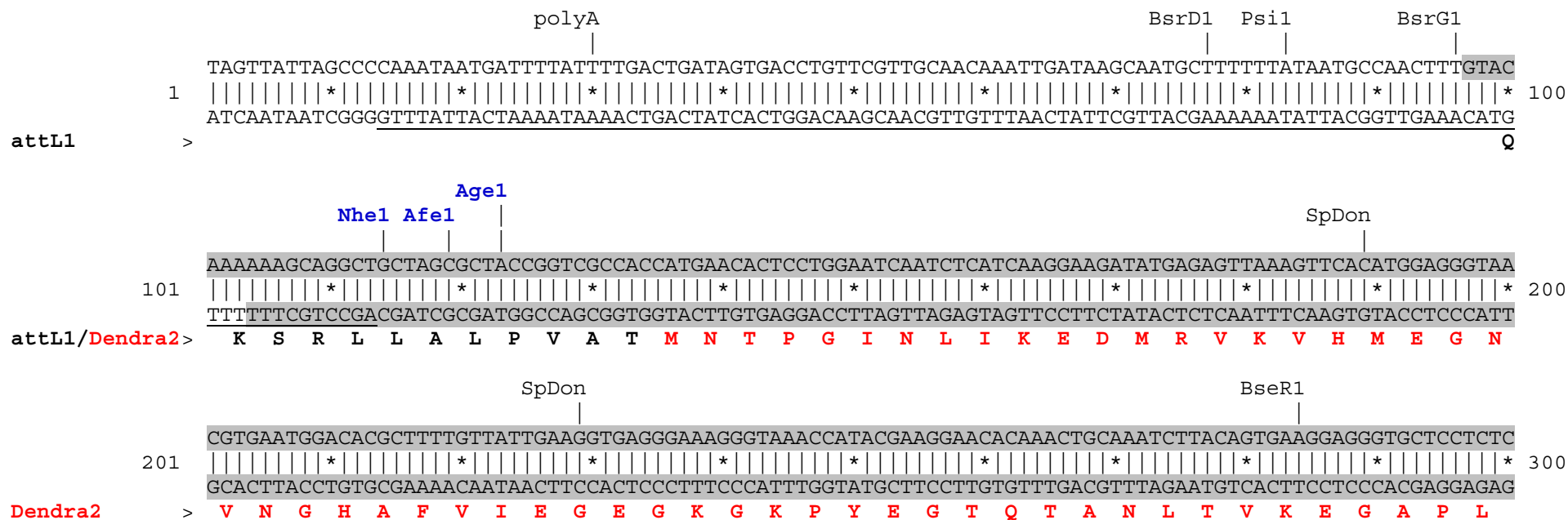
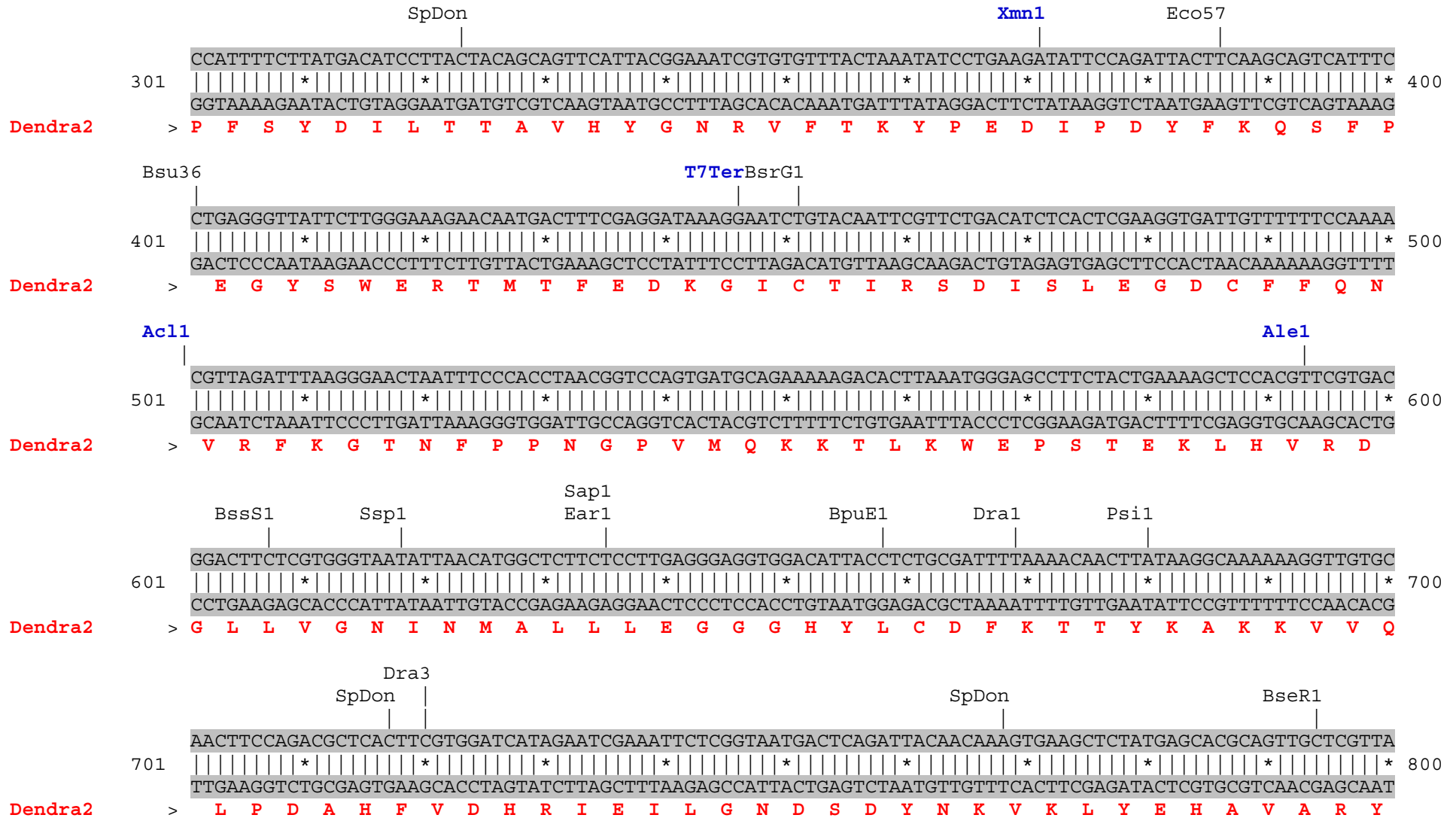


