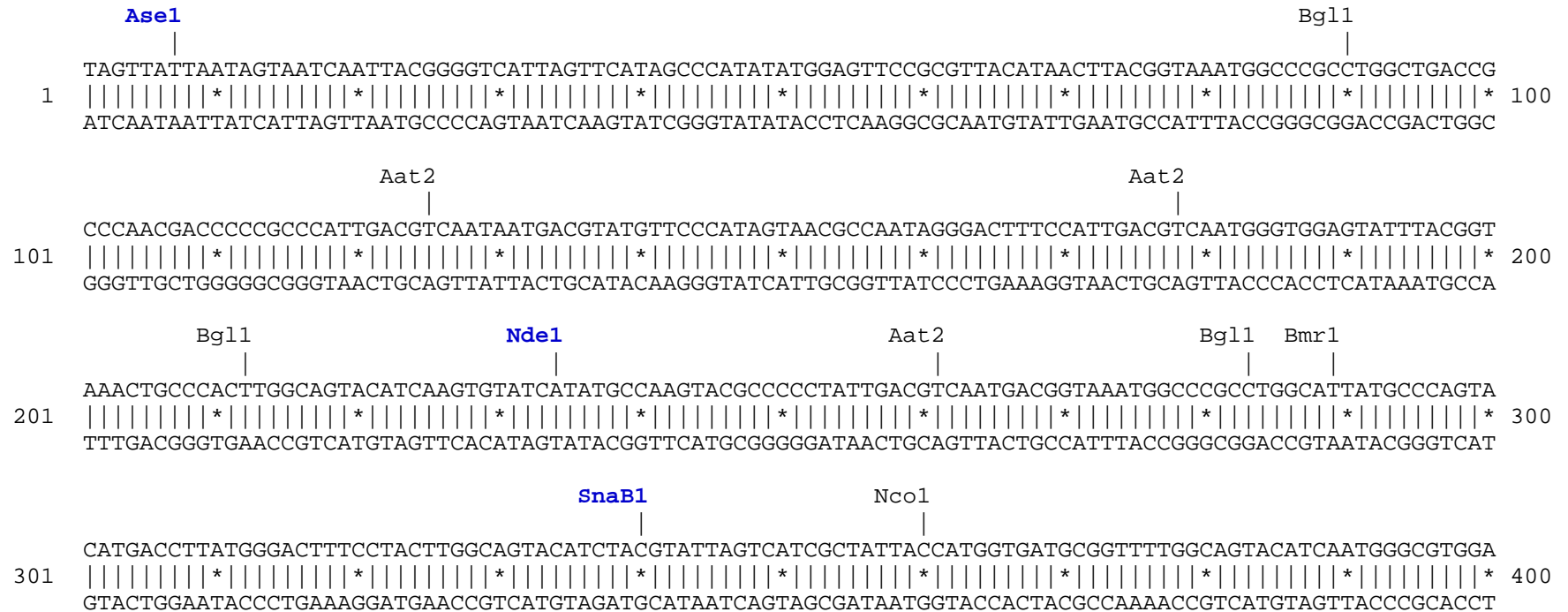


pCop-Green-mito vector restriction map

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) and amino acids added to the C-terminal of CopGFP to prevent aggregation are shown in bold black.




```
BseY1      Bsg1      Xmn1
|          |          |
ACCCAGCGGCTACGAGAACCCCTTCTGACGCCATCAACAACGGCGGCTACACCAACACCCGCATCGAGAAGTACGAGGACGGCGGGCGTGCTGCACGT
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
TGGGGTCGCCGATGCTCTTGGGGAAGGACGTGCGGTAGTTGTTGCCCGCGATGTGGTTGTGGGCGTAGCTCTTCATGCTCCTGCCGCCGCACGACGTGCA
CopGFP  > Y P S G Y E N P F L H A I N N G G Y T N T R I E K Y E D G G V L H V
```

```
Fse1
|
Nae1 |
Eag1 |
NcoM4 |
|
GAGCTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGCGACTTCAAGGTGGTGGGCACCCGGCTTCCCCGAGGACAGCGTGATCTTCACCGACAAGATC
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCACCACCCGTTGGCCGAAGGGGCTCCTGTGCGACTAGAAAGTGGCTGTTCTAG
CopGFP  > 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 D K I
```

```
Nco1
BspM1
BfuA1      Aar1      Eco57
|          |          |
Bsg1      |          |
|          |          |
ATCCGAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGTGCTGGTGGGCAGCTTCGCCCCGACCTTCAGCCTGCGCGACGGCGGCTACT
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
TAGGCGTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCACGACCACCCGTCGAAGCGGGCGTGGAAGTCGGACCGCTGCCGCCGATGA
CopGFP  > 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 G Y
```

```
Eci1
|
BseY1      Pst1      PspOM      Apal
|          |          |          |
