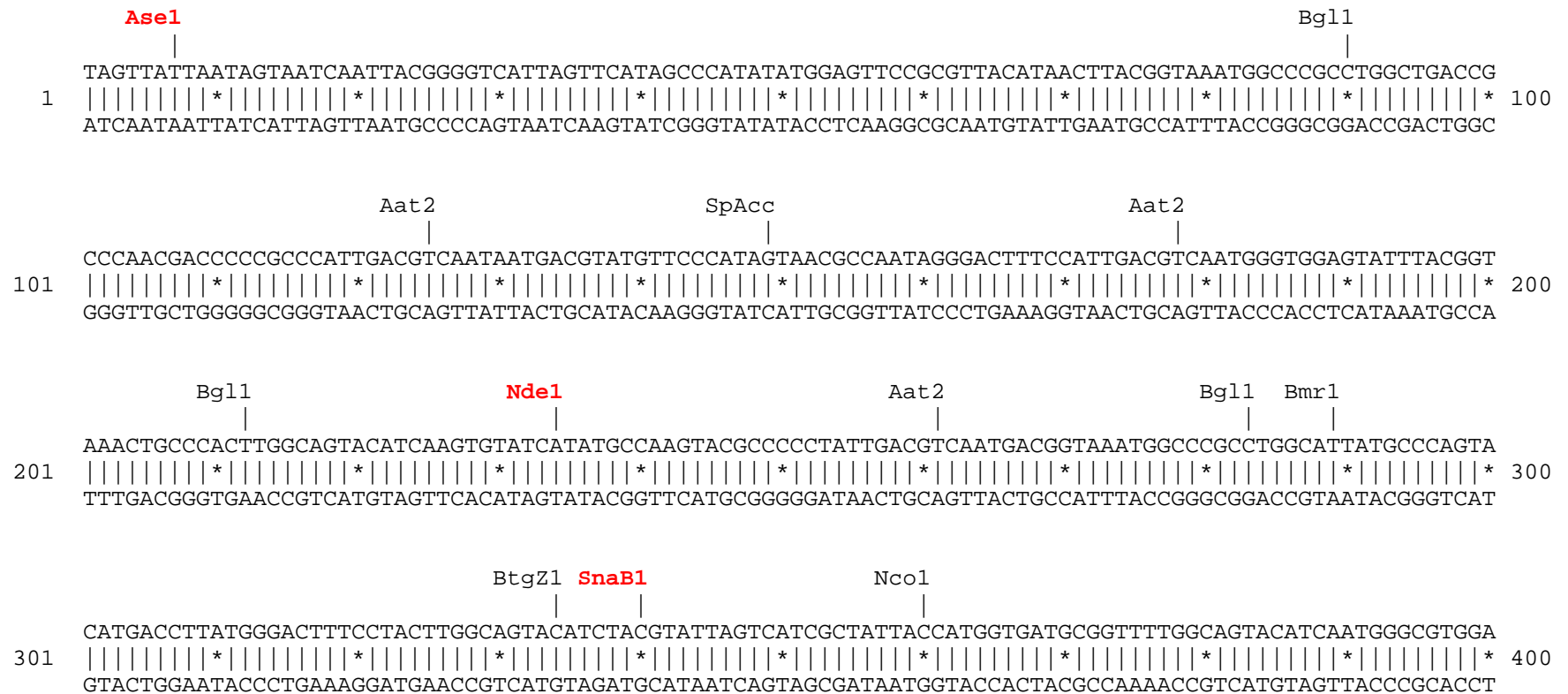
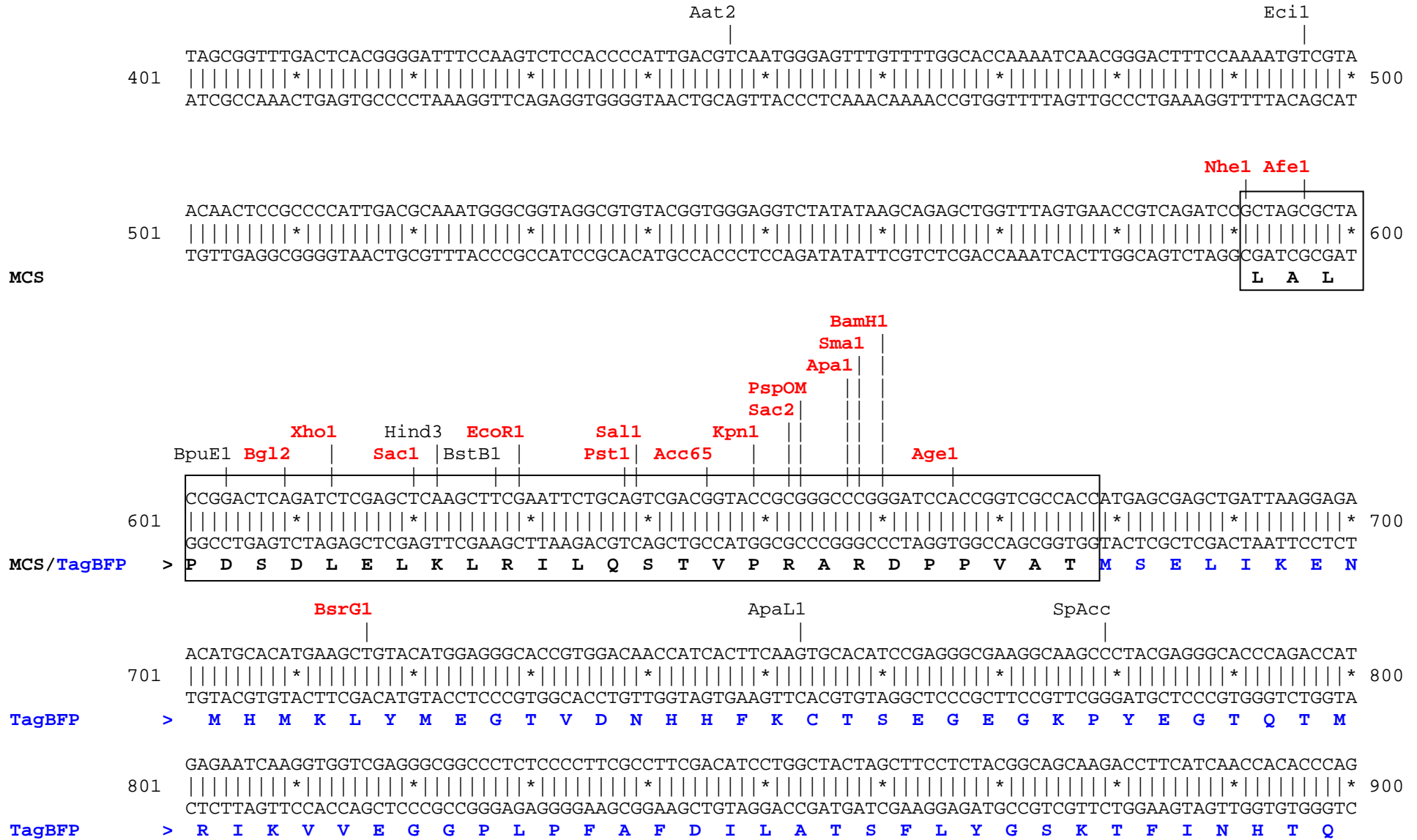


pTagBFP-N vector restriction map

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 are shown in red. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.





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                                     Bsu36      SpDon      Bbs1      Bpm1
                                     |          |          |          |
1001  GGCATCCCCGACTTCTTCAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
      CCGTAGGGGCTGAAGAAGTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGT
TagBFP > G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T

                                     SpDon      BseY1
                                     |          |
1101  CCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTACATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
      GGTCCGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGTGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCT
TagBFP > S L Q D G C L I Y N V K I R G V N F T S N G P V M Q K K T L G W E

      BsmB1
StuI      BglI      BssS1      Eco57
|          |          |          |
1101  GGCTTCACCGAGACGCTGTACCCCGCTGACGGCGGCTTGGAAAGGCAGAAAACGACATGGCCCTGAAGCTCGTGGGCGGGAGCCATCTGATCGCAAACATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
      CCGGAAGTGGCTCTGCGACATGGGGCGACTGCCGCCGGACTTCCGCTTTTGTGCTGTACCGGGACTTCGAGCACCCGCCCTCGGTAGACTAGCGTTTGTAG
TagBFP > A F T E T L Y P A D G G L E G R N D M A L K L V G G S H L I A N I

                                     BpuE1      SpAcc      Bsa1
                                     |          |          |
1201  AAGACCACATATAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCTGGCGTCTACTATGTGGACTACAGACTGGAAAGAATCAAGGAGGCCAACAACG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
      TTCTGGTGTATATCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGACCCGACAGATGATACACCTGATGTCTGACCTTTCTTAGTTCTCCTCCGGTTGTTGC
TagBFP > K T T Y R S K K P A K N L K M P G V Y Y V D Y R L E R I K E A N N E

      PshA1      BssS1      Dra3      Bts1      AlwN1      SpAcc      Hind3      Bmr1      Pac1      Eag1      Xba1
      |          |          |          |          |          |          |          |          |          |
1301  AGACCTACGTCGAGCAGCACGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAAGCTTAATTAAGCGCCGCGACTCTAGATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      TCTGGATGCAGCTCGTCGTGCTCCACCGTCACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTTCGAATTAATTTCCGCCGGCGCTGAGATCTAG
TagBFP > T Y V E Q H E V A V A R Y C D L P S K L G H K L N *

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```
GGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTT
2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
CCC GCGATCCC GCGACCGTTCACATCGCCAGTGC GACGCGCATTGGTGGTGTGGGCGGCGCAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAA

                                     polyA                                     BciV1
                                     |                                     BspH1 |
                                     |                                     BsrB1 | |
                                     |                                     | |

CGGGGAAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAAACCTGATAAAATGCTTCAATAAT
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
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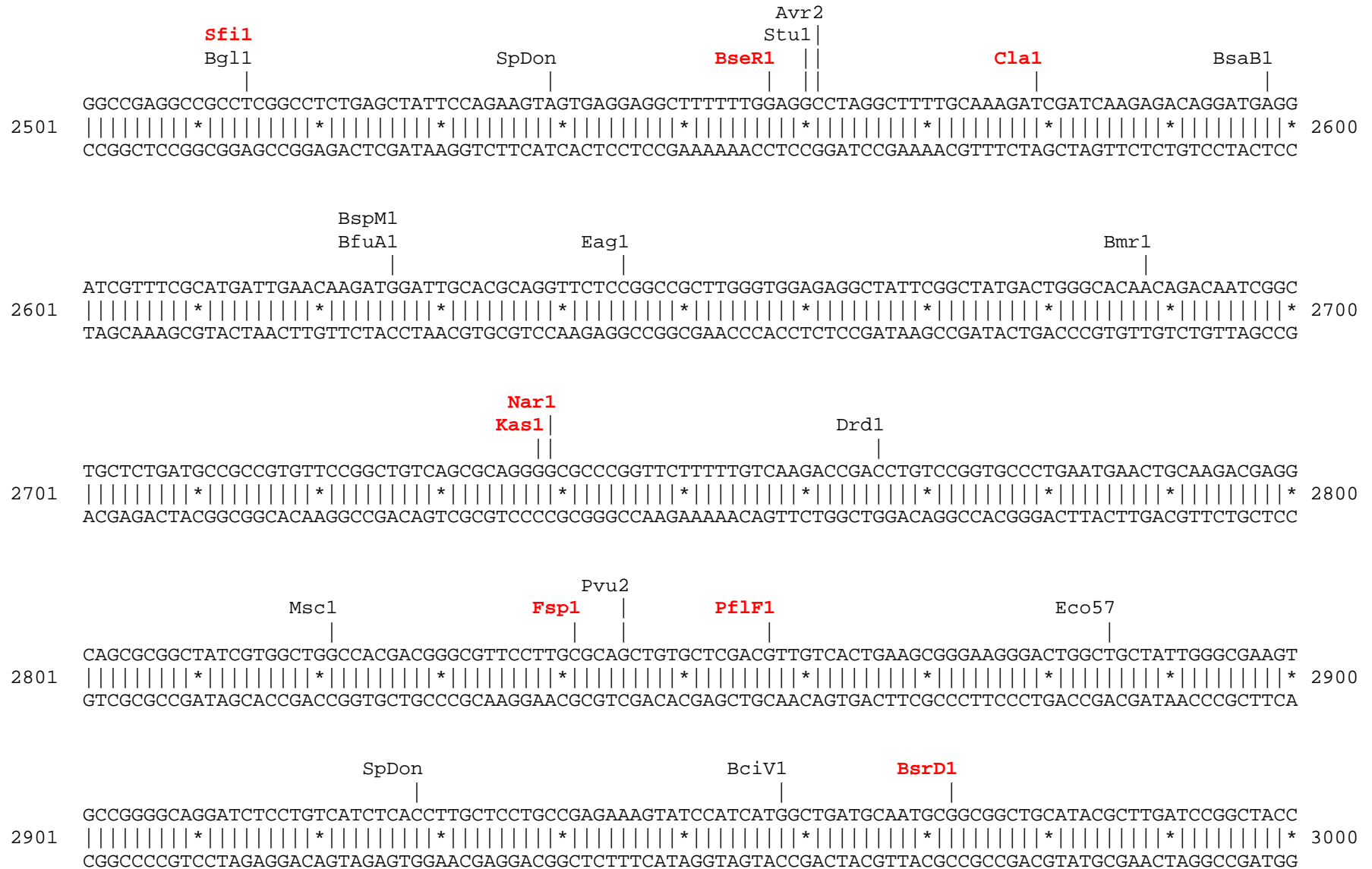
                                     Eci1
                                     | |
Ssp1  Ear1      Bsu36      Pvu2      BseY1
|      |        |          |          |
2201 |      |        |          |          |
ATTGAAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATG
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
