



2501 TCCACCAGCTCCAGATCCTGCTGAGAGATGTTGAAGGTCCTCATGGTGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGAT
 14 E V L E L D Q Q S I N F T K M ← XmnI (2532) AseI (2598)

2601 TAATTGTCAAACACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCACAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCA
 ← SacI (2655)

2701 TTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGG
 ← SpeI (2753)

2801 AAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTAAGTCCAA
 ← SnaBI (2881)

2901 GTAGGAAAGTCCCATAAGGTCATGTACTGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTGGCATATGATACACTT
 ← NdeI (2986)

3001 GATGTACTGCCAAGTGGGCGAGTTTACCGTAAATACTCCACCCATTGACGTCAATGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGA

3101 CGTCAATGGGCGGGGTCGTTGGGCGGTACGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCC
 ← PstI (3165) SdaI (3164) Pacl (3172) BspLU11I (3182)

3201 AGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAG
 ← BspLU11I (3182)

3301 GTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCGCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTG

3401 TCCGCTTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGC
 ← ApaLI (3496)

3501 ACGAACCCCCGTTACGCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCAC

3601 TGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGTACACTAGAAGAACAGTATTTGGTATC

3701 TGGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGC

3801 AGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTT

3901 GGTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAATCGTAACTAA
 ← Pacl (3912) SmaI (3921) EagI (3932) NotI (3931)

4001 CATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGCAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA