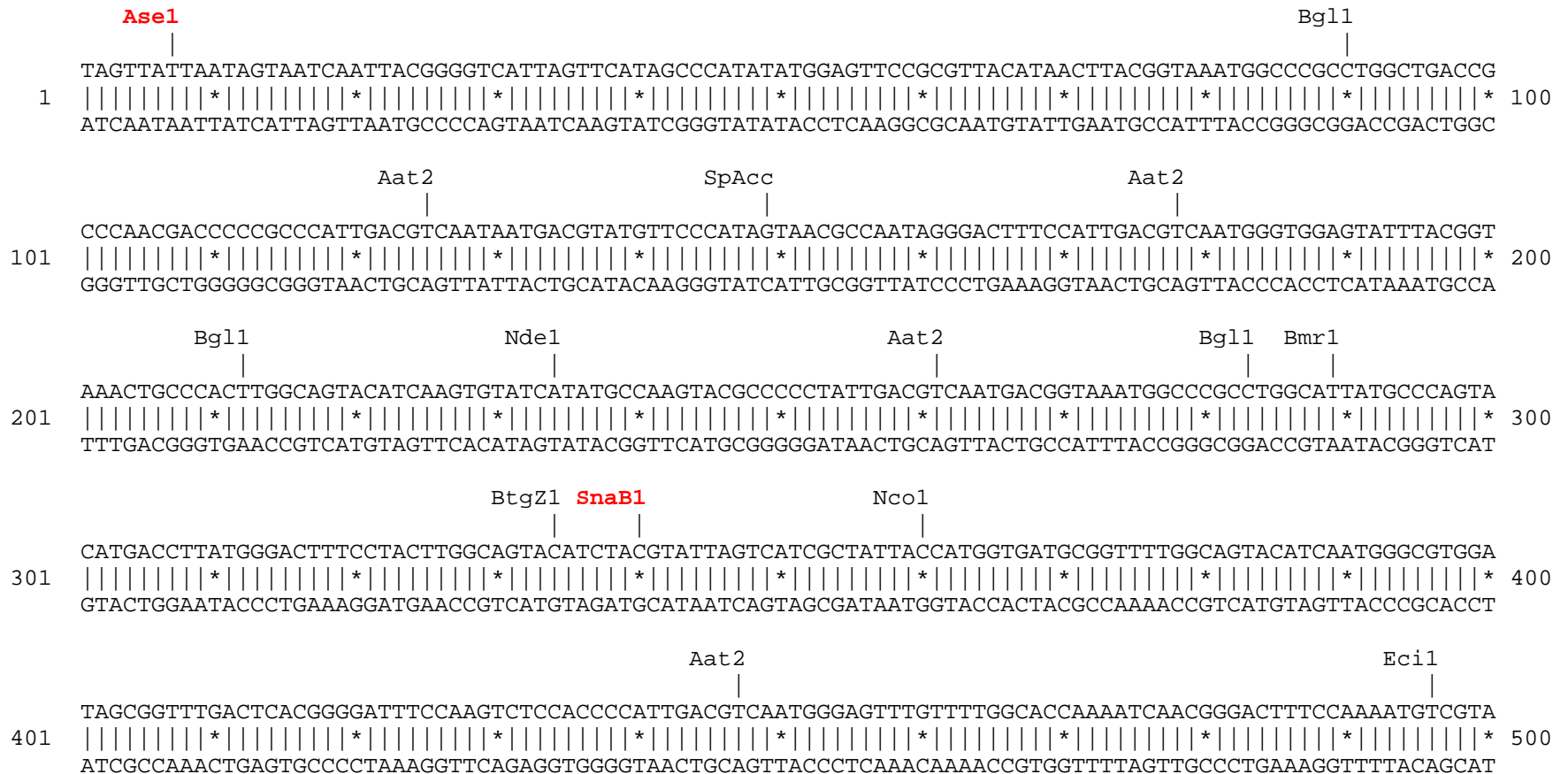


pTagBFP-tubulin vector restriction map.

