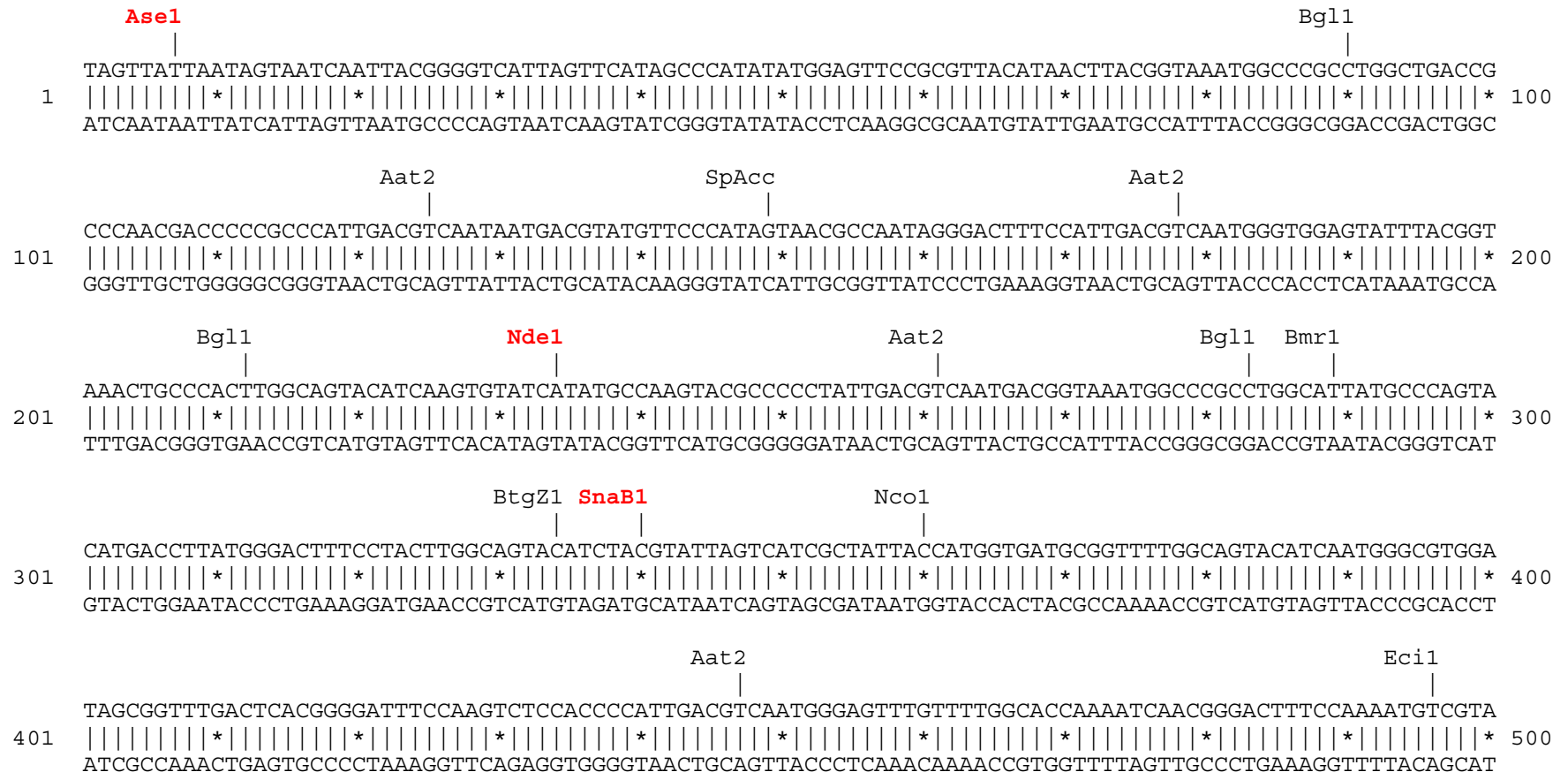


### pTagCFP-mito vector restriction map

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 red. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site).

Mitochondrial targeting sequence (MTS) is shown in bold black.



