





2500 GACTTGAAATCCCCGTGAGTCAAACCGCTATCCACGCCATTGATGTAAGTCCAAAACCGCATCATCATGGTAATAGCGATGACTAATACGTAGATGTA **SnaBI (2587)**

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2600 CTGCCAAGTAGGAAAGTCCATAAGGTCATGTACTGGGCATAATGCCAGGCGGGCCATTTACCGTCATTGACGTCAATAGGGGGCGTACTTGGCATATGA **NdeI (2692)**

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2700 TACACTTGATGTAAGTGGCAGTTTACCGTAAATACTCCACCATTGACGTCAATGAAAGTCCCTATTGGCGTTACTATGGGAACATACGTCA

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2800 TTATTGACGTCAATGGGCGGGGTCGTTGGGCGGTGAGCCAGGCGGGCCATTTACCGTAAAGTTATGTAACGCCTGCAGGTTAA TTAAGAACATGTGAG **PstI (2871)**  
**SdaI (2870)** **PacI (2878)** **BspLU11I (2888)**

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2898 CAAAAGGCCAGCAAAAAGGCCAGGAACCGTAAAAAGGCCGCTTGTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAATAATCGACGCTC

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2998 AAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAGGCGTTTTCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCCTGCCGTTACC

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3098 GGATACCTGTCCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGTTCCGCTCCAAGCTGG

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3198 GCTGTGTGCACGAACCCCGTTCAGCCCGACCCTGCGCCTTATCCGGTAACTATCGTCTTGTAGTCCAAACCCGTAAGACACGACTTATCGCCACTGGC **ApaLI (3202)**

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3298 AGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTA

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3398 TTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAACACCCTGGTAGCGGTGGTTTTTTTG

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3498 TTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGTTA

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3598 AGGGATTTTGGTTCATGGCTAGTTAATTAACATTTAAATC AGCGGCCGAATAAAATATCTTTATTTTTCATTACATCTGTGTGTTGGTTTTTTGTGTGAAT **EagI (3638)**  
**PacI (3618)** **SwaI (3627)** **NotI (3637)**

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3698 CGTAACTAACATACGCTCTCCATCAAACAACGAAACAACAACTAGCAAATAGGCTGTCCCGAGTGAAGTGCAGGTGCCAGAACATTTCTCTA

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3798 TCGAA