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



```

                                                                                                                                                               Nhe1
                                                                                                                                                               |
501  ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGGTC 600
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    TGTGAGGCGGGGTAAGTGCCTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAG

                                                                                                                                                               BsrG1
                                                                                                                                                               |
                                                                                                                                                               ApaL1
                                                                                                                                                               |
601  GCCACCATGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCCTGGACAACCATCACTTCAAGTGCACATCCGAGGGCGAAG 700
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CGGTGGTACTCGCTCGACTAATTCCTTGTACGTGTACTTTCGACATGTACCTCCCGTGGCACCTGTTGGTAGTGAAGTTCACGTGTAGGCTCCCGCTTC
TagBFP >      M S E L I K E N M H M K L Y M E G T V D N H H F K C T S E G E G

                                                                                                                                                               SpAcc
                                                                                                                                                               |
701  GCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCTTCGCTTCGACATCCTGGCTACTAGCTTCTCTACGG 800
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGATCGAAGGAGATGCC
TagBFP >      K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F L Y G

                                                                                                                                                               Bsu36
                                                                                                                                                               |
                                                                                                                                                               SpDon
                                                                                                                                                               |
801  CAGCAAGACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTCAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGAC 900
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    GTCGTTCTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAGTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTG
TagBFP >      S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D

                                                                                                                                                               Bbs1
                                                                                                                                                               |
                                                                                                                                                               Bpm1
                                                                                                                                                               |
                                                                                                                                                               SpDon
                                                                                                                                                               |
901  GGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACCTTACATCCAACGGCCCTG 1000
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    CCCCCGCACGACTGGCGATGGGTCTGTGGTCCGGAGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGTGTAGGTTGCCGGGAC
TagBFP >      G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F T S N G P V

                                                                                                                                                               BsmB1
                                                                                                                                                               |
                                                                                                                                                               BseY1
                                                                                                                                                               |
                                                                                                                                                               StuI
                                                                                                                                                               |
                                                                                                                                                               Bgl1
                                                                                                                                                               |
                                                                                                                                                               BssS1
                                                                                                                                                               |
1001 TGATGCAGAAGAAAACACTCGGCTGGGAGGCCCTTCACCGAGACGCTGTACCCCGCTGACGGCGGCCCTGGAAGGCAGAAACGACATGGCCCTGAAGCTCGT 1100
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
    ACTACGTCTTCTTTGTGAGCCGACCCTCCGGAAGTGGCTCTGCGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTTGCTGTACCGGGACTTCGAGCA
TagBFP >      M Q K K T L G W E A F T E T L Y P A D G G L E G R N D M A L K L V

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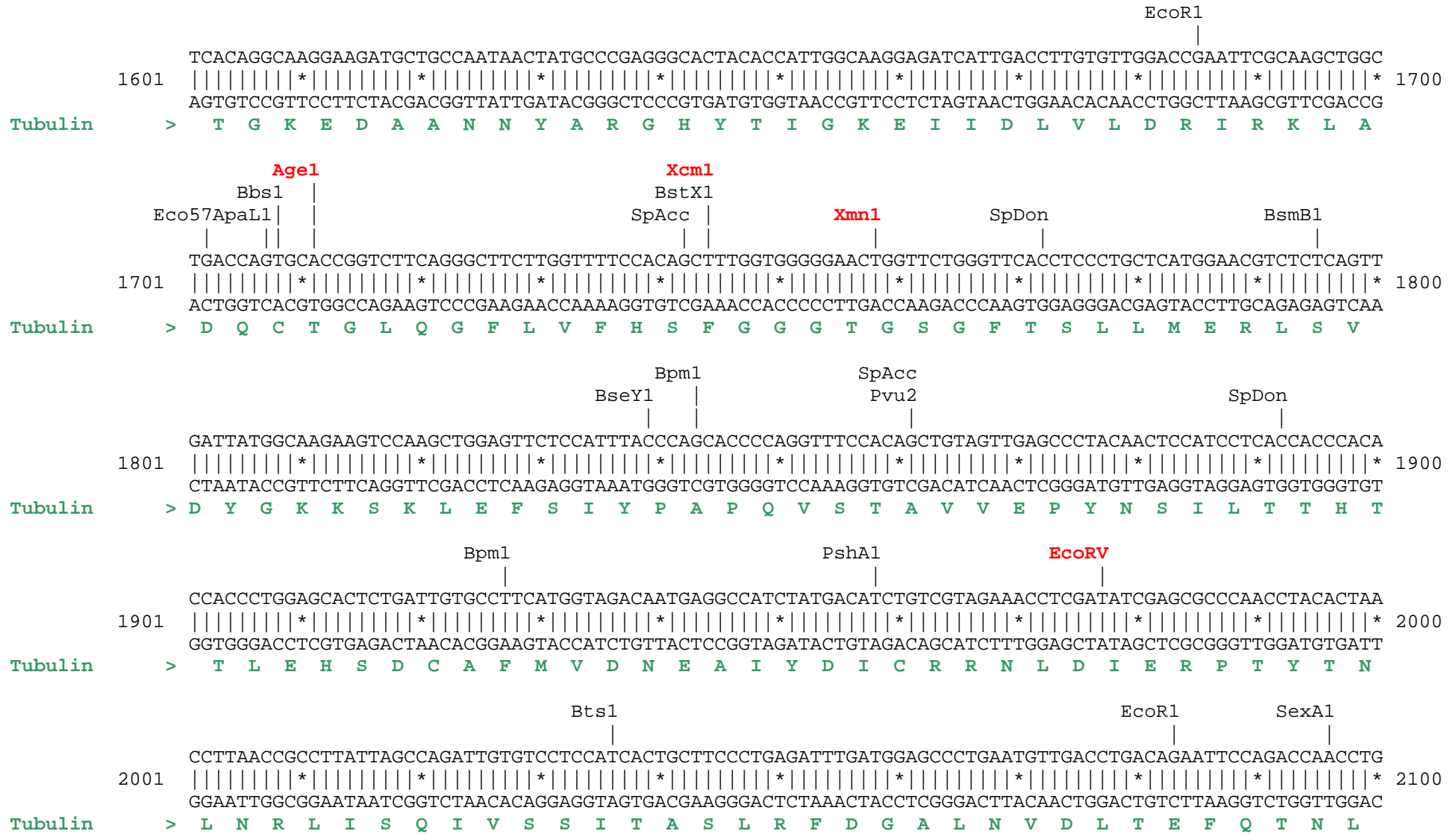
Eco57 BpuE1
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1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CCC GCCCTCGGTAGACTAGCGTTTGTAGTTCTGGTGTATATCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGACCGCAGATGATACACCTGATGTCT
TagBFP > G G S H L I A N I K T T Y R S K K P A K N L K M P G V Y Y V D Y R

SpAcc Bsa1 PshA1 BssS1 Dra3 Bts1 Msc1 AlwN1 SpAcc Hind3 Bmr1
CTGGAAAAGAATCAAGGAGGCCAACAACGAGACCTACGTCGAGCAGCACGAGGTGGCAGTGGCCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAAGC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GACCTTTCTTAGTTCTCCGTTGTTGCTCTGGATGCAGCTCGTCGTGCTCCACCGTCACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTTCG
TagBFP > L E R I K E A N N E T Y V E Q H E V A V A R Y C D L P S K L G H K L

BspE1 Bgl2 Xho1 Msc1 BseY1 BsrD1 Sac1 BstAP Ecl2
TTAATFCCGGACTCAGATCTCGAGTGCCTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTGCTGGGAGCTCTACTGCCT
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
AATTAAGGCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGTCCGACCACAGGTCTAACCGTTACGGACGACCCTCGAGATGACGGA
TagBFP/Tubulin N S G L R S R V R E C I S I H V G Q A G V Q I G N A C W E L Y C L

BstX1 Msc1 Eco57 BseR1 BsmB1 SpAcc
GGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTTCAGTGAGACGGGCGCTGGC
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
CCTTGTGCCGTAGGTTCGGGCTACCGGTCTACGGTTCACTGTTCTGGTAACCCCTCCTCTACTGAGGAAGTTGTGGAAGAAGTCACTCTGCCCGCGACCG
Tubulin > E H G I Q P D G Q M P S D K T I G G G D D S F N T F F S E T G A G

Pml1 Sma1 Bpu10 Sap1 Ear1
AAGCACGTGCCCGGGCTGTGTTTGTAGACTTGGAAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAGCTCA
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
TTCGTGCACGGGCCCCGACACAAACATCTGAACCTTGGGTGTGAGTAAGTCAAGCGTGACCGTGGATGGCGGTCGAGAAGGTGGGACTCGTCGAGT
Tubulin > K H V P R A V F V D L E P T V I D E V R T G T Y R Q L F H P E Q L I




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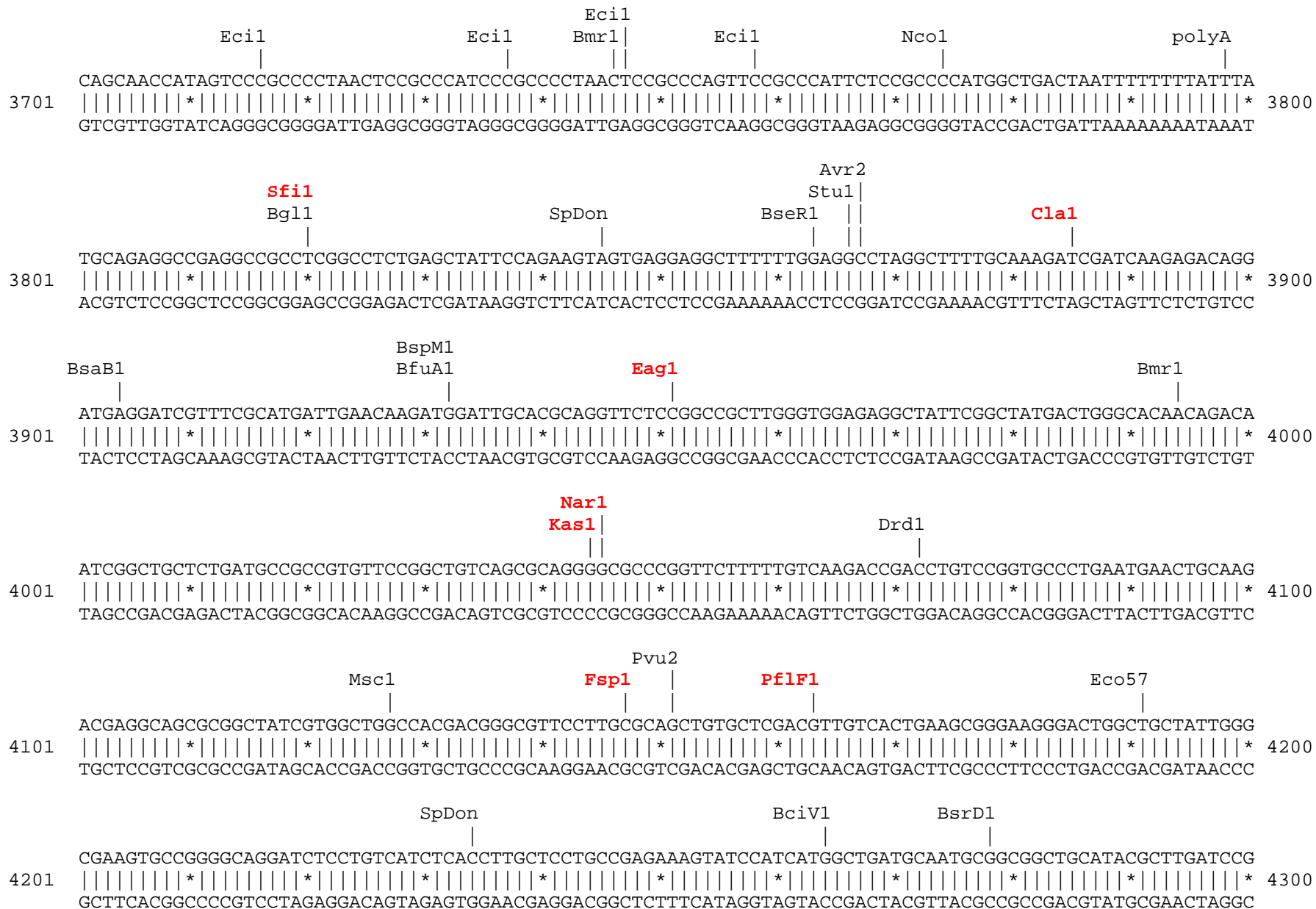
                                     SpAcc
                                     |
                                     NaeI
                                     |
                                     NgoM4
                                     |
3201  GCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
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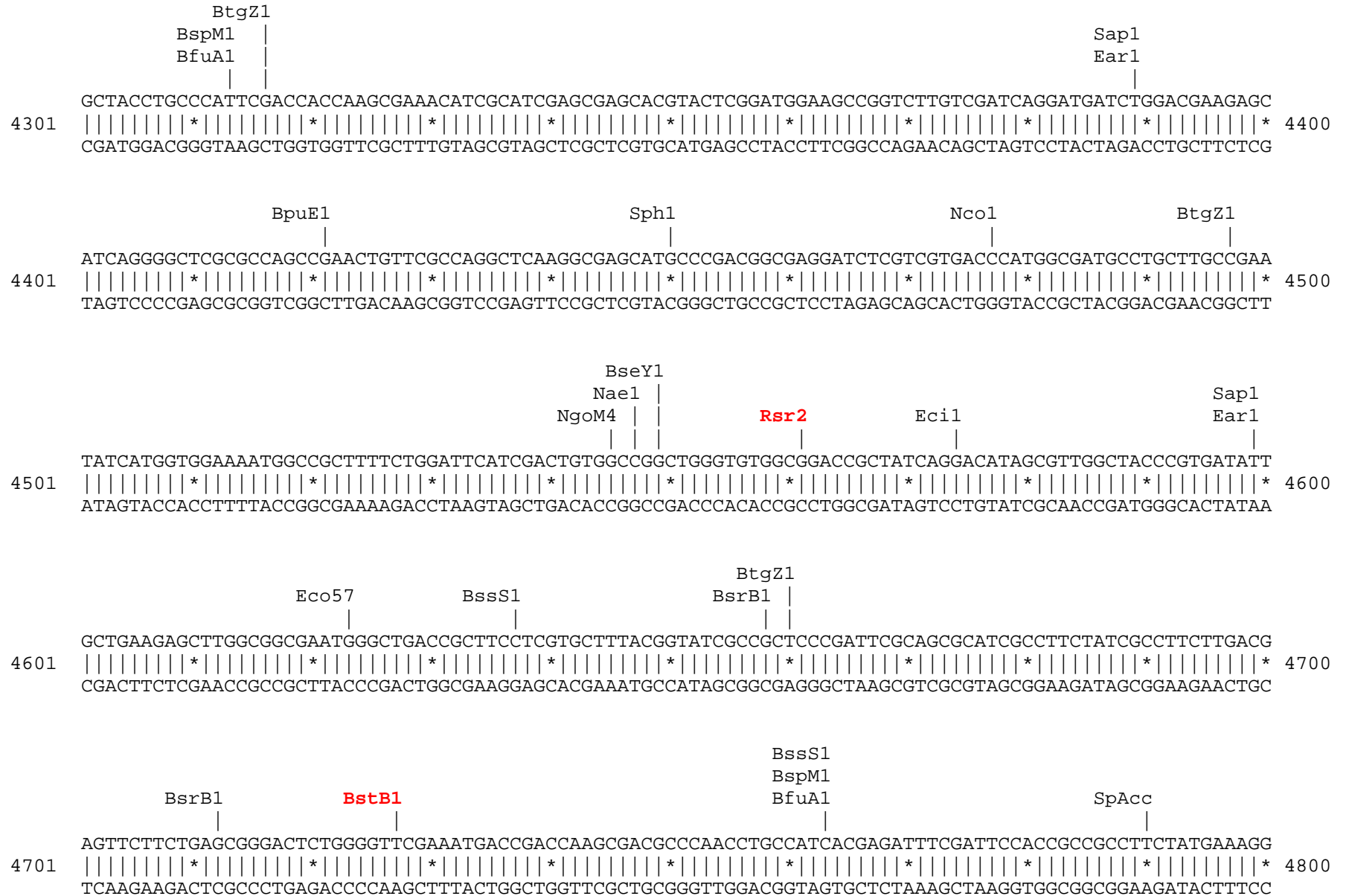
BsrB1
|
3301  AGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      TCCTCGCCCGGATCCCGCGACCGTTCACATCGCCAGTGCAGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCG

                                     polyA
                                     |
                                     BciV1
                                     |
                                     BspH1
                                     |
                                     BsrB1
                                     |
3401  ACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
      TGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAG

                                     Ssp1
                                     |
                                     Ear1
                                     |
                                     Bsu36
                                     |
                                     Ecil
                                     |
                                     Pvu2
                                     |
                                     BseY1
                                     |
3501  AATAATATTGAAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
      TTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCT

                                     NsiI
                                     |
                                     Sph1
                                     |
                                     BfrB1
                                     |
                                     BstAP
                                     |
                                     SexA1
                                     |
                                     BseY1
                                     |
                                     NsiI
                                     |
                                     Sph1
                                     |
                                     BfrB1
                                     |
                                     BstAP
                                     |
3601  AGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
      TCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCA
```





```
        NaeI                      BpmI                      SpAcc
      NgoM4 |                      Avr2 |                      BpmI |
      BpmI |                      |                      |
      | |                          |                      |
4801 TTGGGCTTCGGAATCGTTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTG 4900
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
      AACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGAC

                                  polyA                    polyA
                                  |                          |
4901 AAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGTTTTGTTCATAAACGCGG 5000
