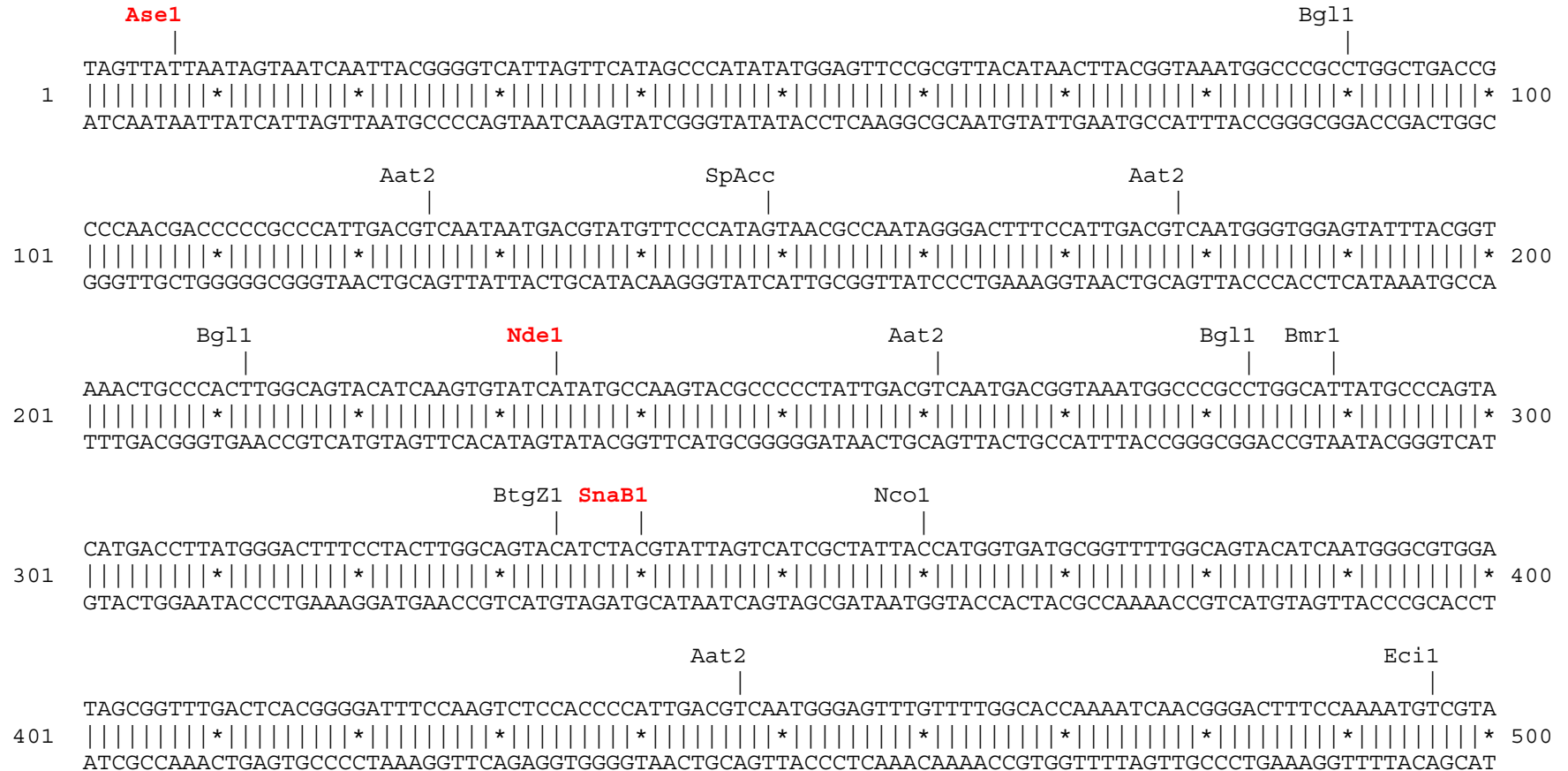