|          |          |          |
ACAGCTTCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCCAGCATCCTGCAGAACGGGGGCCCCATGTTTCGCCTTCCGCCGCTGGAGGA
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
TGTCGAAGCACCACTGTCTGGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTTCGTAGGACGTCTTCCCCCGGGGTACAAGCGGAAGGCGGGCGCACCTCCT
CopGFP  > 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 V E E
```

```

                                Bsm1
                                Pvu1 |
                                BseR1  BseY1
                                |      |
1301 GCTGCACAGCAACACCGAGCTGGGCATCGTGGAGTACCAGCACGCCTTCAAGACCCCGATCGCATTTCGCCAGATCCAGAGCCCAGGCCAGCAACTCCGCC
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1400
    CGACGTGTCGTTGTGGCTCGACCCGTAGCACCTCATGGTCGTGCGGAAGTTCTGGGGCTAGCGTAAGCGGTCTAGGTCTCGGGTCCGGTTCGTTGAGGCGG
CopGFP > L H S N T E L G I V E Y Q H A F K T P I A F A R S R A Q A S N S A

                                Rsr2    Eag1    Xba1    BsaB1    Dra1
                                |      |      |      |      |
1401 GTGGATGGCACAGCCGGACCCGGGATCGGCCCGGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACAC
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1500
    CACCTACCGTGTTCGGCCTGGCCCTAGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTG
CopGFP > V D G T A G P G S A A T L D H N Q P Y H I C R G F T C F K K P P T

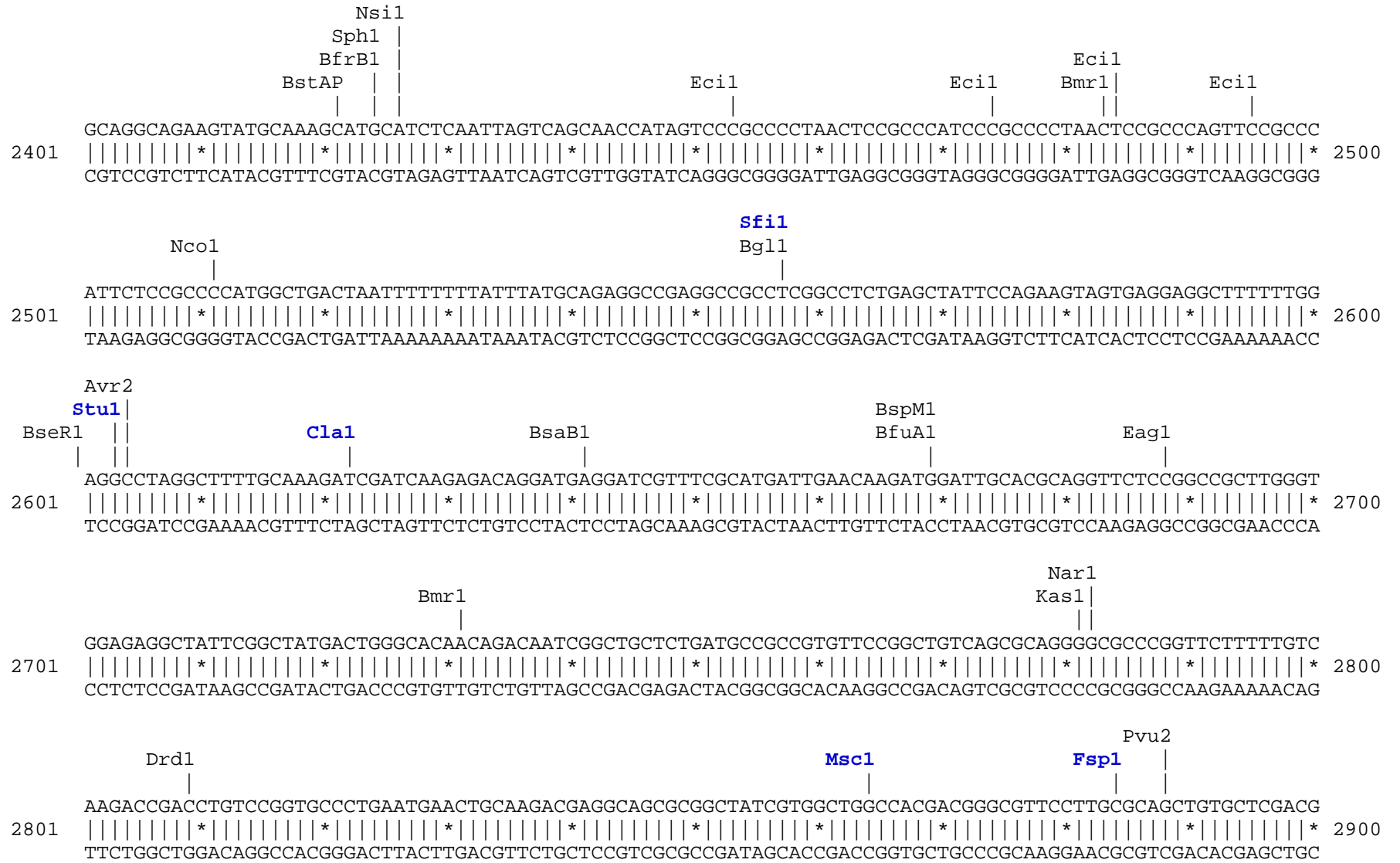
                                Bsm1
                                Mfe1 |      Hpa1 |      Pst1 |
                                ||      |      |
