



100

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC
301 GCCATCCACGCCGTTGAGTCCGCTTCTGCCGCTCCCGCTGTGGTGCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

BspHI (560)

AgeI (552)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCTACCTGAGATCACCGGTCATCATGAACTGTGTTTGCCTGGTCTGGTGGTGTGAG
1 M N C V C R L V L V V L S
601 CCTCTGGCCAGATAGAGTCGTTGCCCTGGCCACCAGCTGGCTCCCTCGAGTCTCTCAGACCCTCGAGCAGATCTGGACAGCGTGTCTCCTAACC
13 L W P D R V V A P G P P A G S P R V S S D P R A D L D S A V L L T
701 CGATCCCTCCTGGCAGACACACGGCAACTAGCTGCACAGATGAGAGACAAATCCCAGCTGACGGAGATCACAGTCTGGACTCCCTGCCACCTTGGCCA
47 R S L L A D T R Q L A A Q M R D K F P A D G D H S L D S L P T L A
801 TGAGCGCTGGGACATTGGGATCTTGCAGCTTCTGGTGTGCTGACAAGGCTTCGAGTAGACTTGATGTCCTACCTCCGGCATGTACAATGGCTGCGCCG
80 M S A G T L G S L Q L P G V L T R L R V D L M S Y L R H V Q W L R R
901 TGCAGGTGGTCTCCCTAAAGACTCTGGAGCCAGAGCTGGTGCCCTGCAAGCCGACTGGAACGGCTACTCCGCGTTTACAGCTCTTGATGTCTCGC
113 A G G P S L K T L E P E L G A L Q A R L E R L L R R L Q L L M S R
1001 CTGGCCTTGGCCAGGACGCCAGACCAACCTGTGATCCCTCGGGCCTCTGCCTCAGCTGGGGAAGCATCCGGGCAGCTCATGCCATCCTAGGAG
147 L A L P Q A A P D Q P V I P L G P P A S A W G S I R A A H A I L G

NheI (1186)

1101 GGCTGCACCTGACCTGGACTGGGCCGTGCGGGCCTGCTGTTGTTAAAGACTCGACTGTGACTCGGGACTGAAAACCACCATCGAGCTAGCTGGCCAGA
180 G L H L T L D W A V R G L L L L K T R L •
1201 CATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTA
1301 ACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAA
1401 ACCTCTACAAATGTGGTATGGAATCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAG
1501 GCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTCATGGAGTTAAGATATAGTGTATTTTCCAAGTGTGAAC
1601 TAGCTCTCATTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTAGAAAATAATTTAAATACATCATTGCAATGAAAAT
1701 AAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGAACCTTTAATAGAAA
1801 TTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAA
141 • N R T Y K L P I L E E I T T K V L K G N M E I
1901 TGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGG
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
2001 GTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTCAGCAGACAGTACCCTGCCAATGTAG
84 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
2101 GCCTCAATGTGGACAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTTGTGCTCATAGAGCATGGTATCTTCTCAG
50 A 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
2201 TGGCAGCTCCACAGCTCCAGATCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATG
17 A V E V L E L D Q Q S I N F T K M
2301 CCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTACTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCT
2401 ACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGGGTGG
2501 AGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGT
2601 ACTGCAAAGTAGGAAAGTCCATAAGGTCATGTAAGTCCAGGCGGGCCATTTACCGTCAATGAGGCGGCTACTTGGCATATG
2701 ATACACTGATGTAAGTCCCAAGTGGGAGTTTACCCTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTC
2801 ATTATTGACGTCAATGGGCGGGGTCGTTGGGCGTCCAGCAGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAGC
2901 AAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGTTGCTGGCCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAATCGACGCTCA
3001 AGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGCGCTTCCCTCGTGAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCG
3101 GATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGG

3201 CTGTGTGCACGAACCCCGTTAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCA
3301 GCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTAT
3401 TTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTGT
3501 TTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAA
3601 GGGATTTTGGTCATGGCTAGTTAATTAACATTTAATCAGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATC
3701 GTAACAAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTAT
3801 CGAA