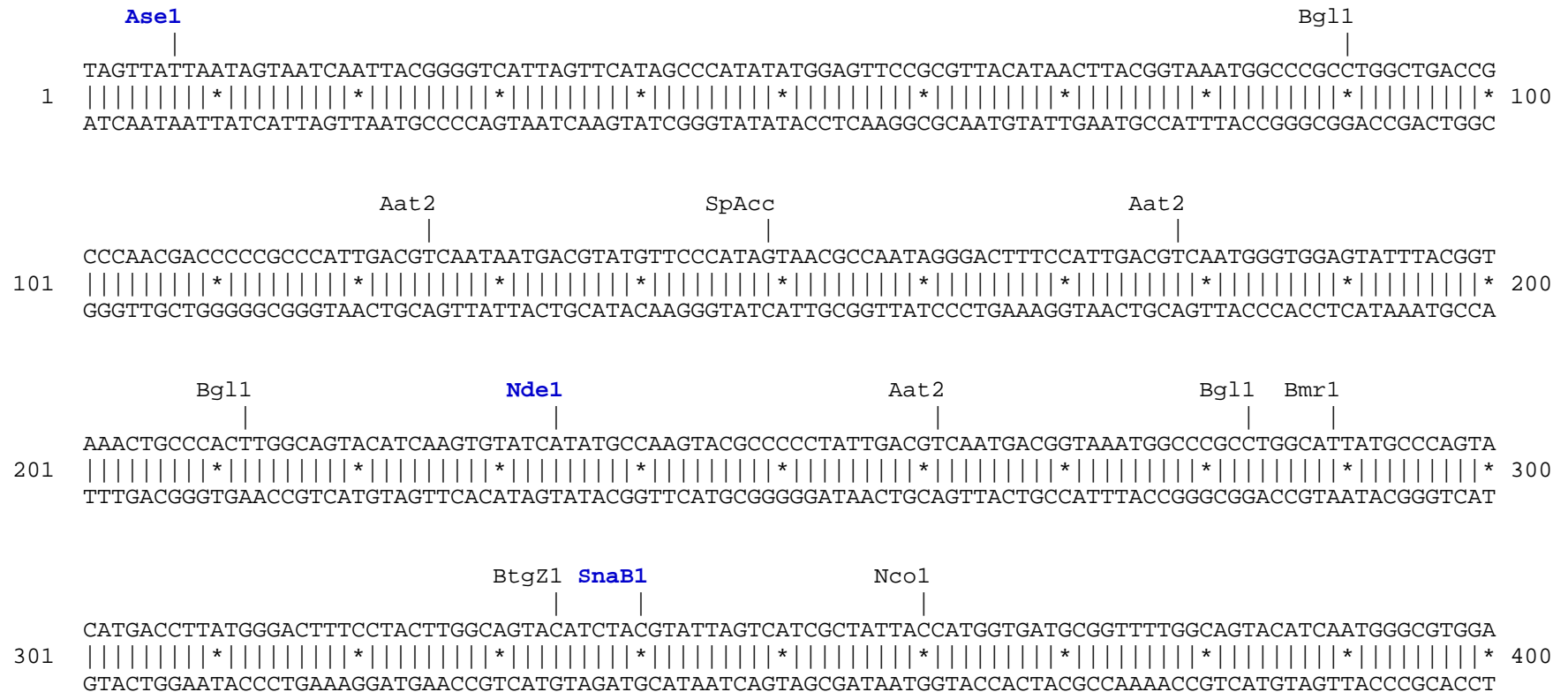


pTagRFP-Cx43 vector restriction map

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 base pairs 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). TagRFP amino acids are shown in red, Connexin 43 amino acids are shown in green, linker amino acids are shown in black.



```

                                     Aat2                                     Eci1
                                     |                                     |
TAGCGGTTTGACTCACGGGATTTCOAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGGTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 500
ATCGCCAAACTGAGTGCCCTAAAGGTTCCAGAGGTGGGGTAACTGCAGTTACCCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                               Nhe1 Afe1
                                               |       |
ACAACCTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 600
TGTGAGGCGGGGTAACCTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTTCGTCTCGACCAAAATCACTTGGCAGTCTAGGCGATCGCGAT

           Xho1      Hind3    EcoR1
           |      |      |      |
BpuE1 Bgl2 |      |      |      |
           |      |      |      |
CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCGGCAGCACTTTTCTTTTTCATTGGGGGGAAGGCGTGAGGAAAGTACCAAACAGCAGCAGACTTTTAAA
601 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 700
GGCTGAGTCTAGAGCTCGAGTTTCAAGCTTAAAGCCGTCGTGAAAAGAAAGTAACCCCCCTTCCGCACTCCTTTTCATGGTTTTGTCTGTCGTCTGAAAATTT

                                               Nae1
                                               |
                                               NgoM4 |
BssH2 |
Asc1 |
Dra1   |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
           |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
CTTTAAACAGACAGGTCTGAGAGCCTGAAGTCTCATTTCATTTTCCTTTGACTTTCAGCCTCCAAGGAGTTCCACCAACTTTGGCGCGCCGGCTTCACTTTTTCATT
701 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 800
GAAATTTGTCTGTCCAGACTCTCGGACTTGAGAGTAAAAAGGAAACTGAAAGTCGGAGGTTTCTCAAGGTGGTTGAAACCGCGCGGCCGAAGTGAAAGTAA

           Hind3  Bpm1  PflF1               BsaXaSpAcc
           |     |     |     |               |     |
AAGTGAAAGAGAGGGTGCCAGACATGGGTGACTGGAGTGCCTTGGGGAAGCTTCTGGACAAGGTCCAAGCCTACTCCACCGCTGGAGGGAAGGTGTGGCT
801 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 900
TTCAC TTTCTCTCCACGGGCTGTACCCACTGACCTCACGGAACCCCTTCAAGACCTGTTCCAGGTTTCGGATGAGGTGGCGACCTCCCTTCCACACCGGA

Cx43    >          M G D W S A L G K L L D K V Q A Y S T A G G K V W L

```

BsaXb Sap1
Bpm1 | Ear1 Pvu2
GTCAGTGCCTTCATATTCAGAATCCTGCTCCTGGGGACAGCTGTTGAGTCAGCTTGGGGTGATGAACAGTCTGCCTTTTCGCTGTAACACTCAACAACCT
901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
CAGTCACGAGAAGTATAAGTCTTAGGACGAGGACCCCTGTCGACAACCTCAGTCGAACCCCACTACTTGTGACGCGAAAGCGACATTGTGAGTTGTTGGA
Cx43 > S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P

Eco57
SpAcc Pml1
GGCTGCGAAAACGTCTGCTATGACAAGTCCCTTCCCCATCTCTCACGTGCGCTTCTGGGTCCCTTCAGATCATATTCGTGTCTGTGCCACACTCCTGTACT
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CCGACGCTTTTGCAGACGATACTGTTTCAGGAAGGGGTAGAGAGTGCACGCGAAGACCCAGGAAGTCTAGTATAAGCACAGACACGGGTGTGAGGACATGA
Cx43 > G C E N V C Y D K S F P I S H V R F W V L Q I I F V S V P T L L Y L

Ear1 Ear1 Sac1 BseR1 PflF1
TGGCCCATGTGTTCTATGTGATGAGGAAGGAAGAGAAGCTAAACAAGAAAAGAAGAGGAGCTCAAAGTGGCCCAGACTGACGGGGTCAACGTGGAGATGCA
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
ACCGGGTACACAAGATACTACTCCTTCTCTTCTCGATTTGTTCTTTCTTCTCCTCGAGTTTCACCGGGTCTGACTGCCCCAGTTGCACCTCTACGT
Cx43 > A H V F Y V M R K E E K L N K K E E E L K V A Q T D G V N V E M H

