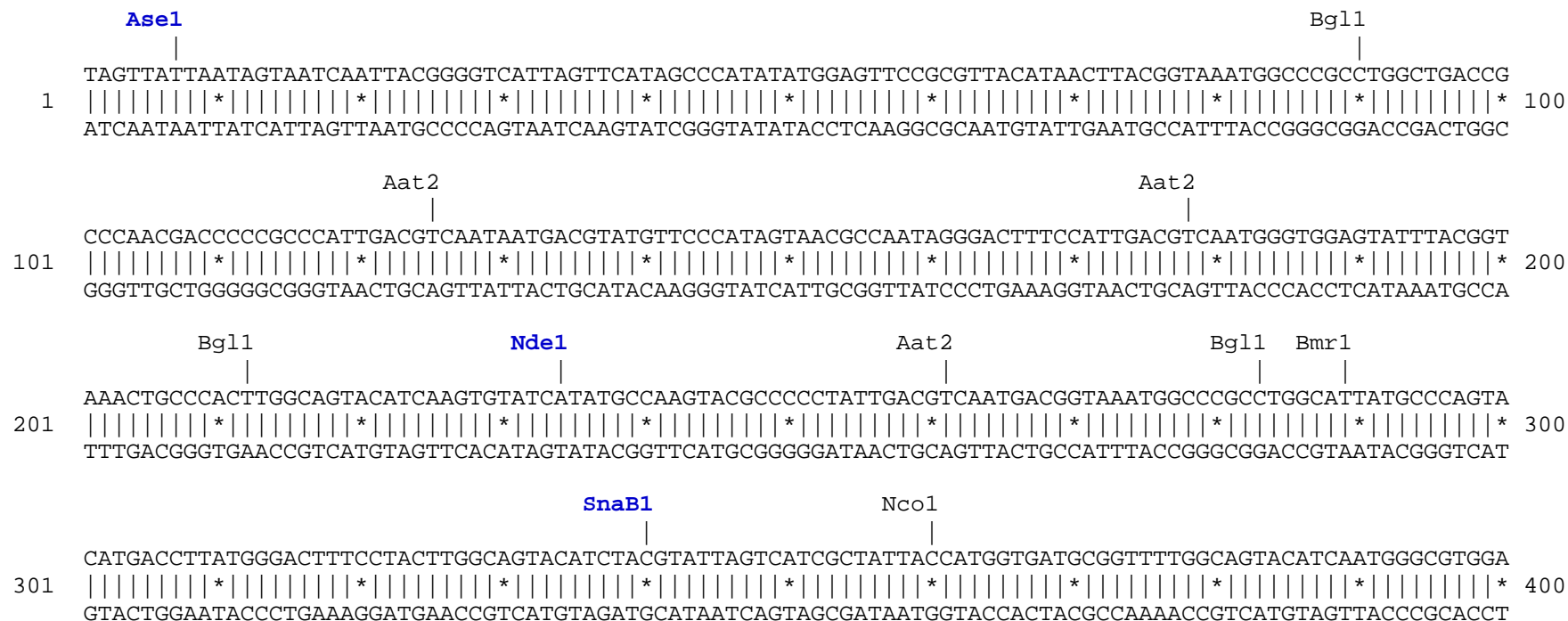
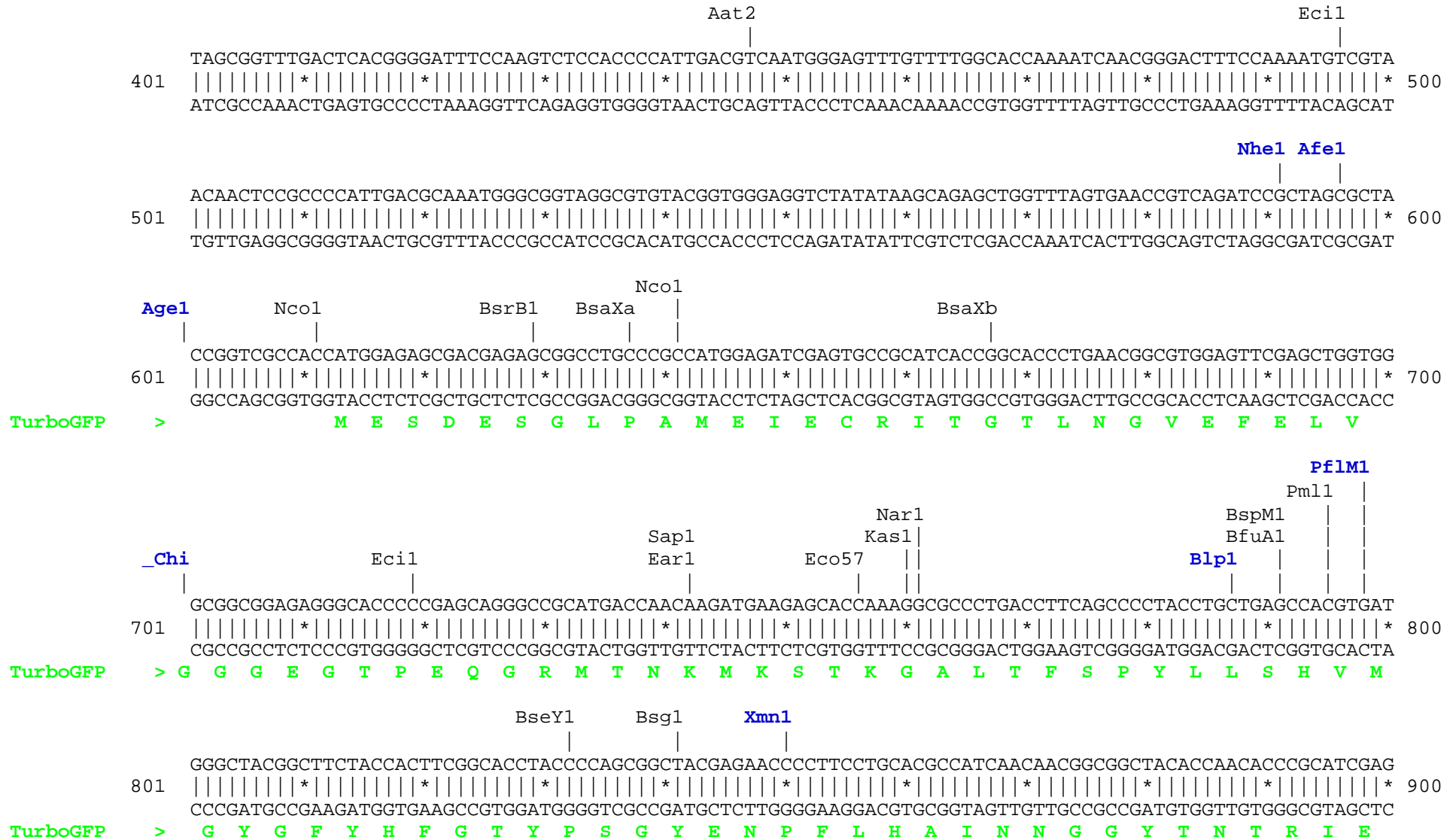


