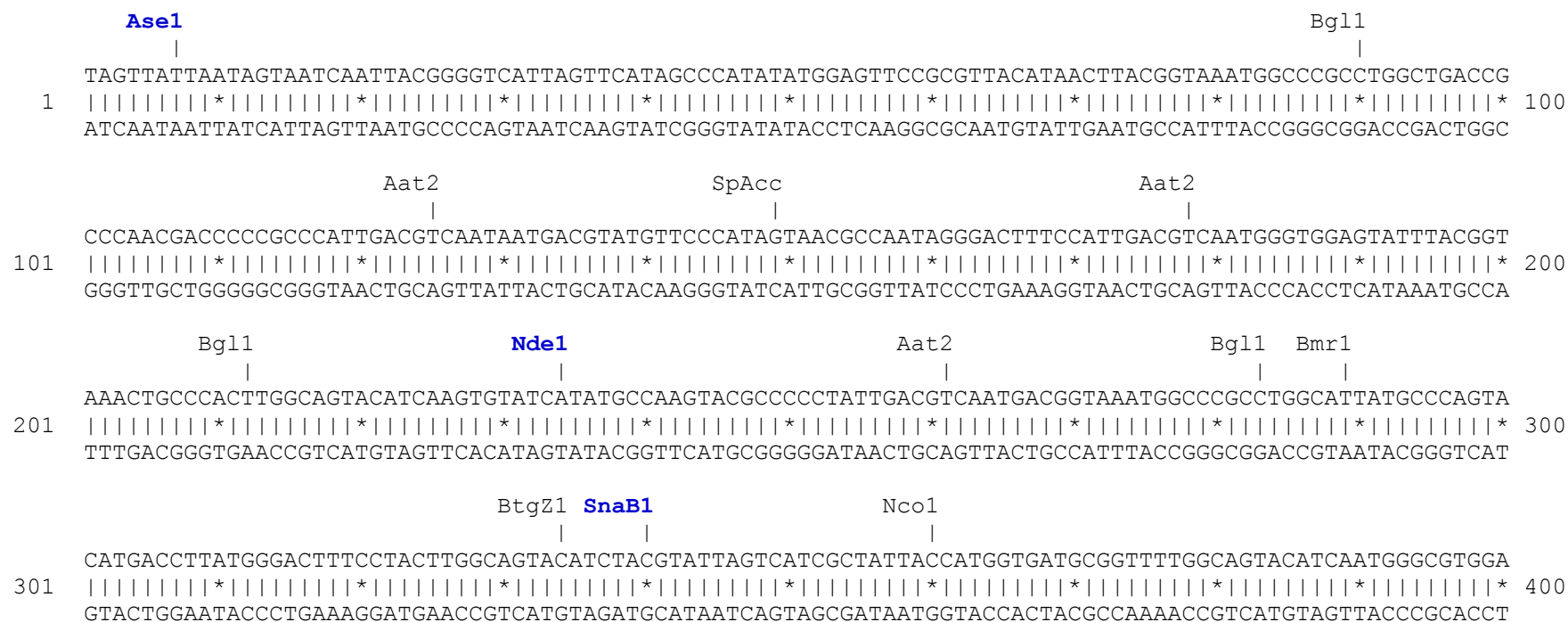


pTagFP635-C vector restriction map

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 basepairs 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). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.



```

                                Aat2                                Eci1
                                |                                |
TAGCGGTTTGACTCACGGGGATTTC AAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGT TTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 500
ATCGCCAAACTGAGTGCCCTAAAGGTT CAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGT TTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                Nhe1 Afe1
                                | |
ACA ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGT TTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 600
TGTTGAGGCGGGGTA ACTTGC GTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Agel      Ale1      Sap1      BsrG1      ApaL1
|          | |      |          |          |
CCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACCTTCAAGT
601 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 700
GGCCAGCGGTGGTACCACAGATTCCC GCTTCTCGACTAATTCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCA
TagFP635 > M V S K G E E L I K E N M H M K L Y M E G T V N N H H F K C

                                SpAcc
                                |
GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGC
701 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 800
CGTGTAGGCTCCCGCTTCCGTTCCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCG
TagFP635 > T S E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A

                                Bsu36      SpDon
                                |          |
TACCAGCTTCATGTACGGCAGCAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
801 | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 900
ATGGTCGAAGTACATGCCGTTCGTTTGG AAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
TagFP635 > T S F M Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R

```

```

          Bbs1          Bpm1          SpDon
          |             |             |
GTCACCACATACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACT
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
CAGTGGTGTATGCTTCTGCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCTCGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
TagFP635  > V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F

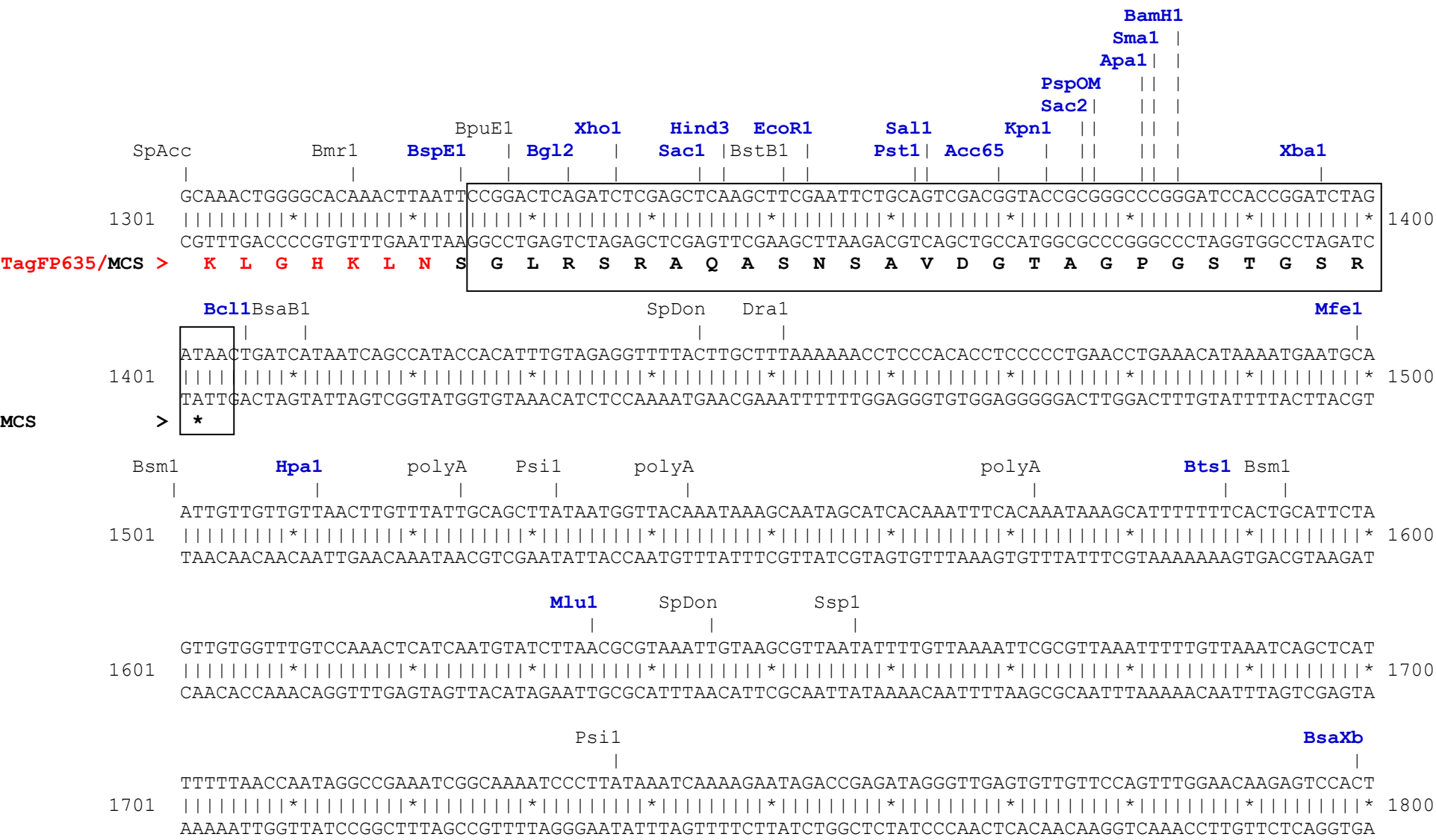
          BseY1  Stu1          Bgl1
          |      |             |
TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
AGGGTAGGTTGCCGGGACACTACGTCTTCTTTGTGAGCCGACCCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
TagFP635  > P S N G P V M Q K K T L G W E A S T E M L Y P A D G G L E G R S D

          BssS1  Eco57          Bbs1  BpuE1
          |      |             |      |
CATGGCCCTGAAGCTCGTGCGGGCGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCCGGCGTC
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
GTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAG
TagFP635  > M A L K L V G G G H L I C N L K T T Y R S K K P A K N L K M P G V

          Bbs1
          |
          SpAcc  |
          |      |
TACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
ATGATACACCTGTCTTCTGACCTTTCTTAGTTCCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
TagFP635  > Y Y V D R R L E R I K E A D K E T Y V E Q H E V A V A R Y C D L P S

          Bbs1  Bsa1  PshA1  BssS1  Dra3  Msc1  AlwN1
          |      |      |      |      |      |      |

