATGCCAAGA GCTTCAGATG TGCCTTGCTC TCCCACCGGG ATGGTGCCAA
     N  A  K  S   F  R  C   A  L  L   S  H  R  D   G  A  K     Frame 2

3301 AGTTCACTTG GGCACCAGGC CTACAGAGAA GCAGTATGAG ACCCTGGAGA
      V  H  L   G  T  R  P   T  E  K   Q  Y  E   T  L  E  N    Frame 2

3351 ACCAGCTGGC ATTCCTGTGC CAACAAGGCT TCTCCCTGGA AAATGCCTTG
       Q  L  A   F  L  C   Q  Q  G  F   S  L  E   N  A  L      Frame 2
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3401 TATGCCCTCT CTGCTGTGGG CCACTTCACC TTGGGCTGTG TGCTGGAGGA
      Y  A  L  S   A  V  G   H  F  T   L  G  C  V   L  E  D    Frame 2

3451 CCAGGAGCAC CAAGTTGCCA AGGAGGAGAG GGAGACCCCC ACCACTGACT
       Q  E  H  Q  V  A  K   E  E  R   E  T  P   T  T  D  S    Frame 2

3501 CCATGCCACC ACTGCTGCGG CAAGCTATTG AGTTGTTTGA CCACCAAGGG
        M  P  P   L  L  R  Q  A  I  E   L  F  D   H  Q  G      Frame 2

                                        BclI
3551 GCTGAGCCTG CATTCCTTTT TGGCCTGGAA CTGATCATCT GTGGCCTGGA
     A  E  P  A   F  L  F   G  L  E   L  I  I  C   G  L  E    Frame 2
                                              *  R   H  G  P    Frame 6

3601 AAAGCAGCTG AAATGTGAGT CTGGCTCTCA CGTGCCCAAA AAGAGAAAGC
      K  Q  L   K  C  E  S   G  S  H   V  P  K   K  R  K  H    Frame 2
      F  A  A   S  I  H  T   Q  S  E   R  A  W   F  S  F  A    Frame 6

3651 ACGTGCCTGC TGATGCCTTG GATGATTTTG ACCTGGACAT GCTGCCTGCT
       V  P  A   D  A  L   D  D  F  D   L  D  M   L  P  A      Frame 2
       R  A  Q   Q  H  R   P  H  N  Q   G  P  C   A  A  Q      Frame 6

3701 GATGCCCTGG ATGACTTTGA TTTGGACATG CTCCCTGCTG ATGCACTTGA
     D  A  L  D   D  F  D   L  D  M   L  P  A  D   A  L  D    Frame 2
     Q  H  G  P   H  S  Q   N  P  C   A  G  Q  Q   H  V  Q    Frame 6

3751 TGATTTTGAC CTGGATATGC TGTGATGGAT CCAGACATGA TAAGATACAT
      D  F  D   L  D  M  L   *  Frame 2
      H  N  Q   G  P  Y  A   T  I  S   G  S  M   I  L  Y  M    Frame 6

3801 TGATGAGTTT GGACAAACCA CAACTAGAAT GCAGTGAAAA AATGCTTTA
       S  S  N   P  C  V   V  V  L  I   C  H  F   F  H  K      Frame 6

3851 TTTGTGAAAT TTGTGATGCT ATTGCTTTAT TTGTAACCAT TATAAGCTGC
     I  Q  S  I   Q  S  A   I  A  K   N  T  V  M   I  L  Q    Frame 6

              HpaI          MfeI
3901 ATAAACAAGT TAACAACAAC AATTGCATTC ATTTTATGTT TCAGGTTCAG
      M  F  L   N  V  V  V   I  A  N   M  K  H   K  L  N  L    Frame 6

3951 GGGGAGGTGT GGGAGGTTTT TTAAAGCAAG TAAAACCTCT ACAAATGTGG
       P  L  H   P  L  N   K  L  A  L   L  V  E   V  F  T      Frame 6

4001 TATGGCTGAT TATGATCCTG CAAGCCTCGT CGTCCTGGCC GGACCACGCT
     T  H  S  I   I  I  R   C  A  E   D  D  Q  G   S  W  A    Frame 6

4051 ATCTGTGCAA GGTCCCCGGC CCCGGACGCG CGCTCCATGA GCAGAGCGCC
      I  Q  A   L  D  G  A   G  S  A   R  E  M  Frame 6

                                SfoI
                                NarI
                                KasI
                     BbsI       BbeI
4101 CGCCGCCGAG GCGAAGACTC GGGCGGCGCC CTGCCCGTCC CACCAGGTCA

4151 ACAGGCGGTA ACGTAACCGG CCTCTTCATC GGGAATGCGC GCGACCTTCA
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4201 GCATCGCCGG CATGTCCCCC TGGCGGACGG GAAGTATCCA GCTCGACCAA

                           XmaI
                           SmaI
4251 GCTTCTCGAC GATAGATCTC CCGGGTGGCA TCCCTGTGAC CCCTCCCCAG

                                         CspCI
                                         CspCI
4301 TGCCTCTCCT GGCCCTGGAA GTTGCCACTC CAGTGCCCAC CAGCCTTGTC

                                    AhdI
4351 CTAATAAAAT TAAGTTGCAT CATTTTGTCT GACTAGGTGT CCTTCTATAA

                                                    BbsI
4401 TATTATGGGG TGGAGGGGGG TGGTATGGAG CAAGGGGCAA GTTGGGAAGA

4451 CAACCTGTAG GGCCTGCGGG GTCTATTGGG AACCAAGCTG GAGTGCAGTG

4501 GCACAATCTT GGCTCACTGC AATCTCCGCC TCCTGGGTTC AAGCGATTCT

4551 CCTGCCTCAG CCTCCCGAGT TGTTGGGATT CCAGGCATGC ATGACCAGGC

4601 TCAGCTAATT TTTGTTTTTT TGGTAGAGAC GGGGTTTCAC CATATTGGCC

4651 AGGCTGGTCT CCAACTCCTA ATCTCAGGTG ATCTACCCAC CTTGGCCTCC

                              AloI
                              AloI
4701 CAAATTGCTG GGATTACAGG CGTGAACCAC TGCTCCCTTC CCTGTCCTTC

                                  ZraI
                                  AatII
4751 TGATTTTAAA ATAACTATAC CAGCAGAGGA CGTCCAGACA CAGCATAGCT

4801 ACCTGGCCAT GCCCAACCGG TGGGACATTT GAGTTGCTTG CTTGGCACTG

                                                  KpnI
                                                  Acc65I
4851 TCCTCTCATG CGTTGGGTCC ACTCAGTAGA TGCCTGTTGA TTCGGTACCG

4901 AGCTCGACTT TCACTTTTCT CTATCACTGA TAGGGAGTGT AAACTCGACT

4951 TTCACTTTTC TCTATCACTG ATAGGAGTGT AAACTCGACT TTCACTTTTC

5001 TCTTATCTGA TAGGGAGTGG TAAACTCCAC TTTAAATTTC TACTCCGCGG

                               XhoI
5051 ACCCGACTTC CTGCAATTAA AGCTTCTCGA GTCTAGATCT GCACCGGTCG

5101 CCACCATGGT GAGCAAGGGC GAGGAGCTGT TCACCGGGGT GGTGCCCATC
           M  V   S  K  G   E  E  L   F  T  G   V  V  P   I   Frame 3

5151 CTGGTCGAGC TGGACGGCGA CGTAAACGGC CACAAGTTCA GCGTGTCCGG
      L  V  E   L  D  G  D   V  N  G   H  K  F   S  V  S   G   Frame 3

5201 CGAGGGCGAG GGCGATGCCA CCTACGGCAA GCTGACCCTG AAGTTCATCT
      E  G  E   G  D  A  T   Y  G  K   L  T  L   K  F  I   C   Frame 3
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5251 GCACCACCGG CAAGCTGCCC GTGCCCTGGC CCACCCTCGT GACCACCCTG
        T  T  G   K  L  P   V  P  W  P   T  L  V   T  T  L      Frame 3

5301 ACCTACGGCG TGCAGTGCTT CAGCCGCTAC CCCGACCACA TGAAGCAGCA
      T  Y  G  V   Q  C  F   S  R  Y   P  D  H  M   K  Q  H     Frame 3

5351 CGACTTCTTC AAGTCCGCCA TGCCCGAAGG CTACGTCCAG GAGCGCACCA
       D  F  F   K  S  A  M   P  E  G   Y  V  Q   E  R  T  I    Frame 3

5401 TCTTCTTCAA GGACGACGGC AACTACAAGA CCCGCGCCGA GGTGAAGTTC
        F  F  K   D  D  G   N  Y  K  T   R  A  E   V  K  F      Frame 3

5451 GAGGGCGACA CCCTGGTGAA CCGCATCGAG CTGAAGGGCA TCGACTTCAA
      E  G  D  T   L  V  N   R  I  E   L  K  G  I   D  F  K     Frame 3

5501 GGAGGACGGC AACATCCTGG GGCACAAGCT GGAGTACAAC TACAACAGCC
       E  D  G   N  I  L  G   H  K  L   E  Y  N   Y  N  S  H    Frame 3

5551 ACAACGTCTA TATCATGGCC GACAAGCAGA AGAACGGCAT CAAGGTGAAC
        N  V  Y   I  M  A   D  K  Q  K   N  G  I   K  V  N      Frame 3

5601 TTCAAGATCC GCCACAACAT CGAGGACGGC AGCGTGCAGC TCGCCGACCA
      F  K  I  R   H  N  I   E  D  G   S  V  Q  L   A  D  H     Frame 3

5651 CTACCAGCAG AACACCCCCA TCGGCGACGG CCCCGTGCTG CTGCCCGACA
       Y  Q  Q   N  T  P  I   G  D  G   P  V  L   L  P  D  N    Frame 3

5701 ACCACTACCT GAGCACCCAG TCCGCCCTGA GCAAAGACCC CAACGAGAAG
        H  Y  L   S  T  Q   S  A  L  S   K  D  P   N  E  K      Frame 3

5751 CGCGATCACA TGGTCCTGCT GGAGTTCGTG ACCGCCGCCG GGATCACTCT
      R  D  H  M   V  L  L   E  F  V   T  A  A  G   I  T  L     Frame 3

                          BsrGI
5801 CGGCATGGAC GAGCTGTACA AGTCCGGTAC AGCTCTCGAC GGAGAAAGCT
       G  M  D   E  L  Y  K   S  G  T   A  L  D   G  E  S  S    Frame 3

5851 CAGGCTCTGG CTCAGAGTCT GACTCCATGG CCAATTTACT GACCGTACAC
        G  S  G   S  E  S   D  S  M  A   N  L  L   T  V  H      Frame 3

5901 CAAAATTTGC CTGCATTACC GGTCGATGCA ACGAGTGATG AGGTTCGCAA
      Q  N  L  P   A  L  P   V  D  A   T  S  D  E   V  R  K     Frame 3

5951 GAACCTGATG GACATGTTCA GGGATCGCCA GGCGTTTTCT GAGCATACCT
       N  L  M   D  M  F  R   D  R  Q   A  F  S   E  H  T  W    Frame 3

6001 GGAAAATGCT TCTGTCCGTT TGCCGGTCGT GGGCGGCATG GTGCAAGTTG
        K  M  L   L  S  V   C  R  S  W   A  A  W   C  K  L      Frame 3

                                      XmnI     NruI
6051 AATAACCGGA AATGGTTTCC CGCAGAACCT GAAGATGTTC GCGATTATCT
      N  N  R  K   W  F  P   A  E  P   E  D  V  R   D  Y  L     Frame 3

6101 TCTATATCTT CAGGCGCGCG GTCTGGCAGT AAAAACTATC CAGCAACATT
       L  Y  L   Q  A  R  G   L  A  V   K  T  I   Q  Q  H  L    Frame 3

                                 RsrII
6151 TGGGCCAGCT AAACATGCTT CATCGTCGGT CCGGGCTGCC ACGACCAAGT
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         G  Q  L   N  M  L   H  R  R  S   G  L  P   R  P  S     Frame 3

          BsrDI                                            AclI
6201 GACAGCAATG CTGTTTCACT GGTTATGCGG CGGATCCGAA AAGAAAACGT
     D  S  N  A   V  S  L   V  M  R   R  I  R  K   E  N  V     Frame 3

                                               BstBI
6251 TGATGCCGGT GAACGTGCAA AACAGGCTCT AGCGTTCGAA CGCACTGATT
      D  A  G   E  R  A  K   Q  A  L   A  F  E   R  T  D  F    Frame 3

                                          PvuI
                                         AsiSI            SnaBI
6301 TCGACCAGGT TCGTTCACTC ATGGAAAATA GCGATCGCTG CCAGGATATA
       D  Q  V   R  S  L   M  E  N  S   D  R  C   Q  D  I      Frame 3

                                                   SnaBI
6351 CGTAATCTGG CATTTCTGGG GATTGCTTAT AACACCCTGT TACGTATAGC
     R  N  L  A   F  L  G   I  A  Y   N  T  L  L   R  I  A     Frame 3

                                EcoRV
6401 CGAAATTGCC AGGATCAGGG TTAAAGATAT CTCACGTACT GACGGTGGGA
      E  I  A   R  I  R  V   K  D  I   S  R  T   D  G  G  R    Frame 3

6451 GAATGTTAAT CCATATTGGC AGAACGAAAA CGCTGGTTAG CACCGCAGGT
       M  L  I   H  I  G   R  T  K  T   L  V  S   T  A  G      Frame 3

6501 GTAGAGAAGG CACTTAGCCT GGGGGTAACT AAACTGGTCG AGCGATGGAT
     V  E  K  A   L  S  L   G  V  T   K  L  V  E   R  W  I     Frame 3

6551 TTCCGTCTCT GGTGTAGCTG ATGATCCGAA TAACTACCTG TTTTGCCGGG
      S  V  S   G  V  A  D   D  P  N   N  Y  L   F  C  R  V    Frame 3

6601 TCAGAAAAAA TGGTGTTGCC GCGCCATCTG CCACCAGCCA GCTATCAACT
       R  K  N   G  V  A   A  P  S  A   T  S  Q   L  S  T      Frame 3

6651 CGCGCCCTGG AAAGGATTTT TGAAGCAACT CATCGATTGA TTTACGGCGC
     R  A  L  E   R  I  F   E  A  T   H  R  L  I   Y  G  A     Frame 3

             PshAI
6701 TAAGGATGAC TCTGGTCAGA GATACCTGGC CTGGTCTGGA CACAGTGCCC
      K  D  D   S  G  Q  R   Y  L  A   W  S  G   H  S  A  R    Frame 3

6751 GTGTCGGAGC CGCGCGAGAT ATGGCCGCGC TGGAGTTCAT ACCGGAGATC
       V  G  A   A  R  D   M  A  A  L   E  F  I   P  E  I      Frame 3

6801 ATGCAGCTGG TGCTGGACCA TGTAATATGT CATGACTATA TCGTACTGAT
     M  Q  L  V   L  D  H   V  I  C   H  D  Y  I   V  L  I     Frame 3

                                                     MluI
6851 AGTGAACAGG CATGTGCGCT GCTGAAGATG GCGATTAGCC ATTAACGCGT
      V  N  R   H  V  R  C   *  Frame 3

6901 AAATGATTGC TCTAGAGTGA GGGTCCCCAC CTGGGACCCT TGAGAGTATC

6951 AGGTCTCCCA CGTGGGAGAC AAGAAATCCC TGTTTAATAT TTAAACAGCA

7001 GTGTTCCCCA TCTGGGTCCT TGCACCCCTC ACTCTGGCCT CAGCCGACTG
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7051 CACAGCGGCC CCTGCATCCC CTTGGCTGTG AGGCCCCTGG ACAAGCAGAG

7101 GTGGCCAGAG CTGGGAGGCA TGGCCCTGGG GTCCCACGAA TTTGCTGGGG

                     AflII
7151 AATCTCGTTT TTCTTCTTAA GACTTTTGGG ACATGGTTTG ACTCCCGAAC

           BmgBI
7201 ATCACCGACG TGTCTCCTGT TTTTCTGGGT GGCCTCGGGA CACCTGCCCT

7251 GCCCCCACGA GGGTCAGGAC TGTGACTCTT TTTAGGGCCA GGCAGGTGCC

7301 TGGACATTTG CCTTGCTGGA CGGGGACTGG GGATGTGGGA GGGAGCAGAC

7351 AGGAGGAATC ATGTCAGGCC TGTGTGTGAA AGGAAGCTCC ACTGTCACCC

                                                         BarI
                                                         BarI
7401 TCCACCTCTT CACCCCCCAC TCACCAGTGT CCCCTCCACT GTCACATTGT

7451 AACTGAACTT CAGGATAATA AAGTGTTTGC CTCCAAAAAA AAAAAAAAAA

                           NotI
7501 ACCGAATTCA GCTTGAAGTT CGCGGCCGCG ACTCTAGATC ATAATCAGCC

7551 ATACCACATT TGTAGAGGTT TTACTTGCTT TAAAAAACCT CCCACACCTC

                                  MfeI        HpaI
7601 CCCCTGAACC TGAAACATAA AATGAATGCA ATTGTTGTTG TTAACTTGTT

7651 TATTGCAGCT TATAATGGTT ACAAATAAAG CAATAGCATC ACAAATTTCA

7701 CAAATAAAGC ATTTTTTTCA CTGCATTCTA GTTGTGGTTT GTCCAAACTC

                AflII
7751 ATCAATGTAT CTTAAGGCGT AAATTGTAAG CGTTAATATT TTGTTAAAAT

7801 TCGCGTTAAA TTTTTGTTAA ATCAGCTCAT TTTTTAACCA ATAGGCCGAA

7851 ATCGGCAAAA TCCCTTATAA ATCAAAAGAA TAGACCGAGA TAGGGTTGAG

                                            AloI
                                            AloI
7901 TGTTGTTCCA GTTTGGAACA AGAGTCCACT ATTAAAGAAC GTGGACTCCA

                                               DraIII
7951 ACGTCAAAGG GCGAAAAACC GTCTATCAGG GCGATGGCCC ACTACGTGAA

8001 CCATCACCCT AATCAAGTTT TTTGGGGTCG AGGTGCCGTA AAGCACTAAA

8051 TCGGAACCCT AAAGGGAGCC CCCGATTTAG AGCTTGACGG GGAAAGCCGG

8101 CGAACGTGGC GAGAAAGGAA GGGAAGAAAG CGAAAGGAGC GGGCGCTAGG

8151 GCGCTGGCAA GTGTAGCGGT CACGCTGCGC GTAACCACCA CACCCGCCGC

8201 GCTTAATGCG CCGCTACAGG GCGCGTCAGG TGGCACTTTT CGGGGAAATG
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8251 TGCGCGGAAC CCCTATTTGT TTATTTTTCT AAATACATTC AAATATGTAT

