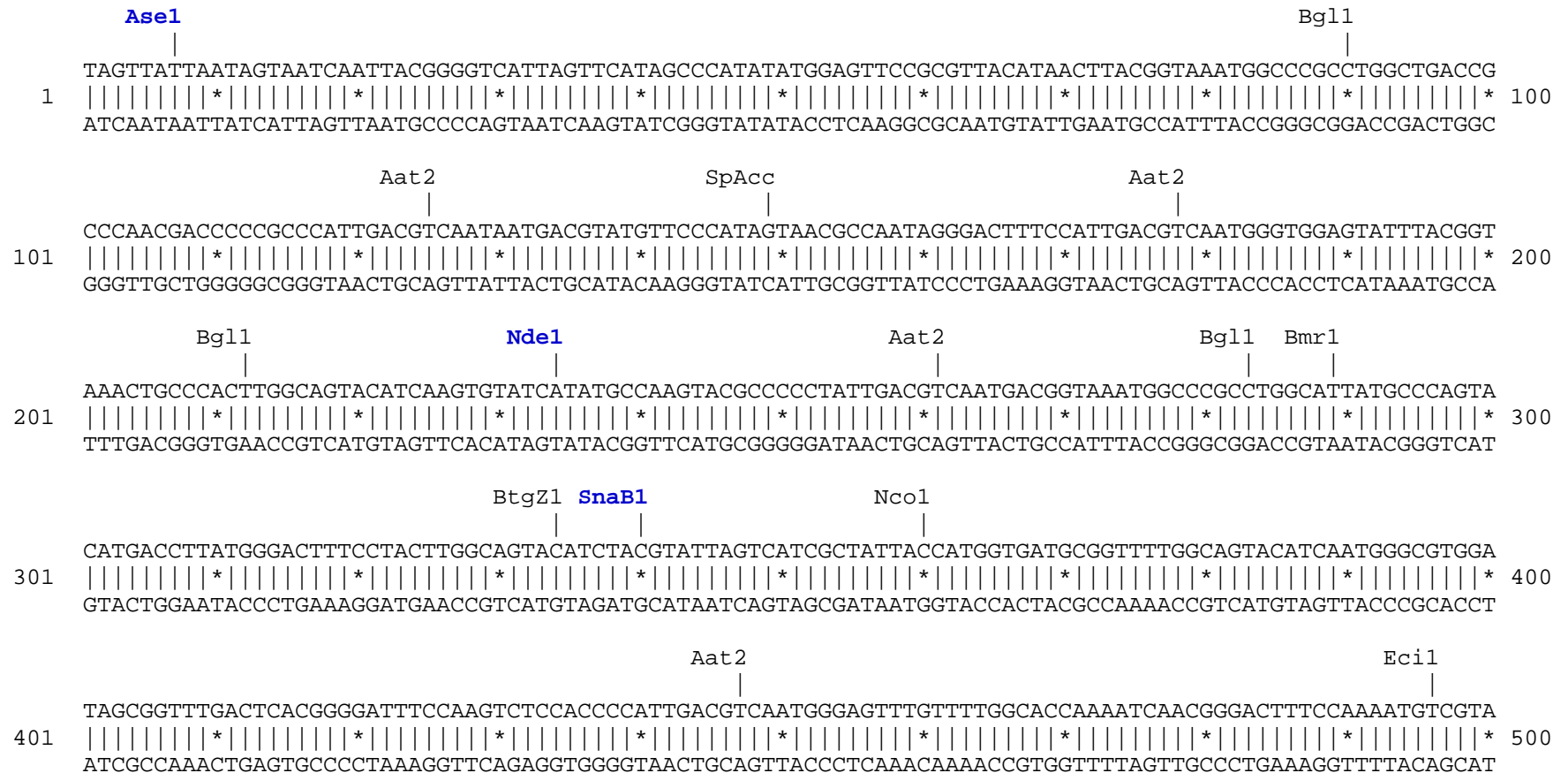
