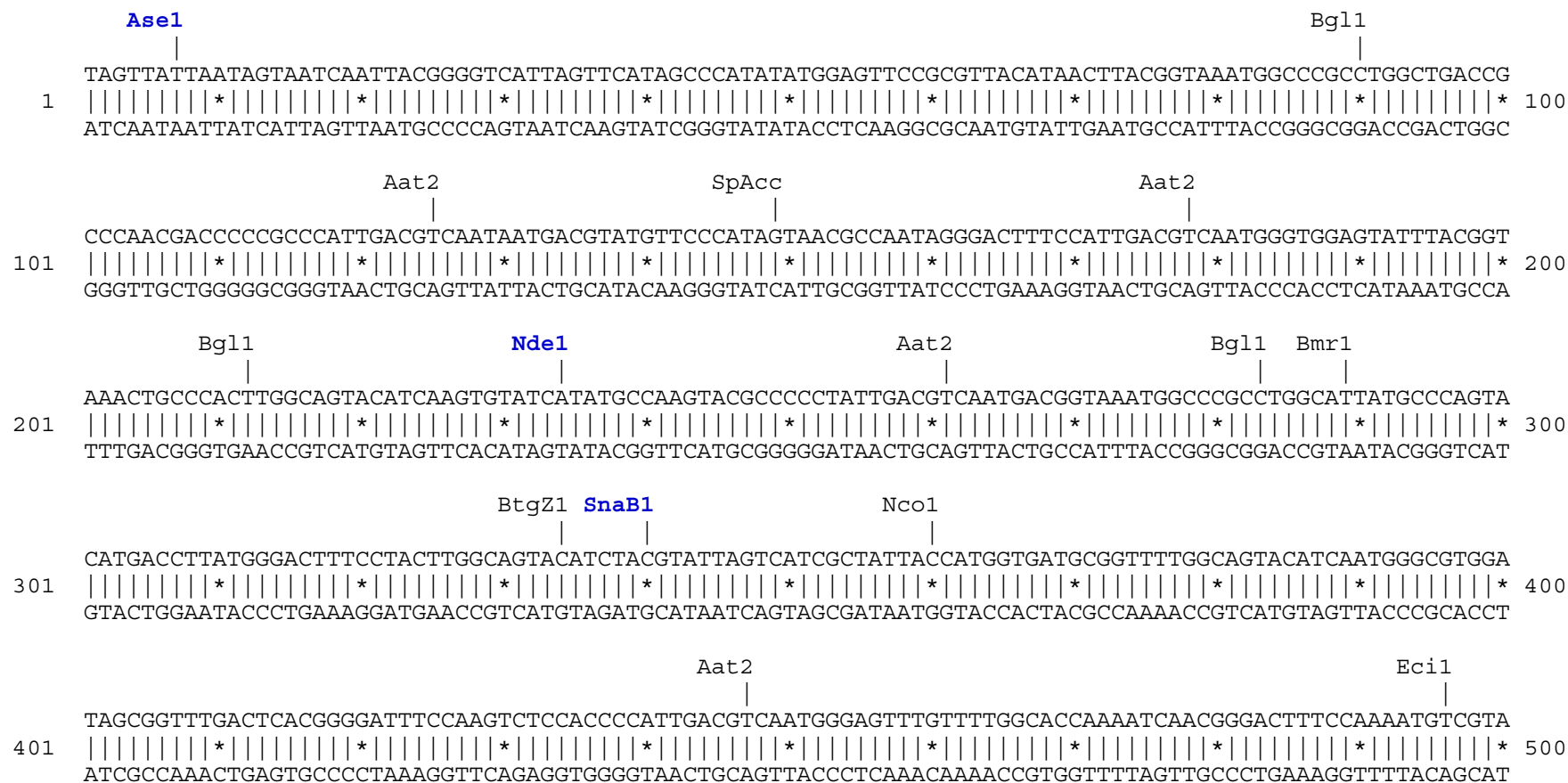
