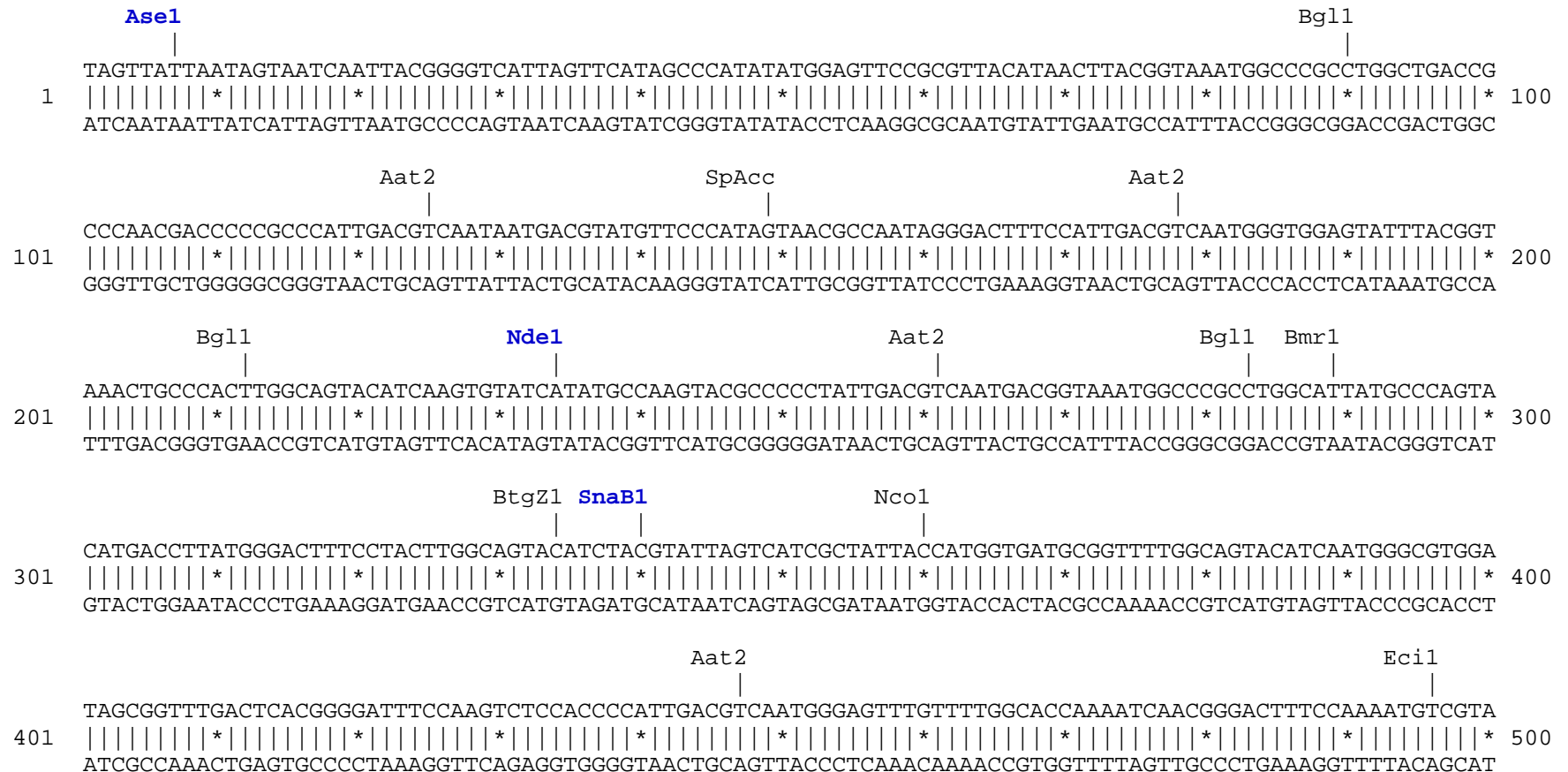


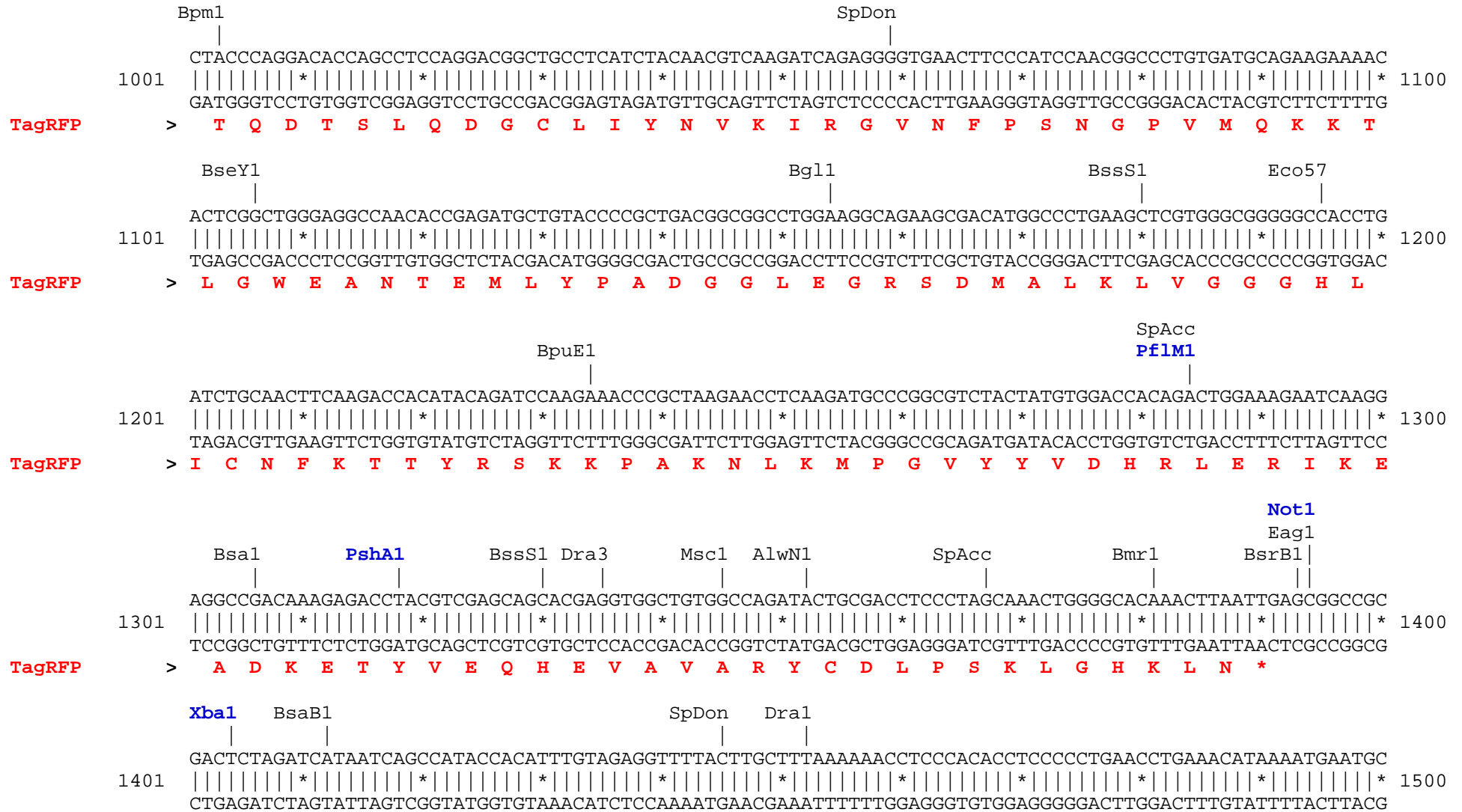
### pTagRFP-N vector restriction map

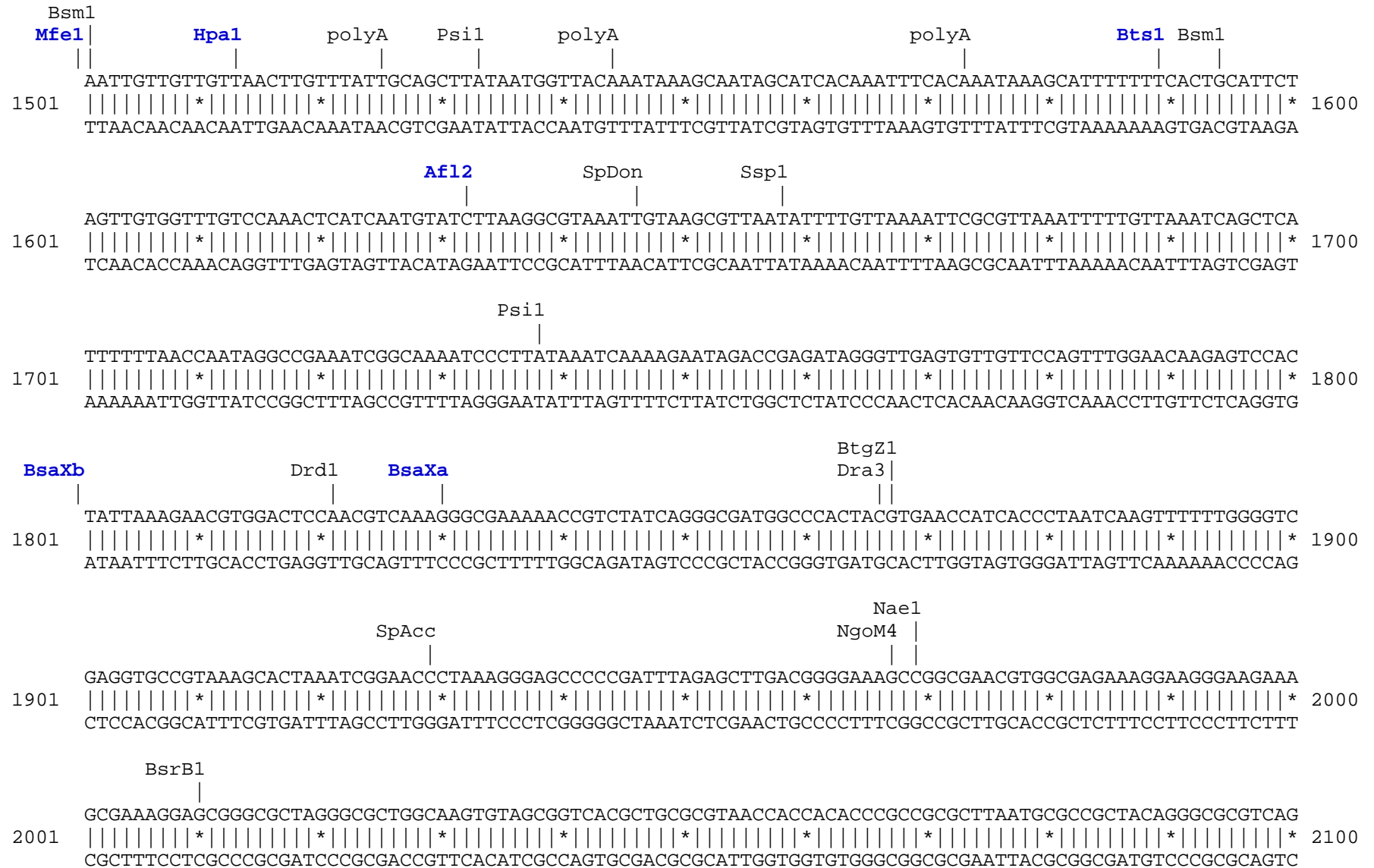
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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

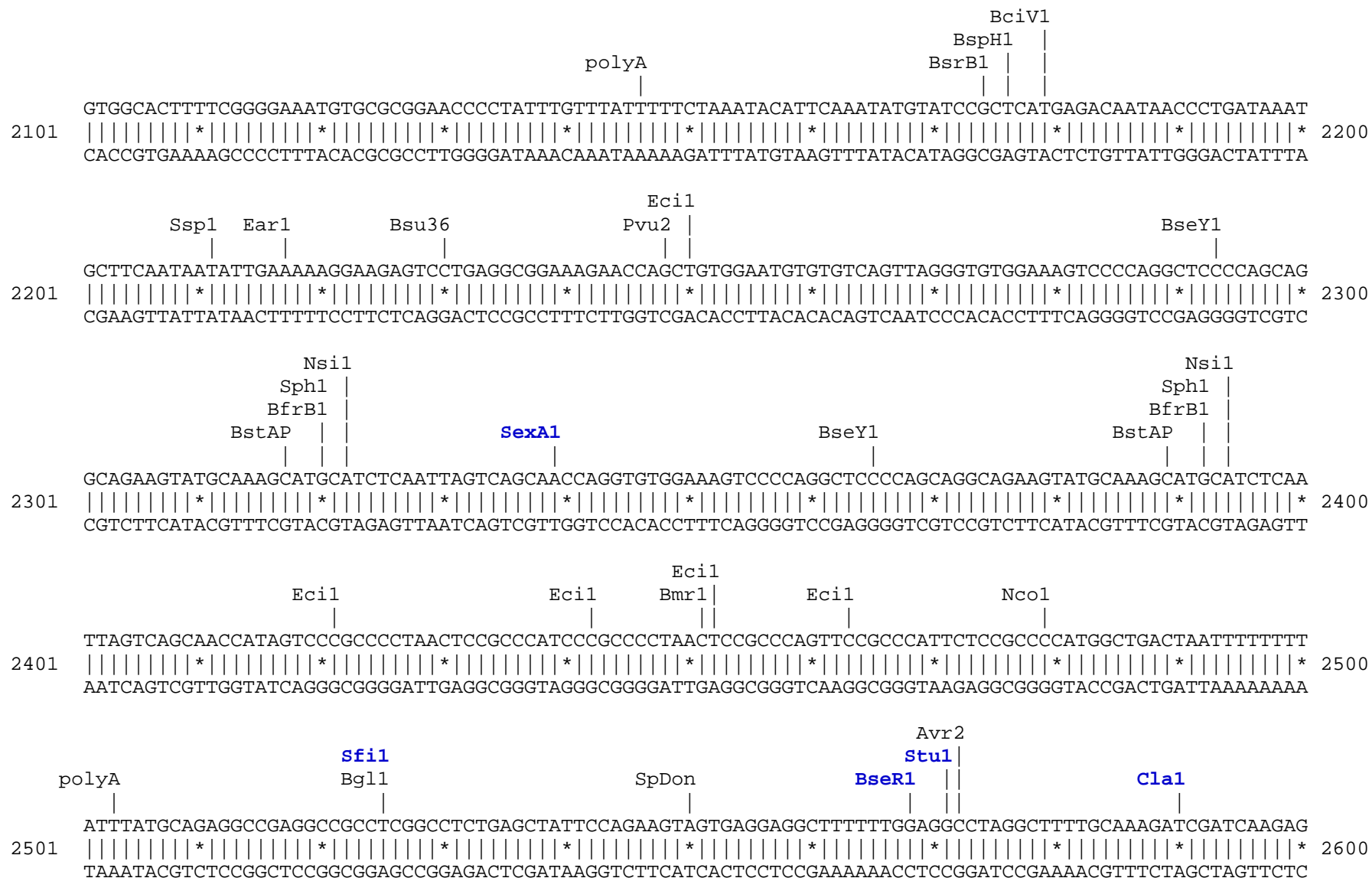
Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.

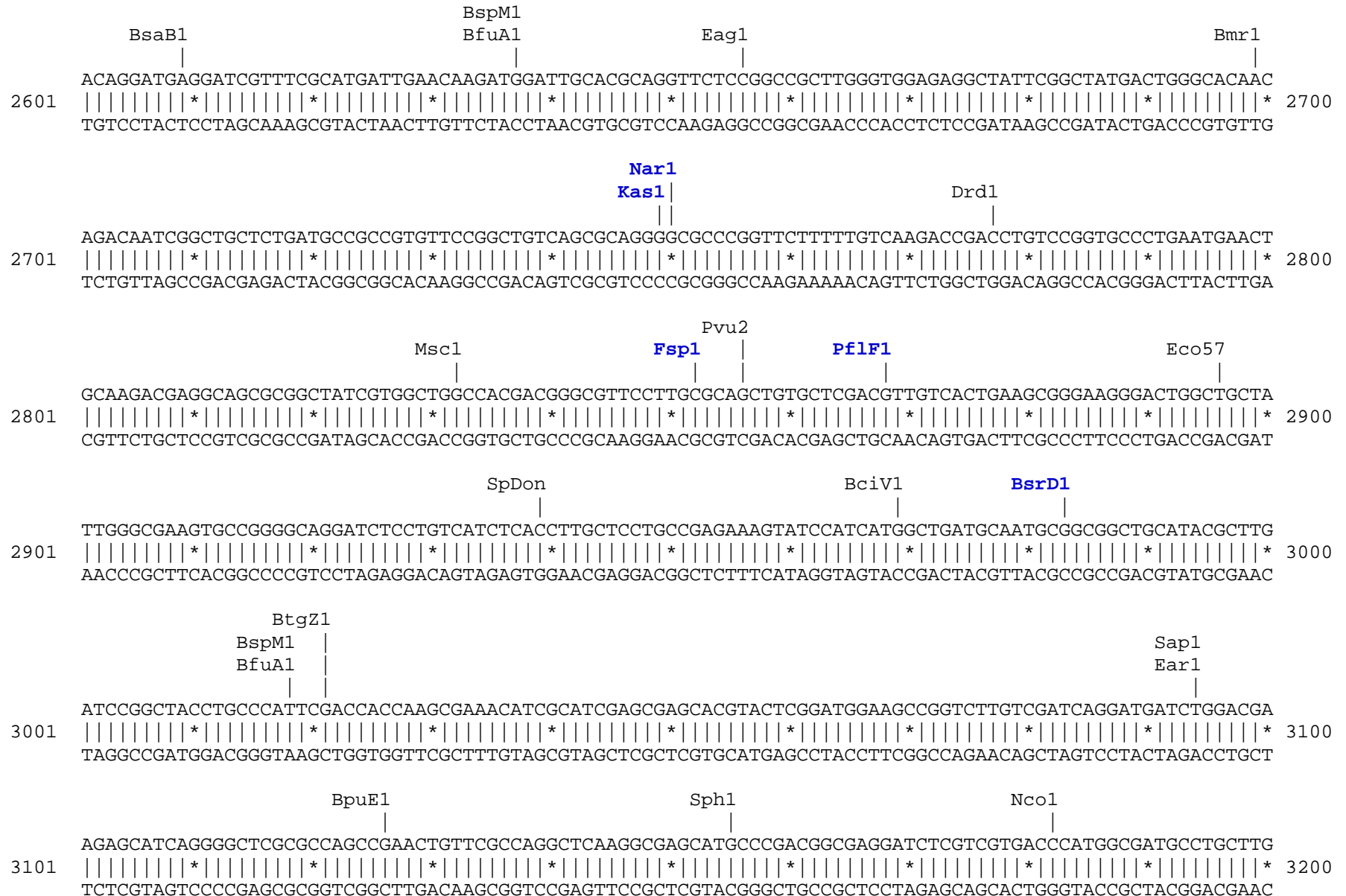


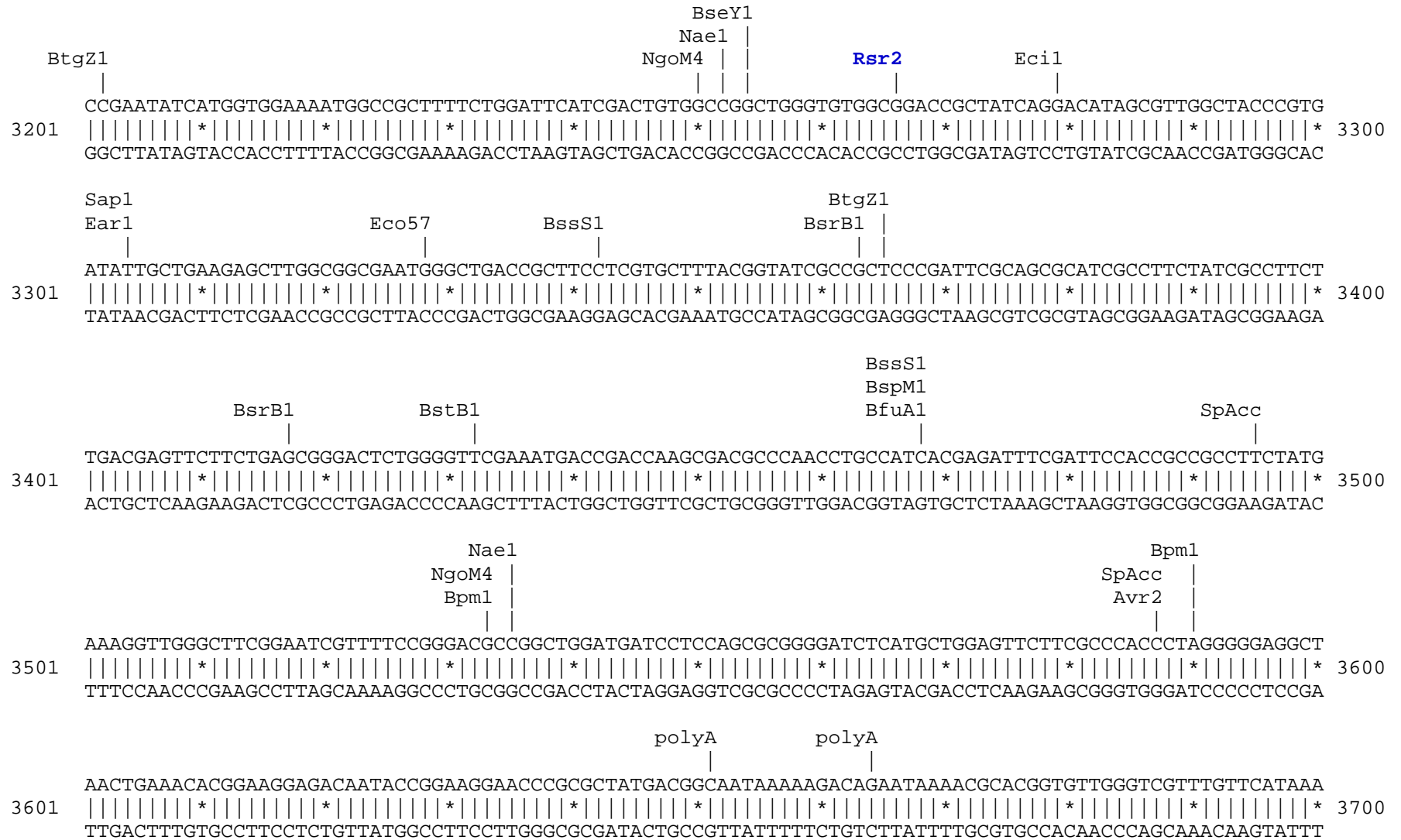












```

                                     Bsa1
                                     |
3701 CGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCC GCGTTTTCTTCCTTTTCCCCACCCACCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
   GCGCCCAAGCCAGGGTCCCAGCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGG

                                     BstAP
                                     |
                                     AlwN1
                                     |
                                     Bsu36
                                     |
                                     Dra1
                                     |
3801 CAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
   GTTCAAGCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGA

                                     Dra1
                                     |
                                     BspH1
                                     |
3901 TCATTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
   AGTAAAAATTAATTTTCTTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGG

                                     BpuE1
                                     |
4001 GTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
   CATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCCGACCAAACAACG

                                     Eco57
                                     |
                                     SpAcc
                                     |
4101 CGGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
   GCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGT

                                     AlwN1
                                     |
                                     BpuE1
                                     |
4201 CTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
   GAAGTTCCTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTG
```



```

                                     ApaL1      BseY1
                                     |           |
TCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGAT
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
AGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTCTGGGTCTGAACCTCGCTTGCTGGATGTGGCTTGACTCTA

                                     BciV1
                                     |           |
                                     Eci1           BssS1
                                     |           |           |
ACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAG
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
TGGATGTCGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTTCGCGCTGTCCATAGGCCATTTCGCGTCCCAGCCTTGTCTCTCGCGTGCTC