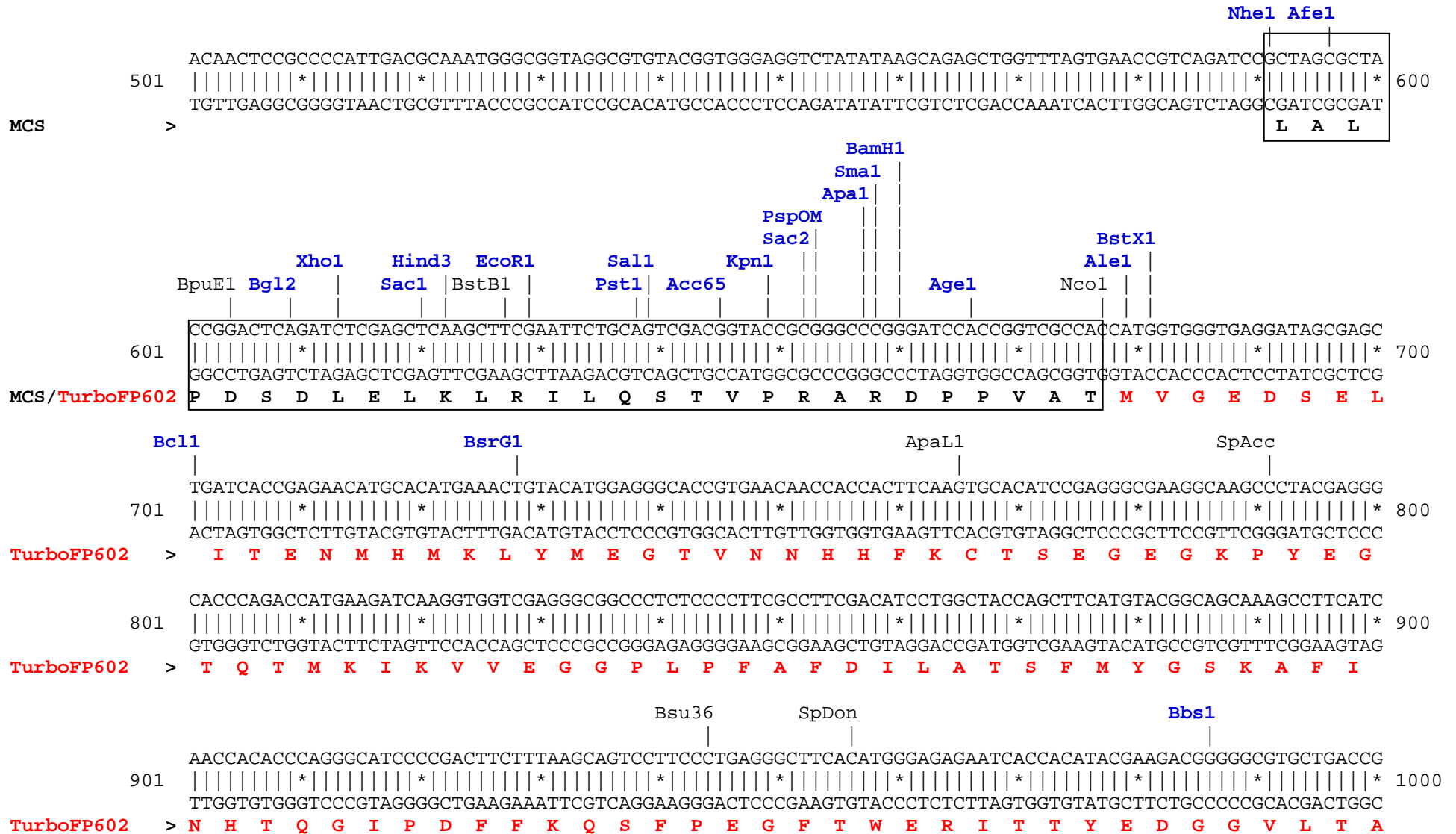


**pTurboFP602-N vector restriction map**

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 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, amino acids encoded by MCS are shown in black.





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Bpm1
|
CTACCCAGGACACCAGCCTCCAGAACGGCTGCCTCATCTACAACGTCAAGATCAACGGGGTGAACCTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAAC
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
GATGGGTCCTGTGGTCGGAGGTCCTTGCCGACGGAGTAGATGTTGCAGTTCTAGTTGCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTG
TurboFP602 > T Q D T S L Q N G C L I Y N V K I N G V N F P S N G P V M Q K K T

Nco1
Sfi1 | Bsg1 Eco57
Bgl1 | Msc1 | BssS1 | BpuE1
BseY1
|
ACTCGGCTGGGAGGCCAGCACCCGAGATGCTGTACCCCGCTGACAGCGGCCTGAGAGGCCATGGCCAGATGGCCCTGAAGCTCGTGGGCGGGGGCTACCTG
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
TGAGCCGACCCTCCGGTCGTGGCTCTACGACATGGGGCGACTGTCGCCGACTCTCCGGTACCGGTCTACCGGGACTTCGAGCACCCGCCCCCGATGGAC
TurboFP602 > L G W E A S T E M L Y P A D S G L R G H G Q M A L K L V G G G Y L

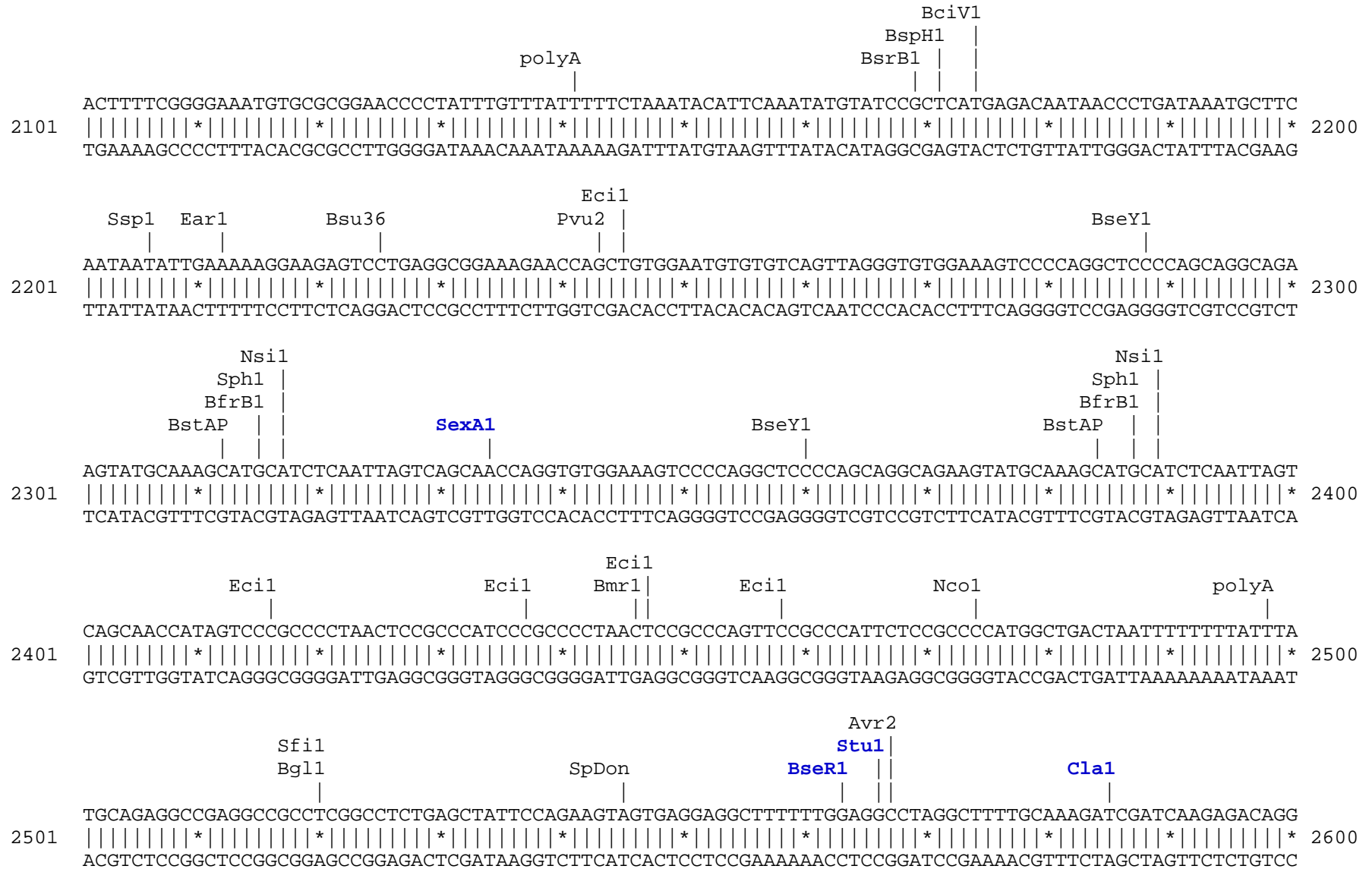
BspM1 PflM1 SpAcc
Bts1BfuA1 | BpuE1 | Dra3 | PflM1
|
CACTGCTCCCTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCTTCCACTTTCGTGGACCACAGACTGGAAAGAATCAAGG
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GTGACGAGGGAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAAGGTGAAGCACCTGGTGTCTGACCTTTCTTAGTTCC
TurboFP602 > H C S L K T T Y R S K K P A K N L K M P G F H F V D H R L E R I K E

Pvu2 Not1
Bsa1 PshA1 BssS1 Msc1 Scal SpAcc Bmr1 | Eag1 Xba1
|
AGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGATGGCTGTGGCCAAGTACTGCGACCTCCCTAGCAAACCTGGGGCACAGCTGATGCGGCCGCGACTC
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
TCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCTACCGACACCGGTTTCATGACGCTGGAGGGATCGTTTGACCCCGTGTGCGACTACGCCGGCGCTGAG
TurboFP602 > A D K E T Y V E Q H E M A V A K Y C D L P S K L G H S *

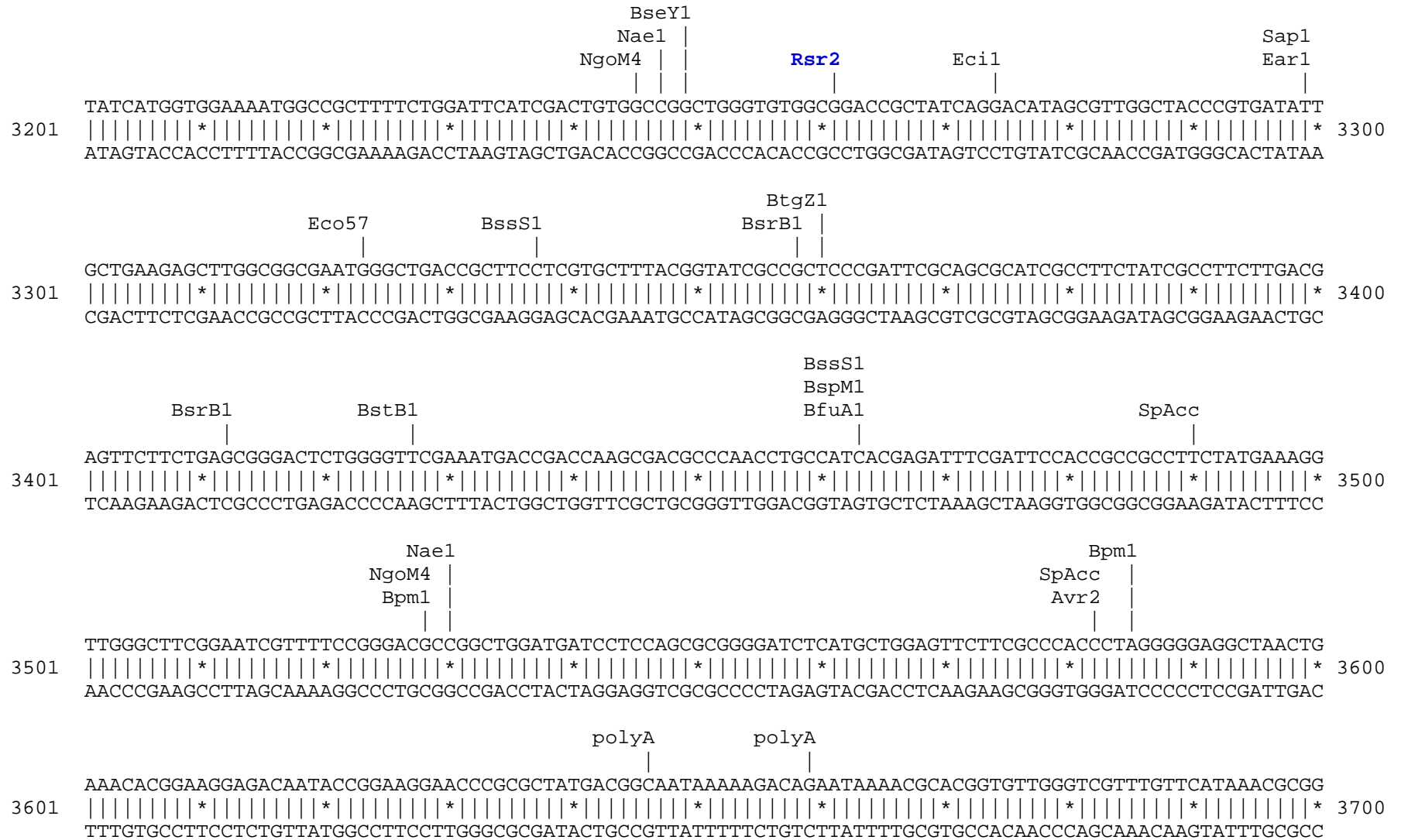
BsaB1 SpDon Dra1 Bsm1 MfeI
|
TAGATCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTG
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
ATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAAC

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                                Bsa1
                                |
3701 GGTTCGGTCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCATTGGGGCCAATACGCCCGGTTTCTTCTTTTCCCCACCCACCCCCCAAGT
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3800
    CCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCA

                                BstAP
                                |
                                AlwN1        Bsu36
                                |             |
3801 TCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATT
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3900
    AGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAA

                                Dral
                                |
                                BspH1
                                |
3901 TTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTGGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGA
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4000
    AAATTTAAATTTTCCTAGATCCACTTCTAGGAAAAAATAATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCT

                                BpuE1
                                |
4001 AAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAACCACCGTACCAGCGGTGGTTTGTGTTGCCGGAT
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4100
    TTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTA

                                Eco57
                                |
                                SpAcc
                                |
4101 CAAGAGCTACCAACTCTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTCTTAGTGTAGCCGTAGTTAGGCCACCACTTCA
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4200
    GTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGT

                                AlwN1        BpuE1
                                |             |
4201 AGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAG
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4300
    TCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTGACGACAGAAATGGCCCCAACCTGAGTTC

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                                     ApaL1   BseY1
                                     |         |
4301 ACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCTGTCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
   TGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTCTGGGTCTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGAT

                                     BciV1
                                     |         |
          SpAcc                      Eci1         BssS1
          |                             |         |
4401 CAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCTGGAACAGGAGAGCGCACGAGGGGAGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
   GTCGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTGCGCCGTCAGCCTTGTCTCTCGCGTGCTCCCTCG

                                     SpAcc          Drd1          BpuE1          SpAcc
                                     |              |              |              |
4501 TTCCAGGGGAAACGCCTGGTATCTTTATAGTCTTCTGTCGGGTTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
   AAGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGA

                                     SpDon
                                     |         |
          Eci1                      BspLU
          |                             |         |
4601 ATGGAAAAACGCCAGCAACGCGCCTTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
   TACCTTTTTGCGGTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTTACAAGAAAGGACGCAATAGGGGACTAAGACACCTA

          Nsil
          BfrB1 |
          |     |
4701 AACCGTATTACCGCCATGCAT
   |||||*|||||*|| 4721
   TTGGCATAATGGCGGTACGTA
```

Found:

Aat2	<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	AlwN1	<b>Apa1</b>	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	<b>Bbs1</b>	BciV1
<b>Bcl1</b>	BfrB1	BfuA1	Bgl1	<b>Bgl2</b>	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	BseY1
<b>Bsg1</b>	Bsm1	BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	BssS1	BstAP	BstB1	<b>BstX1</b>	Bsu36	BtgZ1
Bts1	<b>Clal</b>	Dra1	Dra3	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>	Msc1	Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1	<b>PflF1</b>	PflM1	polyA
<b>PshA1</b>	Psi1	<b>PspOM</b>	<b>Pst1</b>	Pvu2	<b>Rsr2</b>	<b>Sac1</b>	<b>Sac2</b>	<b>Sall</b>	Sap1	<b>Scal</b>	<b>SexA1</b>	Sfi1	<b>Sma1</b>
<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>						

Unique:

<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	<b>Apa1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bbs1</b>	<b>Bcl1</b>	<b>Bgl2</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>
<b>Bsg1</b>	<b>BspLU</b>	<b>BsrD1</b>	<b>BsrG1</b>	<b>BstX1</b>	<b>Clal</b>	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Nar1</b>
<b>Nde1</b>	<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>PshA1</b>	<b>PspOM</b>	<b>Pst1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sac2</b>	<b>Sall</b>	<b>Scal</b>	<b>SexA1</b>	<b>Sma1</b>
<b>SnaB1</b>	<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>										

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Blp1	BmgB1	Bpu10	BsiW1
BsmB1	BspE1	BssH2	BstE2	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP
Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Sgf1	SgrA1	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	Bsl1	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													