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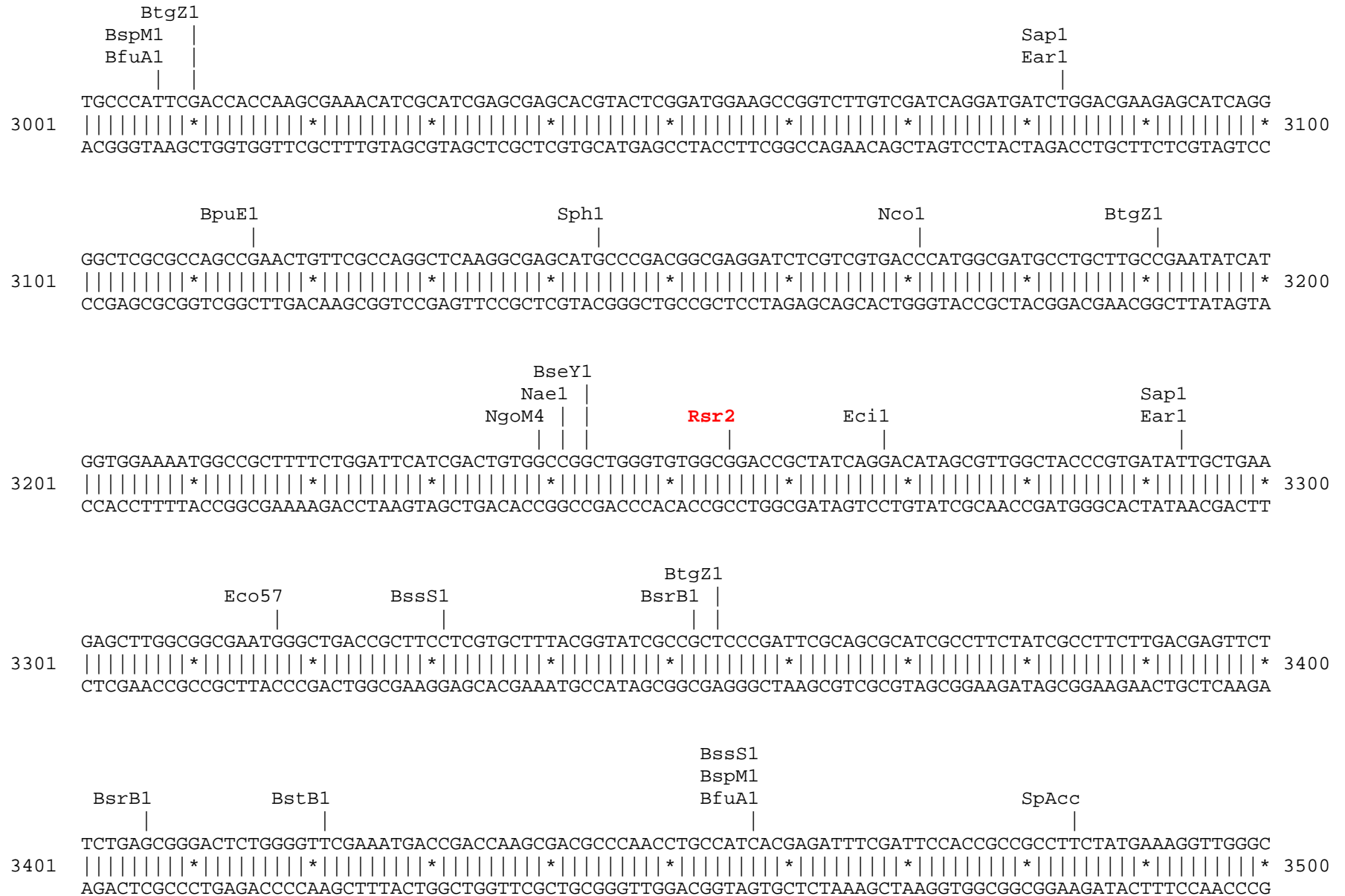
                                     Nsil
                                     Sph1 |
                                     BfrB1 |
                                     BstAP | |
                                     |
                                     SexA1
                                     |
                                     BseY1
                                     |
                                     BstAP | |
                                     BfrB1 |
                                     Sph1 |
                                     Nsil

CAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAA
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
GTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTTTCGTACGTAGAGTTAATCAGTCGTT

                                     Eci1
                                     Eci1  Bmr1 |
                                     |      |
                                     Eci1  Nco1
                                     |      |
                                     polyA
                                     |

CCATAGTCCC GCCCTAACTCCGCCCATCCC GCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCAGA
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
GGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATACGTCT
```





NaeI
NgoM4
BpmI

BpmI
SpAcc
Avr2

3501 TTCGGAATCGTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGGCTAACTGAAACAC
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
AAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTG

polyA polyA

3601 GGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGTTTTGTTTCATAAACCGGGGTTTCG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CCTTCTCTGTTATGGCCTTCCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCAGCAAACAAGTATTTGCGCCCCAAGC

BsaI

3701 GTCCCAGGGCTGGCACTCTGTTCGATACCCACCGAGACCCCAATTGGGGCCAATACGCCCGGTTCCTTCTTTCCACCCACCCCAAGTTTCGGGT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
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BstAP
AlwNI Bsu36 DraI

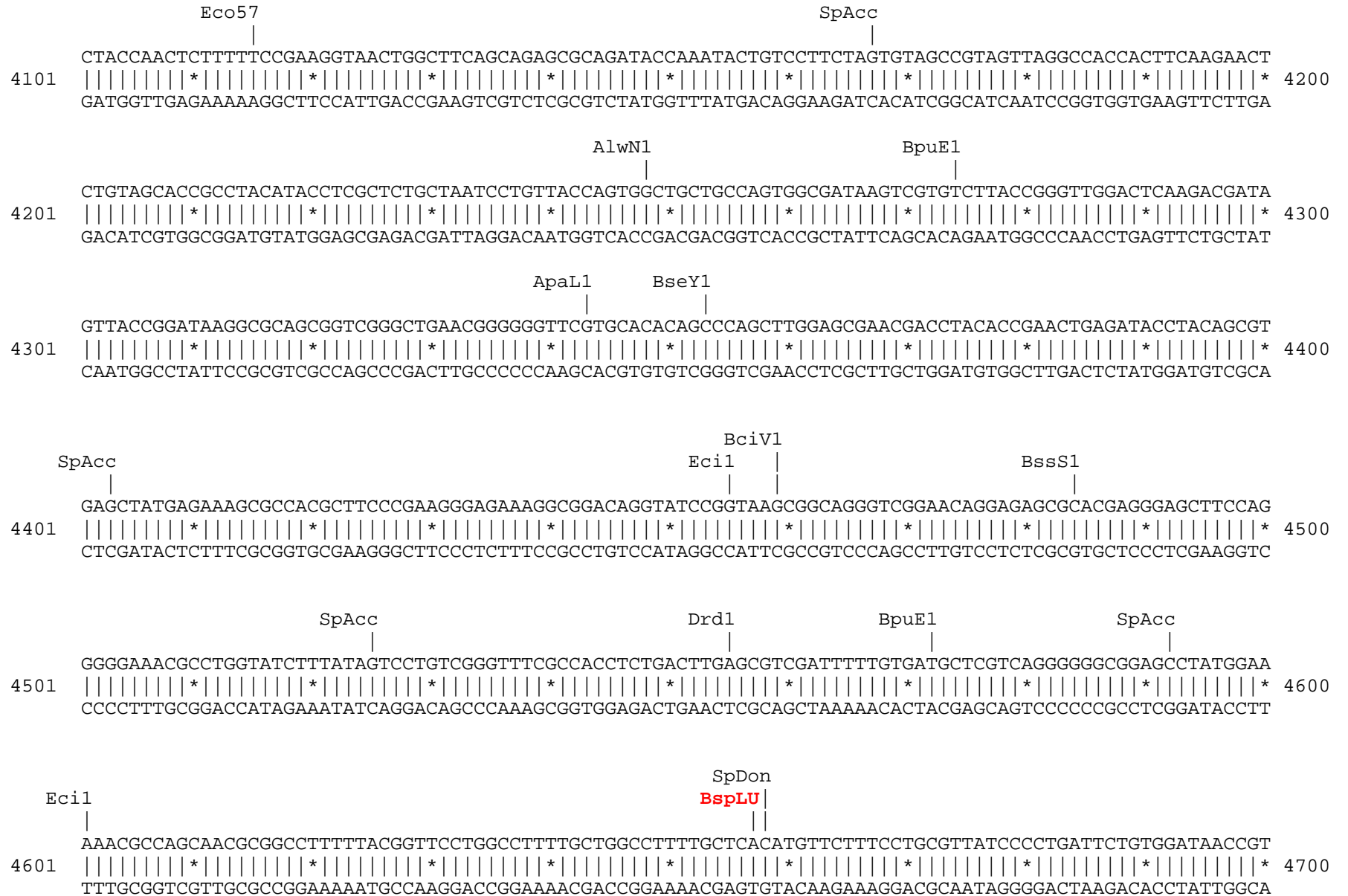
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|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
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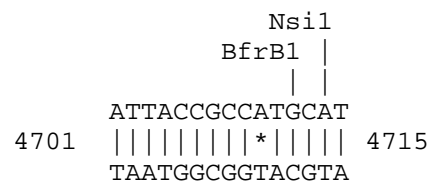
DraI BspH1

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AATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTA

BpuE1

4001 CAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAAACAAAAAACCCAGCCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
GTTTCTTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTTCGCCACCAAAACAAACGGCCTAGTTCTC





Found:

Aat2	Acc65	Afe1	Afl2	Age1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	BfrB1
BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	BsmB1
BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Cla1	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1
Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	Pac1	PflF1	polyA	PshA1	Ps11	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1
Ssp1	Stu1	Xba1	Xho1										

Unique:

Acc65	Afe1	Afl2	Age1	Apa1	Ase1	BamH1	Bbs1	Bgl2	BsaXa	BsaXb	BseR1	BsmB1	BspLU
BsrD1	BsrG1	Cla1	EcoR1	Fsp1	Hpa1	Kas1	Kpn1	Mfe1	Nar1	Nde1	Nhe1	Not1	Pac1
PflF1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SexA1	Sfi1	Sma1	SnaB1	Xba1	Xho1

Not found:

Aar1	Acl1	Ahd1	Ale1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1	Bcglb	Bcl1	Blp1	BmgB1
Bpu10	Bsg1	BsiW1	BspE1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL
FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	PflM1	Pme1	Pml1	Pvu1	R4atB
R4atL	R4atP	R4atR	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter
PISce	Xcm1	Xmn1											

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													