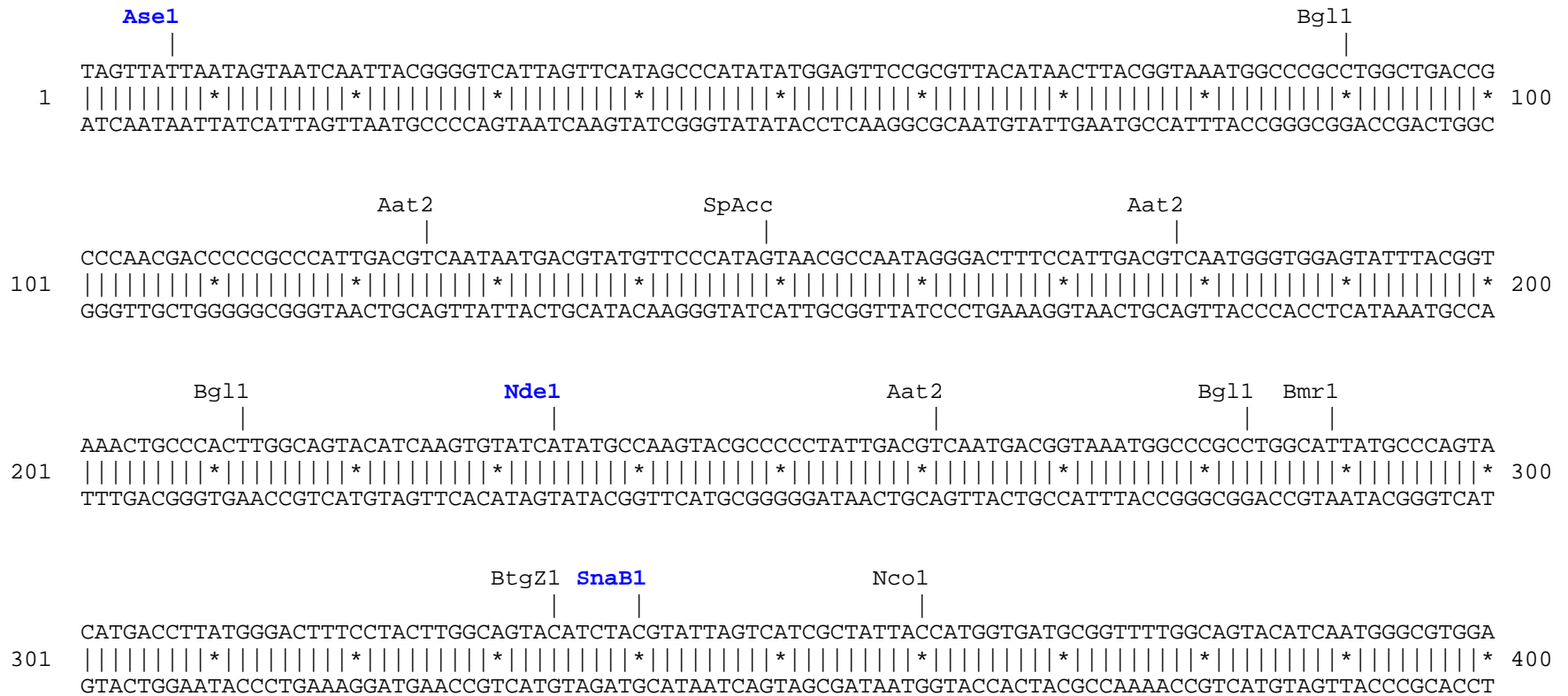


pFusionRed-zyxin vector restriction map

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).

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



BseR1
BseR1 |
Bpm1 |

Pvu1 Xmn1 SpAcc Bgl2 BseR1 BspE1

901 TGGGAGGTGCCTTCCCCGCGCCCCCTCCCCGATCGAGGAATCATTTCCCCCTGCGCCTCTGGAGGAGGAGATCTTCCCTTCCCCGCGCCTCCTCCGGA 1000
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
 ACCCTCCACGGAAGGGCGGCGGGGGAGGGGGCTAGCTCCTTAGTAAAGGGGGACGCGGAGACCTCCTCCTCTAGAAGGGAAGGGGCGGCGGAGGAGGCCT

Zixin > G G A F P P P P P I E E S F P P A P L E E E I F P S P P P P P E

BseR1
Bsu36 |
BseR1 |

SpDon Ahd1 Bts1

1001 GGAGGAGGGAGGGCCTGAGGCCCCCATACCGCCCCACACAGCCCAGGGAGAAGGTGAGCAGTATTGATTTGGAGATCGACTCTCTGTCTCACTGCTG 1100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
 CCTCCTCCCTCCCGGACTCCGGGGGTATGGCGGGGGTGGTGTCTGGTCCCTCTTCCACTCGTCATAACTAAACCTCTAGCTGAGAGACAGGAGTGACGAC

Zixin > E E G G P E A P I P P P P Q P R E K V S S I D L E I D S L S S L L

Sma1 Msc1

1101 GATGACATGACCAAGAATGATCCTTTCAAAGCCCCGGGTGTCATCTGGATATGTGCCCCACCAGTGGCCACTCCATTTCAGTTCCAAGTCCAGTACCAAGC 1200
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
 CTACTGTACTGGTTCTTACTAGGAAAGTTTCGGGCCCACAGTAGACCTATACACGGGGGTGGTCACCGGTGAGGTAAGTCAAGGTTTCAGGTCATGGTTTCG

Zixin > D D M T K N D P F K A R V S S G Y V P P P V A T P F S S K S S T K P

Pst1 BseY1 SpAcc AlwN1

1201 CTGCAGCCGGGGGCACAGCACCCCTGCCTCCTTGAAGTCCCCTTCCAGCTCCCAGCCTCTGCCCCAGGTTCCGGCTCCGGCTCAGAGCCAGACACAGTT 1300
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
 GACGTCGGCCCCGTGTCGTGGGGACGGAGGAACCTTCAGGGGAAGGTCGAGGGTCGGAGACGGGGTCCAAGGCCGAGGCCGAGTCTCGGTCTGTGTCAA

Zixin > A A G G T A P L P P W K S P S S S Q P L P Q V P A P A Q S Q T Q F

Apa1
PspOM
Bgl1

BseY1 BseY1 Bsu36 BseY1 BseY1

```

1301  CCATGTTTCAGCCCCAGCCCCAGCCCAAGCCTCAGGTCCAACCTCCATGTCCAGTCCCAGACCCAGCCTGTGTCTTTGGCTAACACCCAGCCCCGAGGGCCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGTACAAGTCGGGGTCGGGGTCGGGTTCGGAGTCCAGGTTGAGGTACAGGTTCAGGGTCTGGGTTCGGACACAGAAACCGATTGTGGGTTCGGGGCTCCCGGG
Zixin  > H V Q P Q P Q P K P Q V Q L H V Q S Q T Q P V S L A N T Q P R G P
    
```

Bpm1 SpAcc

BseY1 Bpm1

```

1401  CCAGCTCATCTCCGGCTCCAGCCCCAAGTTTTCTCCAGTGACTCCTAAGTTTACTCCTGTGGCTTCCAAGTTCAGTCTCGGAGCCCCAGGTGGATCTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGTTCGAGTAGAGGCCGAGGTTCGGGGATTCAAAGAGGTCCTGAGGATTCAAATGAGGACACCGAAGGTTCAAGTCAGGACCTCGGGGTCCACCTAGAC
Zixin  > P A S S P A P A P K F S P V T P K F T P V A S K F S P G A P G G S G
    
```

Bpm1 BseY1 BseY1

```

1501  GGTCAACAACCAATCAAAAATTGGGGCACCCCGAAGCTCTTTCTGCTGGCACAGGCTCCCCTCAACCTCCCAGCTTACCTATGCCAGCAGAGGGAGAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCAGTGTGGTTTAGTTTTTAACCCCGTGGGGCTTCGAGAAAGACGACCGTGTCCGAGGGGAGTTGGAGGGTTCGAAGTGGATACGGGTTCGTCTCCCTCTT
Zixin  > S Q P N Q K L G H P E A L S A G T G S P Q P P S F T Y A Q Q R E K
    
```

Bsg1 Dra3 BstAP SexA1 PspOM Apa1 PspOM Apa1 PspOM SpAcc

```

1601  GCCCGAGTGCAGGAGAAGCAGCACCCCGTCCCCCACC GGCTCAGAACCAAAACCAGGTGCGCTCCCCTGGGGCCCCAGGGCCCCCTGACTCTGAAGGAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGGGGCTCACGTCTCTTCGTCGTGGGGCACGGGGGTGGCCGAGTCTTGGTTTTGGTCCACGCGAGGGGACCCCGGGGTCCCGGGGACTGAGACTTCCTC
Zixin  > P R V Q E K Q H P V P P P A Q N Q N Q V R S P G A P G P L T L K E
    
```

