PLNT 2530 - Plant Biotechnology March 22, 2024

Name

Student ID number

Assignment 3

**1. (6 points) Demonstrate the effect of sequence topology on restriction digests.**

a) *Answer question a here. The data in the boxes is dummy data. Replace it with your actual results.*

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| ----------------------------------------------------------- BACHREST Version 09/30/2012pBS\_SK-GUS Topology: CIRCULAR Length: 5978 bp-----------------------------------------------------------Search parameters: Recognition sequences between 6 and 21 bp Ends: 5' protruding, Blunt, 3' protruding Type: Symmetric, Asymmetric Minimum fragments: 0 Maximum fragments: 6000 Maximum fragments to print: 30----------------------------------------------------------- # ofEnzyme Recognition Sequence Sites Sites Frags Begin EndAarI CACCTGC(4/8) 4 6448 7225 13981 6447 7178 3609 7178 10786 10787 3194 10787 13980 13981 730 6448 7177OliI CACNN^NNGTG 3 6392 10798 10352 6391 6410 3942 6410 10351 10352 18 6392 6409 |

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| ----------------------------------------------------------- BACHREST Version 09/30/2012pBS\_SK-GUS.fsn Topology: LINEAR Length: 5978 bp-----------------------------------------------------------Search parameters: Recognition sequences between 6 and 21 bp Ends: 5' protruding, Blunt, 3' protruding Type: Symmetric, Asymmetric Minimum fragments: 0 Maximum fragments: 6000 Maximum fragments to print: 30----------------------------------------------------------- # ofEnzyme Recognition Sequence Sites Sites Frags Begin EndAarI CACCTGC(4/8) 4 6448 7225 13981 6447 7178 3609 7178 10786 10787 3194 10787 13980 13981 730 6448 7177OliI CACNN^NNGTG 3 6392 10798 10352 6391 6410 3942 6410 10351 10352 18 6392 6409 |

b) *Answer question b here.*

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**2. (6 points) Create a construct using pBluescript SK(+), for comparison with the construct made using pBluescript SK(-). KEEP BOTH MAPS ON THIS PAGE. You may need to resize.**

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**3. (6 points) Use BACHREST to find restriction digests that would allow us to determine which of the two Bluescript vectors was used in the real construct.** *The data in the boxes is dummy data. Replace it with your actual results.*

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| ----------------------------------------------------------- BACHREST Version 09/30/2012pBS\_SK+GUS Topology: CIRCULAR Length: 5978 bp-----------------------------------------------------------Search parameters: Recognition sequences between 6 and 21 bp Ends: 5' protruding, Blunt, 3' protruding Type: Symmetric, Asymmetric Minimum fragments: 0 Maximum fragments: 6000 Maximum fragments to print: 30----------------------------------------------------------- # ofEnzyme Recognition Sequence Sites Sites Frags Begin End--------------------------------------------------------------------------------PstI CTGCA^G 3 3020 7888 4967 12854 4967 4923 12855 3019 12855 1947 3020 4966PvuI CGAT^CG 3 4025 10677 8106 4024 7730 3705 4025 7729 8106 376 7730 8105PvuII CAG^CTG 5 3073 5081 12750 3072 4772 4218 8532 12749 8075 3303 4772 8074 8532 1699 3073 4771 12750 457 8075 8531 |

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| ----------------------------------------------------------- BACHREST Version 09/30/2012pBS\_SK-GUS Topology: CIRCULAR Length: 5978 bp-----------------------------------------------------------Search parameters: Recognition sequences between 6 and 21 bp Ends: 5' protruding, Blunt, 3' protruding Type: Symmetric, Asymmetric Minimum fragments: 0 Maximum fragments: 6000 Maximum fragments to print: 30----------------------------------------------------------- # ofEnzyme Recognition Sequence Sites Sites Frags Begin End--------------------------------------------------------------------------------PstI CTGCA^G 3 3020 7888 4967 12854 4967 4923 12855 3019 12855 1947 3020 4966PvuI CGAT^CG 3 4025 10677 8106 4024 7730 3705 4025 7729 8106 376 7730 8105PvuII CAG^CTG 5 3073 5081 12750 3072 4772 4218 8532 12749 8075 3303 4772 8074 8532 1699 3073 4771 12750 457 8075 8531 |

*Discussion of data for question 3 here.*

**KEEP BOTH MAPS ON THIS PAGE. You may need to resize.**

