

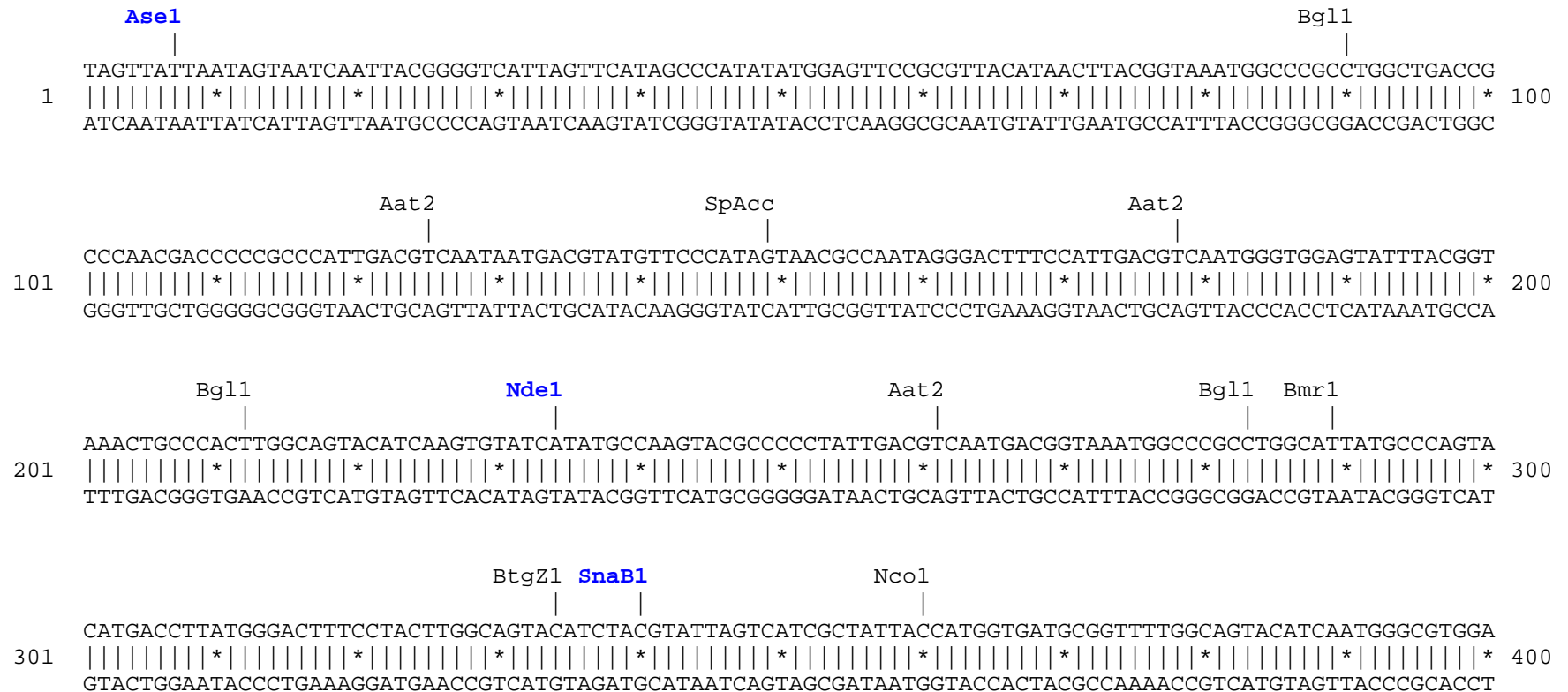
### pFusionRed-Cx43 vector restriction map

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.