BsaB1 Eco57 Sap1 SpDon
CCTGAAGCAGATTGAAATCAAGAAGTTCAAGTACGGGATTGAAGAGCACGGCAAGGTGAAAATGAGGGGCGGCTTGCTGAGAACCTACATCATCAGCATC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GGACTTCGTCTAACTTTAGTTCTTCAAGTTCATGCCCTAACTTCTCGTGCCGTTCCACTTTTACTCCCCGCCGAACGACTCTTGATGTAGTAGTCGTAG
Cx43 > L K Q I E I K K F K Y G I E E H G K V K M R G G L L R T Y I I S I

```
Ear1 Bbs1 | SpAcc BpuE1 BfuA1 Aar1 |
CTCTTCAAGTCTGTCTTCGAGGTGGCCTTCCTGCTCATCCAGTGGTACATCTATGGGTTTCAGCTTGAGCGCGGTCTACACCTGCAAGAGAGATCCCTGCC
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
GAGAAGTTCAGACAGAAGCTCCACCGAAGGACGAGTAGGTCACCATGTAGATACCCAAGTCGAACTCGCGCCAGATGTGGACGTTCTCTCTAGGGACGG
Cx43 > L F K S V F E V A F L L I Q W Y I Y G F S L S A V Y T C K R D P C P
```

```
SexA1 BmgB1 _Chi |
CCCACCAGGTAGACTGCTTCCTCTCACGTCCCACGGAGAAAACCATCTTCATCATCTTCATGCTGGTGGTGTCCCTTGGTGTCTCTCGCTTTGAACATCAT
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
GGGTGGTCCATCTGACGAAGGAGAGTGCAGGGTGCCTCTTTTGGTAGAAGTAGTAGAAGTACGACCACCACAGGAACCACAGAGAGCGAAACTTGTAGTA
Cx43 > H Q V D C F L S R P T E K T I F I I F M L V V S L V S L A L N I I
```

```
Sap1 Ear1 Bbs1 | SpDon Xcm1 |
TGAGCTCTTCTACGTCTTCTTCAAGGGCGTTAAGGATCGCGTGAAGGGAAGAAGCGATCCTTACCACGCCACCCTGGCCCACTGAGCCCATCAAAAGAC
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
ACTCGAGAAGATGCAGAAGAAGTTCCCGCAATTCCTAGCGCACTTCCCTTCTTCGCTAGGAATGGTGCGGTGGTGCACCGGGTACTCGGGTAGTTTTCTG
Cx43 > E L F Y V F F K G V K D R V K G R S D P Y H A T T G P L S P S K D
```

```
BseR1 BseR1 |
TGCGGATCTCCAAAATACGCCTACTTCAATGGCTGCTCCTCACCAACGGCTCCACTCTCGCCTATGTCTCCTCCTGGGTACAAGCTGGTTACTGGTGACA
1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
ACGCCTAGAGGTTTTATGCGGATGAAGTTACCGACGAGGAGTGGTTGCCGAGGTGAGAGCGGATACAGAGGAGGACCCATGTTTCGACCAATGACCACTGT
Cx43 > C G S P K Y A Y F N G C S S P T A P L S P M S P P G Y K L V T G D R
```



```

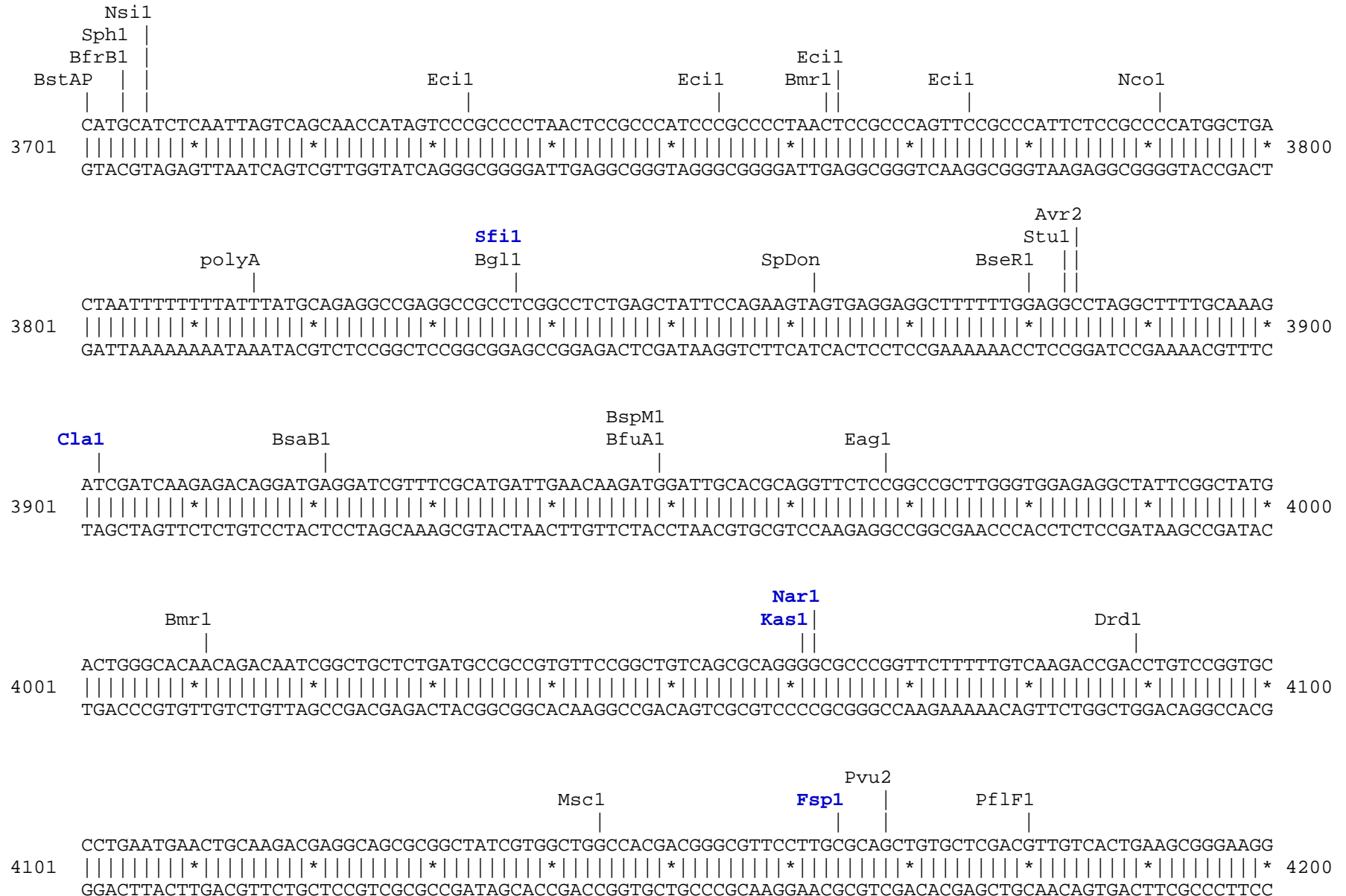
