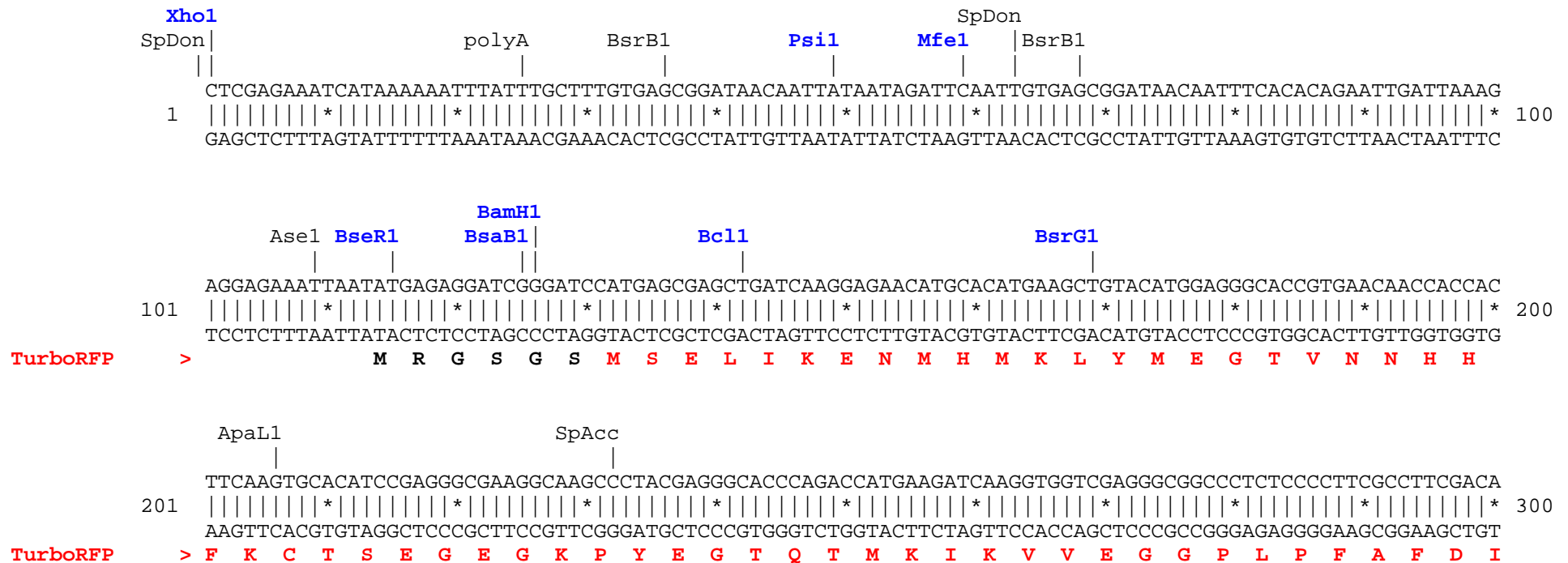
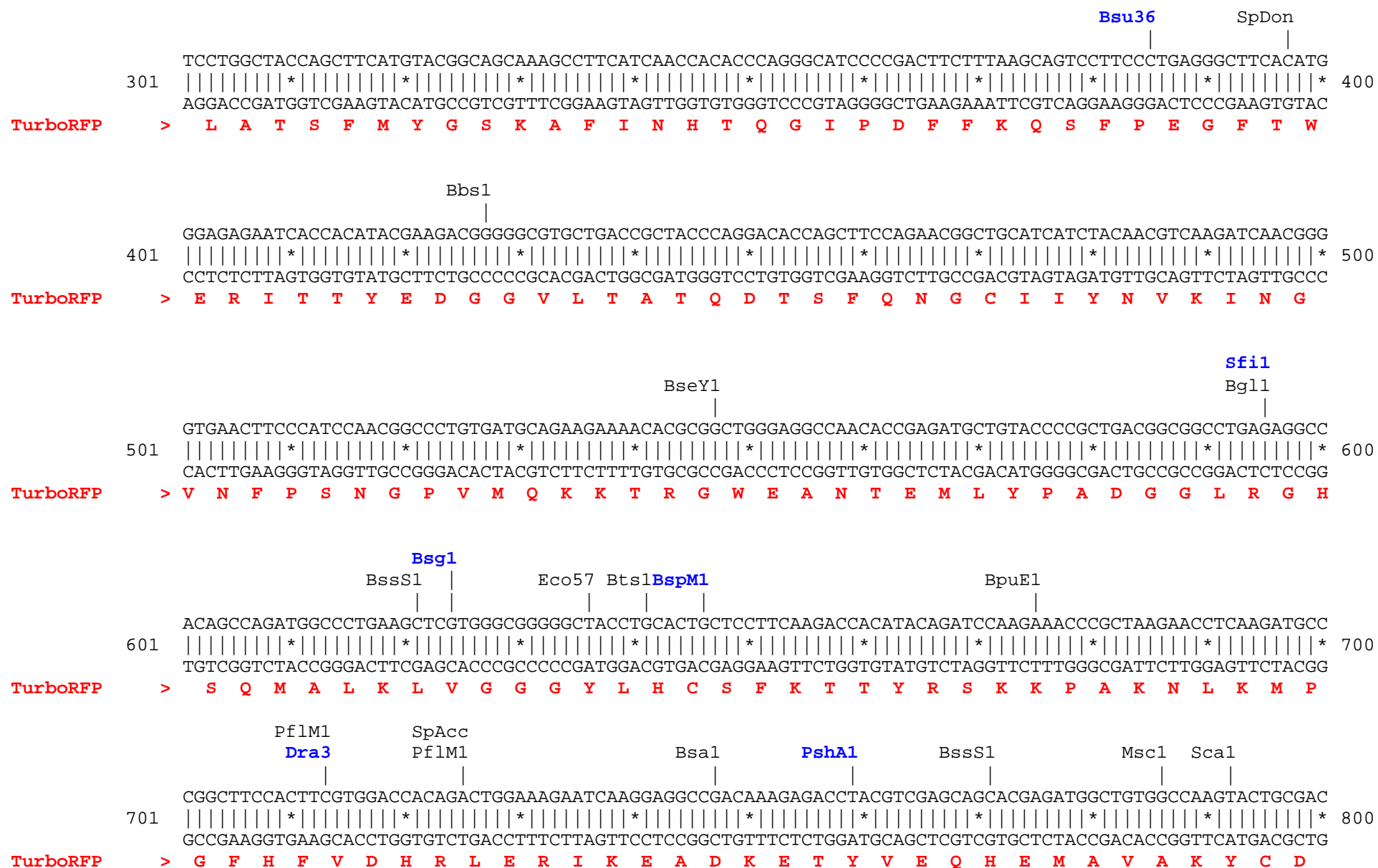


pTurboRFP-B vector restriction map

The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Amino acids encoded by vector's backbone sequence are shown in black.





```

      SpAcc      Bmr1Hind3      Blp1
      |          |          |
      CTCCCTAGCAAACCTGGGGCACAGATGAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTC
801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
      GAGGGATCGTTTGACCCCGTGTCTACTTTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCTAAACAAG
TurboRFP > L P S K L G H R *

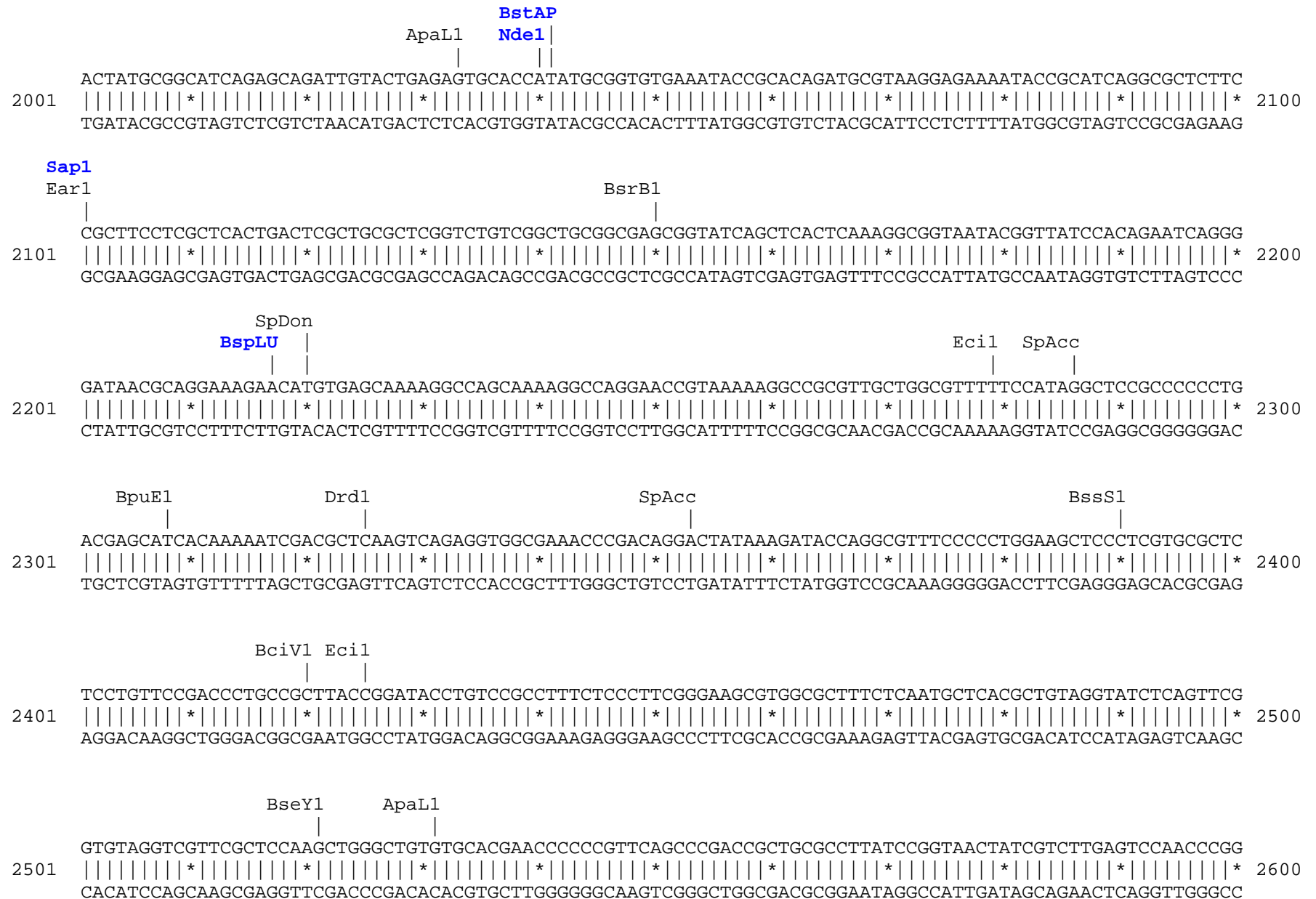
                                polyA      Nhe1      Bpu10      SpAcc
                                |          |          |          |
                                AGAACGCTCGGTTGCCCGCGGGCGTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATC
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
