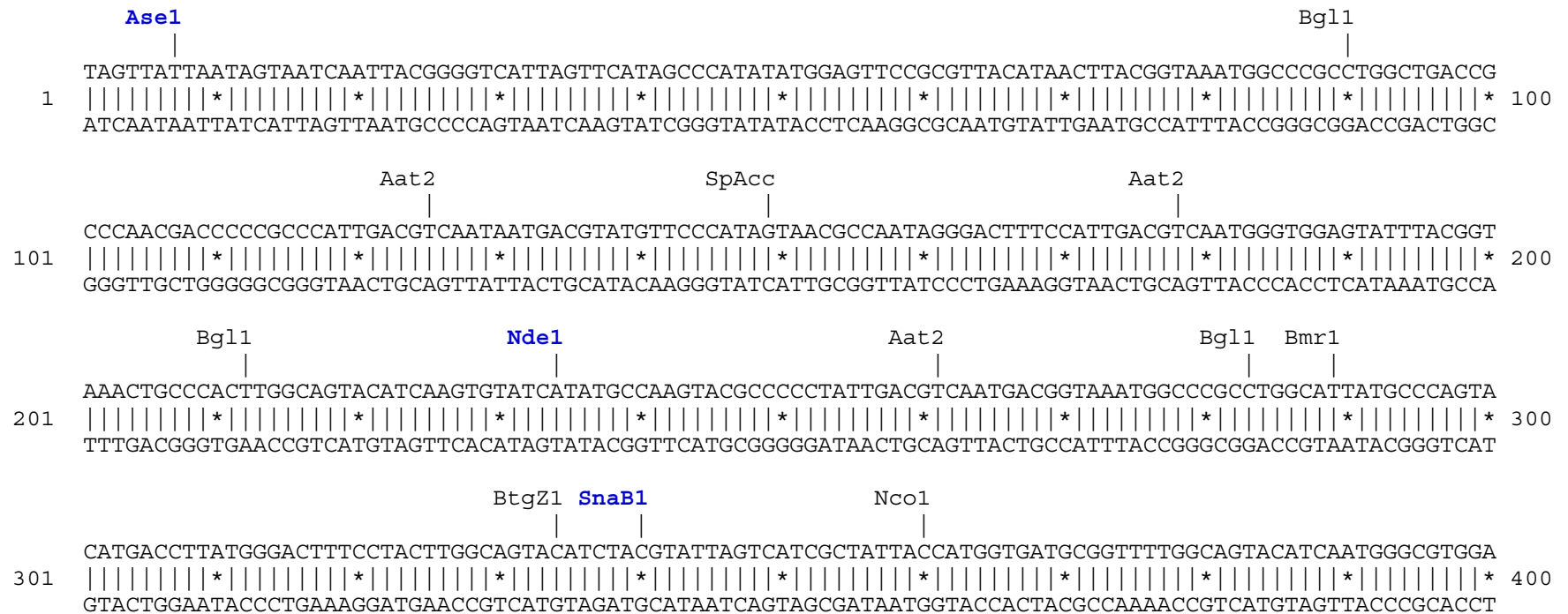