**NheI**

501 ACAACTCCGCCCATTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCATGT 600  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 600  
 TGTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTACA  
**MTS** > M S

BmrI **BssH2** PflM1 **BamH1** **AgeI**

601 CCGTCCTGACGCCGCTGCTGCTGCGGGGCTTGACAGGCTCGGCCCCGGCGGCTCCCAGTGCCGCGCGCAAGATCCATTTCGTTGGGGGATCCACCGGTTCGC 700  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 700  
 GGCAGGACTGCGGCGACGACGACGCCCCGAAGTGTCCGAGCCGGGCCGCGAGGGTACGGCGCGCGGTTCTAGGTAAGCAACCCCCTAGGTGGCCAGCG  
**MTS** > V L T P L L L R G L T G S A R R L P V P R A K I H S L G D P P V A

BsrB1 BseR1 **BmgB1** ApaL1

701 CACCATGAGCGGGGCGAGGAGCTGTTTCGCTGGCCTCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGC CGGTGAG 800  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 800  
 GTGGTACTCGCCCCGCTCCTCGACAAGCGACCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAGTTCGACGCGCCACTC  
**TagCFP** > T M S G G E E L F A G I V P V L I E L D G D V H G H K F S V R G E

BsaXa BsgI BpmI **BstE2** AleI

801 GGAGAGGGCGACCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCCACCCCTGGTGACCACCCCTCGCCT 900  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 900  
 CCTCTCCCGCTGCGGCTGATGCCGTTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGACCGGGTGGGACCACTGGTGGGAGCGGA  
**TagCFP** > G E G D A D Y G K L E I K F I C T T G K L P V P W P T L V T T L A W

BstAP **XmnI**

901 GGGGCATCCAGTGCTTCGCCGCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATCCA 1000  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1000  
 CCCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGTCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCGTGGTAGGT  
**TagCFP** > G I Q C F A R Y P E H M K M N D F F K S A M P E G Y I Q E R T I H

Sac2 SpDon Ale1 SpDon Eco57  
 CTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTTCGAGGGCGACACCCCTGGTGAACCCGCTCGAGCTGAAGGGCGAGGGCTTCAAGGAG  
 1001 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1100  
 GAAGGTCTGCTGCCGTTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCCTTGGCGCAGCTCGACTTCCCGCTCCCGAAGTTCCTC  
 TagCFP > F Q D D G K Y K T R G E V K F E G D T L V N R V E L K G E G F K E

PflM1 BsrG1 Xcm1 Eci1  
 GACGGCAACATCCTGGGCCACAAGTTGGAGTACAGCGCCATCAGCGACAACGTGTACATCATGCCCGACAAGGCCAACAACGGCCTGGAGGGCAACTTCA  
 1101 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1200  
 CTGCCGTTGTAGGACCCGGTGTTC AACCTCATGTTCGCGGTAGTTCGCTGTTGCACATGTAGTACGGGCTGTTCCGGTTGTTGCCGGACCTCCGCTTGAAGT  
 TagCFP > D G N I L G H K L E Y S A I S D N V Y I M P D K A N N G L E A N F K

Bpm1 Pvu2 Bsg1 Xcm1 BtgZ1BsaB1  
 AGATCCGCCACAACATCGAGGGCGGCGGCTGCAGCTGGCCGACCCTACCAGACCAACGTGCCCTGGGCGATGGCCCCGTGCTGATCCCCATCAACCA  
 1201 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1300  
 TCTAGGCGGTGTTGTAGCTCCCGCCGCGCACGTTCGACCGGCTGGTGTATGGTCTGGTTGCACGGGGACCCGCTACCGGGGCGACACTAGGGGTAGTTGGT  
 TagCFP > I R H N I E G G G V Q L A D H Y Q T N V P L G D G P V L I P I N H