                                TCTTGCGAGCCAACGGCGGCCGCAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTAAAAGTCTCGATTCTTCGATTTTACCTCTTTTTTTAG

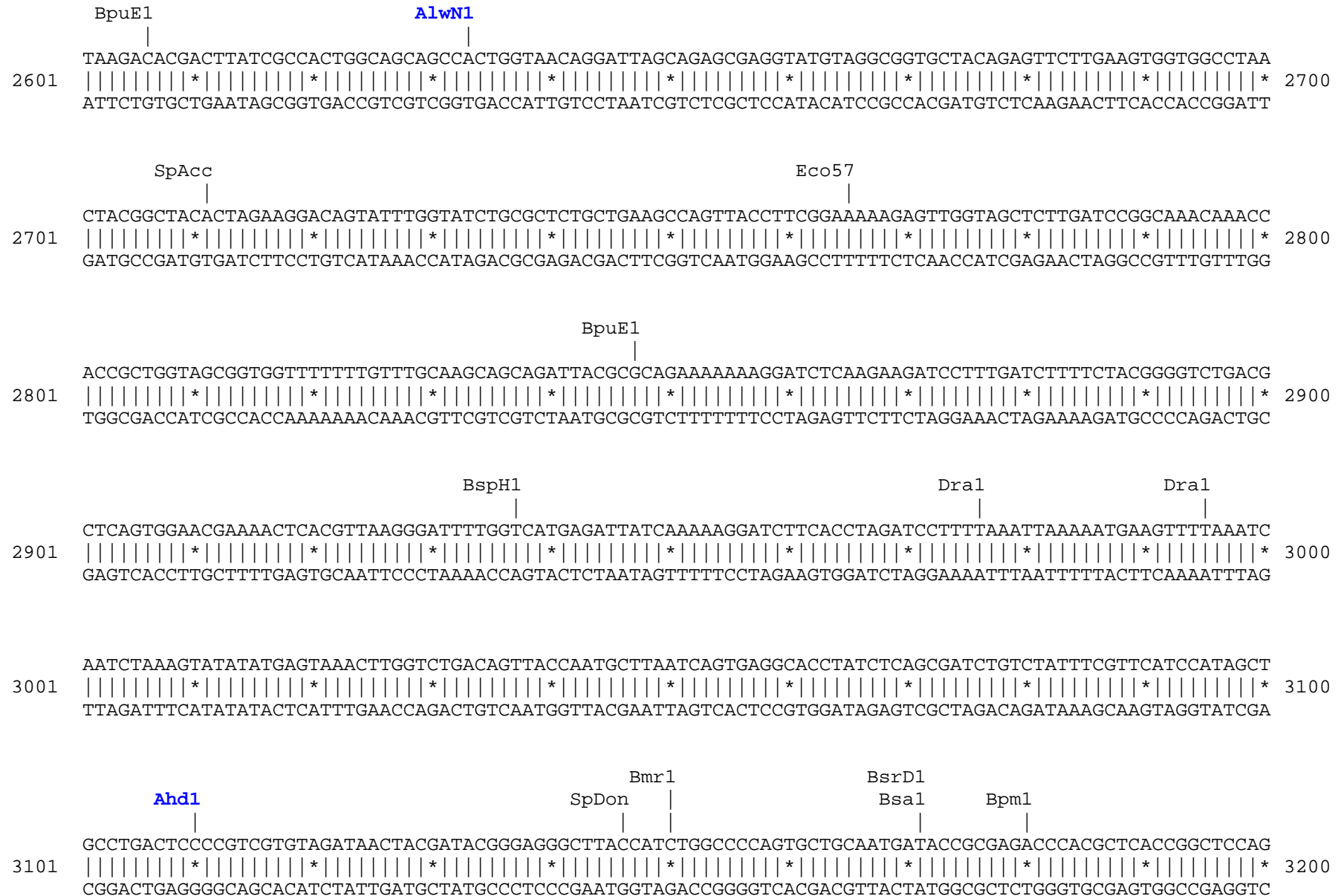
                                                                Pvu2
                                                                |
                                                                ACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTTCAGC
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
                                                                TGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTGTAAAACCTCCGTAAAGTCAGTCAACGAGTTACATGGATATTGGTCTGGCAAGTCG

                                                                SpDon      BspE1
                                                                |          |          |          |
                                                                TGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTATTCACATTCTTGCCCGCCTGATGAATGCTCATCCGGA