                                     SpAcc
                                     |
                                     Drd1           BpuE1
                                     |           |           |
GGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGG
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
CCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCC

                                     SpDon
                                     |           |
SpAcc      Eci1           BspLU
|           |           |
AGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTG
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
TCGGATACCTTTTTGCGGTCTTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGAC

                                     NsiI
                                     |
                                     BfrB1
                                     |
TGGATAACCGTATTACCGCCATGCAT
4701 |||||*|||||*||||| 4726
ACCTATTGGCATAATGGCGGTACGTA

```

**Found:**

Aat2   **Acc65**   **AfeI**   **Afl2**   **AgeI**   **AleI**   AlwN1   **ApaI**   ApaL1   **AseI**   Avr2   **BamHI**   **BbsI**   BciV1  
BfrB1   BfuA1   Bgl1   **Bgl2**   Bmr1   Bpm1   BpuE1   Bsa1   BsaB1   **BsaXa**   **BsaXb**   **BseR1**   BseY1   Bsm1

BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	BssS1	BstAP	BstB1	Bsu36	BtgZ1	<b>Bts1</b>	<b>Cla1</b>	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	Msc1
Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1	<b>PflF1</b>	<b>PflM1</b>	polyA	<b>PshA1</b>	Psi1	<b>PspOM</b>
<b>Pst1</b>	Pvu2	<b>Rsr2</b>	<b>Sac1</b>	<b>Sac2</b>	<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>	<b>Xho1</b>										

**Unique:**

<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	<b>Apa1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bbs1</b>	<b>Bgl2</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	<b>BspLU</b>
<b>BsrD1</b>	<b>BsrG1</b>	<b>Bts1</b>	<b>Cla1</b>	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Nar1</b>	<b>Nde1</b>	<b>Nhe1</b>
<b>Not1</b>	<b>PflF1</b>	<b>PflM1</b>	<b>PshA1</b>	<b>PspOM</b>	<b>Pst1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sac2</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>											

**Not found:**

Aar1	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	BcglA	Bcglb	Bcl1	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BspE1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1
FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1
Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1					

**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	Faul	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													