



2201 TGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAA
SacI (2216)

2301 AGTCCC GTTGATTTACTAGTCAAAAACAACTCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGAT
SpeI (2314)

2401 GTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCACTGACTGGGCATAATGC
SnaBI (2442)

2501 CAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACTCCA
NdeI (2547)

2601 CCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTCAGCCAGGCGG
NdeI (2547)

2701 GCCATTTACCGTAAGTTATGTAACGCCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGG
PacI (2733)
PstI (2726)
SdaI (2725) **BspLU11I (2743)**

2801 CGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTT
BspLU11I (2743)

2901 TCCCCCTGGAAGCTCCCTCGTGCCTCTCTGTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGAAGCGTGGCGCTTTCTCAT
BspLU11I (2743)

3001 AGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTTCCAGCCGACCGCTGCGCCTTATCCG
ApaLI (3057)

3101 GTAACATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGCGGTTGC
ApaLI (3057)

3201 TACAGAGTTCTTGAAGTGGTGGCCTAACTACGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTT
ApaLI (3057)

3301 GGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTGTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATC
ApaLI (3057)

3401 CTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATCAGCGGCCG
EagI (3493)
PacI (3473) **Swal (3482)** **NotI (3492)**

3501 AATAAAATATCTTTATTTTATTACATCTGTGTGTTGGTTTTTTGTGTAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAAAC
EagI (3493)

3601 TAGCAAAATAGGCTGTCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA
EagI (3493)