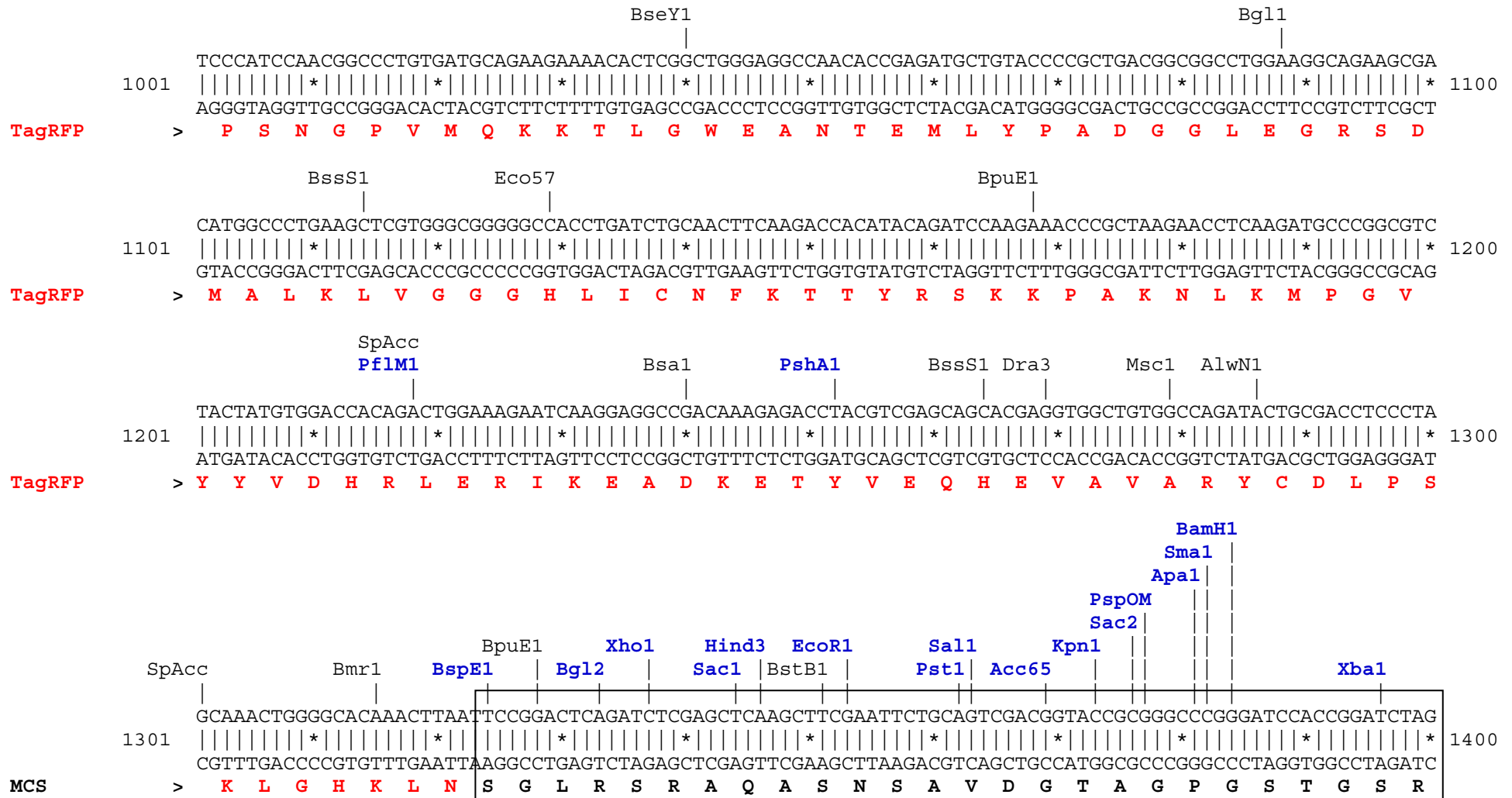


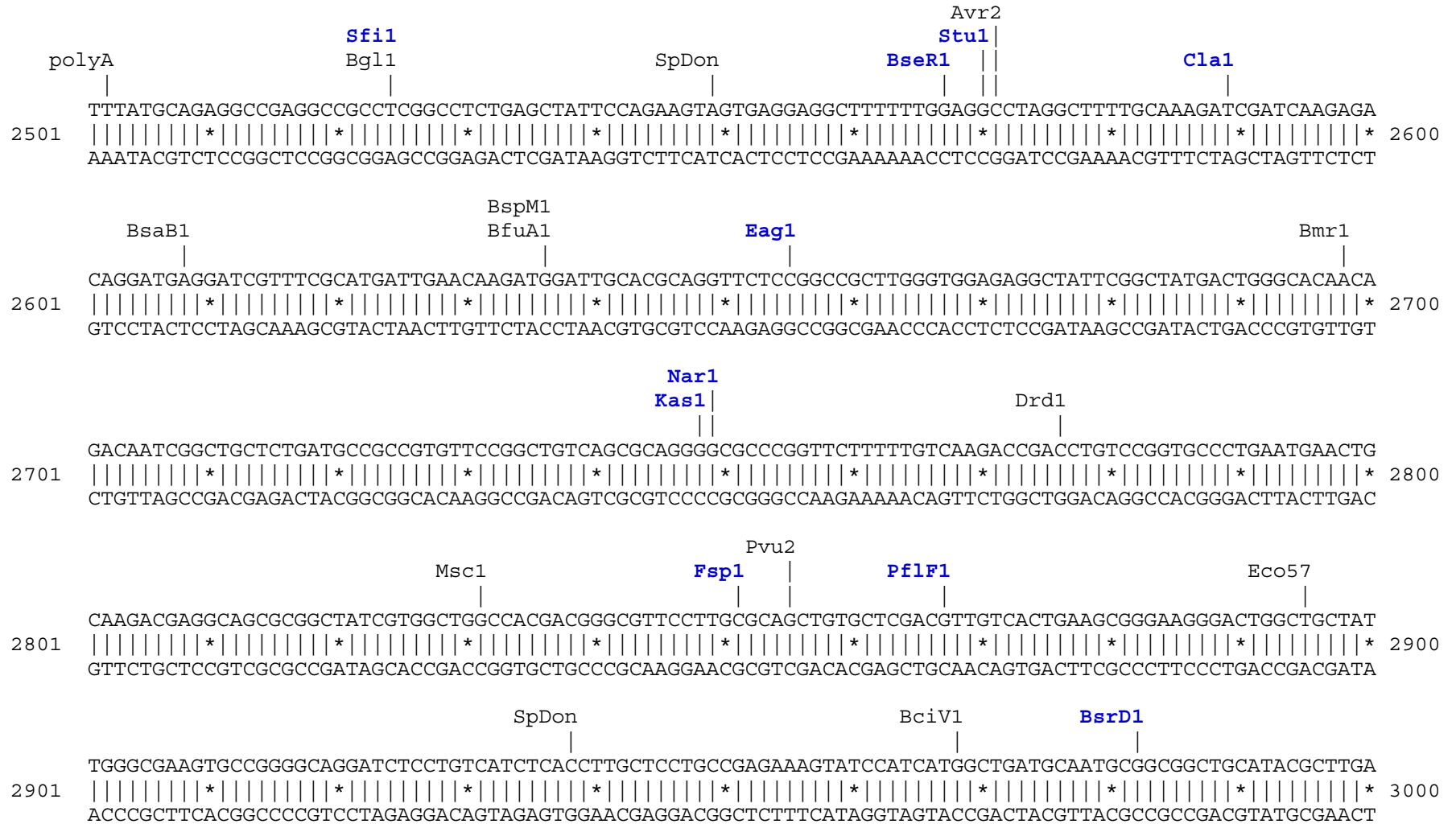
pTagRFP-C vector restriction map

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.







```

          BtgZ1
        BspM1 |
        BfuA1 |
          |
3001 TCCGGCTACCTGCCCATTCGACCACCAAGCGAAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTTCGATCAGGATGATCTGGACGAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
   AGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTT

          BpuE1 |
          Sph1 |
          Nco1 |
3101 GAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
   CTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCGAGTTCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACG

          BseY1 |
          Nae1 |
          NgoM4 |
          Rsr2 |
          Eci1 |
3201 CGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCCGGACCGCTATCAGGACATAGCGTTGGCTACCCGCTGA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
   GCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTCTGTATCGCAACCGATGGGCACT

          Sap1 |
          Ear1 |
          Eco57 |
          BssS1 |
          BsrB1 |
          BtgZ1 |
3301 TATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
   ATAACGACTTCTCGAACCGCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAA

          BssS1 |
          BspM1 |
          BfuA1 |
          SpAcc |
          BsrB1 |
          BstB1 |
3401 GACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
   CTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACT

```



```

                NsiI
                BfrB1 |
                |
                |
    4701  GGATAACCGTATTACCGCCATGCAT  4725
          |||||*|||||*|||||
          CCTATTGGCATAATGGCGGTACGTA
    
```

Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal
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	PshA1	Psi1
PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon
Sph1	Ssp1	Stu1	Xba1	Xho1									

Unique:

Acc65	Afe1	Age1	Ale1	Apa1	Ase1	BamH1	Bbs1	Bcl1	Bgl2	BsaXa	BsaXb	BseR1	BspE1
BspLU	BsrD1	BsrG1	Bts1	Clal	Eag1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1
Nar1	Nde1	Nhe1	PflF1	PflM1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SexA1	Sfi1
Sma1	SnaB1	Stu1	Xba1	Xho1									

Not found:

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Bcg1a	Bcg1b	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1
I_Ceu	loxP	Not1	Nru1	Pac1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1
Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1	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	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													