



**PvuI (7)**  
**SgfI (6)**  
 1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA  
 101 GAGAAAGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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**HindIII (245)**  
**Psp1406I (203)** **PvuII (239)** **Bsu36I (291)**  
 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCGCCCTACCTGAGGGCC  
 301 GCCATCCACGCCGGTTGAGTTCGGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

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**NgoMIV (441)**  
 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

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**BstEII (555)**  
**AgeI (552)** **NcoI (560)**  
 501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACCTGAGATCACCGGTCACCATGGCTGCCCTCGCTGTAACAAGCCGGAGCCGGAGT  
 1 M A A L A V N K P G A G V  
 BbsI (670)

601 AGACAGTGGGCGGCAGGGCAGCCGGGGACGGCTGTGGTGAAGTTTCTGGAGTGTGGGTTTTGTGAAGATGCTTCTCTTTGCAAGGAGATAAAGTTCCT  
 13 D S G R Q G S R G T A V V K V L E C G V C E D V F S L Q G D K V P

**MscI (714)** **SapI (761)**  
 701 CGCTCCTCCTCTGTGGCCACACAGTCTGTCATGACTGTCTTACTCGTTGCCTCTGCATGGAAAGCAATACGTTGCCATTGATCGACAAGTAACAG  
 47 R L L L C G H T V C H D C L T R L P L H G R A I R C P F D R Q V T

**AvrII (801)** **Psp1406I (860)**  
 801 ACCTAGGAGACTCAGGTGTATGGGGTTTAAAAAGAACTTTGCTTACTGGAGCTTTTAGAACGTTTGCAAAATGGGCACATTGGTCAGTATGGAGCTGC  
 80 D L G D S G V W G L K K N F A L L E L L E R L Q N G H I G Q Y G A A  
 901 AGAAGAGCCATTGGACATCTGGAGAGAGCATCATTTCGCTGTGATGAAGTGAAGCTCACGTTGCATCTGTATATTGCAGTGTGTGCAACTCACTTG  
 113 E E A I G T S G E S I I R C D E A H V A S V Y C T V C A T H L  
 1001 TGCTCAGACTGTTCTCAAGTTACTCATTCTACAAGACATTAGCAAAGCATAGGCGTGTGCCTTAGCTGATAAACCTCATGAGAAAACCTATGTGCTGTC  
 147 C S D C S Q V T H S T K T L A K H R R V P L A D K P H E K T M C C

**SphI (1110)** **BstAPI (1101)** **SpeI (1150)**  
 1101 AGCACCAGGTGCATGCCATTGAGTTTGTGTTGCTTGAAGAAGTTGTCAAACCTAGTCCACTCATGTGCTGTGTCTGCAAAGAATATGGAAAGCACCAAGG  
 180 Q H Q V H A I E F V C L E E G C Q T S P L M C C V C K E Y G K H Q G

**ScaI (1212)**  
 1201 TCACAAGCATTAGTACTGGAACAGAAAGTAAATCAGATCCGAGCATCAATTTTAGACATGGCTCACTGCATACGGACCTTCACTGAGGAAATCTCAGAT  
 213 H K H S V L E P E A N Q I R A S I L D M A H C I R T F T E E I S D

**BspLU11I (1386)**  
 1301 TATTCCAGAAAATTAGTTGGGATTGTTTCAGCACATTGAAGGAGGAGAACAATAGTAGAAGATGGAATTGGAATGGCTCACACAGAACATGTCCCAGGTA  
 247 Y S R K L V G I V Q H I E G G E Q I V E D G I G M A H T E H V P G

**BstAPI (1402)**  
 1401 CTGCAGAGAATGCCGATCATGTGTCAGAGCTTATTTTTCTGATTTACATGAAACTCTTTGTCGTCAGAAGAAGAAATGGCTCTAAGTGTGTTGATGCCCA  
 280 T A E N A R S C V R A Y F S D L H E T L C R Q E E M A L S V V D A H  
 1501 TGTTCCGAGAAAACCTGATTTGGCTTAGGCAGCAACAAGAGGATATGACTATTCTCTTGTCCCAGGTCTCAACAGCCTGTCTCCACTGTGAAAAACCTCTG  
 313 V R E K L I W L R Q Q Q E D M T I L L S Q V S T A C L H C E K T L  
 1601 CAGCAGGATGATTGCAGAGTTGTCTTGGCAAAAACAAGAAATACAAGATTACTAGAAAACACTGCAGAAAACAGCAGCAGCAGTTTACAGAGGTTGCAGATC  
 347 Q Q D D C R V V L A K Q E I T R L L E T L Q K Q Q Q Q F T E V A D  
 1701 ATATTCAGTTGGATGCCAGTATCCAGTCACTTTTACAAGGACAATAGAGTTCATATTGGACCCAAAATGGAAATCCGAGTAGTCACATTAGGATTAGA  
 380 H I Q L D A S I P V T F T K D N R V H I G P K M E I R V V T L G L D  
 1801 TGGTGCTGAAAAAATACCATTTTGTCAAGTTAAAACAAGATGAATTTATGCAACCTATTCCAACAATTGGTTTTAATGTGGAACCTGTGGAATACAAA  
 413 G A G K T T I L F K L K Q D E F M Q P I P T I G F N V E T V E Y K

