



PvuI (7) SgfI (6) MfeI (82)  
 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAGTGATGCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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Psp1406I (203) HindIII (245)  
 201 GTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCC  
 301 GCCATCCACGCGGGTTGAGTCGCGTTTCTGCCGCCTCCCGCTGTGGTGCCTCCTGAAGCTCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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NgoMIV (441)  
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCCTGTTGCTCAACTCTACGCTTTTGTTCGTTT

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KasI (535) AgeI (552) SphI (560)  
 501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTA CTTGAGATCACCGGTGAGCTGAGCTGAGAAAATGCAGACCATCAAAAAGGAGCC  
 601 CGCACCCCTAGATCCTACCAGCAGCTCAGACAAGATGCTGCTGCTGAAGTCTGCCTTAGCTGAGGTGGCCGAGGACCTAGCCTCAGGTGAAGATTTGCTC  
 13▶ A P L D P T S S S D K M L L L N S A L A E V A E D L A S G E D L L  
 701 CTGAACGAAGGGAGCATGGGAAAAACAATCCTCGGCGTGTGGGAGAAAAACGGGAATTCATTCCGGACGAGAAGAAAGACGCCATGTATTGGGAGAAAAC  
 47▶ L N E G S M G K N K S S A C R R K R E F I P D E K K D A M Y W E K  
 BglII (826)  
 801 GCGGAAAAACAACGAAGCTGCCAAAAGATCTCGGGAGAAGCGCCGCTCAATGACCTGGTTTTGGAGAACAAGCTGATIGCCCTGGGAGAAGAAAATGC  
 80▶ R R K N N E A A K R S R E K R R L N D L V L E N K L I A L G E E N A  
 901 CACTTTAAAGCTGAGCTGCTCTCCCTGAAATTAAGTTTGGTTAATAGCTCCACGGCGTATGCCAAGAAATCCAGAAAACCTCAGTAATCCACAGCT  
 113▶ T L K A E L L S L K L K F G L I S S T A Y A Q E I Q K L S N S T A  
 1001 GTCTACTTTCAGGACTACCAGACATCCAAGGCTGCCGTGAGCTTTTTGTGGACGAGCATGAGCCTGCATGGTAGCCGGAAGTTGCATCTCAGTCATCA  
 147▶ V Y F Q D Y Q T S K A A V S S F V D E H E P A M V A G S C I S V I  
 1101 AGCACTCCCCAGAGCTCGCTCCGATGTGTCAAGAGGTGCTCCGTTGGAGCACACTCAGGAAAAGCCCGCACAGGGAGGCTGCCGGAGCCCTGAGAA  
 180▶ K H S P Q S S L S D V S E V S S V E H T Q E S P A Q G G C R S P E N  
 BsrBI (1264)  
 1201 CAAGTTCCTGTGATCAAGCAGGAGCCCGTGGAGTTGGAGAGCTTTGCCAGGGAGGCCAGGGAGGAGCGGGGCACGTATTCCACCTCCATCTACCAGAGC  
 213▶ K F P V I K Q E P V E L E S F A R E A R E E R G T Y S T S I Y Q S  
 NcoI (1353)  
 1301 TACATGGGAAGCTCTTCTCCACTTACTCCCACTCCCCACCCCTTTGCAAGTCCATGGTCCACTAGCAACTCCCAAGAACCTCAGAGGCCGATGAGG  
 247▶ Y M G S S F S T Y S H S P P L L Q V H G S T S N S P R T S E A D E  
 Bsp120I (1449)  
 1401 GTGTAGTGGGCAAGTCTTCTGATGGGGAAGACGAACAACAGTCCCTAAGGCCCCATCCATTCTCAGTGGAGCTGCAACGGGTTCAGGCCACGGTGGT  
 280▶ G V V G K S S D G E D E Q Q V P K G P I H S P V E L Q R V H A T V V  
 BspEI (1506) HindIII (1537)  
 1501 GAAGGTTCCGGAAGTGAACCCCTTGCCTTACCGCACAGCTTCGGATTAAAGCCAAGGCCATGCAGGTCAAAGTGGAGGCTTTGGACAGCGAGTTTGAA  
 313▶ K V P E V N P S A L P H K L R I K A K A M Q V K V E A L D S E F E  
 PvuI (1631) SgfI (1630)  
 1601 GGCATGCAGAAAACCTCTTACCCCGCCGATGCGATCGCCAAAAGACATTTTGACCTGGAGAAAACATGGAACCTCGGGTATGGCCATTCTCCCTCCCTC  
 347▶ G M Q K L S S P A D A I A K R H F D L E K H G T S G M A H S S L P  
 1701 CTTTCTCAGTGCAGGTGACGAACATTCAAGATTGGTCCCTCAAATCGGAACACTGGCATCACAAGAAGCTGAGCAGAAAACCTCAGAGTAGCTCAAAAC  
 380▶ P F S V Q V T N I Q D W S L K S E H W H H K E L S S K T Q S S F K T  
 PstI (1883)  
 1801 AGGTGTGGTGAAGTCAAAGACGGTGGCTATAAGGTTTTCCGAAGCTGAGAATTTGATTTGAAGCAGGGAATAGCAAACCTTATCTGCAGAGGTGGTCTCG  
 413▶ G V V E V K D G G Y K V S E A E N L Y L K Q G I A N L S A E V V S  
 MseI (1990)  
 1901 CTCAAGAGATTCATAGCCACACAACCGATCTCGGCTTCGGACTCCAGGTAAATGGCTGCTGACCGAGCTATGCATGGAGGAGGAGCTAGCTGGCCAGACA  
 447▶ L K R F I A T Q P I S A S D S R •  
 2001 TGATAAGATACATTGATGAGTTTGACAAACCACAACCTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAAC

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HpaI (2122) MfeI (2133)  
 2101 CATTATAAGCTGCAATAAACAAGTTAAACAACAACCAATTGCATTCATTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAAC

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EcoRI (2218)  
 2201 CTCTACAAATGTGGTATGGAATTTCTAAAATACAGCATAGCAAACCTTTAACTCCAAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGC  
 2301 ATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTCATGGAGTTTAAAGATATAGTGTATTTTCCCAAGGTTTGAAC

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SspI (2457) SmaI (2471)  
 2401 GCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGAAAATAA  
 2501 ATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATT  
 2601 GGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGGAGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCATTCTCATCTCAATG  
 141▶ N R T Y K L P I L E E I T T K V L K G N M E I

2701 AGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGTAGGGGT  
116 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 H **BstXI (2761)**

2801 GCCTGACAGCCACAATGGTGTCAAAGTCCTTCTGCCCGTTGCTCACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGC  
83 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 **StuI (2896)**

2901 CTC AATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGCTTGTGTCTCATAGAGCATGGTGATCTTCTCAGTG  
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 **BspHI (3046)**

3001 GCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGATGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCC  
16 A V E V L E L D Q Q S I N F T K M **AseI (3104)**

3101 GATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTAC  
**SpeI (3259)**

3201 CGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAG  
**SnaBI (3387)**

3301 ACTTGAAATCCCCTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAC  
**NdeI (3492)**

3401 TGCCAAGTAGAAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGAT  
3501 ACACCTTGATGTA CTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAT

3601 TATTGACGTCAATGGGCGGGGTCGTTGGGCGGT CAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAGCAA  
3701 AAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAG  
3801 TCAGAGGTGGCAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGTCCCTCGTGCGCTCTCTGTTCCGACCTGCCGCTTACCGGA  
3901 TACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCT  
**ApaLI (4002)**

4001 GTGTGCACGAACCCCGTT CAGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGC  
4101 AGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTT  
4201 GGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCCGCTGGTAGCGGTGGTTTTTTTGT  
4301 GCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGG  
**EagI (4438)**

4401 GATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTCATTACATCTGTGTGTTGTTTTTGTGTAATCGT  
**PacI (4418) SmaI (4427) NotI (4437)**

4501 AACTAACATACGCTCTCCATCAAAAACAAAACGAAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCG  
4601 AA