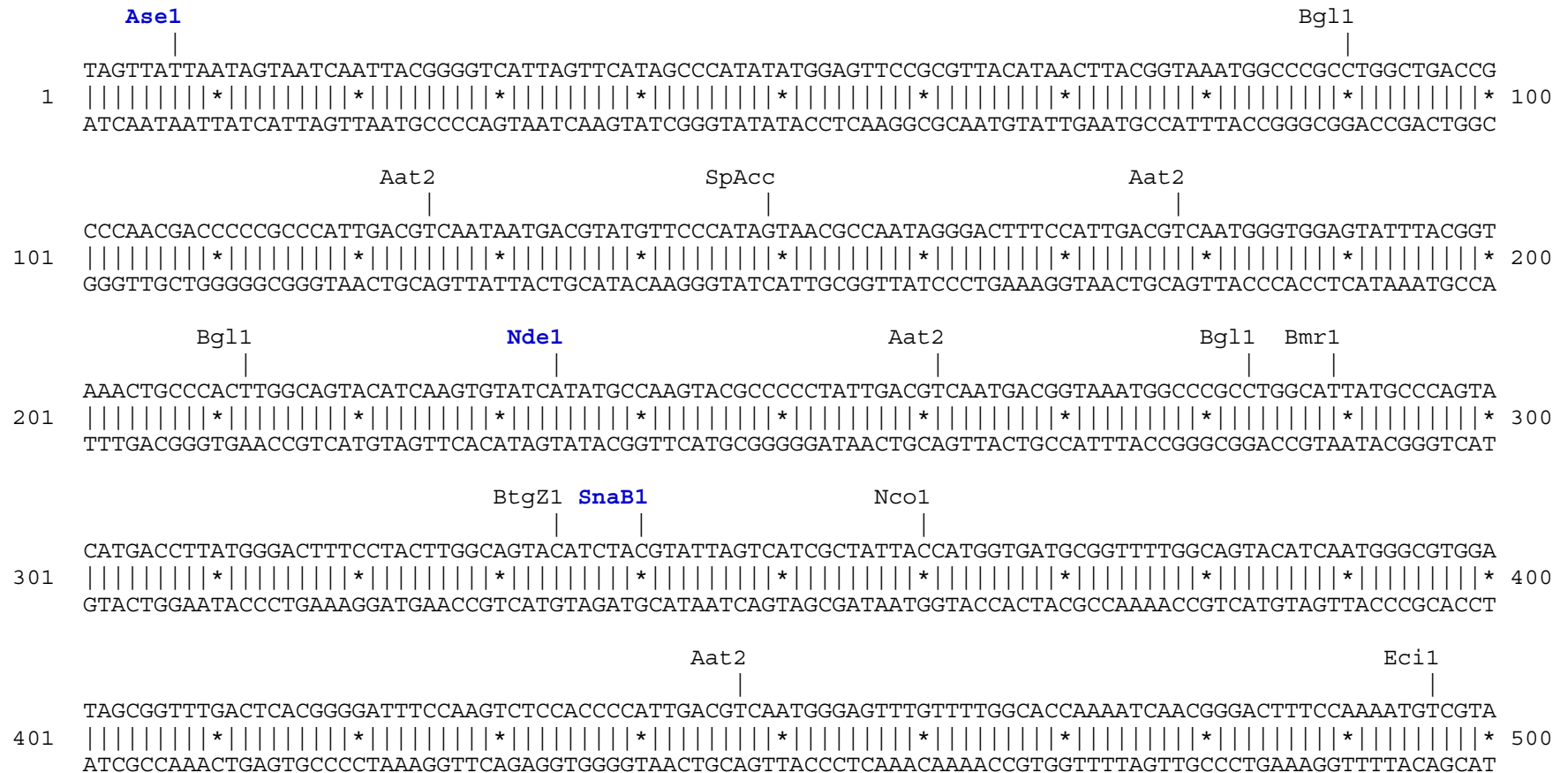
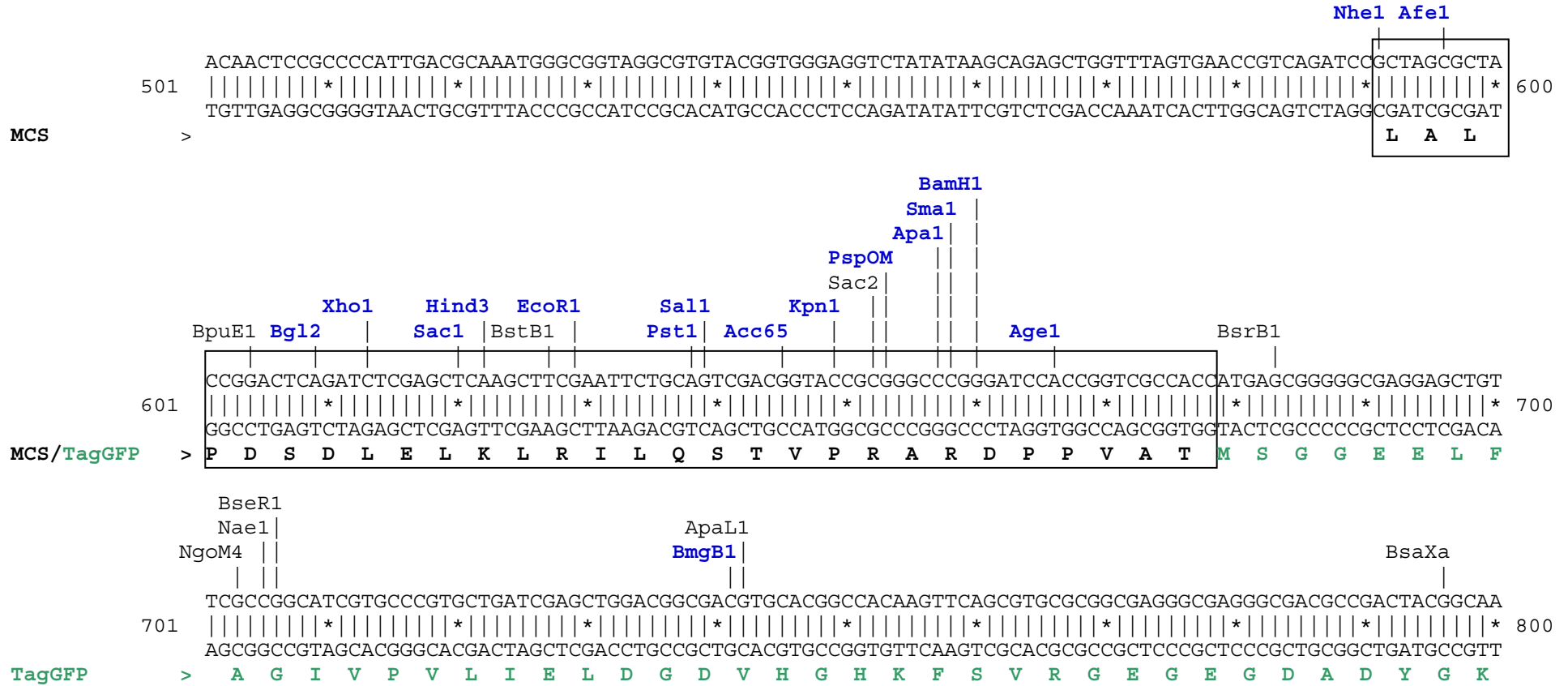


pTagGFP-N vector restriction map

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). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.






```

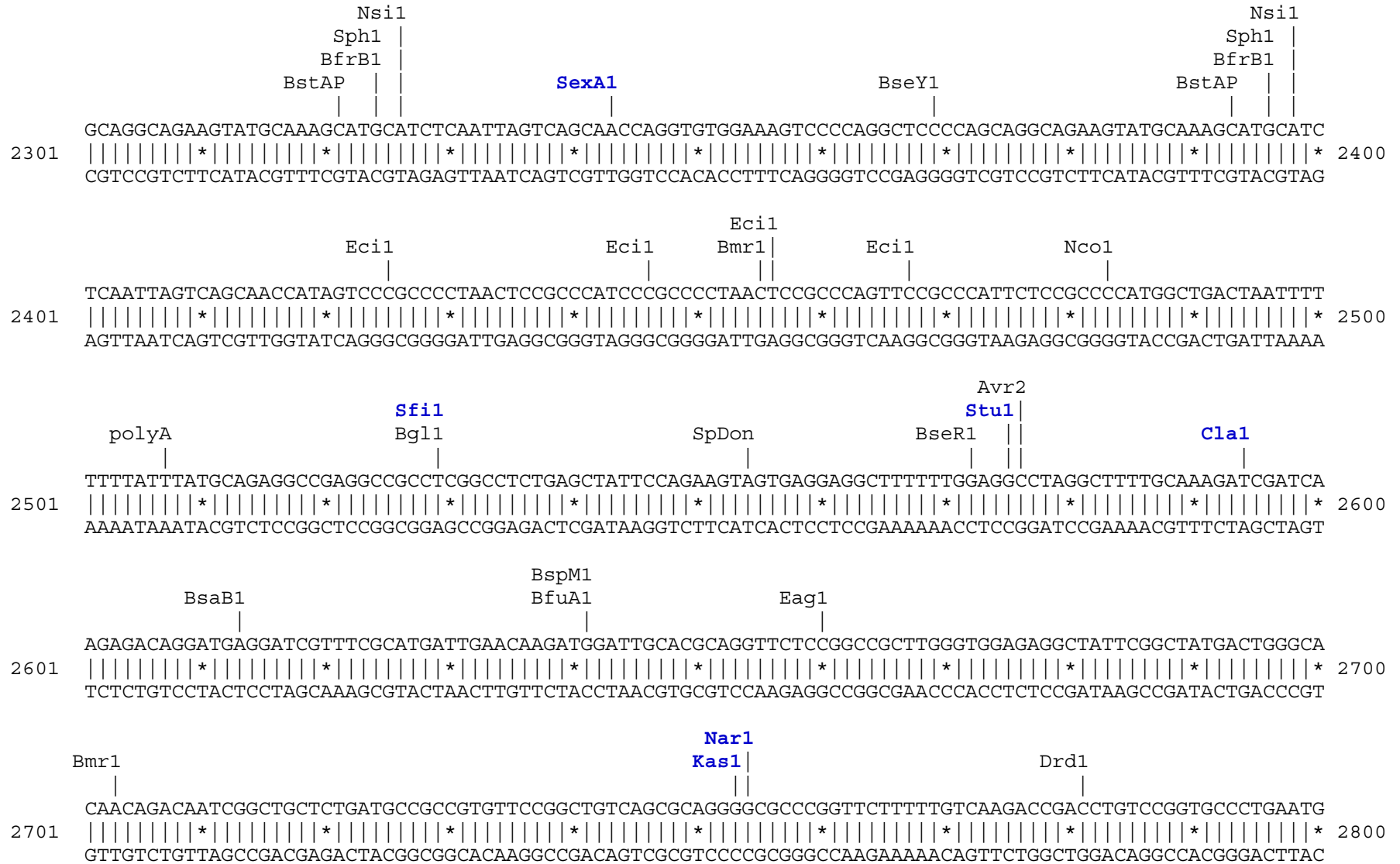
                                Eco57                                     NotI
                                Dra3                                     EagI
                                AlwNI Bpm1                             PflMI   BsrGI   SpDon
1301   GCAAGGACCGCAACGAGGCCCGGACCACATGGTGTCTCTGGAGTCCTTCAGCGCCTGCTGCCACACCCACGGCATGGACGAGCTGTACAGGTAAAGCGG 1400
       |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*
TagGFP >   K D R N E A R D H M V L L E S F S A C C H T H G M D E L Y R *
                                XbaI   BsaBI                             SpDon   DraI
1401   CCGCGACTCTAGATCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGA 1500
       |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*
GCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACT

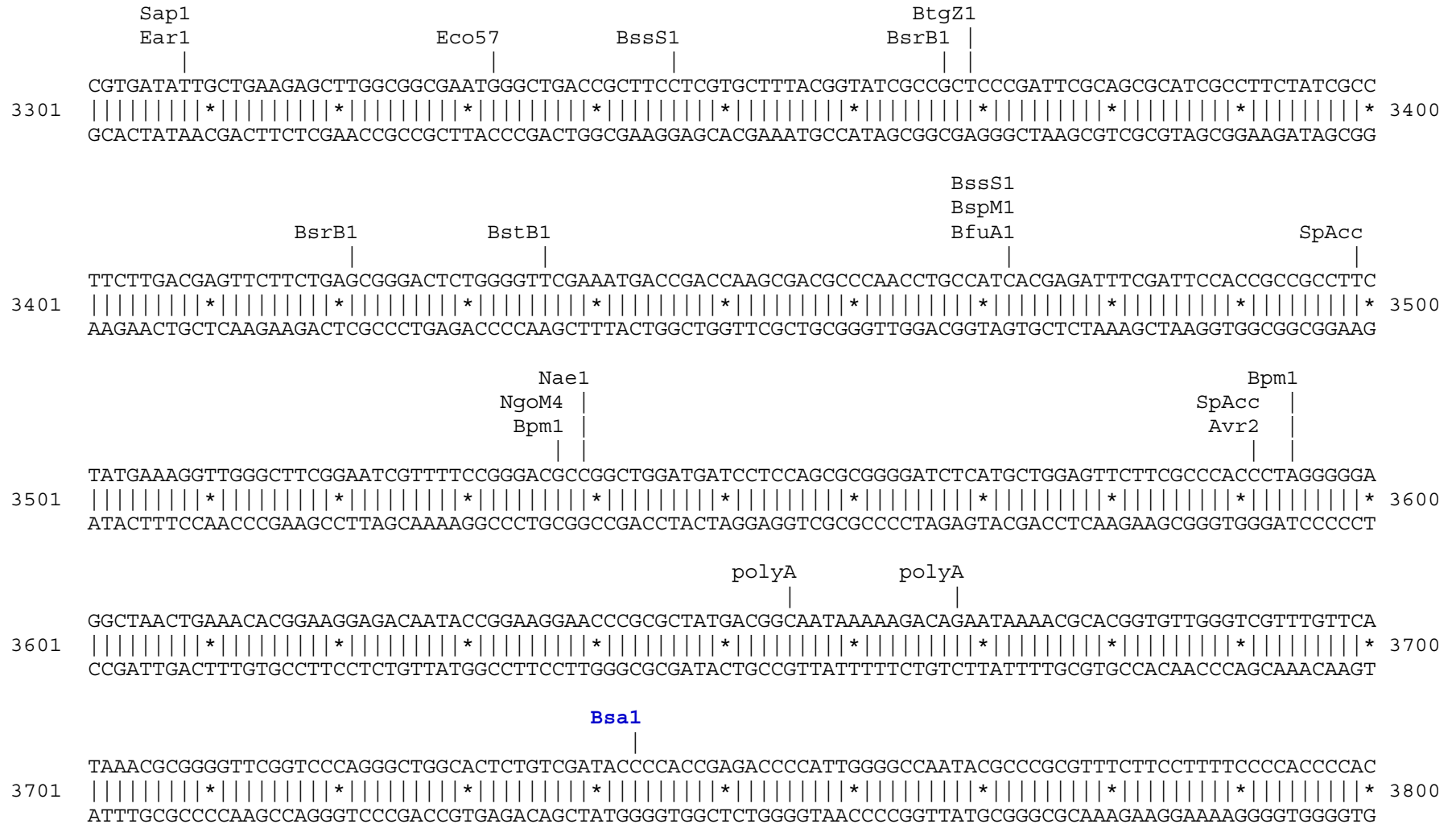
                                BsmI
MfeI |                               HpaI   polyA   PsaI   polyA                                   polyA                               BtsI BsmI
||  ||                               |||  |       |       |       |       |       |       |       |       |       |       |
1501   ATGCAATTGTTGTTGTTAACTTGTATTGTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCAGTCA 1600
       |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*
TACGTTAACCAACAACAATTGAACAAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTAAAGTGTAAATTTTTCGTAATAAAGTGACGT

                                AflII   SpDon                               SspI
1601   TTCTAGTTGTGGTTTGTCCAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGTTAAATCAG 1700
       |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*
AAGATCAACACCAAACAGGTTTGGAGTAGTTACATAGAATTCCGCATTTAACAATTCGCAATTATAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTC

                                PsaI
|
1701   CTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTCCAGTTTGAACAAGAGT 1800
       |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*
GAGTAAAAAATGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCA

```



SpAcc
BciV1
Eci1
BssS1

```

AGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCAGGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCA
4401 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4500
TCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCCTCTCGCGT

              SpAcc                Drd1                BpuE1
CGAGGGGAGCTTCCAGGGGGAAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGG
4501 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4600
GCTCCCTCGAAGGTCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCC

              SpAcc      Eci1                SpDon
GCGGAGCCTATGGA AAAACGCCAGCAACGCGGCCCTTTTACGGTTTCTGGCCTTTTGTGTCCTTTTGTGTCACATGTTTCTTTCTGCGTTATCCCCTGAT
4601 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4700
CGCCTCGGATACCCTTTTTGCGGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGGACTA

              Nsi1
              BfrB1 |
              |
TCTGTGGATAACCGTATTACCGCCATGCAT
4701 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4730
AGACACCTATTGGCATAATGGCGGTACGTA
    
```

Found:

- | | | | | | | | | | | | | | |
|-------------|--------------|-------------|--------------|-------------|-------------|--------------|-------------|-------------|--------------|--------------|--------------|--------------|-------------|
| Aat2 | Acc65 | Afe1 | Afl2 | Age1 | Ale1 | AlwN1 | Apa1 | ApaL1 | Ase1 | Avr2 | BamH1 | BciV1 | BfrB1 |
| BfuA1 | Bgl1 | Bgl2 | BmgB1 | Bmr1 | Bpm1 | Bpu10 | BpuE1 | Bsa1 | BsaB1 | BsaXa | BsaXb | BseR1 | BseY1 |
| Bsg1 | Bsm1 | BspH1 | BspLU | BspM1 | BsrB1 | BsrD1 | BsrG1 | BssS1 | BstAP | BstB1 | BstE2 | Bsu36 | BtgZ1 |
| Bts1 | Cla1 | Dra1 | Dra3 | Drd1 | Eag1 | Ear1 | Eci1 | Eco57 | EcoN1 | EcoR1 | Fsp1 | Hind3 | Hpa1 |
| Kas1 | Kpn1 | Mfe1 | Msc1 | Nae1 | Nar1 | Nco1 | Nde1 | NgoM4 | Nhe1 | Not1 | Nsi1 | PflF1 | PflM1 |

polyA PstI **PspOM** **PstI** Pvu2 **Rsr2** **SacI** Sac2 **SalI** Sap1 **SexA1** **SfiI** **SmaI** **SnaB1**
 SpAcc SpDon Sph1 Ssp1 **StuI** **XbaI** Xcm1 **XhoI** **XmnI**

Unique:

Acc65 **AfeI** **Afl2** **AgeI** **ApaI** **AseI** **BamHI** **Bgl2** **BmgB1** **Bpu10** **BsaI** **BspLU** **BsrD1** **BstE2**
Bts1 **ClaI** **EcoNI** **EcoRI** **FspI** **Hind3** **HpaI** **KasI** **KpnI** **MfeI** **MscI** **NarI** **NdeI** **NheI**
NotI **PflF1** **PspOM** **PstI** **Rsr2** **SacI** **SalI** **SexA1** **SfiI** **SmaI** **SnaB1** **StuI** **XbaI** **XhoI**
XmnI

Not found:

Aar1 Acl1 Ahd1 Asc1 AsiS1 BaeIa BaeIb Bbs1 BbvC1 Bcg1a Bcg1b Bcl1 Blp1 BsiW1
 BsmB1 BspE1 BssH2 BstX1 BstZ1 _Chi EcoK EcoRV ScFRT FseI FspA1 I_Ceu loxP Mlu1
 Nru1 Pac1 Pme1 Pml1 PshA1 Pvu1 SanD1 Sbf1 Sca1 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