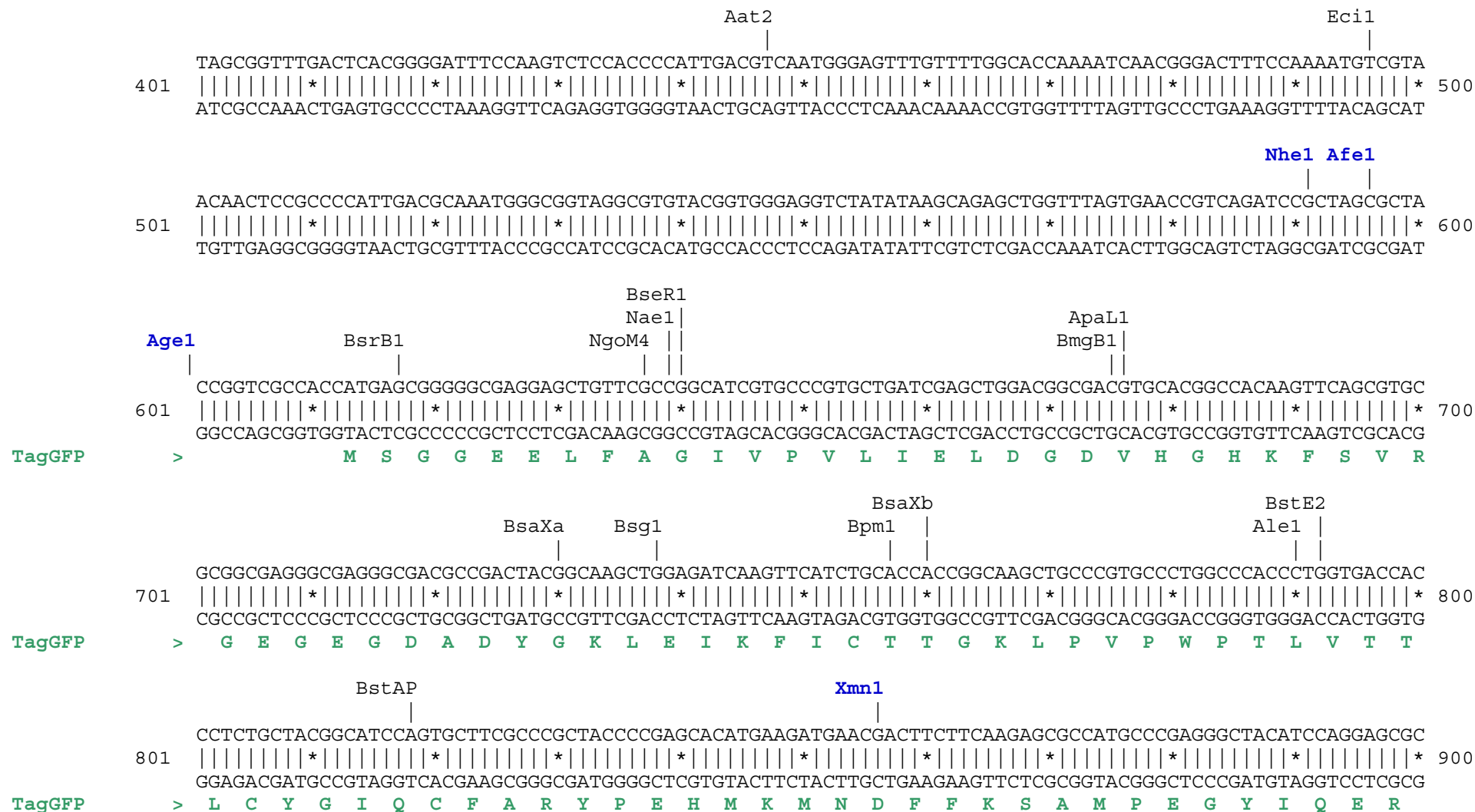


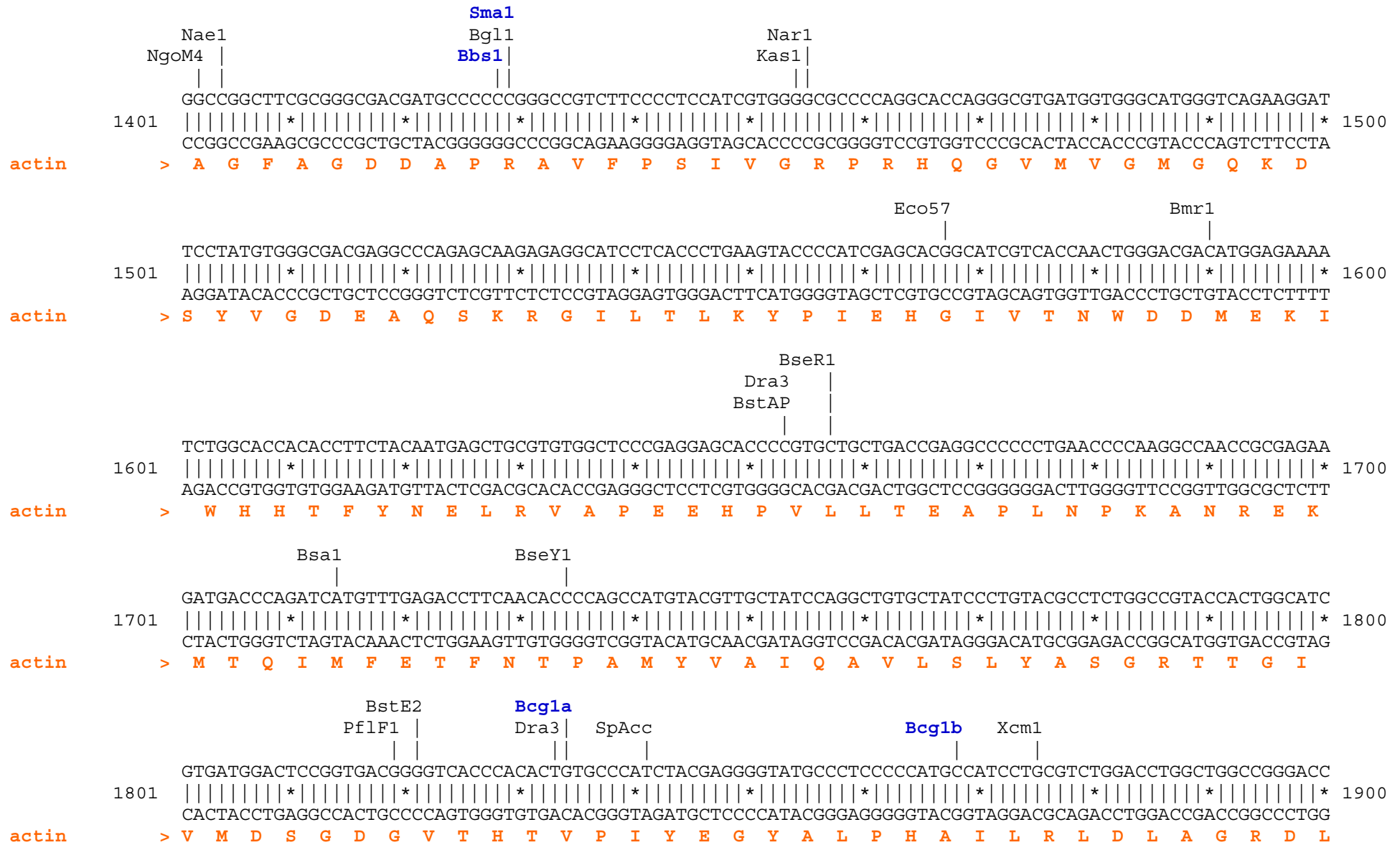
pTagGFP-actin vector restriction map

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). TagGFP amino acids are shown in green, beta-actin amino acids are shown in orange, linker amino acids are shown in black.







