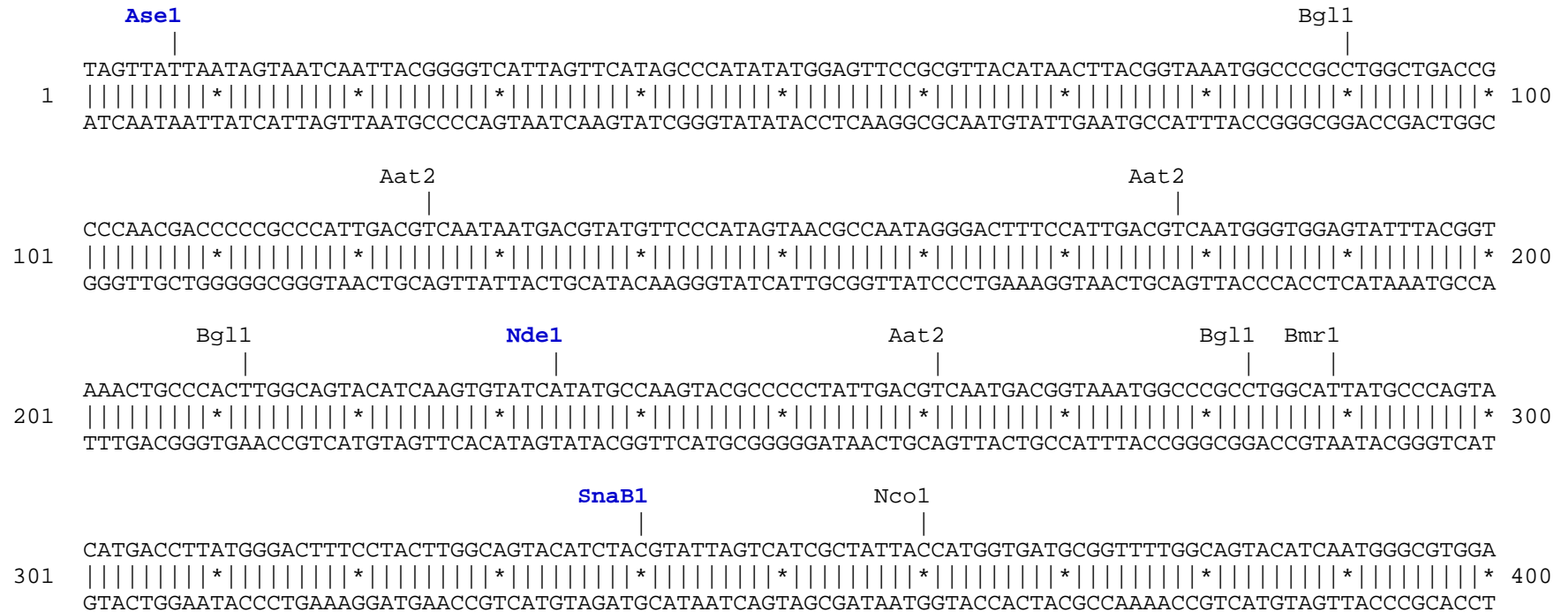


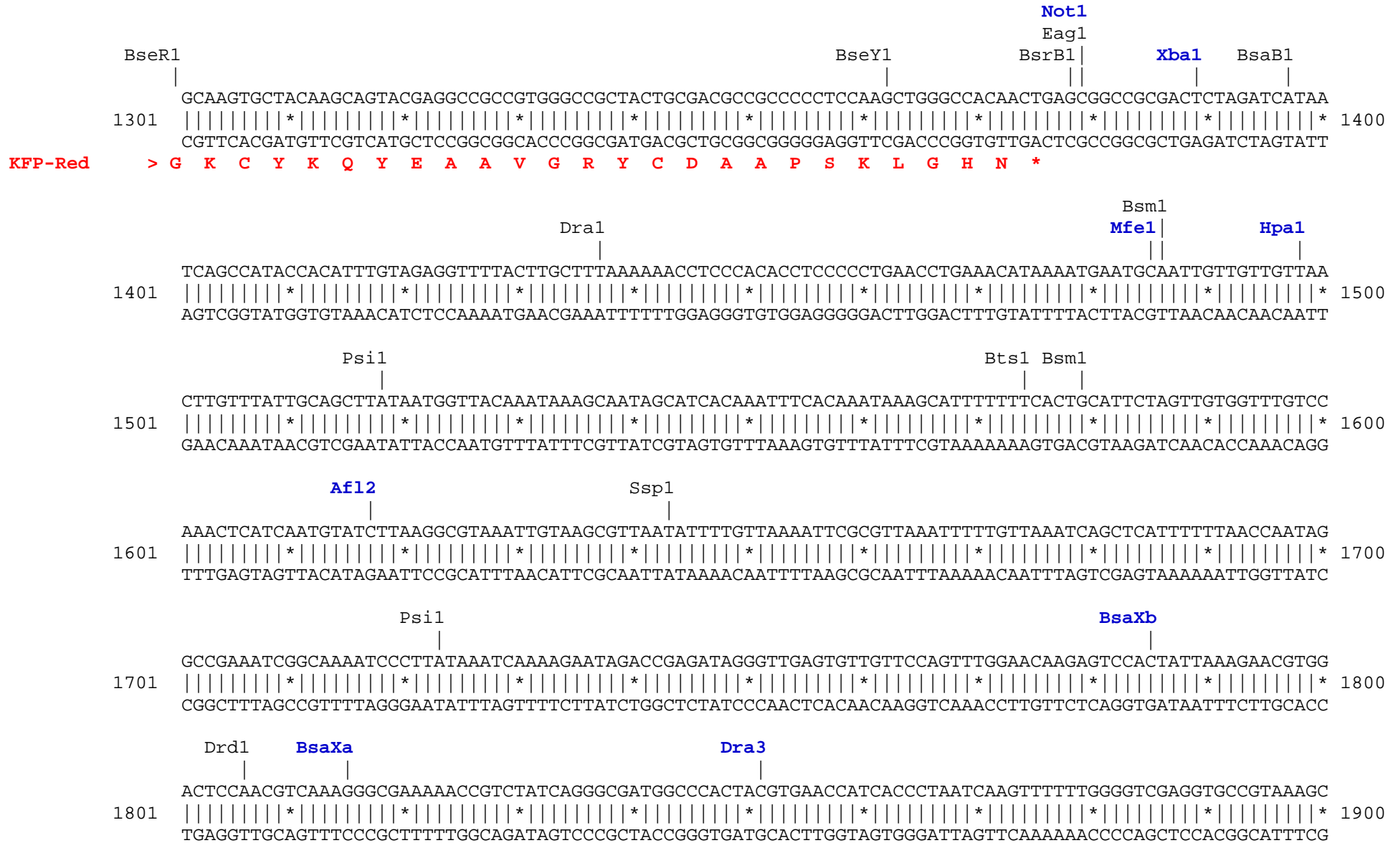
pKindling-Red-N vector restriction map

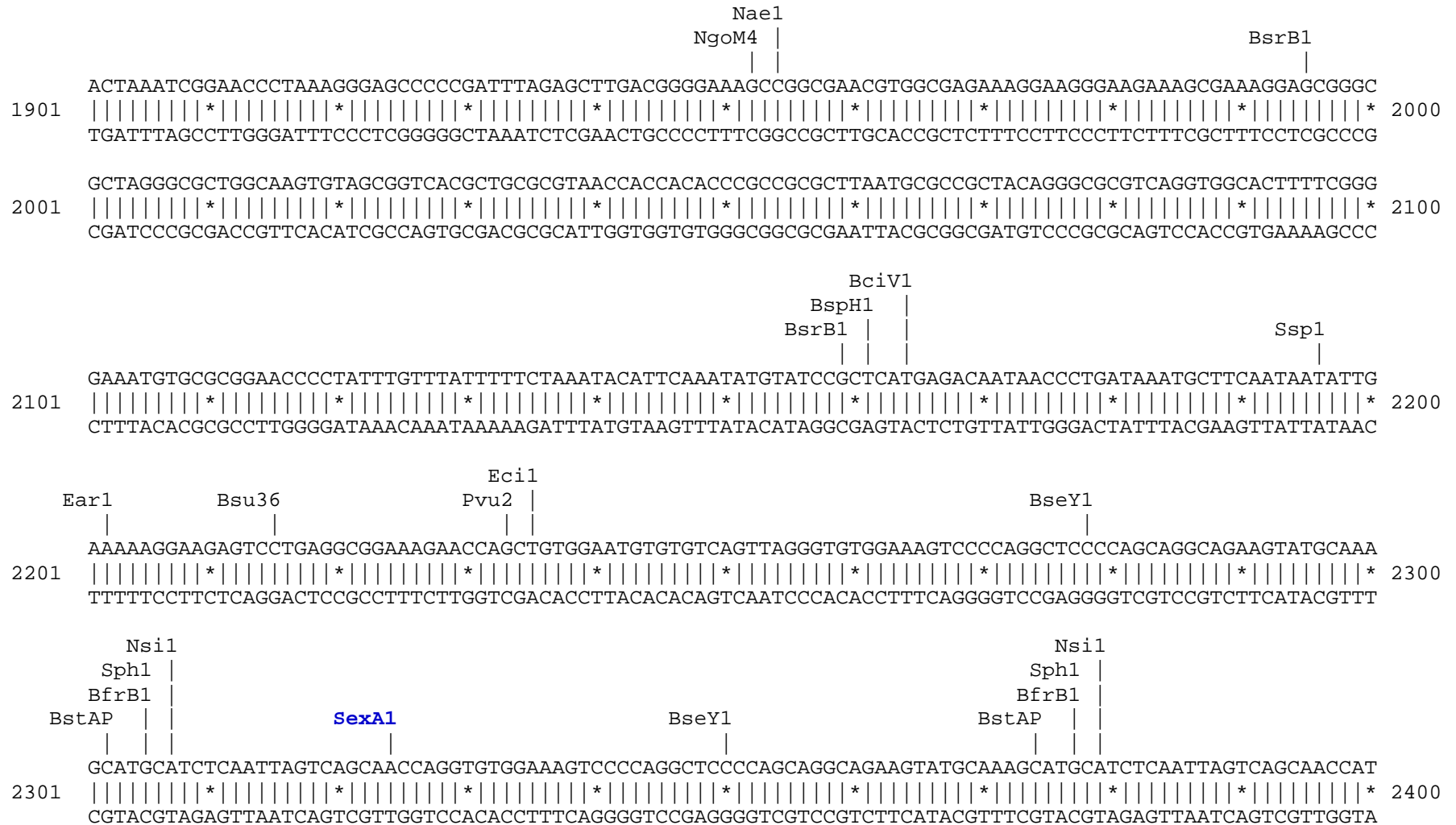
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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








```

                NaeI
              NgoM4 |
              Bpm1 |
                |
GAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCCTAGGGGGAGGCTAACTGAAACACGGAA
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
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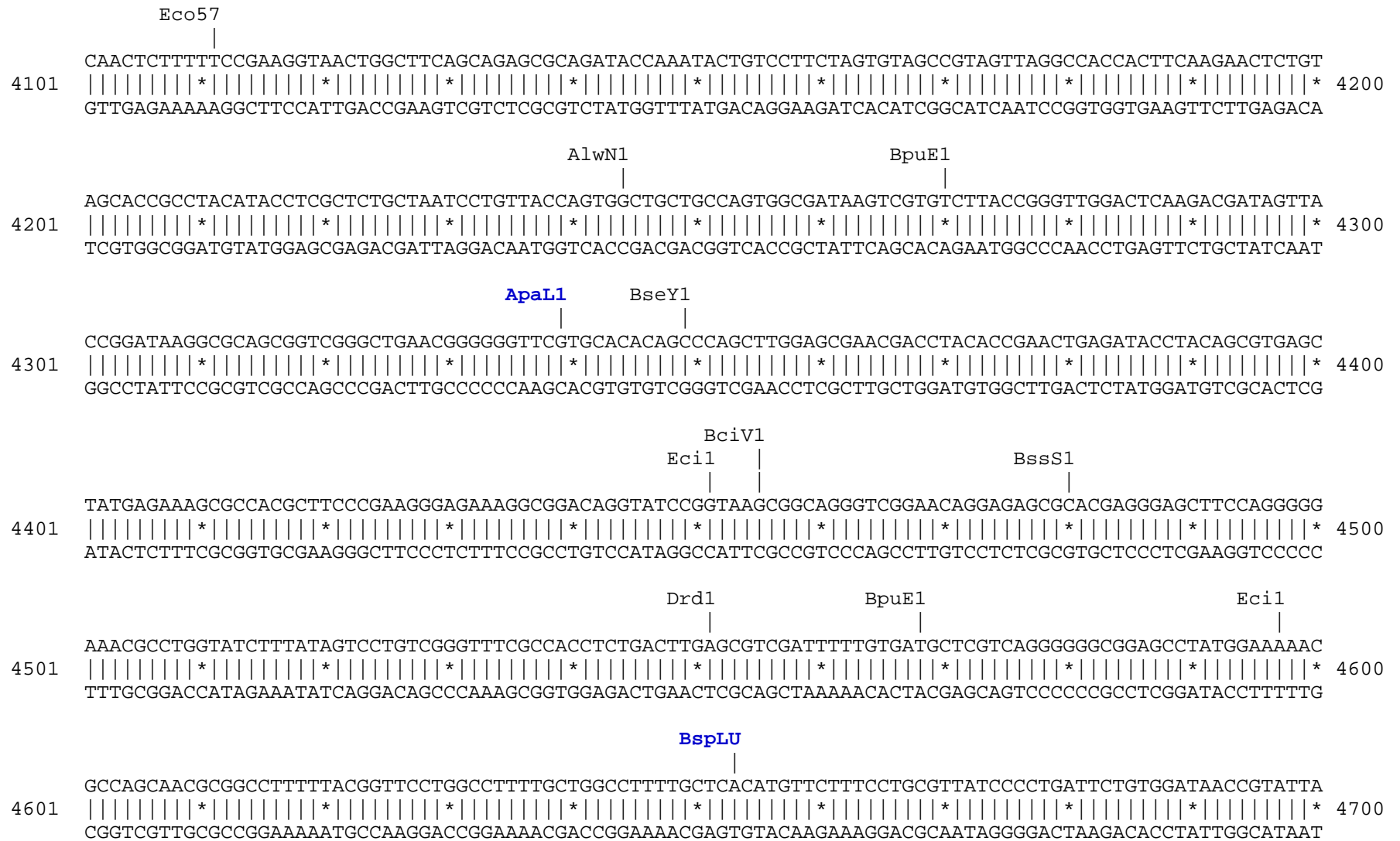
GGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCGTTTGTTCATAAACCGGGGGTTCGGTCC
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CCTCTGTTATGGCCTTCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGG

                BsaI
                |
CAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGCGTTTCTTCTTTTCCCCACCCACCCCAAGTTTCGGGTGAAG
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
GTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTC

                BstAP
                AlwNI
                Bsu36
                DraI
                DraI
GCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAA
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
CGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTT

                BspH1
                |
AAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAA
3901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
TTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTT

                BpuE1
                |
GGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTTGCTTGCAAACAAAAAACCCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTAC
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
CCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGCGGATGGTCCACCAAACAACGGCCTAGTTCTCGATG
```

```
      NsiI
      BfrB1 |
          | |
4701  CCGCCATGCAT
      |||||*| 4711
      GCGGTACGTA
```

Found:

Aar1	Aat2	Acc65	Afe1	Afl2	Age1	AlwN1	Apa1	Apal1	Ase1	Avr2	BamH1	Bcg1a	Bcg1b
BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	Bts1	Clal
Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1
Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	Psi1	PspOM	Pst1	Pvu2
Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	Sph1	Ssp1	Stu1	Xba1	Xho1

Unique:

Aar1	Acc65	Afe1	Afl2	Age1	Apa1	ApaL1	Ase1	BamH1	Bcg1a	Bcg1b	Bgl2	BsaXa	BsaXb
Bsg1	BspLU	BsrD1	BsrG1	Clal	Dra3	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1
Nar1	Nde1	Nhe1	Not1	PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1
SnaB1	Stu1	Xba1	Xho1										

Not found:

Acl1	Ahd1	Ale1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcl1	Blp1	BmgB1	Bpu10	BsiW1
BsmB1	BspE1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu
loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	Pml1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1
Spe1	Srf1	Swal	PISce	Xcm1	Xmn1								

Excluded by site complexity:

Acc1	Acil	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													