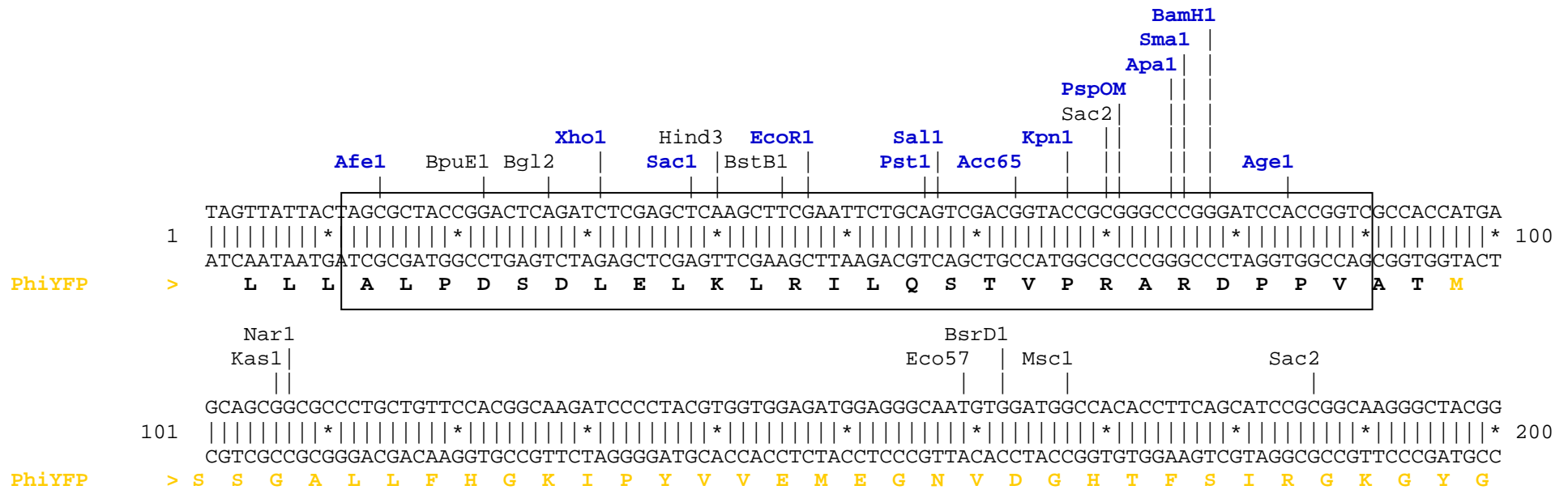


pPhi-Yellow-PRL vector restriction map

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 black.



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                                     Bsg1
                                     Bmr1
                                     SgrA1
                                     BstE2
                                     Ale1
                                     Bpm1
                                     Kas1
                                     Nar1
                                     Bmr1
201  CGATGCCAGCGTGGGCAAGGTGGATGCCAGTTCATCTGCACCACCGGCGATGTGCCCGTGCCCTGGAGCACCCCTGGTGTACCACCCCTGACCTACGGCGCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 300
    GCTACGGTCGCACCCGTTCCACCTACGGGTCAAGTAGACGTGGTGGCCGCTACACGGGCACGGGACCTCGTGGGACCACTGGTGGGACTGGATGCCCGGG
PhiYFP >  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
    GTCACGAAGCGGTTTCATGCCGGGGCTCGACTTCTAAAGATGTTCTCGACGTACGGGCTACCGATGCACGTCCTCGCGTGGTAGTGAAGCTCCCGCTAC
PhiYFP >  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
    CGTTAAAGTTCTGGGCGGGCTCCACTGGAAGCTCTTACCGTTCGCACATGTTAGCGCACTTCGACTTACCGGTCCCAGTTCCTTCTTACCAGGTGCACGA
PhiYFP >  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  GGGCAAGAATCTGGAGTTCAATTTACCCCCCACTGCCTGTACATCTGGGGCGATCAGGCCAATCACGGCCTGAAGAGCGCCTTCAAGATCTGCCACGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
    CCCGTTCTTAGACCTCAAGTTAAAGTGGGGGGTGACGGACATGTAGACCCCGCTAGTCCGGTTAGTGCCGGACTTCTCGCGGAAGTTCTAGACGGTGCTC
PhiYFP >  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

