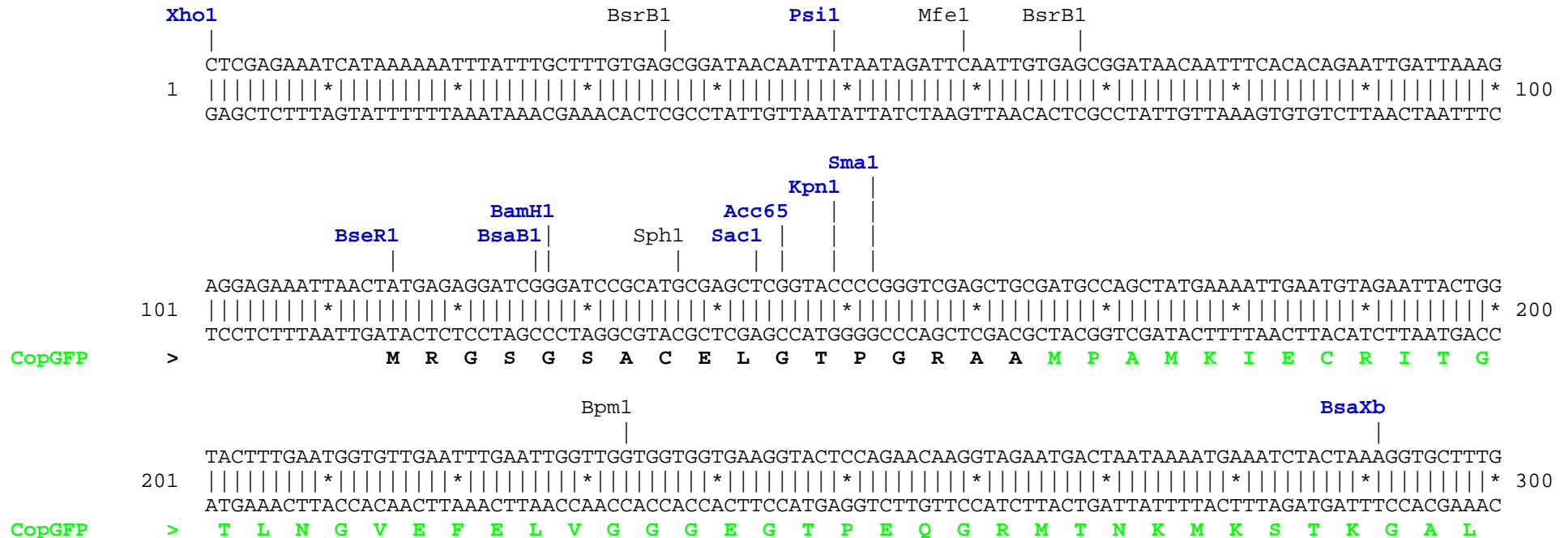
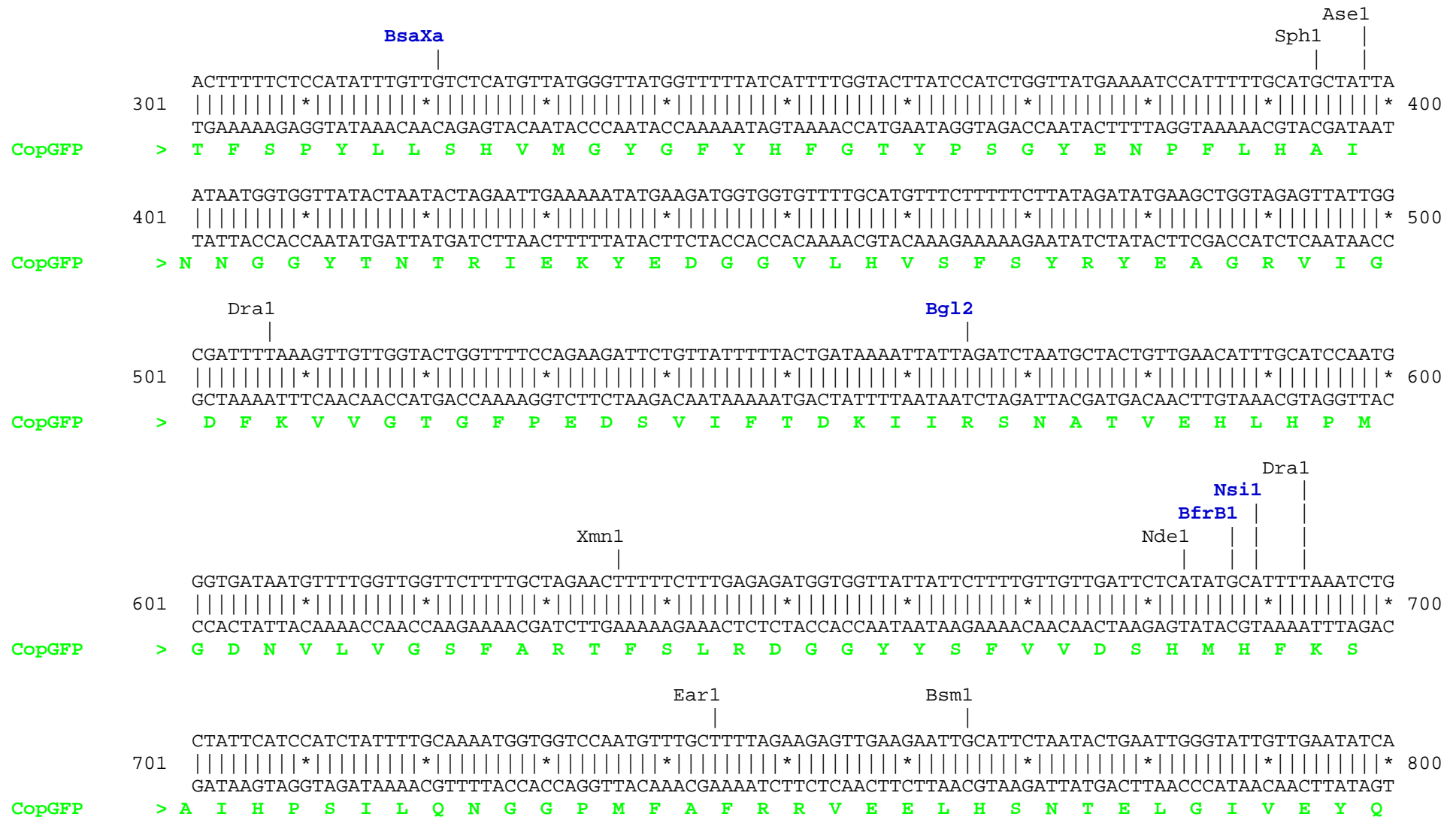


