

PvuI (7)
SgfI (6) 1 GGATCTGCATCGCTCCGGTGCCGTCAGTGGGAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAAGTATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

Psp1406I (203) 201 GTGAACGTTCTTTTTTCGAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGCTCGCATCTCTCCTTACCGCGCCCGCCCTACCTGAGGCC

HindIII (245) 301 GCCATCCACGCCGGTTGAGTCGGTTCGCGCCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

Bsu36I (291) 401 GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTACGCTTTTGTTCGTTT

501 TCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACCTGAGATCACCGGTGAGCATGCTGGTAGCCGGTTCCTGCTGGCGCTGCCGCCGAG

AgeI (552) **SphI (560)** 1 M L V A G F L L A L P P S

NotI (639) 601 CTGGGCCGCGGGCGCCCGAGGGCGGGCAGGCGCCCGCGCGGGGCTGCGCGGACCGCGGAGGAGCTACTGGAGCAGCTGTACGGCGCCTG

RsrII (656) 13 W A A G A P R A G R R P A R P R G C A D R P E E L L E Q L Y G R L

PstI (733) 701 GCGGCCGGCTGCTCAGTGCCTTCCACCACAGCTGCAGCTGGGGCCGCTGAGCAGCGCGCAACCGGAGCTGCCCGCAGGGGGCAGGCCCGCCGACC

BssHIII (757) 47 A A G V L S A F H H T L Q L G P R E Q A R N A S C P A G G R P A D

FspI (824) 801 GCCGTTCCGGCCGCCACCACTGCGCAGCTGTGCCCTGGGCTACAGAATCTCTACGACCCGGGAGGTACCCAGGTACCTGCCTGAAGCCTA

80 R R F R P P T N L R S V S P W A Y R I S Y D P A R Y P R Y L P E A Y

901 CTGCTGTGCCGGGCTGCTGACCGGGCTGTTGCGGAGGAGAGCTGCGCTTCCGAGCGCCCTGTCTACATGCCACCCTGCTCCTGCGCCGACC

113 C L C R G C L T G L F G E E D V R F R S A P V Y M P T V V L R R T

SgrAI (1008) 1001 CCCGCTGCGCCGGCGCGGTTCCGTCTACACCAGGCTACGTCACCATCCCGTGGGCTGCACCTGCTCCCCGAGCCGAGAAGGACGCAGACAGCA

StuI (1034) **BstXI (1046)** 147 P A C A G G R S V Y T E A Y V T I P V G C T C V P E P E K D A D S

Bsu36I (1166) 1101 TCAACTCCAGCATCGACAAACAGGGCGCAAGCTCCTGCTGGGCCCAACGACGCGCCGCTGGCCCTGAGCGCGTCTGCCCGGGAGGTCTCCCCG

XcmI (1127) **Bsp120I (1140)** **SfiI (1162)** **XmaI (1183)** 180 I N S S I D K Q G A K L L L G P N D A P A G P •

MscI (1228) 1201 GCCCGCATCCCGAGGCGCCCAAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTGAATAAATGCTTT

NheI (1222) 1301 ATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTATTTATGTTTCAGGTTCC

HpaI (1360) **MfeI (1371)** 1401 AGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTTAAAATACAGCATAGCAAACTTTAACCTCAAATCAA

EcoRI (1456) 1501 GCCTCTACTTGAATCCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGG

1601 AGTTTAAGATATAGTGTATTTTCCCAAGGTTTGAACAGTCTTTCATTCTTTATGTTTTAAATGCACTGACCTCCCACATTCCTTTTATGTAATAAT

SapI (1638) **SspI (1695)** 1701 TCAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTA

SwaI (1709) 1801 GTTGGACTTAGGGAACAAGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCTGGTGTACTTGAGGGGATGAGTTCCT

141 N R T Y K L P I L E E

SacI (1970) **BstXI (1999)** 1901 CAATGGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGCACATGCCACAGGGGCTGAC

129 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 C P S V

2001 CACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCGTTGCTCAGCAGACCCAATGGCA

96 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 S G I A

StuI (2134) 2101 ATGGCTTCAGCACAGACAGTACCCTGCCAATGATGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGTCTGATGGCCGCCCGACATGGT

62 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 A G V H H


BbsI (2280) 2201 GCTTGTGCTCATAGAGCATGGTGTCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTTCATGGTGGCCCTCCT

XmnI (2276) 29 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 (2342) 2301 ATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACC

SacI (2399)

2401 AGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACGCCCATTTGCGTCAATGGGGCGGAGTTGTACGACATTTTGAAAGTCCCGTTGATTTACT **SpeI (2497)**

2501 **AGTCAAACAAACTCCCATTGACGTCAATGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCA**


SnaBI (2625)

2601 TCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTACC

NdeI (2730)

2701 GTCATTGACGTCAATAGGGGGCGTACTTGCCATATGATACACTTGATGTACTGCCAAGTGGGCGAGTTACCGTAAATACTCCACCCATTGACGTCAATGG

2801 AAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGGTCTGTTGGGCGGTGAGCCAGGCGGGCCATTACCCTAAGTT

PaeI (2916)

PstI (2909)

SdaI (2908)

BspLU11I (2926)

2901 ATGTAACG**CTGCAGGTTAATTAAGAACATGTGAGCAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGGCCGCTTGCTGGCGTTTTCCATAGGCTC**

3001 CGCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCC

3101 TCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTAGGTA

ApaLI (3240)

3201 TCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGAG

3301 TCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGT

3401 GGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGG

3501 CAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACG

PaeI (3656) SwaI (3665) NotI (3675)

3601 GGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAAATATCTTTATT

3701 TTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTC

3801 CCCAGTCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA