



**EcoRI (23) Sdal (38) SpeI (45)**  
**NotI (2) Sall (9) XbaI (19) BamHI (29) Bsp120I (39)**

1 CCGCGCCGCTCGACGATATCTAGAATTCGGATCCTGCAGGGCCACTAGTGCCAACAGATGAGGTTACAATCTCTCCACAAAACATGCAGTAAATAT  


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101 CTGAGGATATTACAGGACTTGGATTTGGTGGCAGGAGATCAACATAAACCAAGACAAGGAAGAAGTCAAAGAAATGAATCAAGTAGATTCTCTGGGATAT  


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201 AAGGTAGGGGATTGGGGGTTGGATAGTGCAGAGTATGGTACTGGCCTAAGGCACTGAGGATCATCTTTTCCACACCCACCAGAGAAGGCTTAGGCT  


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301 CCCGAGTCAACAGGGCATTACCCGCCTGGGGCGCTGAGTCATCAGGACACTGCCAGGAGACAGAACCCCTAGATGCCCTGCAGAATCCTTCTGTATC  


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401 GG|CCCCCTCCCTGAAACATCCTTCATTGCAATATTTCCAGGAAAGGAAGGGGCTGGCTCGGAGGAAGAGAGGTGGGGAGGTGATCAGGTTACAGAG  


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501 GAGGGAATGAATGACATCCCAGGATTACATAAACTGTCAGAGGCAGCGAAGAGTTCACAAGTGTGAAGCCTGGAAGCCGGCGGGTCCGCTGTGTAGG  


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601 AAAGAAGCTAAAGCACTTCCAGAGCCTGTCCGGAGCTCAGAGGTTCCGGAAGACTTATCGACCATGGAATCAAGGTGCTGTTTGCCTCATCTGTATTGC  


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701 TGTGCTGAGGCAAAACCCACTGAAATCAATGAAGACCTCAATATAGCTGCTGTGGCCTCAAACCTTGGCACCACAGATCTTGAGACTGACCTGTTACC  
13▶ V A E A K P T E I N E D L N I A A V A S N F A T T D L E T D L F T  
801 AACTGGGAGACCATGAATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGGCAAGCTGCCTGGCAAAAACCTCCCCCAGATGTCC  
47▶ N W E T M N V I S T D T E Q V N T D A D R G K L P G K K L P P D V  
901 TGAGGGAGCTGGAGGCCAATGCCAGAAGGGCTGGTTGCACAAGAGGCTGCCTCATTGCTCTCCACATTAAGTGCACCCCTAAGATGAAGAAATTTAT  
80▶ L R E L E A N A R R A G C T R G C L I C L S H I K C T P K M K K F I  
1001 CCCTGGCAGGTGCCACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGGCAATTTGTTGATATCCCAGAGATTCTGGCTTCAAGGAT  
113▶ P G R C H T Y E G E K E S A Q G G I G E A I V D I P E I P G F K D  
1101 AAGGAGCCACTGGACCAGTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCAGTGGCTGTCTGAAGGGCCTTGCCAATGTCCAGTGTCTGACCTCC  
147▶ K E P L D Q F I A Q V D L C A D C T T G C L K G L A N V Q C S D L  


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1201 TGAAGAAGTGGCTTCCCAGAGGTGTACCACCTTTTCCAGCAAGATTCAGGGTAGGGTGGACAAAATCAAGGGTCTGGCTGGGGACAGATGATAGCTAGC  
180▶ L K K W L P Q R C T T F A S K I Q G R V D K I K G L A G D R •  
1301 TGGCCAGACATGATAAGATACATTGATGAGTTTGGACAAAACCAACTAGAATGCAGTGAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTT  


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1401 TATTTGTAACCATTATAAGTGAATAAACAAGTTAACAACAACAATTGCATTCAATTTATGTTTCAGGTTACAGGGGAGGTGTGGGAGGTTTTTAAAG  


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1501 CAAGTAAAACCTCTACAATGTGGTATGGAATTAATTCTAAAATACAGCATAGCAAACTTTAACCTCAAATCAAGCCTCTACTTGAATCCTTTTCTGA  


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1601 GGGATGAATAAGGCATAGGCATCAGGGGCTGTTGCCAATGTGCATTAGCTGTTTGCAGCCTCACCTTCTTTCATGGAGTTTAAAGATATAGTGTATTTTCC  
1701 CAAGGTTTGAAGTACTGCTCTTCAATTTCTTATGTTTTAAATGCCTGACCTCCCACATTCCTTTTATAGTAAATATTCAGAAAATATTTAAATACATCAT  
1801 TGCAATGAAAATAAATGTTTTTATTAGGCAGAATCCAGATGCTCAAGGCCCTTCATAATATCCCCAGTTTAGTAGTTGGACTTAGGGAACAAAGGAAC  
1901 CTTAATAGAAATTTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCC|TCAGTCTGCTCCTG|GCCACAAAGTG|CAGCGAGTTGCCGGCCGGTCCGCGCAG  
125◀ • D Q E E A V F H V C N G A P D R L  
2001 GGCGAACTCCCGCCCCACGGCTGCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGTCCCGGAAGTTCTGGACACGACCTCCGACCCTCGGCGTAC  
107◀ A F E R G W P Q E G I E T M A P G S A D R F N T S V V E S W E A Y  
2101 AGCTCGTCCAGGCGCGCACCCACACCAGGCCAGGGTGTGTCGGCACCACCTGGTCTGGACCGCGCTGATGAACAGGGTACGTCGTCGGGACCA  
73◀ L E D L G R V W V W A L T N D P V V Q D Q V A S I F L T V D D R V V  
**SgrAI (2202)**  
2201 CACCGCGAAGTCTGCTCCACGAAGTCCCGGAGAACCCGAGCCGGTCCGACTCGAAGTCCGACCGCTCCGGCAGCTCGCGCGGGTGGACCCGGAAC  
40◀ G A F D D E V F D R S F G L R D T W F E V A G A V D R A T L V P V  
2301 GGCACTGGTCAACTTGGCCATGATGGCTCCTCTGTGAGGAGGAAAGAGAAGGTTAGTACAATTGCTATAGTGGTGTATTATACTATGCAGAT  
7◀ A S T L K A M ◀  
2401 ATACTATGCCAATGATTAATTGTCAA|ACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCG  


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2501 TTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACC  


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2601 AGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCT  


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2701 TTCTCATAGCTCAGCTGAGGTATCTCAGTTCGGTGTAGGCTGTTCCGCTCAAGCTGGGCTGTGTGCACGAACCCCGTTACGCCGACCGCTGCGCC  


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2801 TTATCCGGTAACTATCGTCTTGAAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAG  


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2901 GCGGTGTACAGATTTCTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAA  


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3001 AAGAGTTGGTAGCTCTTGATCCGGCAACAAACCACCGCTGGTAGCGGTGTTTTTTTTGTTTGAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAA  


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3101 GAAGATCCTTTGATCTTTCTACGGGGTCTGACGCTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTATGGCTAGTGAATTAACATTTAAATCA