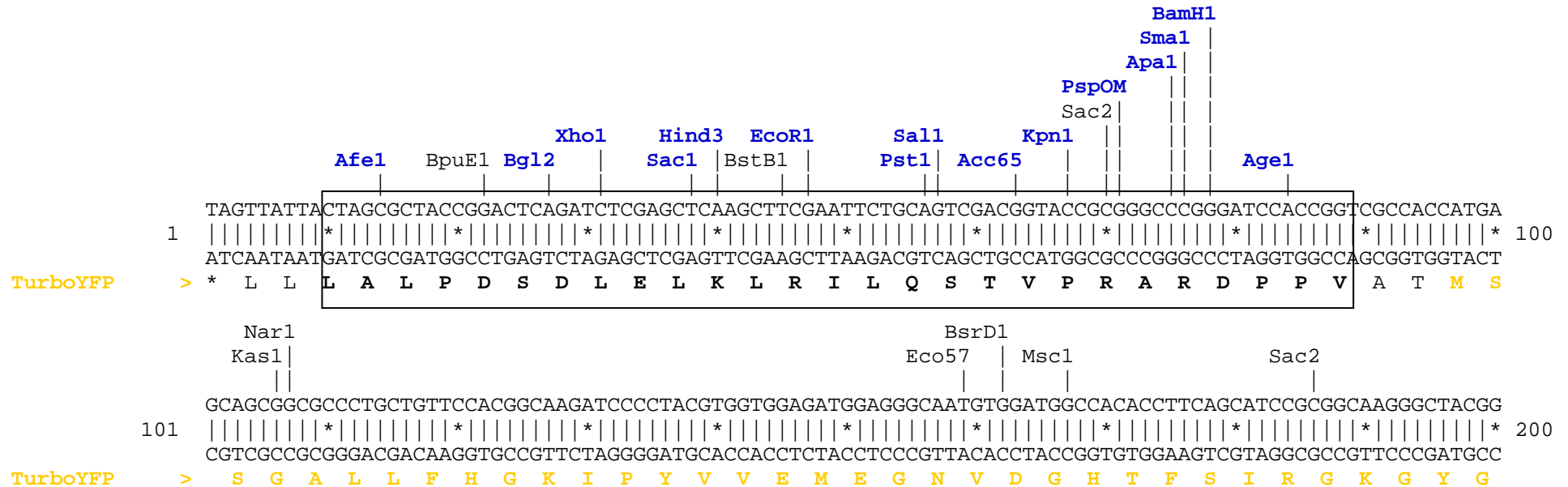


pTurboYFP-PRL vector restriction map

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 bold black.



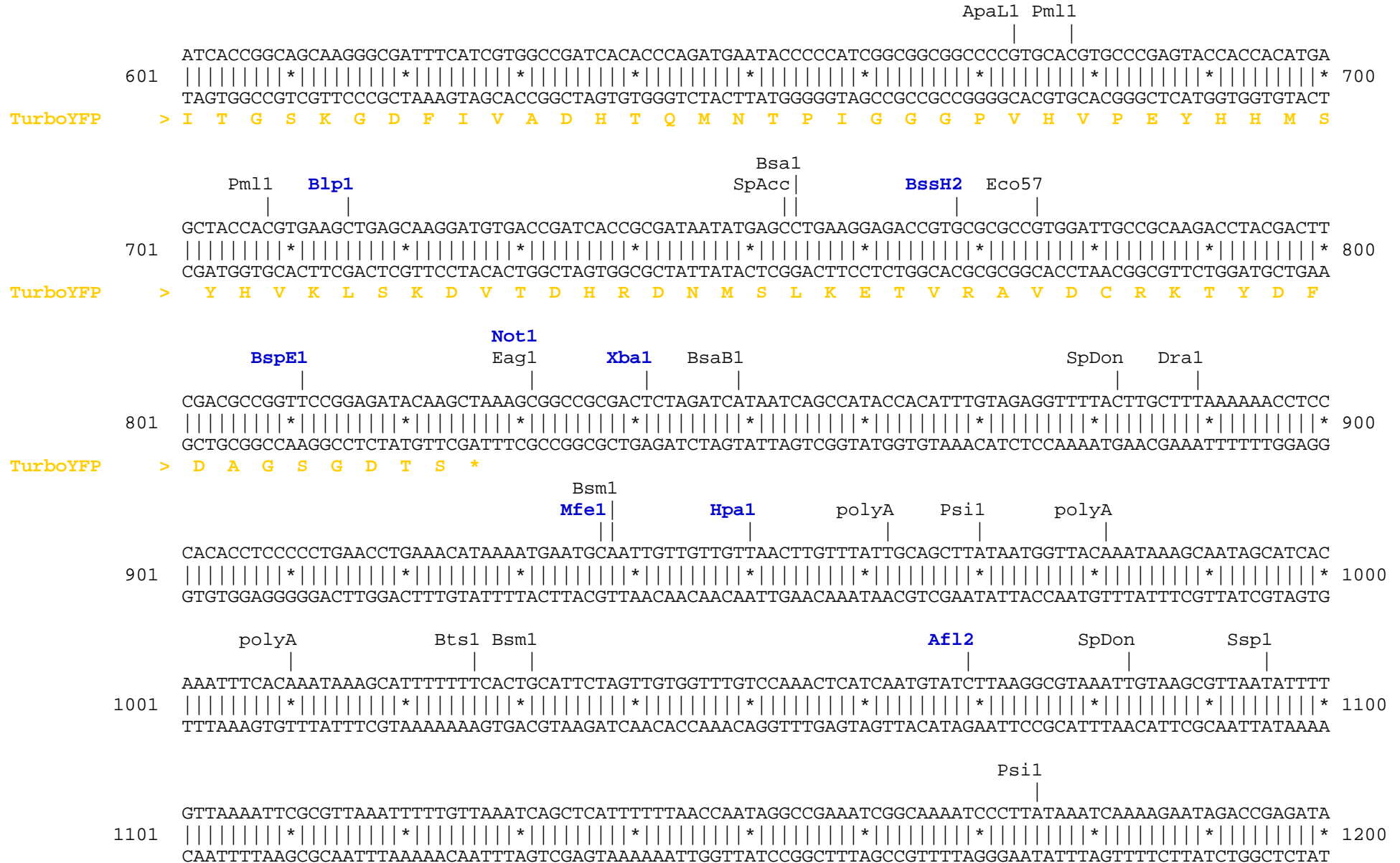
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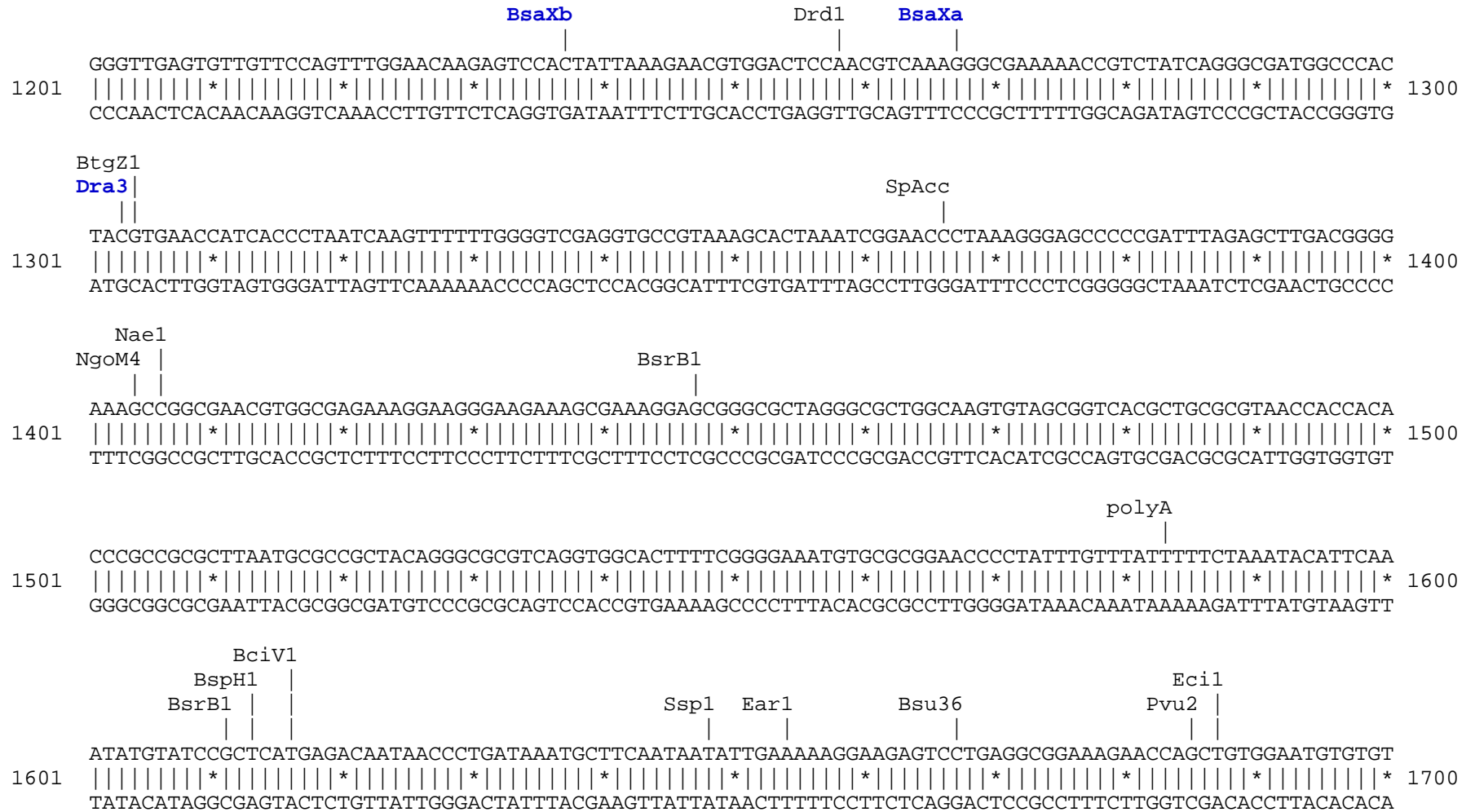
                                     Bsg1
                                     Bmr1
          BtgZ1          SgrA1          BtgZ1          BstE2          Bpm1          Nar1
                                     Kas1
                                     Bmr1
CGATGCCAGCGTGGGCAAGGTGGATGCCAGTTTCATCTGCACCACCGGCGATGTGCCCGTGCCCTGGAGCACCCCTGGTGTACCACCCTGACCTACGGCGCC
201  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 300
GCTACGGTCGCACCCGTTCCACCTACGGGTCAAGTAGACGTGGTGGCCGCTACACGGGCACGGGACCTCGTGGGACCACTGGTGGGACTGGATGCCGCGG
TurboYFP > D A S V G K V D A Q F I C T T G D V P V P W S T L V T T L T Y G A

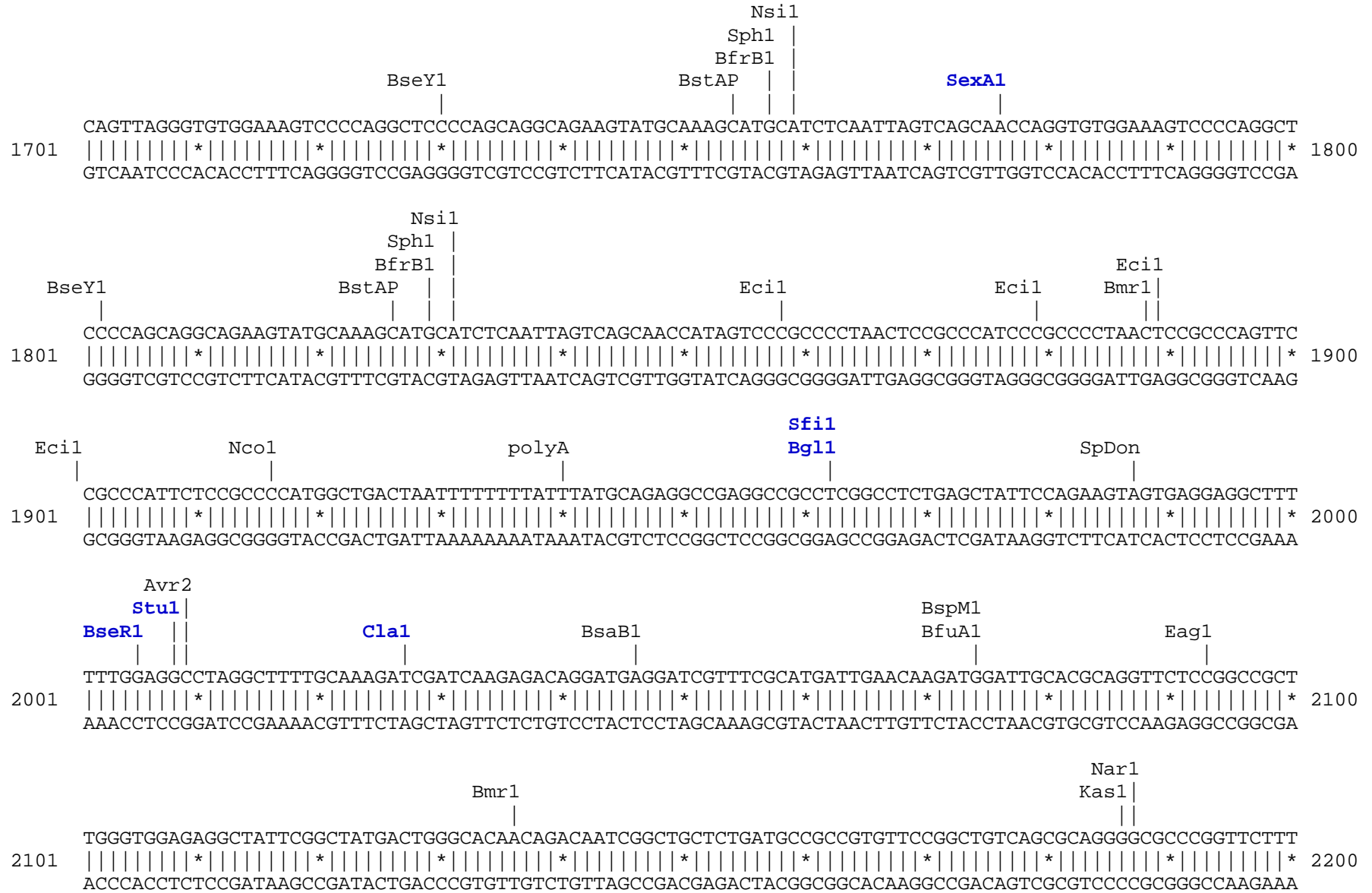
                                     SpAcc
                                     Xmn1          Eco57 Sph1          Bsg1
CAGTGTTCGCCAAGTACGGCCCCGAGCTGAAGGATTTCTACAAGAGCTGCATGCCCGATGGCTACGTGCAGGAGCGCACCATCACCTTCGAGGGCGATG
