



PvuI (7)
SgfI (6)
MfeI (82) **EcoNI (96)**

1 GGATCTGCATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTA

101 GAGAAGGTGGCGCGGGTAAACTGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCC

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

201 GTGAACGTTCTTTTTTCGCAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACCGCGCCCGCCGCTACCTGAGGCC

301 GCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACC

401 GGGCCTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCCTGCTTGTCTAACTCTACGCTTTTGTTCGTTT

NcoI (560)
BstEII (555) **XmnI (571)** **BsaBI (589)**

501 TCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGGCCCTACCTGAGATCACCGGTCACCATGGAAGGGGAAGGGTTCAACCCCTGGATGAGAATCT

601 GAAAAACGGATCAAGGCCAAGATTCAAGTGAAGAAAGACGCTAAGGCTGGTGGTCTCTGGGATCAAGGGAGCAGGGATGCTTCTGTGCTTCATCTATGTC

701 TGCCTGCAACTCTCTTCCCTCCGGCAAAGGACCTCCAATCCAAGACTCAGAGGAGCAGTTACCAGATGTGAGGATGGGCAACTATTCATCAGCTCAT

801 ACAAGAATGAGTATCAAACCTATGGAGGTGACAGAACATTCGGTTGTCAAGTGCATGAGGCTTATATCATCTACCTGAAGGGCTCTTTTTCCAGGA

901 GGTCAAGATTGACCTTCATTTCCGGGAGGATCATAATCCCATCTCTATTCCAATGCTGAACGATGGTGAAGGATGTCTTCACTGTGGTGGCCTCTTG

1001 GCTTTCAAAGATAAAGTTTACCTGACTGTAATGCTCCTGATACTCTCTGCAACACCTCCAGATAAATGATGGGGAGCTGATTGTTGCCAGCTAACCC

1101 CTGGATACTGTGCTCCTGAAGGATCTTACCACAGCACTGTGAACCAAGTACCCTGTGAATCCACTCTGAGGGTGGACGGGACACAGGTTCTTTCTCGA

MscI (1224)
EcoRI (1157) **XhoI (1195)**

1201 GAGAGATGAGTGCATCCTGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTAAAAAATGCTTTATTT

1301 GTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTAAACAACAACATTGCATTCTTTATGTTTCAGGTTACGGG

1401 GGAGGTGTGGAGGTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGAAATCTAAATACAGCATAGCAAACCTTTAACCTCCAATCAAGCCT

1501 CTACTGAACTCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCTCACCTTCTTTCATGGAGTT

1601 TAAGATATAGTGTATTTTCCAAGGTTTGAAGTACTGCTCTTCTTATGTTTAAATGCACTGACCTCCACATTCCCTTTTATGATAAATATTAG

1701 AAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTG

1801 GACTTAGGGAACAAAGAACCTTAAATAGAAATGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTACTTGAGGGGATGAGTTCCTCAAT

1901 GGTGGTTTTGACCAGCTTGCCATTCATCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTGACATGCCACAGGGGCTGACCAC

2001 CTGATGGATCTGTCCACCTCATCAGAGTAGGGGCTGCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCCCTGCTCACAGCAGACCAATGGCAATGG

2101 CTTACGACAGACAGTGACCTGCCAATGTAGGCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCCGCCCCGACATGGTGCTT

2201 GTTGCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGCTTCTATGGTGGCCCTCCTATAG

2301 TGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTCTACTAAACGAGCT

2401 CTGCTTATATAGACCTCCCACCGTACACGCTACCGCCATTTGCGTCAATGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTGTTGATTTACTAGTC

2501 AAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCAT

2601 CATGGTAATAGCGATGACTAATACGTAGATGTA
SnaBI (2621) TACTGCCAAGTAGGAAAGTCCCATAAGGTCATGTA
2701 TTGACGTCAATAGGGGCGTACTTGGCATATGATACACTT
NdeI (2726) TACTGCCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAG
2801 TCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGT
CAGCCAGGCGGGCCATTTACCGTAAGTTATGT
Pacl (2912)
PstI (2905)
SdaI (2904) BspLU11I (2922)
2901 AACGCTGCAGGTTAATTAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTTTTCCATAGGCTCCGCC
3001 CCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTCCCCCTGGAAGCTCCCTCGT
3101 GCGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTC
ApaLI (3236)
3201 AGTTCGGGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTCAGCCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCA
3301 ACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTG
3401 GCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAA
3501 CAAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTCTACGGGGT
EagI (3672)
Pacl (3652) SmaI (3661) NotI (3671)
3601 CTGACGCTCAGTGAACGAAAACCTCACGTTAAGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCAATAAAATATCTTTATTTCA
3701 TTACATCTGTGTGGTTTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCA
3801 GTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA