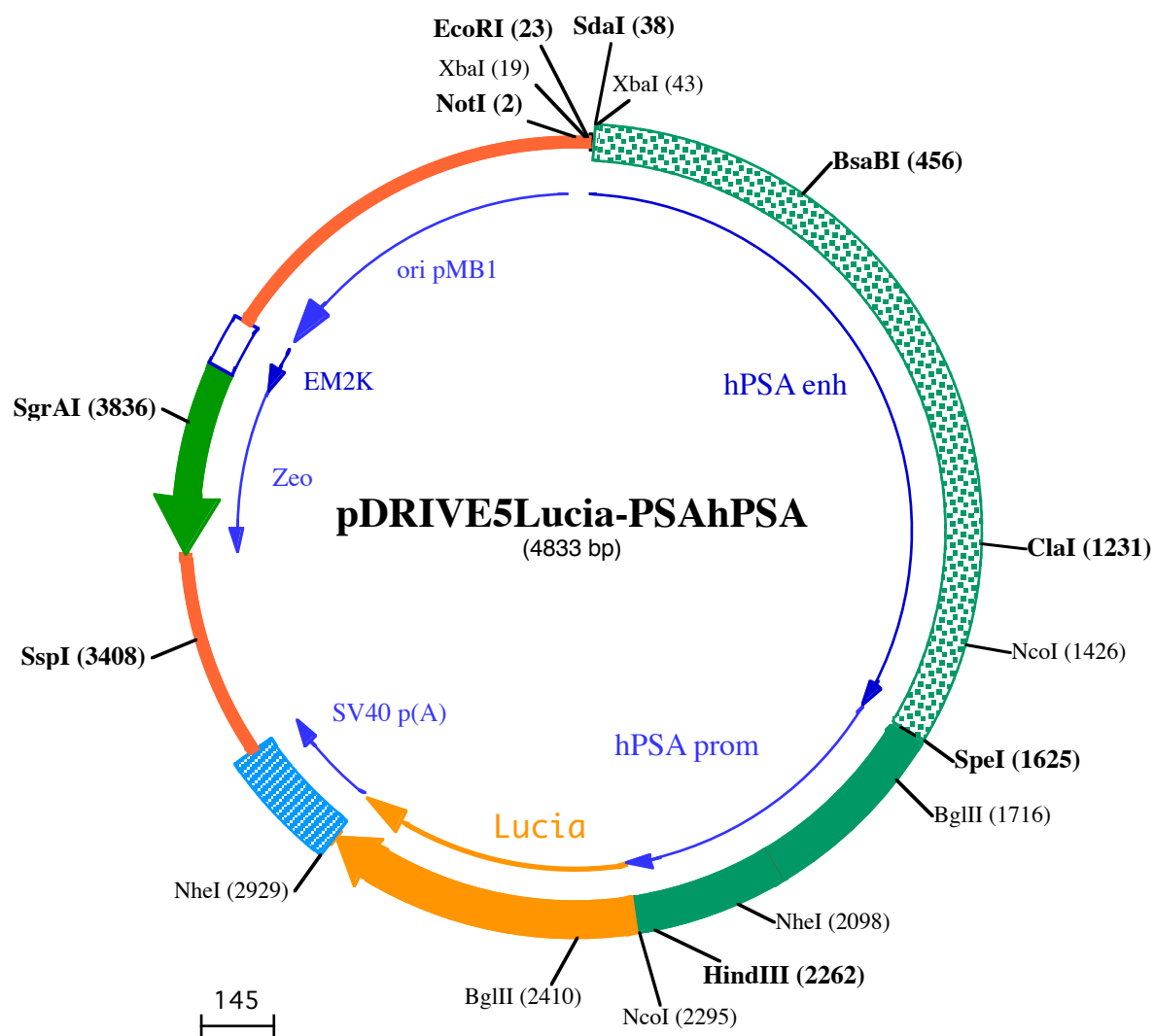




EcoRI (23)

NotI (2) XbaI (19) **SdaI (38)** XbaI (43)

1 CGGCCCGCGTCGACGATATCTAGAATTCGGATCCTGCAAGGCTCTAGAAATCTAGCTGATATAGTGTGGCTCAAAACCTTCAGCACAAATCACACCGTTA

101 GACTATCTGGTGTGGCCAAACCTTCAGGTGAACAAAGGCACTCTAATCTGGCAGGATATTCCAAAGCATTAGAGATGACCTCTTGCAAGAAAAAGAAA

201 TGGAAAAGAAAAAGAAAGAAAGAAAAAAGAGATGACCTCTCAGGCTCTGAGGGAAACGCCTGAGGTCTTTGAGCAAGTCAGTCCTC

301 TGTTCACAGTCTCCCTCACAGGTCATTGTGACGATCAATGTGGTCACGTGTATGAGGCACGACATGCCTGGCTCTGGGAGTGCCGTGAAGTG

BsaBI (456)

401 TATGCTTGCACTGCTGAATGGCTGGGATGTGTCAGGGATTATCTTCAGCACTTACAGATGCTCATCTCATCCTCACAGCATCACTATGGGATGGGTATTA

501 CTGGCCTCATTGATGGAGAAAGTGGCTGTGGCTCAGAAAGGGGGACCACTAGACCAGGACACTCTGGATGCTGGGACTCCAGAGACCATGACCACT

601 CACCAACTGCAGAGAAATTAATTGTGGCTGATGTCCTGTCTGGAGAGGGTGGAGGTGGACCTTCACTAACCTCTACCTTGACCTCTCTTTTAGGG

701 CTCTTTCTGACCTCCACCATGATACTAGGACCCATTGTATTCTGTACCCTCTTGACTCTATGACCCCACTGCCACTGCATCCAGCTGGTCCCTCC

801 TATCTCTATCCAGCTGGCCAGTGCAGTCTCAGTCCCACCTGTTTGTGAGTAAGTCTGAAGGGCTGACATTTTACTGACTTGCAACAAATAAGTA

901 ACTTTCAGAGTTTGTGAATGCTGGCAGAGTCCATGAGACTCCTGAGTCAGAGGCAAGGCTTTTACTGCTCACAGCTTAGCAGACAGCATGAGGTTCA

1001 TGTTCACATTAGTACACCTTGCCCCCCCCAAATCTGTAGGGTGACCAGAGCAGTCTAGGTGGATGCTGTGCACAGGGGTTGTGCCACTGGTGAGAA

1101 ACCTGAGATTAGGAATCCTCAATCTTATACTGGGACAACTTGCAAACCTGCTCAGCCTTTGTCTCTGATGAAGATATTATCTCATGATCTTGGATTGAA

ClaI (1231)

1201 AACAGACCTACTCTGGAGAACATATTGTATCGATTGTCCTTGACAGTAACAAATCTGTTGAAGAGACATTATCTTTATTATCTAGGACAGTAAGCAA

1301 GCCTGGATCTGAGAGAGATATCATCTTGAAGGATGCCTGCTTTACAAACATCCTTGAAACAACATCCAGAAAAAAGGTGTTGCTGTCTTTGCTCA

NcoI (1426)

1401 GAAGACACACAGATACGTGACAGAACCATGGAGAATTGCCTCCCAACGCTGTCAGCCAGAGCCTTCCACCCTTGCTGCAGGACAGTCTCAACGTTCCA

1501 CCATTAATACTTCTTCTATCACATCCTGCTTCTTTATGCCTAACCAAGGTTCTAGGTCCGATCGACTGTGTCTGGCAGCACTCCACTGCCAAACCCAG

SpeI (1625)

1601 AATAAGGCAGCGCTCAGGATCCCGACTAGTACATTGTTTGTGTCACGTTGGATTTTGAATGCTAGGGAACCTTGGGAGACTCATATTTCTGGCTAGAG

BglII (1716)

1701 GATCTGTGGACCACAAGATCTTTTATGATGACAGTAGCAATGTATCTGTGGAGCTGGATTCTGGGTTGGGAGTGAAGGAAAAGAAATGTACTAAATGCC

1801 AAGACATCTATTTAGGAGCATGAGGAATAAAAGTTCTAGTTTCTGGTCTCAGAGTGGTGCAGGGATCAGGGAGTCTACAATCTCCTGAGTCTGGTGT

1901 CTTAGGGCAGCTGGGTCTTGGAGTGCAAGGATCTAGGCACGTGAGGCTTTGTATGAAGAATCGGGGATCGTACCCACCCCTGTTTCTGTTTCATCCT

NheI (2098)

