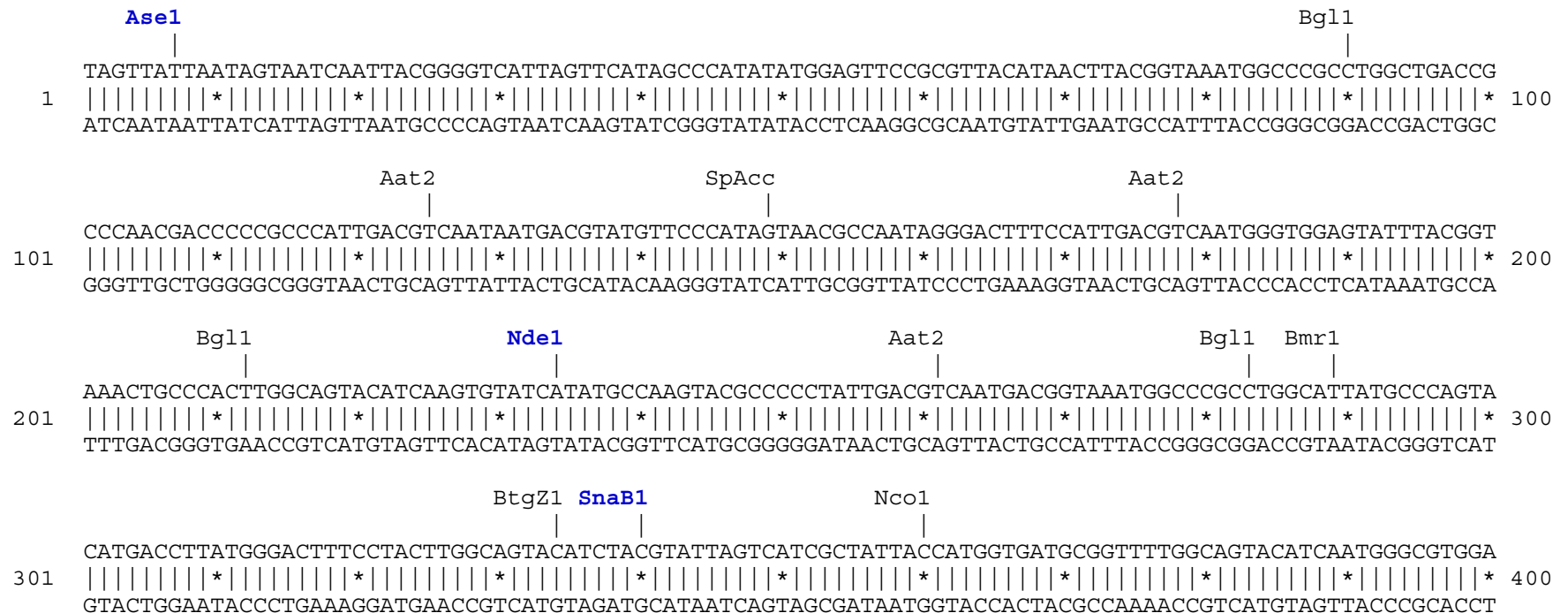


pKillerRed-dMito vector restriction map

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 shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Mitochondrial targeting sequences (MTS-1 and MTS-2) are shown in bold blue and bold green.



ApaL1
Bsa1
PflM1

```

          |
          |
          |
    GCAGCAGCAAGTTCCCCACGGCGACTTCAACGTGCACGCCGTGTGCGAGACCGGCAAGCTGCCCATGAGCTGGAAGCCCATCTGCCACCTGATCCAGTA
101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
    CGTCGTCGTTCAAGGGGGTGCCGCTGAAGTTGCACGTGCGGCACACGCTCTGGCCGTTTCGACGGGTACTCGACCTTCGGGTAGACGGTGGACTAGGTCAT
KillerRed >  S S K F P H G D F N V H A V C E T G K L P M S W K P I C H L I Q Y
  
```

Bpu10

```

          |
    CGGCGAGCCCTTCTTCGCCCCGTACCCCCGACGGCATCAGCCATTTTCGCCCAGGAGTGCTTCCCCGAGGGCCTGAGCATCGACCGCACCGTGCGCTTCGAG
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    GCCGCTCGGAAGAAGCGGGCGATGGGGCTGCCGTAGTCGGTAAAGCGGGTCTCACGAAGGGGCTCCCGGACTCGTAGCTGGCGTGGCACGCGAAGCTC
KillerRed >  G E P F F A R Y P D G I S H F A Q E C F P E G L S I D R T V R F E
  
```

BspM1
BfuA1
Aar1
Ale1SpDon

```

          |
          |
          |
    AACGACGGCACCATGACCAGCCACcACACCTACGAGCTGGACGACACCTGCGTGGTGAGCCGCATCACCGTGAAGTGCAGCGGCTTCCAGCCCGACGGCC
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    TTGTGCGCGTGGTACTGGTTCGGTGTgTGTGGATGCTCGACCTGCTGTGGACGCACCACTCGGCGTAGTGGCACTTGCAGCTGCCGAAGGTGGGGTGCCTGG
KillerRed >  N D G T M T S H H T Y E L D D T C V V S R I T V N C D G F Q P D G P
  
```

_Chi
PflM1
Pvu2
Bsa1
BspLU
Pvu2

```

          |
          |
          |
    CCATCATGCGCGACCAGCTGGTGGACATCCTGCCCAACGAGACCCACATGTTCCCCCACGGCCCCAACGCCGTGCGCCAGCTGGCCTTCATCGGCTTCAC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    GGTAGTACGCGCTGGTTCGACCACCTGTAGGACGGGTTGCTCTGGGTGTACAAGGGGGTTCGGGGGTTGCGGCACGCGGTTCGACCGGAAGTAGCCGAAGTG
KillerRed >  I M R D Q L V D I L P N E T H M F P H G P N A V R Q L A F I G F T
  
```

SpDon
Dra3

```

          |
          |
          |
    CACCGCCGACGGCGGCCTGATGATGGGCCACTTTCGACAGCAAGATGACCTTCAACGGCAGCCGCGCCATCGAGATCCCCGGCCCACACTTCGTGACCATC
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    GTGGCGGCTGCCCGGACTACTACCCGGTGAAGCTGTCGTTCTACTGGAAGTTGCCGTGCGGCGCGGTAGCTCTAGGGGCCGGGTGTGAAGCACTGGTAG
KillerRed >  T A D G G L M M G H F D S K M T F N G S R A I E I P G P H F V T I
  
```

```

                                     Pml1                                Dra3
                                     |                                |
ATCACCAAGCAGATGAGGGACACCAGCGACAAGCGCACCACGTGTGCCAGCGCAGGTGGCCTACGCCACAGCGTGTCCCGCATCACCAGCGCCATCG
1401 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1500
TAGTGGTTCGTCTACTCCCTGTGGTCGCTGTTTCGCGCTGGTGCACACGGTCGCGCTCCACCGGATGCGGGTGTTCGCACGGGGCGTAGTGGTTCGCGGTAGC
KillerRed > I T K Q M R D T S D K R D H V C Q R E V A Y A H S V P R I T S A I G

                                 Not1
                                 |
                                Eag1      Xba1      BsaB1
                                |          |          |
gtagcgacgaggattaaagcggccgcGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCC
1501 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1600
catcgctgctcctaatttcgccggcgCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTTGGAGGGTGTGGAGGGG
KillerRed > S D E D *

                                 Bsm1
                                 |
                                Mfe1      Hpa1      polyA      Pst1      polyA      polyA
                                ||      |          |          |          |          |          |
CTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTATTGTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAA
1601 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1700
GACTTGGACTTTGTATTTTACTTTACGTTAAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTT

                                Bts1 Bsm1
                                |      |
                                |      |
ATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAATTTCG
1701 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1800
TATTTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGTAGTAGTTACATAGAATTCGCATTTAACATTTCGCAATTATAAAACAATTTTAAGC

                                                                 Pst1
                                                                 |
CGTTAAATTTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGT
1801 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1900
GCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTTCTTATCTGGCTCTATCCCAACTCACA

```



```

                        Nsi1
                      Sph1
                    BfrB1
                   BstAP
                BseY1
          TGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGC
2401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
          ACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCG

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                    Nsi1
                  Sph1
                BfrB1
               BstAP
          AGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCCGCCCTAACTCCGCCATCCC GCCCTAACTCCGCCCAGTTCCGCCATTCTC
2501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
          TCTTCATACGTTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAG

```

```

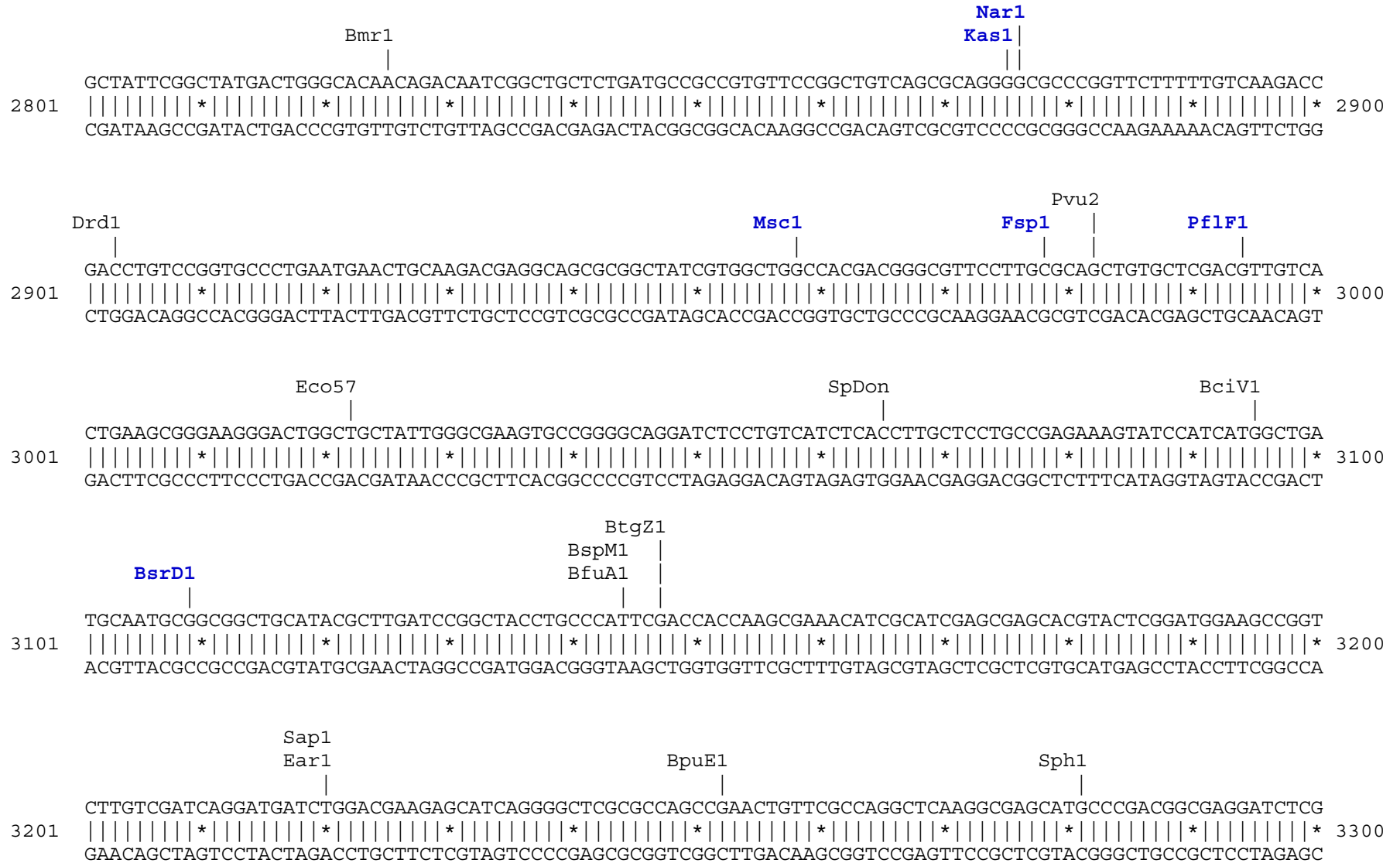
                                Avr2
                              Stu1
                             BseR1
                            SpDon
                      Nco1
                polyA
                Sfi1
              Bgl1
          CGCCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCT
2601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
          GCGGGTACCGACTGATTAATAAAAAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAACCTCCGGA

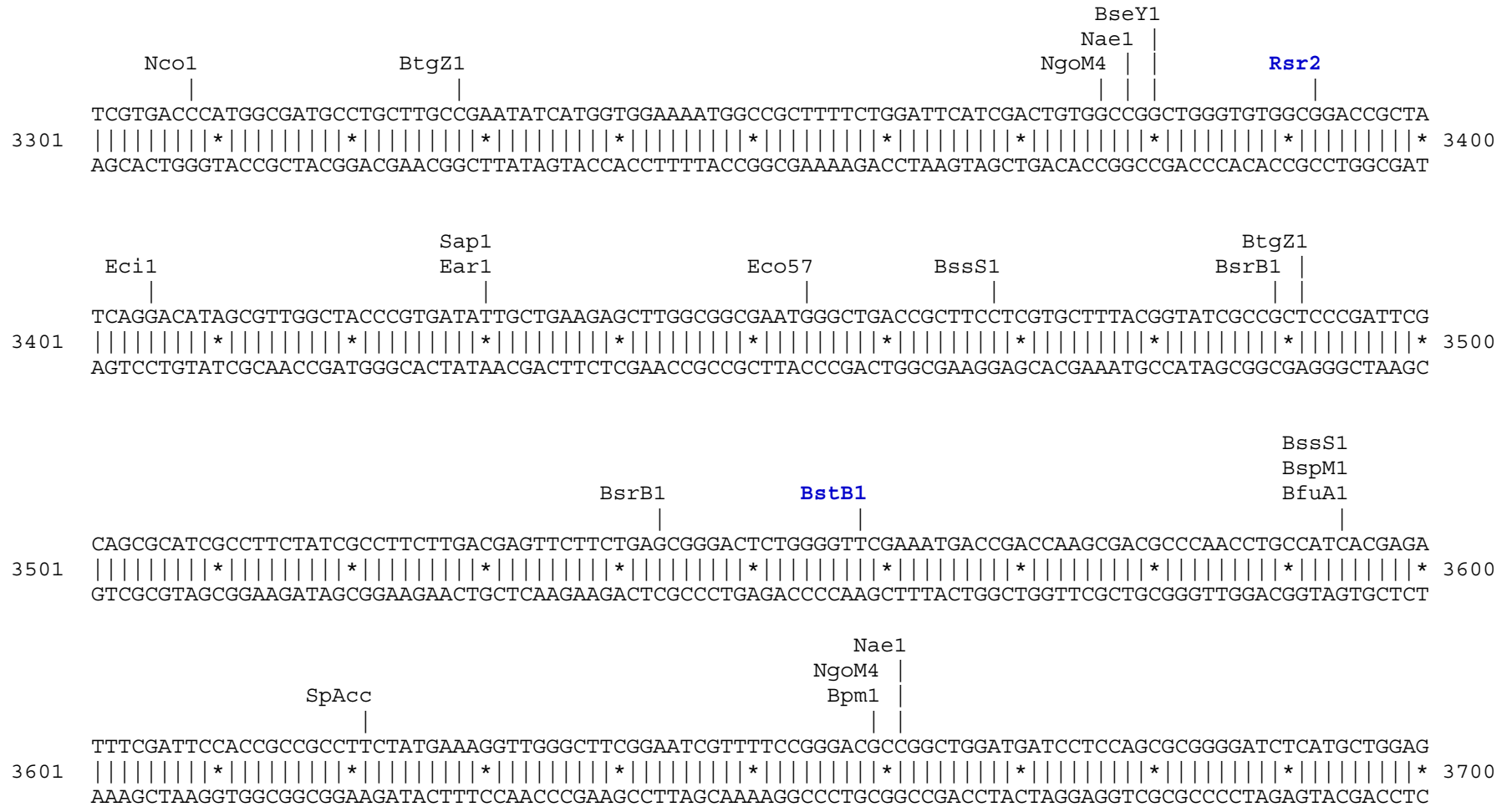
```

```

                    BspM1
                  BfuA1
                 Eag1
                Cla1
              BsaB1
          AGGCTTTTGC AAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTTGGGTGGAGAG
2701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
          TCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTTAACCTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTC

```






```
SpAcc                                     AlwN1
|                                         |
CTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCG
4301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4400
GATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGC

      BpuE1                                     ApaL1      BseY1
      |                                         |         |
ATAAGTCGTGTCCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGGA
4401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4500
TATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGCTTGCCCCCAAGCACGTGTGTTCGGGTGCAACCT

                                         SpAcc                                     BciV1
                                         |                                         |
GCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGC
4501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4600
CGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTTCGCCG

      BssS1                                     SpAcc                                     Drd1
      |                                         |                                         |
AGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTTCGCCACCTCTGACTTGAGCGTTCGAT
4601 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4700
TCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCCAAAGCGGTGGAGACTGAACTCGCAGCTA

      BpuE1      SpAcc      Eci1                                     SpDon
      |         |         |                                         |
TTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTGCTCACATGTT
4701 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4800
AAAACTACTACGAGCAGTCCCCCGCTCGGATACCTTTTTTGGCGTGGTTCGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAA
```

```

                                NsiI
                                BfrB1 |
                                | |
4801 CTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
      |||||*|||*|||*|||*|||*||| 4852
      GAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
  
```

Found:

Aar1	Aat2	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	BciV1	BfrB1	BfuA1	Bgl1
Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	BspH1	BspLU	BspM1
BsrB1	BsrD1	BssH2	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	_Chi	Cla1	Dra1	Dra3	Drd1
Eag1	Ear1	Eci1	Eco57	Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4
Nhe1	Not1	Nsi1	PflF1	PflM1	Pml1	polyA	Psi1	Pvu2	Rsr2	Sap1	SexA1	Sfi1	SnaB1
SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1								

Unique:

Aar1	Afl2	Age1	Ase1	BamH1	Bpu10	BsaXa	BsaXb	BseR1	BsrD1	BstB1	Bts1	_Chi	Cla1
Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nar1	Nde1	Nhe1	Not1	PflF1	Pml1	Rsr2	SexA1	Sfi1
SnaB1	Stu1	Xba1											

Not found:

Acc65	Acl1	Afe1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1
Bgl2	Blp1	BmgB1	Bsg1	BsiW1	BsmB1	BspE1	BsrG1	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoR1
EcoRV	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	PshA1	PspOM
Pst1	Pvu1	Sac1	Sac2	Sal1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal
T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xho1	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													