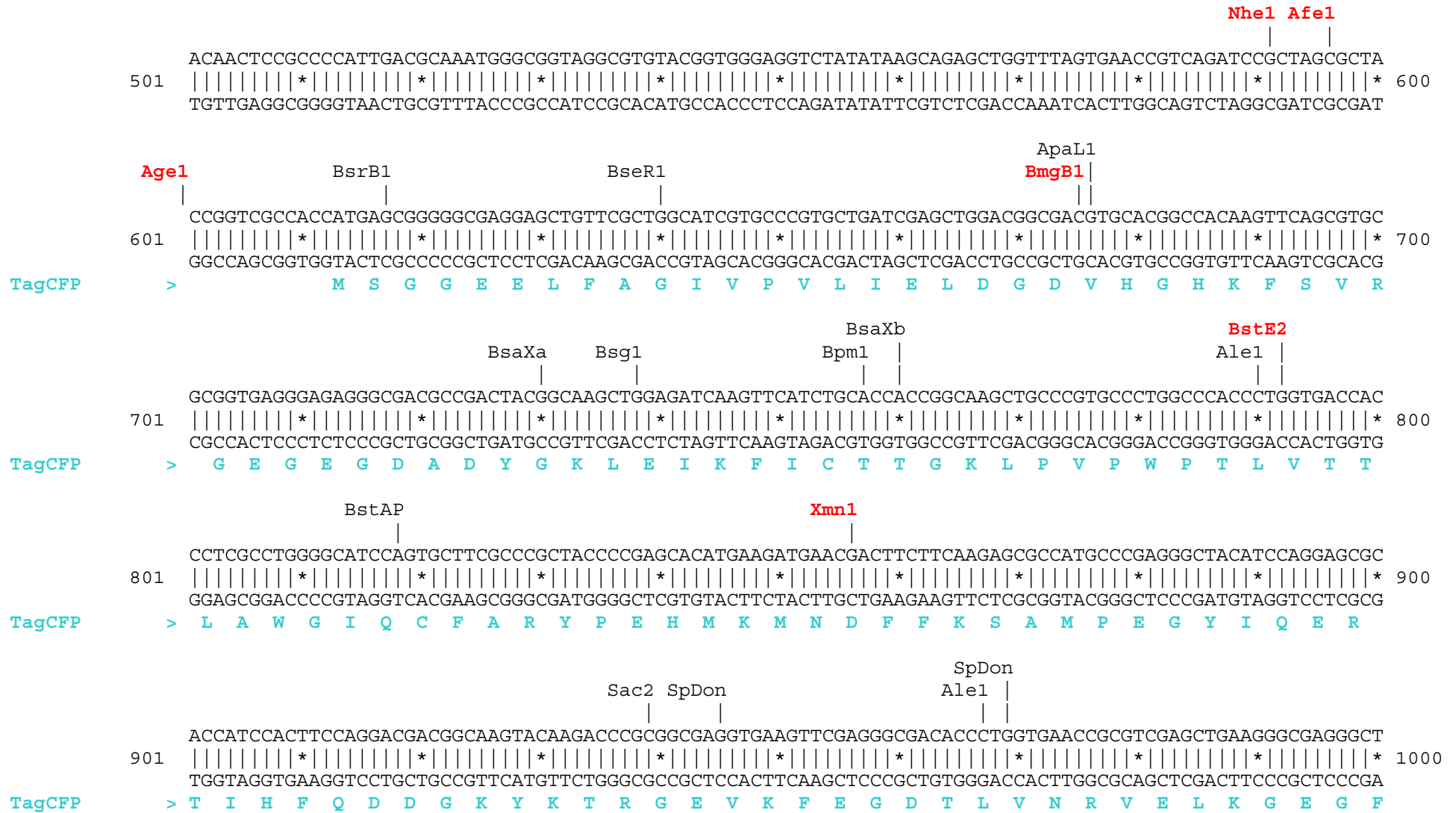


