



**EcoRI (23)**

**NotI (2)**                      **XbaI (19)**                      **SdaI (38)**                      **SpeI (45)**

1 **CGGGCCGCGTCGACGATATCTAGAATTCGGATCCTGCAGGGCCCAGTACTAGTATCTGCAGAGGGCCCTGCGTATGAGTGAAGTGGGTTTTAGGACCAGGAT**

101 **GAGGCGGGTGGGGTGCCTACCTGACGACCGACCCCGACCCACTGGACAAGCACCAACCCCATTCGCCAAATTGCGCATCCCCTATCAGAGAGGGGG**

201 **AGGGGAAACAGGATGCGGCGAGGCGCTGCGCACTGCCAGCTTACGACCCGCGGACAGTGCCTTCGCCCCGCGCTGGCGGCGCGGCCACCGCCGCTCA**

301 **GCACTGAAGGCGGCTGACGTCACTCGCCGGTCCCGCGAAACTCCCCTTCCCGCCACCTTGGTCGCGTCCGCGCCGCGCCGCCCAGCCGGACCGCA**

**Eco47III (466)**

401 **CCACGCGAGGCGGAGATAGGGGGGACGGGCGGACCATCTGCGCTGCGGCGCGGCGACTCAGCGCTGCCTCAGTCTGCGGTGGGCGAGCGGAGGAGTC**

**AvrII (575)**

501 **GTGTCGTGCCTGAGAGCGCAGTGTGCTCCTGGGCACCGCGCAGTCCGCCCCCGGGTCTCTGGCCAGACCACCCCTAGGACCCCTGCCCAAGTCGCA**

**NcoI (602)**

601 **GCCATGGAAATCAAGGTGCTGTTTGCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCCACTGAAATCAATGAAGACCTCAATATAGCTGCTGTGGCCT**  
→ M E I K V L F A L I C I A V A E A K P T E I N E D L N I A A V A

**BglIII (717)**

701 **CCAACTTTGCCACCACAGATCTTGAGACTGACCTGTTACCAACTGGGAGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGA**  
33▶ S N F A T T D L E T D L F T N W E T M N V I S T D T E Q V N T D A D

801 **CAGGGCAAGCTGCCTGGCAAAAACTCCCCAGATGTCCTGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTGCACAAGAGGCTGCCTCATTTC**  
66▶ R G K L P G K K L P P D V L R E L E A N A R R A G C T R G C L I C

901 **CTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAG**  
100▶ L S H I K C T P K M K K F I P G R C H T Y E G E K E S A Q G G I G

1001 **AGGCAATTGTTGATATCCAGAGATTCTGGCTTCAAGGATAAGGAGCCACTGGACCAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCACTGG**  
133▶ E A I V D I P E I P G F K D K E P L D Q F I A Q V D L C A D C T T G

1101 **CTGTCTGAAGGGCCTTGCCAAATGTCCAGTGTCTGACCTCTGAAGAAGTGGCTTCCCGAGAGGTGTACCACCTTTTCCAGCAAGATTTCAGGGTAGGGTG**  
166▶ C L K G L A N V Q C S D L L K K W L P Q R C T T F A S K I Q G R V

**NheI (1236)**

1201 **GACAAAATCAAGGGTCTGGCTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTG**  
200▶ D K I K G L A G D R •

1301 **AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAATTGCATTCAATTT**

1401 **ATGTTTCAGGTTCAGGGGAGGTGTGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAAAC**  
→

1501 **TTTAACTCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGC**

1601 **CTCACCTTCTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTACTGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTC**

**SspI (1715)**

1701 **CCTTTTTAGTAAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAA**

1801 **TATCCCCAGTTTAGTAGTTGGACTTAGGGAAACAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCTGCTCC**  
125▶ • D Q E

1901 **TCTGCCACAAAGTGACGCAAGTTGCCGGCCGGTGCAGGCGGAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGT**  
120▶ E A V F H V C N G A P D R L A F E R G W P Q E G I E T M A P G S A D

2001 **CCCGGAAGTTCTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACAGCCAGGGTGTGTCGGCACCACCTGGTC**  
87▶ R F N T S V V E S W E A Y L E D L G R V W V W A L T N D P V V Q D

2101 **CTGACCGCGTGTGAACAGGTCACGTGTCGCGGACCAACCGGCAAGTCTGCTCCACGAAGTCCCGGGAGAACCAGCCGGTCCGTCAGAAC**  
54▶ Q V A S I F L T V D R V V G A F D D E V F D R S F G L R D T W F

2201 **TCGACCGTCCGGCAGCTCGCGCGGGTGAACCCGGAACGGCACTGGTCAACTGGCCATGATGGCTCCTCTGTCAGGAGAGGAAAGAGAAGGTT**  
20▶ E V A G A V D R A T L V P V A S T L K A M ←

2301 **TAGTACAATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAA**ACTAGGGCTGCAGGTTAATTAAGAACATGTGAG  
←

2401 **CAAAAGGCCAGAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTC**

2501 **AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCGTGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGCTTACC**

2601 **GGATACCTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGCTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGG**

2701 **GCTGTGTGCACGAACCCCGTTCAGCCGACCGTGCCTTATCCGGTAACTATCGTCTTGTAGTCAACCCGGTAAGACACGACTTATCGCCACTGGC**

2801 **AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA**

2901 **TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGTATCCGGCAAAACAAACCACCGCTGGTAGCGGTGTTTTTTTG**

3001 **TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTA**

3101 **AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCA**