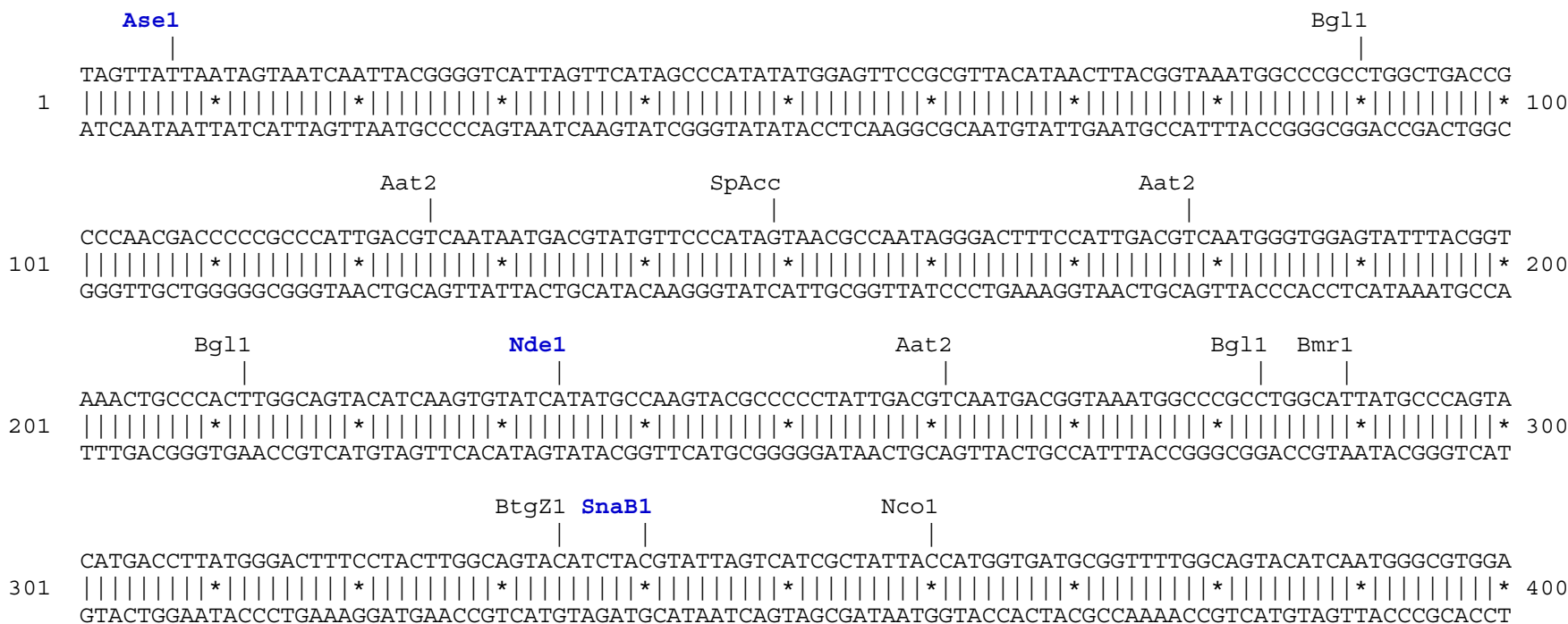
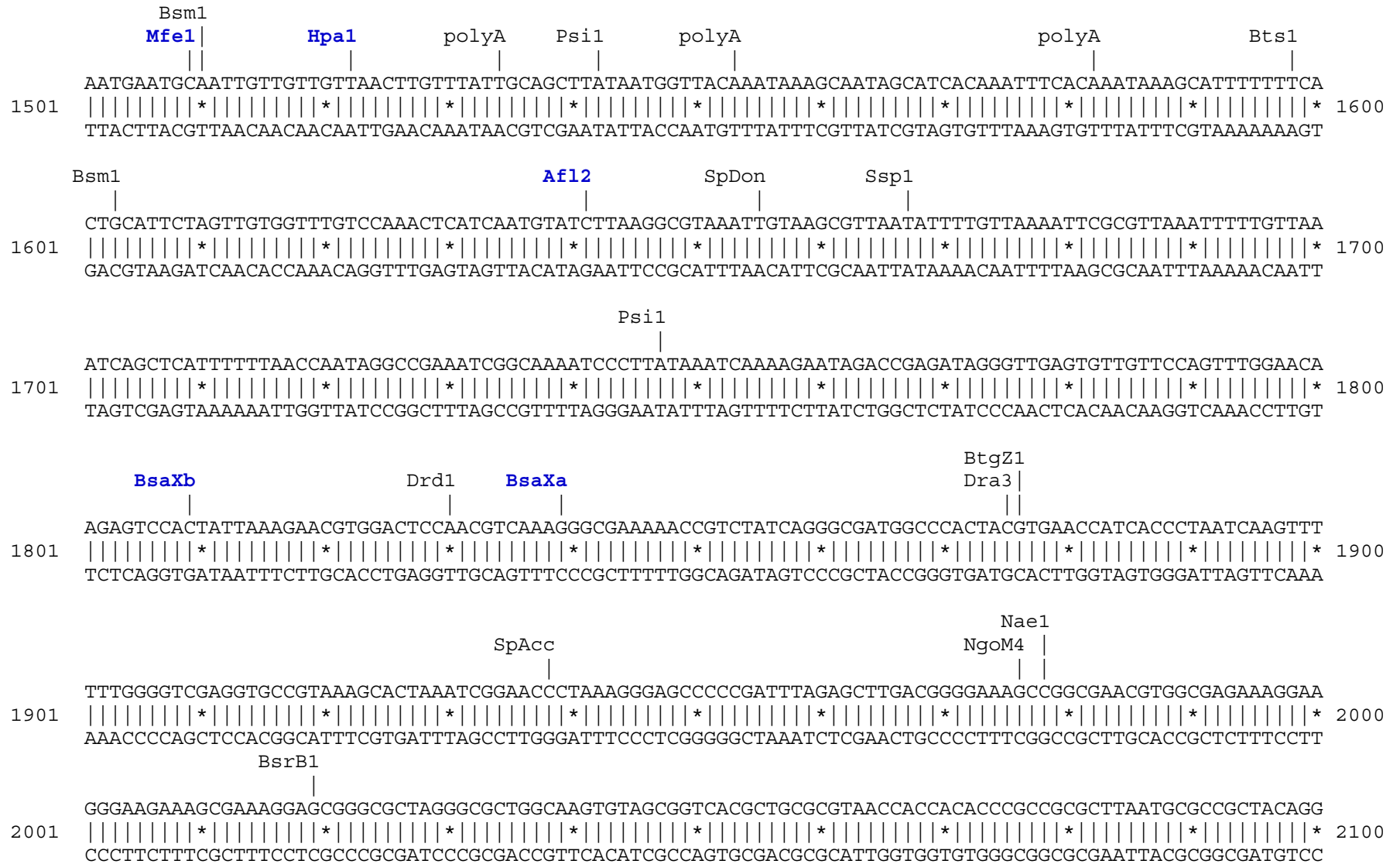


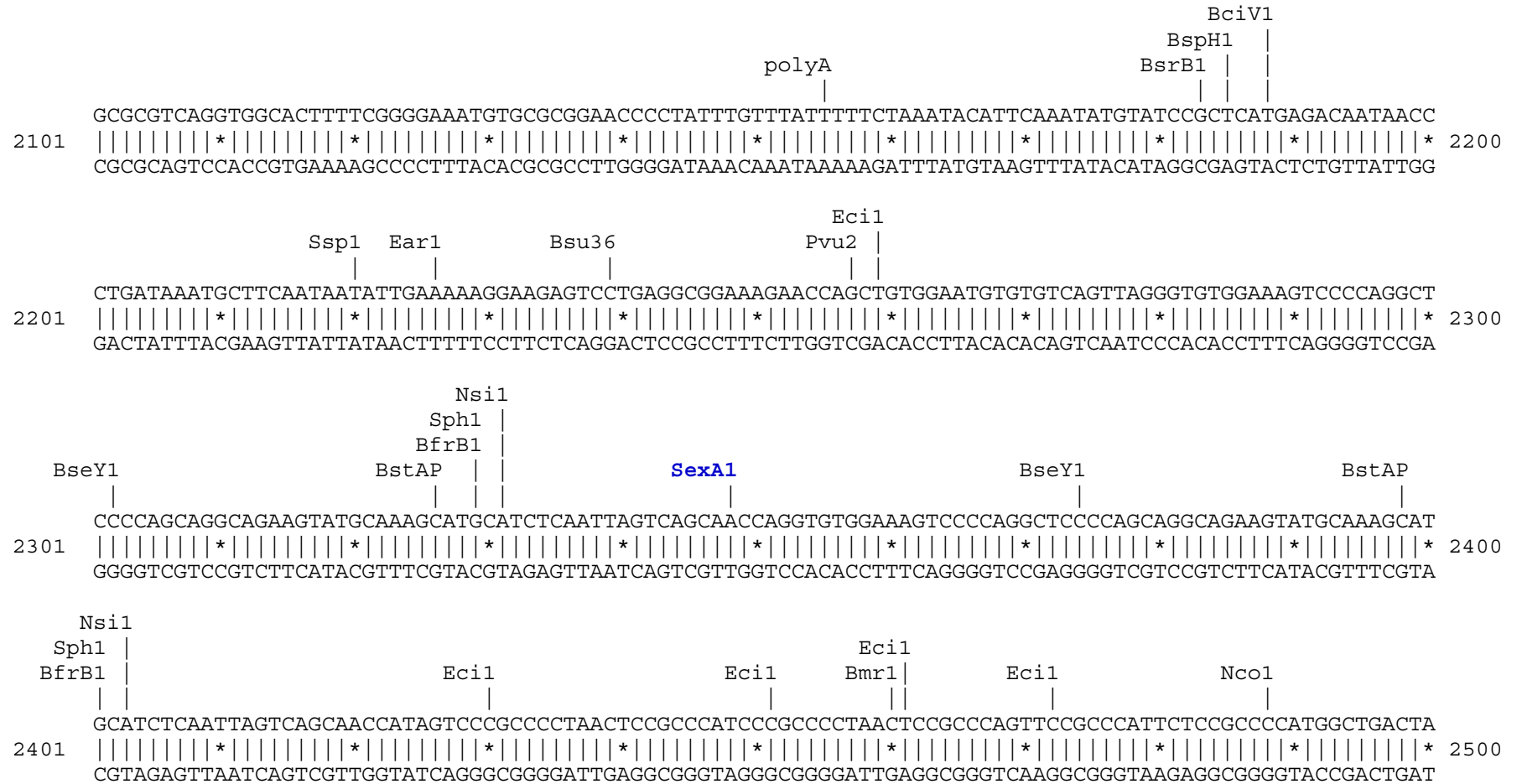
pTurboRFP-mito vector restriction map

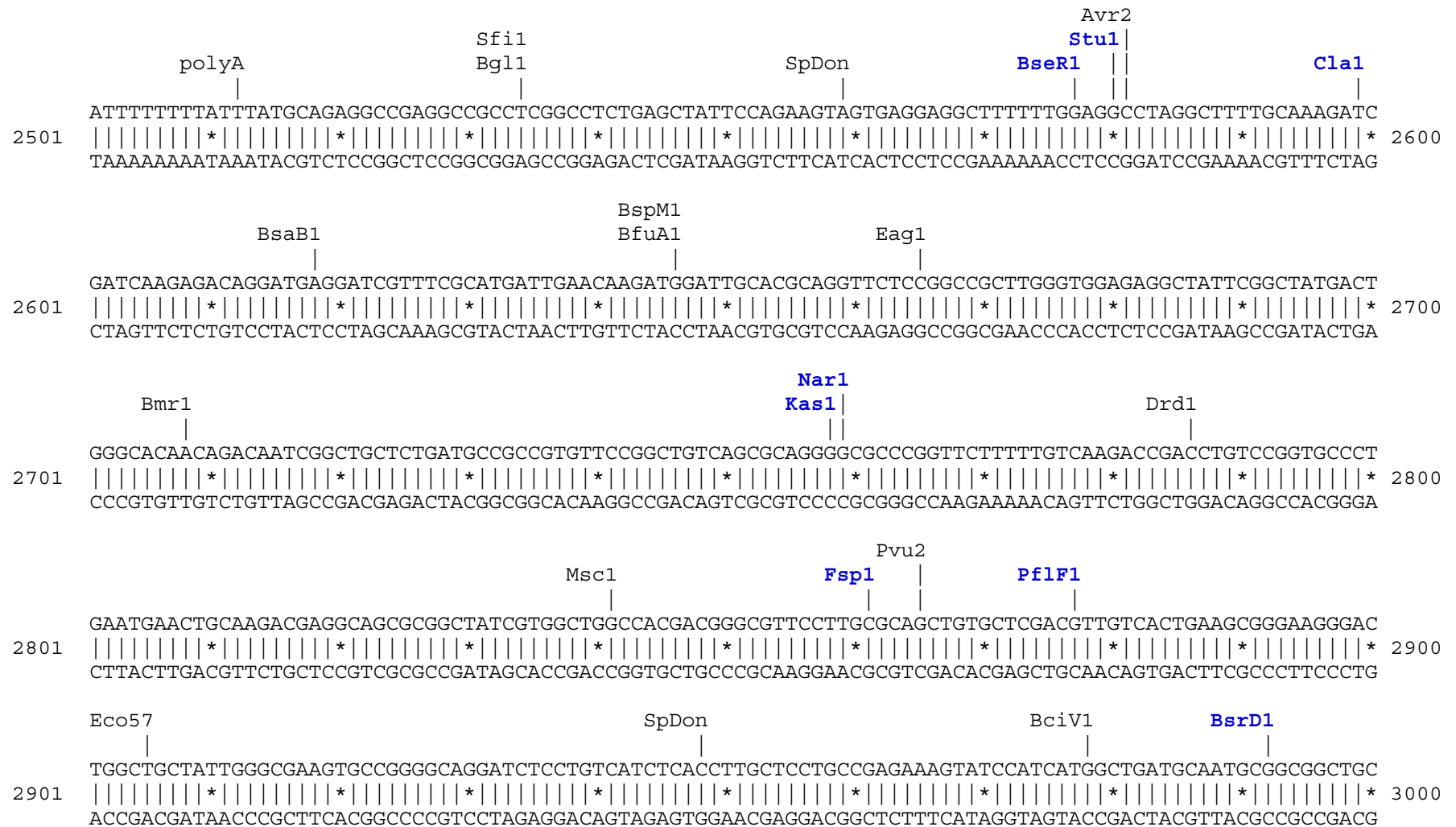
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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

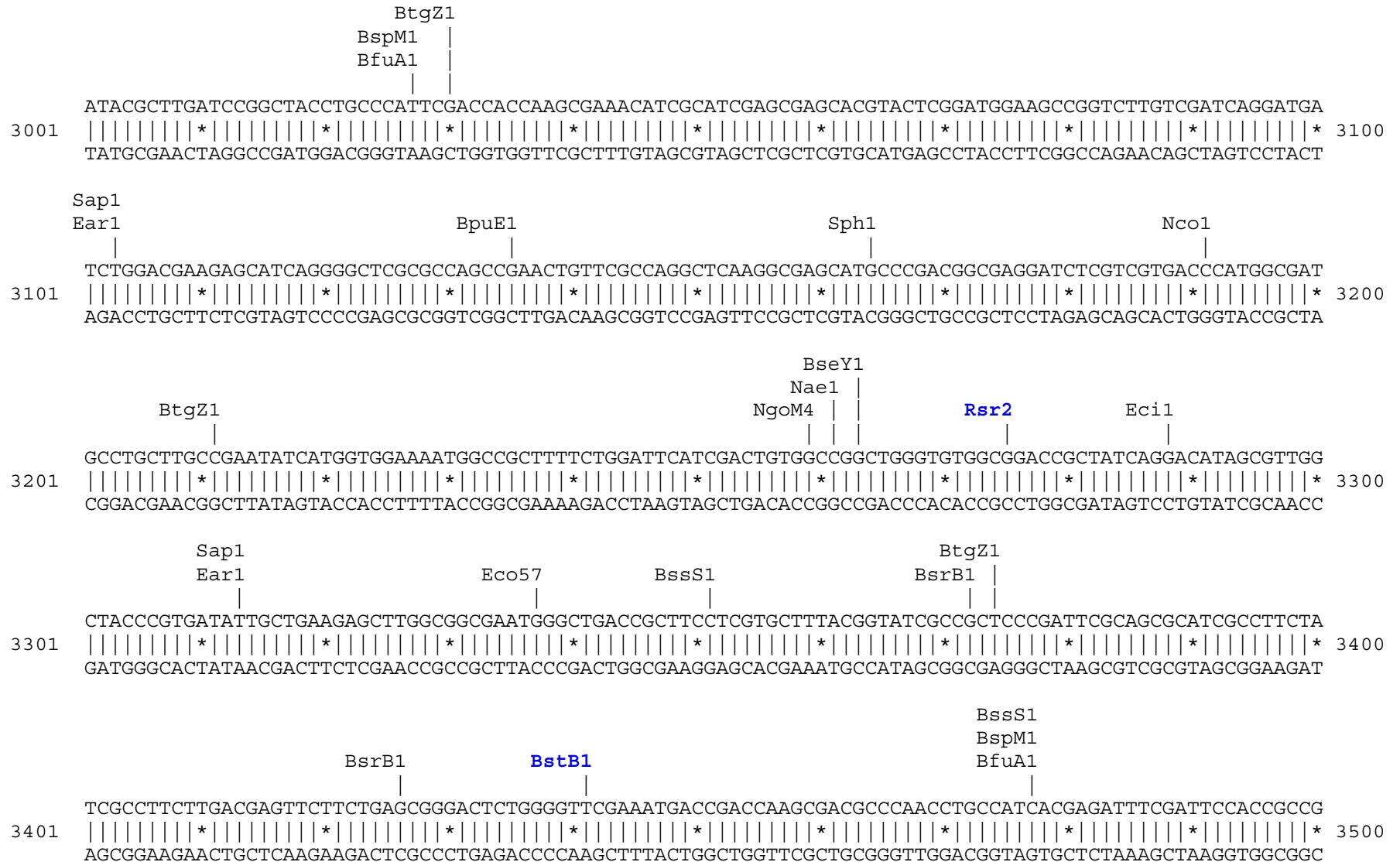
Unique sites shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Mitochondrial targeting sequence (MTS) shown in bold black.












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TTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTT
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
AAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAA

                                     AlwN1                                     BpuE1
                                     |                                     |
AGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACC
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
TCCGGTGGTGAAGTTCCTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGG

                                     ApaL1       BseY1
                                     |         |
GGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCG
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
CCCAACCTGAGTTCCTGCTATCAATGGCCTATTCCGCGTCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTTCGAACCTCGCTTGTGATGTGGC

                                     BciV1
                                     |
                                     Eci1
                                     |
AACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGA
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
TTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCT

BssS1                                     SpAcc                                     Drd1                                     BpuE1
|                                     |                                     |                                     |
GCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCA
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
CGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGT

                                     SpDon
                                     |
                                     BspLU
                                     |
GGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGCGTTATCCC
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
CCCCCGCCTCGGATACCTTTTTGCGGTGCTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGG
```

```

                                     NsiI
                                   BfrB1 |
                                     | |
4701 CTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4735
      |||||*|||||*|||||*|||||
      GACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Afl2	Age1	AlwN1	Apal1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1	BfrB1	BfuA1	Bgl1
Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	BspLU	BspM1
BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Cla1	Dra1	Dra3	Drd1
Eag1	Ear1	Eci1	Eco57	Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4
Nhe1	Not1	Nsi1	PflF1	PflM1	polyA	PshA1	Psi1	Pvu2	Rsr2	Sap1	Sca1	SexA1	Sfi1
SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1							

Unique:

Afl2	Age1	Ase1	BamH1	Bbs1	Bcl1	BsaXa	BsaXb	BseR1	Bsg1	BspLU	BsrD1	BsrG1	BssH2
BstB1	Cla1	Fsp1	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1	Not1	PflF1	PshA1	Rsr2	Sca1
SexA1	SnaB1	Stu1	Xba1										

Not found:

Aar1	Acc65	Ac11	Afe1	Ahd1	Ale1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b
Bgl2	Blp1	BmgB1	Bpu10	BsiW1	BsmB1	BspE1	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoR1
EcoRV	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PspOM
Pst1	Pvu1	Sac1	Sac2	Sal1	SanD1	Sbf1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA
T7RNA	T7Ter	PISce	Xcm1	Xho1	Xmn1								

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	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													