                                     ApaL1
                                     Pml1
601  ATCACCGGCAGCAAGGGCGATTTTCATCGTGGCCGATCACACCCAGATGAATACCCCCATCGGCGGGCGCCCCGTGCACGTGCCCGAGTACCACCACATGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
    TAGTGGCCGTCGTTCCCGCTAAAGTAGCACCGGCTAGTGTGGGTCTACTTATGGGGGTAGCCGCCGCGGGGCACGTGCACGGGCTCATGGTGGTGTACT
PhiYFP >  I T G S K G D F I V A D H T Q M N T P I G G G P V H V P E Y H H M

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          Pml1   Bln1           Bsa1       BssH2   Eco57
          |     |             |           |       |
701  GCTACCACGTGAAGCTGAGCAAGGATGTGACCGATCACCGCGATAATATGAGCCTGAAGGAGACCGTGC GCGCCGTGGATTGCCGCAAGACCTACCTGTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
    CGATGGTGCACCTTCGACTCGTTCCTACACTGGCTAGTGGCGCTATTATACTCGGACTTCCTCTGGCACGCGCGGCACCTAACGGCGTTCTGGATGGACAC
PhiYFP > S Y H V K L S K D V T D H R D N M S L K E T V R A V D C R K T Y L *

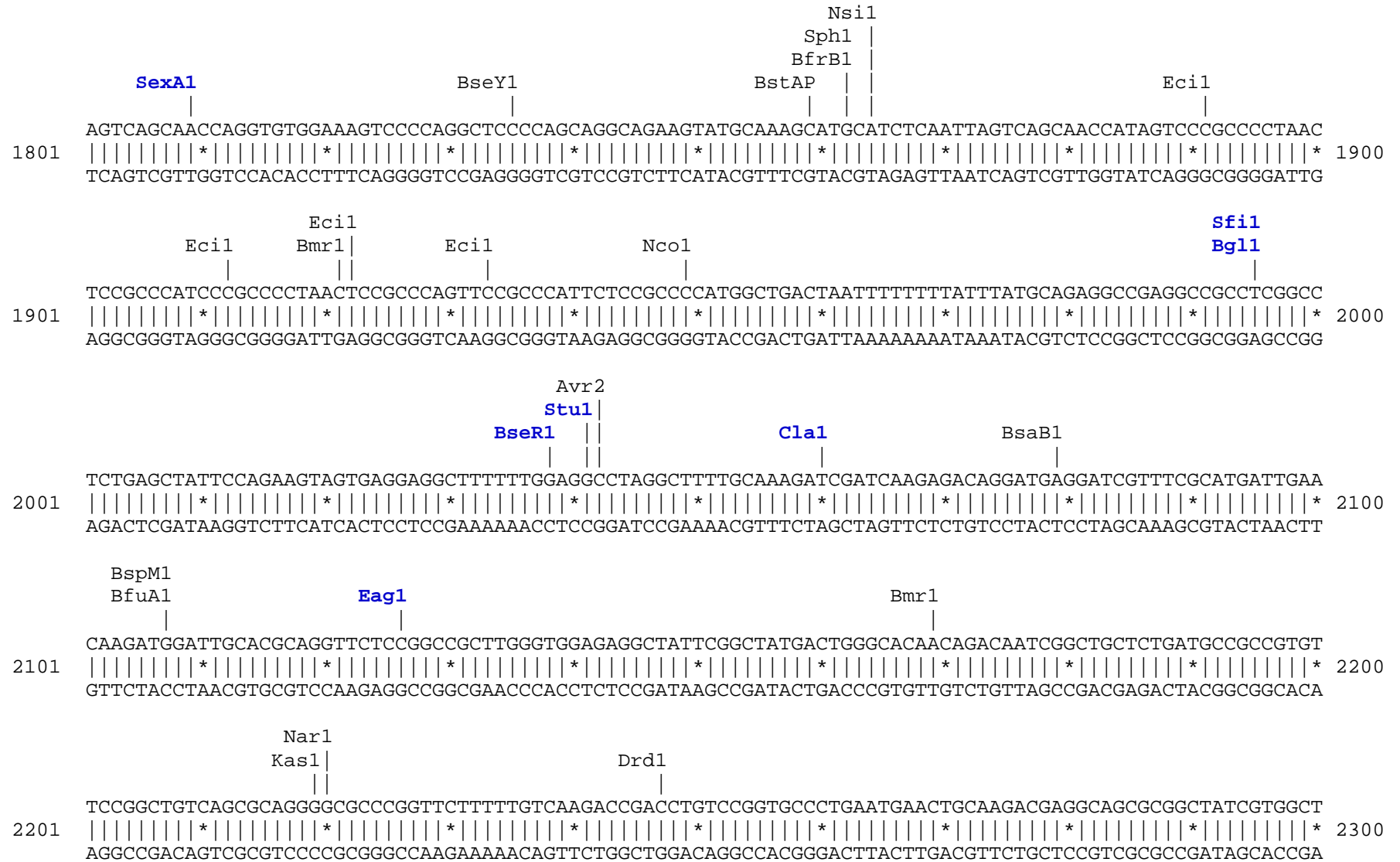
Hind3     Bln1                               Xba1   BsaB1
|         |                                 |       |
801  AAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGCCGCGACTCTAGATCATAATCAGCCATAACACAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
    TTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTG

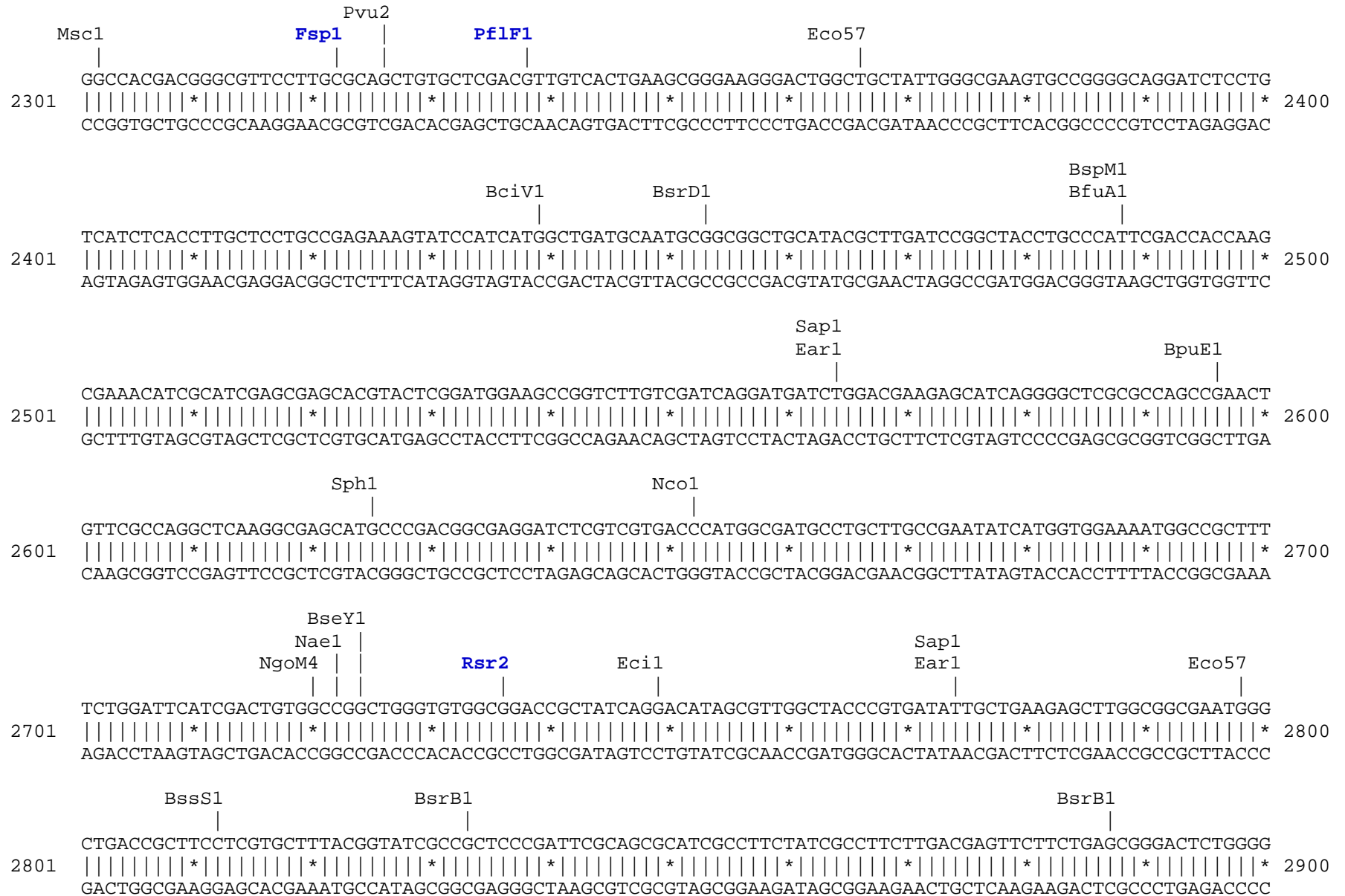
                               Dra1           Bsm1       Hpa1
                               |           ||         |
901  TTGTAGAGGTTTTACTTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
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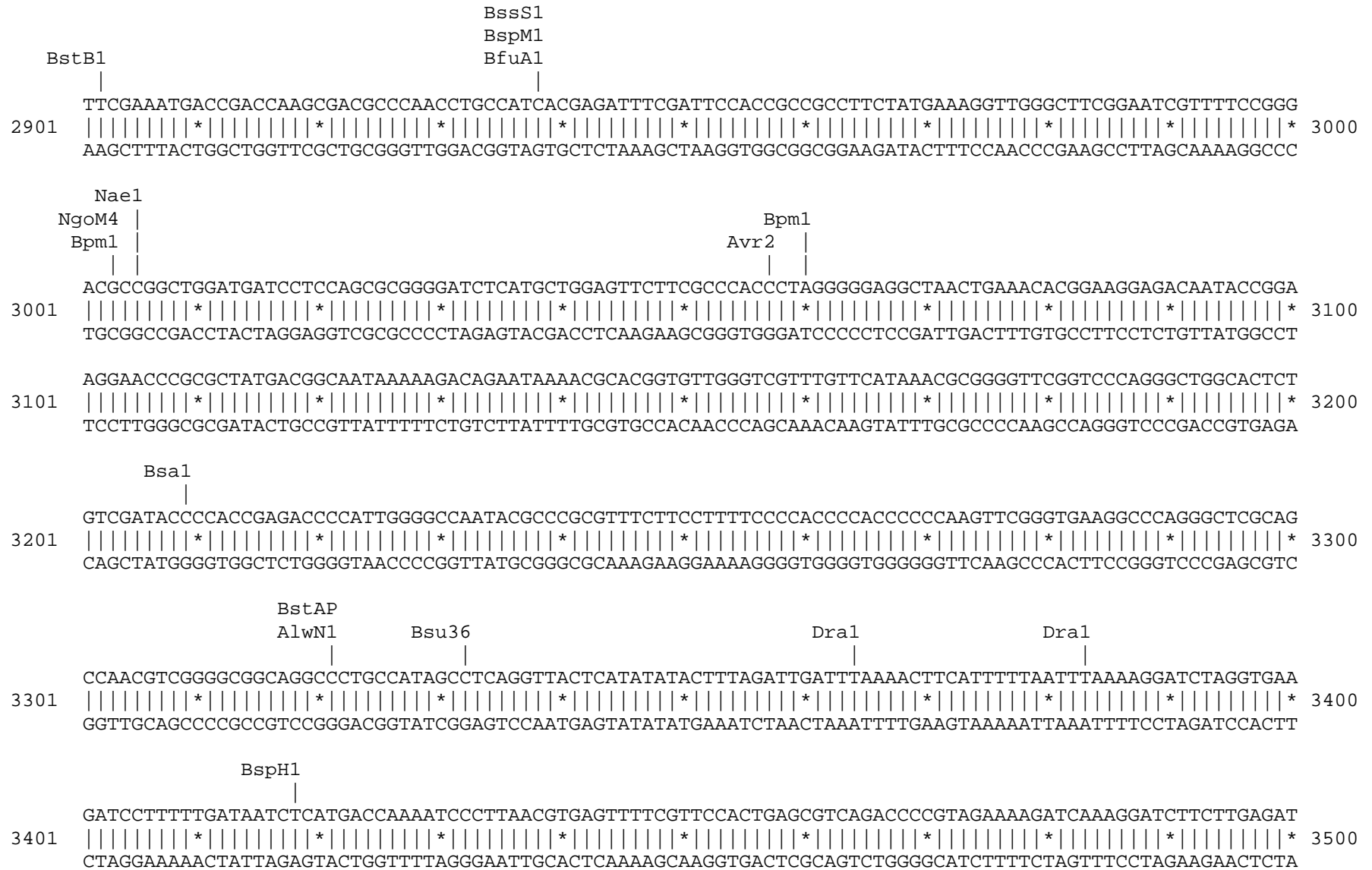
PstI                                           Bts1 Bsm1
|                                               |   |
1001 TTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    AATATTACCAATGTTTATTTCGTTATCGTAGTGTAAAGTGTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGTAGTAGTTACAT

Afl2                               Ssp1
|                                   |
1101 TCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    AGAATTCGCGATTTAACATTCGCAATTATAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTT

PstI                                           BsaXb                               Drr1
|                                               |           |
1201 ATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    TAGGGAATATTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTC
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          BpuE1                                     Eco57
          |                                         |
CCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTCCGA
3501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3600
GGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTTGGTGCGGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCT

AGGTAAGTGGCTTCAGCAGAGCGCAGATAACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCGCCTACATA
3601 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3700
TCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTAT

          AlwN1                                     BpuE1
          |                                         |
CCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAG
3701 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3800
GGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGCT

          ApaL1      BseY1
          |         |
CGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCA
3801 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3900
GCCAGCCCAGACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGT

          BciV1
          |
          Eci1      |      BssS1
          |         |         |
CGCTTCCCAGGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCT
3901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4000
GCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGA

          Drd1      BpuE1      Eci1
          |         |         |
TTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCC
4001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4100
AATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTGCTTGCGCCGG

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                                     BspLU                                     NsiI  
                                     |                                     BfrB1 |  
                                     |                                     |  
4101 TTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGGCTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4196  
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||  
      AAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apal	ApaL1	Avr2	BamH1	BciV1	BfrB1	BfuA1	Bgl1
Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1
BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	BstE2	Bsu36	Bts1	Cla1	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1
Nae1	Nar1	Nco1	NgoM4	Nsi1	PflF1	PflM1	Pml1	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1
Sac2	Sall	Sap1	SexA1	Sfi1	SgrA1	Sma1	Sph1	Ssp1	Stu1	Xba1	Xho1	Xmn1	

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apal	BamH1	Bgl1	BsaXa	BsaXb	BseR1	BspLU	BssH2	Cla1
Dra3	Eag1	EcoR1	Fsp1	Hpa1	Kpn1	Mfe1	PflF1	PflM1	PspOM	Pst1	Rsr2	Sac1	Sall
SexA1	Sfi1	SgrA1	Sma1	Stu1	Xba1	Xho1	Xmn1						

Not found:

AarI	Aat2	AclI	AhdI	AscI	AseI	AsiSI	Baela	Baelb	BbsI	BbvCI	BcgIa	BcgIb	BclI
BmgBI	BpuI0	BsiWI	BsmBI	BspEI	BstXI	BstZI	_Chi	EcoK	EcoNI	EcoRV	ScFRT	FseI	FspAI
I_Ceu	loxP	MluI	NdeI	NheI	NotI	NruI	PacI	PmeI	PshAI	PvuI	SanDI	SbfI	Scal
SgfI	SnaBI	SpeI	SrfI	Swal	PISce	XcmI							

Excluded by site complexity:

AccI	Acil	Afl3	AluI	AlwI	ApoI	AvaI	Ava2	BanI	Ban2	BbvI	BceAI	BfaI	BmeI5
BsaAI	BsaHI	BsaJI	BsaWI	BseM2	BsiE1	BsiH1	BsII	BsmAI	BsmF1	Bsp12	BspCa	BspCb	BsrI
BsrF1	BssK1	BstF5	BstN1	BstU1	BstY1	Btg1	Cac8	CviJ1	DdeI	EaeI	EcoO1	FauI	Fnu4H
FokI	Hae2	Hae3	HgaI	HhaI	Hinc2	Hinf1	HinP1	Hpa2	Hph1	Hpy99	Hpy1	Hpy3	HpyC3
HpyC4	HpyC5	Mae3	Mbo2	Mnl1	MseI	Msl1	MspAI	MwoI	NciI	Nla3	Nla4	Nsp1	PleI
PpuM1	RsaI	Sau3A	Sau96	SfaNI	SfcI	Sml1	Sty1	TaqI	TatI	TfiI	TseI	Tsp45	Tsp50
TspR1													