2001 GGGCGTGTCTCTCTGCCTTTGTCCTCTAGATGAAGTCTCCATGAGCTACAGGGCCTGGTGCATCCAGGGTATCTAGTAATTGCAGAACAGCAAGTGCT

2101 AGCTCTCCCTCCCTCCACAGCTCTGGGTGTGGAGGGGTTGTCCAGCTCCAGCAGCATGGGAGGGCTTGGTCAGCCTCTGGGTGCCAGCAGGGC

HindIII (2262) **NcoI (2295)**

2201 AGGGGCGGAGTCTGGGGAATGAAGGTTTTATAGGGCTCTGGGGAGGCTCCCGAGCCCAAGCTTACCACCTGCACCCGAGAGCTGTGTACCATGG

2301 AAATCAAGGTGCTGTTTGCCCTCATCTGTATTGCTGTTGCTGAGGCAAAACCACTGAAATCAATGAAGACCTCAATATAGCTGCTGTGGCTCCAACCT

2401 TGCCACCACAGATCTTGAGACTGACCTGTTCACTGAGGAGGAGGATGATGTGATTAGCACTGACACAGAGCAGGTGAACACAGATGCTGACAGGGG

2501 AAGCTGCCTGGCAAAAACTCCCCAGATGCTCTGAGGGAGCTGGAGGCAATGCCAGAGGGCTGGTTGCAGAGGCTGCCTCATTTGCCTCTCCC

2601 ACATTAAGTGCACCCCTAAGATGAAGAAATTTATCCCTGGCAGGTGCCACACTTATGAAGGTGAAAAGGAGTCTGCTCAGGGAGGGATTGGAGAGGCAAT

2701 TGTGTATATCCAGAGATTTCTGGCTTCAAGGATAAGGAGGCACTGGACCACTTTATTGCTCAAGTGGACCTCTGTGCTGATTGCACCACTGGCTGTCTG

2801 AAGGGCCTTGCCAATGTCCAGTGTCTGACCTCCTGAAGAGGTGGCTTCCCGAGAGGTGTACCACTTTTGCCAGCAAGATTGAGGTAGGGTGGCAAAA

2901 TCAAGGGTCTGGCTGGGACAGATGATAGCTAGCTGGCCAGACATGATAAGATACATTGATGAGTTTGGACAACCACTAGAAATGCAGTGAAAAAA

3001 TGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTAAGCTGCAATAAACAAGTTAACAACAACATTGCATTCATTTTATGTTTC

3101 AGGTTTCAGGGGAGGTGTGGGAGGTTTTTAAAGCAAGTAAACCTCTACAAATGTGGTATGGAATTAATTCTAAATACAGCATAGCAAACTTTAACC

3201 TCCAAATCAAGCCTCTACTTGAATCTTTTCTGAGGGATGAATAAGGCATAGGCATCAGGGCTGTTGCCAATGTGCATTAGCTGTTTGAGCCTCACCT

3301 TCTTTCATGGAGTTAAGATATAGTGTATTTTCCCAAGGTTTGAAGTGTCTTCTTCTTTATGTTTAAATGCACTGACCTCCACATTCCTCTTTT

3401 AGTAAATATTAGAAATAATTTAAATACATCATTGCAATGAAATAAATGTTTTTATTAGGCAGAAATCCAGATGCTCAAGGCCCTTCATAATATCCCC

3501 CAGTTTAGTAGTTGGACTTAGGGAACAAAGGAACCTTTAATAGAAATTGGACAGCAAGAAAGCGAGCTTCTAGCTTATCCTCAGTCCTGCTCCTTGCCA
125 • D Q E E A V

3601 CAAAGTGACGCAGTTGCCGGCCGGTCGCGCAGGGCGAACTCCGCCCCACGGCTGCTCGCCGATCTCGGTCATGGCCGGCCGGAGGCGTCCCGAA
118 F H V C N G A P D R L A F E R G W P Q E G I E T M A P G S A D R F

3701 GTTCGTGGACACGACCTCCGACCACTCGGCGTACAGCTCGTCCAGGCCGCGCACCCACCCAGGCCAGGGTGTGTCCGGCACCACCTGGTCCTGGACC
85 N T S V V E S W E A Y L E D L G R V W V W A L T N D P V V Q D Q V

SgrAI (3836)

3801 GCGCTGATGAACAGGGTCACGTCGTCCCGACCACACCGCGAAGTCGTCTCCACGAAGTCCCGGGAGAACCAGCCGGTCGGTCCAGAAGTCCGACCG
51 A S I F L T V D D R V V G A F D D E V F D R S F G L R D T W F E V A

3901 CTCGGCGACGTCGCGCGGGTGAGCACCAGGCAACGGCACTGGTCAACTGGCCATGATGGCTCCTCCTGTGAGGAGAGGAAAGAGAAGAAGGTTAGTACA
18 G A V D R A T L V P V A S T L K A M

4001 ATTGCTATAGTGAGTTGTATTATACTATGCAGATATACTATGCCAATGATTAATTGTCAACTAGGGCTGCAGGTTAATTAAGAACATGTGAGCAAAAGG
◀

4101 CCAGCAAAAGGCCAGGAACCGTAAAAAGCCGCGTTGTGGCGTTTTTCCATAGGCTCCGCCCTGACGAGCATCACAATAATCGACGCTCAAGTCAG
◀

4201 AGGTGGCGAAACCCGACAGGACTATAAGATACCAGGCGTTTCCCCTGGAAGCTCCCTCGTGCCTCTCCTGTTCCGACCTGCCGCTTACCGGATACC
◀

4301 TGTCCGCTTTCTCCCTTCGGAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGT
◀

4401 GCACGAACCCCGTTGAGCCGACCGCTGCGCCTTATCCGGTAAGTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCC
◀

4501 ACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTCTTGAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTA
◀

4601 TCTGCGCTCTGCTGAAGCCAGTTACCTTCGAAAAAGAGTTGGTAGCTCTTGATCCGGCAACAAACCCCGCTGGTAGCGGTGTTTTTTGTTTGCAA
◀

4701 GCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTACGGGGTCTGACGCTCAGTGGAACGAAAACCTACGTTAAGGGATT
◀

4801 TTGGTCATGGCTAGTTAATTAACATTTAAATCA
◀