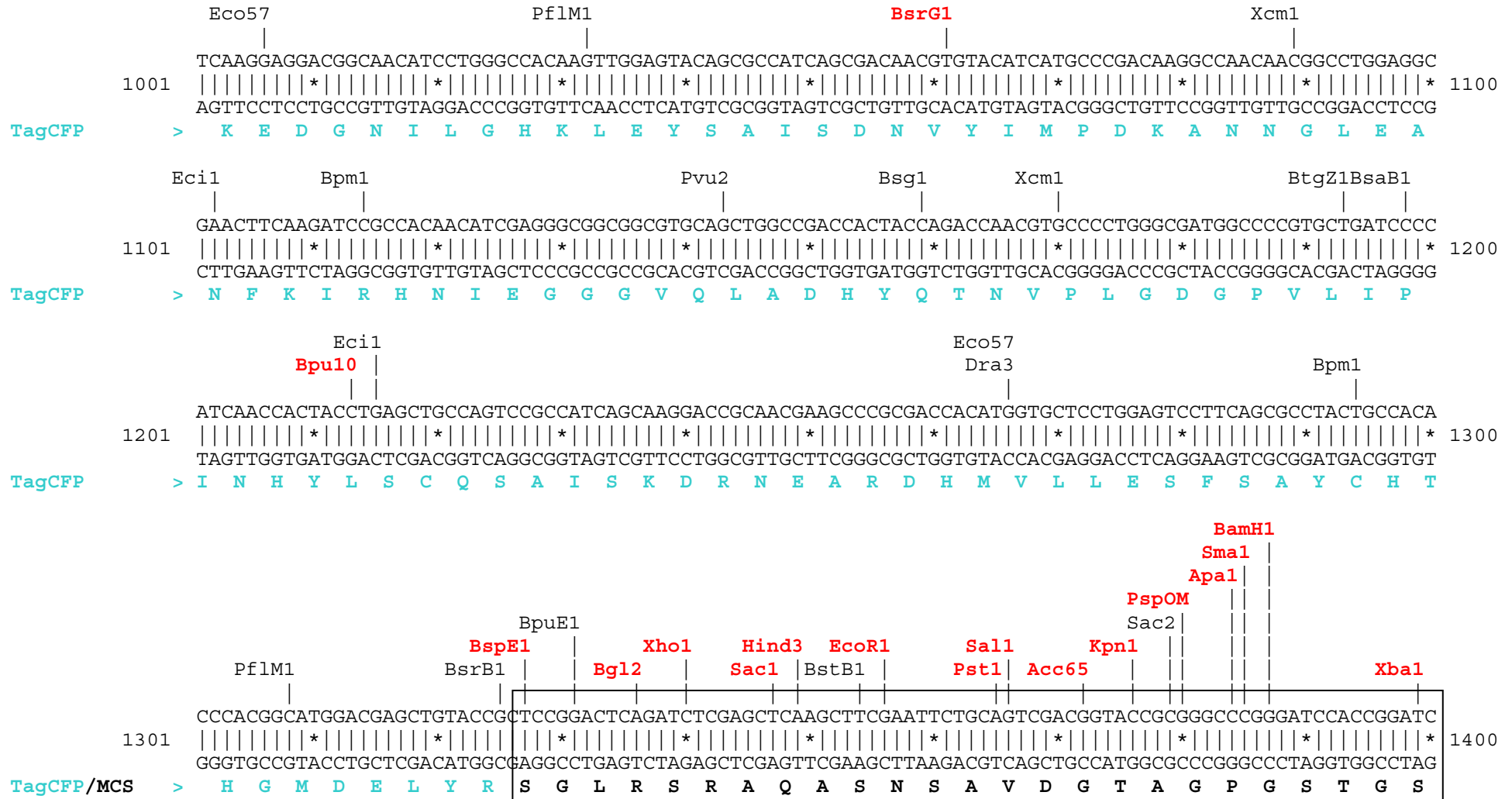
### pTagCFP-C vector restriction map

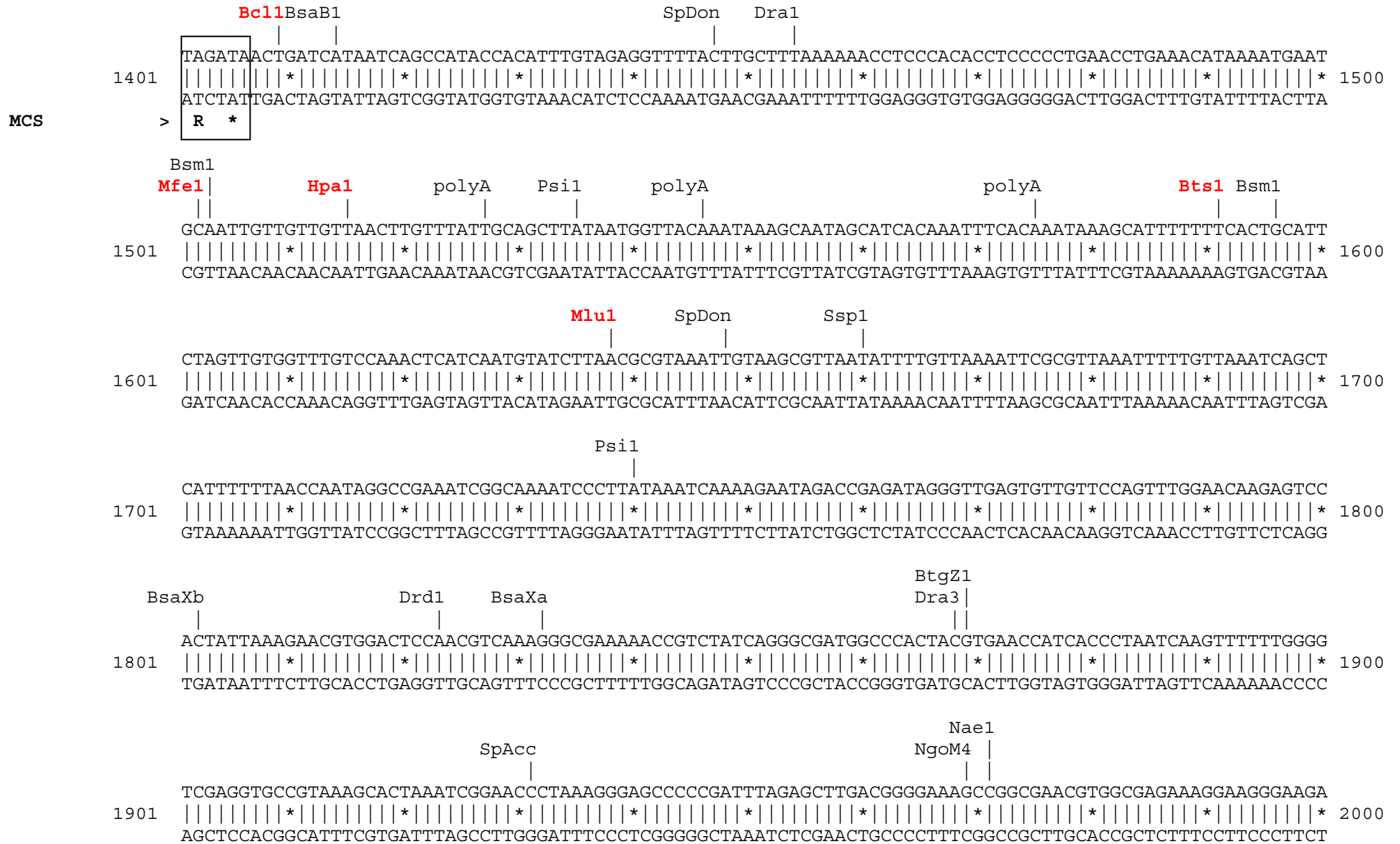
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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

