



2761 CAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGA

2881 CTATAAAGATACCAGGCGTTCCCTCGGAAGCTCCCTCGTGGCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTCTCCCTTCGGGAAGCGTGGCGTTTTCTCAT

ApaI (3057)

3001 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCGTTACGCCGACCGCTGCGCTTATCCGGTAACTATCGTCTTGAGTCC

3121 AACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACT

3241 AGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTCGGAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAACCACCGCTGGTAGCGGTGGTTTTTTGTTGCAAG

PacI (3473)

3361 CAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTA

EagI (3493)

SwaI (3482) NotI (3492)

3481 ACATTTAAATCAGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAAAC

3601 TAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA