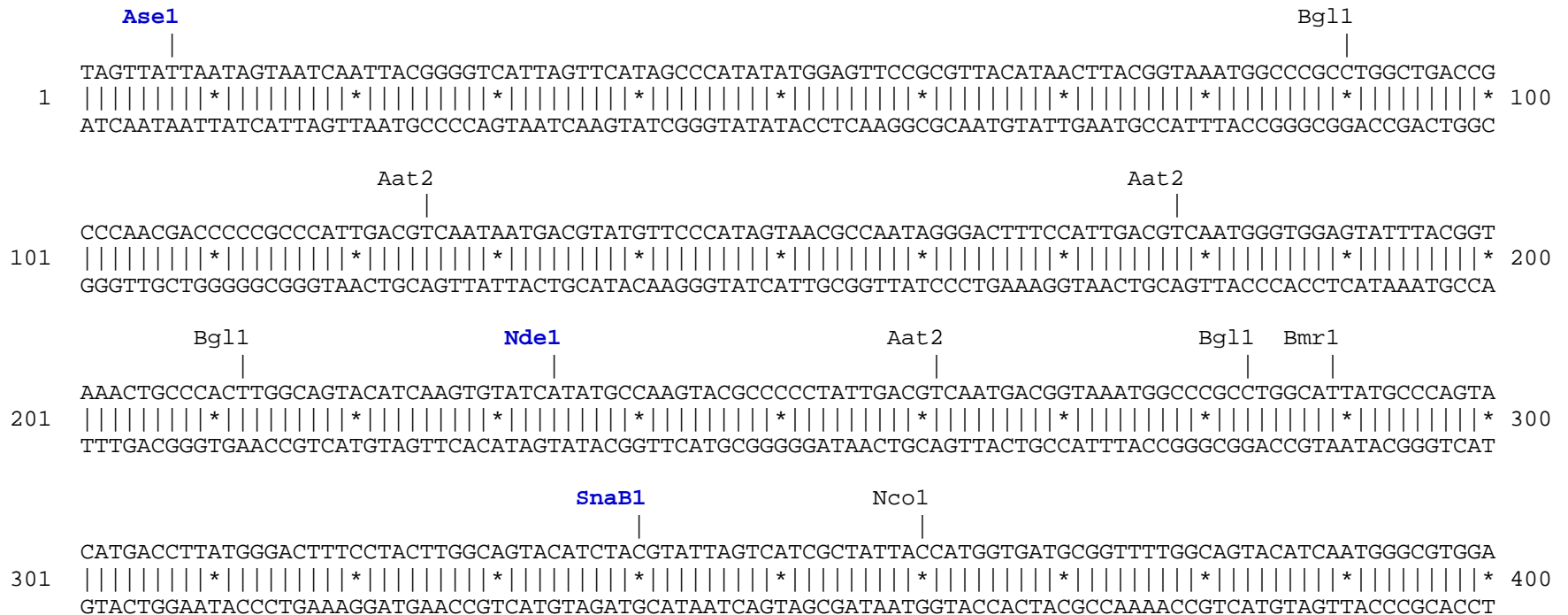


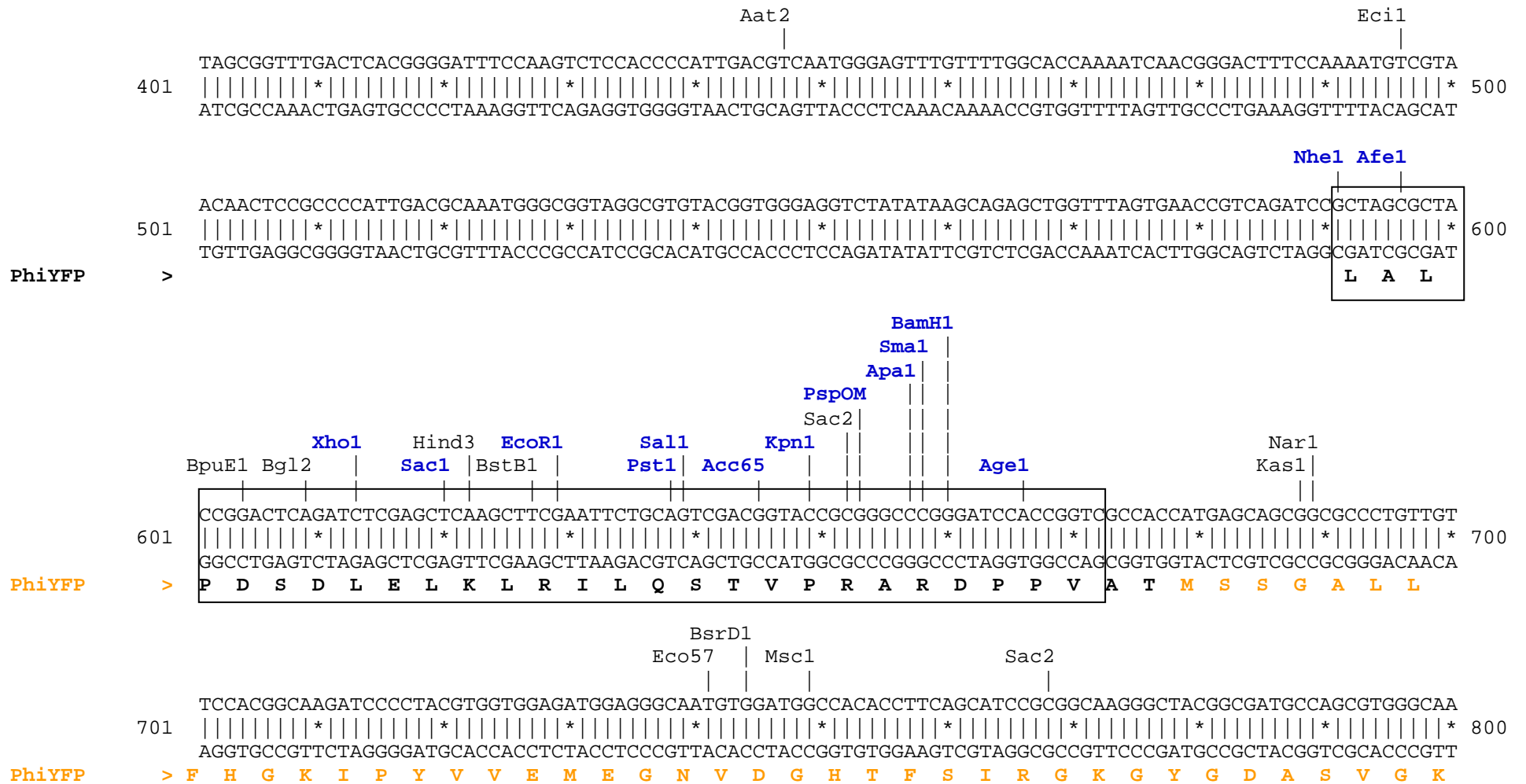
pPhi-Yellow-N vector restriction map

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 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 shown in frame, amino acids coded by MCS shown in black.






```

                                     Bsa1      BssH2      Eco57      Hind3      Bln1
GCAAGGATGTGACCGATCACCGCGATAATATGAGCCTGAAGGAGACCGTGC GCGCCGTTGGATTGCCGCAAGACCTACCTGTGAAGCTTAATTAGCTGAGC
