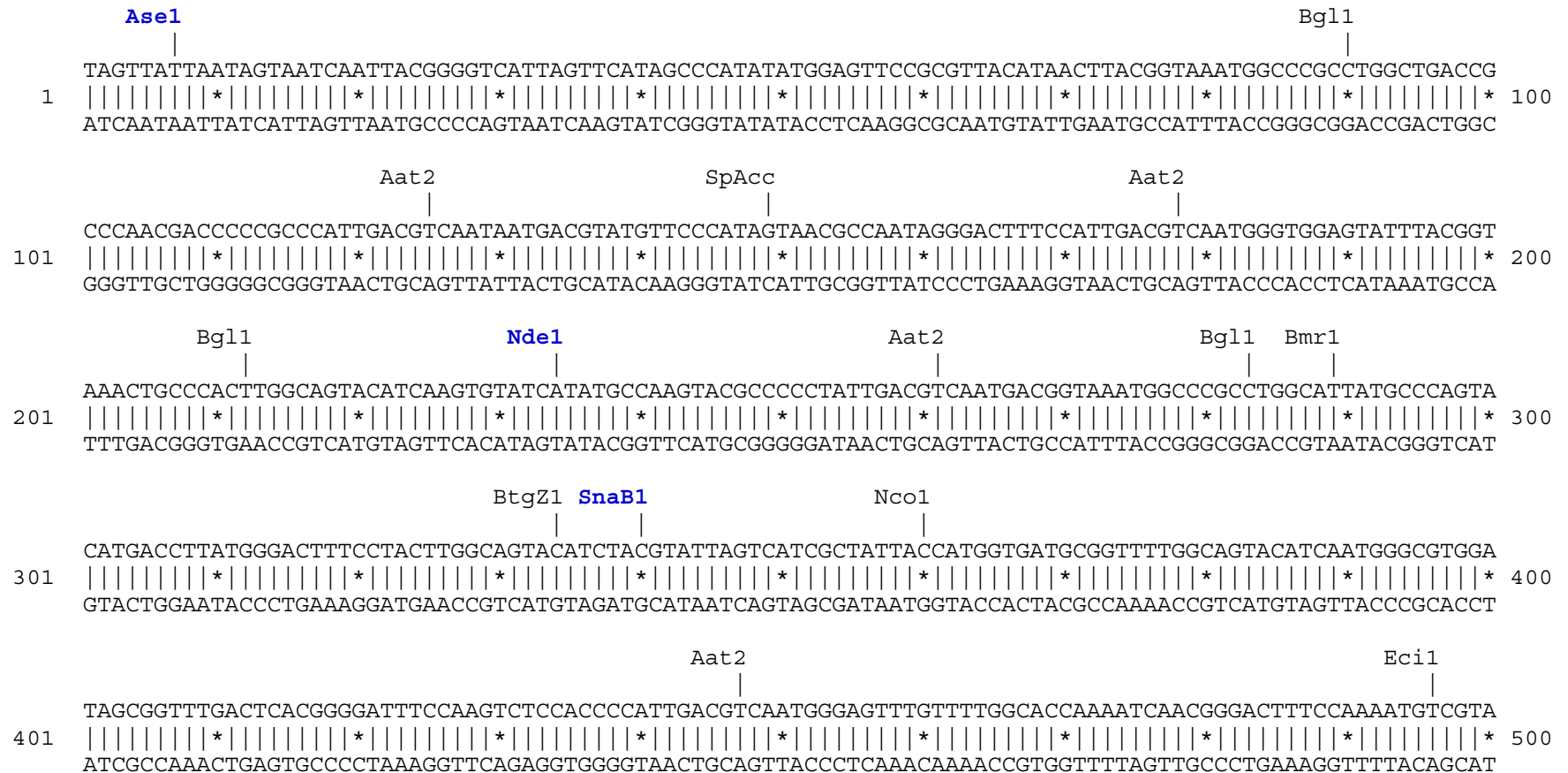