301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 400
GTCACGAAGCGGTTTCATGCCGGGGCTCGACTTCTAAAGATGTTCTCGACGTACGGGCTACCGATGCACGTCCTCGCGTGGTAGTGGAAGCTCCCGCTAC
TurboYFP > Q C F A K Y G P E L K D F Y K S C M P D G Y V Q E R T I T F E G D G

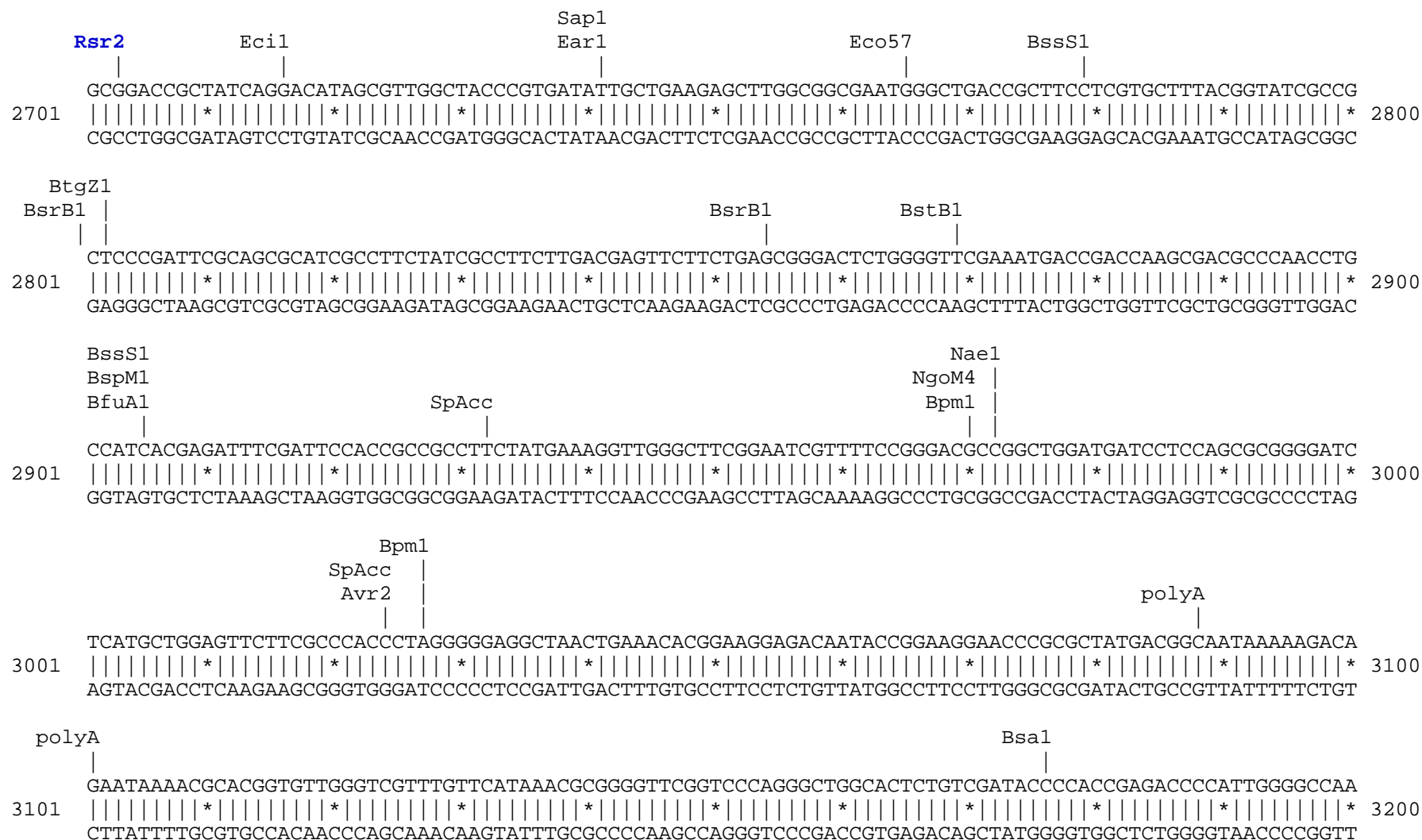
                                     BstE2          BsrG1          Msc1          PflM1
                                     BseY1
          BtgZ1          Bpm1          Pml1
          BstE2          BsrG1          Msc1          BseY1
          Pml1
GCAATTTCAAGACCCGCGCCGAGGTGACCTTCGAGAATGGCAGCGTGTACAATCGCGTGAAGCTGAATGGCCAGGGCTTCAAGAAGGATGGCCACGTGCT
401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
CGTTAAAGTTCTGGGCGGGCTCCACTGGAAGCTTTACCGTCGCACATGTTAGCGCACTTCGACTTACCGGTCCC GAAGTTCTTCTACCGGTGCACGA
TurboYFP > N F K T R A E V T F E N G S V Y N R V K L N G Q G F K K D G H V L

                                     Bpm1          Sap1          BssS1
                                     Bts1          Earl          Eco57
          SpDon          BsrG1
          Bpm1          Bts1          BsrG1          Sap1          Earl          BssS1
          Eco57
GGGCAAGAATCTGGAGTTCAATTTACCCCCACTGCCTGTACATCTGGGGCGATCAGGCCAATCACGGCCTGAAGAGCGCCTTCAAAATCTGCCACGAG
501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
CCCGTTCTTAGACCTCAAGTTAAAGTGGGGGTGACGGACATGTAGACCCCGCTAGTCCGGTTAGTGCCGGACTTCTCGCGGAAGTTTTAGACGGTGCTC
TurboYFP > G K N L E F N F T P H C L Y I W G D Q A N H G L K S A F K I C H E
```









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                                     SpDon
                                     |
                                     BstAP
                                     AlwN1
                                     Bsu36
3201 TACGCCGCGTTTCTTCTTTTCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
    ATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCAGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGA

                                     DraI
                                     DraI
                                     BspH1
3301 CAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
    GTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGG

                                     BpuE1
3401 TTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
    AATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTT

                                     Eco57
                                     |
3501 ACAAAAAAACACCAGCTACCAGCGGTGGTTTGGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
    TGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTT

                                     SpAcc
                                     |
                                     AlwN1
3601 ATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
    TATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACCGACG

                                     BpuE1
                                     |
                                     ApaL1
3701 TGCCAGTGGCGATAAGTCGTGTTTACCGGGTTGGAAGTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGGGGTTTCGTGCACACAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
    ACGGTCACCGCTATTGACACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTC
```



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BseY1                               SpAcc
|                                   |