```
                BspH1                               SpDon   Eag1   BsrB1                               BsaXa
                |                                 |         |         |                                 |
1901  TGACTGACTACCTCATGAAGATCCTCACCGAGCGCGGCTACAGCTTCACCACCACGGCCGAGCGGGAAATCGTGCCTGACATTAAGGAGAAGCTGTGCTA
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2000
actin > T D Y L M K I L T E R G Y S F T T T A E R E I V R D I K E K L C Y
```

```

                                Sap1
                                Ear1
                                SpAcc
          BsaXb          Msc1    BseR1          Xcm1   |   |   |          Bpm1          Drd1
          |             |         |             |       |   |           |             |
2001  CGTCGCCCTGGACTTCGAGCAAGAGATGGCCACGGCTGCTTCCAGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACCGCCAGGTCATCACCATTGGC
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2100
actin > V A L D F E Q E M A T A A S S S S L E K S Y E L P D G Q V I T I G
```

```

        BsrD1              SpAcc
        BsrB1          Bsu36      Ear1  |
        |              |         |   |
2101  AATGAGCGGTTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCTTCCCTGGGCATGGAGTCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGT
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2200
actin > N E R F R C P E A L F Q P S F L G M E S C G I H E T T F N S I M K C
```

```

        BmgB1                                     BsrD1                                     Bts1
        |                                         |                                         |
2201  GTGACGTGGACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCAC
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2300
actin > D V D I R K D L Y A N T V L S G G T T M Y P G I A D R M Q K E I T
```

```

                                BsrD1
          BseY1          BseR1   BsaB1 |         Bpu10         Scal
          |             |         |   |         |         |
2301  TGCCCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCCGGCTCCATCCTGGCCTCGCTGTCCACC
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2400
actin > A L A P S T M K I K I I A P P E R K Y S V W I G G S I L A S L S T
```

```

                BsaB1                               BamH1           Xba1           Bcl1