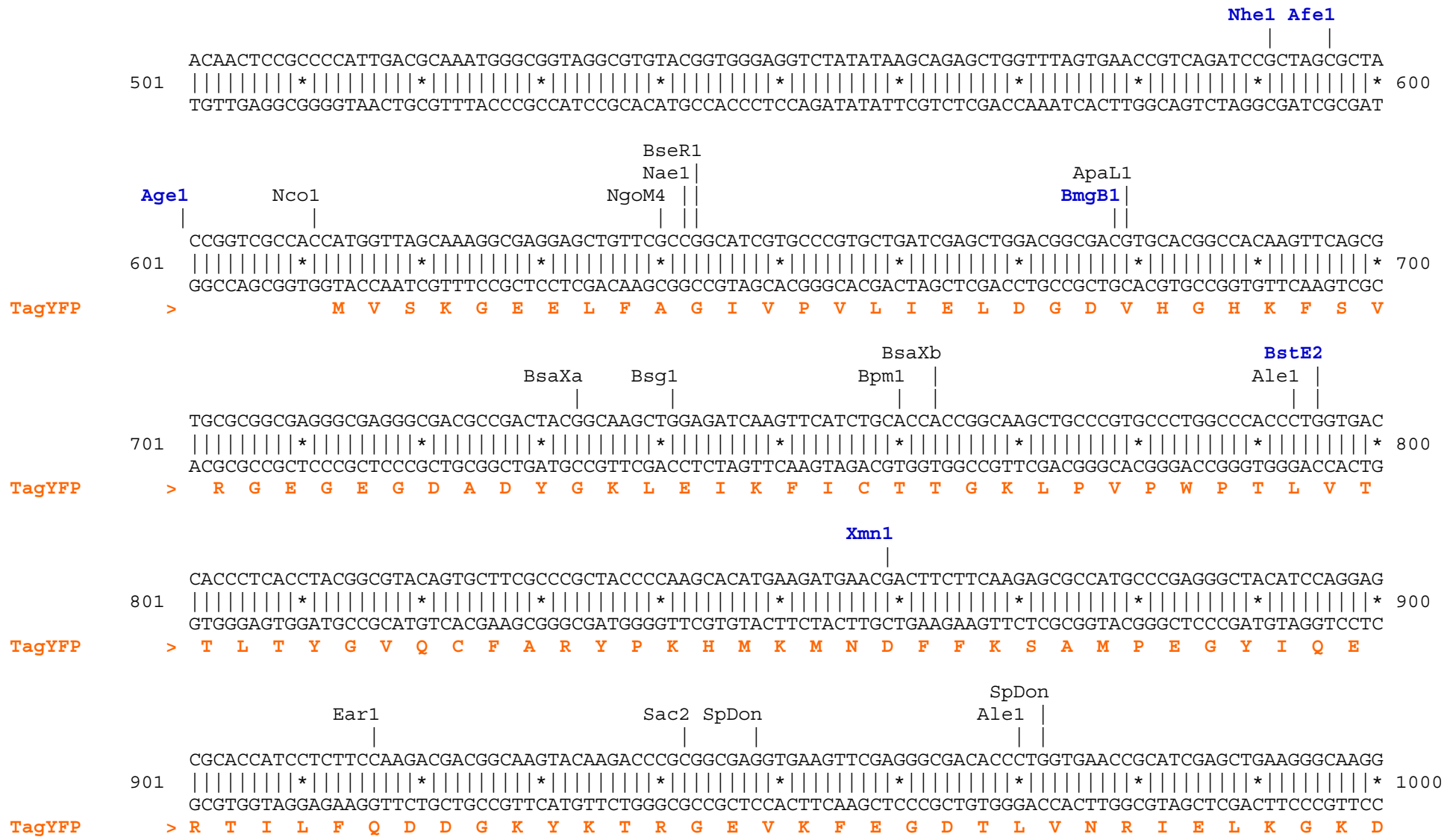


