

pTagFP635-Cx26 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). TagFP635 amino acids are shown in red, Connexin 26 amino acids are shown in green, linker amino acids are shown in black.



Aat2Eci1

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TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
    
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Nhe1 Afe1

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ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
    
```

Bcg1b BseR1

Xho1 Hind3 EcoR1 | Not1 |

BpuE1 Bgl2 | Sac1 | BstB1 | | Eag1 |

Bcg1a

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CCGGACTCAGATCTCGAGCTCAAGCTTTCGAATTCGCGGCCGCACGCTCCTCGGGACACAGTGCCAACCATCCAGAGGACAAGATGGATTGGGGCACACTA
601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
GGCCTGAGTCTAGAGCTCGAGTTTCGAAGCTTAAGCGCCGGCGTGCGAGGAGCCCTGTGTACGGTTGGTAGGTCTCCTGTTCTACCTAACCCCGTGTGAT
    
```

Cx26 > M D W G T L

BsaXb _Chi BsaXa Ear1 BspH1 BssS1

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CAGAGCATCCTCGGGGGTGTCAACAAGCACTCCACCAGCATTGGGAAAATCTGGCTCACTGTCTCTTCATCTTCCGCATCATGATCCTCGTGGTGGCCG
701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
GTCTCGTAGGAGCCCCACAGTTGTTTCGTGAGGTGGTTCGTAACCCTTTTAGACCGAGTGACAGGAGAAGTAGAAGGCGTAGTACTAGGAGCACCACCGGC
    
```

Cx26 > Q S I L G G V N K H S T S I G K I W L T V L F I F R I M I L V V A A

Bpm1 SpAcc

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CGAAGGAGGTGTGGGGAGATGAGCAAGCCGATTTTGTGTTTGCAACACTCTCCAGCCTGGCTGTAAGAATGTGTGCTACGACCACTACTTCCCCATCTCTCA
801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
GCTTCTCCACACCCCTCTACTCGTTCGGCTAAAACAAACGTTGTGAGAGGTCCGACCGACATTCTTACACACGATGCTGGTGATGAAGGGGTAGAGAGT
    
```

Cx26 > K E V W G D E Q A D F V C N T L Q P G C K N V C Y D H Y F P I S H

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                    Bcl1
                    Pvu2 |
                    Pst1 |
SpDon |                 |                 |                 |                 |                 |                 |                 |
          CATCCGGCTCTGGGCTCTGCAGCTGATCATGGTGTCCACGCCGCCCTCTGGTAGCTATGCACGTGGCCTACCGGAGACACGAAAAGAAACGGAAGTTC
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
          GTAGGCCGAGACCCGAGACGTCGACTAGTACCACAGGTGCGGCCGGGAGGACCATCGATACGTGCACCGGATGGCCTCTGTGCTTTTCTTTGCCTTCAAG
Cx26 > I R L W A L Q L I M V S T P A L L V A M H V A Y R R H E K K R K F

                    Ear1
                    SanD1
                    _Chi
1001 ATGAAGGGAGAGATAAAGAACGAGTTTAAAGGACATCGAAGAGATCAAAACCCAGAAGGTCCGTATCGAAGGGTCCCTGTGGTGGACCTACACCACCAGCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
      TACTTCCCTCTCTATTTCTTGCTCAAATTCCTGTAGCTTCTCTAGTTTTGGGTCTTCCAGGCATAGCTTCCCAGGGACACCACCTGGATGTGGTGGTTCGT
Cx26 > M K G E I K N E F K D I E E I K T Q K V R I E G S L W W T Y T T S I

                    Bbs1
                    BstB1 |
                    SpDonBsrG1
                    AlwN1 |
                    SpDon
1101 TCTTCTTCCGGGTCATCTTCGAAGCTGTCTTCATGTATGTCTTTTACATCATGTACAATGGCTTCTTTCATGCAGCGTCTGGTGAAGTGTAACGCCTGGCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
      AGAAGAAGGCCCAGTAGAAGCTTCGACAGAAGTACATACAGAAAATGTAGTACATGTTACCGAAGAAGTACGTGCGCAGACCACTTACATTGCGGACCGG
Cx26 > F F R V I F E A V F M Y V F Y I M Y N G F F M Q R L V K C N A W P

                    BstX1
                    Bbs1
                    BspH1
1201 TTGTCCAATACAGTGGACTGCTTTCATTTCCAGGCCACAGAAAAGACTGTCTTCACGGTGTTCATGATCTCTGTGTCTGGAATTTGCATCCTGCTAAAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
      AACAGGGTTATGTACCTGACGAAGTAAAGGTCCGGGTGTCTTTTCTGACAGAAGTGCCACAAGTACTAGAGACACAGACCTTAAACGTAGGACGATTTG
Cx26 > C P N T V D C F I S R P T E K T V F T V F M I S V S G I C I L L N

                    T7Ter
                    Bpu10
                    BamH1
                    Age1
                    Ale1
                    Nco1
                    Sap1
                    Ear1
1301 ATCACAGAGCTGTGCTATCTGTTCATTAGGTATTGCTCAGGGAAGTCCAAAAGACCAGTTCGCGGATCCACCGGTCCGCCACCATGGTGTCTAAGGGCGAAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      TAGTGTCTCGACACGATAGACAAGTAATCCATAACGAGTCCCTTCAGGTTTTCTGGTCAGCGCCTAGGTGGCCAGCGGTGGTACCACAGATTCCCGCTTC
Cx26/TagFP635> I T E L C Y L F I R Y C S G K S K R P V A D P P V A T M V S K G E E
  
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BsrG1 ApaL1 SpAcc

1401 AGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
 TCGACTAATTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTGTTGGTGGTGAAGTTTCACGTGTAGGCTCCCGCTTCCGTTTCGGGATGCT

TagFP635 > L I K E N M H M K L Y M E G T V N N H H F K C T S E G E G K P Y E

Bsu36 SpDon Bbs1

1501 GGGCACCACAGACCATGAGAATCAAGGTGGTCGAGGGCGGCCCTCTCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAACCTTC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 CCCGTGGGTCGTTACTTCTAGTTCCACCAGCTCCCGCGGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCGTTTTGGAAG

TagFP635 > 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 M Y G S K T F

Bpm1

1601 ATCAACCACACCAGGGCATCCCCGACTTCTTTAAGCAGTCCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATAACGAAGACGGGGCGTGCTGA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 TAGTTGGTGTGGGTCCTGTAGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCGGACACGACT

TagFP635 > 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 G G V L T

Bpm1

1701 CCCGTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 GGCGATGGGTCCTGTGGTTCGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTT

TagFP635 > A T Q D T S L Q D G C L I Y N V K I R G V N F P S N G P V M Q K K

BseY1 Stu1 Bgl1 BssS1 Eco57

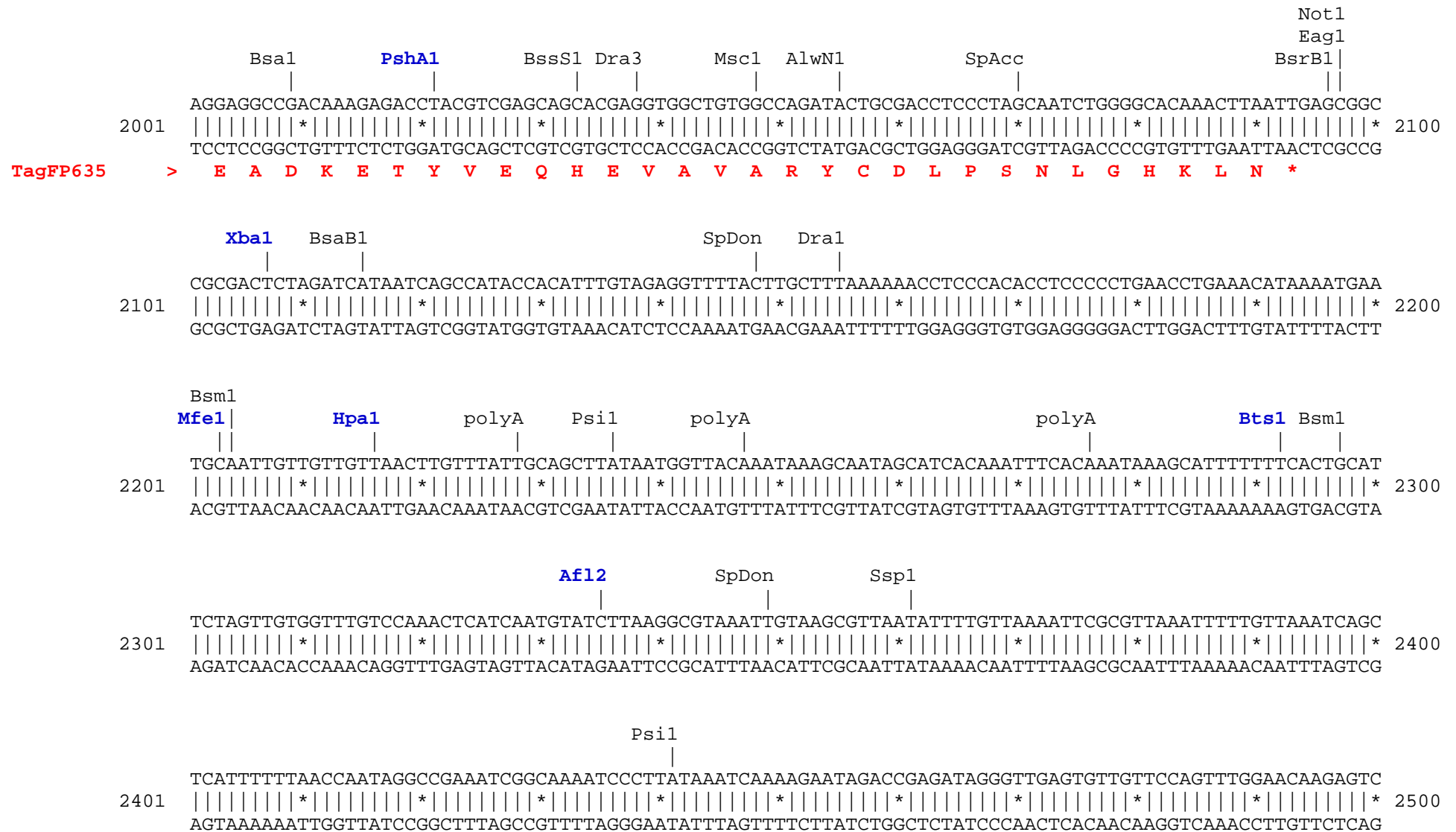
1801 AACACTCGGCTGGGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCAC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
 TTGTGAGCCGACCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCCGGGACCTTCCGTCCTCGCTGTACCGGGACTTCGAGCACCCTGGGGGGGCGTG

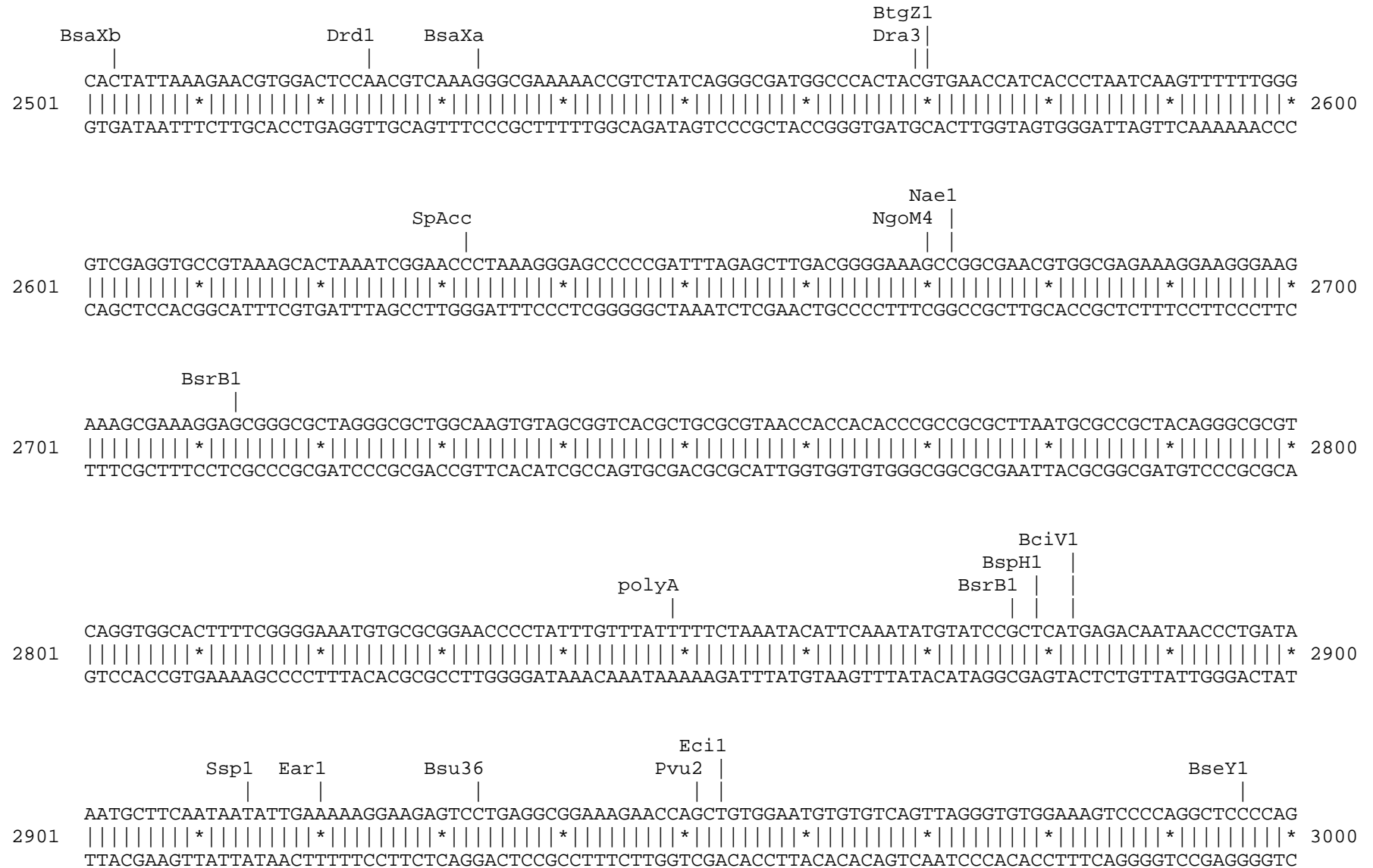
TagFP635 > T L G W E A S T E M L Y P A D G G L E G R S D M A L K L V G G G H

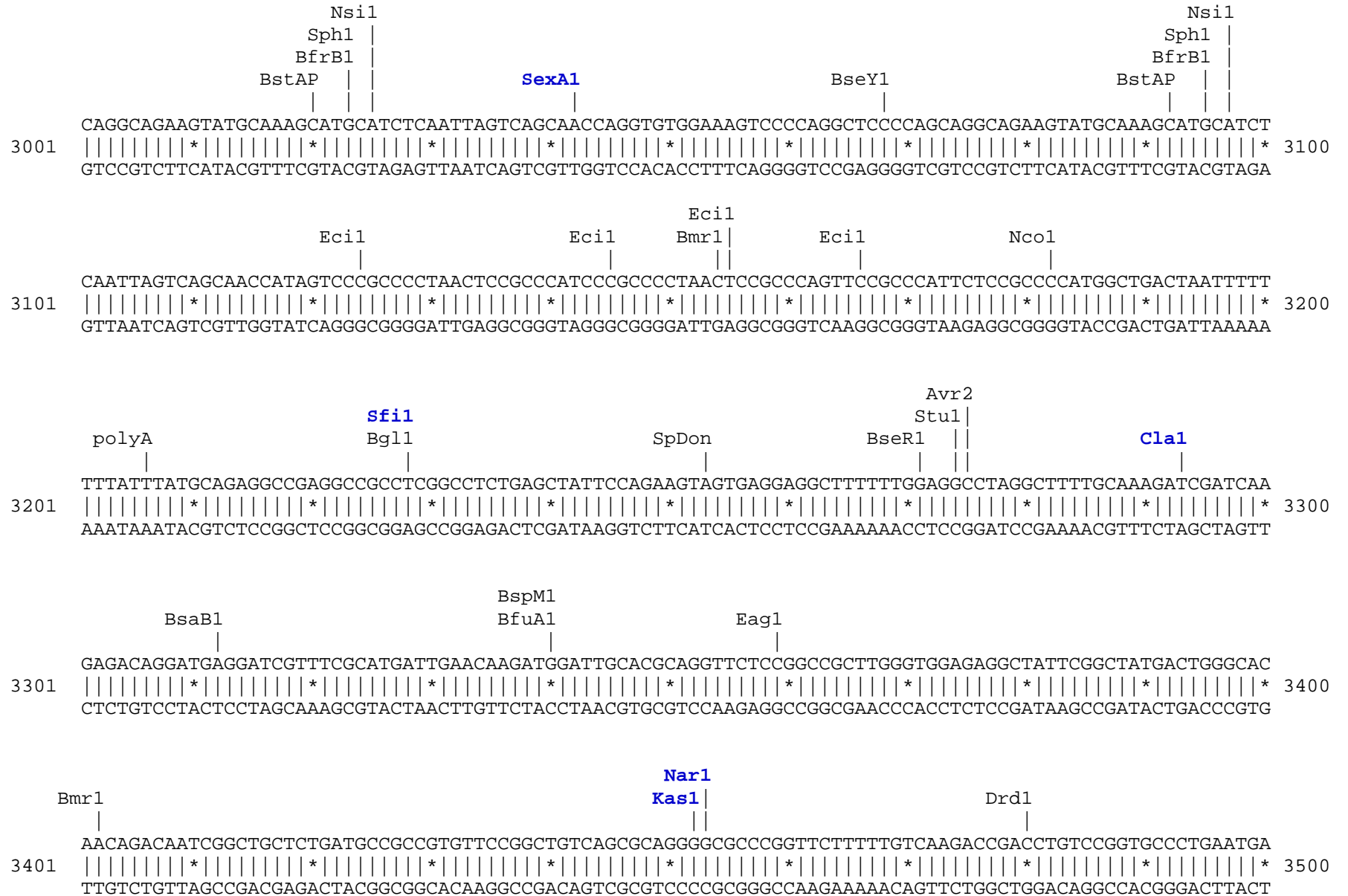
Bbs1 BpuE1 SpAcc Bbs1

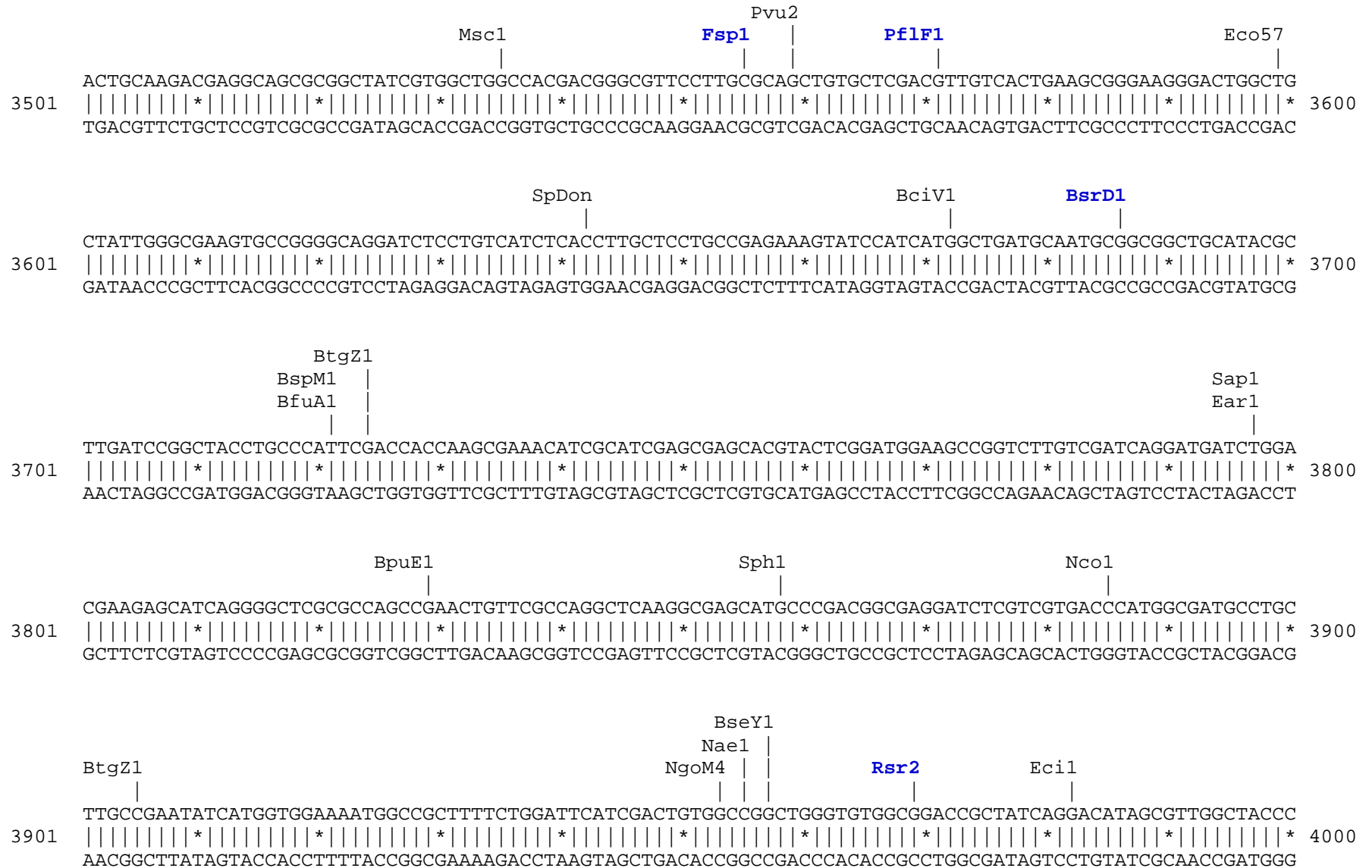
1901 CTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
 GACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGTCTTCTGACCTTCTTAGT

TagFP635 > L I C N L K T T Y R S K K P A K N L K M P G V Y Y V D R R L E R I K










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                                     BstAP
                                     AlwN1
                                     Bsu36
                                     DraI
4501  CCCC AAGTTCGGGTGAAGGCC CAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
      GGGGTTC AAGCCCACTTCCGGGTCCC GAGCGTCGGTTGCAGCCCCGCCGTCGGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTT

      DraI
      BspH1
4601  ACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
      TGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTG

                                     BpuE1
4701  CCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACACCCTACCAGCGGTGGTTTGTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
      GGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCCGCCACCAAACAA

                                     Eco57
                                     SpAcc
4801  TGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
      ACGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGT

                                     AlwN1
                                     BpuE1
4901  CCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
      GGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCAACCGCTATTGAGCAGAGAATGGCCCAAC

                                     ApaL1
                                     BseY1
5001  GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAAGTGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
      CTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCACCAAGCACGTGTGTGGGTTCGAACCTCGCTTGTGATGTGGCTTGACT
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                                           BciV1
                                           |
          SpAcc                            Eci1  |                            BssS1
          |                               |           |                           |
5101  GATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCCGGAACAGGAGAGCGCAC 5200
       |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*  |||||||*
       CTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGGCCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTG

                                     SpAcc                            Drd1  BpuE1
                                     |                               |           |
5201  GAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGG 5300
       |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*  |||||||*
       CTCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCC

                                           SpDon
                                           |
          SpAcc    Eci1                            BspLU
          |         |                               |
5301  CGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGCGTTATCCCCTGATT 5400
       |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*  |||||
       GCCTCGGATACCTTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAA

                                     Nsi1
                                     |
          BfrB1
          |
5401  CTGTGGATAACCGTATTACCGCCATGCAT 5429
       |||||||*|||||||*|||||||  |||
       GACACCTATTGGCATAATGGCGGTACGTA
  
```

Found:

Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	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	Pml1	polyA
PshA1	Psil	Pst1	Pvu2	Rsr2	Sac1	SanD1	Sap1	SexA1	Sfil	SnaB1	SpAcc	SpDon	Sph1
Ssp1	Stul	T7Ter	Xba1	Xho1									

Unique:

Afe1	Afl2	Age1	Ale1	Ase1	BamH1	Bcg1a	Bcg1b	Bcl1	Bgl2	Bpu10	BspLU	BsrD1	BstX1
Bts1	Clal	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1	PflF1	Pml1	PshA1
Pst1	Rsr2	Sac1	SanD1	SexA1	Sfil	SnaB1	T7Ter	Xba1	Xho1				

Not found:

Aar1	Acc65	Ac11	Ahd1	Apal	Asc1	AsiS1	Baela	Baelb	BbvC1	Blp1	BmgB1	Bsg1	BsiW1
BsmB1	BspE1	BssH2	BstE2	BstZ1	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	PspOM	Pvu1	R4atB	R4atL	R4atP
R4atR	Sac2	Sall	Sbf1	Scal	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA	PISce
Xcm1	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	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													