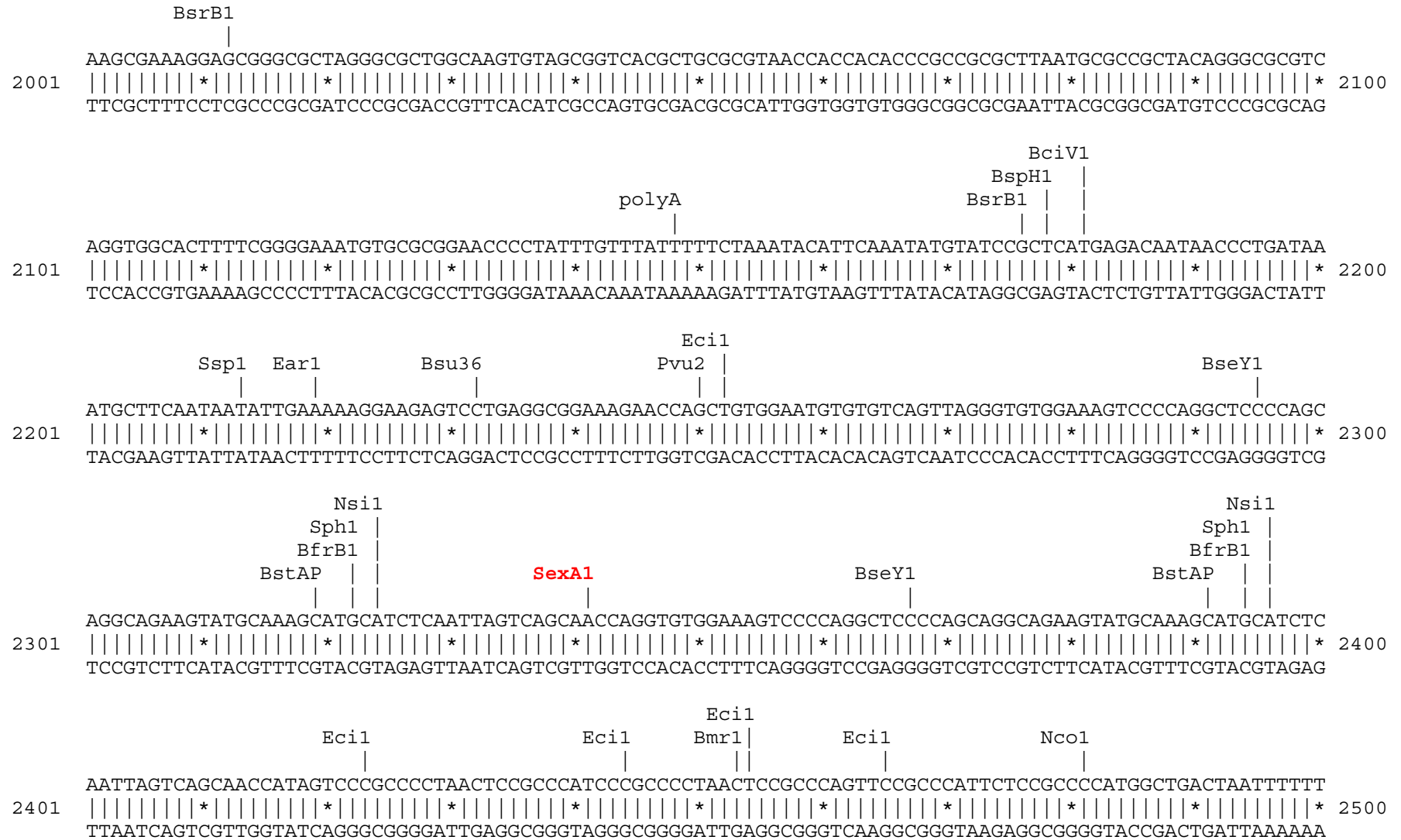
Unique sites shown in bold red. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). MCS sequence shown in frame, amino acids coded by MCS shown in black.



