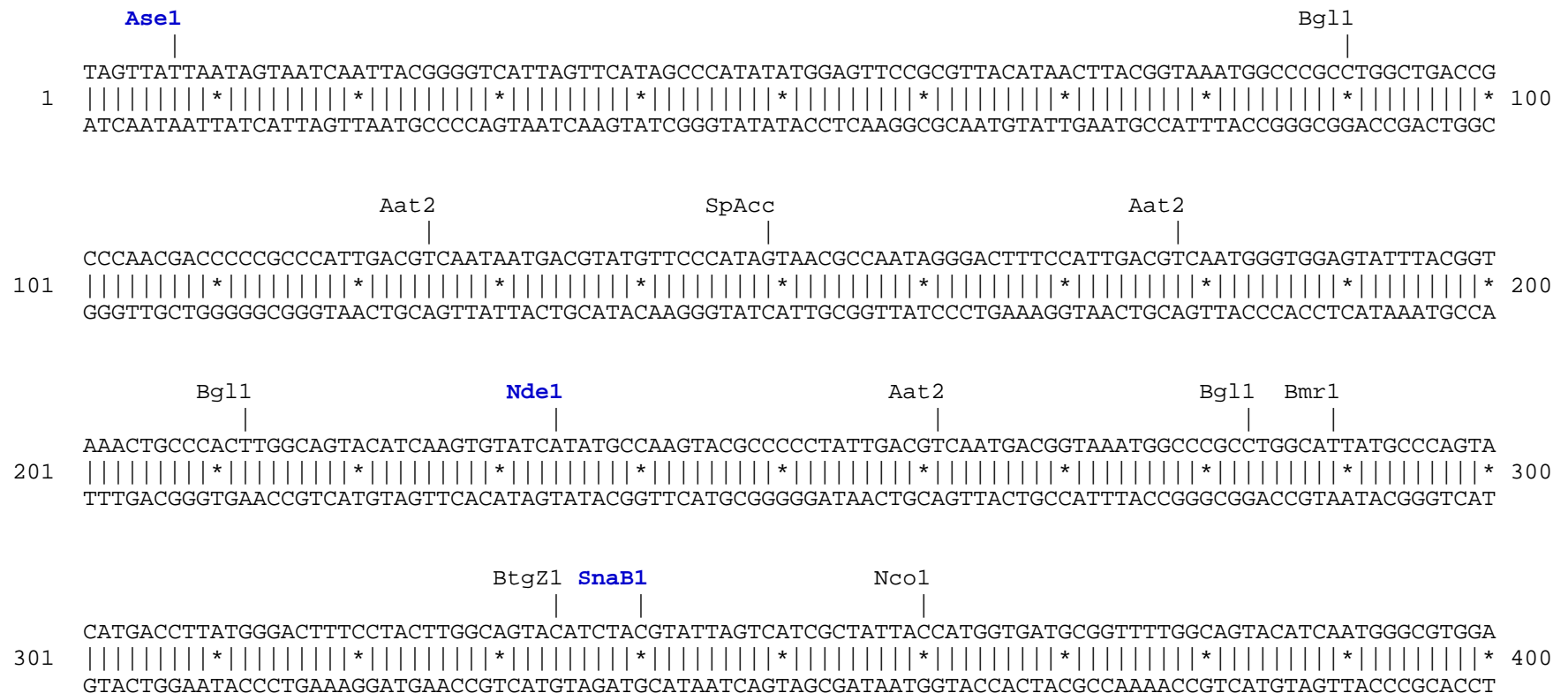


**pTagFP635-zyxin** vector restriction map

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). TagFP635 amino acids are shown in red, Zyxin amino acids are shown in green, linker amino acids are shown in black.



Aat2 Eci1

401 TAGCGGTTTACTCACGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAAATCAACGGGACTTTCCAAAATGTCGTA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 500  
 ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

Nhe1 Afel

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 600  
 TGTGAGGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Xho1 Hind3 EcoR1  
 BpuE1 Bgl2 Sac1 BstB1 Nco1 BsmB1 Bsa1

601 CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCATGGCGGCCCCCGCCCGTCTCCCGCGATCCCCGTTTCGGTCTCGGCTCCGGCTTTTTACGCCCC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 700  
 GGCTTGAGTCTAGAGCTCGAGTTTCAAGCTTAAAGGTACCGCCGGGGGGCGGGCAGAGGGCGCTAGGGGCAAAGCCAGAGCCGAGGCCGAAAAATGCGGGG

Zyxin > M A A P R P S P A I P V S V S A P A F Y A P

BssH2  
 Apa1  
 BseY1  
 PspOM  
 Sma1

Xmn1 SpDon Xmn1

701 GCAGAAGAAGTTCGGCCCTGTGGTGGCCCCAAAGCCAAAGTGAATCCCTTCCGGCCCAGGGACAGCGAGCCTCCCCCGGCACCCGGGGCCCAGCGCGCA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 800  
 CGTCTTCTTCAAGCCGGGACACCACCGGGGTTTCGGGTTTCACTTAGGGAAGGCCGGGTCCCTGTGCGCTCGGAGGGGGCCGTGGGCCCCGGGTTCGCGCGT

Zyxin > Q K K F G P V V A P K P K V N P F R P R D S E P P P A P G A Q R A

Bbs1  
 Bgl1 Xmn1 BseY1 BstAP

801 CAGATGGGCCGGGTGGGCGATATTCCCCCGCCCGCCCCGGAAGACTTTCCCTGCCTCCACCTCCCCTTGCTGGGGATGGCGACGATGCAGAGGGTGCTC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 900  
 GTCTACCCGGCCACCCGCTATAAGGGGGCGGGGGGCTTCTGAAAGGGGACGGAGGTGGAGGGGAACGACCCTACCGCTGCTACGTCTCCACGAG

