





2501 **SacI (2531)**  
CGTCTCCAGCTTATCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGT

2601 **SpeI (2629)**  
TACGACATTTTGGAAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTA

2701 **SnaBI (2757)**  
TCCACGCCATTGATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCCATAAGGTCATG

2801 **NdeI (2862)**  
TACTGGGCATAATGCCAGGCGGGCCATTACCCTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTT

2901  
ACCGTAAATACTCCACCCATTGACGTCAATGAAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGGCGGGGGTCTTGGG

3001 **PstI (3041)** **PacI (3048)** **SdaI (3040)** **BspLU11I (3058)**  
CGGTCAGCCAGGCGGGCCATTTACCCTAAGTTATGTAACGCTGCAGGTTAAITTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAA

3101  
AGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA

3201  
AAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGAAGC

3301 **ApaLI (3372)**  
GTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCCGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCCGACC

3401  
GCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAG

3501  
GTATGTAGCGGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACC

3601  
TTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAG

3701 **PacI (3788)** **SwaI (3797)**  
GATCTCAAGAAGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATT

3801 **EagI (3808)**  
**NotI (3807)**  
TAAATCAGCGGCCGCAATAAAATATCTTTATTTTTCATTACATCTGTGTGTGGTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAA

3901  
CGAAACAAAACAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGACGGTGCCAGAACATTTCTCTATCGAA