



**PvuI (7)**  
**SgfI (6)** 1 GGATCTGGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

MfeI (82) EcoNI (96)  
101 GAGAAGTGGCGGGGTAAACTGGAAAGTGATGTCGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

HindIII (245) **Bsu36I (291)**  
**Psp1406I (203)** 201 GTGAACGTTCTTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCTTACCGCCGCCCGCCCTACCTGAGGCC

**PvuII (239)** EcoNI (287)  
301 GCCATCCACGCCGGTTGAGTCGCGTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

NgoMIV (441)  
401 GGGCCTTTGTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGTTGCTCAACTCTACGTCTTTGTTTCGTTT

**NcoI (560)**  
**BstEII (555)**  
**AgeI (552)**  
501 TCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCCACATGGAGAGCAAGGCGCTGCTGCTGCTGCTGTGTT

1 M E S K A L L A V A L W F  
601 CTGCGTGGAGACCCGAGCCCTGTGGGTTTGCCTGGCGATTTTCCATCCCCCAAGCTCAGCACAGAAAGACATACGACAATTTTGGCAAAT  
13 C V E T R A A S V G L P G D F L H P P K L S T Q K D I L T I L A N  
701 ACAACCCCTCAGATTACTTGCAGGGGACAGCGGACCTGGACTGGCTTTGGCCAATGCTCAGCGTGATTCTGAGGAAAGGTTTGGTACTGAATGCG  
47 T T L Q I T C R G Q R D L D W L W P N A Q R D S E E R V L V T E C

XcmI (833) **SalI (889)**  
801 GCGTGGTACAGTATCTTCTGAAAACACTCACCATCCAGGGTGGTTGAAATGATACTGGAGCCTACAAGTGTCTGACCAGGACGTCGACATAGC  
80 G G G D S I F C K T L T I P R V V G N D T G A Y K C S Y R D V D I A  
901 CTCCACTGTTTATGTCTATGTTGAGATTACAGATCACCATTATCGCCTGTGACTGACCAGCATGGCATGTGTACATCACGAGAACAAAGAAAA  
113 S T V Y V Y V R D Y R S P F I A S V S D Q H G I V Y I T E N K N K

**BspEI (1080)**  
1001 ACTGTTGATCCCTGCCGAGGGTCTGATTTCAAACCTCAATGTGTCTCTTGCCTAGGTATCCAGAAAAGAGATTTGTTCCGGATGGAAACAGAATTT  
147 T V V I P C R G S I S N L N V S L C A R Y P E K R F V P D G N R I

NgoMIV (1150)  
1101 CCTGGACAGCGAGATAGGCTTTACTCTCCCACTTACATGATCAGTATGCCGCGATGGTCTTCTGTGAGGCAAAGATCAATGATGAAACCTATCAGTC  
180 S W D S E I G F T L P S Y M I S Y A G M V F C E A K I N D E T Y Q S  
1201 TATCATGTACATAGTTGTTGGTTGTAGGATATAGGATTTATGATGTGATTCTGAGCCCCCGCATGAAATTTGAGCTATCTGCCGAGAAAACTGTCTTA  
213 I M Y I V V V V G Y R I Y D V I L S P P H E I E L S A G E K L V L  
1301 AATTGTACAGCGAAGACAGAGCTCAATGTGGGGCTTATTTCACCTGGCACTTCCACCTTCAAAGTCTCATATAAGAGATTGTAACCGGGATGTGA  
247 N C T A R T E L N V G L D F T W H S P P S K S H H K K I V N R D V  
1401 AACCTTTCTGGACTGTGGCAAGATGTTTTGAGCAGCTTGAACATAGAAAGTGTACCAAGAGTACCAAGGGGAATACACCTGTAGCGTCCAG  
280 K P F P G T V A K M F L S T L T I E S V T K S D Q G G E Y T C V A S S  
1501 TGGACGGATGATCAAGAGAAATAGAATTTGTCGAGTTCACACAAAGCCTTTTATTGCTTTGGTAGTGGGATGAAATCTTGGTGGAAAGCCACAGTG  
313 G R M I K R N R T F V R V H T K P F I A F G S G M K S L V E A T V

**EcoRV (1648)**  
1601 GGCAGTCAAGTCCGAATCCCTGTGAAGTATCTCAGTTACCCAGCTCCTGATATCAAATGGTACAGAAAAGGAAGGCCATTGAGTCCAACCTACACAATGA  
347 G S Q V R I P V K Y L S Y P A P D I K W Y R N G R P I E S N Y T M

**BstXI (1775)**  
1701 TTGTTGGCGATGAACCTCACCATCATGGAAGTACTGAAAGAGATGCAGGAAACTACACGGTCACTCCACCAACCCATTCAATGGAGAAAACAGAGCCA  
380 I V G D E L T I M E V T E R D A G N Y T V I L T N P I S M E K Q S H  
1801 CATGGTCTCTGTTGTAATGTCCACCCAGATCGGTGAGAAAGCCTTGATCTCGCTATGGATTCTACAGTATGGGACATGCAGACATTGACA  
413 M V S L V V N V P P Q I G E K A L I S P M D S Y Q Y G T M Q T L T  
1901 TGCACAGTCTACGCCAACCTCCCTGCACCACATCCAGTGGTACTGGCAGCTAGAAGAAGCCTGCTCTACAGACCCGGCCAAACAAGCCCGTATGCTT  
447 C T V Y A N P L H H I Q W Y W Q L E E A C S Y R P G Q T S P Y A