Zyxin > Q M G R V G D I P P P P P E D F P L P P P P L A G D G D D A E G A L

```

                                     BseR1
                                     BseR1 |
                                     Bpm1 |
                                     BseR1 |
          Pvu1   Xmn1           SpAcc   Bgl2   BseR1   |   BspE1
          |       |           |         |       |   |
          |       |           |         |       |   |
          |       |           |         |       |   |
TGGGAGGTGCCTTCCCCGCCGCCCTCCCCGATCGAGGAATCATTTCCCCCTGCGCCTCTGGAGGAGGAGATCTTCCCTTCCCCGCCGCCTCCTCCGGA
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
ACCTCCACGGAAGGGCGGCGGGGAGGGGGCTAGCTCCTTAGTAAAGGGGACGCGGAGACCTCCTCCTCTAGAAGGGAAGGGGCGGCGGAGGAGGCCT
Zyxin > 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
          |       |
          |       |
          |       |
GGAGGAGGGAGGGCCTGAGGCCCCCATACCGCCCCACACAGCCCAGGGAGAAGGTGAGCAGTATTGATTTGGAGATCGACTCTCTGTCTACTGCTG
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CCTCCTCCCTCCCGGACTCCGGGGTATGGCGGGGTGGTGTCTGGGTCCCTCTTCCACTCGTTCATAACTAAACCTCTAGCTGAGAGACAGGAGTGACGAC
Zyxin > 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
          |
          |
          |
GATGACATGACCAAGAATGATCCTTTCAAAGCCCGGGTGTCTTGGATATGTGCCCCACCAGTGGCCACTCCATTTCAGTTCCAAGTCCAGTACCAAGC
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTACTGTACTGGTTCTTACTAGGAAAGTTTCGGGCCCACAGTAGACCTATACACGGGGTGGTTCACCGGTGAGGTAAGTCAAGGTTTCAGGTCATGGTTTCG
Zyxin > 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
          |
          SpAcc   BseY1   AlwN1
          |       |       |
          |       |       |
          |       |       |
CTGCAGCCGGGGCACAGCACCCCTGCCTCCTTGAAGTCCCCTTCCAGCTCCCAGCCTCTGCCCCAGGTTCCGGCTCCGGCTCAGAGCCAGACACAGTT
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GACGTCGGCCCCGTGTCGTGGGGACGGAGGAACCTTCAGGGGAAGGTCGAGGGTCGGAGACGGGGTCCAAGGCCGAGGCCGAGTCTCGGTCTGTGTCAA
Zyxin > A A G G T A P L P P W K S P S S Q P L P Q V P A P A Q S Q T Q F
```

```
                                     BseY1 BseY1          Bsu36          BseY1          BseY1          PspOM          Apal
                                     |   |           |           |           |           |   |           |
1301 CCATGTTTCAGCCCCAGCCCCAGCCCCAAGCCTCAGGTCCAACCTCCATGTCCAGTCCCAGACCCAGCCTGTGTCTTTGGCTAACACCCAGCCCCGAGGGCCC 1400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGTACAAGTCGGGGTCGGGGTCGGGTTCGGAGTCCAGGTTGAGGTACAGGTTCAGGGTCTGGGTTCGGACACAGAAACCGATTGTGGGTTCGGGGCTCCCGGG
Zyxin > 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
BseY1 |           Bpm1           SpAcc
      |           |           |
1401 CCAGCCTCATCTCCGGCTCCAGCCCCTAAGTTTTTCTCCAGTGACTCCTAAGTTTACTCCTGTGGCTTCCAAGTTCAGTCTGGAGCCCCAGGTGGATCTG 1500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGTCGGAGTAGAGGCCGAGGTTCGGGGATTCAAAAAGAGGTCACTGAGGATTCAAATGAGGACACCGAAGGTTCAAGTCAGGACCTCGGGGTCCACCTAGAC
Zyxin > 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 GGTCACAACCAAATCAAAAATTGGGGCACCCCGAAGCTCTTTCTGCTGGCACAGGCTCCCCTCAACCTCCCAGCTTACCTATGCCAGCAGAGGGAGAA 1600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCAGTGTGGTTTAGTTTTTAACCCCGTGGGGCTTCGAGAAAGACGACCGTGTCCGAGGGGAGTTGGAGGGTCAAGTGGATAACGGGTTCGTCTCCCTCTT
Zyxin > 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          Apal          PspOM          SpAcc
          |           |           |           |           |           |           |           |
1601 GCCCGAGTGCAGGAGAAGCAGCACCCCGTGGCCCCACCGGCTCAGAACCAAAACCAGGTGCGCTCCCCTGGGGCCCCAGGGCCCCCTGACTCTGAAGGAG 1700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGGGGCTCACGTCTCTTCGTTCGTGGGGCACGGGGTGGCCGAGTCTTGGTTTTGGTCCACGCGAGGGGACCCCGGGGTCCCAGGGGACTGAGACTTCTC
Zyxin > 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
  CACCTCCTCGACCTCGTCGACTGGGTCGTCGATTACGTCTGTACCTCGTAGGAGTCTCCGTCTTACACCGACAGTTGCTTGAGACGCCGGCTACGGTAG
Zyxin > 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
          BfuA1
          Srf1
          Sma1
          BtgZ1
          Pvu2
          SpDon
          Aar1
          Fsp1
1801 AACCCCTGGCCCGGGCGCAGCCAGCCGTCGCGCTCTAGGGCAGCTGTTCCACATCGCCTTGCCTTACCTGCCACCAGTGTGCGCAGCAGCTCCAGGGCCA
  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
  TTGGGGACCGGGCCCGCTCGGTCGCGCAGGCGCGAGATCCCGTCGACAAGGTGTAGCGGACGAAGTGGACGGTGGTTCACACGCGTCGTCGAGGTCCCGGT
Zyxin > 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
          BfuA1
          Aar1
          Nar1
          SpAcc
          Kas1
          SpAcc
          Bpm1
          SpAcc
          SpAcc
          Bpm1
          Aar1
1901 GCAGTTCTACAGTCTGGAGGGGGCGCCGTACTIONTACTGCGAGGGCTGTTACTACTGACACCCTGGAGAAGTGTAACACCTGCGGGGAGCCCATCACTGACCGCATG
  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
  CGTCAAGATGTCAGACCTCCCCCGGCATGACGCTCCCGACAATGTGACTGTGGGACCTCTTACATTGTGGACGCCCCTCGGGTAGTGACTGGCGTAC
Zyxin > 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
          Ale1
          Bpm1
2001 CTGAGGGCCACGGGCAAGGCCTATCACCCGCACTGCTTACCTGTGTGGTCTGCGCCCGCCCTGGAGGGCACCTCCTTCATCGTGGACCAGGCCAACC
  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
  GACTCCCGGTGCCCCGTTCCGGATAGTGGGCGTGACGAAGTGGACACACCAGACGCGGGCGGGGACCTCCCGTGAGGAAGTAGCACCTGGTCCGGTTGG
Zyxin > 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
```

```

                                     Bpu10
                                     |
GGCCCCACTGTGTCCCCGACTACCACAAGCAGTACGCCCCGAGGTGCTCCGTCTGCTCTGAGCCCATCATGCCTGAGCCTGGCCGAGATGAGACTGTGCG
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
CCGGGGTGACACAGGGGCTGATGGTGTTCGTCATGCGGGGCTCCACGAGGCAGACGAGACTCGGGTAGTACGGACTCGGACCGGCTCTACTCTGACACGC
Zyxin > P H C V P D Y H K Q Y A P R C S V C S E P I M P E P G R D E T V R

                                     SpAcc
                                     |
AGTGGTCGCCCTGGACAAGAACTTCCACATGAAGTGTTACAAGTGTGAGGACTGCGGGAAGCCCCTGTTCGATTGAGGCAGATGACAATGGCTGCTTCCCC
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
TCACCAGCGGGACCTGTTCTTGAAGGTGTACTTCACAATGTTCACTCCTGACGCCCTTCGGGGACAGCTAACTCCGTCTACTGTTACCGACGAAGGGG
Zyxin > V V A L D K N F H M K C Y K C E D C G K P L S I E A D D N G C F P

                                     Pml1          Bts1          BamH1  Agel          Ale1          Sap1
                                     |          |          |          |          |          |
CTGGACGGTCACGTGCTCTGTTCGGAAGTGCCACACTGCTAGAGCCCAGACGGATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGG
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
GACCTGCCAGTGCACGAGACAGCCTTTCACGGTGTGACGATCTCGGGTCTGCCTAGGTGGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCC
Zyxin/TagFP635>L D G H V L C R K C H T A R A Q T D P P V A T M V S K G E E L I K E

                                     BsrG1          ApaL1          SpAcc
                                     |          |          |
AGAACATGCACATGAAGCTGTACATGGAGGGCACCCTGAACAACCACACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCAGCCAGAC
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
TCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCCGGGATGCTCCCGTGGGTCTG
TagFP635 > 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 G T Q T

                                     Bsu36          SpDon          Bbs1          Bpm1
                                     |          |          |          |
CAGGGCATCCCCGACTTCTTTAAGCAGTCCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGCGTGCTGACCGCTACCCAGG
2601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
GTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCGCACGACTGGCGATGGGTCC
TagFP635 > 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 A T Q D

