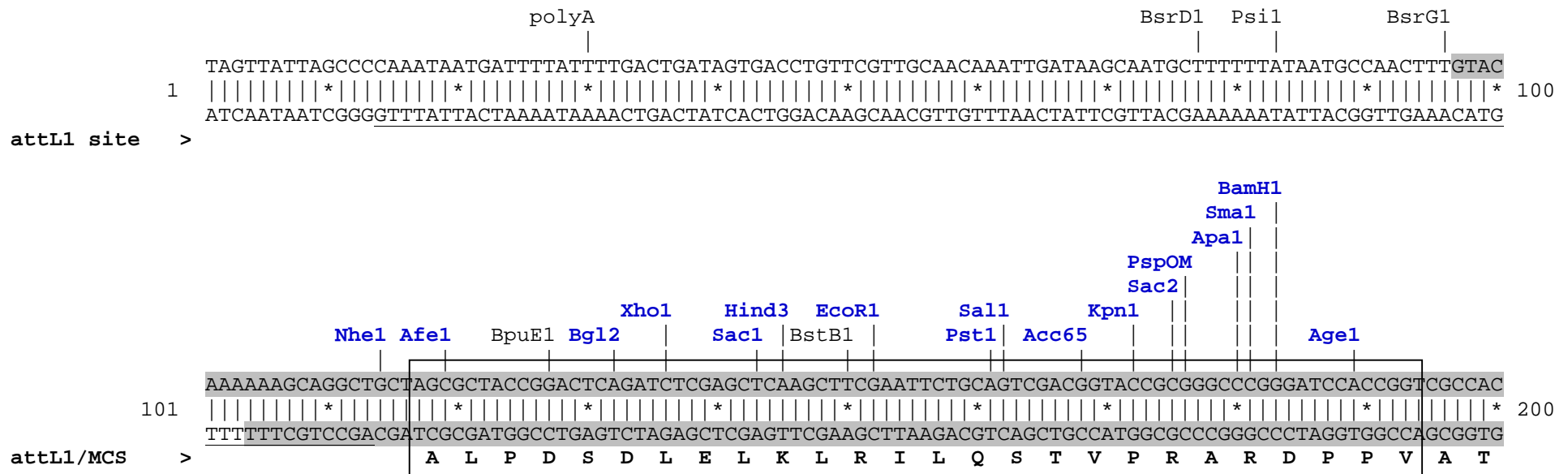
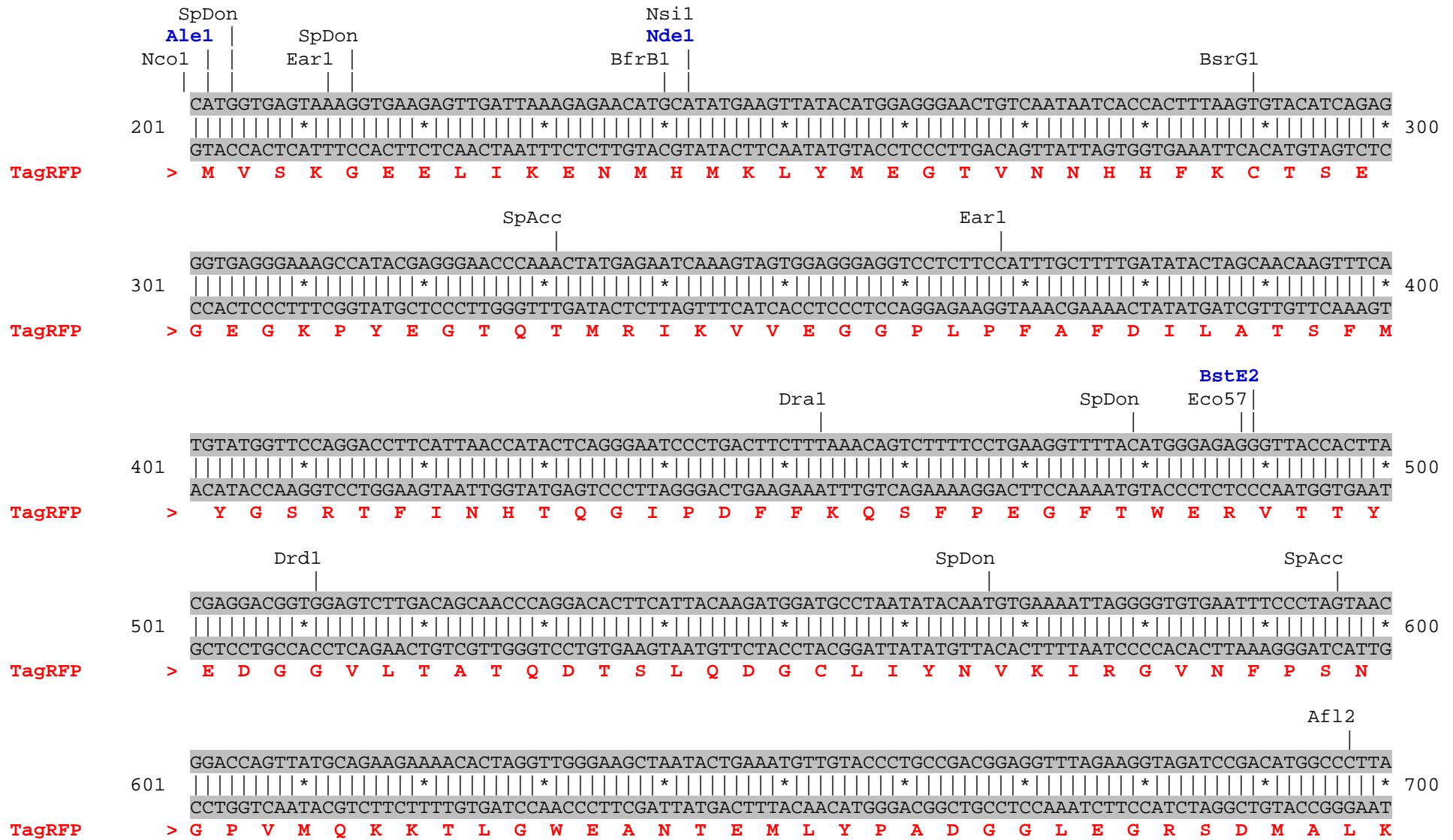