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
                                                                ACCTATAATGCCGGAATAATTTCTGGCATTCTTTTTTATTTCGTGTTCAAATAGGCCGGAATAAGTGTAAAGAACGGGCGGACTACTTACGAGTAGGCCT

                                                                BsrD1      BtgZ1      Acl1
                                                                |          |          |          |
                                                                ATTTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTACCCCTTGTTACACCGTTTTCCATGAGCAAACCTGAAACGTTTTTCATCGCTC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
                                                                TAAAGCATAACCGTTACTTTCTGCCACTCGACCACTATAACCTATCACAAGTGGGAACAATGTGGCAAAGGTTACTCGTTTTGACTTTGCAAAAGTAGCGAG

                                                                Bpm1
                                                                |
                                                                TGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTA
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
                                                                ACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAATGCCACTTTTGGACCGGATAAAGGGATTTCCCAAAT
```



SpDon SpDon
| |
CTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACT
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
GAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTATGAGTATGA

Earl Ssp1 BspH1 BciV1 BsrB1 polyA
| | | | |
CTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCG
3901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
GAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCAAGGC

Aat2 BspH1 SpAcc BssS1 Bbs1
| | | | |
CGCACATTTCCCGAAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTC
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
GCGTGTAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAG

AC
4101 || 4102
TG

