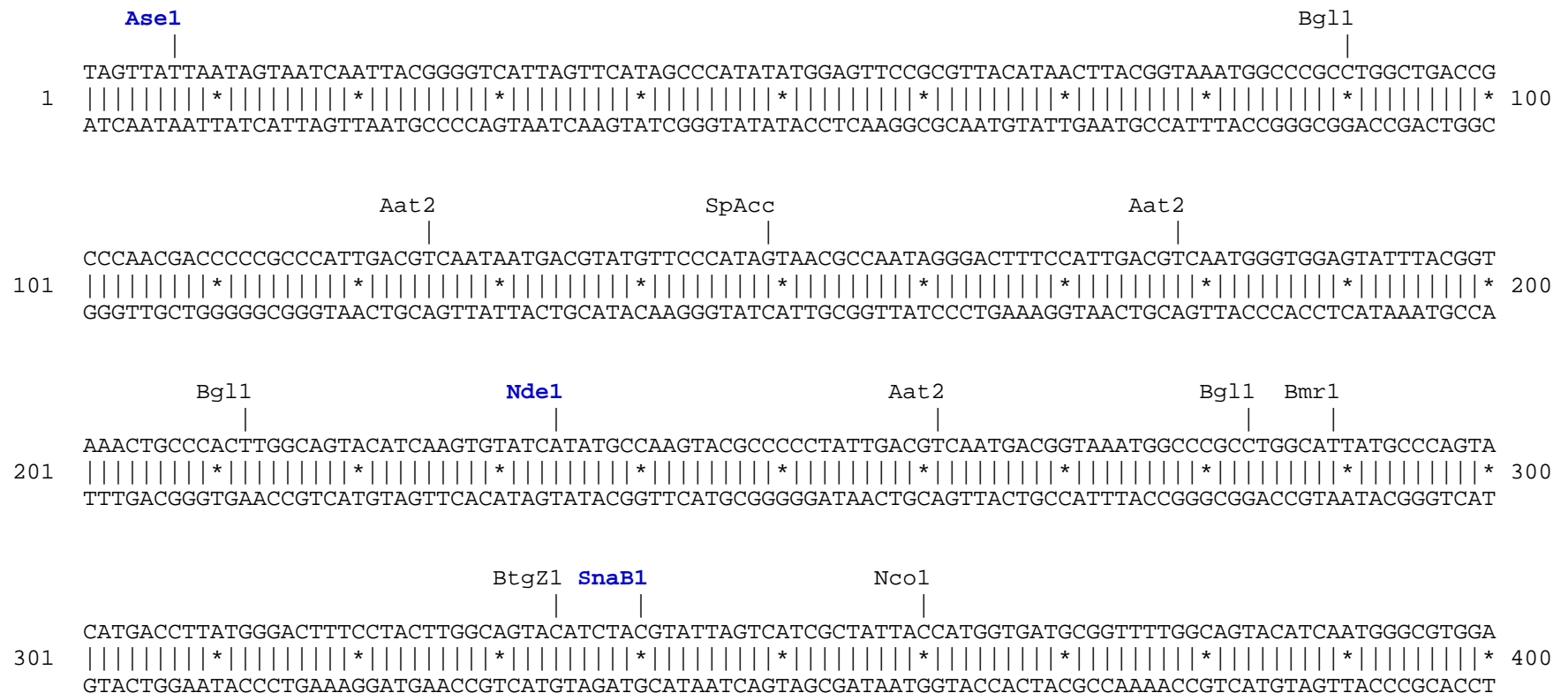


pTagRFP-H2B vector restriction map

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 base pairs long are not included – for the more complete enzyme list please refer to the Table of restriction sites.

Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagRFP amino acids are shown in red, H2B amino acids are shown in green, linker amino acids are shown in black.