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
      TTTGTGCCTTCTCTGTTATGGCCTTCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTGC GTGCCACAACCAGCAAACAAGTATTTGCGCC

                                           BsaI
                                           |
5001 GGTTCGGTCCCAGGGCTGGCACTCTGTGCGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGT TTTCTTCC TTTTCCCCACCCACCCCCCAAGT 5100
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
      CCAAGCCAGGGTCCCAGCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGT TATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCA

                                                BstAP             Bsu36
                                                AlwNI             DraI
                                                |                  |
5101 TCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATT 5200
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
      AGCCCACTTCGGGTCCCAGCGTCGGTTGCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAA

          DraI                  BspH1
          |                        |
5201 TTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGA 5300
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
      AAATTTAAATTTTCTAGATCCA CTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCT

                                     BpuE1
                                     |
5301 AAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTGCCGGAT 5400
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
      TTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTTCGCCACCAAAACAAACGGCCTA
```

```

        Eco57                                SpAcc
        |                                     |
5401 CAAGAGCTACCAACTCTTTTTCCGAAGGTAACGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCA 5500
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
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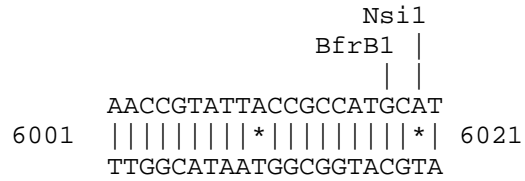
                AlwN1                                BpuE1
                |                                     |
5501 AGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAG 5600
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      TCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTC

                ApaL1                                BseY1
                |                                     |
5601 ACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAAGTGGAGATACCTA 5700
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      TGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTTCGGGTCTGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGAT

                                BciV1
                                |
                                Eci1                                BssS1
                                |                                     |
5701 CAGCGTGAGCTATGAGAAAGCGCCACGCTTCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGGAGC 5800
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      GTCGACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCGCCAGCCTTGTCTCTCGCGTGCTCCCTCG

        SpAcc                                Drd1                                BpuE1                                SpAcc
        |                                     |                                     |                                     |
5801 TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCT 5900
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      AAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACTACGAGCAGTCCCCCGCCTCGGA

        Eci1                                SpDon
        |                                     |
5901 ATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTCCTGGCCTTTTGGCTGGCCTTTTGGCTCACATGTTCTTTTCCTGCGTTATCCCCTGATTCTGTGGAT 6000
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      TACCTTTTTGCGGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTA
  
