



EcoRI (23)

EcoRV (17)

NotI (2) SalI (9) XbaI (19) SdaI (38)

1 GCGGCCGCGTCAACGATATCTAGAATTCCGATCCTGCAGGCGCTGCTCGGGAGGCTGAGGCAGGAGAATCACTTGAACAGGGAGGCAGAGGTTGTGG
101 TGAGCAGAGATCGCGCCATTGCTCTCCAGCCTGGGCAACAAGAGCAAAGTTCTGTTAAAAAAGTCCTTTTCGATGTGACTGTCTCTCCCAA
201 ATTTGTAGACCTCTTAAGATCATGCTTTTTCAGATACTTCAAAGATTCCAGAAGATATGCCCGGGGTCTGGAAGCCACAAGGTAACACAACACATC
301 CCCCTCTTGACTATCAATTTTACTAGAGGATGTGGTGGGAAACCATTATTTGATATTAACAATAAGGCTTGGGATGGAGTAGGATGCAAGCTCCCC

AvrII (452)

401 AGGAAAGTTTAAGATAAACCTGAGACTTAAAAGGTGTTAAGAGTGGCAGCCTAGGGAATTTATCCGGACTCCGGGGAGGGGGCAGAGTACCAGCC
501 TCTGCATTAGGATTCTCCGAGGAAAAGTGTGAGAACGGCTGCAGGCAACCCAGGCGTCCCGGCTAGGAGGGACGCCAGGCTCGCGGAAGAGA
601 GGGAGAAAGTGAAGCTGGGAGTTGCCACTCCAGACTTGTGGAATGCAGTTGGAGGGGGCAGCTGGGAGCGCGCTTGTCCCAATCACAGGAGAAGGA
701 GGAGGTGGAGGAGGAGGCTGCTTGGAGGAAGTATAAGAATGAAGTTGTGAAGCTGAGATCCCTCCATTGGGACCGGAGAAACCAGGGGAGCCCCCGG
801 GCAGCCGCGCCCCCTTCCACGGGCGCTTACTGCGCCGCGCGCCCGCCCCACCCCTCGCAGCACCCCGCGCCCGCGCCCTCCAGCCGGGTCCA

NeoI (934)

901 GCGGAGCGCTGGGGCCGGAGCCGAGTGAGCACCATGGTTCGGGGCCCTGCATGCTGCTGCTGCTGCTGCTGGGCTGAGGCTACAGCTCTCCCT
1001 GGGCATCATCCAGTTGAGGAGGAGAACCCGGACTTCTGGAACCGCGAGGAGCCGAGGCCCTGGGTGCCGCAAGAAGCTGCAGCTGCACAGACAGCC
22> G I I P V E E E N P D F W N R E A A E A L G A A K K L Q P A Q T A
1101 GCCAAGAACCTCATCATCTTCTGGGCGATGGGATGGGGTGTCTACGGTACAGCTGCCAGGATCCTAAAAGGGCAGAAGAAGGACAACTGGGGCCTG
56> A K N L I I F L G D G M G V S T V T A A R I L K G Q K K D K L G P

NdeI (1229)

1201 AGATACCCCTGGCTATGGACCGCTTCCCATATGTGGCTCTGTCCAAGACATACAATGTAGACAAACATGTGCCAGACAGTGGAGCCACAGCCACGGCCTA
89> E I P L A M D R F P Y V A L S K T Y N V D K H V P D S G A T A T A Y
1301 CCTGTGCGGGTCAAGGGCACTTCCAGACCTTGGCTTGGTGCAGCCCGCTTAAACAGTGAACACGACACCGGGCAACGAGGTCATCTCCGTG
122> L C G V K G N F Q T I G L S A A A R F N Q C N T T R G N E V I S V
1401 ATGAATCGGGCAAGAAAGCAGGGAAGTCAAGTGGGAGTGGTAACCACCACAGTGCAGCAGCCCTGCCAGCCGGCACCTACGCCACACGGTGAACC
156> M N R A K K A G K S V G V V T T T R V Q H A S P A G T Y A H T V N
1501 GCAACTGGTACTCGGACCGCAGCTGCCTCGGCCCGCCAGGAGGGTGCAGGACATCGCTACGCAGCTCATCTCCAATGGACATTGATGTGAT
189> R N W Y S D A D V P A S A R Q E G C Q D I A T Q L I S N M D I D V I
1601 CCTGGGTGGAGGCCGAAAGTACATGTTTTCGCATGGGAACCCAGACCTGAGTACCAGATGACTACAGCCAAAGTGGGACAGGCTGGACGGGAAGAA
222> L G G G R K Y M F R M G T P D P E Y P D D Y S Q G G T R L D G K N
1701 CTGGTGCAGGAATGGCTGGCAAGCGCCAGGGTGCCTGGTATGTGTGAACCGCACTGAGCTCATGCAGGCTTCCCTGGACCCGTCTGTGACCCATCTCA
256> L V Q E W L A K R Q G A R Y V W N R T E L M Q A S L D P S V T H L
1801 TGGTCTCTTTGAGCCTGGAGACATGAAATACGAGATCCACCGAGACTCCACATGGACCCCTCCCTGATGGAGATGACAGAGGCTGCCCTGCGCCTGT
289> M G L F E P G D M K Y E I H R D S T L D P S L M E M T E A A L R L L