### Gateway® TagRFP-AS-N entry clone restriction map

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 bold blue. 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, the attL sites are underlined. Shaded region corresponds to DNA sequence transferred from the entry clone into the destination vector following recombination. Non-TagRFP amino acids are shown in black, TagRFP amino acids are shown in red.





DraI SpDon

```

1001 AGCTAGTTCGGAGGTGGACTTGTCTGTAACCTTTAAAAACCACATATAGGTCTAAGAAGCCAGCAAAGAATCTAAAAATGCCTGGTGTACTATGTGGA
1002 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
1003 TCGATCAGCCTCCACCTGTGAACTAGACATTGAAATTTTTGGTGTATATCCAGATTCTTCGGTTCGTTCTTAGATTTTTTACGGACCACAAATGATACACCT
TagRFP > L V G G G H L I C N F K T T Y R S K K P A K N L K M P G V Y Y V D

```

SpAcc SpDon

```

801 CCATAGACTAGAAAAGGATAAAAAGAAGCAGACAAAGAAACTTACGTGGAGCAACATGAGGTTCGCCGTCGCTAGGTATTGCGACTTACCTTCCAAGCTAGGT
802 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
803 GGTATCTGATCTTTCTATTTTTCTTCGTCTGTTTTCTTTGAATGCACCTCGTTGTACTCCAGCGGCAGCGATCCATAACGCTGAATGGAAGGTTTCGATCCA
TagRFP > H R L E R I K E A D K E T Y V E Q H E V A V A R Y C D L P S K L G

```

NotI BseY1  
EagI Eco57 BsrG1 PstI BsrD1

```

901 CACAAATTGAACTGAAGCGGCCGCGACTCTAGGACCCAGCTTTCTTTGTACAAAGTTGGCATTATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACA
902 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
903 GTGTTTAACTTGAAGTTTCGCCGCGCTGAGATCCTGGGTCGAAAGAACATGTTTCAACCGTAATATTCTTTTCGTAACGAATAGTTAAACAACGTTGCTTGT
TagRFP/attL2 > H K L N *

```

polyA BsaB1 SpDon DraI

```

1001 GGTCACTATCAGTCAAAATAAAAATCATTATTTTGCTAGATCATAATCAGCCATAACACATTTGTAGAGGTTTACTTTGCTTTAAAAAACCTCCCACACCTC
1002 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
1003 CCAGTGATAGTCAGTTTTATTATTAGTAATAAACGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAATGAACGAAATTTTTTGGAGGGTGTGGAG
attL2 site

```

BsmI HpaI polyA PstI polyA

```

1101 CCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCATCACAAATTTCA
1102 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
1103 GGGGACTTGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGT

```

polyA Bts1 BsmI AflII SpDon SspI

```

1201 CAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTTGTAAGCGTTAATATTTTGTAAAT
1202 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
1203 GTTATTTCGTAAAAAAAGTGACGTAAGATCAACACCAACAGGTTTGGAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAACAATTTTA

```

```

                                     Psil
                                     |
1301 TCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAAATCAAAAGAATAGACCGAGATAGGGTTGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    AGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTC

                                     BsaXb          Drd1          BsaXa          BtgZ1
                                     |             |             |             |
1401 TGTGTTCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
    ACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTT

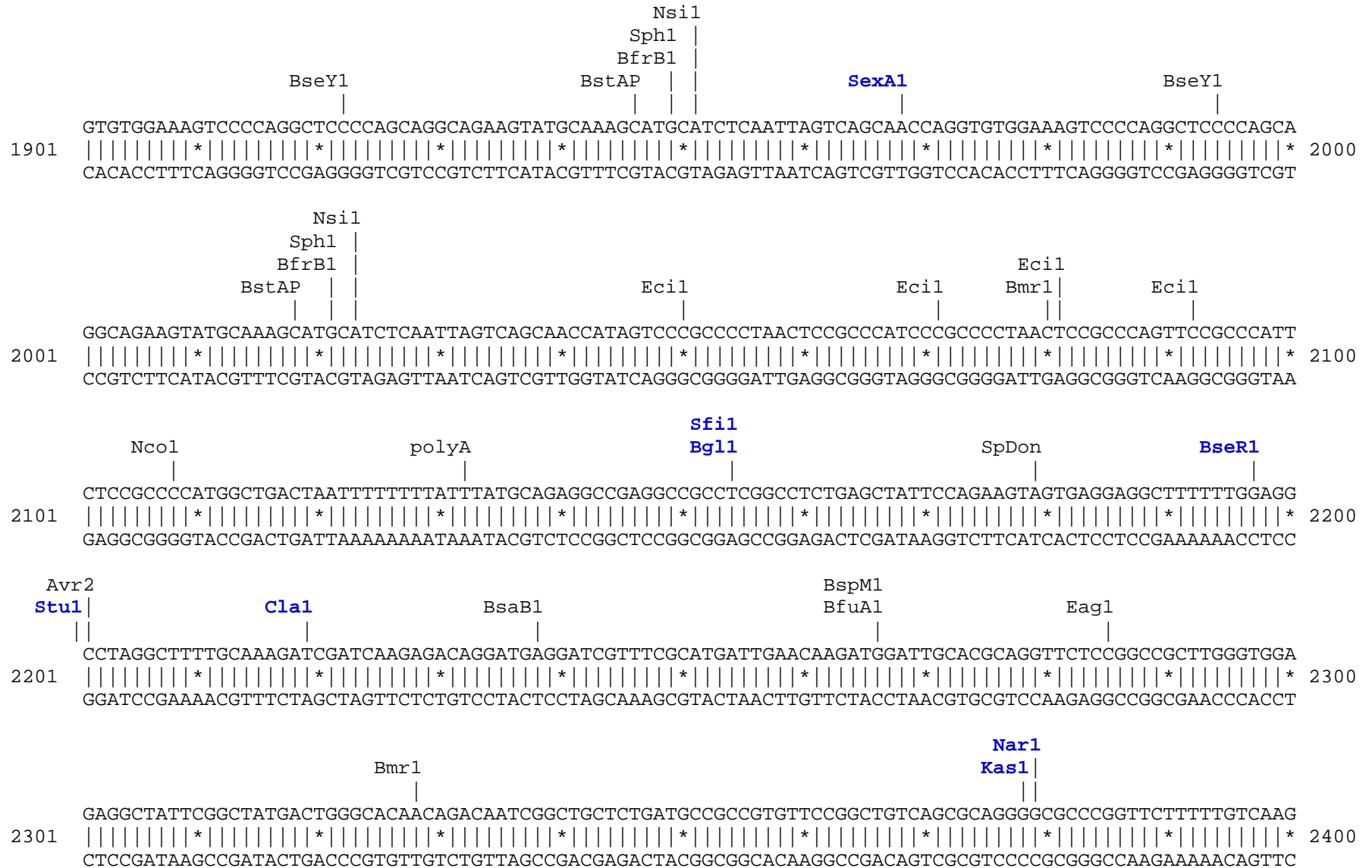
                                     SpAcc          NaeI
                                     |             |
1501 CCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCCGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
    GGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCC

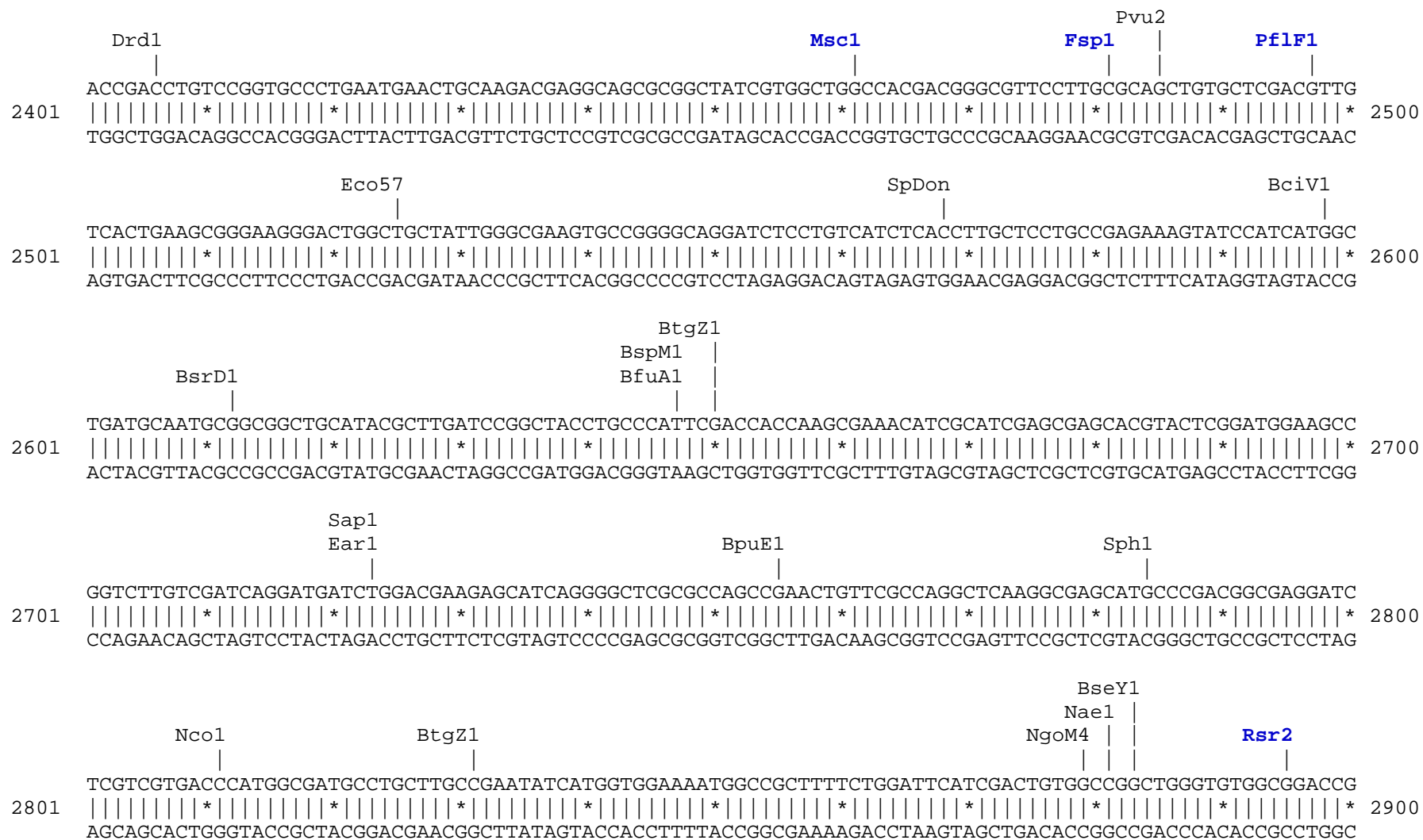
                                     BsrB1
                                     |
1601 CGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
    GCTTGCACCGCTTTTCCTTCCCTTCTTTCGCTTTTCTCGCCCGGATCCCGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGGC

                                     polyA
                                     |
1701 GCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
    CGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCCTTACACGCGCCTTGGGGATAAACAATAAAAAGATTTATGTAAGTTTATACATA

                                     BciV1          BspH1          BsrB1          Ssp1          Ear1          Bsu36          Pvu2          Eci1
                                     |             |             |             |             |             |             |             |
1801 CCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
    GGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCC

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                Ecil              SapI              Eco57              BssSI              BtgZ1
                |                |                |                |                |
                |                |                |                |                |
          2901  CTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGAT
                |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
          GATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTA

                                                BsrB1              BstB1              BssSI
                                                |                |                |
                                                |                |                |
          3001  TCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACG
                |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
          AGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGC

                                                NaeI
                                                |
                                                |
                SpAcc              NgoM4              Bpm1
                |                |                |
                |                |                |
          3101  AGATTTTCGATTCCACCGCCGCTTCTATGAAAAGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTG
                |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
          TCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGAC

                Bpm1              SpAcc              Avr2              polyA              polyA
                |                |                |                |                |
                |                |                |                |                |
          3201  GAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAA
                |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
          CTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTT

                                                BsaI
                                                |
                                                |
          3301  CGCACGGTGTGGGTCGTTTGTTCATAAACCGGGGTTGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCCG
                |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
          GCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGC

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                                                                 BstAP
                                                                 AlwN1
                                                                 Bsu36
3401 CGTTTCTTCCTTTTCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTAC 3500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATG

          DraI          DraI          BspH1
          |             |             |
3501 TCATATATACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTG 3600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      AGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCAC

                                                                 BpuE1
                                                                 |
3601 AGTTTTCTGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGTAATCTGCTGCTTGCAAACAAAAAA 3700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTT

                                                                 Eco57
                                                                 |
3701 ACCACCGTACCAGCGGTGGTTTGTGGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTC 3800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAG

          SpAcc          AlwN1
          |             |
3801 CTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTG 3900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCAAC

          BpuE1          ApaI1          BseY1
          |             |             |
3901 GCGATAAGTCGTGCTTACCAGGTTGGACTCAAGACGATAGTTACCAGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTT 4000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTGGGTTCGAA
```



```

                                     SpAcc
                                     |
GGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGC
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
CCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCTGTCCATAGGCCATTTCG

                                     BssS1
                                     |
                                     SpAcc
                                     |
                                     Drd1
                                     |
GGCAGGGTTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTC
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
CCGTCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAG

                                     BpuE1
                                     |
                                     SpAcc
                                     |
                                     Ecil
                                     |
                                     SpDon
                                     |
                                     BspLU
                                     |
GATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTCCTGGCCTTTTGGCTGGCCTTTTGTCTCACAT
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTA

                                     NsiI
                                     |
                                     BfrB1
                                     |
GTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4355
CAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

<b>Acc65</b>	<b>Afe1</b>	Afl2	<b>Age1</b>	<b>Ale1</b>	AlwN1	<b>Apa1</b>	<b>Apal1</b>	Avr2	<b>BamH1</b>	BciV1	BfrB1	BfuA1	<b>Bgl1</b>
<b>Bgl2</b>	Bmr1	Bpm1	BpuE1	<b>Bsa1</b>	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	BseY1	Bsm1	BspH1	<b>BspLU</b>	BspM1
BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	<b>BstE2</b>	Bsu36	BtgZ1	<b>Bts1</b>	<b>Clal</b>	Dra1	<b>Dra3</b>	Drd1
Eag1	Ear1	Eci1	Eco57	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Msc1</b>	Nae1	<b>Nar1</b>
Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1	<b>PflF1</b>	polyA	Psi1	<b>PspOM</b>	<b>Pst1</b>	Pvu2	<b>Rsr2</b>	<b>Sac1</b>
<b>Sac2</b>	<b>Sall</b>	Sap1	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xho1</b>		

Unique:

<b>Acc65</b>	<b>Afe1</b>	<b>Age1</b>	<b>Ale1</b>	<b>Apa1</b>	<b>Apal1</b>	<b>BamH1</b>	<b>Bgl1</b>	<b>Bgl2</b>	<b>Bsa1</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	<b>BspLU</b>
<b>BstE2</b>	<b>Bts1</b>	<b>Clal</b>	<b>Dra3</b>	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Msc1</b>	<b>Nar1</b>	<b>Nde1</b>
<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>PspOM</b>	<b>Pst1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sac2</b>	<b>Sall</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>Stu1</b>	<b>Xho1</b>

Not found:

Aar1	Aat2	Acl1	Ahd1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcgl1a	Bcgl1b	Bcl1
Blp1	BmgB1	Bpu10	Bsg1	BsiW1	BsmB1	BspE1	BssH2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	PflM1	Pme1
Pml1	PshA1	Pvu1	R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Sca1	Sgf1	SgrA1	SnaB1	Spe1
Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xba1	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	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													