8301 CCGCTCATGA GACAATAACC CTGATAAATG CTTCAATAAT ATTGAAAAAG

8351 GAAGAGTCCT GAGGCGGAAA GAACCAGCTG TGGAATGTGT GTCAGTTAGG

8401 GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC

8451 ATCTCAATTA GTCAGCAACC AGGTGTGGAA AGTCCCCAGG CTCCCCAGCA

8501 GGCAGAAGTA TGCAAAGCAT GCATCTCAAT TAGTCAGCAA CCATAGTCCC

8551 GCCCCTAACT CCGCCCATCC CGCCCCTAAC TCCGCCCAGT TCCGCCCATT

                                                       SfiI
8601 CTCCGCCCCA TGGCTGACTA ATTTTTTTTA TTTATGCAGA GGCCGAGGCC

8651 GCCTCGGCCT CTGAGCTATT CCAGAAGTAG TGAGGAGGCT TTTTTGGAGG

     AvrII
8701 CCTAGGCTTT TGCAAAGATC GATCAAGAGA CAGGATGAGG ATCGTTTCGC

8751 ATGATTGAAC AAGATGGATT GCACGCAGGT TCTCCGGCCG CTTGGGTGGA
     M  I  E  Q  D  G   L   H  A  G   S  P  A  A   W  V  E     Frame 3

8801 GAGGCTATTC GGCTATGACT GGGCACAACA GACAATCGGC TGCTCTGATG
      R  L  F   G  Y  D   W  A  Q   Q   T  I  G   C  S  D  A   Frame 3

                                  SfoI
                                  NarI
                                  KasI
                                  BbeI
8851 CCGCCGTGTT CCGGCTGTCA GCGCAGGGGC GCCCGGTTCT TTTTGTCAAG
       A  V  F   R  L  S   A  Q  G  R   P  V  L   F  V  K      Frame 3

8901 ACCGACCTGT CCGGTGCCCT GAATGAACTG CAAGACGAGG CAGCGCGGCT
     T  D  L  S   G  A  L   N  E  L   Q  D  E  A   A  R  L     Frame 3

                                   FspI             Tth111I
8951 ATCGTGGCTG GCCACGACGG GCGTTCCTTG CGCAGCTGTG CTCGACGTTG
      S  W  L   A  T  T  G   V  P  C   A  A  V   L  D  V  V    Frame 3

9001 TCACTGAAGC GGGAAGGGAC TGGCTGCTAT TGGGCGAAGT GCCGGGGCAG
       T  E  A   G  R  D   W  L  L  L   G  E  V   P  G  Q      Frame 3

9051 GATCTCCTGT CATCTCACCT TGCTCCTGCC GAGAAAGTAT CCATCATGGC
     D  L  L  S   S  H  L   A  P  A   E  K  V  S   I  M  A     Frame 3
                 *  R  V   K  S  R  G   L  F  Y   G  D  H      Frame 6

         BsrDI
9101 TGATGCAATG CGGCGGCTGC ATACGCTTGA TCCGGCTACC TGCCCATTCG
      D  A  M   R  R  L  H   T  L  D   P  A  T   C  P  F  D    Frame 3
     S  I  C  H   P  P  Q   M  R  K   I  R  S   G  A  W  E     Frame 6

9151 ACCACCAAGC GAAACATCGC ATCGAGCGAG CACGTACTCG GATGGAAGCC
       H  Q  A   K  H  R   I  E  R  A   R  T  R   M  E  A      Frame 3
      V  V  L   R  F  M  A   D  L  S   C  T  S   P  H  F  G    Frame 6
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                                        SapI
9201 GGTCTTGTCG ATCAGGATGA TCTGGACGAA GAGCATCAGG GGCTCGCGCC
     G  L  V  D   Q  D  D   L  D  E   E  H  Q  G   L  A  P    Frame 3
       T  K  D   I  L  I   I  Q  V  F   L  M  L   P  E  R    Frame 6

9251 AGCCGAACTG TTCGCCAGGC TCAAGGCGAG CATGCCCGAC GGCGAGGATC
      A  E  L   F  A  R  L   K  A  S   M  P  D   G  E  D  L  Frame 3
     W  G  F  Q   E  G  P   E  L  R   A  H  G  V   A  L  I   Frame 6

9301 TCGTCGTGAC CCATGGCGAT GCCTGCTTGC CGAATATCAT GGTGGAAAAT
       V  V  T   H  G  D   A  C  L  P   N  I  M   V  E  N    Frame 3
      E  D  H   G  M  A  I   G  A  Q   R  I  D   H  H  F  I  Frame 6

                                                      RsrII
9351 GGCCGCTTTT CTGGATTCAT CGACTGTGGC CGGCTGGGTG TGGCGGACCG
     G  R  F  S   G  F  I   D  C  G   R  L  G  V   A  D  R   Frame 3
       A  A  K   R  S  E   D  V  T  A   P  Q  T   H  R  V    Frame 6