**pCop-Green-YB vector** restriction map

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 shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Amino acids coded by vector's backbone sequence are shown in black.





```

                                Dral   MfeI   Hind3   Sac2   Bsp1
                                |       |       |       |       |
801 ACATGCTTTTAAAACTCCAATTGCTTTTGGCTTAACCGCGGAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
   TGTACGAAAATTTTGAGGTTAACGAAAACGAATTGGCGCCTTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGG
CopGFP > H A F K T P I A F A *

                                NheI   Bpu10
                                |       |
901 ATCTGGATTTGTTTCAGAACGCTCGGTTGCCGCGGGCGTTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
   TAGACCTAAACAAGTCTTGCGAGCCAACGGCGGCCCGCAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTAAAAGTCTCGATTCTTCGATTTT

1001 TGGAGAAAAAAATCACTGGATATAACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
   ACCTCTTTTTTTAGTGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTGTA AAACTCCGTAAAGTCAGTCAACGAGTTACATGGATATT

                                Pvu2   Dral
                                |       |
1101 CCAGACCGTTCAGCTGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTTATTACATTCTTGCCCGCCTGATG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
   GGCTCGCAAGTCGACCTATAATGCCGAAAAATTTCTGGCATTCTTTTTTATTTCGTGTTCAAATAGGCCGAAATAAGTGTAAGAACGGGCGGACTAC

                                BspE1
                                Bsm1   BsrD1
                                |       |       |
1201 AATGCTCATCCGGAATTTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTTCACCCCTTGTTACACCGTTTTCCATGAGCAAACCTGAAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
   TTACGAGTAGGCCTTAAAGCATAACCGTTACTTTCTGCCACTCGACCACTATAACCTATCACAAAGTGGGAACAATGTGGCAAAAGGTA CTGTTTGACTTT

Ac11   Bpm1
|       |
1301 CGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
   GCAAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAAATGCCACTTTTGACCGGATAAA

```

```

                                     BsmB1   PflM1
                                     |       |
CCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACCTTCTTC
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
GGGATTTCCCAAATAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAAACTAAATTTGCACCGGTTATACCTGTTGAAGAAG

                                     Nco1       Ssp1
                                     |         |
GCCCCCGTTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGCTCTGTGATGGCTTCCATG
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
CGGGGGCAAAGTGGTACCCGTTTATAATATGCGTTCGGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGACACTACCGAAGGTAC

                                     Bsm1       Scal
                                     |         |
TCGGCAGAAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATTGGTGCCCTTAAACGCCTGGGGT
1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
AGCCGTCTTACGAATTACTTAATGTTGTCATGACGCTACTCACCGTCCCGCCCCGCATTAATAAATTCCGTCAATAACCACGGGAATTTGCGGACCCCA

                                     BpuE1       Bmr1
                                     |         |
AATGACTCTCTAGCTTGAGGCATCAAATAAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTTCGGTGAACGCTCTCCTGAG
1701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
TTACTGAGAGATCGAACTCCGTAGTTTTATTTTGCTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTC

                                     Xba1
Eci1       BsrB1 |       BsmB1
|         |   |       |
TAGGACAAATCCGCCGCTCTAGAGCTGCCTCGCGCTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTG
1801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
ATCCTGTTTAGGCGGCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAGTGTGCAACAGAC

                                     Drd1       Bmr1 PflF1
                                     |         |       |
TAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTTCGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAG
1901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
ATTCGCCTACGGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCCACAACCGCCACAGCCCCGCGTCGGTACTGGGTGAGTGCATCGCTATCGCCTC
```



```
                BpuE1                AlwN1
                |                      |
2601 TGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
   ACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAAC

                                                Eco57
                                                |
2701 AAGTGGTGGCCTAACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
   TTCACCACCGGATTGATGCCGATGTGATCTTCCTGTGATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTA

                                                BpuE1
                                                |
2801 CCGGCAAACAACCACCGCTGGTAGCGGTGGTTTTTTTTGTTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
   GGCCGTTTGTGGTGGCGACCATCGCCACCAAAAAACAACGTTTCGTCGTCTAATGCGCGTCTTTTTTTTCTAGAGTTCTTCTAGGAAACTAGAAAAG

                                                BspH1                DraI
                                                |                      |
2901 TACGGGGTCTGACGCTCAGTGGAAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTAATAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
   ATGCCCAGACTGCGAGTCACTTGCTTTTGTGAGTGCAATTCCCTAAAACCAGTACTCTAATAGTTTTTCTAGAAAGTGATCTAGGAAAATTTAATTTTT

                DraI
                |
3001 TGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
   ACTTCAAAATTTAGTTAGATTTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAG

                Ahd1                Bmr1                BsrD1                Bsa1                Bpm1
                |                      |                      |                      |                      |
3101 GTTCATCCATAGCTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
   CAAGTAGGTATCGACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGTACGACGTTACTATGGCGCTCTGGGTGC
```







Unique:

Aat2	Acc65	Ahd1	AlwN1	BamH1	Bbs1	Bcg1a	Bcg1b	BfrB1	Bgl1	Bgl2	Blp1	Bpu10	Bsa1
BsaB1	BsaXa	BsaXb	BseR1	BseY1	BspE1	BspLU	BstAP	BstZ1	EcoK	Fsp1	Hind3	Kpn1	Msc1
Nco1	Nhe1	Nsi1	PflF1	PflM1	Psi1	Pvu1	Pvu2	Sac1	Sac2	Sap1	Sma1	Xba1	Xho1

Not found:

Aar1	Afe1	Afl2	Age1	Ale1	Apal	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfuA1
BmgB1	Bsg1	BsiW1	BspM1	BsrG1	BssH2	BstB1	BstE2	BstX1	Bsu36	_Chi	Clal	Dra3	Eag1
EcoN1	EcoR1	EcoRV	ScFRT	Fse1	FspA1	Hpa1	I_Ceu	Kas1	loxP	Mlu1	Nae1	Nar1	NgoM4
Not1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM	Pst1	Rsr2	Sall	SanD1	Sbf1	SexA1	Sfi1
Sgf1	SgrA1	SnaB1	Spe1	Srf1	Stu1	Swal	PISce	Xcm1					

Excluded by site complexity:

Acc1	Ac11	Afl3	Alu1	Alw1	Apol	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													