

**pFusionRed-vimentin 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).

FusionRed amino acids are shown in red, vimentin amino acids are shown in green, linker amino acids are shown in black.





Xcm1      SpAcc   Pst1      AlwN1

901      GCGGACGCCATCAACACCGAGTTCAAGAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGC 1000  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*||  
 CGGCTGCGGTAGTTGTGGCTCAAGTTCTTGTGGGCGTGGTTGCTCTTCCACCTCGACGTCCTCGACTTACTGGCGAAGCGGTTGATGTAGCTGTTCCACG

Vimentin > A D A I N T E F K N T R T N E K V E L Q E L N D R F A N Y I D K V R

Sac1  
Xho1  
Bpm1 BpuE1 Ecl2      EcoN1  
SpAcc

1001      GCTTCCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCG 1100  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*||  
 CGAAGGACCTCGTCGTCTTATTCTAGGACGACCGGCTCGAGCTCGTTCGAGTTCCCGGTTCCGTTTCAGCGCGGACCCCTGGAGATGCTCCTCCTCTACGC

Vimentin > F L E Q Q N K I L L A E L E Q L K G Q G K S R L G D L Y E E E M R

Nae1  
NgoM4  
BseR1  
BspM1  
Aar1  
BseR1      EcoN1

1101      GGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCCGCTCGAGGTGGAGCGGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAA 1200  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*||  
 CCTCGACGCGGCCGTCCACCTGGTTCGATTGGTTGCTGTTTTCGGGCGCAGCTCCACCTCGCGCTGTTGGACCGGCTCCTGTAGTACGCGGAGGCCCTCTTT

Vimentin > E L R R Q V D Q L T N D K A R V E V E R D N L A E D I M R L R E K

Eco57      BseR1      Ahd1      BsmB1 BmgB1

1201      TTGCAGGAGGAGATGCTTCAGAGAGAGGAAGCCGAAAACACCTGCAATCTTTTCAGACAGGATGTTGACAATGCGTCTCTGGCACGTCTTGACCTTGAAC 1300  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*||  
 AACGTCTCTCTACGAAGTCTCTCTCCTTCGGCTTTTGTGGGACGTTAGAAAGTCTGTCCTACAACCTGTTACGCAGAGACCGTGCAGAAGTGGAACTTG

Vimentin > L Q E E M L Q R E E A E N T L Q S F R Q D V D N A S L A R L D L E R

Ear1 Ear1 AlwN1 Pst1  
 GCAAAGTGAATCTTTGCAAGAAGAGATTGCCTTTTTGAAGAAACTCCACGAAGAGGAAATCCAGGAGCTGCAGGCTCAGATTTCAGGAACAGCATGTCCA  
 1301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1400  
 CGTTTCACCTTAGAAACGTTCTTCTCTAACGGAAAACTTCTTTGAGGTGCTTCTCCTTTAGGTCTCGACGTCCGAGTCTAAGTCCTTGTCGTACAGGT  
**Vimentin** > K V E S L Q E E I A F L K K L H E E E I Q E L Q A Q I Q E Q H V Q

Cla1 PshA1 BsiW1 SpAcc EcoN1 Pst1 Sbf1 BspM1  
 AATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCCTGCGTGACGTACGTACGCAATATGAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCAGAA  
 1401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1500  
 TTAGCTACACCTACAAAGGTTCCGACTGGAGTGCCGACGGGACGCACTGCATGCAGTCGTTATACTTTACACCCGACGGTTCTTGGACGTCCTCCGTCTT  
**Vimentin** > I D V D V S K P D L T A A L R D V R Q Q Y E S V A A K N L Q E A E

EcoN1 EcoN1  
 GAATGGTACAAATCCAAGTTTGGCTGACCTCTCTGAGGCTGCCAACCCGGAACAATGACGCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGAC  
 1501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1600  
 CTTACCATGTTTAGGTTCAAACGACTGGAGAGACTCCGACGGTTGGCCTTGTTACTGCGGGACGCGGTCCGTTTTCGTCCTCAGGTGACTCATGGCCTCTG  
**Vimentin** > E W Y K S K F A D L S E A A N R N N D A L R Q A K Q E S T E Y R R Q

