

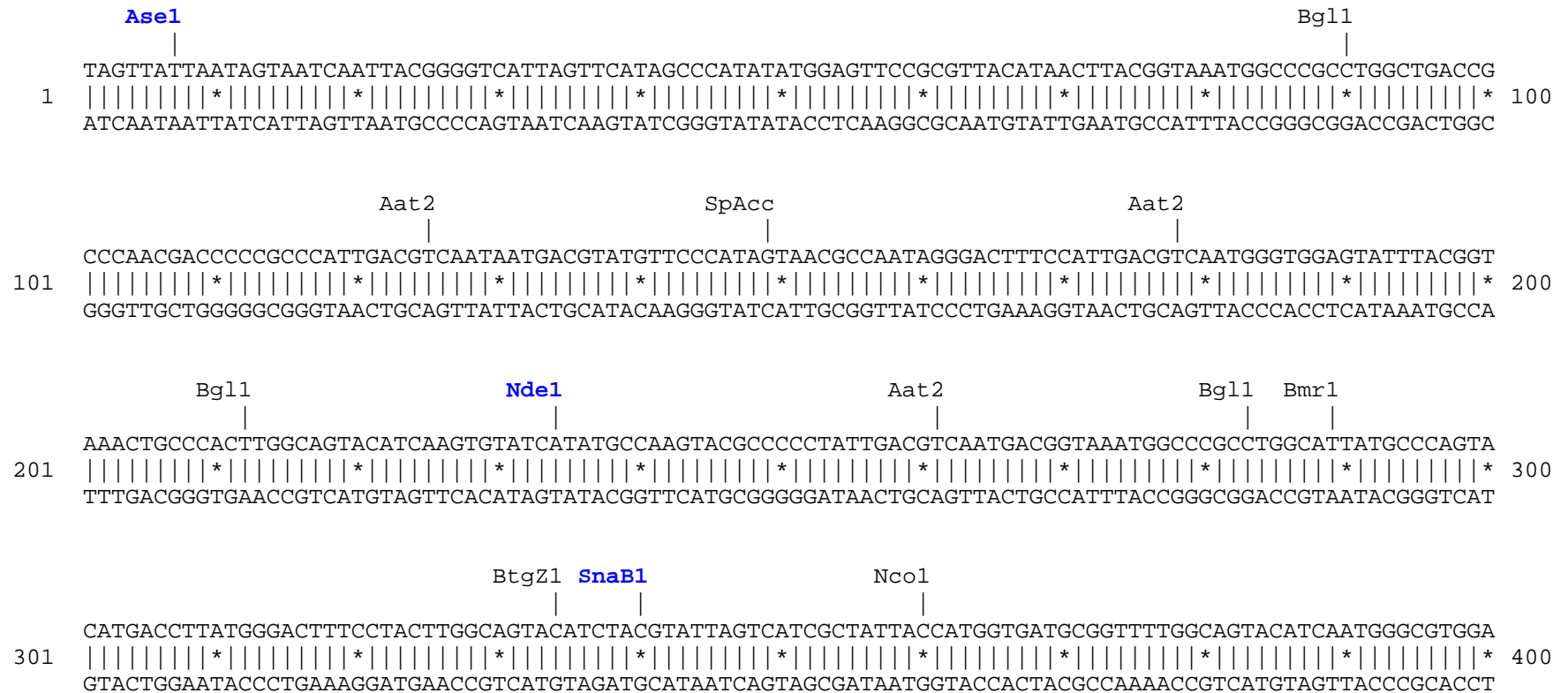
pFusionRed-Cx43 vector restriction map

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).

FusionRed amino acids are shown in red, Connexin 43 amino acids are shown in green, linker amino acids are shown in black.



Aat2Eci1

```
401 TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTGTAGTTGCCCTGAAAGGTTTTACAGCAT
```

Nhe1 **Afe1**

```
501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
TGTTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
```

Hind3
Xho1 Sac1 **EcoR1**

BpuE1 **Bgl2** Ecl2 BstB1Dra1

```
601 CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCGGCAGCACTTTTCTTTTCATTGGGGGAAGGCGTGAGGAAAGTACCAAACAGCAGCAGACTTTTAAA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
GGCCTGAGTCTAGAGCTCGAGTTTCGAAGCTTAAGCCGTCGTGAAAAGAAAAGTAACCCCCCTTCCGCACTCCTTTTCATGGTTTTGTCGTCGTCTGAAAATTT
```

Dra1Eco57Nae1
BssH2
Asc1NgoM4SpDon

```
701 CTTTAAACAGACAGGTCTGAGAGCCTGAACTCTCATTFTTCTTTGACTTCAGCCTCCAAGGAGTTCCACCAACTTTGGCGCGCCGGCTTCACTTTTCATT
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
GAAATTTGTCTGTCCAGACTCTCGGACTTGAGAGTAAAAAGGAAAAGTGAAGTCGGAGGTTCCCTCAAGGTGGTTGAAACCGCGCGCCGAAGTGAAAGTAA
```

Hind3 Bpm1 PflF1BsaXaSpAcc

```
801 AAGTGAAAGAGAGGTTGCCAGACATGGGTGACTGGAGTGCCTTGGGGAAGCTTCTGGACAAGGTCCAAGCCTACTCCACCGCTGGAGGGAAGGTGTGGCT
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
TTCAC TTTCTCTCCACGGGTCTGTACCCACTGACCTCACGGAACCCCTTTCGAAGACCTGTTCCAGGTTTCGGATGAGGTGGCGACCTCCCTTCCACACCGA
```

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

901 | GTCAGTGTCTTCATATTTCAGAATCCTGCTCCTGGGGACAGCTGTTTGAGTTCAGCTTGGGGTATGAACAGTCTGCCTTTTCGCTGTAACACTCAACAACCT 1000
 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
 CAGTCACGAGAAGTATAAGTCTTAGGACGAGGACCCCTGTTCGACAACACTCAGTCGAACCCCACTACTTGTTCAGACGGAAAGCGACATTGTGAGTTGTTGGA
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**

SpAcc
Eco57

Pml1

1001 | GGCTGCGAAAACGTCTGCTATGACAAGTCTTCCCCATCTCTCACGTGCGCTTCTGGGTCTTCAGATCATATTTCGTGTCTGTGCCCCACTCCTGTACT 1100
 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
 CCGACGCTTTTGACAGACGATACTGTTTCAGGAAGGGGTAGAGAGTGCACGCGAAGACCCAGGAAGTCTAGTATAAGCACAGACACGGGTGTGAGGACATGA
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
Ecl2
BseR1
PflF1

1101 | TGGCCCATGTGTTCTATGTGATGAGGAAGGAAGAGAAGCTAAACAAGAAAGAGGAGCTCAAAGTGGCCCAGACTGACGGGGTCAACGTGGAGATGCA 1200
 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
 ACCGGGTACACAAGATACTACTCCTTCCTTCTCTTCGATTTGTTCTTTCTTCTCCTCGAGTTTCACCGGGTCTGACTGCCCCAGTTGCACCTCTACGT
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

Ear1
SpDon

1201 | CCTGAAGCAGATTGAAATCAAGAAGTTCAAGTACGGGATTGAAGAGCACGGCAAGGTGAAAATGAGGGGCGGCTTGCTGAGAACCTACATCATCAGCATC 1300
 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
 GGACTTCGTCTAACTTTAGTTCTTCAAGTTCATGCCCTAACTTCTCGTGCCGTTCCACTTTTACTCCCCCGCCGAACGACTCTTGGATGTAGTAGTCGTAG
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**

Xmn1 BssS1 Nhe1 Bmr1
 1701 GAAACAATTCTCGTGCCGCAATTACAACAAGCAAGCTAGCGAGCAAACTGGGCGAACTACAGCGCAGAGCAAAATCGCATGGGGCAGGCCGGAAGCAC 1800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 CTTTGTAAAGGAGCACGGCGTTAATGTTGTTTCGTTTCGATCGCTCGTTTTGACCCGCTTGATGTGCGGTCTCGTTTTAGCGTACCCCGTCCGGCCTTCGTG
Cx43 > N N S S C R N Y N K Q A S E Q N W A N Y S A E Q N R M G Q A G S T

BseY1 Bsm1 BsaXb Bpm1 BsaXa
 1801 CATCTCCAACCTCGCACGCCCAGCCGTTTCGATTTCCCCGACGACAACCAGAATGCCAAAAAGTTGCTGCTGGACATGAACTCCAGCCATTAGCCATCGTG 1900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 GTAGAGGTTGAGCGTGCGGGTCGGCAAGCTAAAGGGGCTGCTGTTGGTCTTACGGTTTTTTCAACGACGACCTGTACTTGAGGTTCGGTAATCGGTAGCAC
Cx43 > I S N S H A Q P F D F P D D N Q N A K K V A A G H E L Q P L A I V

Stu1 BamH1 Age1 Bpm1 Nco1 SpDon Ale1
 1901 GACCAACGACCTTCCAGCAGAGCCAGCAGCCGCGCCAGCAGCAGGCTCGGCCTGATGACCTGGAGATTGCGGATCCACCGGTCGCCACCATGGTGAGCG 2000
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 CTGGTTGCTGGAAGGTCGTCTCGGTCGTGCGGCGGGTCGTGCTCCGGAGCCGACTACTGGACCTCTAACGCCTAGGTGGCCAGCGGTGGTACCACTCGC
**Cx43/
 FusionRed** > D Q R P S S R A S S R A S S R P R P D D L E I A D P P V A T M V S E

BsrG1 ApaL1 SpAcc
 2001 AGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCCTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGA 2100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 TCGACTAATTCTCTTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCCGGGATGCT
FusionRed > L I K E N M P 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

2101 GGGCACCCAGACCATGAGAATCAAGGTCGTGCGAGGGCGGCCCTCTCCCTTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTC 2200
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 CCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCC GCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCTGTTGGAAG
FusionRed > 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 R T F

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                                     Bsu36      SpDon      Bbs1
                                     |           |           |
2201  ATCAAGCACCCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGGCGTGCTGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
      TAGTTCGTGGGAGGCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACT
FusionRed > I K H P P 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      BseY1
                                     |           |
2301  CCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCAACGGCCCTGTGATGCAGAAGAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      GGCGATGGGTCTGTGGTCCGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTTCGGTTGCCGGGACACTACGTCTTCTT
FusionRed > A T Q D T S L 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

                                     BsmB1
                                     |
                                     BseY1  StuI  Bgl1  BssS1  Eco57
                                     |   |   |   |   |   |
2401  AACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCTGAAGCTCGTGGGCGGGGGCCAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
      TTGTGAGCCGACCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGACCTTCCGCGTACACTGTACCGGGACTTTCGAGCACCCGCCCGGGTG
FusionRed > T L G W E A S 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

                                     BpuE1      SpAcc
                                     |           |
                                     Bsa1  BpuE1  PflM1
                                     |   |   |   |
2501  CTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTGGACCACAGACTGGAAAGAATCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
      GACTAGACGTTGGAACCTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGAGATGTTGCACCTGGTGTCTGACCTTTCTTAGT
FusionRed > L I C N L E T 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

                                     Not1
                                     |
                                     Bsa1  PshA1  BssS1  Dra3  Msc1  SpDon  BsrB1  Eag1
                                     |   |   |   |   |   |   |   |
2601  AGGAGGCCGACGATGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGTATGGAGGTAAATGAGCGGCCGCGAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
      TCCTCCGGCTGCTACTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTACCTCCATTTACTCGCCGGCGCTG
FusionRed > E A D D E T Y V E Q H E V A V A R Y S T G G A G D G G K *
```

Xba1 | BsaB1 | SpDon | Dra1 | Bsm1 | Mfe1 |

2701 | TCTAGATCATAATCAGCCATAACCACATTTGTAGAGGGTTTTACTTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAAT | 2800

AGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGACTTTGGACTTTGTATTTTACTTACGTTA

Hpa1 | polyA | Pst1 | polyA | polyA | Bst1 | Bsm1 |

2801 | TGTGTTTGTTAACTTGTGTTTATTGCAGCTTATAATGGTTACAAAATAAGCAATAGCATCACAAATTTACAAAATAAGCATTTTTTTCACTGCATTCTAGT | 2900

ACAACAACAATTTGAACAATAACGTCGAATATTACCAATGTTTATTTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAATAAAAGTGACGTAAGATCA

Afl2 | SpDon | Ssp1 |

2901 | TGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTTGTTAAAATTTCGCGTTAAATTTTTGTTAAATCAGCTCATT | 3000

ACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAACAATTTTAAAGCGCAATTTAAACAATTTAGTCGAGTAAA

Pst1 | BsaXb |

3001 | TTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTAT | 3100

AAATTTGGTTATCCGCTTTAGCCGTTTTAGGGAATTTTAGTTTTCTTATCTGGCTCTATCCCAACTCACACAAGGTCAAAACCTTGTCTCAGGTGATA

Drd1 | BsaXa | BtgZ1 | Dra3 |

3101 | TAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCCTAATCAAGTTTTTTGGGGTCGAG | 3200

ATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCAGCTC

SpAcc | Nae1 | NgoM4 |

3201 | GTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCG | 3300

CACGGCATTTCGTGATTAGCTTTGGGATTTCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTTCGC

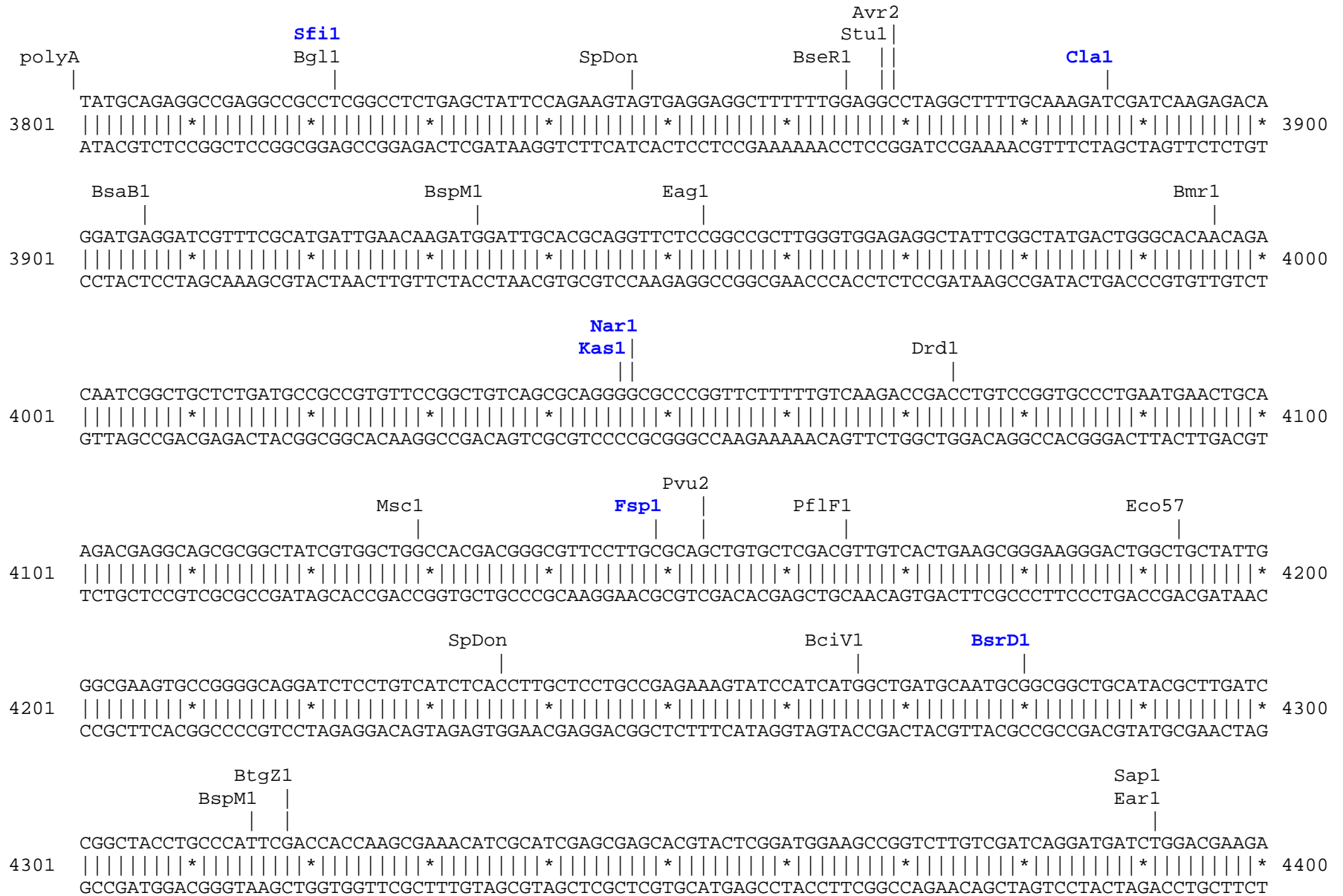
BsrB1
|
AAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTG
3301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
TTTCCTCGCCCGGATCCCGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATGTCCCGCGCAGTCCAC

polyA
|
GCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCT
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
CGTGAAAAGCCCCCTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGA

Ssp1 Ear1 Bsu36 Ecil Pvu2 BseY1
| | | | |
TCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCA
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
AGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCACACCTTTTCAGGGGTCCGAGGGGTCCGTCCGT

Nsil Sph1 BfrB1 BstAP SexA1 BseY1 BstAP Sph1 BfrB1 Nsil
| | | | | | | | | | | | | | |
GAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTA
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CTTCATACGTTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCCGAGGGGTCCGTCCGTCTTCATACGTTTTCGTACGTAGAGTTAAT

Ecil Ecil Bmr1 Ecil Nco1
| | | | |
GTCAGCAACCATAGTCCC GCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCAGTTCCGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTATT
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
CAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAATAA



BpuE1 Sph1 Nco1 BtgZ1
GCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGCCG
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
CGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGC

BseY1
Nae1 |
NgoM4 | | Rsr2 | Eci1 |
AATATCATGGTGGAAAATGGCCGCTTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATA
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
TTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTAT

Sap1 BtgZ1
Ear1 Eco57 BssS1 BsrB1 |
TTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGA
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
AACGACTTCTCGAACCGCGCTTACCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACT

BssS1 BspM1 SpAcc
BsrB1 BstB1 |
CGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAA
4701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
GCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTT

Nae1 Bpm1
NgoM4 | SpAcc |
Bpm1 | Avr2 |
GGTTGGGCTTCGGAATCGTTTTCCGGGACCGCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAAC
4801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
CCAACCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTG

```

                                polyA      polyA
                                |           |
4901  TGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCGTTTGTTCATAAACGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
      ACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCCTGCCACAACCCAGCAAACAAGTATTTGCG

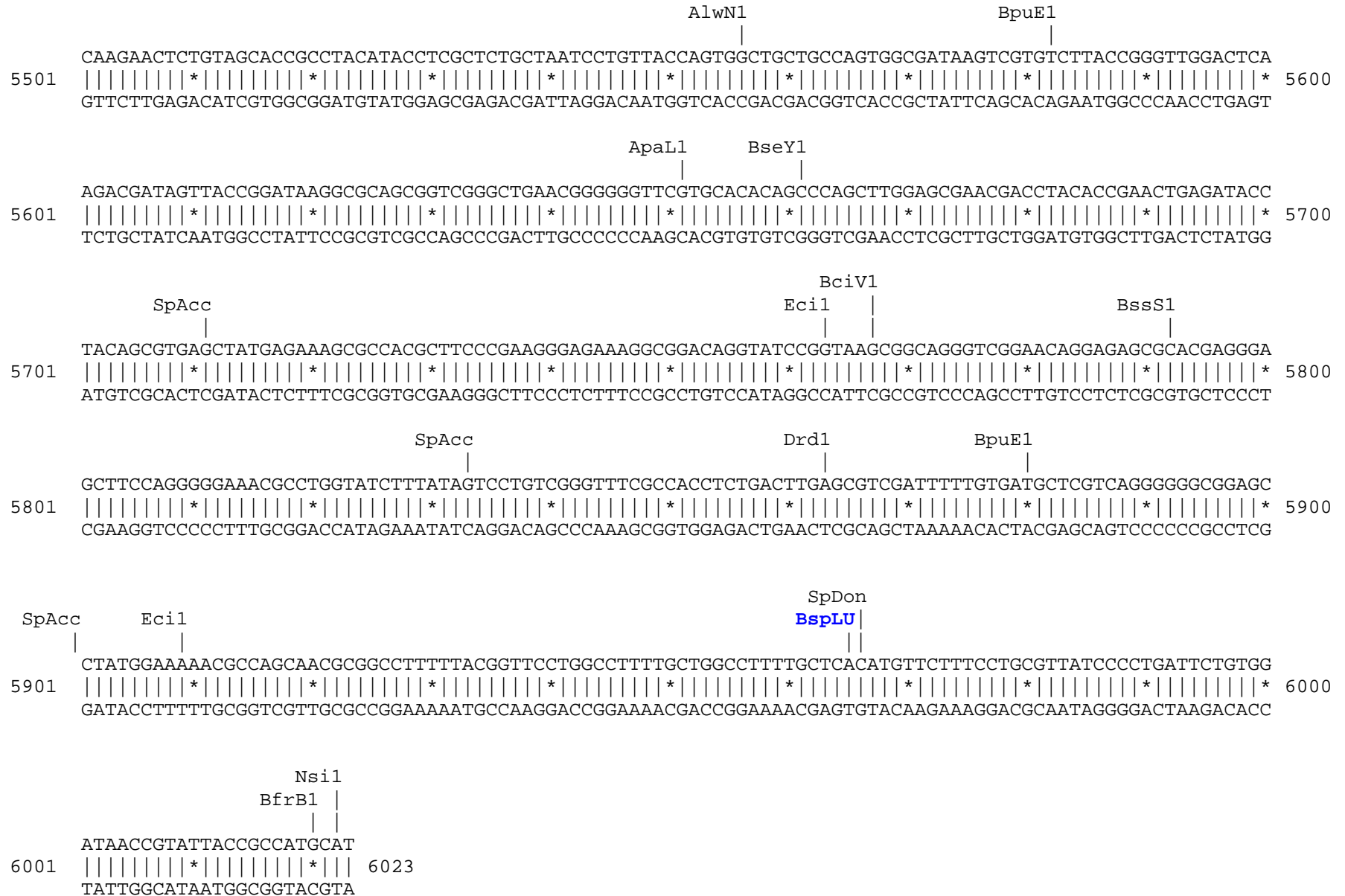
                                Bsa1
                                |
5001  GGGGTTTCGGTCCCAGGGCTGGCACTCTGTTCGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTTCTTCTTTTCCCACCCACCCCCCAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
      CCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTT

                                BstAP      AlwN1      Bsu36      Dra1
                                |           |           |           |
5101  GTTCGGGTGAAGGCCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
      CAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGT

                                Dra1      BspH1
                                |           |
5201  TTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAAAGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
      AAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCAT

                                BpuE1
                                |
5301  GAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
      CTTTTCTAGTTTTCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTGCACCAAAACAAACGGCC

                                Eco57      SpAcc
                                |           |
5401  ATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
      TAGTTCFCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAA
```



Found:

Aar1	Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Asc1	Ase1	Avr2	BamH1	Bbs1	BciV1
BfrB1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BsmB1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
_Chi	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	Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfi1	SnaB1	SpAcc	SpDon	Sph1	Ssp1
Stu1	Xba1	Xcm1	Xho1	Xmn1									

Unique:

Aar1	Afe1	Afl2	Age1	Ale1	Asc1	Ase1	BamH1	Bgl2	BmgB1	BsmB1	BspLU	BsrD1	BsrG1
BssH2	Bts1	_Chi	Clal	EcoR1	Fsp1	Hpa1	Kas1	Mfe1	Nar1	Nde1	Not1	PflM1	Pml1
PshA1	Rsr2	Sfi1	SnaB1	Xba1	Xcm1	Xho1	Xmn1						

Not found:

Acc65	Acl1	Ahd1	Apa1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Bcl1	Blp1	Bpu10	Bsg1
BsiW1	BspE1	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	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	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													