                |                                   |                 |                 |
2401  TTCCAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCTCCATCGTCCACCGCAAATGCTTCTAGGGATCCACCGGATCTAGATAACTGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
    AAGGTCGTCTACACCTAGTCGTTTCGTCCTCATACTGCTCAGGCCGGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTGACT
actin  > F Q Q M W I S K Q E Y D E S G P S I V H R K C F *

                BsaB1           SpDon   Dra1                               Bsm1
                |               |       |                                   |
2501  TCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
    AGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAAACAACA

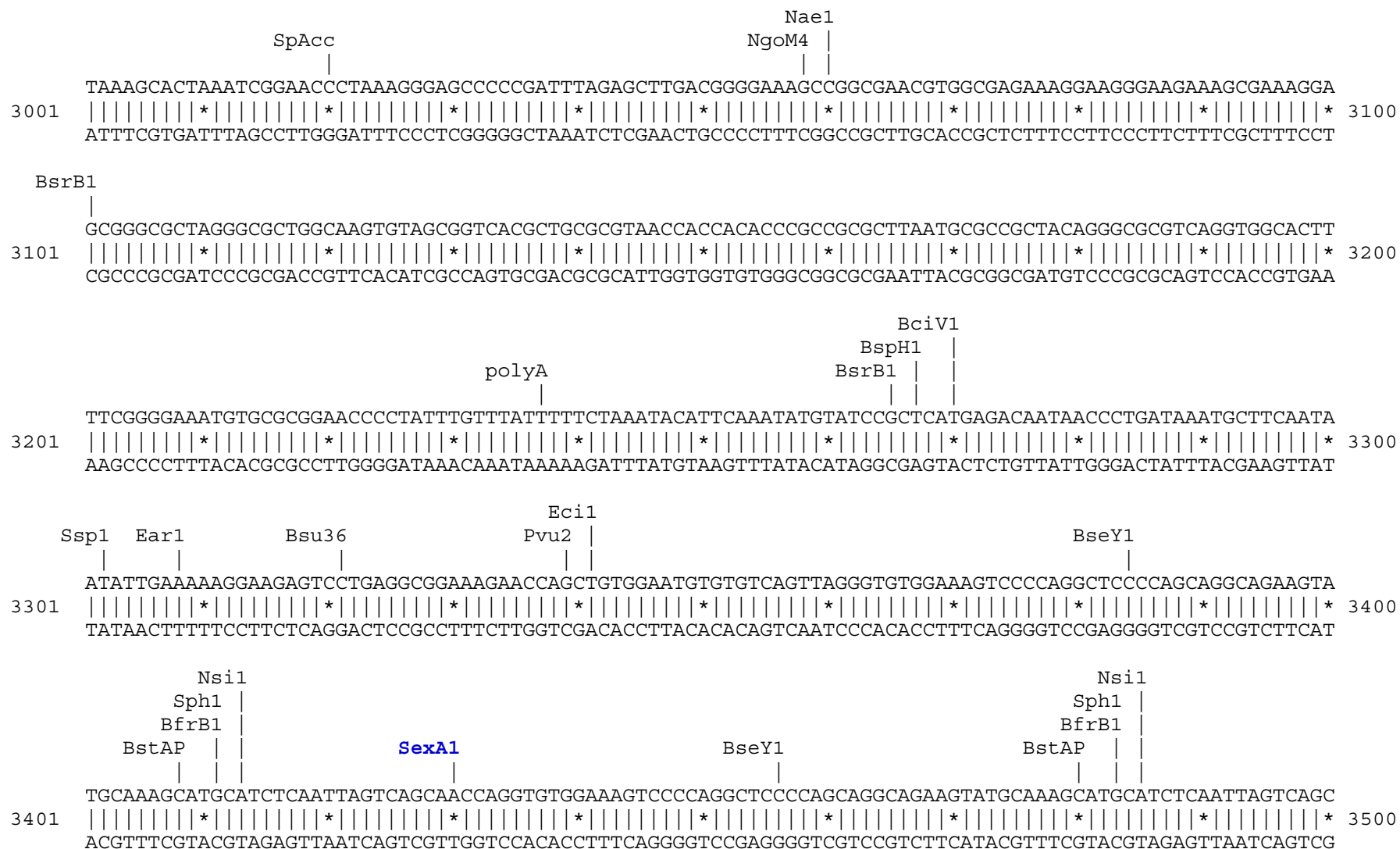
    Hpa1           polyA   Pst1           polyA           polyA           Bts1 Bsm1
    |             |       |               |               |               |       |
2601  TGTTAACCTTGTATTATTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
    ACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTATTTCGTAAAAAAAGTGACGTAAGATCAACACCA

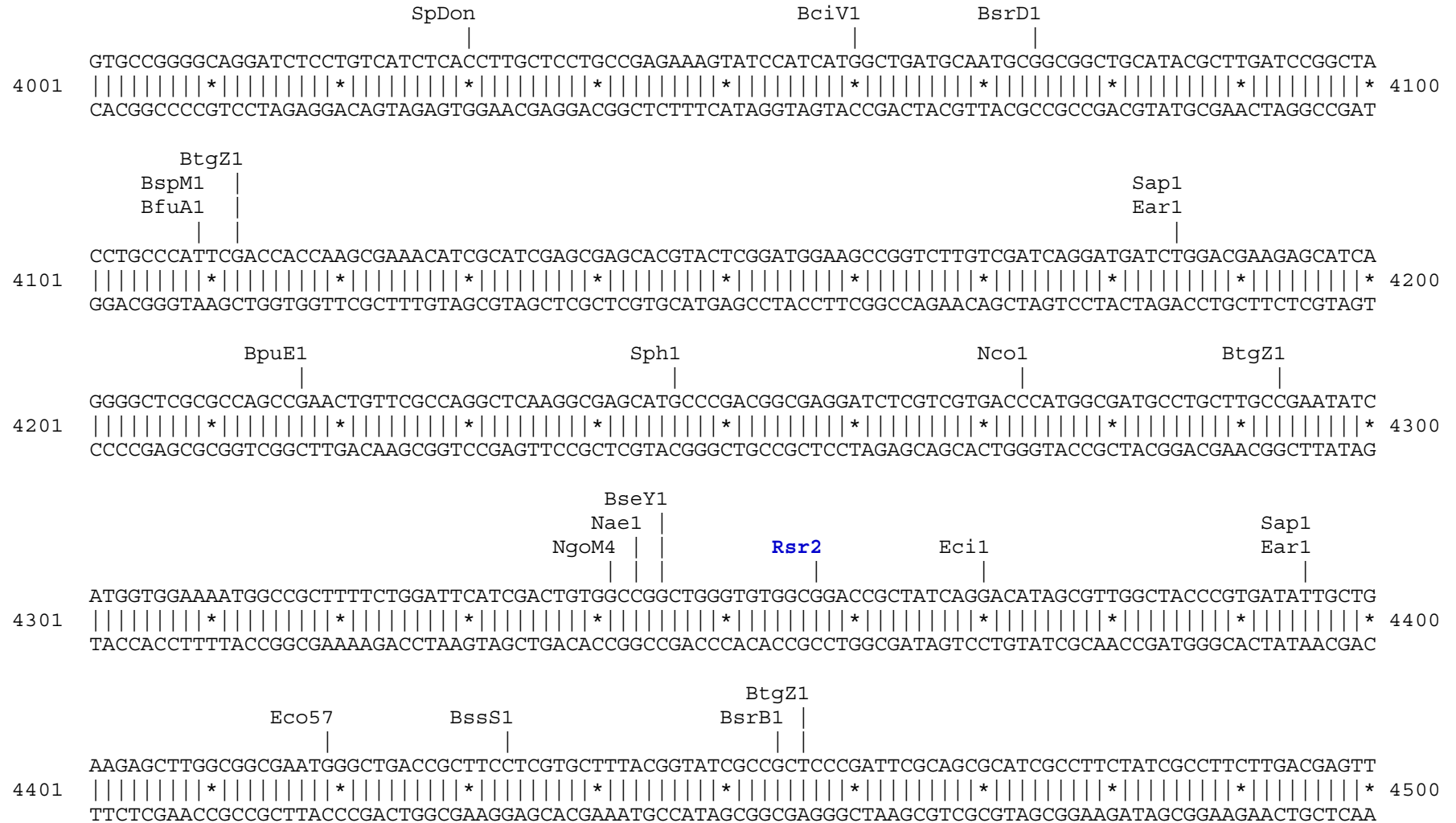
                Mlu1           SpDon           Ssp1
                |               |               |
2701  TTGTCCAAACTCATCAATGTATCTTAAACGCGTAAATTGTAAGCGTTAATATTTTTGTTAAAATTTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
    AACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTTCGCAATTATAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTG

                Pst1                               BsaXb
                |                                   |
2801  CAATAGGCCGAAATCGGC AAAATCCCTTATAAAATCAAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
    GTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAAACAAGGTCAAACCTTGTTCAGGTGATAATTTCT

                Drd1   BsaXa                               BtgZ1
                |     |                                   |       |
2901  ACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCCTAATCAAGTTTTTTGGGGTTCGAGGTGCCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
    TGCACCTGAGGTTGCAGTTTCCCGCTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGC

```






```

                                     BpuE1
                                     |
