



2301 TACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTCCCGTTGATTTACTAGTCAAAAACAACTCCCATTGACGTCAATGGGGTG
SpeI (2362)
←

2401 GAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTACTIONGCAAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATG
SnaBI (2490)

2501 TACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTIONGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATAT
NdeI (2595)

2601 GATACACTTGATGTACTIONGCAAGTGGGCAGTTTACCGTAAATACTCCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGT

2701 CATTATTGACGTCAATGGGGCGGGGTCGTTGGCGGGTCAGCCAGGCGGGCCATTTACCGTAAGTTATGTAACGCTGCAGGTTAATTAAGAACATGTGAG
PstI (2774)
SdaI (2773)
PaeI (2781)
BspLU11I (2791)
←

2801 CAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACA AAAATCGACGCTC

2901 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCTGGAAGCTCCCTCGTGGCTCTCTGTTCCGACCTGCCGCTTACC

3001 GGATACCTGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGG

3101 GCTGTGTGCACGAACCCCGTTTCCAGCCGACCGCTGCGCCTTATCCGGTAACCTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGC
ApaLI (3105)

3201 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

3301 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCCAGCTGGTAGCGGTGGTTTTTTTG

3401 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTA

3501 AGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCGCAATAAATATCTTTATTTTCATTACATCTGTGTGTTGGTTTTTTGTGTAAT
PaeI (3521) **SwaI (3530)** **EagI (3541)** **NotI (3540)**

3601 CGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTA
3701 TCGAA