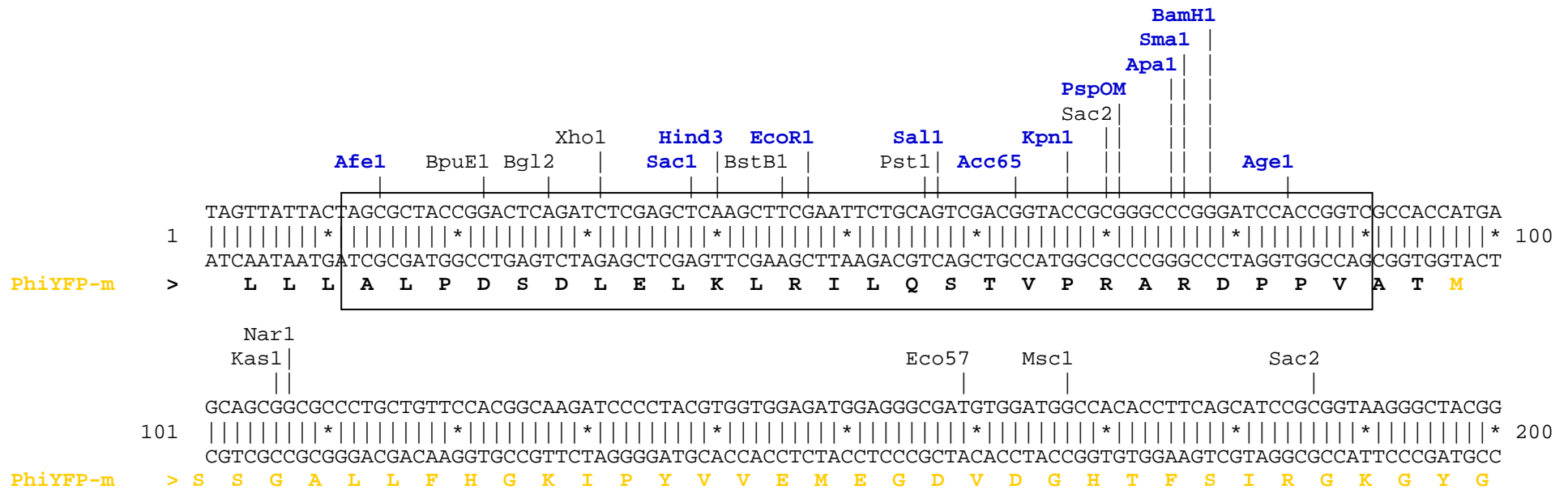


**pPhi-Yellow-PRL-dest1 vector** restriction map

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 and MODC amino acids are shown in bold black.



```

                                     Bsg1
                                     Bmr1
                                     SgrA1
                                     BstE2
                                     Ale1
                                     Bpm1
                                     Nar1
                                     Kas1
                                     Bmr1
201  CGATGCCAGCGTGGGCAAGGTGGATGCCCAGTTCATCTGCACCACCGGCGATGTGCCCGTGCCCTGGAGCACCCCTGGTGTACCACCCCTGACCTACGGCGCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 300
    GCTACGGTCGCACCCGTTCCACCTACGGGTCAAGTAGACGTGGTGGCCGCTACACGGGCACGGGACCTCGTGGGACCACTGGTGGGACTGGATGCCGCGG
PhiYFP-m >  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

                                     Xmn1
                                     Eco57
                                     Sph1
                                     Bsg1
301  CAGTGCTTCGCCAAGTACGGCCCCGAGCTGAAGGATTTCTACAAGAGCTGCATGCCCGATGGCTACGTGCAGGAGCGCACCATCACCTTCGAGGGCGATG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 400
    GTCACGAAGCGGTTTCATGCCGGGGCTCGACTTCTAAAGATGTTCTCGACGTACGGGCTACCGATGCACGTCCTCGCGTGGTAGTGGAAGCTCCCGCTAC
PhiYFP-m >  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

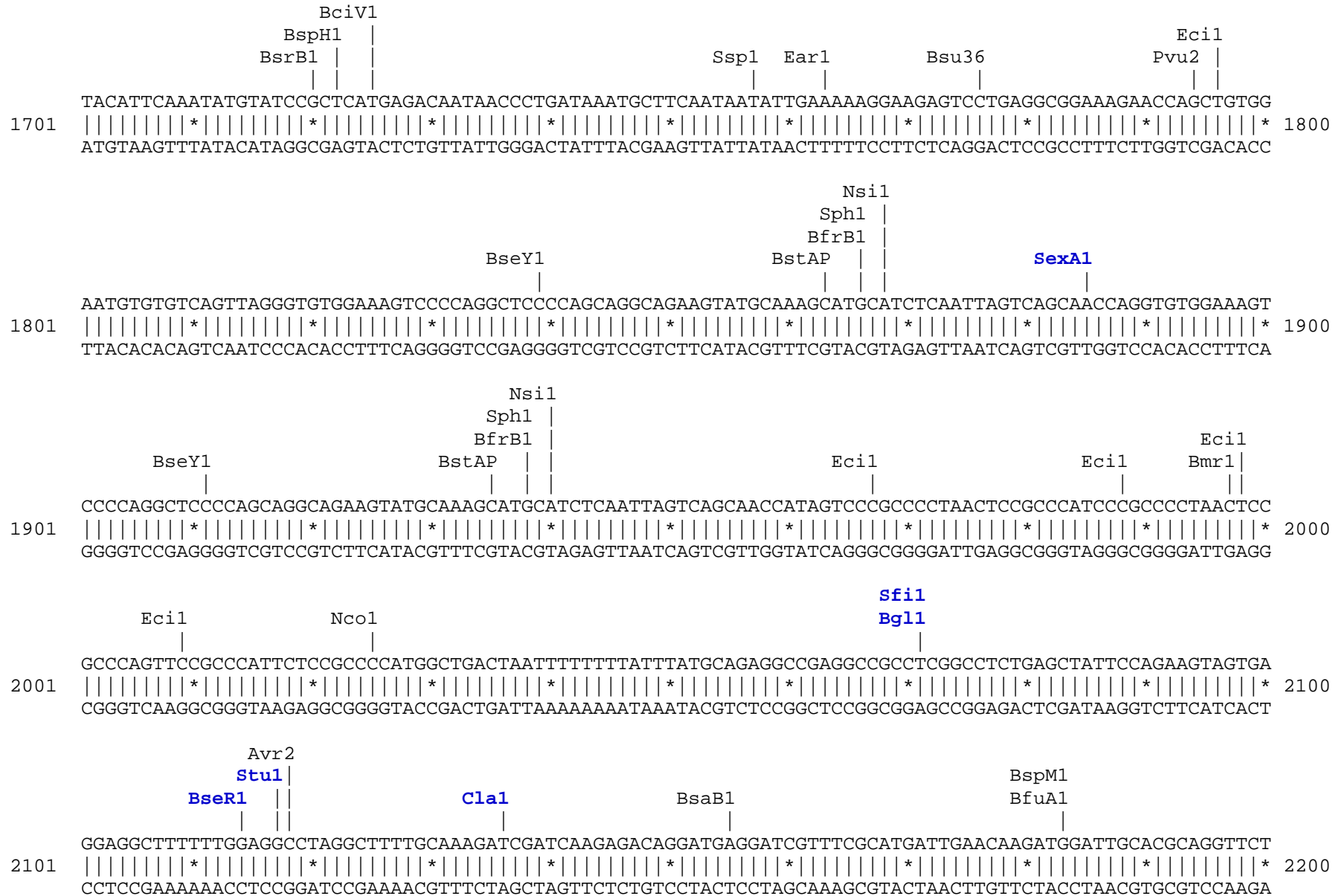
                                     BstE2
                                     BsrG1
                                     Msc1
                                     Msc1
                                     Pml1
                                     BseY1
