



125

1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATGCCACAGTCCCGAGAAGTTGGGGGAGGGTGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC  
201 GTGAACGTTCTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGTTGAGTCCGCTTCCGCCCTCCCGCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
401 GGGCCTTTGTCGGCGCTCCCTTGAGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCTAACTCTACGCTTTGTTTCGTTT

Agel (552) BspHI (567)

501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTAGGAGGCCATGAGTCTCTTAACTGTGAGAACAGCTGCG  
601 GGTCCAGCCAGTCGTCCAGTGACTGCTGCGCTGCCATGGCCGCTCCTGCAGCGCTGCAGTAAAAGATGACAGCGTGAGTGGCTCTGCCAGCACCGGGAA  
111 G S S Q S S S D C C A A M A A S C S A A V K D D S V S G S A S T G N  
701 CCTCTCCAGCTCCTTCATGGAGGATCCAGGGCTACGATGTGGAGTTTGACCCACCTCTGGAGAGCAAGTATGAGTGTCCATCTGCTTGATGGCTTTA  
441 L S S S F M E E I Q G Y D V E F D P P L E S K Y E C P I C L M A L  
801 CGGAAGCAGTCAAACACCATGTGGCCACAGTTCTGCAAAGCTGCATCATCAAATCCATAAGGGATGCAGGGCACAAGTCCAGTTGACAATGAAA  
781 R E A V Q T P C G H R F C K A C I I K S I R D A G H K C P V D N E  
901 TACTGCTGAAAATCAACTGTTCCCGACAATTTGCAAAGCGAGAGATTTCCCTGACGGTAAAGTGGCCAAAATAAGGCTGTTGCAAAGATGGA  
111 I L L E N Q L F P D N F A K R E I L S L T V K C P N K G C L Q K M E  
1001 ACTGAGACATCTCGAGGATCATCAAGTACATTTGTAATTTGCTCTAGTGAATTTGCCAGTCCCAACGCTCTTTCCAGAAGTCCAGGTTAATACACAC  
144 L R H L E D H Q V H C E F A L V N C P Q C Q R P F Q K C Q V N T H  
1101 ATTATTGAGGATGTCCAGGAGCAGGTTTCTGTGTAACCTGTGCTGTGCCATGACATGAAGAGAAAGAGATCCATGATCAAAGCTGTCTCTGG  
178 I I E D C P R R Q V S C V N C A V S M A Y E E K E I H D Q S C P L  
1201 CAAATATCATCTGTAATACTGTGGTACAATCCTCATCAGAGAACAGATGCCTAATCATTATGATCTGGACTGCCAACAGCTCCAATCCCTTGACATT  
211 A N I I C E Y C G T I L I R E Q M P N H Y D L D C P T A P I P C T F  
1301 CAGTGTTTTTGGCTGTATGAAAAGATGCAGAGGAATCACTTGGCAGCAGACTTGAAGAGAATACCCAGTTGCACATGAGACTGTTGGCCAGGCTGTT  
244 S V F G C H E K M Q R N H L A R H L Q E N T Q L H M R L L A Q A V  
1401 CATAATGTTAACCTTGTCTTGGCTCCGTCGATGCCGCTCCTCATCCCGGGATGTCGTCCAGAGGACCCAAATTATGAGGAAAATCAAAACAGTTGG  
278 H N V N L A L R P C D A A S P S R G C R P E D P N Y E E T I K Q L  
1501 AGAGTCGCTAGTAAGACAGGACCATCAGATCCGGGAGCTGACTGCCAAAATGAAAATCAGAGTATGTACGTGGGCGAGCTCAAACGGACCATTCGGAC  
311 E S R L V R Q D H Q I R E L T A K M E T Q S M Y V G E L K R T I R T  
1601 CCTGGAGGACAAGGTTGCCGAAATGGAAGCAGCAGTGTAAACGGGATCTACATTTGGAAGATTGGCAACTTTGGGATGCACCTGAAATCCCAAGAAGAG  
344 L E D K T V A E M E A Q Q C N G I Y I W K I G N F G M H L K S Q E E  
1701 GAAAGACCTGTTGTATCCATAGCCCTGGATTCTACACAGGCAGACCTGGGTACAAGCTGTGCATGCGCCTTCAAGTACCGATGACGACAGCTCAGCGCT  
378 E R P V V I H S P G F Y T G R P G Y A K L C M R L H L Q L L P T A Q R  
1801 GTGCAAATATATATCCCTTTTTGTCCACACAATGCAAGGAGAATATGACAGCCACCTCCCTGGCCCTTCCAGGGTACAATACGCTTACAATTCTCGA  
411 C A N Y I S L F V H T M Q G E Y D S H L P W P F Q G T I R L T I L D  
1901 CCAGTCTGAAGCACTTATAAGGCAAAACACGAAGAGGTCATGGACGCCAAACCGAAGTCTTGCCTTTACGCGACCACAATCCACGGAACCCCAAAA  
444 Q S E A L I R Q N H E E V M D A K P E L L A F Q R P T I P R N P K  
2001 GGTGTTGGCTATGTAACATTTATGCACCTGGAAGCCTTAAGACAGGGAACCTTCATTAAGGATGATACATTACTAGTGCCTGTGAAGTCTCTACCCGCT  
478 G F G Y V T F M H L E A L R Q G T F I K D D T L L V R C E V S T R  
2101 TTGACATGGGCTTCCGAAAGGAGGTTTCCAGCCACGAAGTACTGATGCGGGGTTGAGCGTCCATGTACTTGTGTTCAAAAATAGGAACCATATG  
511 F D M G G L R K E G F Q P R S T D A G V •

NheI (208)

2201 GGAAAACCGTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTTGTGAAATTTG  
2301 TGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAAATTCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGG  
2401 GAGGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAAT  
2501 CCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTTATGAGTAAATTAAGATATAG  
2601 TGTATTTTCCCAAGGTTTGAAGTACTGCTTTCATTTCTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTATGAAAAATTCAGAAAATATTTA  
2701 AATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTATGAGTTGGACTTAGGGA  
2801 ACAAAGGAACCTTAATAGAAATTTGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTG  
141 • N R T Y K L P I L E E I T T K  
2901 ACCAGCTTGCCATTCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATC  
124 V L K G N M E I 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  
3001 TGCCACCTCATCAGAGTAGGGGTCCTGACAGCCACAATGGTGTCAAAGCTTCTGCCCGTTGCTCACAGCAGACCAATGGCAATGGCTTCAGCACA  
91 D V E D S Y P 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  
3101 GACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCGAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGTTGCTCTCA  
58 V T V R G I Y 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

3201 TAGAGCATGGTGATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAGTCGTAT  
24 Y L M T I K E T A V E V L E L D Q Q S I N F T K M  
3301 TATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCACTAAACGAGCTCTGCTTATAT  
3401 AGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAACAAACT  
3501 CCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCGCAAAACCGCATCATCATGGTAATA  
3601 GCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAA  
3701 TAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGG  
3801 CGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGGGGGGTCTTGGGGCGTCCAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGCA  
3901 GGTTAATAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAGGCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGA  
4001 GCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCT  
4101 GTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGT  
4201 AAGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAG  
4301 ACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTAC  
4401 GGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACACCG  
4501 CTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCA  
4601 GTGGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCCAATAAAATATCTTTATTTTCATTACATCTGT  
4701 GTGTTGGTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGAAGTGC  
4801 AAGTGCCAGAACATTTCTATCGAA