### pTurboGFP-C vector restriction map

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 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 shown in frame, amino acids coded by MCS shown in black.





```

                                     Fse1
                                     Nae1 |
                                     Eag1 |
                                     NgoM4 |
    Bsg1      Eco57      Pml1
    |         |         |
    AAGTACGAGGACGGCGGGCGTGCTGCACGTGAGCTTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGGCGACTTCAAGGTGATGGGCACCCGGCTTCCCCG
901 |          * |         * |          * |          * |          * |          * |          * |          * |          * |          * |          * |
    TTCATGCTCCTGCCGCCGACGACGTGCACTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCTACTACCCGTTGGCCGAAGGGGC
TurboGFP > K Y E D G G V L H V S F S Y R Y E A G R V I G D F K V M G T G F P

```

```

                                     Nco1
                                     BspM1
                                     BfuA1
                                     Bsg1
                                     Aar1
                                     BsaB1
                                     Eco57
    AGGACAGCGTGATCTTCACCGACAAGATCATCCGCAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGATCTGGATGGCAGCTTACCCCG
1001 |          * |         * |          * |          * |          * |          * |          * |          * |          * |          * |
    TCCTGTGCACTAGAAAGTGGCTGTTCTAGTAGGCGTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCTAGACCTACCGTTCGAAGTGGGC
TurboGFP > E D S V I F T D K I I R S N A T V E H L H P M G D N D L D G S F T R

```

```

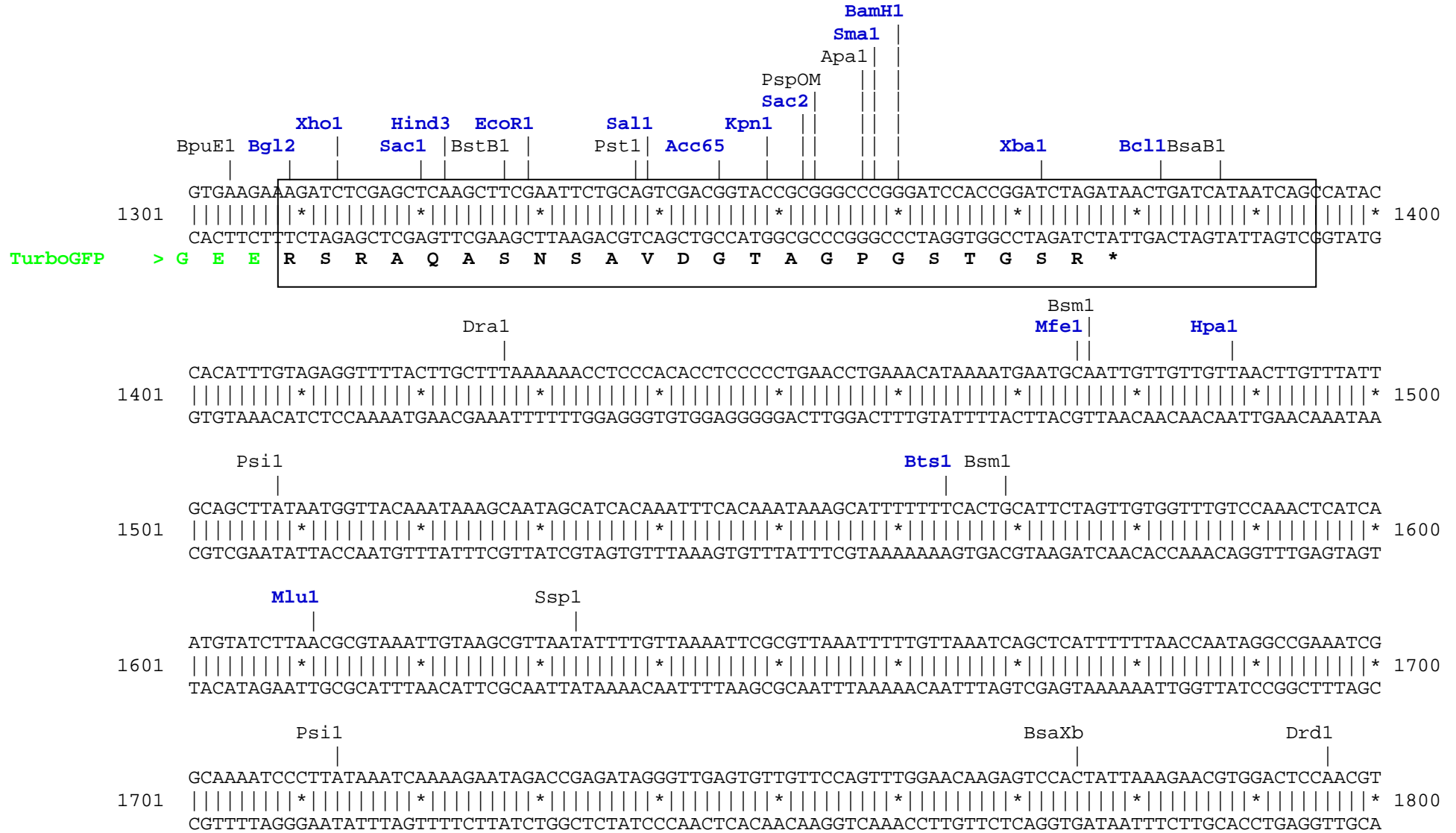
    BsaXb
    |
    CACCTTCAGCCTGCGGACGGCGGCTACTACAGCTCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCCAGCATCTGTGAGAACGGGGGC
1101 |          * |         * |          * |          * |          * |          * |          * |          * |          * |          * |
    GTGGAAGTCGGACGCGCTGCCGCCGATGATGTCGAGGACCCACCTGTCCGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTTCGTAGGACGTCTTGCCCCCG
TurboGFP > T F S L R D G G Y Y S S V V D S H M H F K S A I H P S I L Q N G G