SpDon Bsg1 Xcm1 Ear1  
 AGGTGCAGTCCCTCACCTGTGAAGTGGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAAGTTTGCCGTTGAAGC  
 1601 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1700  
 TCCACGTCAGGGAGTGGACACTTCACCTACGGGAATTTCTTGGTTACTCAGGGACCTTGCGGTCTACGCACTTTACCTTCTCTTGAACGGCAACTTCG  
**Vimentin** > V Q S L T C E V D A L K G T N E S L E R Q M R E M E E N F A V E A

Xcm1 Sbf1 Pst1 Ale1 BspM1  
 TGCTAACTACCAAGACACTATTGGCCGCCTGCAGGATGAGATTTCAGAATATGAAGGAGGAAATGGCTCGTCACCTTCGTGAATACCAAGACCTGCTCAAT  
 1701 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1800  
 ACGATTGATGGTTCTGTGATAACCGGCGGACGTCCTACTCTAAGTCTTATACTTCTCCTTTACCGAGCAGTGAAGCACTTATGGTTCTGGACGAGTTA  
**Vimentin** > A N Y Q D T I G R L Q D E I Q N M K E E M A R H L R E Y Q D L L N



Bsu36 SpDon Bbs1 Bpm1

2301 GCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGC 2400  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2400  
 CGTCAGGAAGGGACTCCCCAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCTGCCGACG

FusionRed > Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C

BseY1 BsmB1 Stul BseY1

2401 CTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGT 2500  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2500  
 GAGTAGATGTTGCAGTTCGAATCTCCCACCTTGAAGGGTCGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACA

FusionRed > L I Y N V K V R G V N F P A N G P V M Q K K T L G W E A S T E T M Y

Bgl1 BssS1 Eco57 Bsa1 BpuE1

2501 ACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAA 2600  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2600  
 TGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGACTTCGAGCACCCGCCCCGGTGGACTAGACGTTGGAAGTCTGGTGTATGTCTAGGTT

FusionRed > P A D G G L E G A C D M A L K L V G G G H L I C N L E T T Y R S K

BpuE1 SpAcc PflM1 Bsa1 PshA1 BssS1

2601 GAAACCCGCTACGAACCTCAAGATGCCCCGGCGTCTACAACGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTTCGAGCAGCAC 2700  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2700  
 CTTTGGGCGATGCTTGGAGTTCTACGGGCCGAGATGTTGCACCTGGTGTCTGACCTTTCTTAGTTCTCCGGCTGCTACTCTGGATGCAGCTCGTTCGTG

FusionRed > K P A T N L K M P G V Y N V D H R L E R I K E A D D E T Y V E Q H

Dra3 Msc1 SpDon BsrB1 Not1 Eagl Xba1 BsaB1

2701 GAGGTGGCTGTGGCCAGATACTTACTGTTGGCGCTGGTGTATGGAGGTAATGAGCGGCCGCGACTCTAGATCATAATCAGCCATAACCACATTTGTAGAG 2800  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2800  
 CTCCACCGACACCGGTCTATGAGATGACCACCGGACCACTACCTCCATTTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTC

FusionRed > E V A V A R Y S T G G A G D G G K \*

```

                                     Bsm1
      SpDon   Dra1                   Mfe1   Hpa1   polyA   Psil
      |       |                       |       |       |       |
2801 GTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
      CAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCTGAATATTAC

      polyA                   polyA       Bts1 Bsm1                   Af12
      |                         |           |       |                   |
2901 GTTACAAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACCTGCAATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
      CAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTATTTTCGTAATAAAGTACGTAAGATCAACACCAAAACAGGTTTGTAGTAGTTACATAGAATTCC

      SpDon       Ssp1
      |           |
3001 CGTAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
      GCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAAT

      Psil
      |
3101 TAAATCAAAAAGAAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      ATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTT

                                     BtgZ1
                                     Dra3
                                     |
                                     |
3201 ACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCTTAAAGGGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
      TGGCAGATAGTCCCCTACCGGGTGTGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCT

                                     Nae1
                                     NgoM4
                                     |
                                     |
3301 GCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      CGGGGGCTAAATCTCGAACTGCCCCCTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTTCGCTTTCCTCGCCCGGATCCCAGGACCGTTACATCG