Gateway® Dendra2-At-C entry clone restriction map

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 regions correspond to DNA sequences transferred from the entry clone into the destination vector following recombination. Non-Dendra2 amino acids coded by those DNA sequences are shown in black, Dendra2 amino acids are shown in red.





Sma1
Apa1

Xho1
Bgl2
Bpm1
BpuE1
BsrG1

Hind3 EcoR1
Sac1 BstB1
Sall Pst1
Acc65
Kpn1
PspOM
Sac2

Xcm1

801 TTCTCCTCTCCCATCACAGGTTTGGTCTGGAGACTCAGGTGTGTACAAAAGATCTCGAGCTCAAGCTTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCCG 900
 AAGAGGAGAGGGTAGTGTCCAAACCAGACCTCTGAGTCCACACATGTTTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGC

Dendra2/MCS > S P L P S Q V W S G D S G V Y K R S R A Q A S N S A V D G T A G P

BamH1

BseY1 BsrG1 PsiI BsrD1

901 GGATCCACCGGATCTAGGTAAGTGAACCCAGCTTTCTTGACAAAAGTTGGCATTATAAGAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTA 1000
 CCTAGGTGGCTAGATCCATTGACTTGGGTCGAAAGAACATGTTTCAACCGTAATATTCTTTTCGTAACGAATAGTTAAACAACGTTGCTTGTCCAGTGAT

MCS/attL2 > G S T G S R *

polyA

Bcl1BsaB1 SpDon Dra1

1001 TCAGTCAAAAATAAAATCATTATTTGCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGGCTTTAAAAAACCTCCCACACCTCC 1100
 AGTCAGTTTTATTTTAGTAATAAACGATCTATTGACTAGTATTAGTCGGTATGGTGTAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGG

attL2 site >

Bsm1
MfeI HpaI polyA PsiI polyA

1101 CCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTATTGTCAGCTTATAATGGTTACAAAATAAAGCAATAGCATCACAAATTTTAC 1200
 GGGACTTGGACTTTGTATTTTACTTACGTTAAACAACAATGGAACAAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTG

polyA

Bts1 Bsm1 MluI SpDon Ssp1

1201 AAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACCGTAAATTGTAAGCGTTAATATTTTGTAAATTT 1300
 TTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAACAGGTTTGTAGTAGTTACATAGAATTGCGCATTTAACATTTCGCAATTATAAAAACAATTTTAA

```

                                     Psil
                                     |
1301 CGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGT 1400
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCA

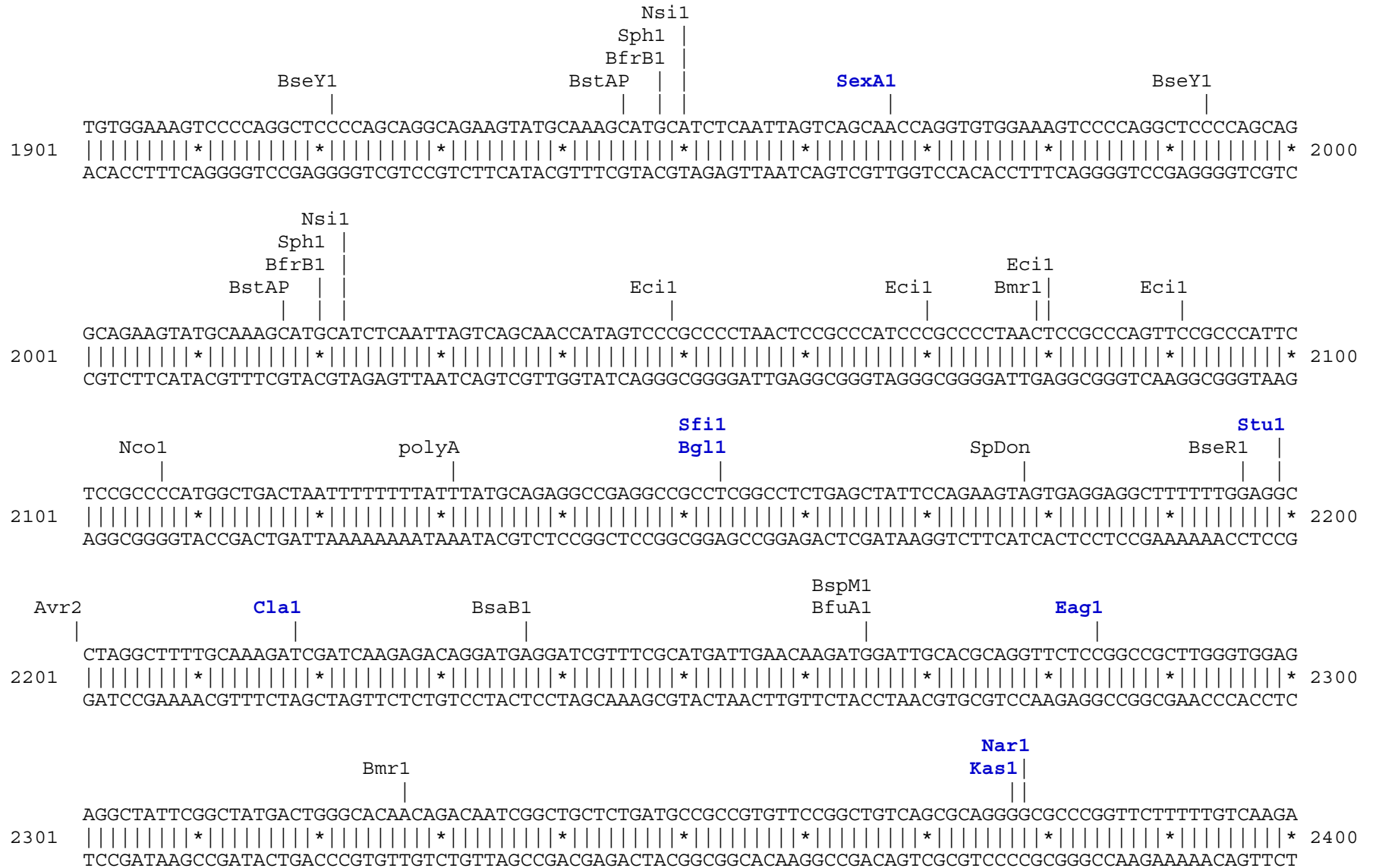
                                     BsaXb          Drd1          BsaXa          BtgZ1
                                     |             |             |             |
1401 GTTGTTCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAAC 1500
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTTCCGCTTTTTGGCAGATAGTCCCCTACCGGGTGATGCACTTG

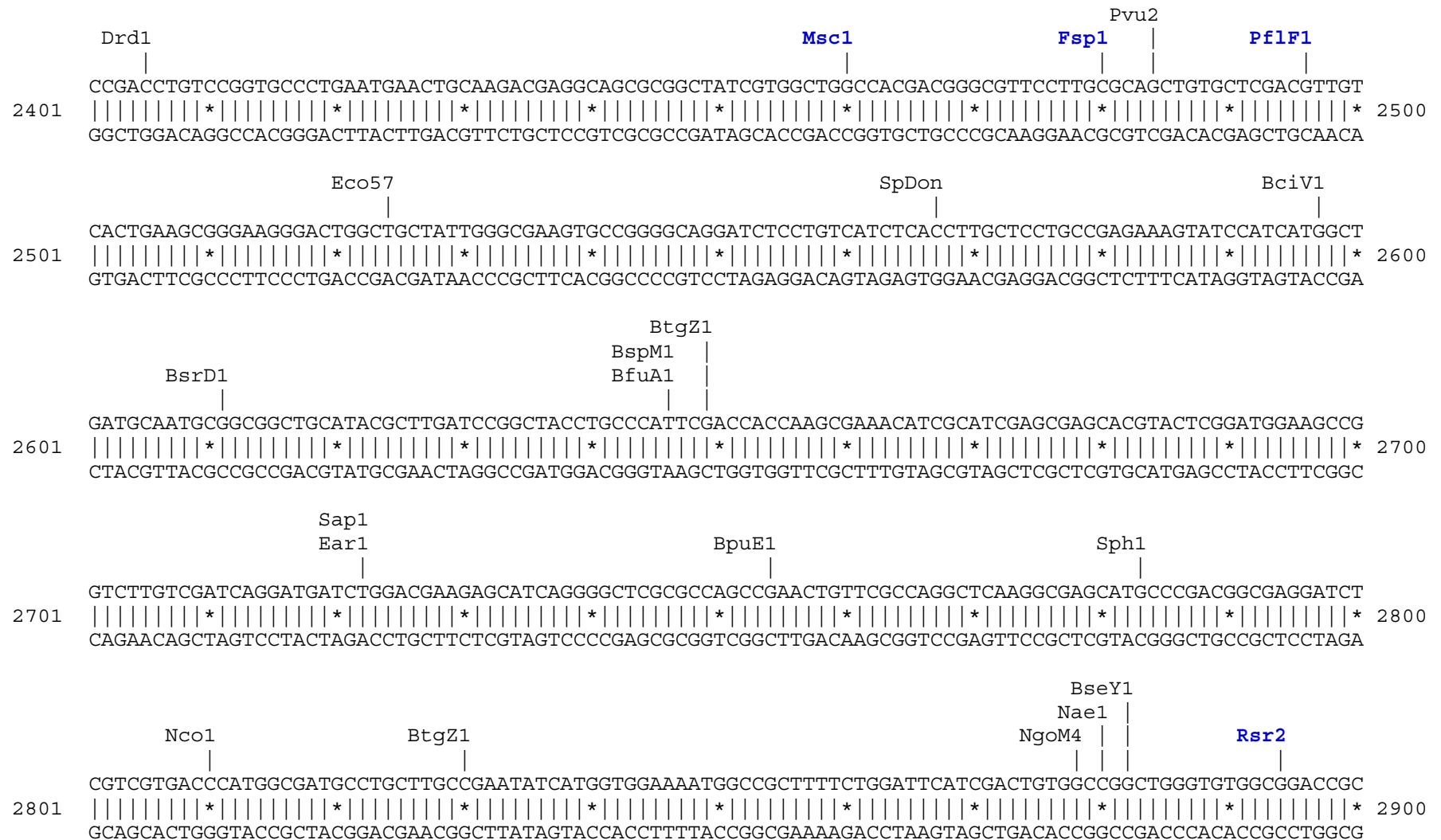
                                     SpAcc          Nae1
                                     |             |
1501 CATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGC 1600
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCG

                                     BsrB1
                                     |
1601 GAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAACCACCACACCCGCCGCG 1700
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCATCCCGCACCCTTACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGC

                                     polyA
                                     |
1701 CTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATC 1800
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GAATTACGCGGCGATGTCCCAGCAGTCCACCGTGAAAAGCCCTTTACACGCGCCTTGGGGATAAAACAAATAAAAAAGATTTATGTAAGTTTATACATAG

    BciV1          BspH1          BsrB1          Ssp1          Ear1          Bsu36          Pvu2          Eci1
    |             |             |             |             |             |             |             |
1801 CGCTCATGAGACAATAACCCGTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCTTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGG 1900
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCTTTCTTGGTGCACACCTTACACACAGTCAATCCC
  
