





**NheI (2835)**

2801 <sup>SapI (2805)</sup> GAGACGCTTTCATAATAGAAGGTGCCTAGAATTC <sup>EcoRI (2829)</sup> **CTAGCTGGCAGACATGATAAGATACATTGATGAGTTTGGACAAACCACAACCTAGAATGCAGTG** <sup>MscI (2841)</sup>  
747 ▶ E T L F I I E G A •

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2901 **AAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAAACAAGTTAAACAACAACAATTGCATTCATTTT**  
**HpaI (2973)** MfeI (2984)

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3001 **ATGTTTCAGGTTCCAGGGGAGGTGTGGGAGTTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTCTAAATACAGCATAGCAAACTTTA**  
EcoRI (3069)

3101 **ACCTCAAATCAAGCCTCTACTTGAATCCTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGACGCCCA**

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3201 **CCTTCTTTCATGGAGTTTAAGATATAGTGATTTTTCCCAAGTTTGAAGTCTCTTCTTTATGTTTTAAATGCACTGACCTCCACATTCCCTT**  
SapI (3251)

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3301 **TTTAGTAAATATTCAGAAATAATTTAAATACATCATTGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATC**  
**SspI (3308)** SwaI (3322)

3401 **CCCCAGTTTAGTAGTTGGACTTAGGGAACAAGGAACCTTAATAGAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTTAGTTCCTGGTGTACTTGAGG**  
141 ◀ • N R T Y K L

3501 **GGGATGAGTTCCTCAATGGTGGTTTTGACCAGCTTGCCATTCTCAATGAGCACAAAGCAGTCAGGAGCATAGTCAGAGATGAGCTCTCTGCACATGC**  
133 ◀ P I L E E I T T K V L K G N M E I L V F C D P A Y D S I L E R C M G

3601 **CACAGGGGCTGACCACCCTGATGGATCTGTCCACCTCATCAGAGTAGGGGTGCCTGACAGCCACAATGGTGTCAAAGTCTTCTGCCGTTGCTCACAGC**  
100 ◀ C P S V V R I S R D V E D S Y P H R V A V I T D F D K Q G N S V A

3701 **AGACCAATGGCAATGGCTTCAGCACAGACAGTACCCTGCCAATGTAGGCCTCAATGTGGACAGCAGAGATGATCTCCCAGTCTTGGTCTGATGGCC**  
67 ◀ 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 A

**XmnI (3889)**

3801 **GCCCCGACATGGTCTTGTGTCCTCATAGAGCATGGTATCTTCTCAGTGGCAGCTCCACCAGCTCCAGATCTGCTGAGAGATGTTGAAGGTCTTCA**  
33 ◀ 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 K M

**AseI (3955)**

3901 **TGGTGGCCCTCTATAGTGAGTCGTATTATACTATGCCGATATACTATGCCGATGATTAATTGTCAAACAGCGTGGATGGCGTCTCCAGCTTATCTGAC**  
0 ◀

4001 **GGTCACTAAACGAGCTCTGCTTATATAGACCTCCACCGTACACGCCTACCGCCATTTGCGTCAATGGGGCGGAGTTGTTACGACATTTTGAAAGTC**

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4101 **CCGTTGATTTACTAGTCAAAACAAACTCCCAATTGACGTCAATGGGGTGGAGACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAC**  
**SpeI (4110)**

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4201 **TGCCAAAACGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTACTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGCATAATGCCAGG**  
**SnaBI (4238)**

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4301 **CGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGATACACTTGTACTGCTGCAAGTGGGCAGTTTACCGTAAATACTCCACCCA**  
**NdeI (4343)**

4401 **TTGACGTCAATGGAAAGTCCTATTGGCGTTACTATGGGAACATACGTCAATTATTGACGTCAATGGCGGGGGTCTTGGCGGTCAGCCAGGCGGGCCA**

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4501 **TTTACCGTAAGTTATGTAACGCCCTGCAGGTTAA** **TAAGAACA** **TGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGCTGGCGTT**  
PacI (4529) **SdaI (4521)** **BspLU11I (4539)**

4601 **TTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCC**

4701 **CCTGGAAGCTCCCTCGTGCCTCTCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCT**

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4801 **CACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCCGCTCAAGCTGGCTGTGTGCACGAACCCCCGTTCCAGCCGACCGCTGCGCCTTATCCGGTAA**  
ApaLI (4853)

4901 **CTATCGTCTTGAGTCCAACCCGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACA**

5001 **GAGTCTTGAAGTGGTGGCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTA**

5101 **GCTCTTGATCCGGCAAACAACCCGCTGGTAGCGGTGGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTT**

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5201 **GATCTTTTCTACGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTCATGGCTAGTTAATTAACATTTAAATC** **AGCGGCCCAATA**  
PacI (5269) SwaI (5278) **EagI (5289)** **NotI (5288)**

5301 **AAATATCTTTATTTTATTACATCTGTGTGGTTTTTTTGTGTGAATCGTAACTAACATACGCTCTCCATCAAACAAAACGAAACAAAACAACTAGC**

5401 **AAAATAGGCTGTCCCAAGTGAAGTGCAGGTGCCAGAACATTTCTTATCGAA**