Aat2 Eci1

```

TAGCGGTTTGACTCACGGGATTTC AAGTCTCCACCCATTGACGTCAATGGGAGTTTGTTTTGGCACC AAAATCAACGGGACTTTCCAAAATGTCGTA
| | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
401 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
ATCGCCAAACTGAGTGCCCTAAAGGTT CAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
    
```

```

ACA ACTCCGCCCATTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
| | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
501 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TGTTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
    
```

Nhe1 **Afe1**

Hind3

**Xho1** Sac1 **EcoR1**

BpuE1 **Bgl2** Ecl2 BstB1 Dra1

```

CCG GACTCAGATCTCGAGCTCAAGCTTCGAATTCGGCAGCACTTTCTTTTCATTGGGGGGAAGGCGTGAGGAAAGTACCAAACAGCAGCAGACTTTTAAA
| | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
601 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GGCCTGAGTCTAGAGCTCGAGTTTCAAGCTTAAGCCGTCGTGAAAAGAAAGTAAACCCCTTCCGCACTCCTTTTCATGGTTTTGTCGTCGTCTGAAAATTT
    
```

Nae1

**BssH2** NgoM4

Dra1 **Asc1** Eco57 SpDon

```

CTTTAAACAGACAGGTCTGAGAGCCTGAACTCTCATTTTTCTTTGACTTCAGCCTCCAAGGAGTTCCACCAACTTTGGCGCGCCGGCTTCACCTTTTCATT
| | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
701 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
GAAATTTGTCTGTCCAGACTCTCGGACTTGAGAGTAAAAAGGAACTGAAGTCGGAGGTTCTCAAGGTGGTTGAAACCGCGCGCCGAAGTGAAAGTAA
    
```

Hind3 Bpm1 PflF1 BsaXaSpAcc

```

AAGTAAAAGAGAGGTGCCAGACATGGGTGACTGGAGTGCCTTGGGGAAGCTTCTGGACAAGGTCCAAGCCTACTCCACCGCTGGAGGGAAGGTGTGGCT
| | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
801 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
TTCACTTTCTCTCCACGGGTCTGTACCCACTGACCTCACGGAACCCCTTCAAGACCTGTTCCAGGTTTCGGATGAGGTGGCGACCTCCCTTCCACACCGGA
    
```

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





Xmn1 BssS1 Nhe1 Bmr1  
GAAACAATTCTCGTGCCGCAATTACAACAAGCAAGCTAGCGAGCAAACTGGGCGAACTACAGCGCAGAGCAAAATCGCATGGGGCAGGCCGGAAGCAC  
1701 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1800  
CTTTGTTAAGGAGCACGGCGTTAATGTTGTTTCGTTTCGATCGCTCGTTTTGACCCGCTTGATGTGCGGTCTCGTTTTAGCGTACCCCGTCCGGCCTTCGTG  
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  
CATCTCCAACCTCGCACGCCAGCCGTTTCGATTTCCCCGACGACAACCAGAATGCCAAAAAAGTTGCTGCTGGACATGAACTCCAGCCATTAGCCATCGTG  
1801 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 1900  
GTAGAGGTTGAGCGTGCGGGTCGGCAAGCTAAAGGGGCTGCTGTTGGTCTTACGGTTTTTTCAACGACGACCTGTACTTGAGGTGCGTAATCGGTAGCAC  
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

StuI BamHI AgeI Bpm1 NcoI SpDon Ale1  
GACCAACGACCTTCCAGCAGAGCCAGCAGCCGCGCCAGCAGCAGGCCTCGGCCTGATGACCTGGAGATTGCGGATCCACCGGTCGCCACCATGGTGAGCG  
1901 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2000  
CTGGTTGCTGGAAGGTCGTCTCGGTGCTCGGC GGGTCTGCTCGGAGCCGGACTACTGGACCTCTAACGCTAGGTGGCCAGCGGTGGTACCACTCGC  
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  
AGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGA  
2001 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2100  
TCGACTAATTCTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCCGGGATGCT  
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