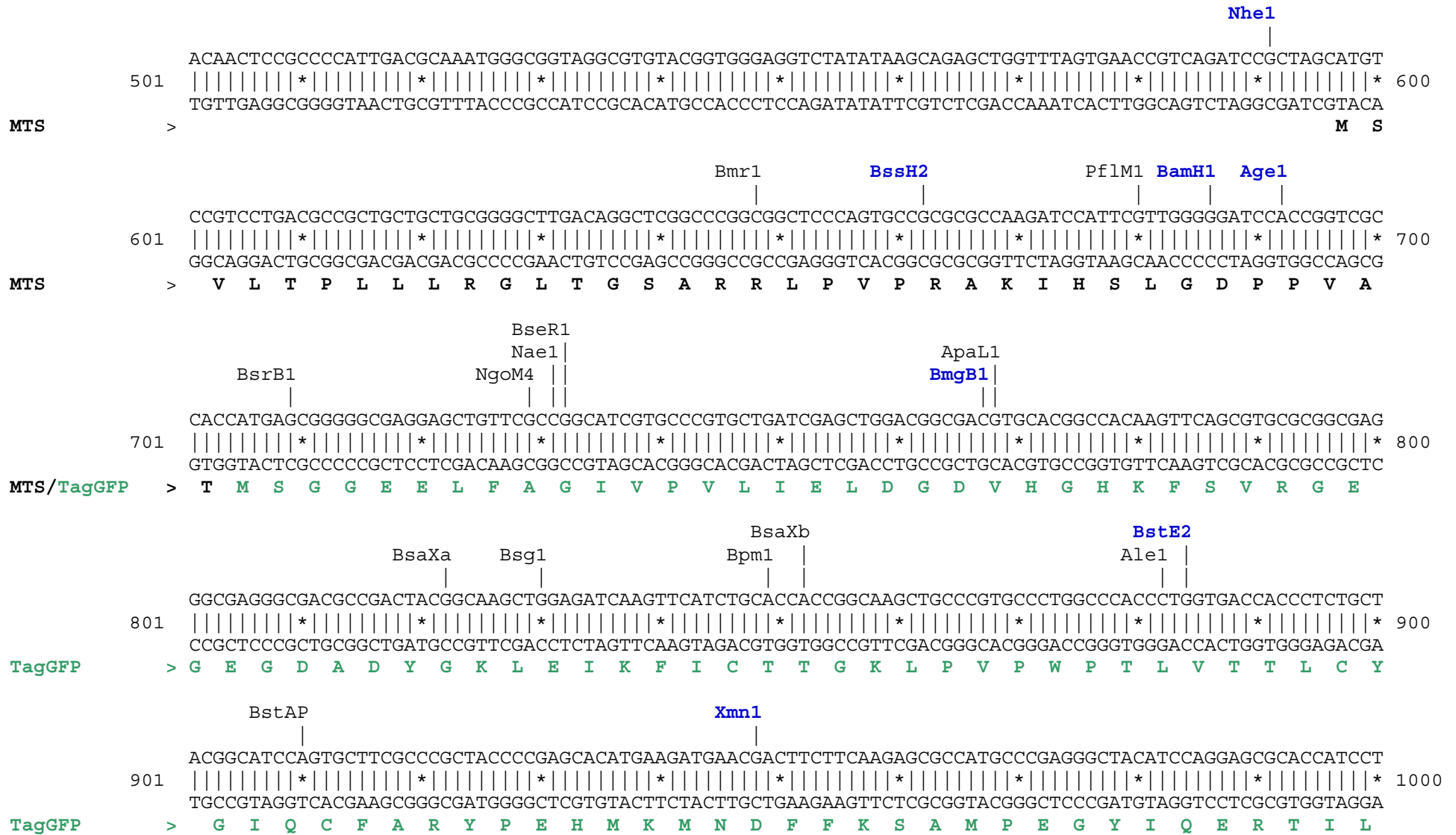


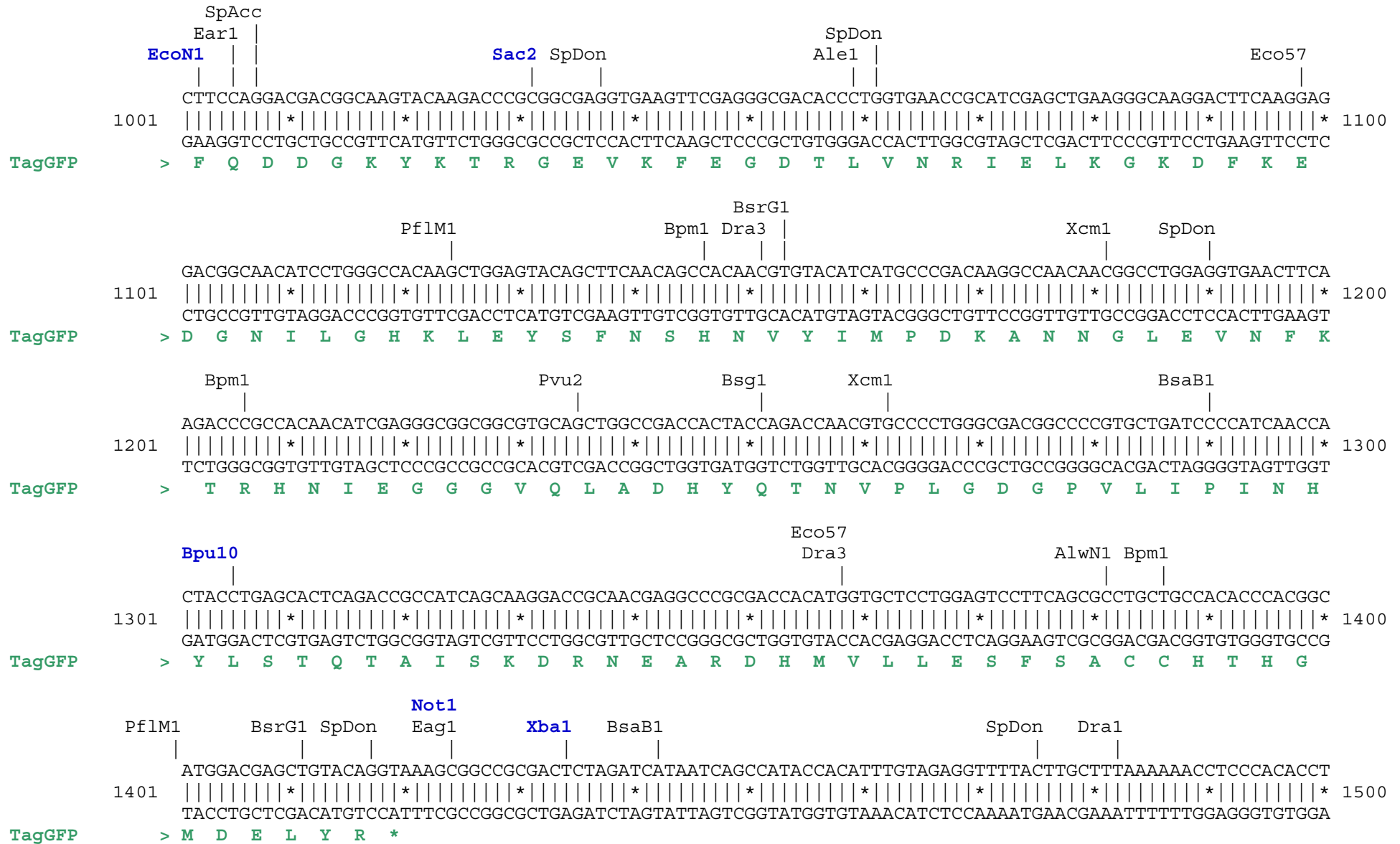
### pTagGFP-mito vector restriction map

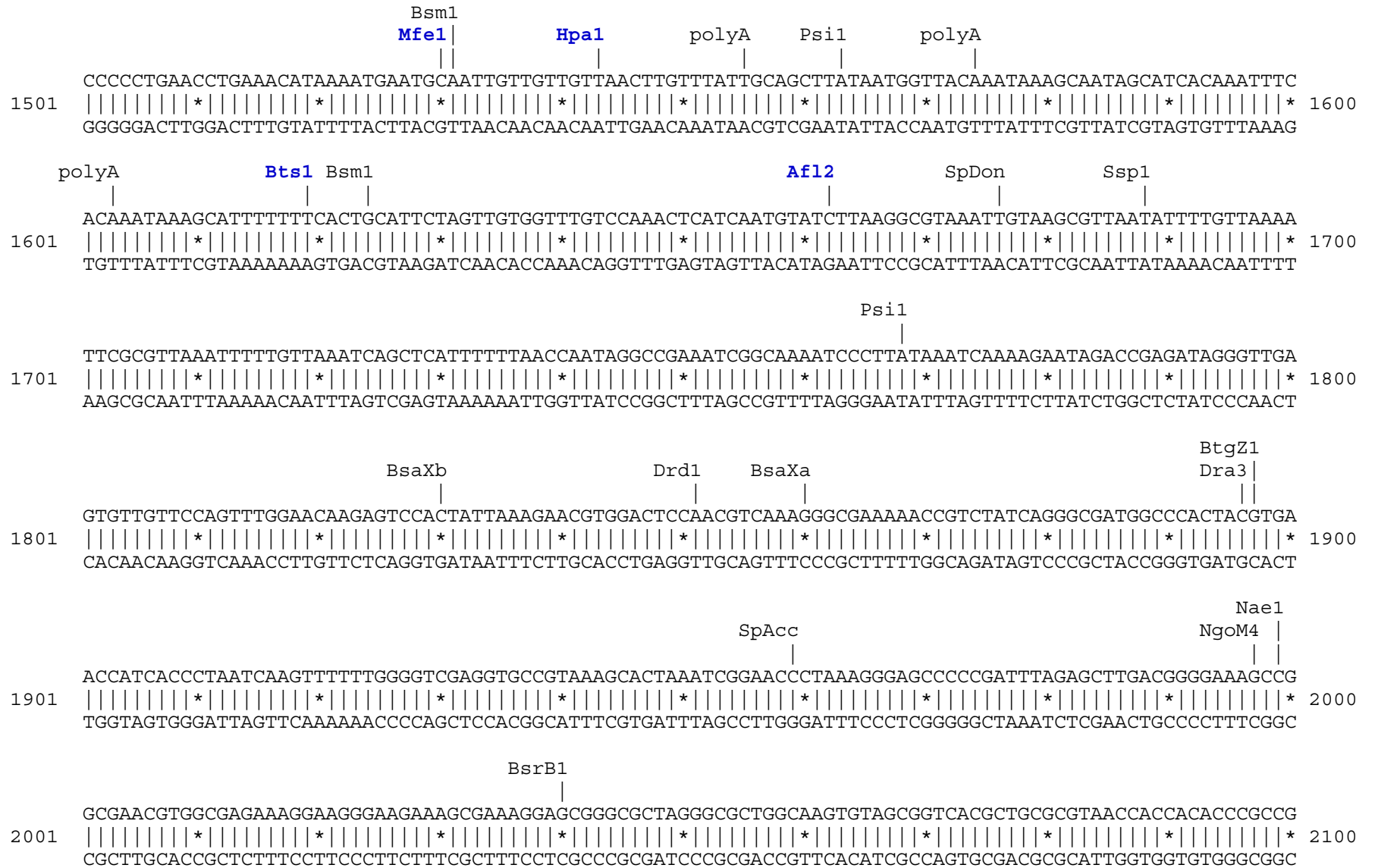
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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