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
CGTTCCTACACTGGCTAGTGGCGCTATTATACTCGGACTTCTCTGGCACGCGCGGCACCTAACGGCGTTCTGGATGGACACTTTCGAATTAATCGACTCG
PhiYFP > S K D V T D H R D N M S L K E T V R A V D C R K T Y L *

                                     Xba1      BsaB1
TTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGG
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
AACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAAC

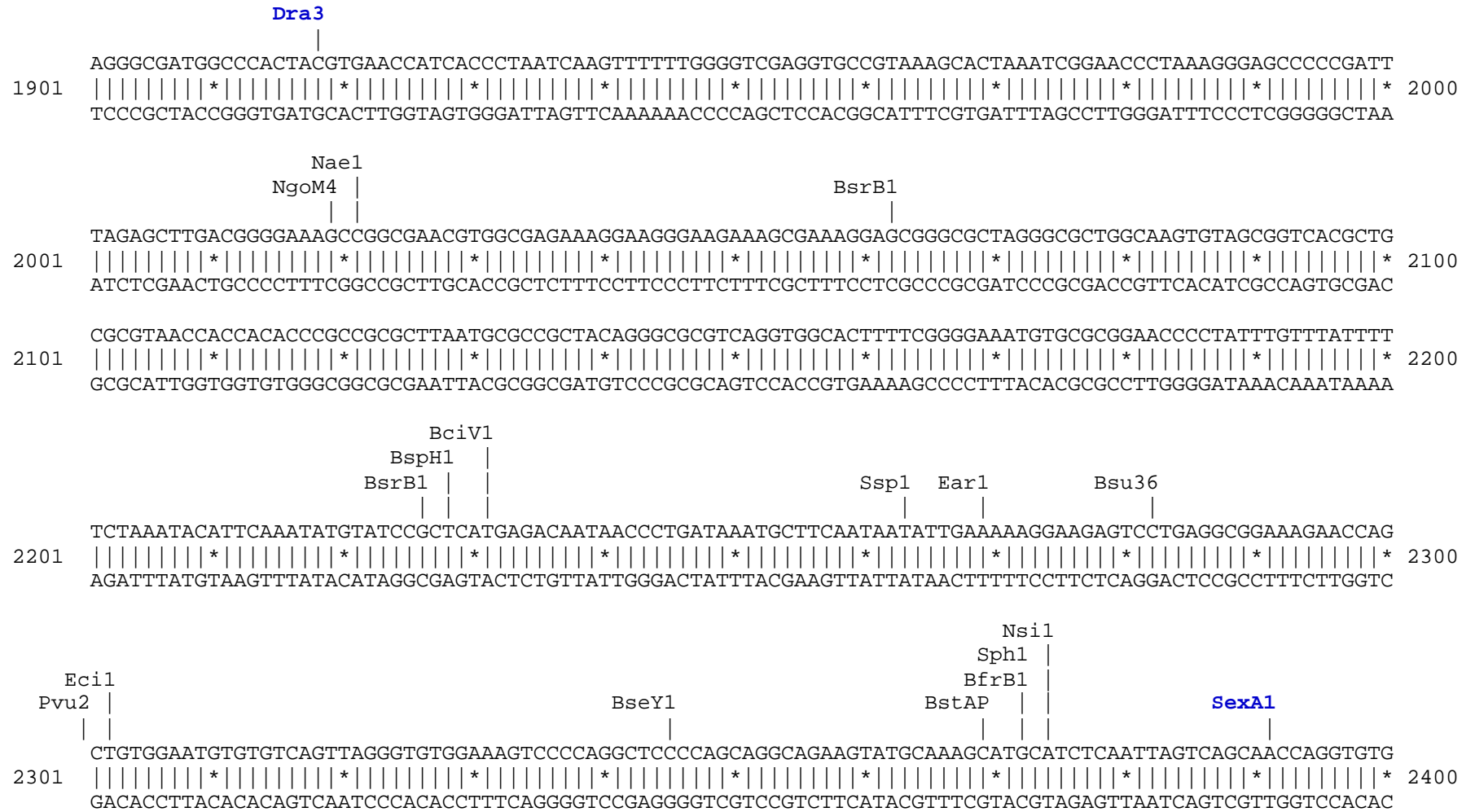
Dra1      Bsm1      Mfe1      Hpa1      Pst1
CTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAAATA
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
GAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAAATAACGTCGAATATTACCAATGTTTAT

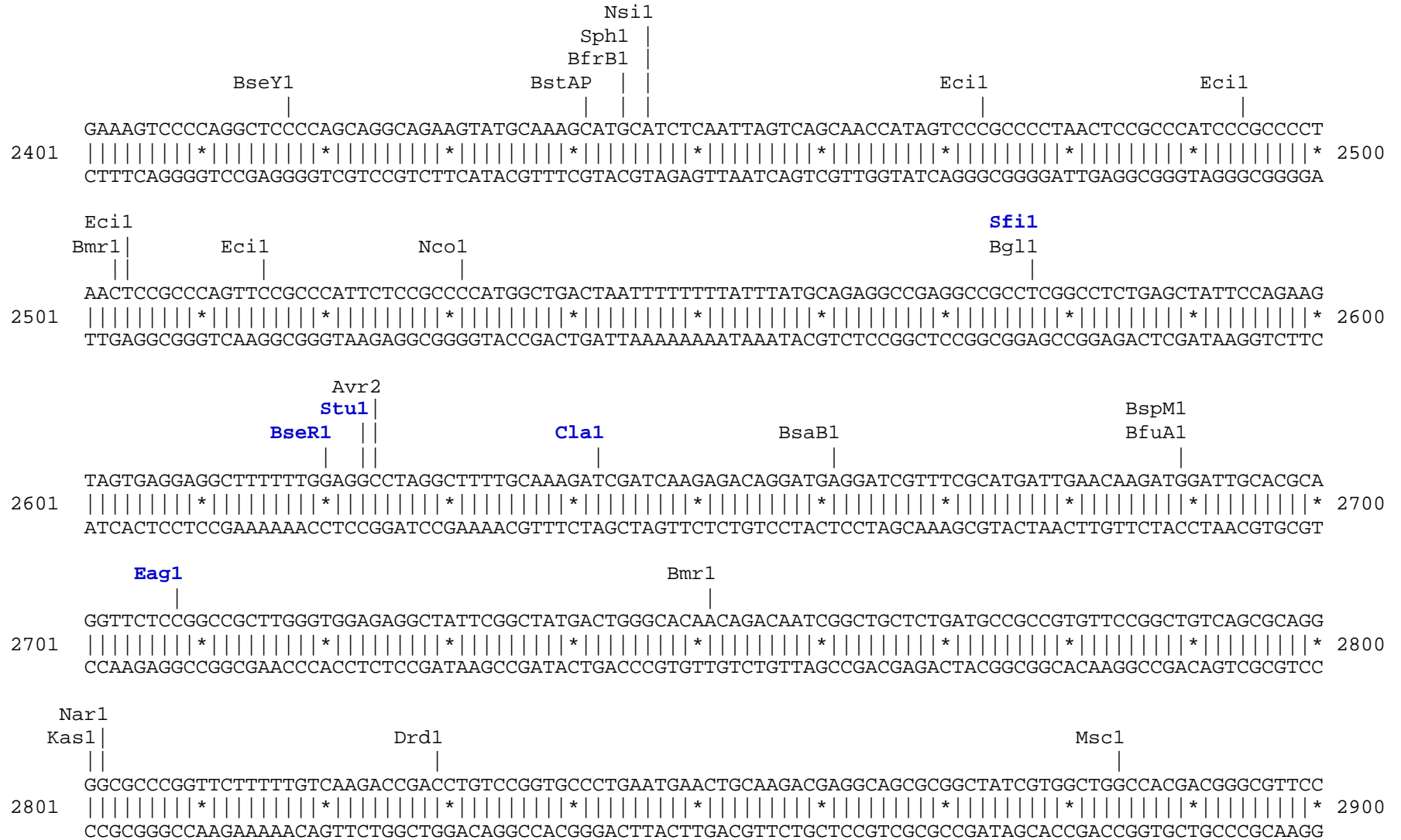
                                     Bts1 Bsm1      Afl12
AAGCAATAGCATCACAAATTTACAAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGT
1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
TTCGTTATCGTAGTGTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGGAGTAGTTACATAGAATTCCGCATTTAACA

Ssp1      Pst1
AAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAA
1701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
TTCGCAATTATAAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTT

                                     BsaXb      Drd1      BsaXa
GAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATC
1801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
CTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCCTTTTTGGCAGATAG

```






```

          BsrB1                      BsrB1          BstB1
          |                          |                |
3401 TTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
    AAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTT

          BssS1                      NaeI
          BspM1                      NgoM4
          BfuA1                      Bpm1
          |                          |
3501 GCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
    CGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGG

          Bpm1
          Avr2
          |
3601 TCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
    AGGTCGCGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTTGGGCGCGATACTG

          Bsa1
          |
3701 GGCAATAAAAAGACAGAATAAAAACGCACGGTGTGGGTCGTTTGTTCATAAACGCGGGGTTCCGGTCCCAGGGCTGGCACTCTGTGATAACCCACCGAGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
    CCGTTATTTTTCTGTCTTATTTTTCGCTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCT

3801 CCCCATTGGGGCCAATACGCCCAGTTTCTTCCTTTTCCCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
    GGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTC

          BstAP
          AlwN1          Bsu36          DraI          DraI
          |              |              |              |
3901 GCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
    CGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGA

```



```

BspH1
|
4001 CATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
GTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCAT

Eco57
|
4101 ATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
TAGACGACGAACGTTTTGTTTTTGGTGGCGATGGTTCGCCACCAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAGGCTTCCATTGACCGAAGTCGT

4201 GAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCCTTCAAGAAGTCTGTAGCACCGCTACATACTCGCTCTGCTAATCCT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGA

AlwN1
|
BpuE1
|
4301 GTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAAGGCGCAGCGGTCCGGGCTGAACGGGG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
CAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCC

ApaL1
|
BseY1
|
4401 GGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
CCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCGACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTT

BciV1
|
EciI
|
BssS1
|
4501 AGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCCGGTT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
TCCGCTGTCCATAGGCCATTTCGCGTCCCAGCCTTGCTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTCGCGGACCATAGAAATATCAGGACAGCCCAA

Drd1
|
BpuE1
|
EciI
|
4601 TCGCCACCTCTGACTTGAGCGTCGATTTTTGTTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTTACGGTTCTTGCC
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
AGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTTCGCCGAAAAAATGCCAAGGACCGG

```

```

                                     NsiI
                                   BfrB1 |
                                   | |
         BspLU
         |
TTTTGCTGGCCTTTTGTACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4701  | | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | | 4778
AAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAAATGGCGGTACGTA

```

Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	BciV1	BfrB1
BfuA1	Bgl1	Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1
Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	BstE2	Bsu36	Bts1
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1
Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1	Pml1	Psi1	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	SgrA1	Sma1	SnaB1	Sph1	Ssp1
Stu1	Xba1	Xho1	Xmn1										

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	Ase1	BamH1	BsaXa	BsaXb	BseR1	BspLU	BssH2	Cla1
Dra3	Eag1	EcoR1	Fsp1	Hpa1	Kpn1	Mfe1	Nde1	Nhe1	PflF1	PflM1	PspOM	Pst1	Rsr2
Sac1	Sall	SexA1	Sfi1	SgrA1	Sma1	SnaB1	Stu1	Xba1	Xho1	Xmn1			

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	BcglA	Bcglb	Bcl1	BmgB1	Bpu10
BsiW1	BsmB1	BspE1	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP
Mlu1	Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	Spe1	Srf1	Swal
PISce	Xcm1												

Excluded by site complexity:

Acc1	Ac11	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													