3801 CCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATC 3900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTTCGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAG

      BciV1
      Eci1 |                               BssS1 |                               SpAcc |
3901 CGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTTCGCCACCTCTGACT 4000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GCCATTCGCCGTCCTCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGA

      Drd1 |                               BpuE1 |                               SpAcc |                               Eci1 |
4001 TGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTT 4100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      ACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTTCGGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAA

      SpDon |                               NsiI |
      BspLU |                               BfrB1 |
      || |                               || |
4101 GCTCACATGTTCTTTCTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4163
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

```

Found:

Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Avr2	BamH1	BciV1	BfrB1	BfuA1	Bgl1
Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspE1
BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	BstE2	Bsu36	BtgZ1	Bts1
Cla1	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1
Mfe1	Msc1	Nae1	Nar1	Nco1	NgoM4	Not1	Nsi1	PflF1	PflM1	Pml1	polyA	Psi1	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfil	SgrA1	Sma1	SpAcc	SpDon	Sph1
Ssp1	Stu1	Xba1	Xho1	Xmn1									

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	BamH1	Bgl1	Bgl2	Blp1	BsaXa	BsaXb	BseR1	BspE1
BspLU	BssH2	Cla1	Dra3	EcoR1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Not1	PflF1	PflM1	PspOM
Pst1	Rsr2	Sac1	Sall	SexA1	Sfil	SgrA1	Sma1	Stu1	Xba1	Xho1	Xmn1		

Not found:

Aar1	Aat2	Acl1	Ahd1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1
BmgB1	Bpu10	BsiW1	BsmB1	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu
loxP	Mlu1	Nde1	Nhe1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SnaB1
Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1						

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apol	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bs11	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													