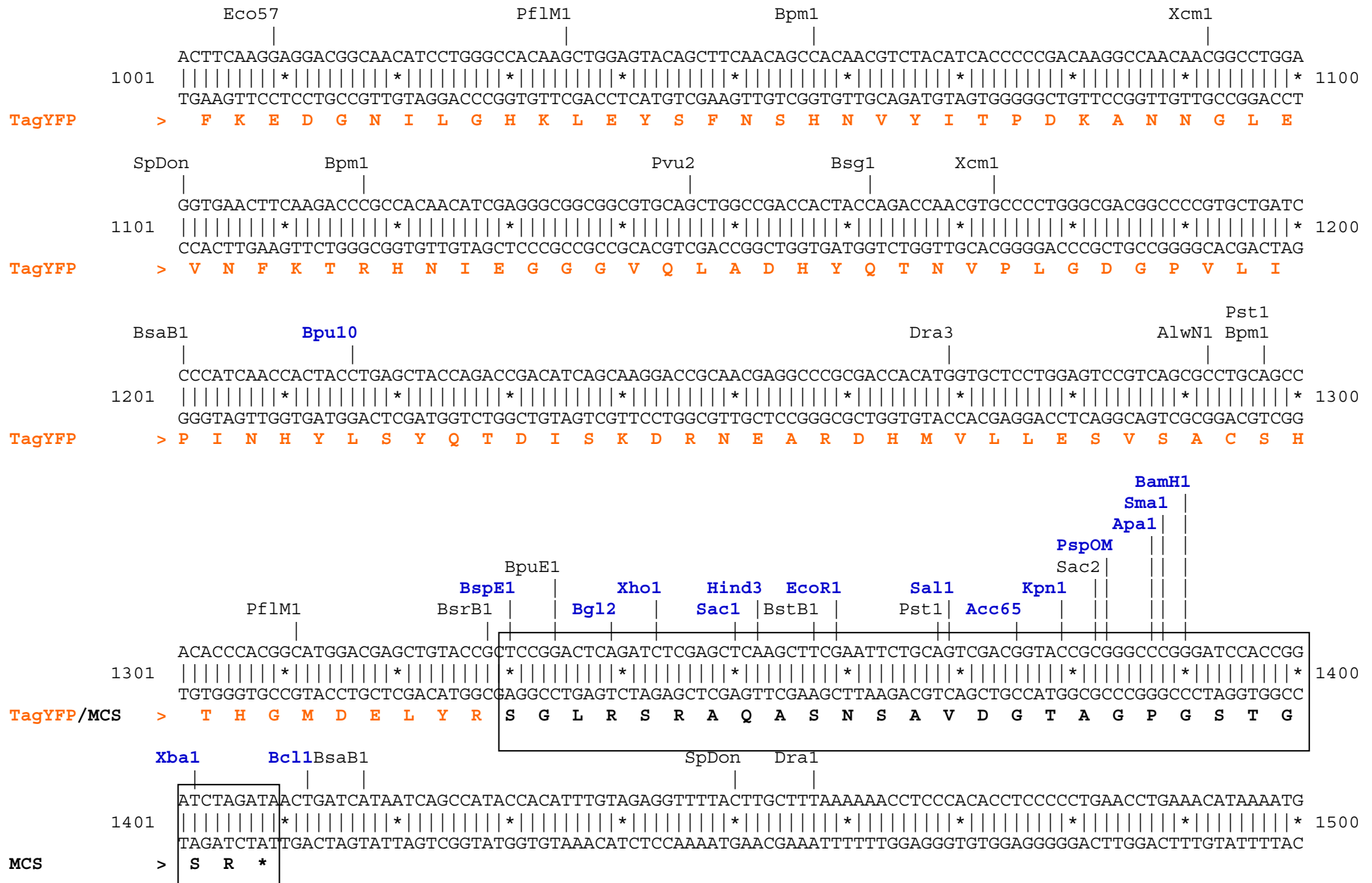
pTagYFP-C vector restriction map

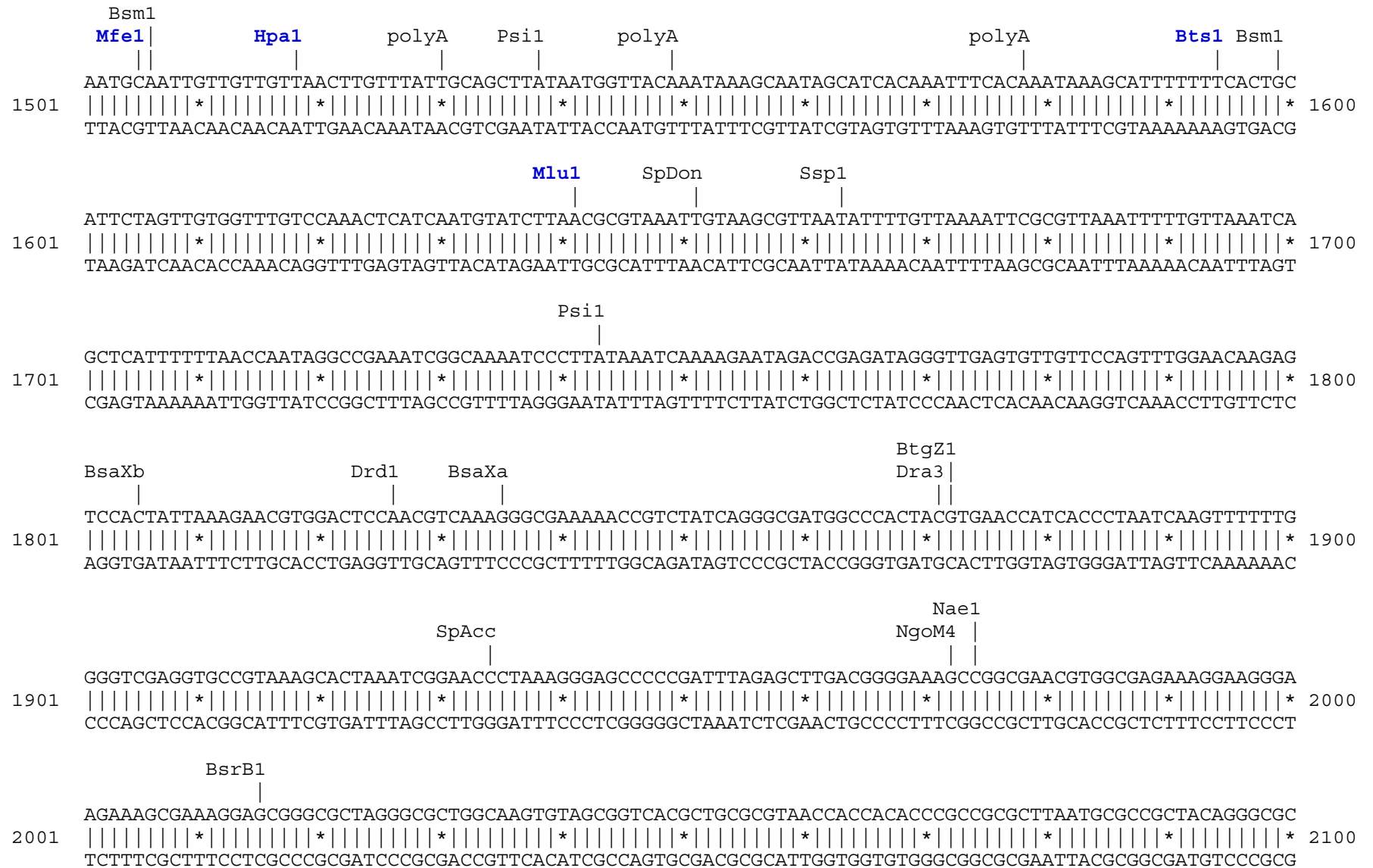
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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