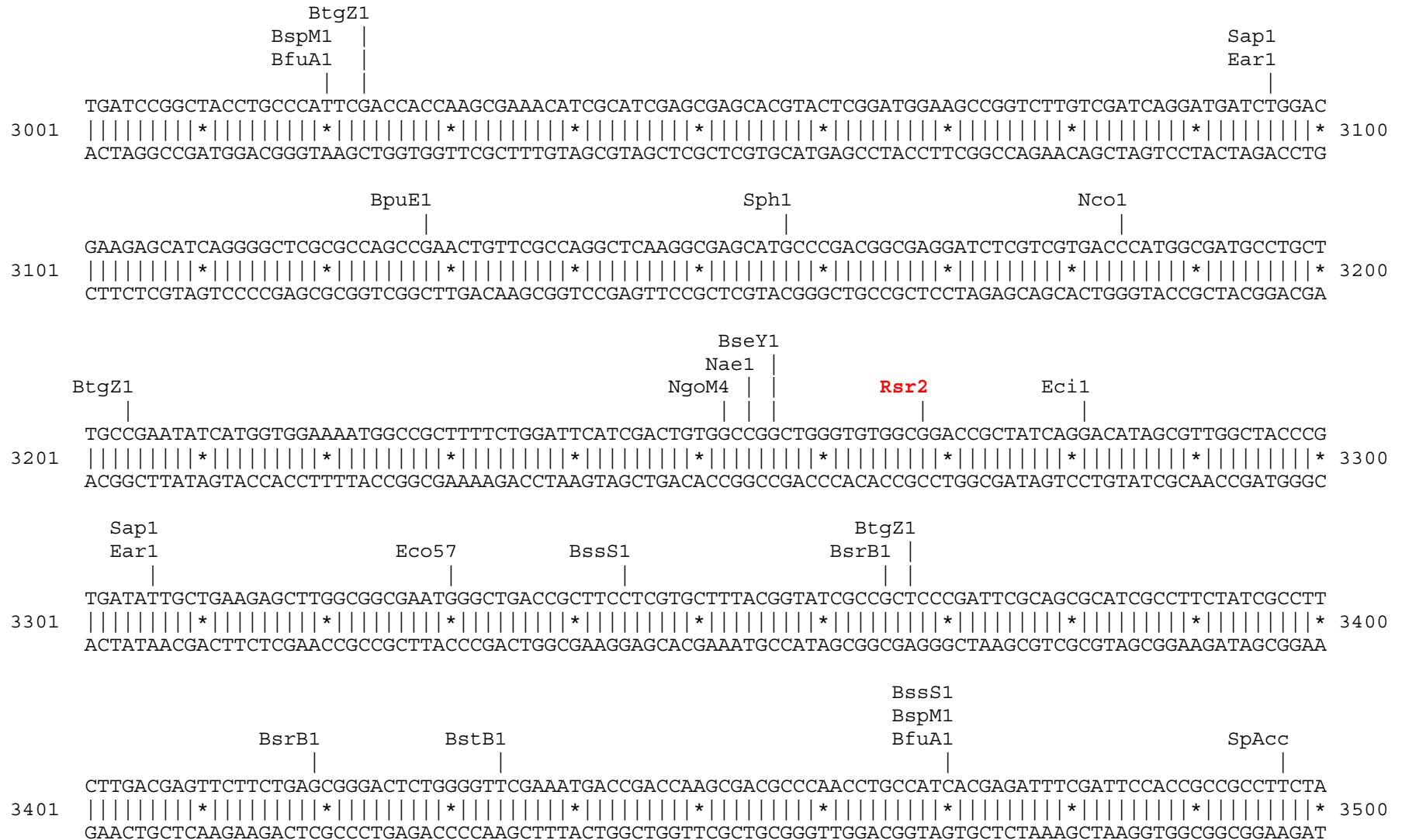












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                               NaeI
                               |
                    NgoM4  |
                    Bpm1  |
                               |
3501  TGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCTTAGGGGAGG
    |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3600
    ACTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCC

                                     polyA         polyA
                                     |             |
3601  CTAACTGAAACACGGAAGGAGACAATAACCGGAAGGAACCCGCGTATGACGGCAATAAAAAAGACAGAATAAAACGCACGGTGTGGGTCGTTTGTTCATA
    |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3700
    GATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTTCGTGCCACAACCCAGCAAACAAGTAT