BseY1
 BseR1
 Eco57 Pvu2 | BstAP
 Bpm1 |
 Eag1

1701 GTGGAGGAGCTGGAGCAGCTGACCCAGCAGCTAATGCAGGACATGGAGCATCCTCAGAGGCAGAATGTGGCTGTCAACGAACTCTGCGGCCGATGCCATC 1800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 CACCTCCTCGACCTCGTCGACTGGGTTCGTCGATTACGTCTGTACCTCGTAGGAGTCTCCGTCTTACACCGACAGTTGCTTGAGACGCCGGCTACGGTAG
Zixin > V E E L E Q L T Q Q L M Q D M E H P Q R Q N V A V N E L C G R C H Q

Ale1
 BspM1 |
 Bpm1 |
 Srf1
 Sma1 | BtgZ1 Pvu2 | SpDon | Aar1 | Fsp1

1801 AACCCCTGGCCCGGGCGCAGCCAGCCGTCCTCGCGCTCTAGGGCAGCTGTTCCACATCGCCTGCTTACCTGCCACCCAGTGTGCGCAGCAGCTCCAGGGCCA 1900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
 TTGGGGACCGGGCCCGTCGGTCGGCAGGCGGAGATCCCGTCGACAAGGTGTAGCGGACGAAGTGGACGGTGGTTCACACGCGTCGTCGAGGTCCCGGT
Zixin > P L A R A Q P A V R A L G Q L F H I A C F T C H Q C A Q Q L Q G Q

BspM1
 Aar1 |
 Nar1
 SpAcc | Kas1 | SpAcc Bpm1 | SpAcc | SpAcc Bpm1 |

1901 GCAGTTCTACAGTCTGGAGGGGGCGCCGTACTIONGCGAGGGCTGTTACACTGACACCCTGGAGAAGTGTAACACCTGCGGGGAGCCCATCACTGACCGCATG 2000
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
 CGTCAAGATGTCAGACCTCCCCCGCGCATGACGCTCCCGACAATGTGACTGTGGGACCTCTTACATTGTGGACGCCCTCGGGTAGTACTGGCGTAC
Zixin > Q F Y S L E G A P Y C E G C Y T D T L E K C N T C G E P I T D R M

Bpu10
 BbvC1
 Sph1 | Stu1 | Bts1 | SpDon | Bpm1

2001 CTGAGGGCCACGGGCAAGGCTATCACCCGCACTGCTTCACTGTGTGGTCTGCGCCCGCCCTGGAGGGCACCTCCTTCATCGTGGACCAGGCCAACC 2100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
 GACTCCCGGTGCCCCGTTCCGGATAGTGGGCGTGACGAAGTGGACACACCAGACGCGGGCGGGGGACCTCCCGTGGAGGAAGTAGCACCTGGTCCGGTTGG
Zixin > L R A T G K A Y H P H C F T C V V C A R P L E G T S F I V D Q A N R


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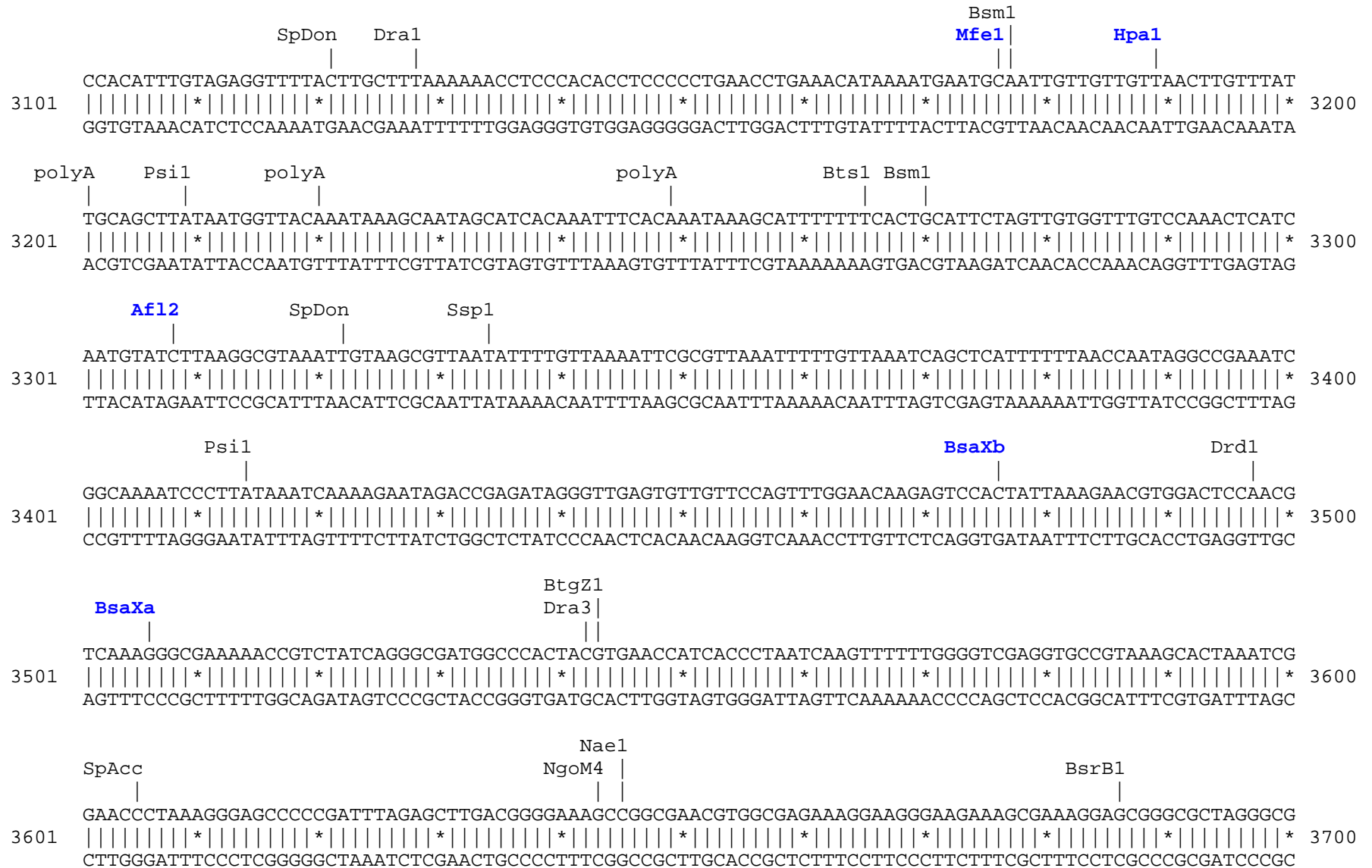
                                     Bsu36      SpDon      Bbs1      Bpm1
2601  CCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCC 2700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTTCGG
FusionRed  > P D F F K 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

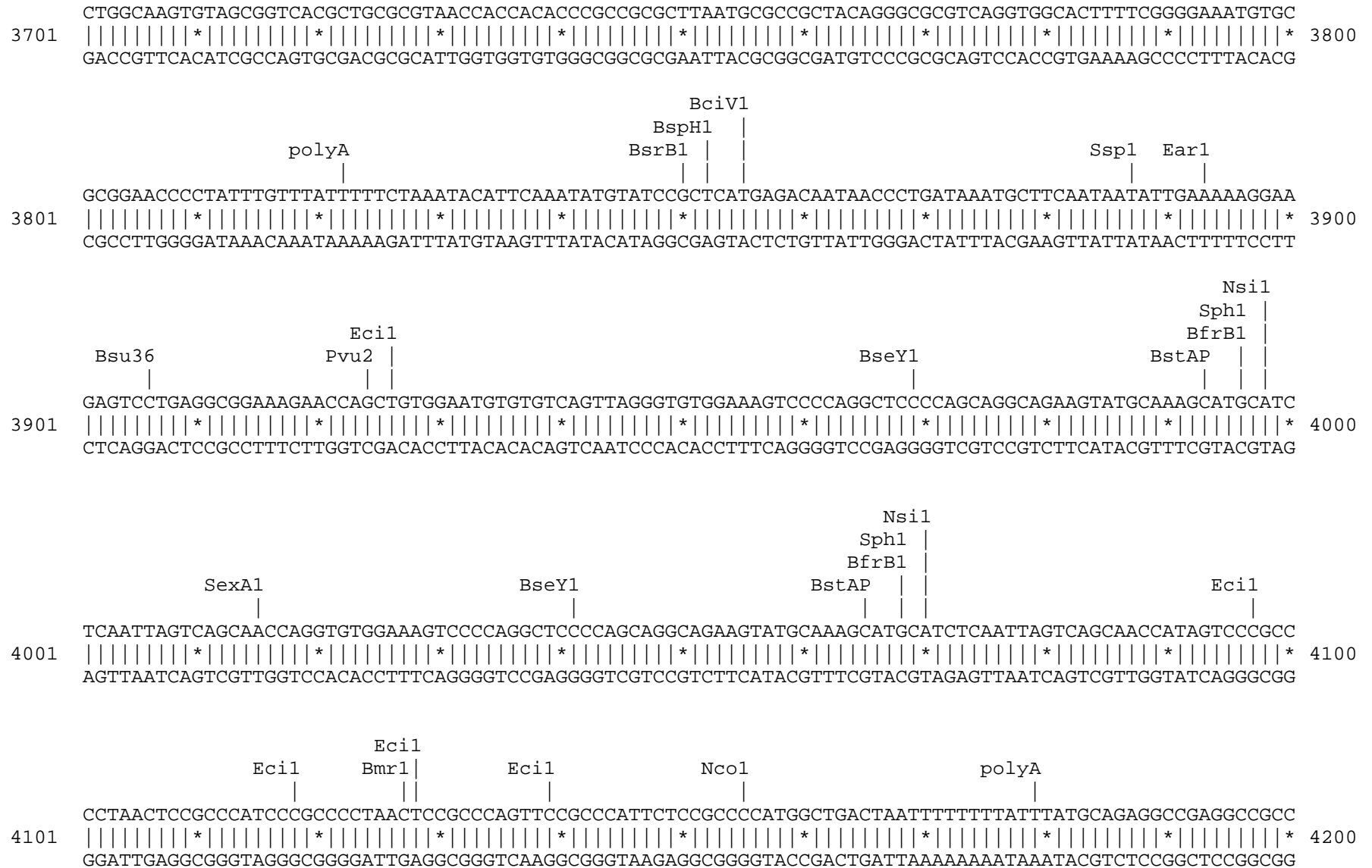
                                     BseY1      BseY1      BsmB1      StuI
2701  TCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTC 2800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      AGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCTTGAAGGGTCGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAG
FusionRed  > Q D G C 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

                                     Bgl1      BssS1      Eco57      Bsa1
2801  CACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACC 2900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GTGGCTCTGCTACATGGGGCGACTGCCGCGCGGACCTTCCGCGTACACTGTACCGGGACTTCGAGCACCCGCCCGGTGGACTAGACGTTGGAACCTCTGG
FusionRed  > T E T M Y 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

                                     BpuE1      SpAcc      Bsa1
                                     BpuE1      PflM1
2901  ACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCCGGCTCTACAACGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCT 3000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCGCAGATGTTGCACCTGGTGTCTGACCTTTCTTAGTTCTCCGGCTGCTACTCTGGA
FusionRed  > T Y R S K 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

                                     Not1      Eag1
                                     PshA1      BssS1      Dra3      Msc1      SpDon      BsrB1      Xba1      BsaB1
3001  ACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGATGGAGGTAATGAGCGGCCGCGACTCTAGATCATAATCAGCCATA 3100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TGCAGTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGGACCACTACCTCCATTTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTAT
FusionRed  > V E Q H E V A V A R Y S T G G A G D G G K *
```






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      NaeI
      NgoM4 |
      BpmI  |
      |
TCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAAT
5201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
AGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTA

                polyA      polyA
                |          |
ACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCGTTTGTTCATAAACGCGGGGTTCGGTCCCAGGGCTGG
5301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
TGGCCTTCCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTTCGCGTCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACC

      BsaI
      |
CACTCTGTCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTCTTCCCTTTTCCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGC
5401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
GTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCG

                BstAP      AlwN1      Bsu36      DraI      DraI
                |          |          |          |          |
TCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAGGATCTA
5501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
AGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGAT

                BspH1
                |
GGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCT
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
CCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGTAAGA

```


Found:

Aar1	Aat2	Afe1	Afl2	Age1	Ahd1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1
BbvC1	BciV1	BfrB1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsg1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP
BstB1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoR1
Fsp1	Hind3	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1
PflF1	PflM1	Pml1	polyA	PshA1	Psi1	PspOM	Pst1	Pvu1	Pvu2	Rsr2	Sac1	Sap1	SexA1
Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Srf1	Ssp1	Stu1	Xba1	Xho1	Xmn1		

Unique:

Afe1	Afl2	Age1	Ahd1	Ase1	BamH1	BbvC1	BsaXa	BsaXb	Bsg1	BspE1	BspLU	BsrD1	BsrG1
BssH2	Clal	Ecl2	EcoR1	Hind3	Hpa1	Mfe1	Nde1	Nhe1	Not1	PflF1	PflM1	Pml1	PshA1
Pst1	Pvu1	Rsr2	Sac1	Sfi1	SnaB1	Srf1	Xba1	Xho1					

Not found:

Acc65	Acl1	Asc1	AsiS1	Baela	Baelb	BcglA	Bcglb	Bcl1	Blp1	BmgB1	BsiW1	BstE2	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT
Fse1	FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	R4atB	R4atL	R4atP	R4atR	Sac2
Sall	SanD1	Sbf1	Scal	Sgfl	SgrA1	Spe1	Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1	

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													