                                                SapI
9401 CTATCAGGAC ATAGCGTTGG CTACCCGTGA TATTGCTGAA GAGCTTGGCG
       Y  Q  D   I  A  L  A   T  R  D   I  A  E   E  L  G  G  Frame 3
     A  I  L  V   Y  R  Q   S  G  T   I  N  S  F   L  K  A   Frame 6

9451 GCGAATGGGC TGACCGCTTC CTCGTGCTTT ACGGTATCGC CGCTCCCGAT
       E  W  A   D  R  F   L  V  L  Y   G  I  A   A  P  D    Frame 3
      A  F  P   S  V  A  E   E  H  K   V  T  D   G  S  G  I  Frame 6

9501 TCGCAGCGCA TCGCCTTCTA TCGCCTTCTT GACGAGTTCT TCTGAGCGGG
     S  Q  R  I   A  F  Y   R  L  L   D  E  F  F   *   Frame 3
       R  L  A   D  G  E   I  A  K  K   V  L  E   E  S  R   Frame 6

               BstBI
9551 ACTCTGGGGT TCGAAATGAC CGACCAAGCG ACGCCCAACC TGCCATCACG
                     M  T   D  Q  A   T  P  N  L   P  S  R    Frame 2
     S  E  P  T   R  F  S   R  G  L   S  A  W  G   A  M   Frame 6

9601 AGATTTCGAT TCCACCGCCG CCTTCTATGA AAGGTTGGGC TTCGGAATCG
       D  F  D   S  T  A  A   F  Y  E   R  L  G   F  G  I  V  Frame 2

9651 TTTTCCGGGA CGCCGGCTGG ATGATCCTCC AGCGCGGGGA TCTCATGCTG
       F  R  D   A  G  W   M  I  L  Q   R  G  D   L  M  L    Frame 2

                     AvrII
9701 GAGTTCTTCG CCCACCCTAG GGGGAGGCTA ACTGAAACAC GGAAGGAGAC
     E  F  F  A   H  P  R   G  R  L   T  E  T  R   K  E  T   Frame 2

9751 AATACCGGAA GGAACCCGCG CTATGACGGC AATAAAAAGA CAGAATAAAA
       I  P  E   G  T  R  A   M  T  A   I  K  R   Q  N  K  T  Frame 2

9801 CGCACGGTGT TGGGTCGTTT GTTCATAAAC GCGGGGTTCG GTCCCAGGGC
       H  G  V   G  S  F   V  H  K  R   G  V  R   S  Q  G    Frame 2

9851 TGGCACTCTG TCGATACCCC ACCGAGACCC CATTGGGGCC AATACGCCCG
     W  H  S  V   D  T  P   P  R  P   H  W  G  Q   Y  A  R   Frame 2

9901 CGTTTCTTCC TTTTCCCCAC CCCACCCCCC AAGTTCGGGT GAAGGCCCAG
       V  S  S   F  S  P  P   H  P  P   S  S  G   E  G  P  G  Frame 2
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 9951 GGCTCGCAGC CAACGTCGGG GCGGCAGGCC CTGCCATAGC CTCAGGTTAC
        L  A  A   N  V  G   A  A  G  P   A  I  A   S  G  Y     Frame 2

