



PvuI (7)
SgfI (6) 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA **MfeI (82)**

101 GAGAAAGTGGCGGGGTAAGTGGAAAGTGTGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC **HindIII (245)** **Bsu36I (291)**

301 GCCATCCACGCGGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTCTCAACTCTACGCTTTTGTTCGTTT **NgoMIV (441)**

501 TCTGTTTGTCCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTGACGATGCCAAGGGTCCCAAGCAACAGCCGCCGAGCCCGA **KasI (535)** **AgeI (552)** **SphI (560)**
1 M P K G P K Q Q P P E P E

601 GTGGATCGGGACGGGAGGGCACGAGCCCGGCAAAAGTGTGAAGAAAGGAAAAAGGACAAGAAGACCAAAAAGACGTTCTTTGAAGAGCTGGCA **SacII (629)**
13> W I G D G E G T S P A D K V V K K G K K D K K T K K T F F E E L A
701 GTAGAGGACAAACAGCTGGGAAAGAGGAAAAATTGCAGAAGGAGAAGGAGCAGCAACAGCAACAGCAGCAACAGAAGAAAAAGCAGACACCCAGGAAAG
47> V E D K Q A G E E E K L Q K E K E Q Q Q Q Q Q Q K K K R D T R K
801 GCCGTCGAAAAAGGATGTGGACGATGATAGTGTGAGAGAGTCTCATGGAGGACTTAAGCAACTGTCTGTGCCAGCCAGTGTGAGGAAGATGAGGT
80> G R R K K D V D D D S D E R V L M E R L K Q L S V P A S D E E D E V
901 GCCTGCCCCATACCCGAGGACGGAAGGCAAGGTTGGAATGTTTTGAAGCCCTGATCAGGATGACAGTGAAGGAGGAGGAGGAGGAAAGAA
113> P A P I P R G R K K A K G G N V F E A L I Q D D S E E E E E E E
1001 AACCGTGTCTCAAGCCCGCAAGCCAGAGAAGAATCGCATCAATAAAGCCGTGGCTGAGGAACCTCTGGGCTCAGGAGTAAAAAGGAAAGGAGGAGA
147> N R V L K P A K P E K N R I N K A V A E E P P G L R S K K G K E E
1101 AATCAAAAAGGAAAGCAAGAGTAAACCTGCTGCTGCAGACAGTGAAGGGAAAGAGGAGGAG GACACAGCTAAAGAAAAGGAGCCTCCTCAGCAAGGAA
180> K S K G K A K S K P A A A D S E G E E E E D T A K E K E P P Q Q G K
1201 GGACAGAGACAAAAGGAGGCTGAGCAGGGCTCAGGGGAAAGAGAAGGAAAGGAAAGGAGGACTTGAAGGCAACGATCCCTATGCCAACCTTAGCAAAA
213> D R D K K E A E Q G S G E E K E E K E G D L K A N D P Y A N L S K

1301 AAGGAAAAGAAAAGCTAAAGAAACAGATGGATTATGAACGACAGGTGGAGTCATTGAAAGCAGCTAATGCTGCAGAAAACGACTTCTGTGTCCAGG **BstAPI (1360)**
247> K E K K K L K K Q M D Y E R Q V E S L K A A N A A E N D F S V S Q

1401 CAGAGGTGCTTCCCGCCAGGCAATGTTAGAAAATGCATCTGACATTAAGTTGAAAAAGTTCAGCATCTCCGCCACGGCAAGGAGCTATTTCGTCATGC **NsiI (1433)**
280> A E V S S R Q A M L E N A S D I K L E K F S I S A H G K E L F V N A