5101 ATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    TAGTTTCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTC

                                     Eco57
                                     |
                                     SpAcc
                                     |
5201 AGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    TCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTT

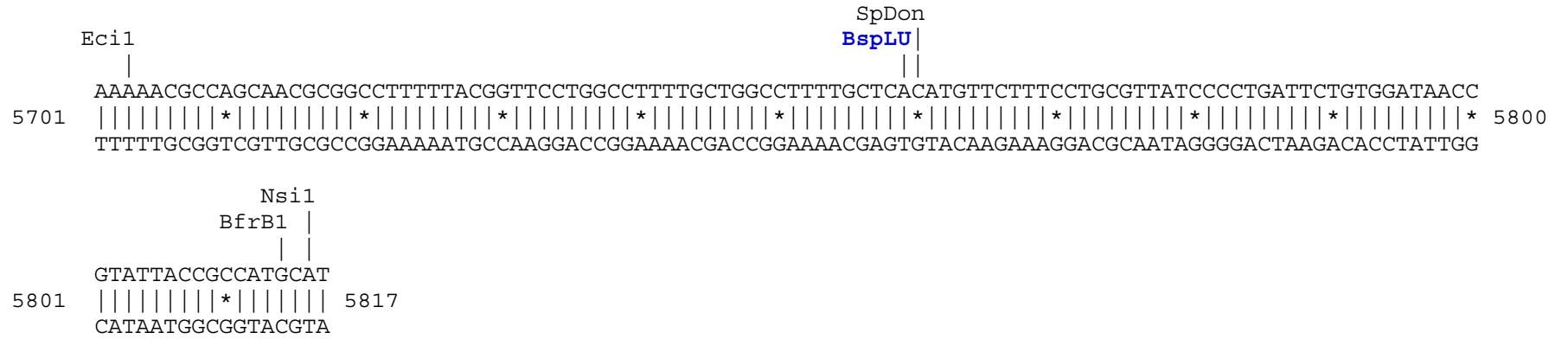
                                     AlwN1
                                     |
                                     BpuE1
                                     |
5301 CTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    GAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTACAGACAGAATGGCCCAACCTGAGTTCTGCT

                                     ApaL1
                                     |
                                     BseY1
                                     |
5401 TAGTTACCGGATAAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
    ATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCG

                                     BciV1
                                     |
                                     Eci1
                                     |
                                     BssS1
                                     |
5501 GTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
    CACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTTCGCCCTCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGG

                                     SpAcc
                                     |
                                     Drd1
                                     |
                                     BpuE1
                                     |
                                     SpAcc
                                     |
5601 AGGGGAAACGCCTGGTATCTTTATAGTCTGTCTGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
    TCCCCCTTTCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACC

```



Found:

| | | | | | | | | | | | | | |
|-------------|-------------|-------------|--------------|-------------|--------------|-------------|-------------|--------------|-------------|--------------|--------------|--------------|-------------|
| Aat2 | Afe1 | Age1 | Ale1 | AlwN1 | ApaL1 | Ase1 | Avr2 | BamH1 | Bbs1 | Bcg1a | Bcg1b | BciV1 | Bcl1 |