401  GCAATTTCAAGACCCGCGCCGAGGTGACCTTCGAGAATGGCAGCGTGTACAATCGCGTGAAGCTGAATGGCCAGGGCTTCAAGAAGGATGGCCACGTGCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
    CGTTAAAGTTCTGGGCGGGCTCCACTGGAAGCTTTACCGTTCGCACATGTTAGCGCACTTCGACTTACCGGTCCCAGGTTCTTCTCCTACCGGTGCACGA
PhiYFP-m >  G 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
                                     Bts1
                                     BsrG1
                                     Sap1
                                     Ear1
                                     Bgl2Eco57
                                     BssS1
501  GGGCAAGAATCTGGAGTTCAATTTCAACCCCCACTGCCTGTACATCTGGGGCGATCAGGCCAATCACGGCCTGAAGAGCGCCTTCAAGATCTGCCACGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
    CCCGTTCTTAGACCTCAAGTTAAAGTGGGGGGTGACGGACATGTAGACCCCGCTAGTCCGGTTAGTGCCGGACTTCTCGCGGAAGTTCTAGACGGTGCTC
PhiYFP-m >  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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```

Eag1                               Bmr1                               Nar1
|                                   |                                   |
|                                   |                                   |
2201 CCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGGCGCC 2300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGG

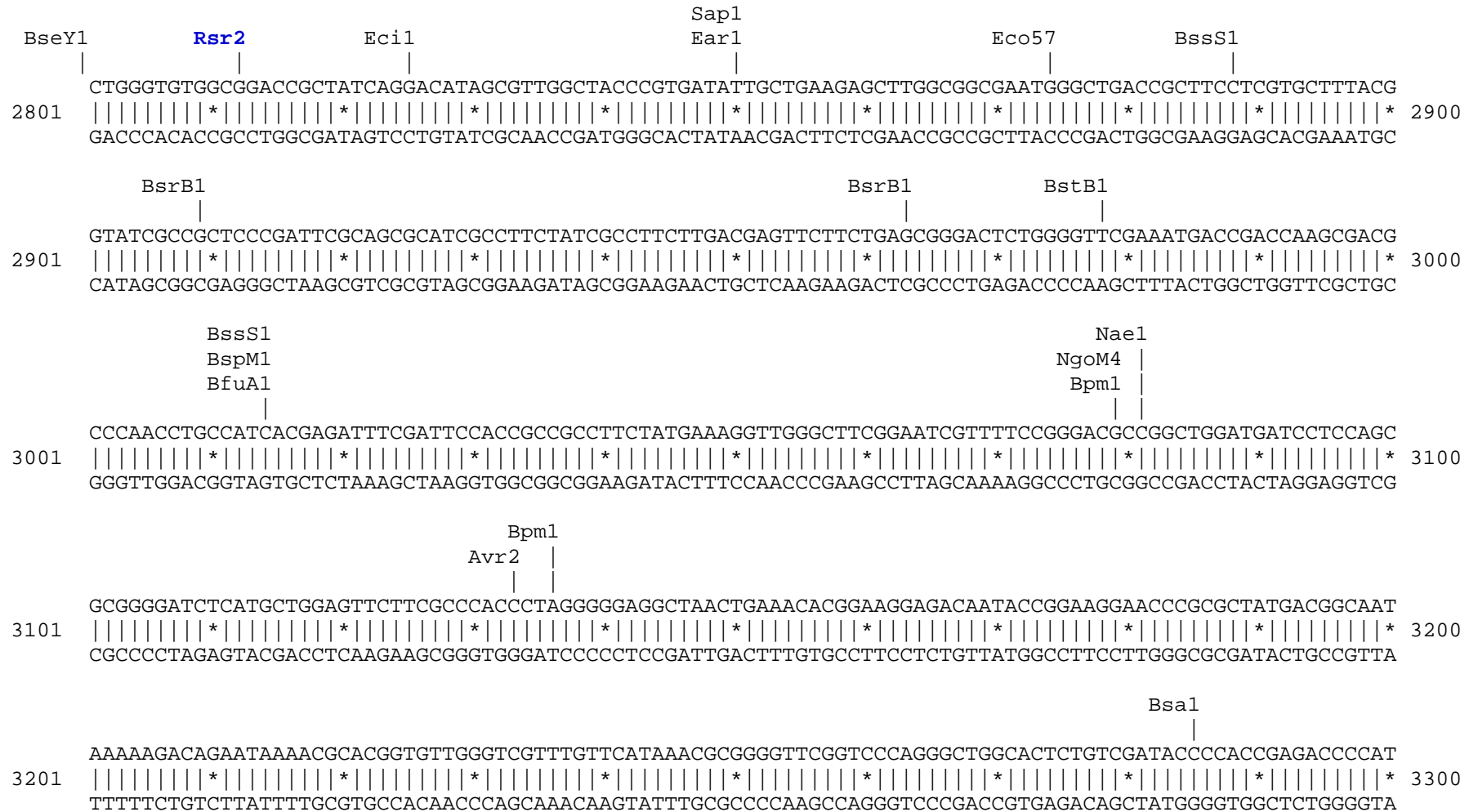
                                Drd1                               Msc1                               Fsp1
                                |                                   |                                   |
                                |                                   |                                   |
2301 CGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGC 2400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCG

Pvu2                               PflF1                               Eco57
|                                   |                                   |
|                                   |                                   |
2401 AGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAG 2500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAAACCCGCTTCACGGCCCCGTCTTAGAGGACAGTAGAGTGGAACGAGGACGGCTC

                                BciV1                               BsrD1                               BspM1
                                |                                   |                                   |
                                |                                   |                                   |
2501 AAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCAC 2600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TTTCATAGGTAGTACCGACTACGTTACGCCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCGTAGCTCGCTCGTG

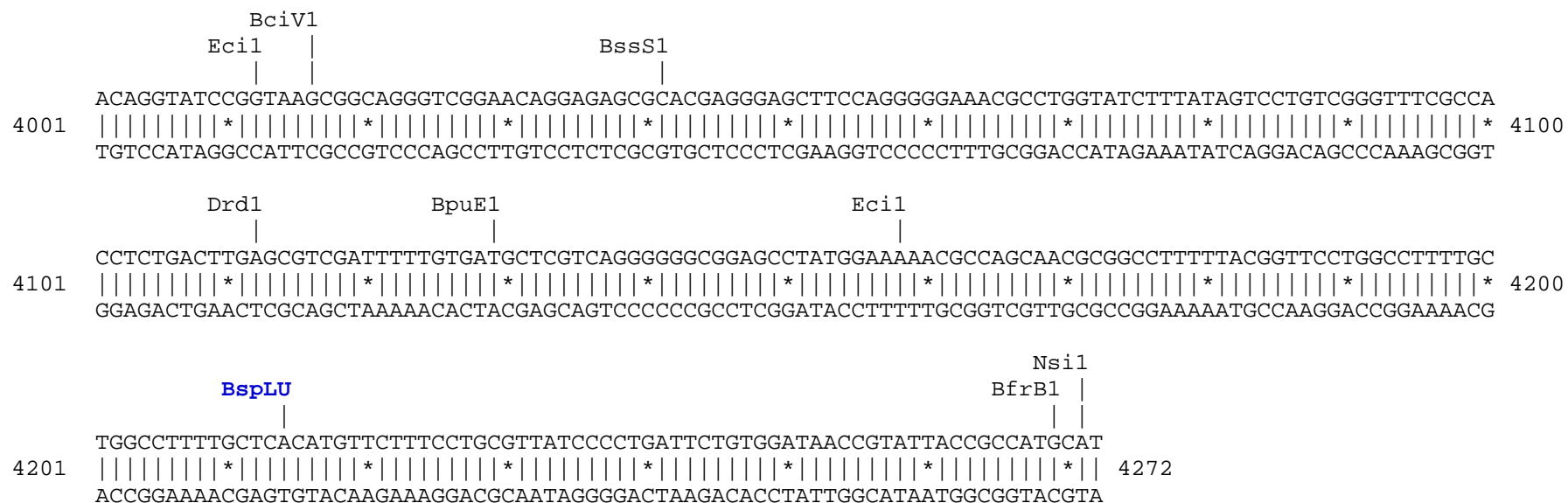
                                Sap1                               Ear1                               BpuE1
                                |                                   |                                   |
                                |                                   |                                   |
2601 GTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGCTCAAGGGCAGCAT 2700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCGAGTTCGCTCGTA

Sph1                               Nco1                               Nae1
|                                   |                                   |
|                                   |                                   |
2701 GCCCGACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGG 2800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCC
```