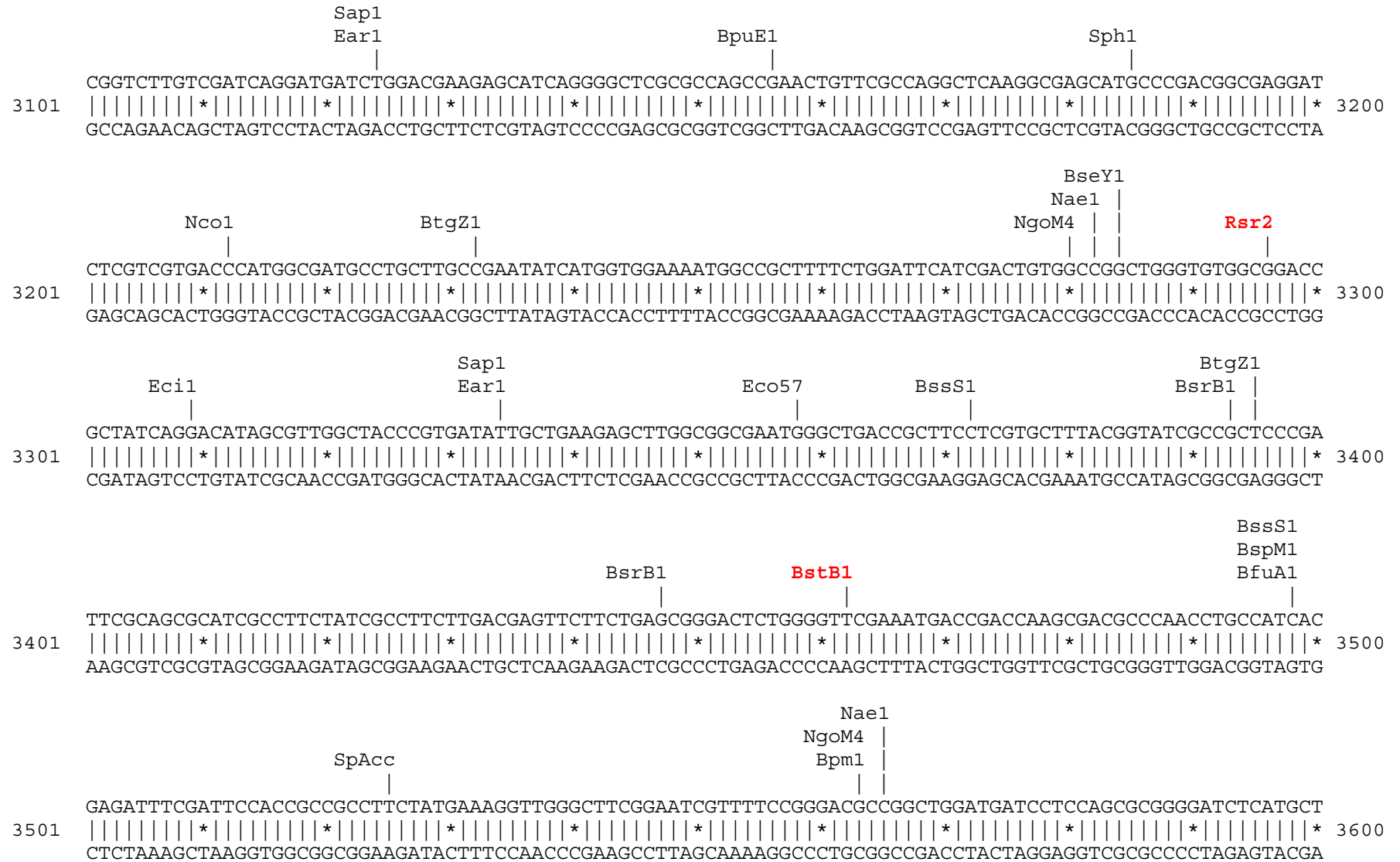
Eci1 Bpu10 Eco57 Dra3 Bpm1  
 CTACCTGAGCTGCCAGTCCGCCATCAGCAAGGACCGCAACGAAGCCCGGACCCACATGGTGTCTCCTGGAGTCCTTCAGCGCCTACTGCCACACCCACGGC  
 1301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1400  
 GATGGACTCGACGGTCAGGCGGTAGTTCGTTCTGGCGTTGCTTCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGATGACGGTGTGGGTGCCG  
 TagCFP > Y L S C Q S A I S K D R N E A R D H M V L L E S F S A Y C H T H G

PflM1 Not1 Eag1 Xba1 BsaB1 SpDon Dra1  
 ATGGACGAGCTGTACCGCTAAAGCGGCCGCGACTCTAGATCATAATCAGCCATAACCATTTGTAGAGGTTTTACTTGGCTTTAAAAAACCTCCCACACCT  
 1401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1500  
 TACCTGCTCGACATGGCGATTTTCGCCGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTGGAGGGTGTGGA  
 TagCFP > M D E L Y R \*









```
                Bpm1
                SpAcc
                Avr2
                polyA
                polyA
3601  GGAGTTCTTCGCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAA
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3700
      CCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTT

                                Bsa1
3701  ACGCACGGTGTGGGTCGTTTGTTCATAAACCGGGGTTCCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTGGGGCCAATACGCCC
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3800
      TGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGG

                                BstAP
                                AlwN1
                                Bsu36
3801  GCGTTTCTTCCTTTTCCCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTA
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3900
      CGCAAAGAAGGAAAAAGGGTGGGGTGGGGGGTTCAAGCCCACTTCGCGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAAT

                Dra1
                Dra1
                BspH1
3901  CTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGT
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4000
      GAGTATATATGAAATCTAACTAAATTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCA

                                BpuE1
4001  GAGTTTTCGTTCCTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAA
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4100
      CTCAAAAGCAAGGTGACTCGCAGTCTGGGCATCTTTTCTAGTTTCTAGAGAAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTT

                                Eco57
4101  AACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGT
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4200
      TTGGTGGCGATGGTCCCAACAAACCGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACA
```



```

                SpAcc                               AlwN1
                |                                   |
CCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGT
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
GGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCA

                BpuE1                               ApaL1           BseY1
                |                                   |               |
GGCGATAAGTCGTGTCCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCT
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
CCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCGTCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTTCGGGTCTGA

                SpAcc                               Eci1
                |                                   |
TGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAG
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
ACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTC

BciV1                BssS1                SpAcc                Drd1
|                   |                   |                   |
CGGCAGGGTTCGGAAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGT
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
GCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTCGCGGACCATAGAAAATATCAGGACAGCCCCAAAGCGGTGGAGACTGAACTCGCA

                BpuE1                SpAcc                Eci1                SpDon
                |                   |                   |                   |
CGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGCGCCTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTTGTGCTCACA
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
GCTAAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTTCGTCGCCGAAAAAATGCCAAGGACCCGAAAAACGACCCGAAAAACGAGTGT

                NsiI                BfrB1
                |                   |
TGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4756
ACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

```

**Found:**

Aat2	<b>Afl2</b>	<b>Age1</b>	Ale1	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	BciV1	BfrB1	BfuA1	Bgl1	<b>BmgB1</b>
Bmr1	Bpm1	<b>Bpu10</b>	BpuE1	<b>Bsa1</b>	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	<b>BspLU</b>
BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	<b>BssH2</b>	BssS1	BstAP	<b>BstB1</b>	<b>BstE2</b>	Bsu36	BtgZ1	<b>Bts1</b>	<b>Cla1</b>	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</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>	PflM1	polyA	Psi1	Pvu2	<b>Rsr2</b>	<b>Sac2</b>	Sap1	<b>SexA1</b>
<b>Sfi1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stu1</b>	<b>Xba1</b>	Xcm1	<b>Xmn1</b>				

**Unique:**

<b>Afl2</b>	<b>Age1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>BmgB1</b>	<b>Bpu10</b>	<b>Bsa1</b>	<b>BspLU</b>	<b>BsrD1</b>	<b>BsrG1</b>	<b>BssH2</b>	<b>BstB1</b>	<b>BstE2</b>	<b>Bts1</b>
<b>Cla1</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Msc1</b>	<b>Nar1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>Rsr2</b>	<b>Sac2</b>	<b>SexA1</b>
<b>Sfi1</b>	<b>SnaB1</b>	<b>Stu1</b>	<b>Xba1</b>	<b>Xmn1</b>									

**Not found:**

Aar1	Acc65	Acl1	Afe1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b
Bcl1	Bgl2	Blp1	BsiW1	BsmB1	BspE1	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoR1	EcoRV	ScFRT
Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pst1
Pvu1	Sac1	Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA
T7Ter	PISce	Xho1											

**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													