10001 TCATATATAC TTTAGATTGA TTTAAAACTT CATTTTTAAT TTAAAAGGAT
      S  Y  I  L   *  Frame 2

10051 CTAGGTGAAG ATCCTTTTTG ATAATCTCAT GACCAAAATC CCTTAACGTG

10101 AGTTTTCGTT CCACTGAGCG TCAGACCCCG TAGAAAAGAT CAAAGGATCT

10151 TCTTGAGATC CTTTTTTTCT GCGCGTAATC TGCTGCTTGC AAACAAAAAA

10201 ACCACCGCTA CCAGCGGTGG TTTGTTTGCC GGATCAAGAG CTACCAACTC

10251 TTTTTCCGAA GGTAACTGGC TTCAGCAGAG CGCAGATACC AAATACTGTC

10301 CTTCTAGTGT AGCCGTAGTT AGGCCACCAC TTCAAGAACT CTGTAGCACC

10351 GCCTACATAC CTCGCTCTGC TAATCCTGTT ACCAGTGGCT GCTGCCAGTG

10401 GCGATAAGTC GTGTCTTACC GGGTTGGACT CAAGACGATA GTTACCGGAT

10451 AAGGCGCAGC GGTCGGGCTG AACGGGGGGT TCGTGCACAC AGCCCAGCTT

10501 GGAGCGAACG ACCTACACCG AACTGAGATA CCTACAGCGT GAGCTATGAG

10551 AAAGCGCCAC GCTTCCCGAA GGGAGAAAGG CGGACAGGTA TCCGGTAAGC

10601 GGCAGGGTCG GAACAGGAGA GCGCACGAGG GAGCTTCCAG GGGGAAACGC

10651 CTGGTATCTT TATAGTCCTG TCGGGTTTCG CCACCTCTGA CTTGAGCGTC

10701 GATTTTTGTG ATGCTCGTCA GGGGGGCGGA GCCTATGGAA AAACGCCAGC

10751 AACGCGGCCT TTTTACGGTT CCTGGCCTTT TGCTGGCCTT TTGCTCACAT

10801 GTTCTTTCCT GCGTTATCCC CTGATTCTGT GGATAACCGT ATTACCGCCA

10851 TGCAT
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pNK-TGCK, 10855 bp. (CIRCULAR)
Restriction analysis 8/6/2009
pDRAW32 revision 1.1.101
Rebase containing 280 enzymes.
56 enzymes match enzyme selection criteria.

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AatII          (G_ACGT'C) [ZraI]
Cuts 1 time.
Cuts at position 4783.

AccI           (GT'mk_AC) [FblI,XmiI]
Cuts 1 time.
Cuts at position 2157.

Acc65I         (G'GTAC_C) [KpnI,Asp718I]
[dcm methylated]
Cuts 2 times.
Cuts at positions 2674, 4894.
Fragment sizes 2220, 8635.

AclI           (AA'CG_TT) [Psp1406I]
Cuts 1 time.
Cuts at position 6247.

AfeI           (AGC'GCT) [Eco47III,Aor51HI]
Cuts 2 times.
Cuts at positions 14, 1337.
Fragment sizes 1323, 9532.

AflII          (C'TTAA_G) [BfrI,BspTI,Bst98I,BstAFI,MspCI,Vha464I]
Cuts 2 times.
Cuts at positions 7166, 7761.
Fragment sizes 595, 10260.

AhdI           (GACnn_n'nnGTC) [Eam1105I,AspEI,BmeRI,DriI]
Cuts 1 time.
Cuts at position 4386.

AjuI           (GAAnnnnnnnTTGGnnnnnn_nnnnn')
Cuts 1 time.
Cuts at position 2675.

AjuI           (CCAAnnnnnnnTTCnnnnnnn_nnnnn')
Cuts 1 time.
Cuts at position 2707.

AloI           (GAACnnnnnnTCCnnnnnnn_nnnnn')
Cuts 2 times.
Cuts at positions 4748, 7961.
Fragment sizes 3213, 7642.
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AloI (GGAnnnnnnGTTCnnnnnnn_nnnnn')
Cuts 2 times.
Cuts at positions 4716, 7929.
Fragment sizes 3213, 7642.

AsiSI (GCG_AT'CGC) [SgfI,RgaI,SfaAI]
Cuts 1 time.
Cuts at position 6335.

AvrII (C'CTAG_G) [AspA2I,BlnI,XmaJI]
Cuts 2 times.
Cuts at positions 8701, 9716.
Fragment sizes 1015, 9840.

BarI (GAAGnnnnnnTACnnnnnnn_nnnnn')
Cuts 1 time.
Cuts at position 7441.

BarI (GTAnnnnnnCTTCnnnnnnn_nnnnn')
Cuts 1 time.
Cuts at position 7473.

BbeI (G_GCGC'C) [NarI,DinI,EgeI,EheI,KasI,Mly113I,SfoI]
Cuts 2 times.
Cuts at positions 4129, 8882.
Fragment sizes 4753, 6102.

BbsI (GAAGACnn'nnnn_) [BpiI,BpuAI,BstV2I]
Cuts 2 times.
Cuts at positions 4120, 4453.
Fragment sizes 333, 10522.

BclI (T'GATC_A) [FbaI,Ksp22I]
[dam methylated]
Cuts 1 time.
Cuts at position [3582].

BmgBI (CAC'GTC) [BtrI,AjiI]
Cuts 2 times.
Cuts at positions 1066, 7209.
Fragment sizes 6143, 4712.

BmtI (G_CTAG'C) [NheI,AsuNHI,BspOI]
Cuts 1 time.
Cuts at position 1203.

BspEI (T'CCGG_A) [AccIII,Aor13HI,BseAI,Bsp13I,Kpn2I,MroI]
[dam methylated]
Cuts 1 time.
Cuts at position 436.

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BsrDI          (GCAATG_nn') [Bse3DI,BseMI]
Cuts 2 times.
Cuts at positions 6212, 9112.
Fragment sizes 2900, 7955.

BsrGI          (T'GTAC_A) [Bsp1407I,BstAUI]
Cuts 2 times.
Cuts at positions 321, 5815.
Fragment sizes 5494, 5361.

BstBI          (TT'CG_AA) [AsuII,Bpu14I,Bsp119I,BspT104I,Csp45I,NspV,SfuI]
Cuts 2 times.
Cuts at positions 6286, 9561.
Fragment sizes 3275, 7580.

BstZ17I        (GTA'TAC) [BssNAI,Bst1107I]
Cuts 1 time.
Cuts at position 2158.