Found:

- Acc65   AfeI   Afl2   AgeI   AleI   AlwNI   ApaI   ApaLI   Avr2   BamHI   BciV1   BfrB1   BfuA1   Bgl1
- Bgl2   BlpI   BmrI   BpmI   BpuE1   BsaI   BsaBI   BsaXI   BsaXB   BseRI   BseY1   BsgI   BsmI   BspHI
- BspLU   BspMI   BsrBI   BsrDI   BsrGI   BssH2   BssS1   BstAP   BstBI   BstE2   Bsu36   Bts1   ClaI   DraI
- Dra3   Drd1   EagI   EarI   EciI   Eco57   EcoRI   EcoRV   FspI   Hind3   HpaI   KasI   KpnI   MfeI
- MscI   NaeI   NarI   NcoI   NgoM4   NsiI   PflFI   PflMI   PmlI   PsiI   PspOM   PstI   Pvu2   Rsr2
- Sac1   Sac2   SalI   SapI   SexAI   SfiI   SgrAI   SmaI   SphI   SspI   StuI   XbaI   XhoI   XmnI

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	BamH1	Bgl1	Blp1	BsaXa	BsaXb	BseR1	BspLU	BsrD1
BssH2	Cla1	Dra3	EcoR1	EcoRV	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	PflF1	PflM1	PspOM	Rsr2
Sac1	Sall	SexA1	Sfi1	Sma1	Stu1	Xba1	Xmn1						

Not found:

Aar1	Aat2	Acl1	Ahd1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	BcglA	Bcglb	Bcl1
BmgB1	Bpu10	BsiW1	BsmB1	BspE1	BstX1	BstZ1	_Chi	EcoK	EcoN1	ScFRT	Fse1	FspA1	I_Ceu
loxP	Mlu1	Nde1	Nhe1	Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Scal	Sgf1
SnaB1	Spe1	Srf1	Swal	PISce	Xcm1								

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													