



100  
|-----|

1 GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATGCCACAGTCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
101 GAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCC  
201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCC  
301 GCCATCCACGCCGTTGAGTCGCGTTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC  
401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGTCTCAACTCTACGCTTTTGTTCGTTT

**BspHI (560)**  
**AgeI (552)**

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACCTGAGATCACCGGTCATCATGAAGGTCTCCGAGCACTTCTGTGGCTGCTGCTCAT  
1 M K V S A A L L W L L L I  
601 AGCAGTGCCTTCAGCCCCAGGGGCTCGTGGCCAGCTTCTGTCCCAACCCTGCTGCTTAACTGGCCAATAGGAAGATACCCCTTCAGGACTA  
13 A A A F S P Q G L A G P A S V P T T C C F N L A N R K I P L Q R L  
701 GAGAGCTACAGGAGAATCACCAGTGGCAAATGTCCCCAGAAAGCTGTGATCTTCAAGACCAAAGTGGCCAAGGATATCTGTGCCGCCCAAGAAGAAGT  
47 E S Y R R I T S G K C P Q K A V I F K T K L A K D I C A D P K K K  
NheI (885)

801 GGGTGCAGGATTCATGAAGTATCTGGACAAAAATCTCCAACCTCAAAGCCATAAATAATCACCATTTTTGAAACCAAACAGAGCTAGTGGCCAGAC  
80 W V Q D S M K Y L D Q K S P T P K P •  
901 ATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAA

1001 CCATTATAAGCTGCAATAAACAAGTTAAACAACAACATTGCATTATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAA  
1101 CCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACCTTAACTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGG  
1201 CATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTTGAAT  
1301 AGCTTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATA  
1401 AATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAAT  
1501 TGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAAT  
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 GAGCAAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGCCACCTCATCAGAGTAGGGG  
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 TGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTACGACAGACAGTACCCTGCCAATGTAGG  
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 CCTCAATGTGGACAGCAGAGATGATCTCCAGTCTTGGTCTGATGGCCGCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGT  
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 GGCACCTCCACAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCTTCATGGTGGCCCTCTATAGTGAAGTCTATTATACTATGCCGATATACTATGC  
17 A V E V L E L D Q Q S I N F T K M  
2001 CGATGATTAATTGTCAAACAGCGTGGATGGCTCTCCAGCTTATCTGACGGTTCACATAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCTA  
2101 CCGCCATTTGCGTCAATGGGGCGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGG  
2201 GACTTGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA  
2301 CTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGA  
2401 TACACTTGATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA  
2501 TTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCTGAGGTTAATTAAGAACATGTGAGCA  
2601 AAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGCCGCGTGTGCGGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAAAAAATCGACGCTCAA  
2701 GTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACC GG  
2801 ATACCTGTCCGCTTTCTCCCTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTCGTTCCGCTCAAGCTGGGC  
2901 TGTGTGCACGAACCCCCGTTACGCCCAGCGTGGCCTTATCCGGTAACTATCGTCTTGTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAG  
3001 CAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATT  
3101 TGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGATTGGTAGCTCTTGTGATCCGGCAAACAAACCCGCTGGTAGCGGTGTTTTTTGTT

3201 TGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAG  
3301 GGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTGTGTGAATCG  
3401 TAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATC  
3501 GAA