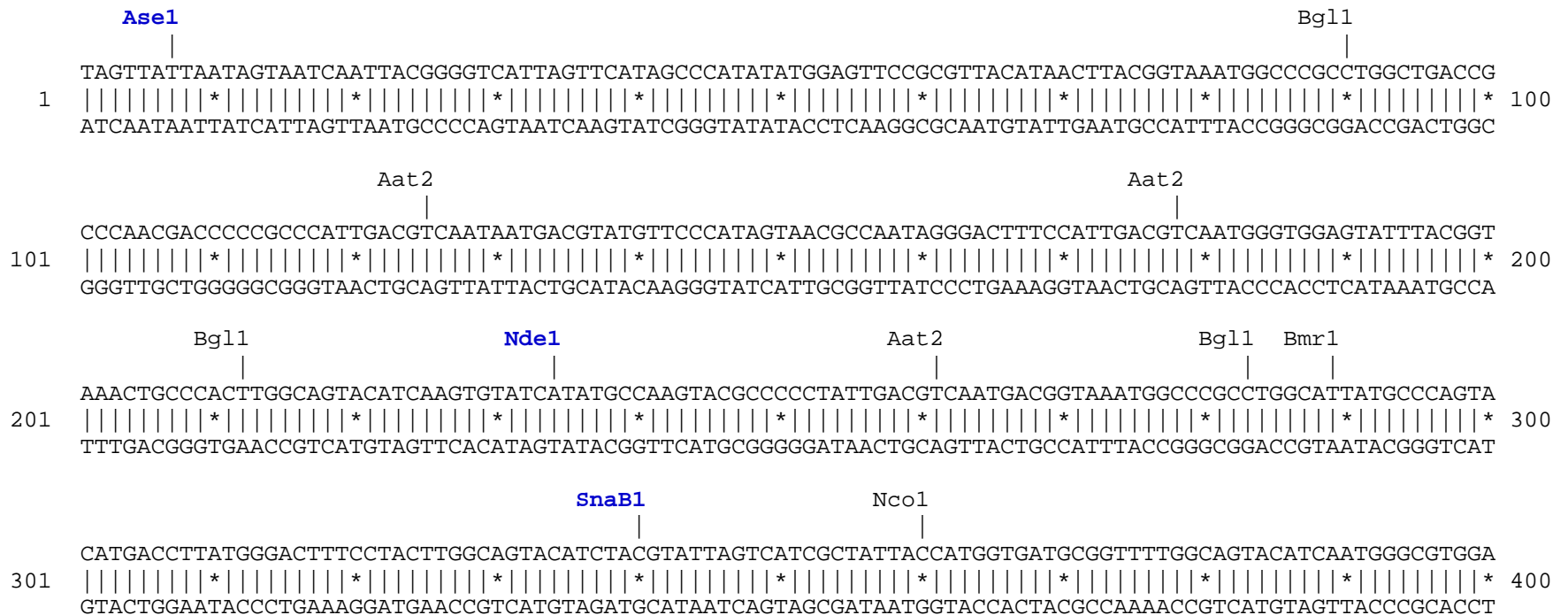


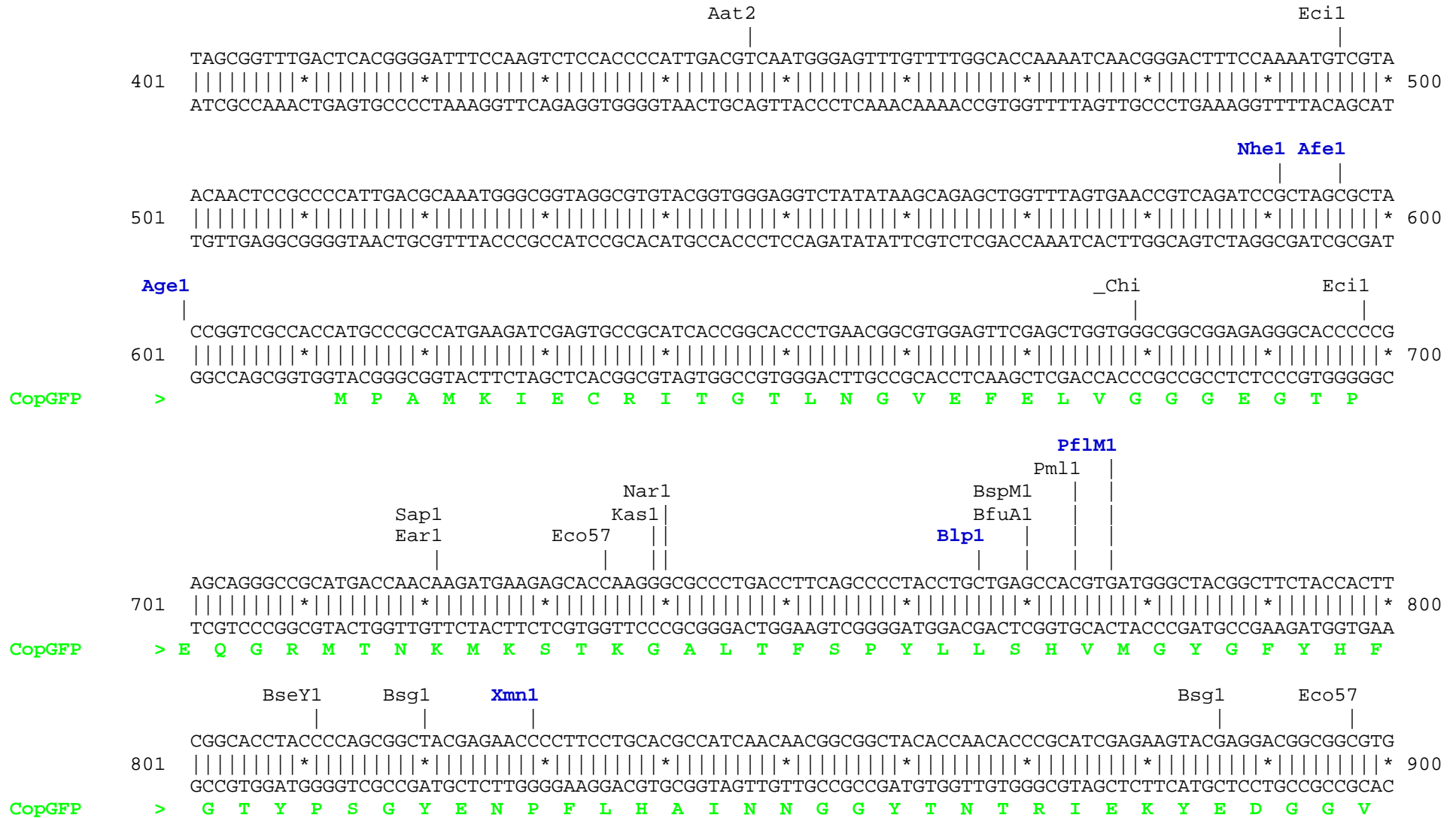
pCop-Green-peroxi vector restriction map

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).

Amino acids of peroxisomal targeting signal are shown in black.



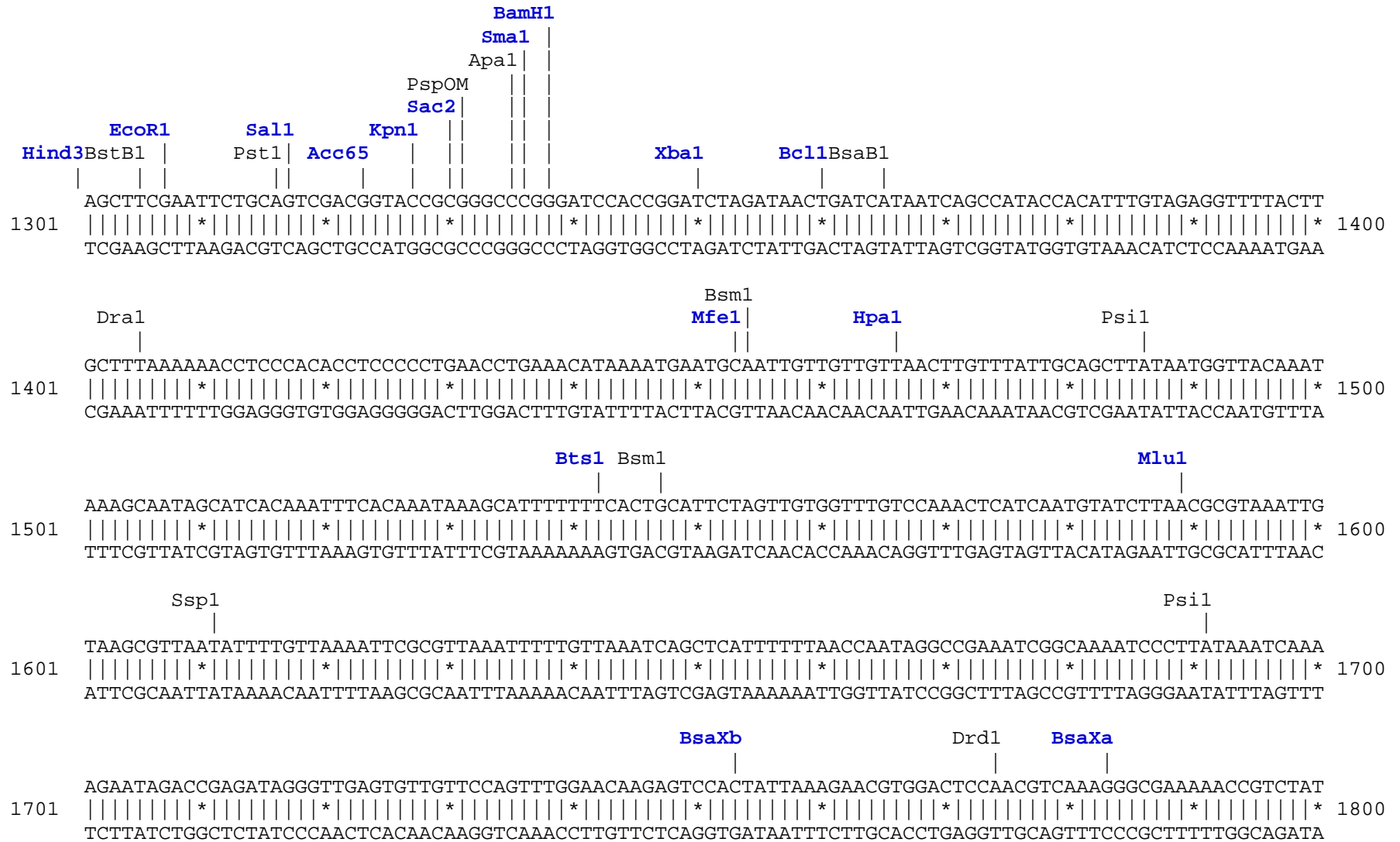


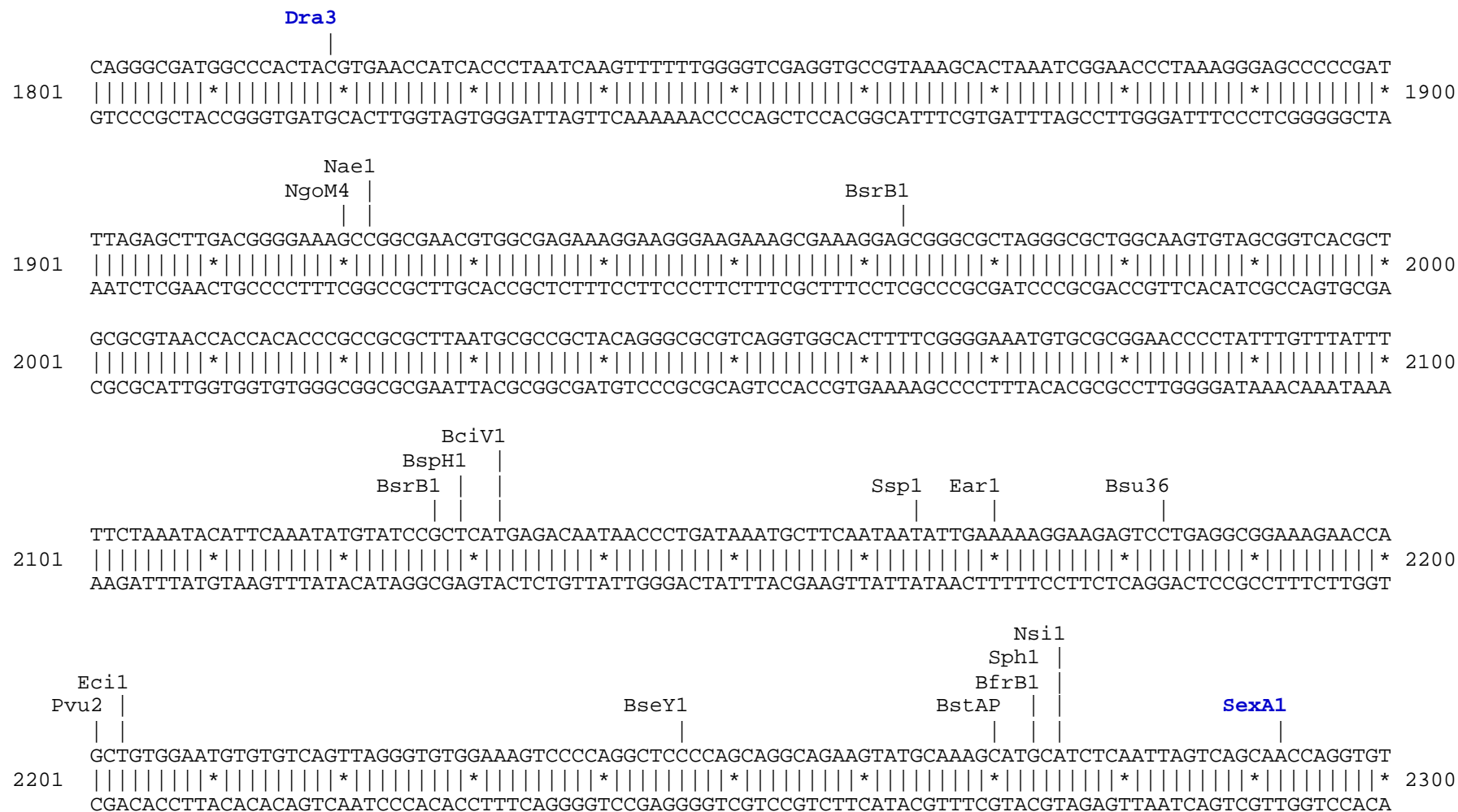
```
                                FseI
                                NaeI
                                EagI
                                PmlI
                                NgoM4
901  CTGCACGTGAGCTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGGCAGCTTCAAGGTGGTGGGCACCGGCTTCCCCGAGGACAGCGTGATCTTCACCG
   |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1000
GACGTGCACTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCACCACCCGTTGGCCGAAGGGGGCTCCTGTGCGACTAGAAGTGCC
CopGFP > L H V S F S Y R Y E A G R V I G D F K V V G T G F P E D S V I F T

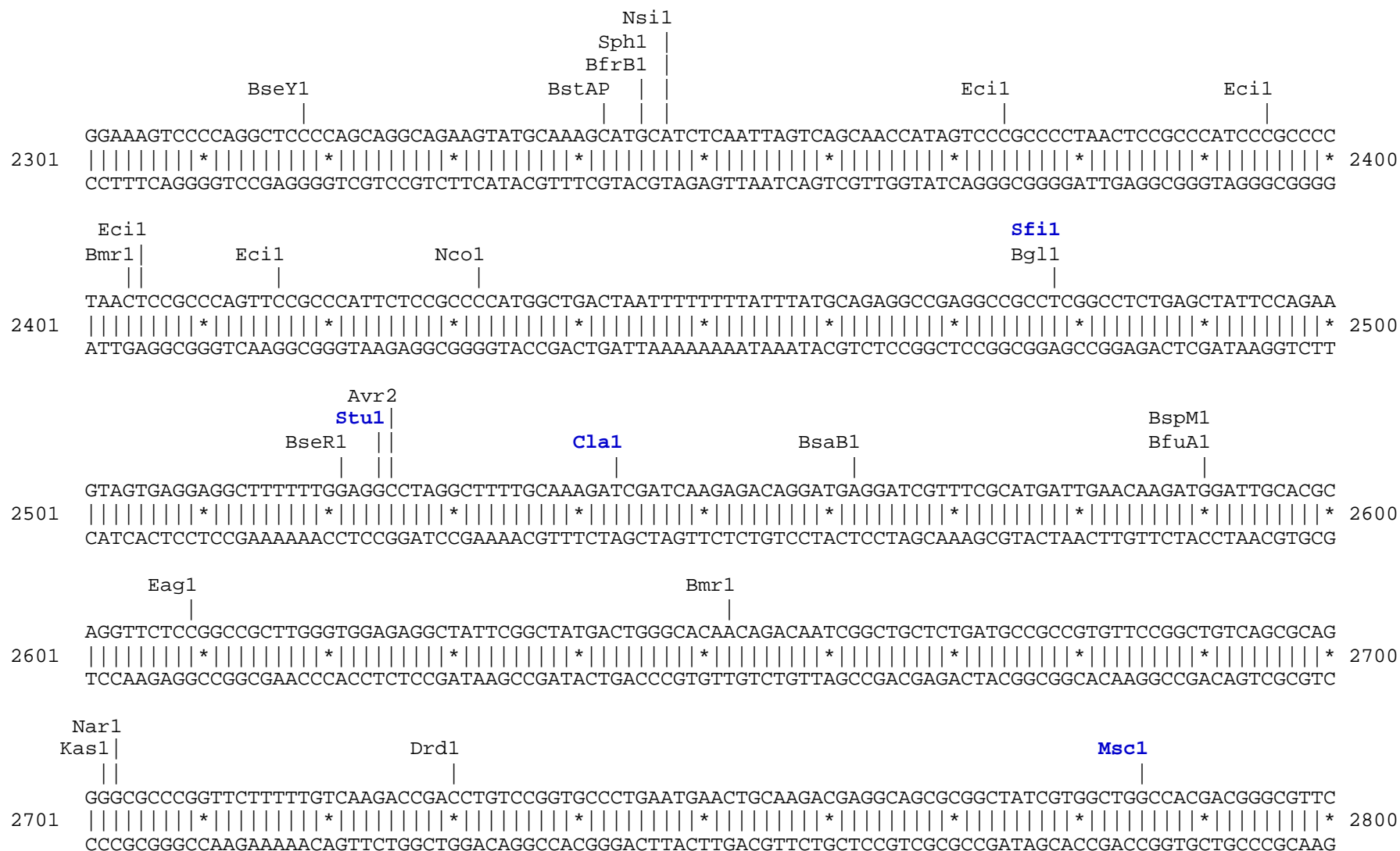
                                NcoI
                                BspM1
                                BfuA1
                                BsgI
                                AarI
                                Eco57
                                _Chi
1001 ACAAGATCATCCGCAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGTGCTGGTGGGCAGCTTCCGCCGCACCTTCAGCCTGCGCGACGG
   |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1100
TGTTCTAGTAGGCGTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCACGACCACCCGTCGAAGCGGGCGTGGGAAGTCGGACGCGCTGCC
