



2501 ACAGCAGACCCAATGGCAATGGCTTCAGCACAGACAGTGACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCCAGTCTTGGCTCTGA
68 V A S G I A I A E A C V T V R G I Y A E I H V A S I I E G T K T R I

2601 TGGCCGCCCCGACATGGTGTCTTGTTCCTCATAGAGCATGGTATCTTCTCAGTGGCGACCTCCACCAGCTCCAGATCTGTGAGAGATGTTGAAGGT
35 A A G V H H K N D E Y L M T I K E T A V E V L E L D Q Q S I N F T

2701 CTTCATGATGGCCCTCCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTA
2 K M

2800 TCTGACGGTTCACTAAACGAGCTCTGCTTATATAGACCTCCCACCGTACACGCCTACCGCCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGG
SacI (2817)

2900 AAAGTCCCGTTGATTTACTAGTCAAAACAAACTCCCATTGACGTCAATGGGGTGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATT
SpeI (2915)

2999 GATGTACTGCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAA
SnaBI (3043)

3099 TGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGATGTACTGCCAAGTGGGCAGTTTACCGTAAATACT
NdeI (3148)

3199 CCACCCATTGACGTCAATGGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCATTATTGACGTCAATGGGCGGGGTCTGTTGGCGGTCAGCCAGG

3299 CGGGCCATTTACCGTAAGTTATGTAACGCCCTGCAGGTTAA TTAAGAACATGTGAGCAAAAGGCCAGGAAACCGTAAAAAGGCCGCTT
PstI (3327) SdaI (3326) PacI (3334) BspLU11I (3344)

3397 GCTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCAG
BspLU11I (3344)

3497 CGGTTTTCCCTGGAAAGCTCCCTCGTGCCTCTCTGTTCCGACCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTT

3597 CTCATAGCTCAGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTGCTCCAAGCTGGGCTGTGTGCACGAACCCCGTTAGCCGACCGCTGCGCCTT
ApaLI (3658)

3697 ATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGC

3797 GGTGCTACAGAGTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAA

3897 GAGTTGGTAGCTCTTGATCCGGCAAACAAACCAGCTGGTAGCGGTGGTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGA

3997 AGATCCTTTGATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAACTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC AGCG
PacI (4074) SwaI (4083) EagI (4094) NotI (4093)

4097 GCCGCAATAAAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAAACAAAACGAAACAAAA
4197 CAAACTAGCAAAATAGGCTGTCCCCAGTGCAAGTGCAGGTGCCAGAACATTTCTCTATCGAA