Aat2 Eci1

TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCAATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAAATCAACGGGACTTTCCAAAATGTGCGTA
 401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
 ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

Nhe1 Afel

ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTGAGGGCGGGTAACTGCCTTTACCGCCATCCGCACATGCCACCCTCCAGATATATTTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Xho1 Hind3 EcoR1 Sall Kpn1
 BpuE1 Bgl2 Sac1 BstB1 Pst1 Acc65

CCGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCCACCATGCCAGAGCCAGCGAAGTCTGCTCCCGCCCCGAAAAGGGCTC
 601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCTGAGTCTAGAGCTCGAGTTTCGAAGCTTAAGACGTCAGCTGCCATGGCGGTTGGTACGGTCTCGGTCGCTTCAGACGAGGGCGGGGCTTTTTCCCGAG

H2B > M P E P A K S A P A P K K G S

BspM1
 BsrG1 BfuA1

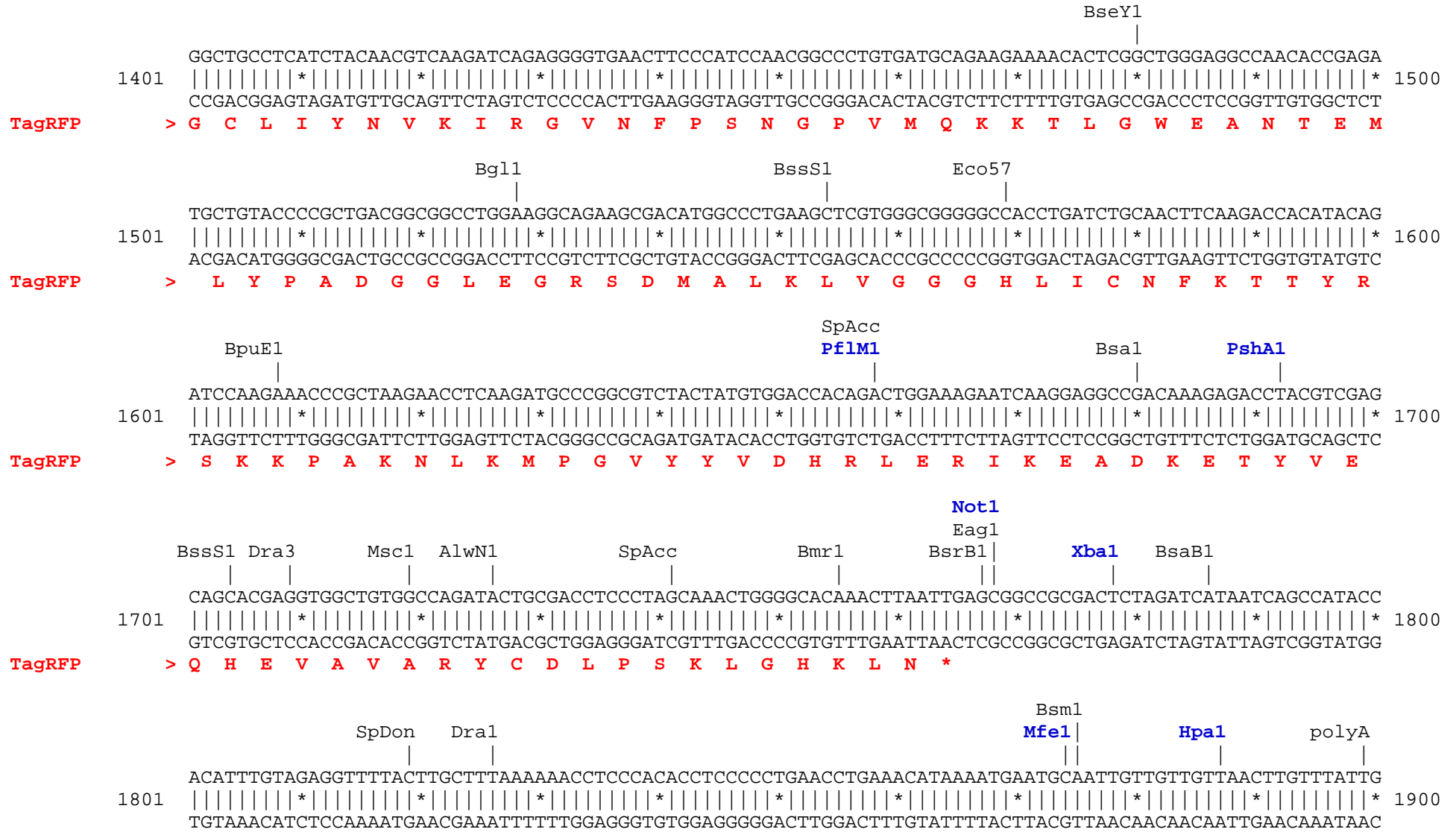
CAAGAAGGCGGTGACTAAGGCGCAGAAGAAAGGCGGCAAGAAGCGCAAGCGCAGCCGCAAGGAGAGCTATTCCATCTATGTGTACAAGGTTCTGAAGCAG
 701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 GTTCTTCCGCCACTGATTCCGCGTCTTCTTTCCGCCGTTCTTTCGCGTTCGCGTCGGCGTTTCTCTCGATAAGGTAGATACACATGTTCCAAGACTTCGTC

H2B > K K A V T K A Q K K G G K K R K R S R K E S Y S I Y V Y K V L K Q

BstX1 EcoR1 BspM1 BfuA1
 Eco57 Nco1 BspH1 BtgZ1 Aar1 SpDon

GTCCACCCTGACACCGCATTTCGTCCAAGGCCATGGGCATCATGAATTCGTTTTGTGAACGACATTTTCGAGCGCATCGCAGGTGAGGCTTCCCGCCTGG
 801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 CAGGTGGGACTGTGGCCGTAAAGCAGGTTCCGGTACCGTAGTACTTAAGCAAACACTTGTCTGTAAAAGCTCGCGTAGCGTCCACTCCGAAGGGCGGACC

H2B > V H P D T G I S S K A M G I M N S F V N D I F E R I A G E A S R L A



```
       Psil      polyA           polyA           Bts1  Bsm1
       |          |                |                |      |
1901  CAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTCACAAATAAAGCATTTCCTACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAA 2000
      |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*
      GTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTT

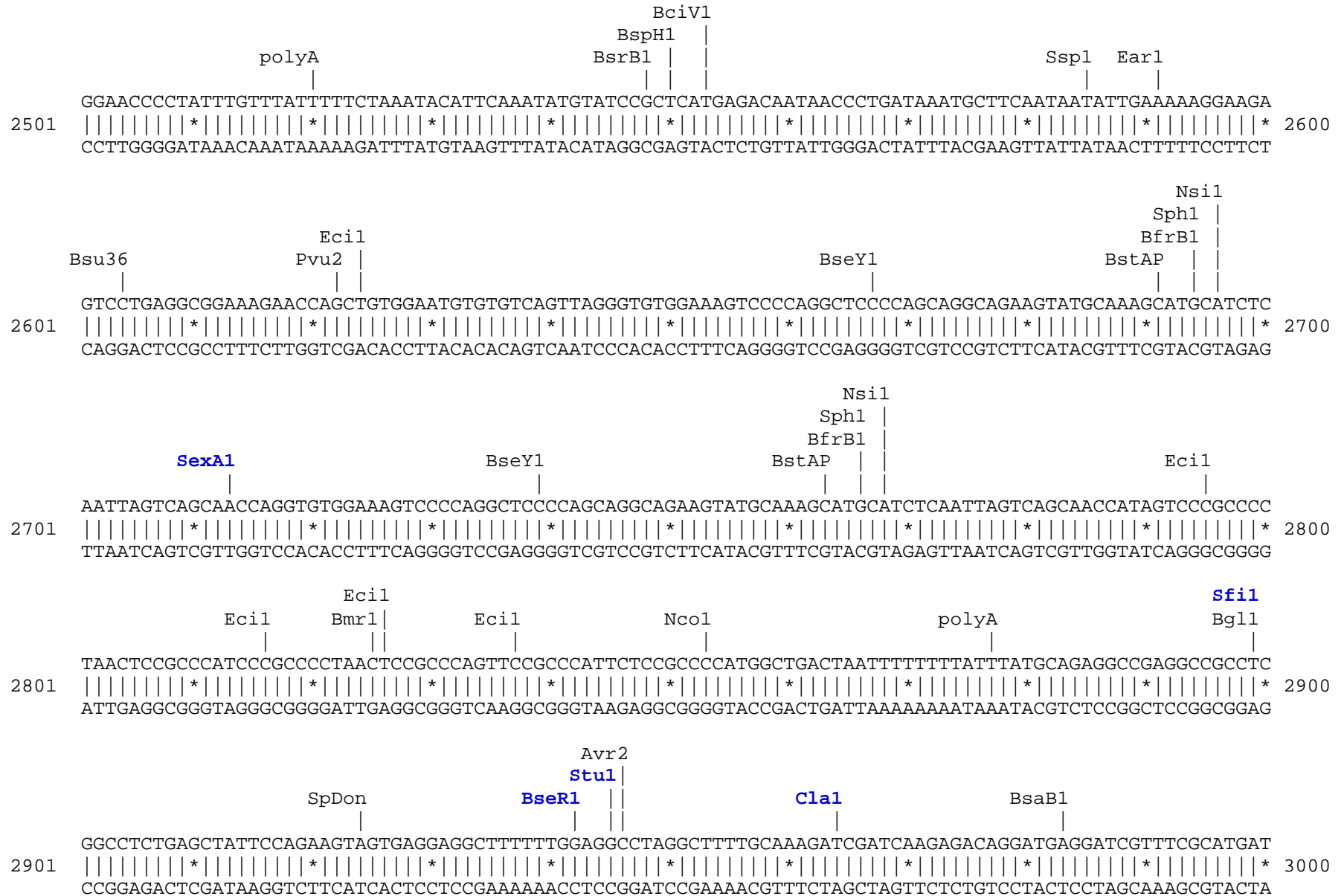
      Af12      SpDon      Ssp1
      |          |          |
2001  TGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGG 2100
      |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*
      ACATAGAATTCCGCATTTAACATTCGCAATTATAAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCC

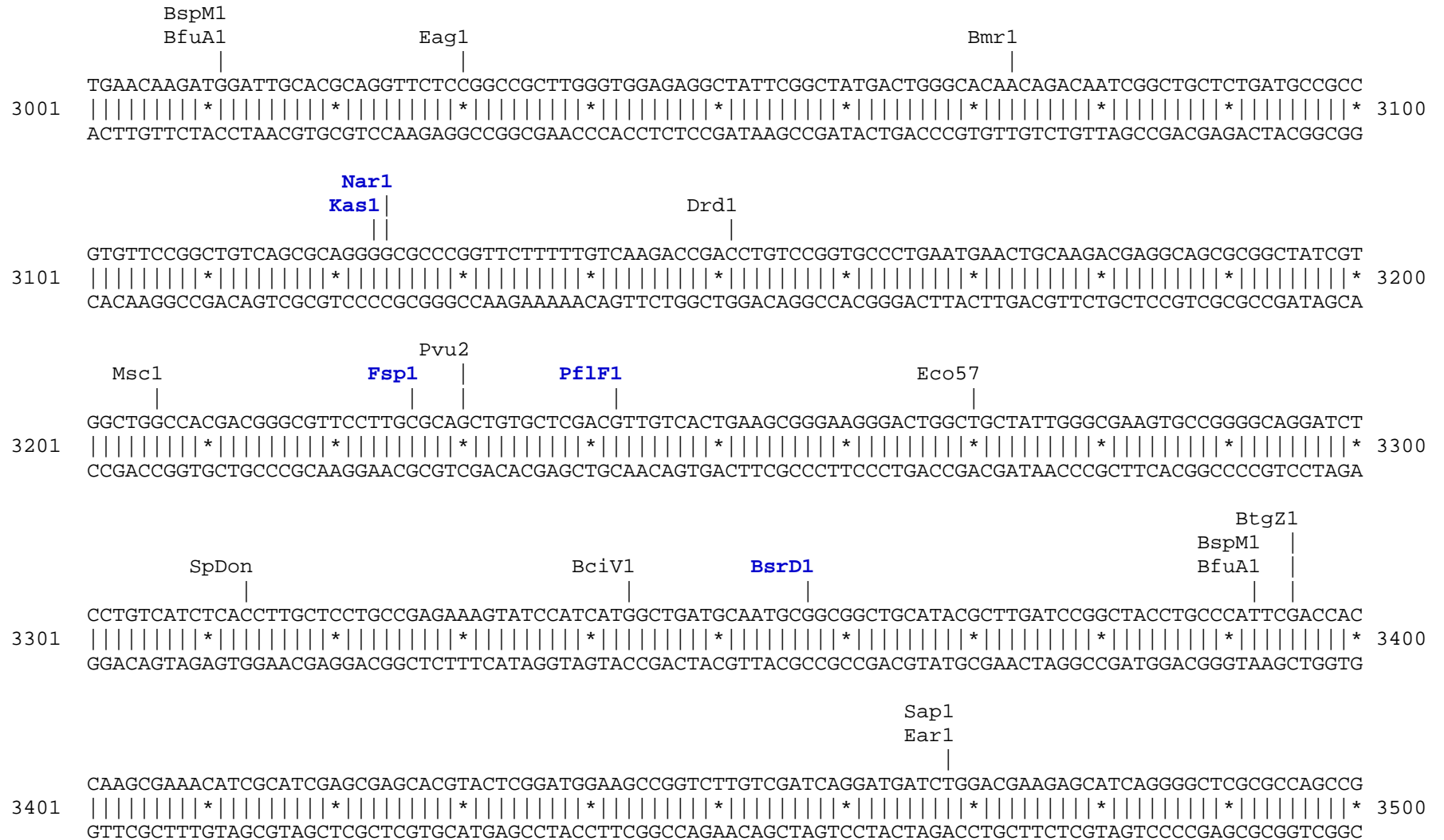
       Psil                                     BsaXb                                     Drd1
       |                                         |                                         |
2101  CAAAATCCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTC 2200
      |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*
      GTTTTAGGGAATATTAGTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAG

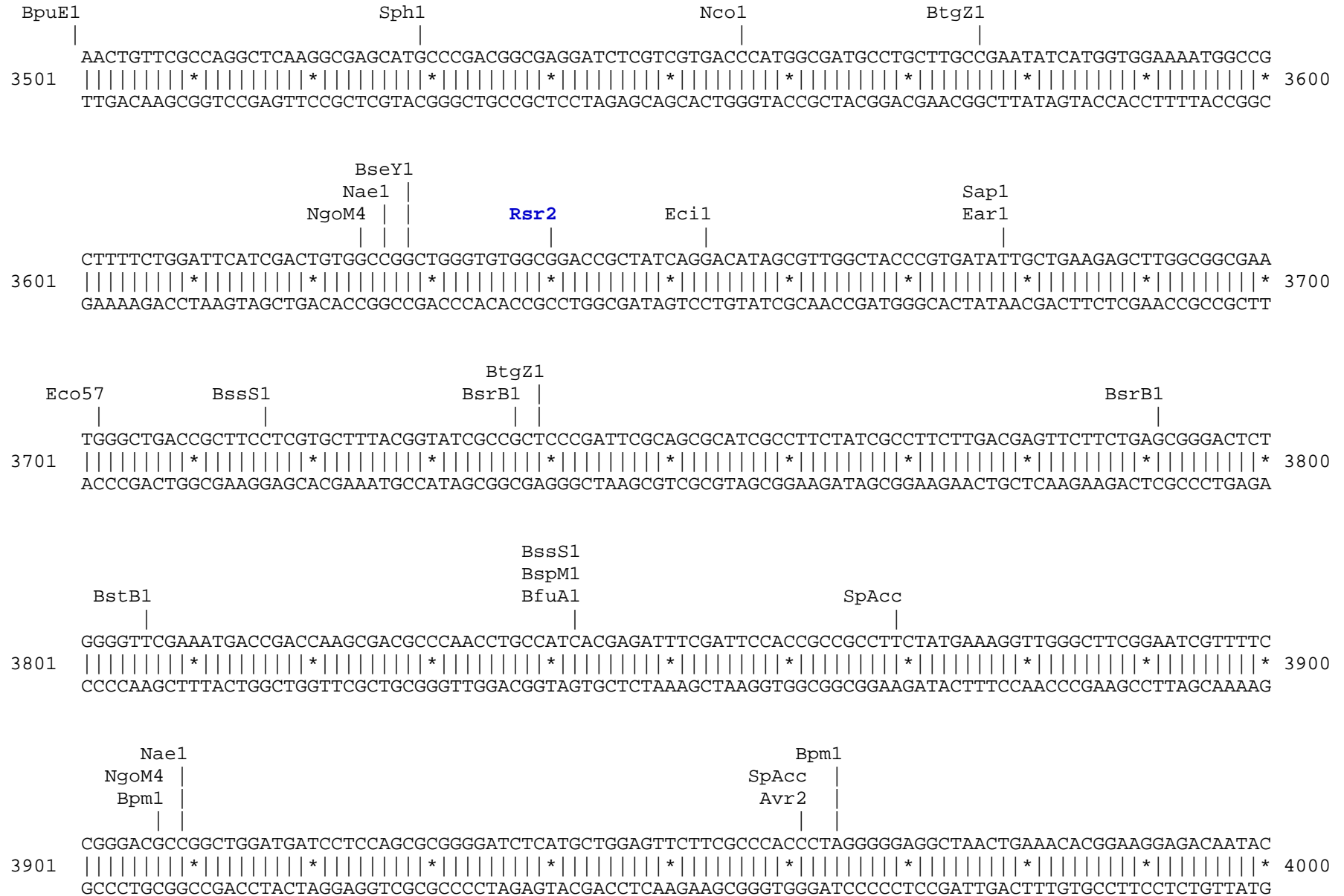
                                           BtgZ1
                                           Dra3 |
BsaXa |
|     |