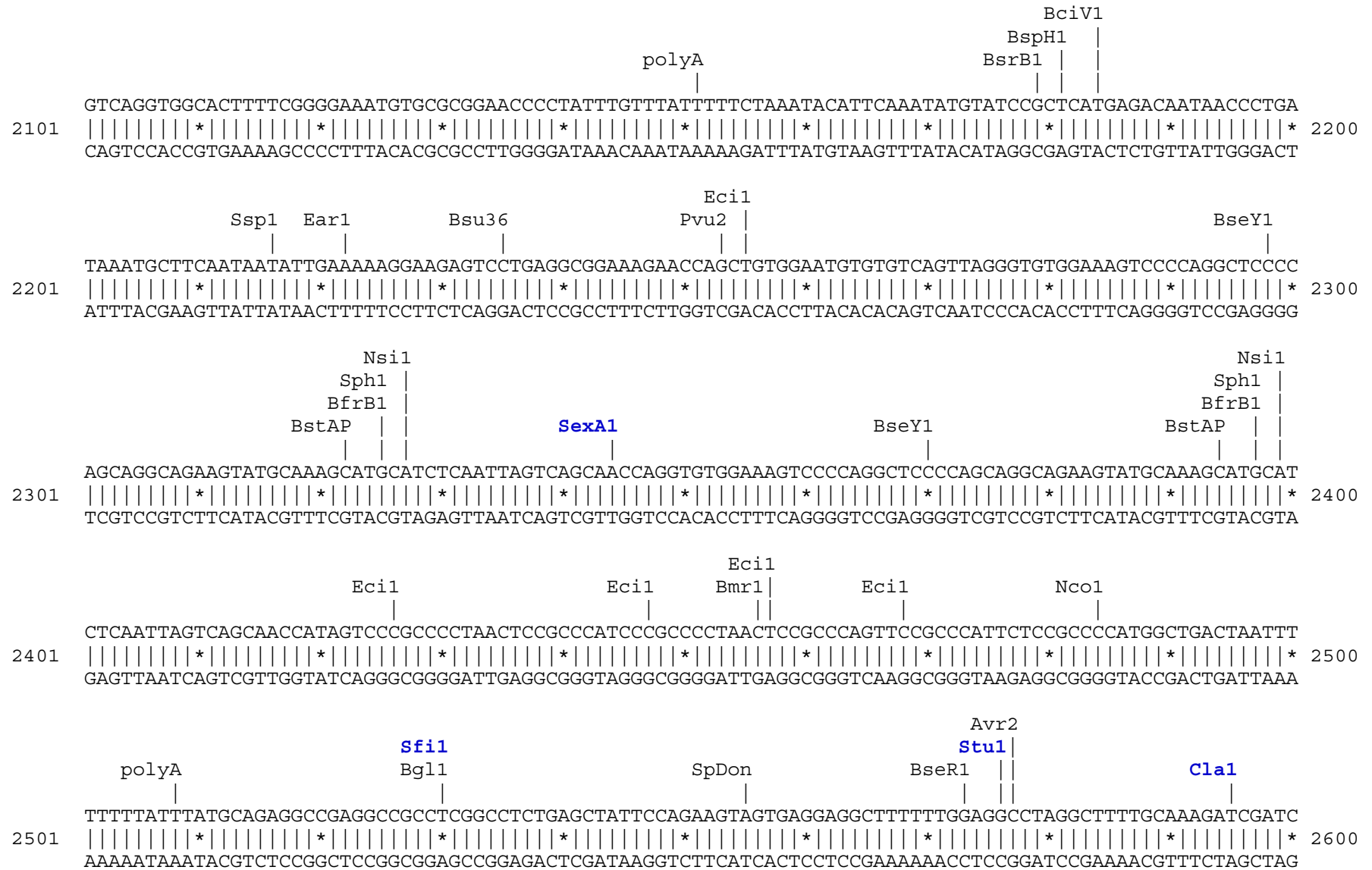
Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.