                                     SpAcc      NaeI      NgoM4
                                     |           |     |
TTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAAG
3201  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 3300
AAAAAACCCAGCTCCACGGCATTTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCCTTTCGGCCGCTTGCACCGCTCTTTC

                                     BsrB1
                                     |
GAAGGGAAGAAAAGCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTAC
3301  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 3400
CTTCCCTTCTTTCGCTTTCCTCGCCCGCATCCCGCGACCGTTTACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATG

                                     polyA      BspH1      BsrB1      BciV1
                                     |           |     |     |
AGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA
3401  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 3500
TCCCGCGCAGTCCACCGTGAAAAGCCCTTTTACACGCGCCTTGGGGATAAACAATAAAAAGATTTATGTAAGTTTATAATAGGCGAGTACTCTGTTAT

                                     Ssp1      Ear1      Bsu36      Pvu2      Eci1
                                     |     |     |     |     |
ACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCTTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAG
3501  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 3600
TGGGACTATTTACGAAGTTATTATAACTTTTCTTCTCAGGACTCCGCTTTTCTTGGTTCGACACCTTACACACAGTCAATCCACACCTTTTCAGGGGTC

                                     NsiI      Sph1      BfrB1
                                     |     |     |
BseY1      BstAP      SexA1      BseY1
|           |           |           |
GCTCCCCAGCAGGCAGAAGTATGCAAAGCATGTCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAG
3601  |||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 3700
CGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTC
```