| BfrB1 | BfuA1 | Bgl1 | Bgl2 | BmgB1 | Bmr1 | Bpm1 | Bpu10 | BpuE1 | Bsa1 | BsaB1 | BsaXa | BsaXb | BseR1 |
| BseY1 | Bsg1 | Bsm1 | BspE1 | BspH1 | BspLU | BspM1 | BsrB1 | BsrD1 | BsrG1 | BssS1 | BstAP | BstB1 | BstE2 |
| Bsu36 | BtgZ1 | Bts1 | Cla1 | Dra1 | Dra3 | Drd1 | Eag1 | Ear1 | Eci1 | Eco57 | EcoN1 | EcoRV | Fsp1 |
| Hpa1 | Kas1 | Mfe1 | Mlu1 | Msc1 | Nae1 | Nar1 | Nco1 | Nde1 | NgoM4 | Nhe1 | Nsi1 | PflF1 | PflM1 |
| polyA | Psi1 | Pvu2 | Rsr2 | Sac2 | Sall1 | Sap1 | Sca1 | SexA1 | Sfi1 | Sma1 | SnaB1 | SpAcc | SpDon |
| Sph1 | Ssp1 | Stu1 | Xba1 | Xcm1 | Xho1 | Xmn1 | | | | | | | |

Unique:

| | | | | | | | | | | | | | |
|--------------|-------------|-------------|--------------|-------------|--------------|--------------|-------------|-------------|--------------|--------------|--------------|-------------|--------------|
| Afe1 | Age1 | Ase1 | BamH1 | Bbs1 | Bcg1a | Bcg1b | Bcl1 | Bgl2 | BspE1 | BspLU | BstB1 | Cla1 | EcoN1 |
| EcoRV | Fsp1 | Hpa1 | Mfe1 | Mlu1 | Nde1 | Nhe1 | Rsr2 | Sac2 | Sall1 | Sca1 | SexA1 | Sfi1 | Sma1 |
| SnaB1 | Stu1 | Xba1 | Xho1 | Xmn1 | | | | | | | | | |

Not found:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------|-------|-------|
| Aar1 | Acc65 | Acl1 | Afl2 | Ahd1 | Apa1 | Asc1 | AsiS1 | Bae1a | Bae1b | BbvC1 | Blp1 | BsiW1 | BsmB1 |
| BssH2 | BstX1 | BstZ1 | _Chi | EcoK | EcoR1 | ScFRT | Fse1 | FspA1 | Hind3 | I_Ceu | Kpn1 | loxP | Not1 |
| Nru1 | Pac1 | Pme1 | Pml1 | PshA1 | PspOM | Pst1 | Pvu1 | Sac1 | SanD1 | Sbf1 | Sgf1 | SgrA1 | Spe1 |
| Srf1 | Swa1 | T3RNA | T7RNA | T7Ter | PISce | | | | | | | | |

Excluded by site complexity:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Acc1 | Aci1 | Afl3 | Alu1 | Alw1 | Apo1 | Ava1 | Ava2 | Ban1 | Ban2 | Bbv1 | BceA1 | Bfa1 | Bme15 |
| BsaA1 | BsaH1 | BsaJ1 | BsaW1 | BseM2 | BsiE1 | BsiH1 | Bsl1 | BsmA1 | BsmF1 | Bsp12 | BspCa | BspCb | Bsr1 |
| BsrF1 | BssK1 | BstF5 | BstN1 | BstU1 | BstY1 | Btg1 | Cac8 | CviJ1 | Dde1 | Eae1 | EcoO1 | Fau1 | Fnu4H |
| Fok1 | Hae2 | Hae3 | Hga1 | Hha1 | Hinc2 | Hinf1 | HinP1 | Hpa2 | Hph1 | Hpy99 | Hpy1 | Hpy3 | HpyC3 |
| HpyC4 | HpyC5 | Mae3 | Mbo2 | Mnl1 | Mse1 | Msl1 | MspA1 | Mwo1 | Nci1 | Nla3 | Nla4 | Nsp1 | Ple1 |
| PpuM1 | Rsa1 | Sau3A | Sau96 | SfaN1 | Sfc1 | Sml1 | Sty1 | Taq1 | Tat1 | Tfi1 | Tse1 | Tsp45 | Tsp50 |
| TspR1 | | | | | | | | | | | | | |