```

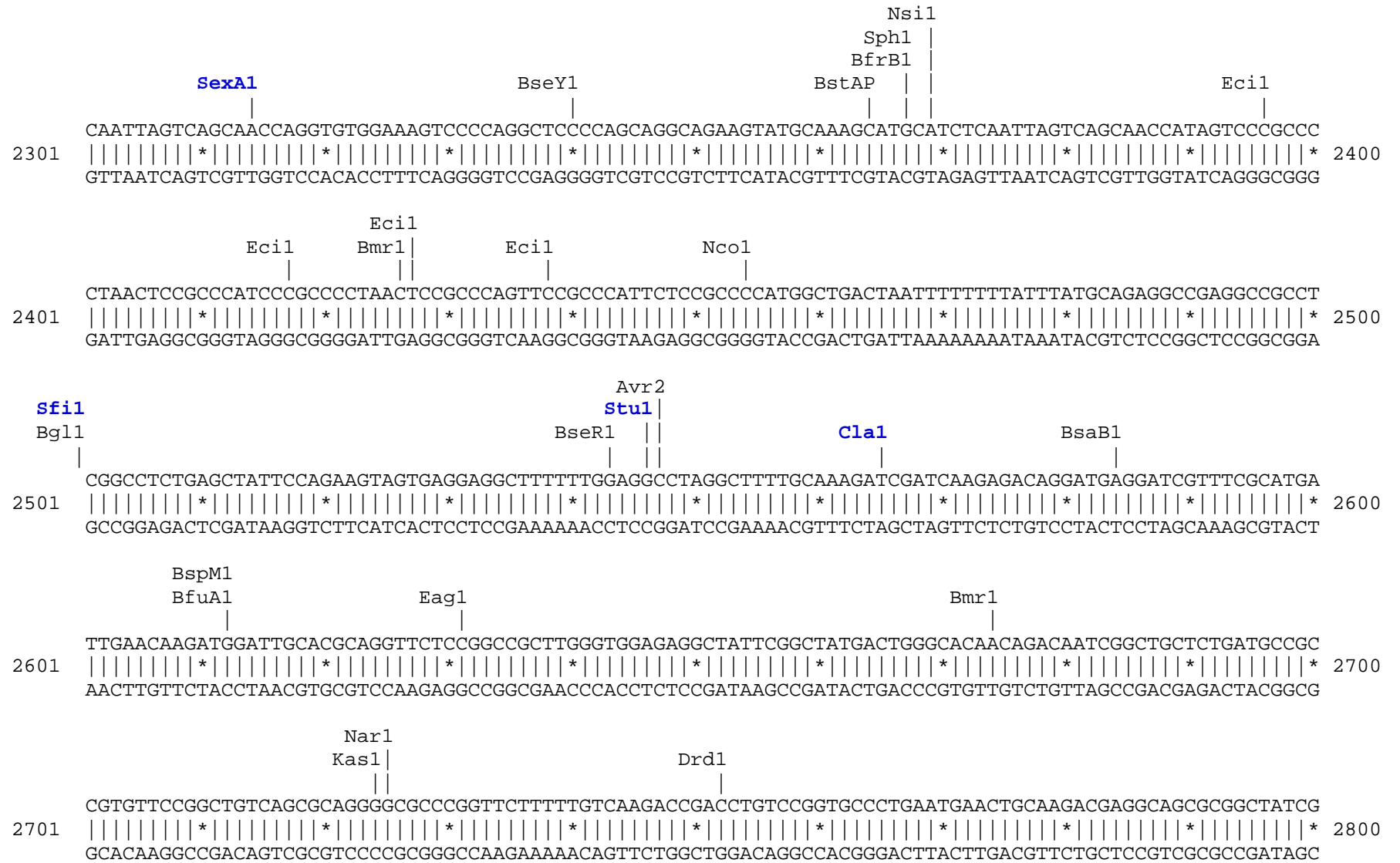
```

    Ecil
    Apa1 |
    |
    CACCTTCAGCCTGCGGACGGCGGCTACTACAGCTCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCCAGCATCTGTGAGAACGGGGGC
1201 |          * |         * |          * |          * |          * |          * |          * |          * |          * |          * |
    GGGTACAAGCGGAAGGCGGGCGCACCTCCTCCTAGTGTCGTTGTGGCTCGACCCGTAGCACCTCATGGTTCGTGCGGAAGTTCTGGGGCTACGTCTACGGC
TurboGFP > P M F A F R R V E E D H S N T E L G I V E Y Q H A F K T P D A D A

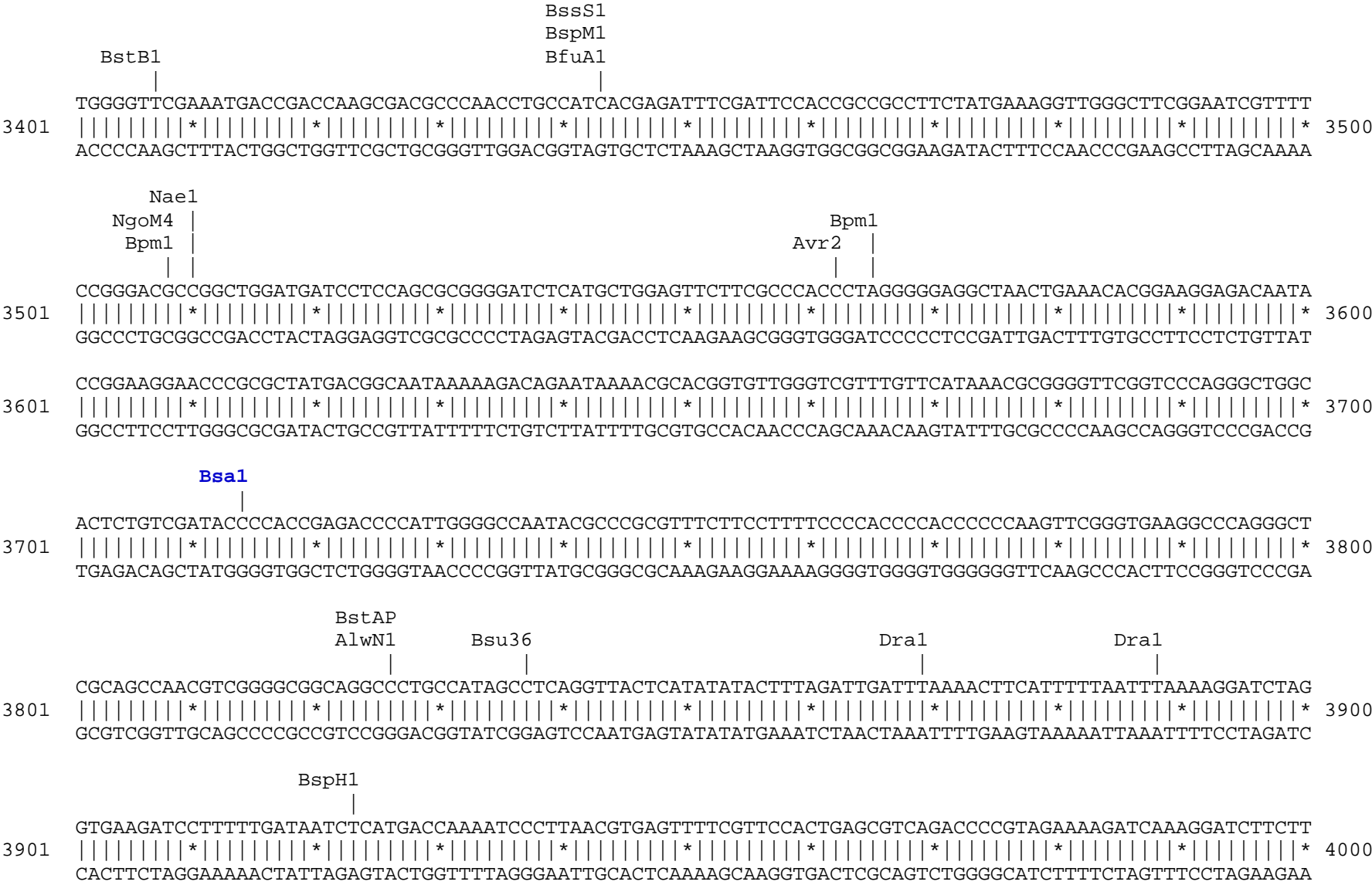
```













```

          BpuE1
          |
GAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTT
4001 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4100
      CTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAA

Eco57
|
TCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCGCCT
4101 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4200
      AGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGA

          AlwN1          BpuE1
          |          |
ACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG
4201 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4300
      TGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTACAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCC

          ApaI1          BseY1
          |          |
CGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAG
4301 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4400
      GCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTTCGAACTCGCTTGCTGGATGTGGCTTACTCTATGGATGTCGCACTCGATACTCTTTC

          BciV1          BssS1
          |          |          |
CGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGCCTGG
4401 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4500
      GCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTGCGCCGTCCAGCCTTGTCCTCTCGCGTGTCTCCCTCGAAGGTCCCCCTTTGCGGACC

          Drd1          BpuE1          EcoI
          |          |          |
TATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG
4501 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4600
      ATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTTCGTTGC

```



Found:

- |             |             |              |             |             |              |              |              |             |              |              |             |             |             |
|-------------|-------------|--------------|-------------|-------------|--------------|--------------|--------------|-------------|--------------|--------------|-------------|-------------|-------------|
| <b>Aar1</b> | Aat2        | <b>Acc65</b> | <b>Afe1</b> | <b>Age1</b> | AlwN1        | Apa1         | <b>ApaL1</b> | <b>Ase1</b> | Avr2         | <b>BamH1</b> | BciV1       | <b>Bcl1</b> | BfrB1       |
| BfuA1       | Bgl1        | <b>Bgl2</b>  | <b>Blp1</b> | Bmr1        | Bpm1         | BpuE1        | <b>Bsa1</b>  | BsaB1       | BsaXa        | BsaXb        | BseR1       | BseY1       | Bsg1        |
| Bsm1        | BspH1       | <b>BspLU</b> | BspM1       | BsrB1       | <b>BsrD1</b> | BssS1        | BstAP        | BstB1       | Bsu36        | <b>Bts1</b>  | <b>_Chi</b> | <b>Cla1</b> | Dra1        |
| <b>Dra3</b> | Drd1        | Eag1         | Ear1        | Eci1        | Eco57        | <b>EcoR1</b> | <b>Fse1</b>  | <b>Fsp1</b> | <b>Hind3</b> | <b>Hpa1</b>  | Kas1        | <b>Kpn1</b> | <b>Mfe1</b> |
| <b>Mlu1</b> | <b>Msc1</b> | Nae1         | Nar1        | Nco1        | <b>Nde1</b>  | NgoM4        | <b>Nhe1</b>  | Nsil        | <b>PflF1</b> | <b>PflM1</b> | Pml1        | Psil        | PspOM       |
| Pst1        | Pvu2        | <b>Rsr2</b>  | <b>Sac1</b> | <b>Sac2</b> | <b>Sal1</b>  | Sap1         | <b>SexA1</b> | <b>Sfi1</b> | <b>Sma1</b>  | <b>SnaB1</b> | Sph1        | Ssp1        | <b>Stu1</b> |
| <b>Xba1</b> | <b>Xho1</b> | <b>Xmn1</b>  |             |             |              |              |              |             |              |              |             |             |             |

Unique:

Aar1	Acc65	Afe1	Age1	ApaL1	Ase1	BamH1	Bcl1	Bgl2	Blp1	Bsa1	BspLU	BsrD1	Bts1
_Chi	Clal	Dra3	EcoR1	Fse1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Mlu1	Msc1	Nde1	Nhe1
PflF1	PflM1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1	SnaB1	Stu1	Xba1	Xho1	Xmn1

Not found:

Acc1	Afl2	Ahd1	Ale1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcg1a	Bcg1b	BmgB1	Bpu10
BsiW1	BsmB1	BspE1	BsrG1	BssH2	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	ScFRT	FspA1	I_Ceu
loxP	Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1
Swal	PISce	Xcm1											

Excluded by site complexity:

Acc1	Ac11	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													