CspCI          (CAAnnnnnGTGGnnnnnnnnnn_nn')
Cuts 1 time.
Cuts at position 4326.

CspCI          (CCACnnnnnTTGnnnnnnnnnnn_nn')
Cuts 1 time.
Cuts at position 4361.

DraIII         (CAC_nnn'GTG) [AdeI]
Cuts 1 time.
Cuts at position 7995.

EcoNI          (CCTnn'n_nnAGG) [BstENI,XagI]
Cuts 1 time.
Cuts at position 3216.

EcoRV          (GAT'ATC) [Eco32I]
Cuts 1 time.
Cuts at position 6428.

FspI           (TGC'GCA) [Acc16I,AviII,NsbI]
Cuts 1 time.
Cuts at position 8981.

HpaI           (GTT'AAC) [KspAI]
Cuts 2 times.
Cuts at positions 3911, 7642.
Fragment sizes 3731, 7124.

KasI           (G'GCGC_C) [NarI,BbeI,DinI,EgeI,EheI,Mly113I,SfoI]
Cuts 2 times.
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Cuts at positions 4125, 8878.
Fragment sizes 4753, 6102.

KpnI          (G_GTAC'C)  [Acc65I,Asp718I]
Cuts 2 times.
Cuts at positions 2678, 4898.
Fragment sizes 2220, 8635.

MfeI          (C'AATT_G)  [MunI]
Cuts 2 times.
Cuts at positions 3920, 7629.
Fragment sizes 3709, 7146.

MluI          (A'CGCG_T)
Cuts 1 time.
Cuts at position 6895.

NarI          (GG'CG_CC)  [BbeI,DinI,EgeI,EheI,KasI,Mly113I,SfoI]
Cuts 2 times.
Cuts at positions 4126, 8879.
Fragment sizes 4753, 6102.

NdeI          (CA'TA_TG)  [FauNDI]
Cuts 1 time.
Cuts at position 1887.

NheI          (G'CTAG_C)  [AsuNHI,BmtI,BspOI]
Cuts 1 time.
Cuts at position 1199.

NotI          (GC'GGCC_GC)  [CciNI]
Cuts 2 times.
Cuts at positions 51, 7523.
Fragment sizes 7472, 3383.

NruI          (TCG'CGA)  [Bsp68I,BtuMI]
[dam methylated]
Cuts 1 time.
Cuts at position 6091.

PshAI         (GACnn'nnGTC)  [BoxI,BstPAI]
Cuts 1 time.
Cuts at position 6712.

PvuI          (CG_AT'CG)  [BpvUI,MvrI,Ple19I]
Cuts 1 time.
Cuts at position 6335.

RsrII         (CG'GwC_CG)  [CpoI,CspI,Rsr2I]
Cuts 2 times.
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Cuts at positions 6178, 9395.
Fragment sizes 3217, 7638.

SapI          (GCTCTTCn'nnn_) [BspQI,LguI,PciSI]
Cuts 2 times.
Cuts at positions 9223, 9433.
Fragment sizes 210, 10645.

ScaI          (AGT'ACT) [AssI,BmcAI,ZrmI]
Cuts 1 time.
Cuts at position 2735.

SfiI          (GGCCn_nnn'nGGCC)
[dcm methylated]
Cuts 1 time.
Cuts at position 8654.

SfoI          (GGC'GCC) [NarI,BbeI,DinI,EgeI,EheI,KasI,Mly113I]
Cuts 2 times.
Cuts at positions 4127, 8880.
Fragment sizes 4753, 6102.

SmaI          (CCC'GGG) [Cfr9I,TspMI,XmaI,XmaCI]
Cuts 2 times.
Cuts at positions 692, 4272.
Fragment sizes 3580, 7275.

SnaBI         (TAC'GTA) [BstSNI,Eco105I]
Cuts 2 times.
Cuts at positions 6351, 6393.
Fragment sizes 42, 10813.

SpeI          (A'CTAG_T) [AhlI,BcuI]
Cuts 1 time.
Cuts at position 64.

Tth111I       (GACn'n_nGTC) [AspI,PflFI,PsyI]
Cuts 2 times.
Cuts at positions 1064, 8997.
Fragment sizes 7933, 2922.

XhoI          (C'TCGA_G) [PaeR7I,Sfr274I,SlaI,StrI,TliI]
Cuts 2 times.
Cuts at positions 31, 5076.
Fragment sizes 5045, 5810.

XmaI          (C'CCGG_G) [SmaI,Cfr9I,TspMI,XmaCI]
Cuts 2 times.
Cuts at positions 690, 4270.
Fragment sizes 3580, 7275.
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XmnI (GAAnn'nnTTC) [Asp700I,MroXI,PdmI]
Cuts 1 time.
Cuts at position 6085.

ZraI (GAC'GTC) [AatII]
Cuts 1 time.
Cuts at position 4781.