Eco57 SpDon BciV1 BsrD1
GACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCCGGCGGC
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CTGACCGACGATAACCCGCTTCACGGCCCCGTCTAGAGGACAGTAGAGTGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCG

BtgZ1
BspM1
BfuA1
TGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA CTGGATGGAAGCCGGTCTTGTGCATCAGGA
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
ACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCT

Sap1
Ear1 BpuE1 Sph1 Nco1
TGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGAGCATGCCCCGACGGCGAGGATCTCGTTCGTGACCCATGGC
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
ACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCG

BtgZ1 BseY1 Nae1 NgoM4 Rsr2 Eci1
GATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGT
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
CTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCA

Sap1
Ear1 Eco57 BssS1 BtgZ1 BsrB1
TGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCCTCGTCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTT
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
ACCGATGGGCACTATAACGACTTCTCGAACC GCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAA


```

                                     SpDon
                                     BspLU|
                SpAcc      Eci1
                |           |
TCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTAT
5901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6000
AGTCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATA

                                     Nsi1
                                     BfrB1 |
                                     | |
CCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6001 |||||*|||||*|||||*|||||*||||| 6038
GGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Asc1	Ase1	Avr2	BamH1	Bbs1	BciV1
BfrB1	BfuA1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	PflM1	Pml1	polyA
PshA1	Psil	Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfil	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1
Xba1	Xcm1	Xho1	Xmn1										

Unique:

Aar1	Afe1	Afl2	Age1	Ale1	Asc1	Ase1	BamH1	Bgl2	BmgB1	BspLU	BsrD1	BsrG1	BssH2
Bts1	_Chi	Clal	EcoR1	Fsp1	Hpa1	Kas1	Mfe1	Nar1	Nde1	Not1	PflM1	Pml1	PshA1
Rsr2	Sfil	SnaB1	Xba1	Xcm1	Xho1	Xmn1							

Not found:

Acc65	Ac11	Ahd1	Apa1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Bcl1	Blp1	Bpu10	Bsg1
BsiW1	BsmB1	BspE1	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT
Fse1	FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	PspOM	Pst1	Pvu1	R4atB	R4atL
R4atP	R4atR	Sac2	Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA
T7RNA	T7Ter	PISce											

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	Bs11	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													