**BbrPI (2014)**  
2001 GTAAAGAATGGAGACACGTGGAGGATTTCCAGGGGGAAACAAGATCGAAGTCAACAAAAACCAATATGCCCTGATTGAAGGAAAAACAAAAGTGAAG  
480 C K E W R H V E D F Q G G N K I E V T K N Q Y A L I E G K N K T V S  
2101 TACGCTGGTCAATCAAGCTGCCAACGTGTCAGCGTTGTACAAATGTGAAGCCATCAACAAAGCGGACGAGGAGAGGGTCACTCCTTCCATGTGATC  
513 T L V I Q A A N V S A L Y K C E A I N K A G R G E R V I S F H V I

**ApaLI (2265)** **BbrPI (2298)**  
2201 AGGGGCTCTGAAATTACTGTGCAACCTGCTGCCAGCCAAGTACAGGAGAGTGTGTCCCTGTTGTGCACTGCAGACAGAAATACGTTTGAACCTCA  
547 R G P E I T V Q P A A Q P T E Q E S V S L L C T A D R N T F E N L

HindIII (2308)  
2301 CGTGGTACAAGCTTGCTCACAGGAACATCGGTCCATGGGCGAATCACTCACACCAGTTTGAAGAAGTTGGATGCTCTTTGAAACTGAATGGCAC  
580 T W Y K L G S Q A T S V H M G E S L T P V C K N L D A L W K L N G T  
2401 CATGTTTTCTAACAGCAAAATGACATCTTATTGTTGGCATTTTGAAGTGCCTCTCTGCAGGACCAAGGCGACTATGTTTGTCTGCTCAAGATAAGAAG  
613 M F S N S T N D I L I V A F Q N A S L Q D Q G D Y V C S A Q D K K  
2501 ACCAAGAAAAGACATTGCTGGTCAAACAGTCACTATCCTAGAGCGCATGGCACCCATGATCACCGGAAATCTGGAGAATCAGACAACCAACATTGGCG  
647 T K K R H C L V K Q L I I L E R M A P M I T G N L E N Q T T T I G

XcmI (2641)  
2601 AGACCATTGAAGTACTTGCCAGCATCTGAAATCCTACCCACACATTACATGGTTCAAAGACAACGAGACCTGGTAGAAGATTGAGGCATTGACT  
680 E T I E V T C P A S G N P T P H I T W F K D N E T L V E D S G I V L

**BsrBI (2795)**  
2701 GAGAGATGGGAACCGAACCTGACTATCCGAGGGTGAAGGAGGATGGAGGCCTCTACACCTGCCAGGCCTGCAATGTCTTGCTGTGCAAGAGCG  
713 R D G N R N L T I R R V R K E D G G L Y T C Q A C N V L G C A R A

**NheI (2835)**

2801 <sup>SapI (2805)</sup> GAGACGCTTTCATAATAGAAAGGTGCCTAGAATTC <sup>EcoRI (2829)</sup> **CTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTG** <sup>MscI (2841)</sup>  
747 ▶ E T L F I I E G A •

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2901 **AAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTCATTTT**  
<sup>HpaI (2973)</sup> <sup>MfeI (2984)</sup>

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3001 **ATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTA**  
<sup>EcoRI (3069)</sup>

3101 **ACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCA**

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3201 **CCTCTTTTCATGGAGTTAAGATATAGTGATTTTTCCCAAGGTTTGAAGTCTCTTCATTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTT**  
<sup>SapI (3251)</sup>

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3301 **TTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATC**  
<sup>SspI (3308)</sup> <sup>SwaI (3322)</sup>

3401 **CCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTTAATAGAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGG**  
141 ◀ • N R T Y K L

3501 **GGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGC**  
133 ◀ P I L E E I T T K 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

3601 **CACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGC**  
100 ◀ C P S V V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V A

3701 **AGACCAATGGCAATGGCTTCAGCACAGACAGTGACCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCC**  
67 ◀ S G I A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I A

**XmnI (3889)**

3801 **GCCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCA**  
33 ◀ A G V H H K N D E 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

**AseI (3955)**

3901 **TGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGAC**  
0 ◀

4001 **GGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTC**

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4101 **CCGTTGATTTACTAGTCAAAACAAACTCCCAATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAC**  
<sup>SpeI (4110)</sup>

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4201 **TGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGG**  
<sup>SnaBI (4238)</sup>

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4301 **CGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCTCAAGTGGGCAGTTTACCGTAAATACTCCACCCA**  
<sup>NdeI (4343)</sup>

4401 **TTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTTGGCGGTCAGCCAGGCGGGCCA**

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4501 **TTTACCGTAAGTTATGTAACGCCGTCAGGTTAA** <sup>PacI (4529)</sup> **TTAAGAACA** <sup>BspLU11I (4539)</sup> **TGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTT**

4601 **TTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC**

4701 **CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCT**

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4801 **CACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCAAGCTGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCTTATCCGGTAA**  
<sup>ApaLI (4853)</sup>

4901 **CTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA**

5001 **GAGTTCCTGAAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTA**

5101 **GCTCTTGATCCGGCAAACAACACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT**

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5201 **GATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC** <sup>EagI (5289)</sup> **AGCGGCCCAATA**  
<sup>PacI (5269)</sup> <sup>SwaI (5278)</sup> <sup>NotI (5288)</sup>

5301 **AAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGC**

5401 **AAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTATCGAA**