



2401 **ATTGTCAA**AACAGCGTGGATGGCGTCTCCAGCTTATCTGACGGTTCATAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCTACCGCCATT
←

2501 TGCCTCAATGGGGCGGAGTTGTTACGACATTTTGGAAAGTCCCCTTGATTT**ACTAGT**CAAAACAACTCCCATTGACGTCAATGGGGTGGAGACTTGGAA
SpeI (2551) ←

2601 ATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGT
SnaBI (2679)

2701 AGGAAAGTCCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGA
NdeI (2784)

2801 TGTA CTGCAAGTGGGCAGTTTACCCTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTACTATGGGAACATACGTCATTATTGACG

2901 TCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACG**CTGCAGGTTAA**TTAAGAACATGTGAGCAAAAGGCCAG
PacI (2970) SdaI (2962) BspLU11I (2980) ←

3001 CAAAAGCCAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGT

3101 GGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAAGTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGCT

3201 CGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCAC
ApaLI (3294)

3301 GAACCCCGTTGAGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTG

3401 GTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTG

3501 CGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGCAAGCAG

3601 CAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGG

EagI (3730)

3701 **TCATGGCTAGTTAATTAACATTTAAATCAGCGCCGCA**AATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTGTGTAATCGTAACTAACA
PacI (3710) SmaI (3719) NotI (3729)

3801 TACGCTCTCCATCAAACAAACGAAACAAACAAACTAGCAAATAGGCTGTCCCAGTGCAAGTGACAGGTGCCAGAACATTTCTCTATCGAA