1501 CTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAAATAAAGCAATAGCATCACAAATT
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1600
    GAGGGGGACTTGGACTTTGTATTTTACTTTACGTTAAACAACAATGAACAAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAA
CopGFP > P P P E P E T *

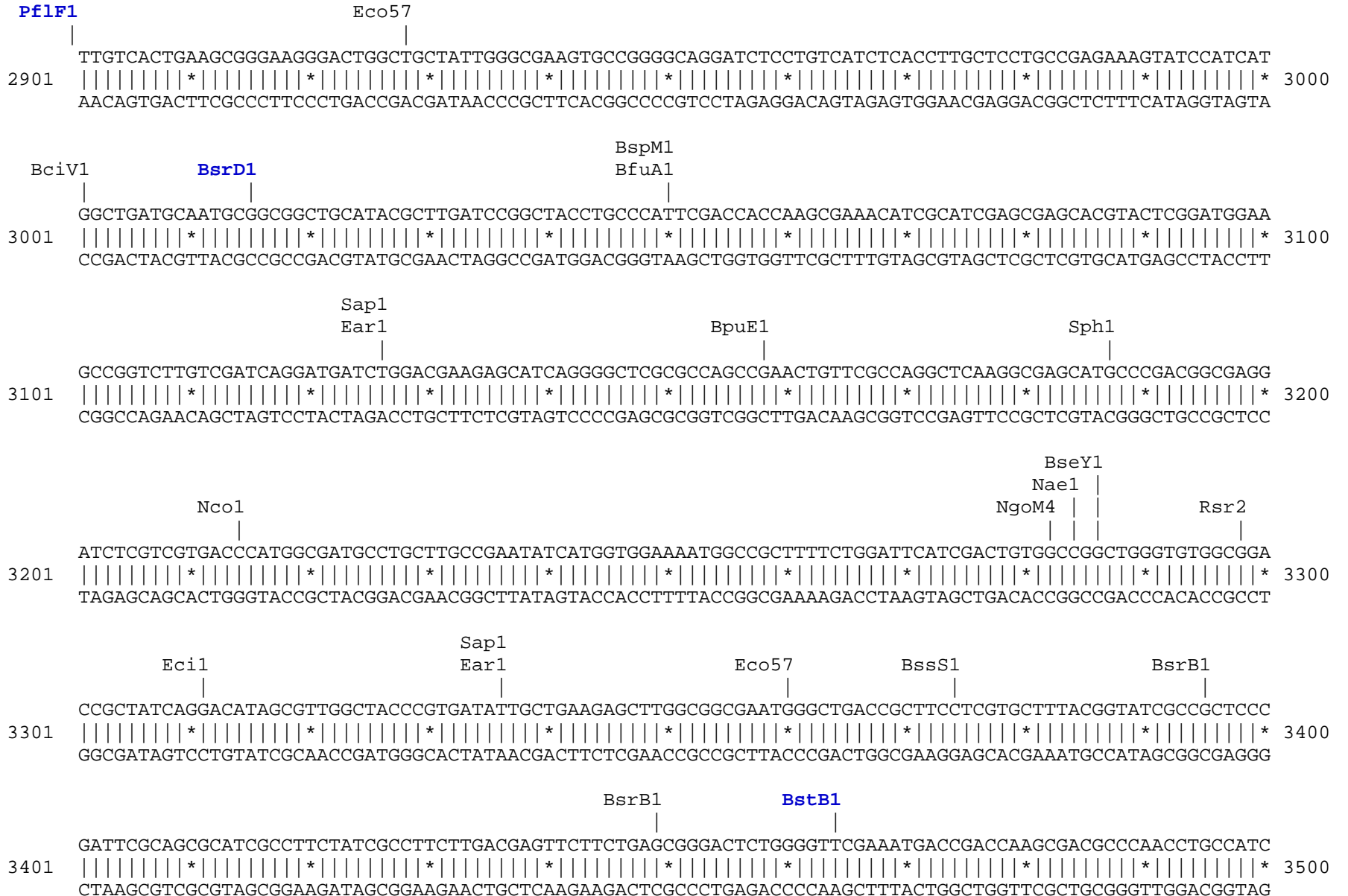
                                Bts1 Bsm1                                Afl12                                Ssp1
                                |      |      |      |      |      |      |
1601 TCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAA
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1700
    AGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGTAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAACAATT

                                Pst1
                                |
1701 AATTCGCGTTAAATTTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTT
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1800
    TTAAGCGCAATTTAAAAACAATTTAGTTCGAGTAAAAAATTTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTTCTTATCTGGCTCTATCCCAA

                                BsaXb                                Drd1    BsaXa                                Dra3
                                |      |      |      |      |      |
1801 GAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGT
    |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1900
    CTCACAACAAGGTCAAACCTTGTTCCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTTGGCAGATAGTCCCGCTACCGGGTGTATGCA