                                     BsaI
                                     |
3701  AACGCGGGTTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCACCGAGACCCCCATTGGGGCCAATACGCCCGCGTTTTCTTCCTTTTCCCCACCCACCC
    |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3800
    TTGCGCCCCAAGCCAGGGTCCCAGCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGG

                                     BstAP      AlwN1        Bsu36                                     DraI
                                     |        |         |                                         |
3801  CCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAA
    |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3900
    GGGTCAAGCCACTTCCGGGTCCCGAGCGTCGGTTCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTT

                                     DraI        BspH1
                                     |        |
3901  CTTTCATTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC
    |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4000
    GAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGG

                                     BpuE1
                                     |
4001  CCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACACGCGGTGGTTTTGTTT
    |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4100
    GGATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTCGCCACCAAACAAA

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                                Eco57                                SpAcc
                                |                                |
4101  GCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCAC 4200
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTG

                                AlwN1                                BpuE1
                                |                                |
4201  CACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGG 4300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACC

                                ApaL1                                BseY1
                                |                                |
4301  ACTCAAGACGATAGTTACCGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAG 4400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTGCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTC

                                BciV1                                Eci1                                BssS1
                                |                                |                                |
4401  ATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACG 4500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCAGCCTTGTCTCTCGCGTGC

                                SpAcc                                Drd1                                BpuE1
                                |                                |                                |
4501  AGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGC 4600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCG

                                SpAcc                                Eci1                                SpDon                                BspLU
                                |                                |                                |                                |
4601  GGAGCCTATGGAAAAACGCCAGCAACGCGGCTTTTTACGGTTCTGGCCTTTTGTGGCCTTTTGTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTC 4700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCTCGGATACCTTTTTCGCGTTCGTCGCGGAAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAG

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                NsiI
                BfrB1 |
                | |
4701  TGTGGATAACCGTATTACCGCCATGCAT 4728
      |||*|||*|||
      ACACCTATTGGCATAATGGCGGTACGTA
  
```

**Found:**

Aat2	<b>Acc65</b>	<b>Afe1</b>	<b>Age1</b>	Ale1	AlwN1	<b>Apa1</b>	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	BciV1	<b>Bcl1</b>	BfrB1	
BfuA1	Bgl1	<b>Bgl2</b>	<b>BmgB1</b>	Bmr1	Bpm1	<b>Bpu10</b>	BpuE1	<b>Bsa1</b>	BsaB1	BsaXa	BsaXb	BseR1	BseY1	
Bsg1	Bsm1	<b>BspE1</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	BssS1	BstAP	BstB1	<b>BstE2</b>	Bsu36	
BtgZ1	<b>Bts1</b>	<b>Cla1</b>	Dra1	Dra3	Drd1	<b>Eag1</b>	Ear1	Eci1	Eco57	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	
	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Mlu1</b>	<b>Msc1</b>	Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	Nsi1	<b>PflF1</b>	PflM1
polyA	Psi1	<b>PspOM</b>	<b>Pst1</b>	Pvu2	<b>Rsr2</b>	<b>Sac1</b>	Sac2	<b>Sall</b>	Sap1	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>SnaB1</b>	
SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xba1</b>	Xcm1	<b>Xho1</b>	<b>Xmn1</b>						

**Unique:**

<b>Acc65</b>	<b>Afe1</b>	<b>Age1</b>	<b>Apa1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bcl1</b>	<b>Bgl2</b>	<b>BmgB1</b>	<b>Bpu10</b>	<b>Bsa1</b>	<b>BspE1</b>	<b>BspLU</b>	<b>BsrD1</b>
<b>BsrG1</b>	<b>BstE2</b>	<b>Bts1</b>	<b>Cla1</b>	<b>Eag1</b>	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Mlu1</b>	<b>Msc1</b>
<b>Nar1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>PflF1</b>	<b>PspOM</b>	<b>Pst1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sall</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>SnaB1</b>	<b>Stu1</b>
<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>											

**Not found:**

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Blp1	BsiW1
BsmB1	BssH2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP	Not1
Nru1	Pac1	Pme1	Pml1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal
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													