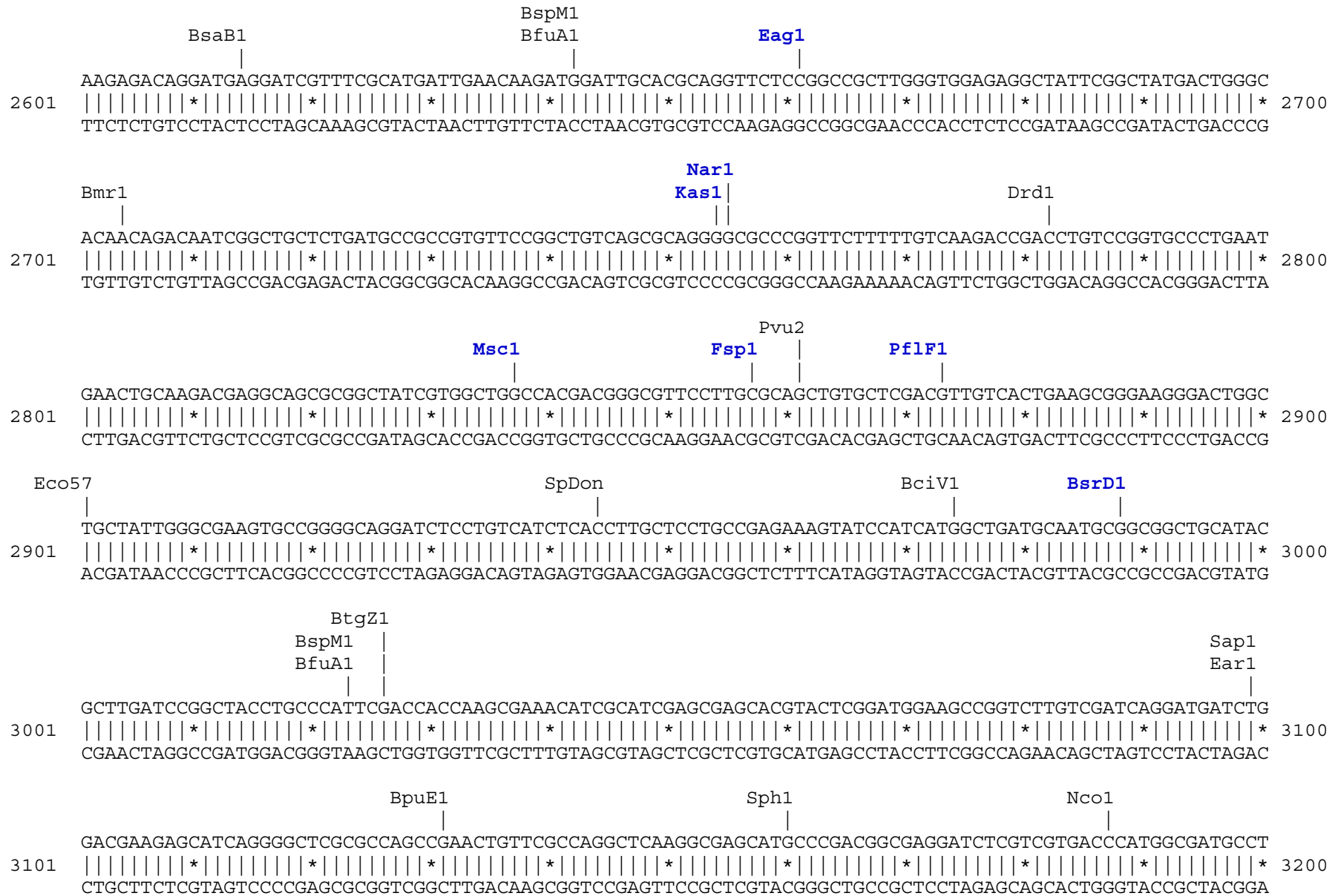


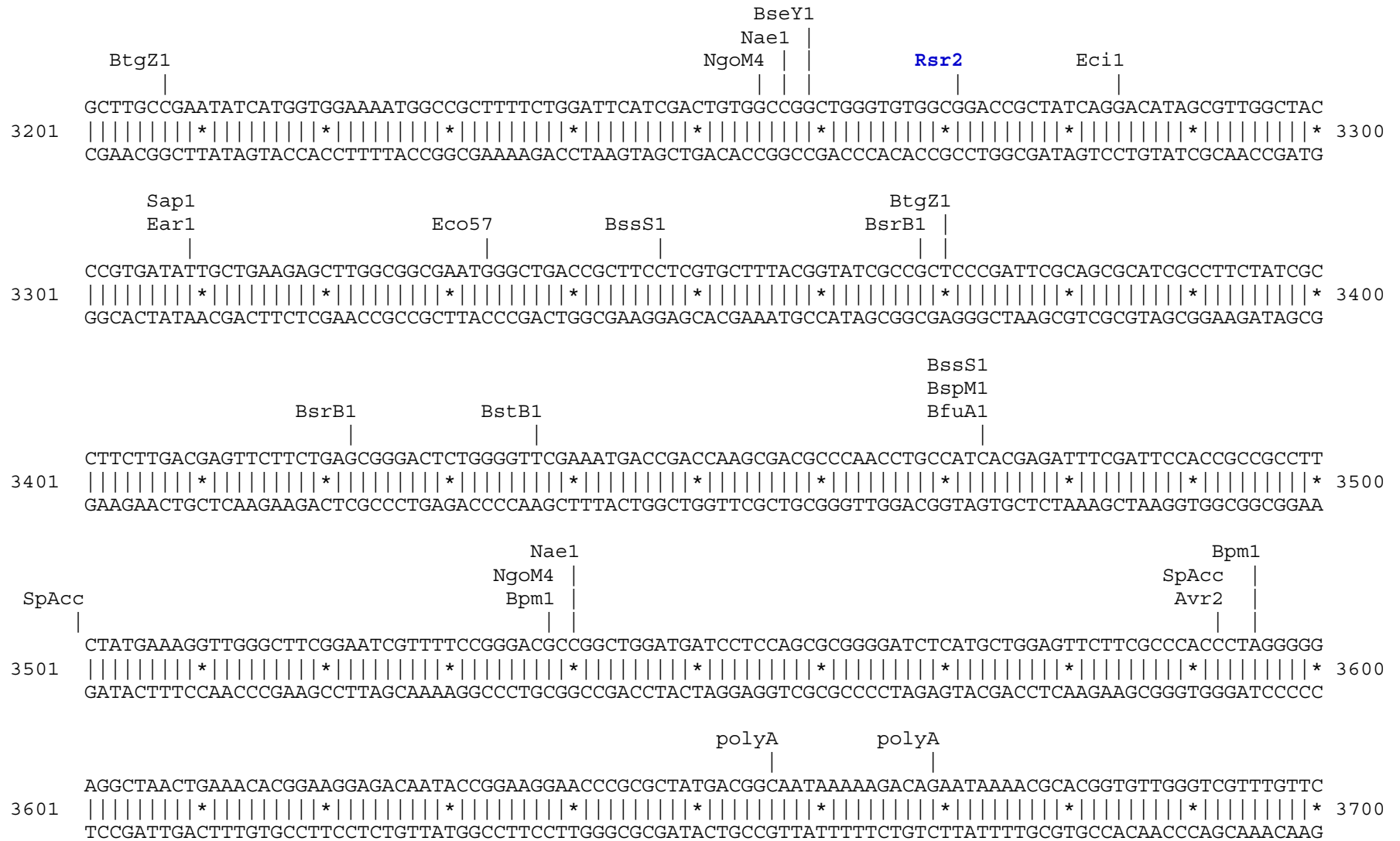


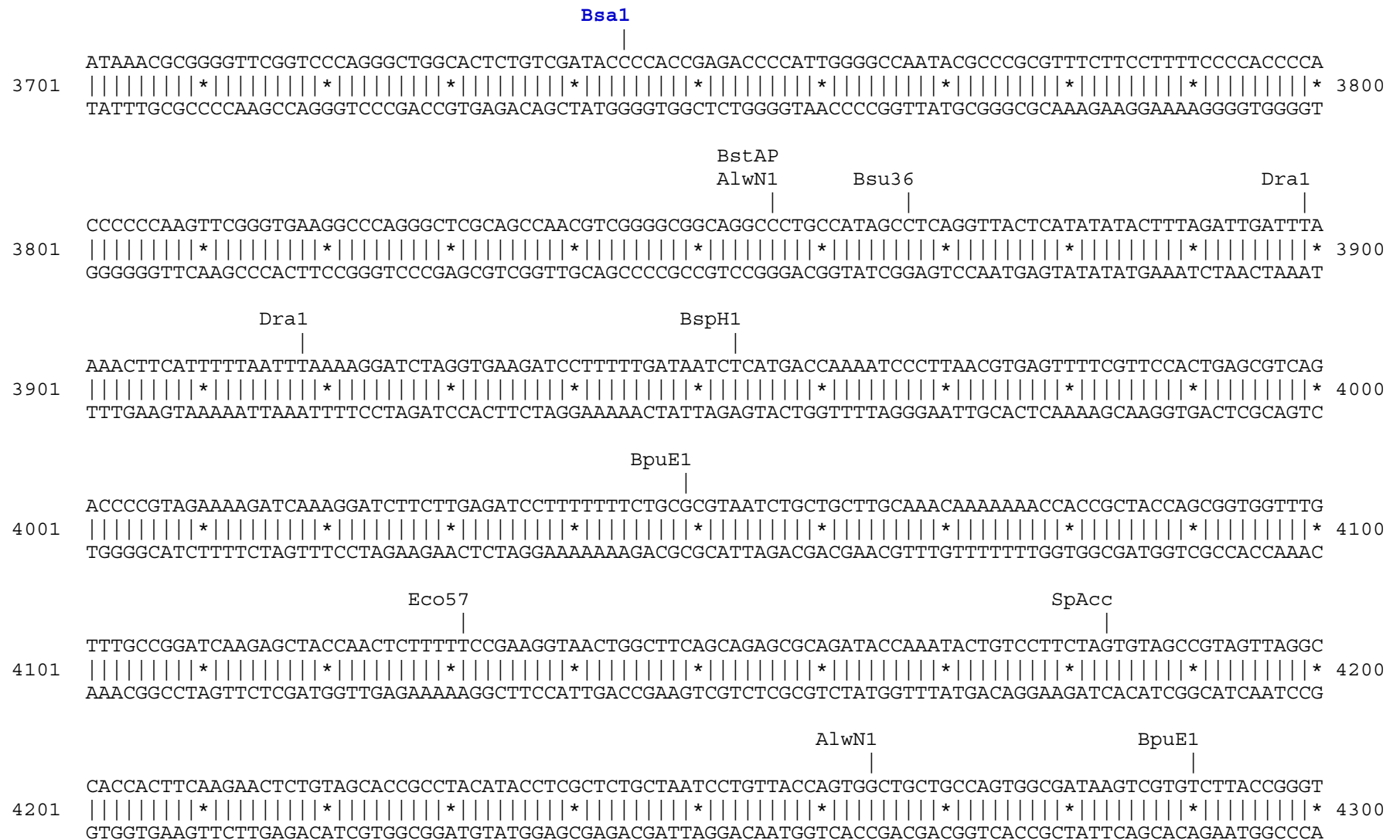













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                                         ApaL1    BseY1
                                         |         |
TGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACT
4301 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4400
ACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTTCGGGTTCGAACCTCGCTTGCTGGATGTGGCTTGA

                                     SpAcc
                                     |
GAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGC
4401 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4500
CTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTCGCCGTCCAGCCTTGTCTCTCGCG

BssS1                                     SpAcc                                     Drd1                                     BpuE1
|                                         |                                         |                                         |
ACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGG
4501 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4600
TGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCC

                                     SpDon
                                     BspLU
                                     |
GGCGGAGCCTATGAAAAACGCCAGCAACGCGGCTTTTTACGGTTCCTGGCCTTTTGGCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCCTGA
4601 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4700
CCGCTCGGATACTTTTTCGCGTTCGTTGCCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACT

                                     NsiI
                                     BfrB1
                                     |
TTCTGTGGATAACCGTATTACCGCCATGCAT
4701 |||||||*|||||||*|||||||* 4731
AAGACACCTATTGGCATAATGGCGGTACGTA

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Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	BciV1	Bcl1	BfrB1
BfuA1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BssS1	BstAP	BstB1	BstE2	Bsu36	BtgZ1

Bts1	Cla1	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Kpn1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1	polyA
Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc
SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xho1	Xmn1						

Unique:

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

Not found:

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Blp1	BsiW1
BsmB1	BsrG1	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													