```




```

                NsiI                NsiI
                SphI |                SphI |
                BfrB1 |                BfrB1 |
                BstAP | |                BstAP | |
                | | |                | | |
2301  CAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      GTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTA

                EciI                EciI                EciI                EciI                NcoI
                |                |                |                |                |
2401  TAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCCAGTTCGCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
      ATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAT

                                Avr2
                                StuI |
polyA                SfiI                SpDon                BseR1                ClaI
|                |                |                |                |
2501  TTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
      AAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCT

                BspM1                EagI                BmrI
                BsaB1                BfuA1                |                |
                |                |                |                |
2601  CAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
      GTCCTACTCCTAGCAAAGCGTACTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGT

                                NarI
                                KasI |                Drd1
                                |                |
2701  GACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAGT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
      CTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGAC

```

[illegible]

SapI
 EarI
 Eco57
 BssS1
 BtgZ1
 BsrB1 |
 |
 |
 3301 TATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
 ATAACGACTTCTCGAACC GCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAA

BssS1
 BspM1
 BfuA1
 SpAcc
 BsrB1
 BstB1
 |
 |
 |
 |
 3401 GACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
 CTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACT

NaeI
 NgoM4 |
 Bpm1 |
 |
 |
 Bpm1
 SpAcc |
 Avr2 |
 |
 |
 3501 AAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
 TTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGAT

polyA
 |
 polyA
 |
 3601 ACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTGCTTTGTTTCATAAAC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
 TGACTTTGTGCCTTCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTG

Bsa1
 |
 3701 GCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGCATACCCACCGAGACCCCATTTGGGGCCAATACGCCCCGCTTTCTTCTTTTCCCCACCCACCCCCC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
 CGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGG

```

                                BstAP
                                AlwN1      Bsu36
                                |            |
    SpDon                      |            |
    |                            |            |
3801 AAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
    TTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAA

                                Dra1
                                |
                                BspH1
                                |
3901 CATTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
    GTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGC

                                BpuE1
                                |
4001 TAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCGGTGGTTTGTGTTGCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
    ATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGG

                                Eco57
                                |
                                SpAcc
                                |
4101 GGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
    CCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTG

                                AlwN1      BpuE1
                                |            |
4201 TTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
    AAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCACCGCTATTGAGCAGAGAATGGCCCAACCTGA

                                ApaL1      BseY1
                                |            |
4301 CAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
    GTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTGGGTGCGAACCTCGCTTGCTGGATGTGGCTTGACTCTAT

```

CCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGG
 4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
 GGATGTGCGACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCTCTCGCGTGCTCC

GAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGA
 4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
 CTCGAAGGTCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCT

GCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGTTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGT
 4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
 CGGATACCTTTTTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTTACAAGAAAGGACGCAATAGGGGACTAAGACA

GGATAACCGTATTACCGCCATGCAT
 4701 |||||*|||||*||||| 4725
 CCTATTGGCATAATGGCGGTACGTA

Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal
Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1
Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	polyA	PshA1	Psi1	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sac2	Sal1	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1
Ssp1	Stu1	Xba1	Xho1										

Unique:

Acc65	Afe1	Age1	Ale1	Apal	Ase1	BamH1	Bcl1	Bgl2	BsaXa	BsaXb	BseR1	BspE1	BspLU
BsrD1	BsrG1	Bts1	Clal	Eag1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Nar1
Nde1	Nhe1	PflF1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sal1	SexA1	Sfi1	Sma1	SnaB1
Xba1	Xho1												

Not found:

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1
I_Ceu	loxP	Not1	Nru1	Pac1	PflM1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1
Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													