CopGFP > D K I I R S N A T V E H L H P M G D N V L V G S F A R T F S L R D G

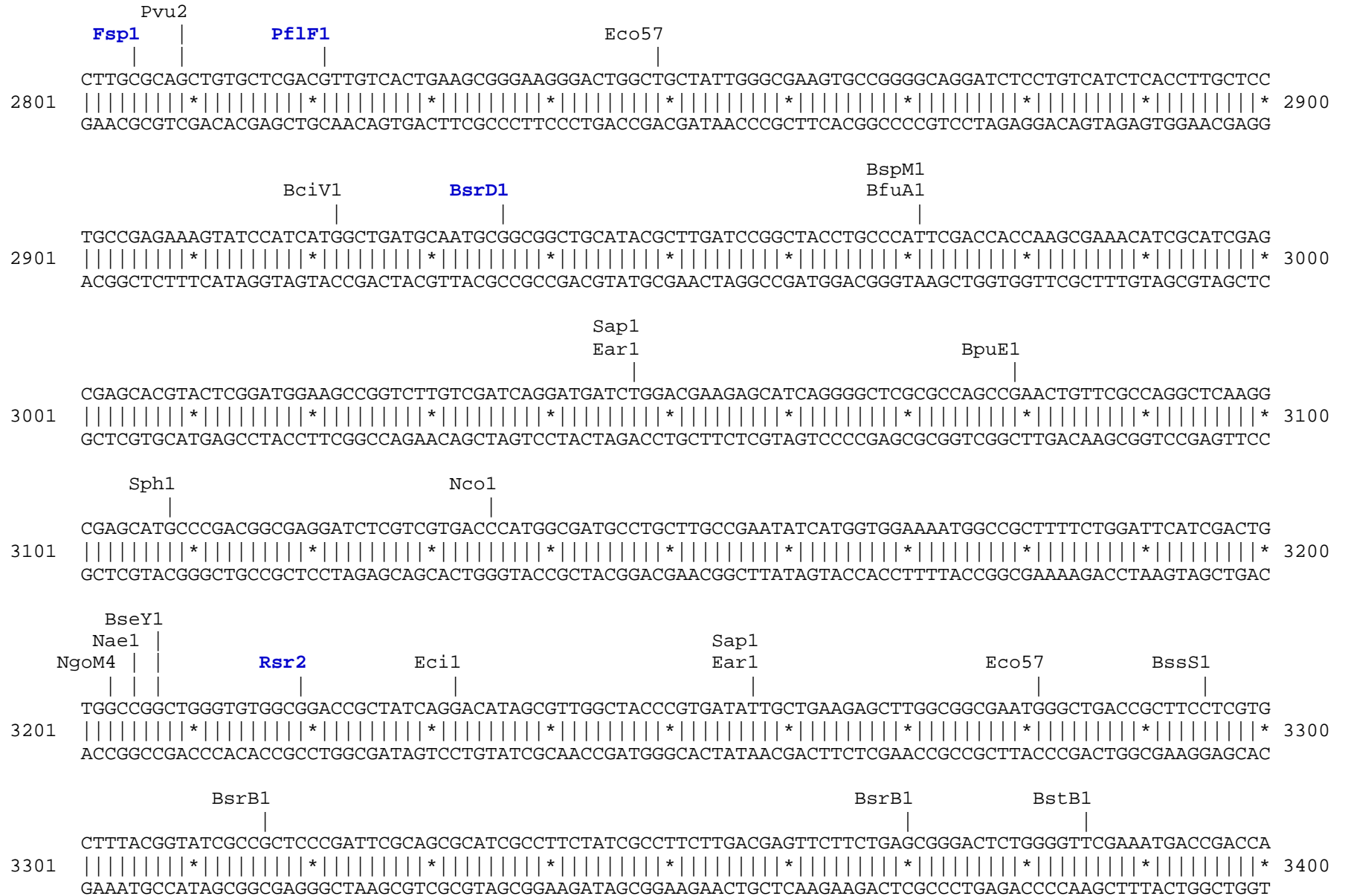
                                BseY1
                                Pst1
                                PspOM
                                Apal
                                Eci1
                                Bsg1
1101 CGGCTACTACAGCTTCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCAGCATCCTGCAGAACGGGGGCCCATGTTCGCCTTCCGCCCGC
   |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1200
GCCGATGATGTCGAAGCACCACTGTCGGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTTCGTAGGACGTCTTGCCCCGGGGTACAAGCGGAAGGCCGGCG
CopGFP > G Y Y S F V V D S H M H F K S A I H P S I L Q N G G P M F A F R R