**XcmI (1913)**  
 1901 AATCTAAAATTCACATTTGGGATGTGGGTGAAAAACAAAATTAAGACCATTGTGGAACATTATTACCTCAATACACAAGCTGTTGATTTGTTGTTG  
 447 N L K F T I W D V G G K H K L R P L W K H Y Y L N T Q A V V F V V

**HpaI (2052)**  
 2001 ATAGTAGTCATAGAGACAGAATTAGTGAAGCACACAGTGAAGTTCGAAAGTTGTTAAACGGAAAAAGAACTCCGAGATGCCTTACTCTTATTTTGTCTAA  
 480 D S S H R D R I S E A H S E L A K L L T E K E L R D A L L L I F A N  
 2101 CAAACAGGATGTAGCTGGAGCACTTTTCACTAGAGAAGAAATCACTGAAGTCTCAGTCTCCATAAATATGCTGTGGAAGGAGTTGGTATATTGAGGGCTGT  
 513 K Q D V A G A L S V E E I T E L L S L H K L C C G R S W Y I Q G C

**MscI (2296)**  
**NheI (2290)**  
 2201 GATGCTCGAAGTGAATGGGGCTCTACGAAGGTTGGACTGGCTGTCCGGCAACTTGTGGCTGCTGGAGTGTGGATGTTGCTTATTGCTAGCTGGCC  
 547 D A R S G M G L Y E G L D W L S R Q L V A A G V L D V A • -  
 2301 CAGACATGATAAGATACATTGATGAGTTGGACAAACCACAACCTAGAATGCAGTGAAGAAAATGCTTTATTGTAATTTGTGATGCTATTGCTTTATT

2401 **HpaI (2428)**  
 TGTAACCATTATAAGCTGCAATAAACAAGTTAAACAACAACAATTGCATTTCATTTTATGTTTCAGGTTTCAGGGGAGGTGTGGGAGGTTTTTTAAAGCAAG

2501 **EcoRI (2524)**  
 TAAAACCTCTACAAATGTGGTATGGAATTCTAAAATACAGCATAGCAAACTTTAACCTCCAATCAAGCCTCTACTTGAATCCTTTTCTGAGGGATGAA

2601 TAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTGCAGCCTCACCTTCTTCATGGAGTTAAGATATAGTGATTTTTCCAAGGTTT

2701 **SapI (2706)** **SspI (2763)** **Swal (2777)**  
 GAACTAGCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTTAGTAAAATATTCAGAAAATAATTTAAATACATCATTGCAATGA

2801 **EcoO109I (2838)**  
 AAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCAATAATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATA

2901 GAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGGGGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCATC  
 141 • N R T Y K L P I L E E I T T K V L K G N M

3001 **SacI (3038)** **BstXI (3067)**  
 TCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCACCTGATGGATCTGTCCACCTCATCAGAGT  
 118 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 D V E D S Y  
 3101 AGGGGTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGCAGACCCAAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAAT  
 85 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 V T V R G I

3201 **StuI (3202)**  
 GTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGTGTGTTGCTCCTCATAGAGCATGGTGTCTTC  
 52 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 Y L M T I K

3301 **BbsI (3348)** **XmnI (3344)**  
 TCAGTGGCGACCTCCACCAGTCCAGATCCTGCTGAGAGATGTTGAAGTCTTCATGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATAC  
 18 E T A V E V L E L D Q Q S I N F T K M

3401 **AseI (3410)** **SacI (3467)**  
 TATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAACGAGCTCTGCTTATATAGACCTCCACCGTACAC

3501 **SpeI (3565)**  
 GCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAACAAACTCCCATTGACGTCAATGGG

3601 **SnaBI (3693)**  
 GTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAG

3701 **NdeI (3798)**  
 ATGTACTGCCAAGTAGGAAAGTCCATAAAGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCA

3801 TATGATACTTGTACTGCTCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATA

3901 **PacI (3984)** **SdaI (3976)** **BspLU11I (3994)**  
 CGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAATAAGAACATGT  
 4001 GAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAGGCCGCTTGTGGCGTTTTCCATAGGCTCCGCCCCCTGACGAGCATCAGAAAATCGACG  
 4101 CTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGCTT  
 4201 ACCGGATACTGTCCGCTTTTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCCGGTGTAGGTGCTTCCGCTCAAGC

4301 **ApaLI (4308)**  
 TGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCAAACCCGTAAGACACGACTTATCGCCACT

4401 GGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACA

4501 GTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTT

4601 TTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGCTGACGCTCAGTGGAAACGAAAACCTCACG

4701 **EagI (4744)** **PacI (4724)** **Swal (4733)** **NotI (4743)**  
 TTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGGCCGCAATAAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTG

4801 AATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAACTAGCAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCT

4901 CTATCGAA