```



Found:

Aat2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	Baela	Baelb	BamH1	Bbs1	BbvC1	BciV1	Bcl1	BfrB1
BfuA1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1
Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoN1	EcoR1	EcoRV	Fsp1	Hind3
Hpa1	Kas1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1	Pml1
polyA	PshA1	Psi1	Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1
Stu1	Xba1	Xcm1	Xho1	Xmn1										

Unique:

Age1	Ale1	Ase1	Baela	Baelb	BamH1	BbvC1	Bcl1	Bgl2	Blp1	BmgB1	BsaXa	BsaXb	BspE1	BspLU
BsrG1	BstB1	Clal	Eag1	Ecl2	EcoRV	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nhe1	PflF1
PflM1	Pml1	Rsr2	Sac1	Sfi1	Sma1	SnaB1	Xba1	Xcm1	Xho1	Xmn1				

Not found:

Aar1	Acc65	Ac11	Afe1	Afl2	Ahd1	Apal	Asc1	AsiS1	BcglA	Bcglb	Bsg1	BsiW1	BssH2	BstE2
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu
Kpn1	loxP	Not1	Nru1	Pac1	Pme1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall
SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce			

Excluded by site complexity:

Acc1	Ac11	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfal	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
Mn11	Mse1	Msl1	MspA1	Mwo1	Nci1	Nla3	Nla4	Nsp1	Ple1	PpuM1	Rsa1	Sau3A	Sau96	SfaN1
Sfc1	Sml1	Sty1	Taq1	Tat1	Tfil	Tse1	Tsp45	Tsp50	TspR1					