```

```

                                                                                                     BseY1
                                                                                                     |
ACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTG
2701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
TGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGAC
TagFP635 > 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 T L G W

StuI           BglI           BssS1           Eco57
|             |             |             |
GGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAAC
2801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
CCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCGCCGACCTTCCGTCTTCGCTGTACCGGGACTTCGAGCACCCCGCCCCGGTGGACTAGACGTTG
TagFP635 > 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 L I C N

                                                                                                     Bbs1
                                                                                                     |
                                                                                                     SpAcc
                                                                                                     |
TTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACA
2901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
AACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGTCTTCTGACCTTTCTTAGTTTCTCCGGCTGT
TagFP635 > 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 E A D K

                                                                                                     Not1
                                                                                                     |
                                                                                                     Eag1
                                                                                                     |
                                                                                                     BsrB1
                                                                                                     |
                                                                                                     XbaI
                                                                                                     |
PshA1           BssS1 Dra3           MscI           AlwN1           SpAcc           BsrB1           XbaI
|             |             |             |             |             |             |             |
AAGAGACCTACGTTCGAGCAGCAGGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAATCTGGGGCACAACTTAATTGAGCGGCCGCGACTCTAGA
3001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
TTCTCTGGATGCAGCTCGTTCGTGCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTAGACCCCGTGTGTTGAATTAAGTTCGCCGGCGCTGAGATCT
TagFP635 > E T Y V E Q H E V A V A R Y C D L P S N L G H K L N *

                                                                                                     Bsm1
                                                                                                     |
                                                                                                     MfeI
                                                                                                     |
BsaB1           SpDon           DraI           MfeI
|             |             |             |             |
TCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTTGCTTTAAAAAACCCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGT
3101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
AGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACA
```

Hpa1 polyA PstI polyA polyA BtsI BsmI  
TGTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTACAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGT  
3201 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3300  
ACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCA

Afl2 SpDon Ssp1  
TTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTTAAC  
3301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3400  
AACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAACAATTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTG

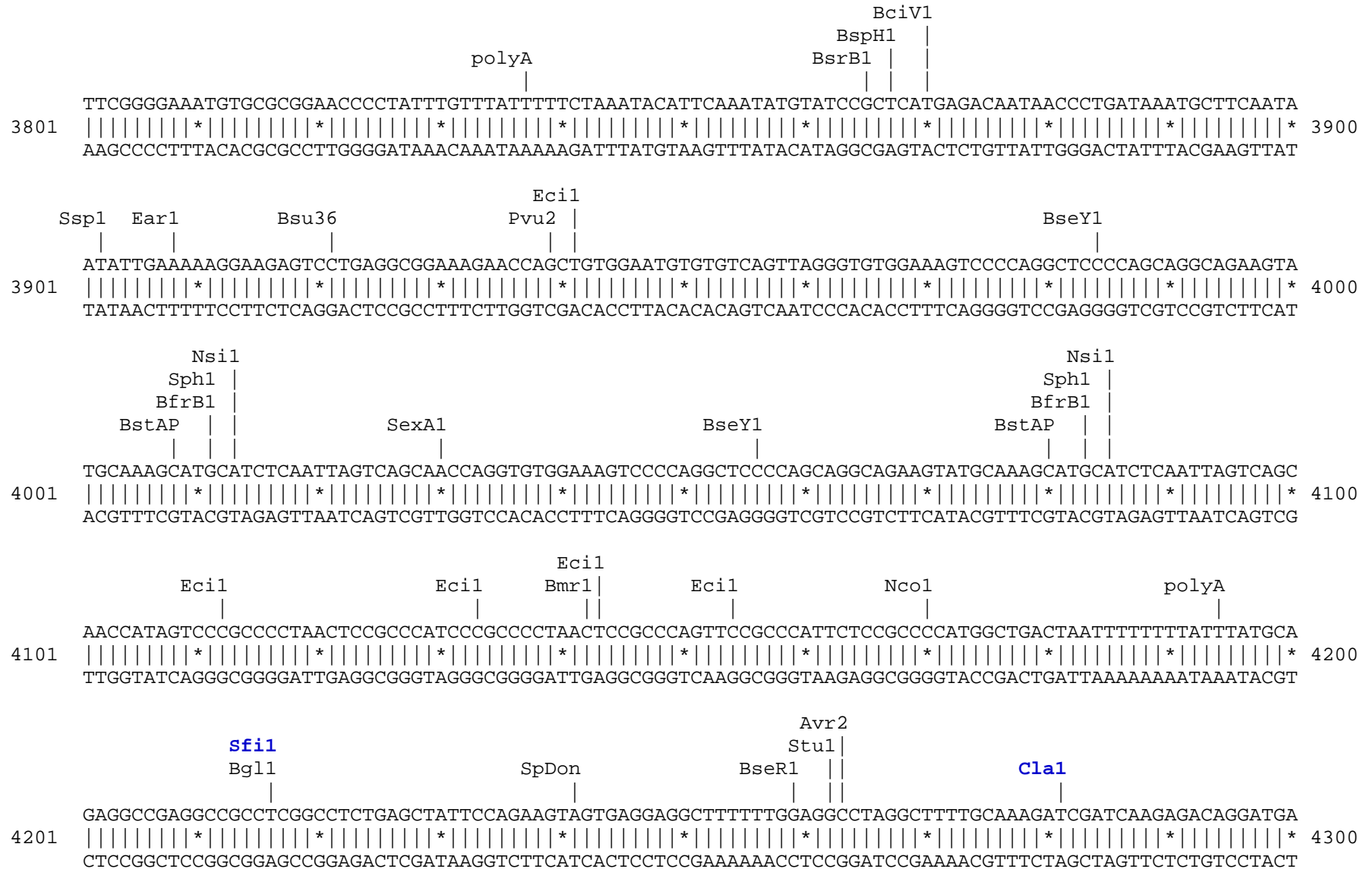
PstI BsaXb  
CAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGA  
3401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3500  
GTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCT

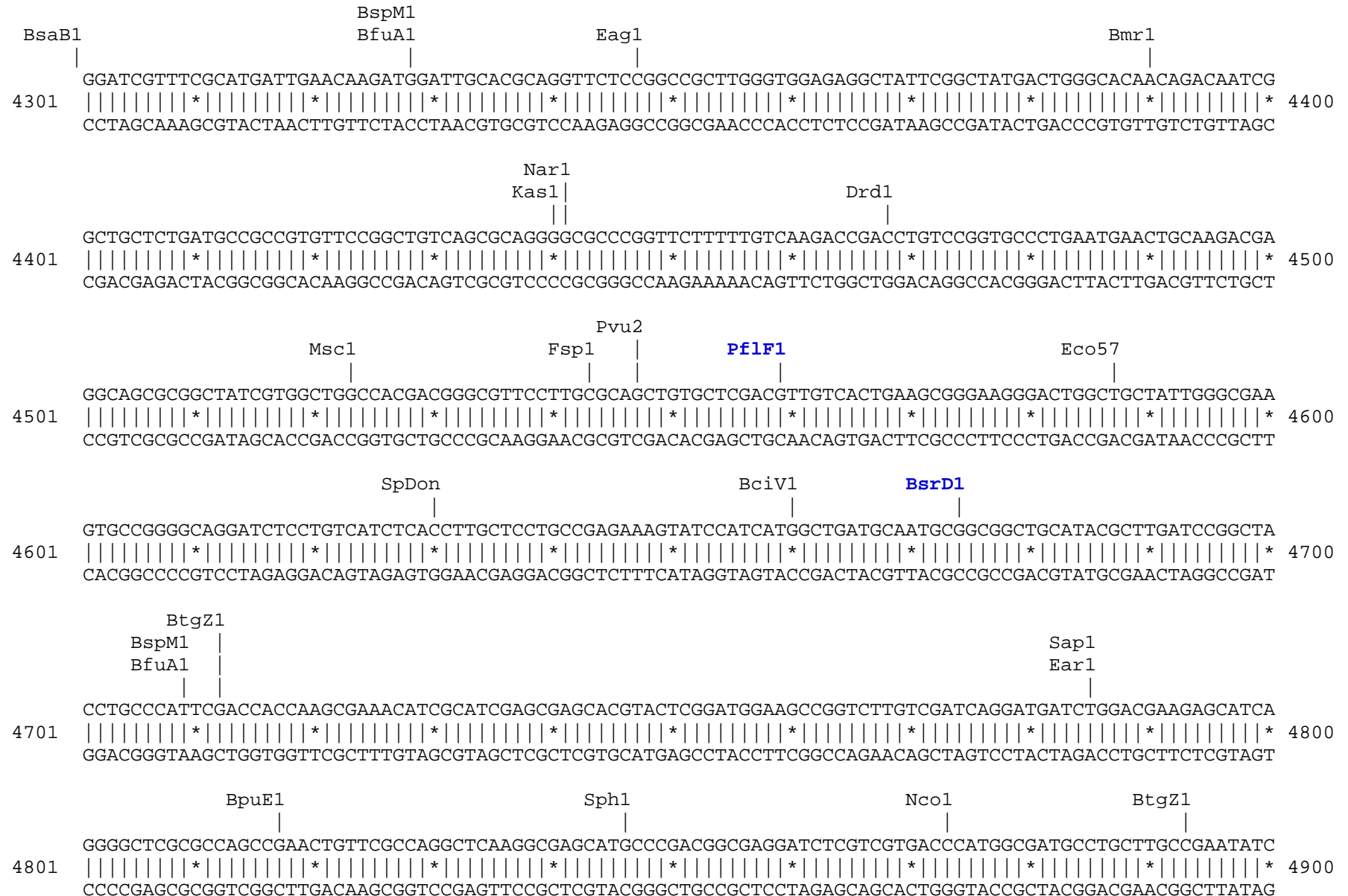
Drd1 BsaXa BtgZ1 Dra3  
ACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCG  
3501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3600  
TGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGC

SpAcc NaeI NgoM4  
TAAAGCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGA  
3601 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3700  
ATTTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGACCCGCTCTTTCTTCCCTTCTTTTCGCTTTTCT

BsrB1  
GCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACCCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTTCAGGTGGCACTT  
3701 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3800  
CGCCCGGATCCCGCGACCGTTACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAA











```

                                     ApaL1   BseY1
                                     |       |
6001 TAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6100
   ATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCTGGGTCTGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCTG

                                     BciV1
                                     |   |
   SpAcc                               Eci1   |                               BssS1
   |                                     |   |                               |
6101 GTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCTGGAACAGGAGAGCGCACGAGGGAGCTTCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6200
   CACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGTCTCCCTCGAAGG

                                     SpAcc                               Drd1   BpuE1                               SpAcc
                                     |                               |   |                               |   |                               |
6201 AGGGGGAAACGCCTGGTATCTTTATAGTCTGTCTCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6300
   TCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATAACC

                                     SpDon
                                     |   |
   Eci1                               BspLU
   |                                   |   |
6301 AAAAAAGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6400
   TTTTTCGCGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGG

                                     Nsil
                                     |   |
   BfrB1
   |   |
6401 GTATTACCGCCATGCAT 6417
   |||||*|||||
   CATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ahd1</b>	Ale1	AlwN1	Apa1	Apal1	<b>Ase1</b>	Avr2	<b>BamH1</b>	Bbs1
<b>BbvC1</b>	BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>
BseR1	BseY1	<b>Bsg1</b>	Bsm1	<b>BsmB1</b>	<b>BspE1</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	<b>BssH2</b>	BssS1
BstAP	BstB1	Bsu36	BtgZ1	Bts1	<b>Clal</b>	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	<b>EcoR1</b>
Fsp1	<b>Hind3</b>	<b>Hpa1</b>	Kas1	<b>Mfe1</b>	Msc1	Nae1	Nar1	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1
<b>PflF1</b>	<b>Pml1</b>	polyA	<b>PshA1</b>	Psil	PspOM	<b>Pst1</b>	<b>Pvu1</b>	Pvu2	<b>Rsr2</b>	<b>Sac1</b>	Sap1	SexA1	<b>Sfi1</b>
Sma1	<b>SnaB1</b>	SpAcc	SpDon	Sph1	<b>Srf1</b>	Ssp1	Stul	<b>Xba1</b>	<b>Xho1</b>	Xmn1			

Unique:

<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ahd1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>BbvC1</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>Bsg1</b>	<b>BsmB1</b>	<b>BspE1</b>	<b>BspLU</b>	<b>BsrD1</b>
<b>BsrG1</b>	<b>BssH2</b>	<b>Clal</b>	<b>EcoR1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Mfe1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>Pml1</b>	<b>PshA1</b>	<b>Pst1</b>
<b>Pvu1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sfi1</b>	<b>SnaB1</b>	<b>Srf1</b>	<b>Xba1</b>	<b>Xho1</b>						

Not found:

Acc65	Acl1	Asc1	AsiS1	Baela	Baelb	BcglA	Bcglb	Bcl1	Blp1	BmgB1	BsiW1	BstE2	BstX1
BstZ1	_Chi	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1
loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1
Sca1	Sgf1	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	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													