SacII (1916)

1901 GAGCAGGAACCCCGCGGCTTCTTCTCTTCTGAGGGTGGTGCATCGACACCGTTCATCACGAAAGCAGGGCTTACCGGCACTGACTGAGACGATC
322> S R N P R G F F L F V E G G R I D H G H H E S R A Y R A L T E T I
2001 ATGTTGAGGACGATGAGAGGGCGGGCAGCTACCAGGAGGACACGCTGAGCCTGTACTGCGGACCTCCAGCTTCTCTTCTGAGG
356> M F D D A I E R A G Q L T S E E D T L S L V T A D H S H V F S F G
2101 GCTACCCCTGCGAGGGAGCTCCATCTTGGGCTGGCCCTGGCAAGGCCGGGACAGGAAGGCTTACACGGTCTCTTATACGAAACGGTCCAGGCTA
389> G Y P L R G S S I F G L A P G K A R D R K A Y T V L L Y G N G P G Y
2201 TGTGCTCAAGGACGGCGCCCGGGATGTTACCGAGAGCGAGAGCGGGAGCCCGAGTATCGGCAGCAGTCAAGTGGCCCTGGACGAGAGACCCAC
422> V L K D G A R P D V T E S E S G S P E Y R Q Q S A V P L D E E T H
2301 GCAGGCGAGGACGTGGCGGTGTTGCGCGCGGCCCGCAGGCGCACCTGGTTCAGGCGTGCAGGAGCAGACCTTATAGCGCACGTGATGGCCTTCCGCG
456> A G E D V A V F A R G P Q A H L V H G V Q E Q T F I A H V M A F A

NheI

2401 CCTGCTGGAGCCCTACACCGCTGCGACCTGGCGCCCCCGCGGACCCAGCAGCCGCGCACCCGGGGCGTCCCGGTCCAAGCGTCTGGATTGAA
489> A C L E P Y T A C D L A P P A G T T D A A H P G R S R S K R L D •
2501 CTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTAT

MfeI (2649)

2601 TGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTCATTATTTTATGTTTCAGGTTTCAGGGGAGGTTGGGAGTTTTT
2701 TAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTT
2801 TCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTCATGGAGTTTAAAGATATAGTGTAT

SspI (2979)

2901 TTTCCCAAGTGTGAACTAGCTCTTCAATTTCTTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTTAGTAAAAATATTAGAAATAATTTAAATAC
3001 ATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAA
3101 GGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCCTCTGCCACAAAGTGCACGAGTTGCCGGCCGGGTGG
125< • D Q E E A V F H V C N G A P D
3201 CGCAGGGCGAACTCCCGCCCCACGGTGTCTCGCCGATCTCGGTGATGCGCCGGGAGGCGTCCCGGAAGTTCTGTGGACACGACCTCCGACCTCGG
108< R L A F E R G W P Q E G I E T M A P G S A D R F N T S N V E S W E A
3301 CGTACAGCTCGTCCAGGCCGCGACCCACACCCAGGCCAGGGTGTGTCCGCGCACCTGGTCTGGACCGGCTGATGAACAGGGTACGTCGTCGCCG
75< Y L E D L G R V W V W A L T N D P V V Q D Q V A S I F L T V D D R

SgrAI (3407)

3401 GACCACACCGCGAAGTCTGCTCCACGAAGTCCCGGGAGAACCCGAGCCGGTCCGATCCAGAACTCGACCGCTCCGGCGACGTGCGCGCGGTGAGCACC
42< V V G A F D D E V F D R S F G L R D T W F E V A G A V D R A T L V

3501 GGAACGGCACTGGTCAACTTGGCCATGATGGCTCCTCCTGTCAGGAGAGGAAAGAGAAGAAGGTTAGTACAATTGCTATAGTGAGTTGTATTATACTATG
8 P V A S T L K A M ←

3601 CAGATATACTATGCCAATGATTAATTGTCAA ACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGG
←

3701 CCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAG
←

3801 ATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTG
←

3901 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCGCT
←

4001 GCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTA
←

4101 TGTAGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTC
←

4201 GGAAAAAGAGTTGGTAGCTTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGAT
←

4301 CTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAA
←

4401 ATCA