1501 TGACCTGTACATAGTAGCCGGCCCGCTATGGGCTGGTGGGACCAACGGCAAAGGCAAACCACGCTTCTGAAGCACATTGCCAACCGTGCCTGAGC **BsrGI (1505)** **EagI (1518)** **NgoMIV (1516)**
313> D L Y I V A G R R Y G L V G P N G K G K T T L L K H I A N R A L S
1601 ATCCCCCTAACATTGACGTGCTGTGTCGAGCAGGAGGTGGTGGCTGATGAAACACACCGCTGCAAGCTGTCTTCGAGCAGATACCAAGCGACTGA
347> I P P N I D V L L C E Q E V V A D E T P A V Q A V L R A D T K R L
1701 GGTGCTAGAGGAGGAGAGACGGCTTACGGGACAGCTGGAGCAGGGGATGACACTGCTGCTGAGAACTAGAAAAGGTGATGAGGAACTGCGAGCTAC
380> R L L E E E R R L Q G Q L E Q G D D T A A E K L E K V Y E E L R A T

1801 CGGGCAGCAGCTGCAGAGGCAAGGCACGGCGGATCTGGCTGGCTTGGGCTTCCGACCTGAGATGCAGAATCGGCCACACAGAAGTTCTTGGGGT **BstAPI (1804)** **BamHI (1832)**
413> G A A A A E A K A R R I L A G L G F D P E M Q N R P T Q K F S G G

1901 TGGAGAATGCGTGTCTCCCTGGCCAGGGCACTGTTTCATGGAGCAACGCTGCTGATGTTGGATGAGCCCACTAACACCTGGACCTCAACGCCGTCATCT **MscI (1919)** **XcmI (1967)**
447> W R M R V S L A R A L F M E P T L L M L D E P T N H L D L N A V I

2001 GGCTCAATAACTACCTTACGGGCTGGAGGAAGACGTTGCTGATTGTCTCCACGACCAGGGCTTTCTGGATGACGTTTGAACCTGATATCATCCACTGGA **EcoRV (2083)**
480> W L N N Y L Q G W R K T L L I V S H D Q G F L D D V C T D I I H L D
2101 CACCCAGCGGCTCCATTACTACAGGGGCAATTACATGACCTTCAAGAAGATGTACCAGCAGAAGCAGAAAAGAGCTGCTAAAGCAGTACGAGAAGCAGGAG
513> T Q R L H Y Y R G N Y M T F K K M Y Q Q K Q K E L L K Q Y E K Q E
2201 AAGAACTGAAGGAGCTGAAGGCTGGGGCAAGTCCACCAAGCAAGCGGAAAAGCAAACAAAGAAAGTCTGACTCGAAAACAGCAGAAGTGGCCGACGGA
547> K K L K E L K A G G K S T K Q A E K Q T K E V L T R K Q Q K C R R
2301 AAAACCAGGATGAAGAGTCTCAGGAGCCCCCTGAGCTCCTGAAGCGTCCCAAGGAGTACACCGTGGCTTACCTTCCAGACCCCCGCTCTCAGCCC
580> K N Q D E E S Q E P P E L L K R P K E Y T V R F T F P D P P P L S P

2401 ACCTGTGCTGGCCCTGCACGGTGTGACGTTTGGCTACGAGGGGAGAAGCCACTCTTTAAGAATCTAGATTTCCGGCATCGACATGGACTCCCGGATTTGC **DraIII (2416)** **XbaI (2463)** **BsaBI (2493)**
613> P V L G L H G V T F G Y E G Q K P L F K N L D F G I D M D S R I C
2501 ATCGTGGTCCCAATGGTGTGGGAAAGAGCACACTACTCTGCTGCTGACTGGCAAGCTGACACCGACCAACGGGAGATGAGGAAGAACCATCGGCTGA
647> I V G P N G V G K S T L L L L L T G K L T P T N G E M R K N H R L
2601 AAATCGGCTTCTTAACAGCAGTACGCAGAGCAGCTGCACATGGAGGAGACGCCACTGAGTACCTGCAGCGGAGCTTCAATCTGCCCTACAGGATGC
680> K I G F F N Q Y A E Q L H M E E T P T E Y L Q R S F N L P Y Q D A

2701 CCGAAAGTCTTGGCCGCTTTGGCCTGGAGAGCCACGCCACACCATCCAGATCTGCAAACCTCCGGTGGGAGAAAAGCCCGAGTTGTGTTTGGCGAG **SfiI (2713)** **BglII (2750)**
713> R K C L G R F G L E S H A H T I Q I C K L S G G Q K A R V V F A E