```



Eco57
|
AAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACT
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
TTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCTCTATGGTTTATGA

AlwN1
|
GTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCA
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGT

BpuE1
|
GTGGCGATAAGTCGTGCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAG
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
CACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCGGGTC

ApaI1
|
BseY1
|
CTTGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTA
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
GAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCAT

BciV1
|
BssS1
|
Drd1
|
AGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGC
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
TCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCG

BpuE1
|
Eci1
|
GTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGCGCCTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTCTCA
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
CAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGT

```

                                     NsiI
                                     BfrB1 |
                                     | |
BspLU |
|
4701 | CATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4758
    |
    GTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

```

Found:

Aar1	Aat2	Afl2	Age1	AlwN1	Apa1	Apal1	Ase1	Avr2	BamH1	BciV1	BfrB1	BfuA1	Bgl1
Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	BspLU
BspM1	BsrB1	BsrD1	BssH2	BssS1	BstAP	BstB1	Bsu36	Bts1	_Chi	Clal	Dra1	Dra3	Drd1
Eag1	Ear1	Eci1	Eco57	Fse1	Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1
NgoM4	Nhe1	Nsi1	PflF1	PflM1	Pml1	Psi1	PspOM	Pst1	Pvu1	Pvu2	Rsr2	Sap1	SexA1
Sfi1	SnaB1	Sph1	Ssp1	Stu1	Xba1	Xmn1							

Unique:

Aar1	Afl2	Age1	Apa1	ApaL1	Ase1	BamH1	Blp1	Bsa1	BsaXa	BsaXb	BspLU	BsrD1	BssH2
BstB1	Bts1	Cla1	Dra3	Fse1	Fsp1	Hpa1	Mfe1	Msc1	Nde1	Nhe1	PflF1	PspOM	Pst1
Pvu1	SexA1	Sfi1	SnaB1	Stu1	Xba1	Xmn1							

Not found:

Acc65	Acc1	Afe1	Ahd1	Ale1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	BcglA	Bcglb	Bcl1
Bgl2	BmgB1	Bpu10	BsiW1	BsmB1	BspE1	BsrG1	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoR1	EcoRV
ScFRT	FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Not1	Nru1	Pac1	Pme1	PshA1	Sac1	Sac2
Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	PISce	Xcm1	Xho1	

Excluded by site complexity:

Acc1	Ac1	Afl3	Alu1	Alw1	Ap01	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													