2201  AAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGA 2300
      |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*
      TTTCCCGCTTTTGGCAGATAGTCCCCTACCGGGTGATGCACCTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCT

                                           Nae1
SpAcc |   NgoM4 |   BsrB1
|       |       |
2301  ACCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCT 2400
      |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*
      TGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGACCCGCTCTTTCTCCCTTTCTTTCGCTTTCTTCGCCCAGATCCCGCGA

                                           Nae1
2401  GGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCGGCTTAATGCGCCGCTACAGGGCGGCTCAGGTGGCACTTTTTCGGGGAAATGTGCGC 2500
      |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*
      CCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATGTCCCAGCAGTCCACCGTGAAAAGCCCCTTTACACGCG
```








```

                                polyA      polyA
                                |          |
CGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACCGGGGTTTCGGTCCCAGGGCTGGCA
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
GCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTTCGCGTCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGT

                                BsaI
                                |
CTCTGTCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCAGTTTCTTCCCTTTTCCCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTC
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
GAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCGAG

                                BstAP      AlwNI      Bsu36      DraI      DraI
                                |          |          |          |          |
GCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAGGATCTAGG
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCC

                                BspH1
                                |
TGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTG
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
ACTTCTAGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAAC

                                BpuE1
                                |
AGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTT
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
TCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTTGTTTTTTGGTGGCGATGGTTCGCCACCAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAA

                                Eco57      SpAcc
                                |          |
CCGAAGGTAACCTGGCTTTCAGCAGAGCGCAGATAACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTA
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
GGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGAT
```

```

                                     AlwN1           BpuE1
                                     |             |
4601 CATACTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGC 4700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCG

                                     ApaL1     BseY1           SpAcc
                                     |         |             |
4701 GCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGC 4800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGTCGCCAGCCCAGCTTGCCCCCAAGCACGTGTGTGCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCGACTCGATACTCTTTTCG

                                     BciV1
                                     |   |
                                     Eci1   BssS1
                                     |   |   |
4801 GCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACAGGGGAGCTTCCAGGGGGAAACGCCTGGT 4900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCA

                                     SpAcc           Drd1           BpuE1           SpAcc     Eci1
                                     |             |             |             |             |
4901 ATCTTTATAGTCCTGTCTGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGC 5000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTGCTTGCG

                                     SpDon           Nsi1
                                     |             |
                                     BspLU           BfrB1
                                     ||           |
5001 GGCCTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTTGTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 5100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1	Bts1
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1
Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsil	PflF1	PflM1	polyA	PshA1
Psil	Pst1	Pvu2	Rsr2	Sac1	Sall	Sap1	SexA1	Sfil	SnaB1	SpAcc	SpDon	Sph1	Ssp1
Stu1	Xba1	Xho1											

Unique:

Aar1	Acc65	Afl2	Age1	Ale1	Ase1	BamH1	Bbs1	Bgl2	Bpu10	BsaXa	BsaXb	BseR1	BspLU
BsrD1	BstX1	Bts1	Clal	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Nar1	Nde1	Nhe1	Not1
PflF1	PflM1	PshA1	Pst1	Rsr2	Sac1	Sall	SexA1	Sfil	SnaB1	Stu1	Xba1	Xho1	

Not found:

Acc1	Ahd1	Apal	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Bcl1	Blp1	BmgB1	Bsg1
BsiW1	BsmB1	BspE1	BssH2	BstE2	BstZ1	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP
ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL
R4atP	R4atR	Sac2	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA
T7Ter	PISce	Xcm1	Xmn1										

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apo1	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													