                                BseR1
                                BseY1
                                Bsm1
                                PvuI
                                BpuE1
                                XhoI
                                SacI
1201 GTGGAGGAGCTGCACAGCAACACCGAGCTGGGCATCGTGGAGTACCAGCACGCTTCAAGACCCCGATCGCATTCGCCTCCAAGCTGTAGCTCGAGCTCA
   |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1300
CACCTCCTCGACGTGTCGTTGTGGCTCGACCCGTAGCACCTCATGGTTCGTGCGGAAGTTCTGGGGCTAGCGTAAGCGGAGGTTTCGACATCGAGCTCGAGT
CopGFP > V E E L H S N T E L G I V E Y Q H A F K T P I A F A S K L *
```










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                                     NsiI
                                     BfrB1 |
                                     | |
          BspLU
          |
CTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4679
GAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

```

Found:

Aar1	Aat2	Acc65	Afe1	Age1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	BciV1	Bcl1	BfrB1
BfuA1	Bgl1	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1
BspH1	BspLU	BspM1	BsrB1	BsrD1	BssS1	BstAP	BstB1	Bsu36	Bts1	_Chi	Cla1	Dra1	Dra3
Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fse1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1
Msc1	Nae1	Nar1	Nco1	Nde1	Ngom4	Nhe1	Nsi1	PflF1	PflM1	Pml1	Psil	PspOM	Pst1
Pvu1	Pvu2	Rsr2	Sac1	Sac2	Sal1	Sap1	SexA1	Sfi1	Sma1	SnaB1	Sph1	Ssp1	Stu1
Xba1	Xho1	Xmn1											

Unique:

Aar1	Acc65	Afe1	Age1	ApaL1	Ase1	BamH1	Bcl1	Blp1	Bsa1	BsaXa	BsaXb	BspLU	BsrD1
Bts1	Clal	Dra3	EcoR1	Fse1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Mlu1	Msc1	Nde1	Nhe1
PflF1	PflM1	Pvu1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1	SnaB1	Stu1	Xba1	Xho1
Xmn1													

Not found:

Acc1	Afl2	Ahd1	Ale1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcgl1a	Bcgl1b	Bgl2	BmgB1
Bpu10	BsiW1	BsmB1	BspE1	BsrG1	BssH2	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	ScFRT	FspA1
I_Ceu	loxP	Not1	Nru1	Pac1	Pme1	PshA1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1
Swal	PISce	Xcm1											

Excluded by site complexity:

Acc1	Acil	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													