



75

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BspHI (560)

AgeI (552)

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCATCATGAGGATCTCTGCCAGCTTCTGTGCTGTGCTCAT
AGCCGCTGCTTTCAGCATCCAAGTGTTGGGCCAACAGATGGGCCAATGCATCCACATGCTGCTATGTCAAGAAACAAAAGATCCCCAAGAGGAATCTC
13▶ A A A F S I Q V W A Q P D G P N A S T C C Y V K K Q K I P K R N L
701 AAGAGCTACAGAAGGATCACCAGTAGTCGGTGTCCCTGGGAAGCTGTTATCTTCAAGACAAAGAGGGCATGGAAGTCTGCGCTGAAGCCCATCAGAAGT
47▶ K S Y R R I T S S R C P W E A V I F K T K K G M E V C A E A H Q K

NheI (885)

801 GGGTCGAGGAGGCTATAGCATACTTAGACATGAAAACCCCACTCAAAGCCTTGAAGAAATGTGCCTGAACAGAAACCACTAGCTAGTGGCCAGAC
80▶ W V E E A I A Y L D M K T P T P K P •
901 ATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAA

1001 CCATTATAAGCTGCAATAACAAGTTAACAACAACAAATTCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAA
1101 CCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGG
1201 CATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAT
1301 AGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATA
1401 AATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAAT

1501 TGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAAT
141 • N R T Y K L P I L E E I T T K V L K G N M E I
1601 GAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGG
117▶ L V F C D P A Y D S I L E R C M G C P S V V R I S R D V E D S Y P
1701 TGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGG
83▶ H R V A V I T D F D K Q G N S V A S G I A I A E A C V T V R G I Y A
1801 CCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGT
50▶ E I H V A S I I E G T K T R I A A G V H H K N D E Y L M T I K E T
1901 GGCACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAAGTCTTATACTATGCCGATATACTATGC
17▶ A V E V L E L D Q Q S I N F T K M
2001 CGATGATTAATTGTCAAACAGCGTGGATGGCTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTA

2101 CCGCCATTTGCGTCAATGGGGCGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGGA
2201 GACTTGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA
2301 CTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGA
2401 TACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA
2501 TTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACCGCTGAGGTTAATTAAGAACATGTGAGCA
2601 AAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAA

2701 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACC GG
2801 ATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCAAGCTGGGC
2901 TGTGTGCACGAACCCCCGTTACGCCCACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAG
3001 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATT
3101 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGATTGGTAGCTCTTGTATCCGGCAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGT

3201 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAG
3301 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCG
3401 TAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATC
3501 GAA