```






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                                     BstAP
                                     AlwN1       Bsu36
                                     |             |
GTTTCTTCCTTTTCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACT
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
CAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGA

                Dra1           Dra1           BspH1
                |             |             |
CATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGA
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
GTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACT

                                     BpuE1
                                     |
GTTTTCGTTCCTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAA
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTT

                                     Eco57
                                     |
CCACCGCTACCAGCGGTGGTTTTGTTTGC CGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCC
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
GGTGGCGATGGTCGCCACCAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTTATGACAGG

                SpAcc           AlwN1
                |             |
TTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGG
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
AAGATCACATCGGCATCAATCCGGTGGTGAAGTTCCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCAAC

                BpuE1           ApaL1           BseY1
                |             |             |
CGATAAGTCGTGTCCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTG
3901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
GCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGCTTGCCCCCAAGCACGTGTGTCCGGTTCGAAC

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                                     SpAcc
                                     |
GAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCG
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
CTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCGACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCTGTCCATAGGCCATTTCGC

                                     BssS1
                                     |
GCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTTCG
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
CGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGC

                                     SpDon
                                     |
                                     BspLU
BpuE1
|
SpAcc
|
Eci1
|
ATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCCTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTGCATG
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
TAAAAAACAACGAGCAGTCCCCCGCTCGGATACCTTTTTGCGGTGCTTTCGCGCCGAAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTAC

                                     Nsi1
                                     |
                                     BfrB1
                                     |
TTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4301 |||||*|||||*|||||*|||||*|||||*|||||*||||| 4354
AAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
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Found:

Acc65	Acl1	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Avr2	BamH1	BciV1	Bcl1	BfrB1	BfuA1
Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	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	Mlu1	Msc1	Nae1
Nar1	Nco1	NgoM4	Nhe1	Nsi1	PflF1	polyA	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2
Sal1	Sap1	SexA1	Sfi1	Sma1	SpAcc	SpDon	Sph1	Ssp1	Stu1	T7Ter	Xcm1	Xho1	Xmn1

Unique:

Acc65	Acl1	Afe1	Age1	Ale1	Apa1	ApaL1	BamH1	Bcl1	Bgl1	Bgl2	Bsa1	BsaXa	BsaXb
BspLU	Bts1	Cla1	Eag1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Msc1	Nar1
Nhe1	PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1	Stu1	T7Ter	Xcm1
Xho1	Xmn1												

Not found:

Aar1	Aat2	Afl2	Ahd1	Asc1	Ase1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Blp1
BmgB1	Bpu10	Bsg1	BsiW1	BsmB1	BspE1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV
ScFRT	Fse1	FspA1	I_Ceu	loxP	Nde1	Not1	Nru1	Pac1	PflM1	Pme1	Pml1	PshA1	Pvu1
SanD1	Sbf1	Sca1	Sgf1	SgrA1	SnaB1	Spe1	Srf1	Swa1	T3RNA	T7RNA	PISce	Xba1	

Excluded by site complexity:

Acc1	Aci1	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													