```

```
GGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATT 3500
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
CCAGTGCGACGCGCATTGGTGGTGTGGGCGGCACGAATTACGCGGCATGTCCCAGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAA

                                  BciV1
                                BspH1
                                BsrB1
                                SspI  EarI  Bsu36
                                |    |    |
                                |    |    |
polyA                                |    |    |
                                |    |    |
TGTTFATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGG
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
ACAAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCC

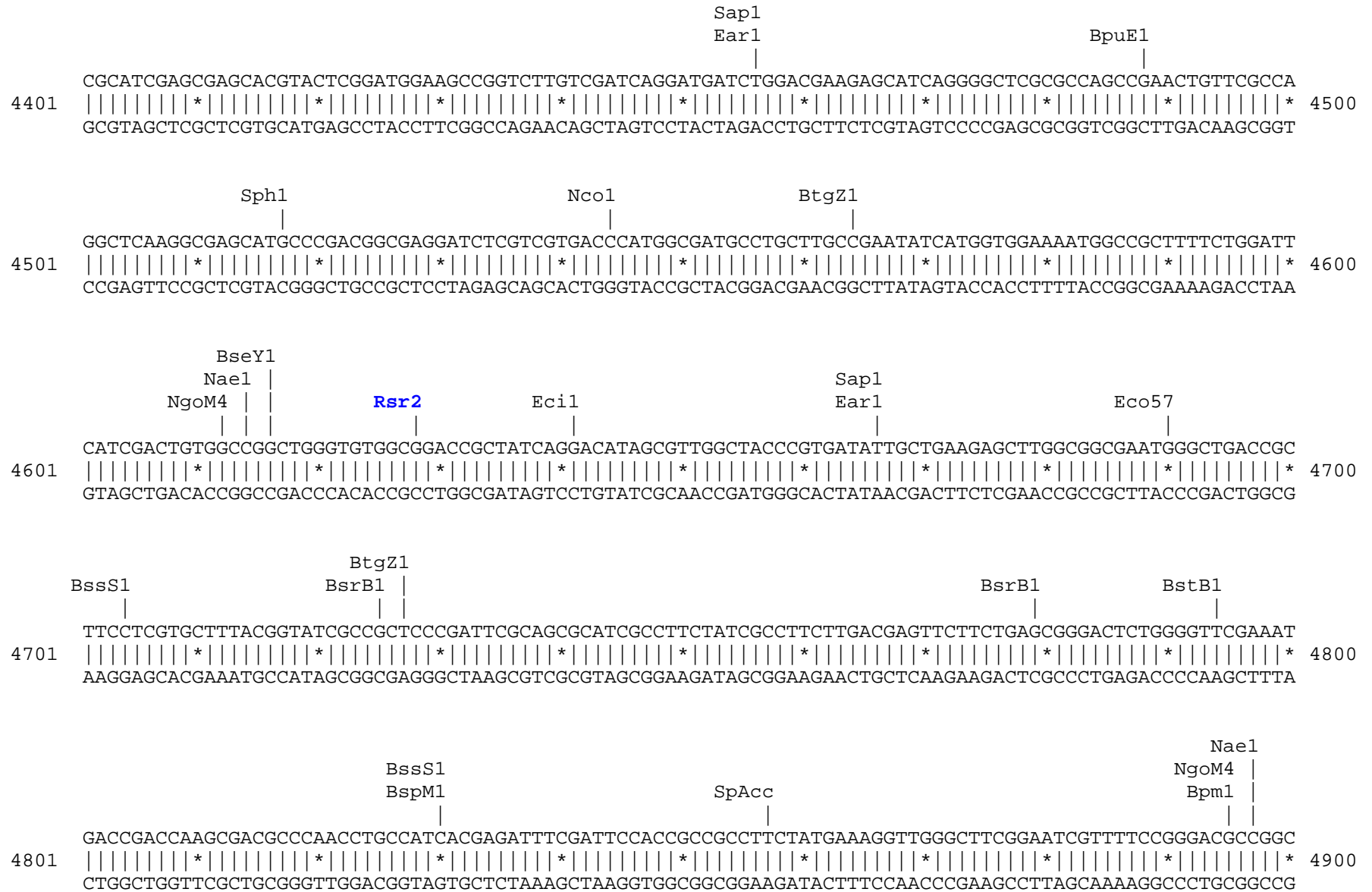
                                                              NsiI
                                                              SphI
                                                              BfrB1
EciI                               BseYI                               BstAP
Pvu2                               |    |    |
|    |                               |    |    |
|    |                               |    |    |
AAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCA
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
TTTTCTTGGTTCGACACCTTACACACAGTCAATCCACACCTTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGT

                                                              NsiI
                                                              SphI
                                                              BfrB1
SexA1                               BseYI                               BstAP                               EciI
|    |                               |    |    |                               |    |    |                               |
|    |                               |    |    |                               |    |    |                               |
|    |                               |    |    |                               |    |    |                               |
ACCAGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCA
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
TGGTCCACACCTTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGT

                                                              NsiI
EciI                               BmrI                               EciI                               NcoI                               polyA                               BglI
|    |                               |    |    |                               |    |    |                               |    |    |                               |
|    |                               |    |    |                               |    |    |                               |    |    |                               |
|    |                               |    |    |                               |    |    |                               |    |    |                               |
TCCCGCCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTTTTATTTATGAGAGGCGGAGCCGCTCGGCCTCTGAGCT
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
AGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAATAAATAACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGA
```











Found:

<b>Aar1</b>	Aat2	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ahd1</b>	Ale1	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	<b>Bbs1</b>	<b>Bcg1a</b>
<b>Bcg1b</b>	BciV1	BfrB1	Bgl1	<b>Bgl2</b>	<b>BmgB1</b>	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	<b>Bsg1</b>	<b>BsiW1</b>	Bsm1	BsmB1	BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	<b>BssH2</b>	BssS1	BstAP
BstB1	Bsu36	BtgZ1	<b>Bts1</b>	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoN1
<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	Msc1	Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>
Nsil	PflF1	<b>PflM1</b>	polyA	PshA1	Psil	Pst1	Pvu2	<b>Rsr2</b>	Sac1	Sap1	Sbf1	SexA1	<b>Sfi1</b>
Sma1	<b>SnaB1</b>	SpAcc	SpDon	Sph1	<b>Srf1</b>	Ssp1	Stul	<b>Xba1</b>	Xcm1	Xho1			

Unique:

<b>Aar1</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ahd1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bbs1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	<b>Bgl2</b>	<b>BmgB1</b>	<b>Bsg1</b>	<b>BsiW1</b>
<b>BspLU</b>	<b>BsrD1</b>	<b>BsrG1</b>	<b>BssH2</b>	<b>Bts1</b>	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Nar1</b>	<b>Nde1</b>	<b>Nhe1</b>
<b>Not1</b>	<b>PflM1</b>	<b>Rsr2</b>	<b>Sfi1</b>	<b>SnaB1</b>	<b>Srf1</b>	<b>Xba1</b>							

Not found:

Acc65	Acc1	Apal	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcl1	Blp1	Bpu10	BspE1	BstE2	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL	R4atP
R4atR	Sac2	Sall	SanD1	Scal	Sgf1	SgrA1	Spe1	Swal	T3RNA	T7RNA	T7Ter	PISce	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													