GGCACCCAGACCATGAGAATCAAGGTCGTGAGGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTC  
2101 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 2200  
CCCGTGGGTCGGTACTCTTAGTTCCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCGTCTTGGGAAG  
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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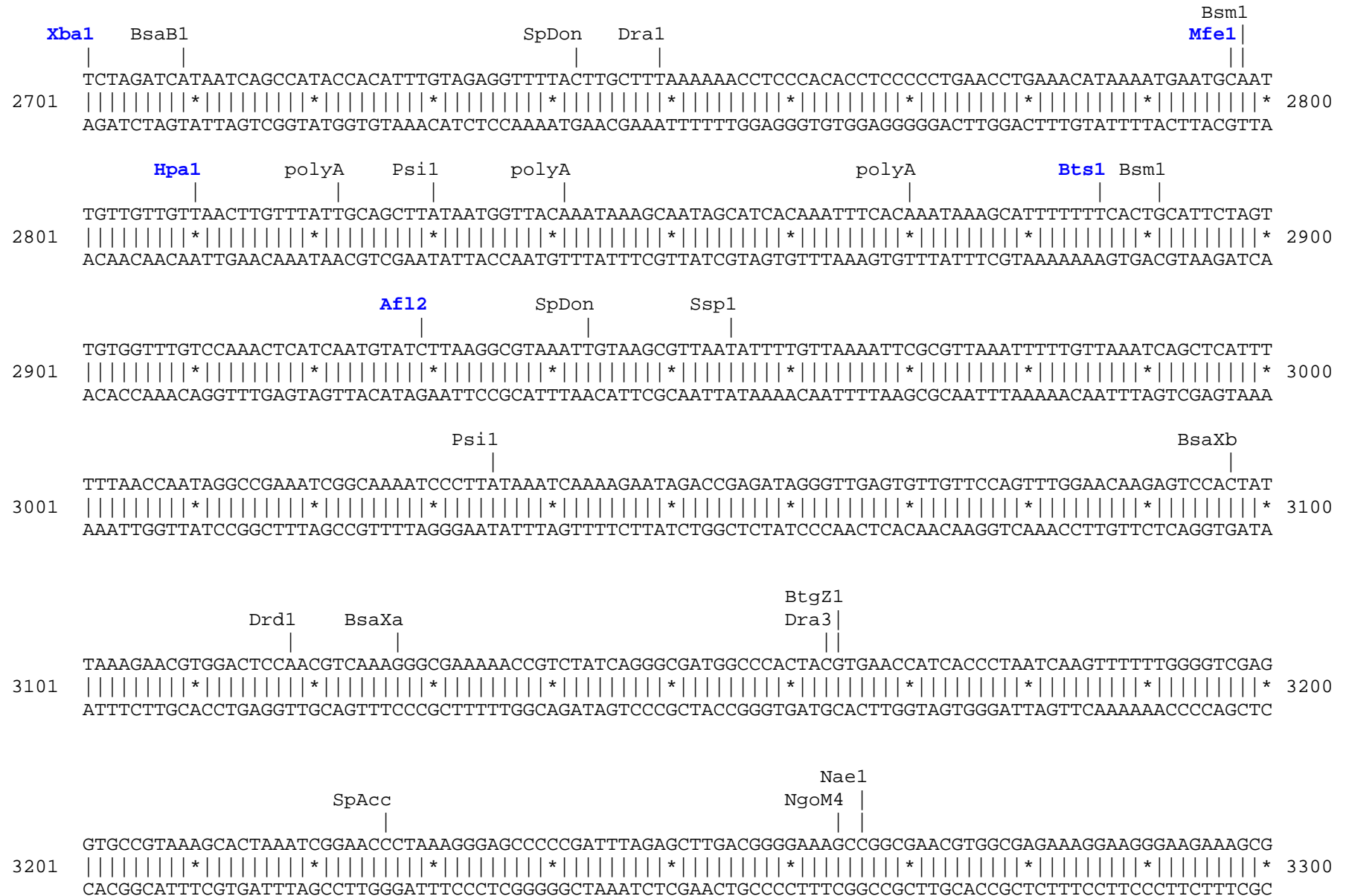
                                     Bsu36      SpDon      Bbs1
                                     |           |           |
2201 ATCAAGCACCCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGGCGTGCTGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
    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
    GGCGATGGGTCTGTGGTTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTTCGGTTGCCGGGACACTACGTCTTCTT
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      BglI      BssS1      Eco57
                                     |   |       |       |       |       |
2401 AACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCTGAAGCTCGTGGGCGGGGGCCAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
    TTGTGAGCCGACCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGACTTTCGAGCACCCGCCCGGGTG
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
                                     |           |
                                     BsaI      BpuE1      PflM1
                                     |   |       |       |
2501 CTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTGGACCACAGACTGGAAAGAATCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
    GACTAGACGTTGGAACCTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGCAGATGTTGCACCTGGTGTCTGACCTTTCTTAGT
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

                                     NotI
                                     |
                                     BsaI      PshA1      BssS1  Dra3      MscI      SpDon      EagI      BsrB1
                                     |   |       |   |       |   |       |       |       |       |       |
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 *
```



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

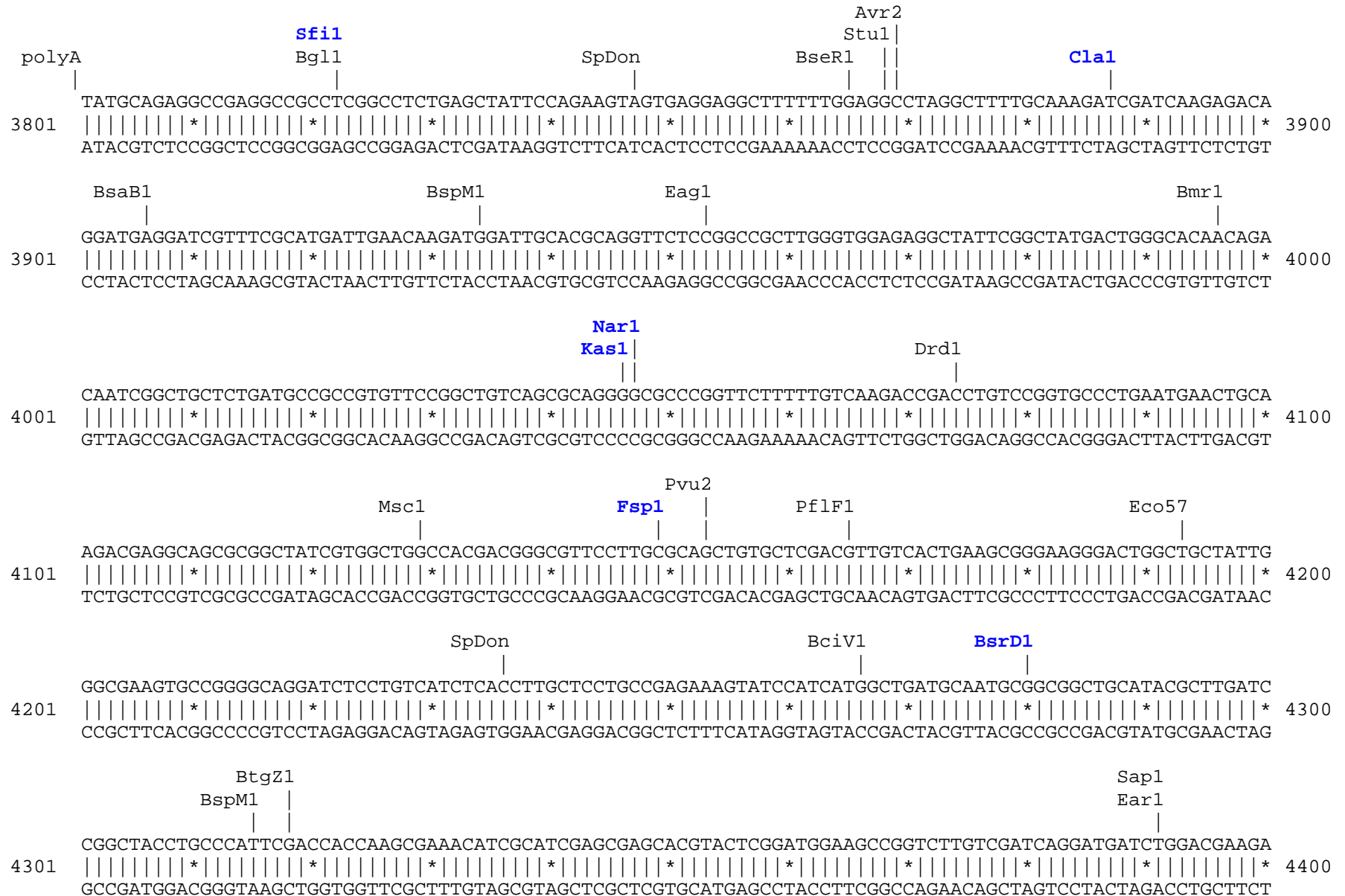
polyA  
|  
GCACTTTTTCGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCT  
3401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3500  
CGTGAAAAGCCCCCTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGA

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

Nsil Sph1 BfrB1 BstAP SexA1 BseY1 BstAP Sph1 BfrB1 Nsil  
| | | | | | | | | | | | | | |  
GAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTA  
3601 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3700  
CTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCCGAGGGGTCCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAAT

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





BpuE1 Sph1 Nco1 BtgZ1  
GCATCAGGGGCTCGCGCCAGCCGAACCTGTTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGCCG  
4401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4500  
CGTAGTCCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGC

BseY1  
Nae1 |  
NgoM4 | | Rsr2 | Ecil |  
AATATCATGGTGGAAAATGGCCGCTTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATA  
4501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4600  
TTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTAT

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

BssS1  
BsrB1 | BstB1 | BspM1 | SpAcc |  
CGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAA  
4701 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4800  
GCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTT

Nae1  
NgoM4 | Bpm1 | Bpm1 | SpAcc | Avr2 |  
GGTTGGGCTTCGGAATCGTTTTCCGGGACCGCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAAC  
4801 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4900  
CCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTG

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                                polyA      polyA
                                |           |
TGA AACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCGTTTGTTCATAAACGC
4901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5000
ACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGC GTGCCACAACCCAGCAAACAAGTATTTGCG

                                Bsa1
                                |
GGGGTTCGGTCCCAGGGCTGGCACTCTGTTCGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTTCTTCTTTTTCCCACCCACCCCCCAA
5001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5100
CCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTT

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

                                Dra1      BspH1
                                |           |
TTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTA
5201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5300
AAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCAT

                                BpuE1
                                |
GAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGG
5301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5400
CTTTTCTAGTTTTCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTGCACCAAAACAAACGGCC

                                Eco57      SpAcc
                                |           |
ATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTT
5401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5500
TAGTTCFCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAA

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                                     AlwN1                               BpuE1
CAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCA
5501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
GTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGT

                                     ApaL1           BseY1
AGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATAACC
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
TCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGG

                                     BciV1
                                     Eci1           BssS1
SpAcc
TACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGA
5701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
ATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCT

                                     SpAcc           Drd1           BpuE1
GCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGC
5801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5900
CGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCG

                                     SpDon
SpAcc           Eci1
CTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTTGGCCTTTTGGCTGGCCTTTTGTCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGG
5901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6000
GATACCTTTTTGCGGTCTTTCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACC

                                     NsiI
                                     BfrB1
ATAACCGTATTACCGCCATGCAT
6001 |||||*|||||*||||| 6023
TATTGGCATAATGGCGGTACGTA

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Found:

<b>Aar1</b>	Aat2	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	AlwN1	ApaL1	<b>Asc1</b>	<b>Ase1</b>	Avr2	<b>BamH1</b>	Bbs1	BciV1
BfrB1	Bgl1	<b>Bgl2</b>	<b>BmgB1</b>	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
<b>BsmB1</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	<b>BsrG1</b>	<b>BssH2</b>	BssS1	BstAP	BstB1	Bsu36	BtgZ1	<b>Bts1</b>
<b>_Chi</b>	<b>Clal</b>	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	<b>EcoR1</b>	<b>Fsp1</b>	Hind3	<b>Hpa1</b>
<b>Kas1</b>	<b>Mfe1</b>	Msc1	Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	Nhe1	<b>Not1</b>	Nsi1	PflF1	<b>PflM1</b>	<b>Pml1</b>
polyA	<b>PshA1</b>	Psi1	Pvu2	<b>Rsr2</b>	Sac1	Sap1	SexA1	<b>Sfi1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1
Stu1	<b>Xba1</b>	<b>Xcm1</b>	<b>Xho1</b>	<b>Xmn1</b>									

Unique:

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

Not found:

Acc65	Acl1	Ahd1	Apa1	AsiS1	Baela	Baelb	BbvC1	BcglA	Bcglb	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													