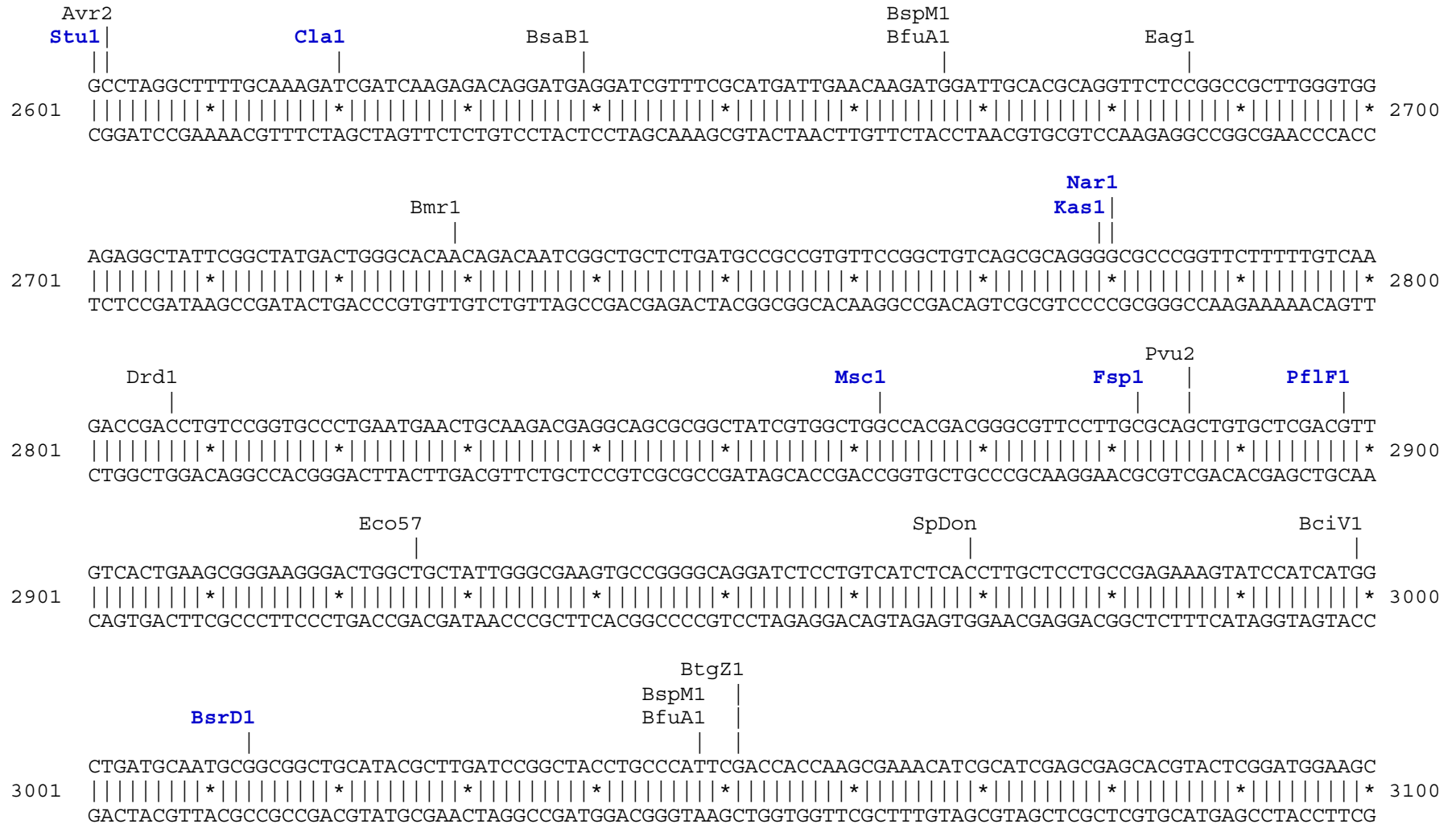














Bpm1  
 SpAcc  
 Avr2  
 polyA  
 polyA

3601 GGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3700  
 CCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTT

Bsa1

3701 ACGCACGGTGTGGGTTCGTTTGTTCATAAACCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGATAACCCACCGAGACCCCATTGGGGCCAATACGCC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3800  
 TGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGG

BstAP  
 AlwN1  
 Bsu36

3801 GCGTTTCTTCCTTTTCCCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3900  
 CGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAAT

Dra1  
 Dra1  
 BspH1

3901 CTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGT  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4000  
 GAGTATATATGAAATCTAACTAAATTTGAAGTAAAAATTAATTTTCCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCA

BpuE1

4001 GAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4100  
 CTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTT

Eco57

4101 AACCACCGCTACCAGCGGTGGTTTTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATAACCAAATACTGT  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4200  
 TTGGTGGCGATGGTCCCAACCAAACCGCCTAGTTCTCGATGGTTGAGAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACA





**Found:**

Aat2	<b>Afl2</b>	<b>Age1</b>	Ale1	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	BciV1	BfrB1	BfuA1	Bgl1	<b>BmgB1</b>
Bmr1	Bpm1	<b>Bpu10</b>	BpuE1	<b>Bsa1</b>	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	<b>BspLU</b>
BspM1	BsrB1	<b>BsrD1</b>	BsrG1	<b>BssH2</b>	BssS1	BstAP	<b>BstB1</b>	<b>BstE2</b>	Bsu36	BtgZ1	<b>Bts1</b>	<b>Cla1</b>	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	<b>EcoN1</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Msc1</b>	Nae1	<b>Nar1</b>
Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1	<b>PflF1</b>	PflM1	polyA	Psi1	Pvu2	<b>Rsr2</b>	<b>Sac2</b>	Sap1
<b>SexA1</b>	<b>Sfi1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xba1</b>	Xcm1	<b>Xmn1</b>			

**Unique:**

<b>Afl2</b>	<b>Age1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>BmgB1</b>	<b>Bpu10</b>	<b>Bsa1</b>	<b>BspLU</b>	<b>BsrD1</b>	<b>BssH2</b>	<b>BstB1</b>	<b>BstE2</b>	<b>Bts1</b>	<b>Cla1</b>
<b>EcoN1</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Msc1</b>	<b>Nar1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>Rsr2</b>	<b>Sac2</b>	<b>SexA1</b>
<b>Sfi1</b>	<b>SnaB1</b>	<b>Stu1</b>	<b>Xba1</b>	<b>Xmn1</b>									

**Not found:**

Aar1	Acc65	Ac11	Afe1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b
Bcl1	Bgl2	Blp1	BsiW1	BsmB1	BspE1	BstX1	BstZ1	_Chi	EcoK	EcoR1	EcoRV	ScFRT	Fse1
FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pst1	Pvu1
Sac1	Sal1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter
PISce	Xho1												

**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													