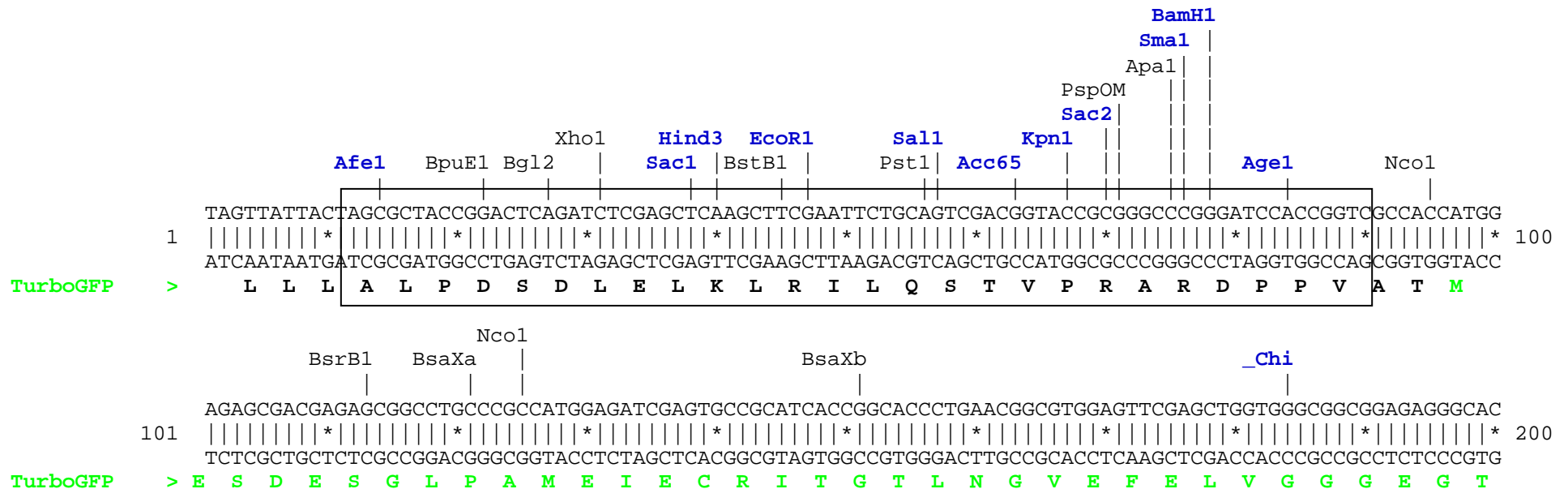


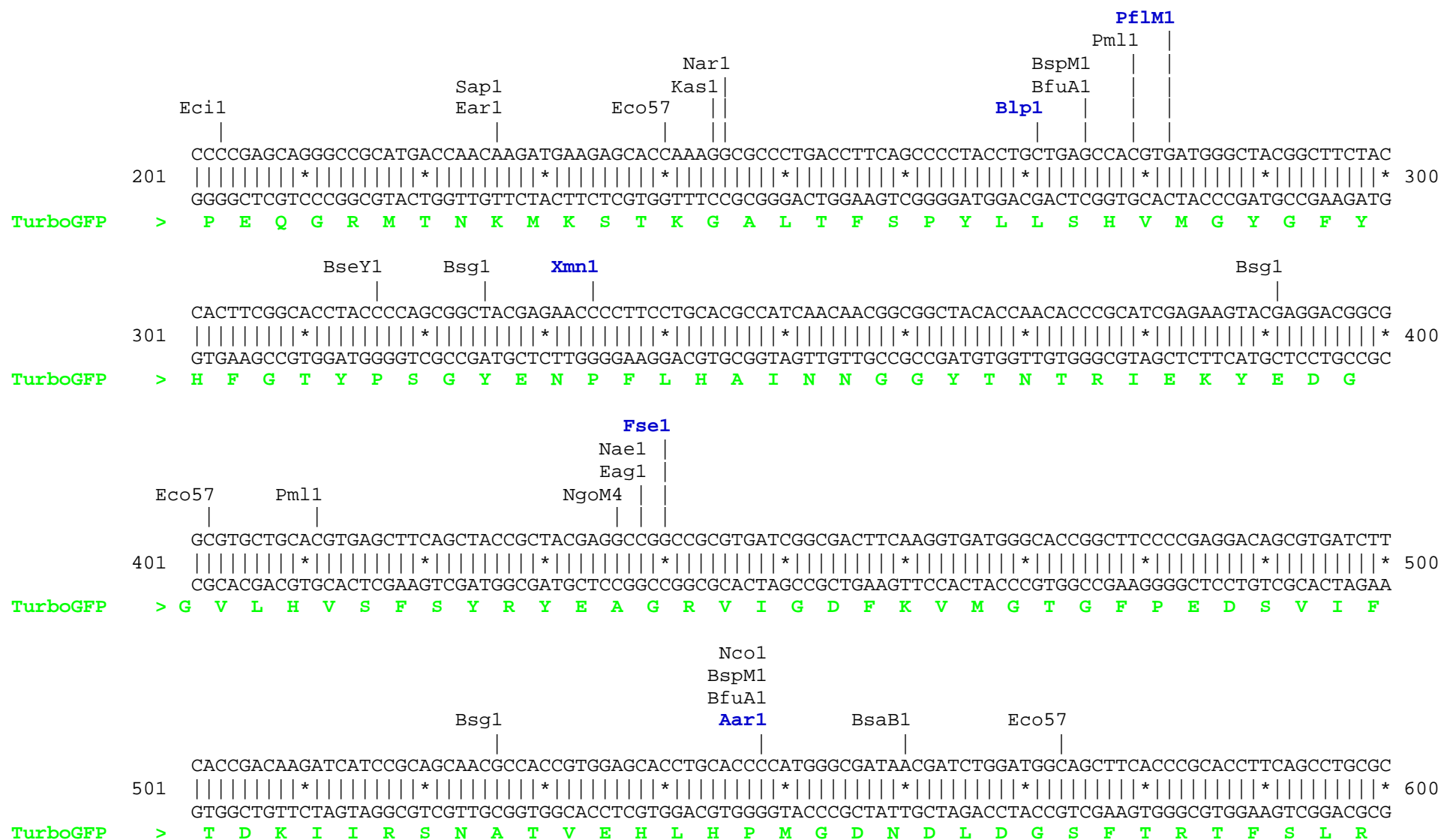
pTurboGFP-PRL-dest1 vector restriction map

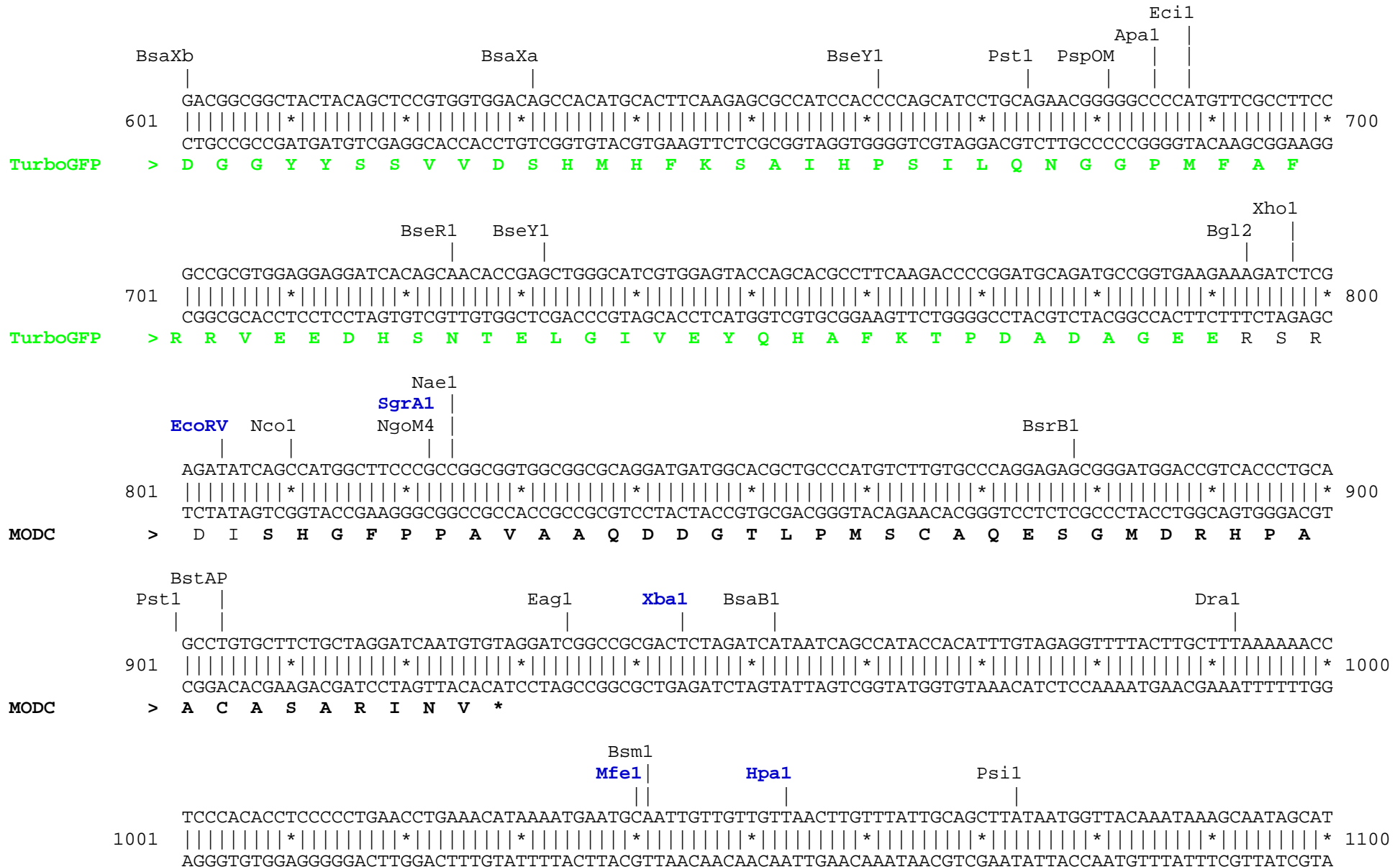
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction 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).

MCS sequence shown in frame, amino acids coded by MCS and MODC amino acids are shown in bold black.







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          Bts1 Bsm1                               Afl2                               Ssp1
          |  |                                   |                                   |
1101 CACAAATTTACAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
   GTGTTTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTCGCAATTATA

                                     Psil
                                     |
1201 TTTGTTAAAAATTCGCGTTAAATTTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAAGAATAGACCGAG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
   AAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTC

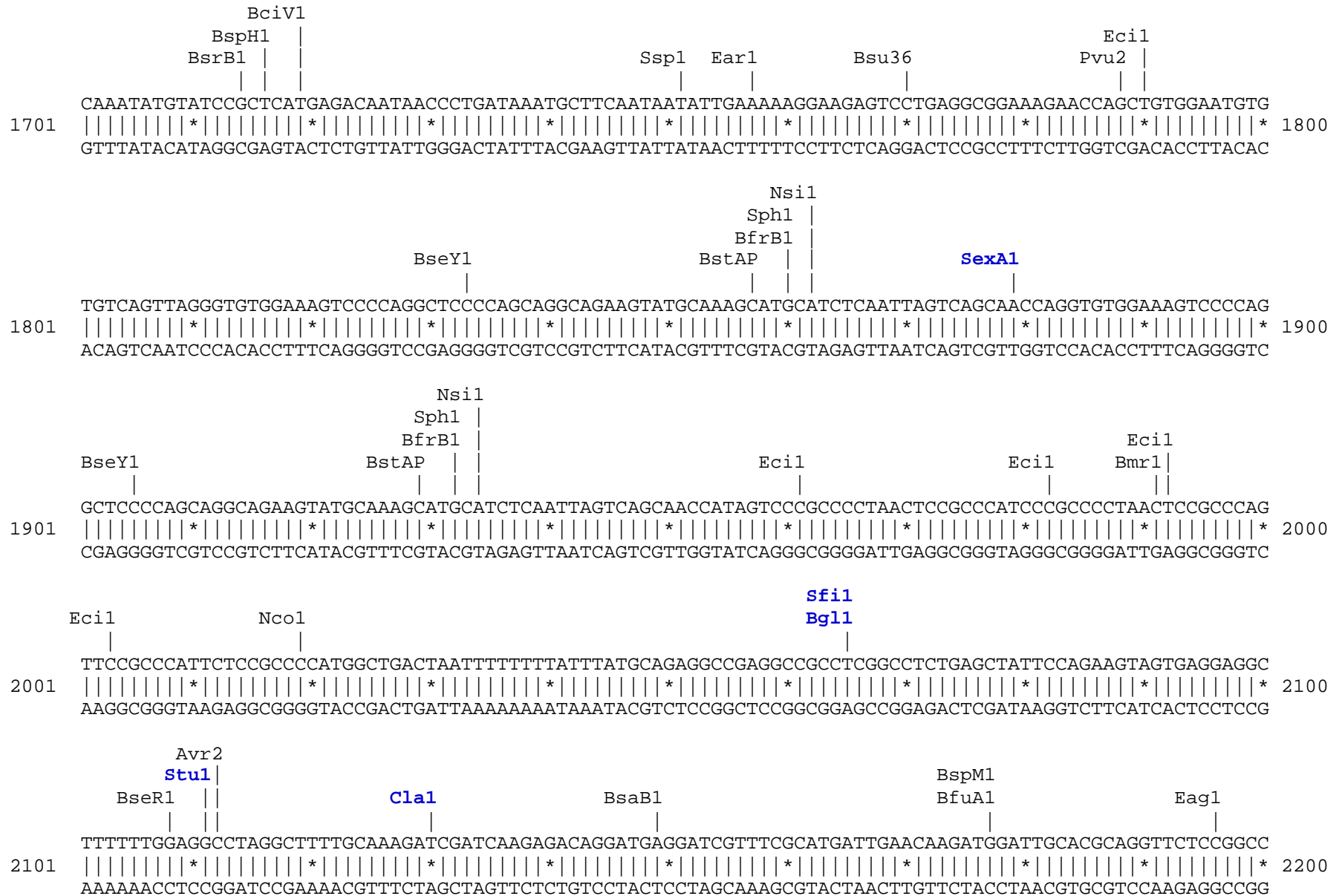
          BsaXb                               Drd1 BsaXa
          |  |                               |  |  |
1301 ATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
   TATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCCTTTTTGGCAGATAGTCCCCTACCGG

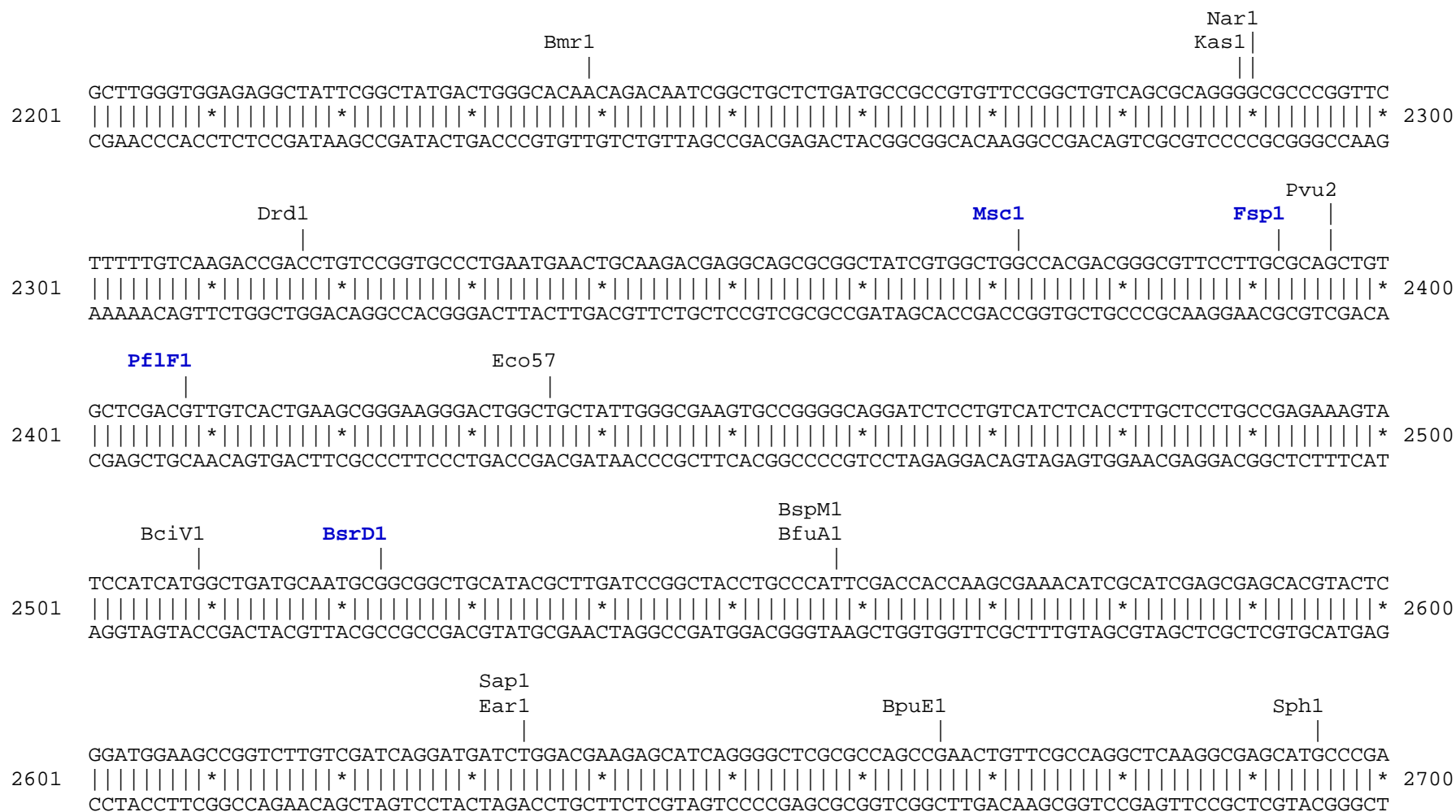
          Dra3
          |
1401 CACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCTTAAAGGGAGCCCCGATTTAGAGCTTGACG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
   GTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGC

          Nae1
          |  |
          NgoM4 |                               BsrB1
          |  |                               |
1501 GGGAAAAGCCGGCGAACGTGGCGAGAAAAGGAAGGAAGAAAAGCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
   CCTTTTCGGCCGCTTGCACCGCTCTTTCCCTTCCCTTCTTTTCGCTTTCCTCGCCCCGCGATCCCCTGACCGTTTACATCGCCAGTGCGACGCGCATTGGTGG

1601 ACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
   TGTGGGCGGCGCAATTACGCGCGATGTCCCCTGACGCTGAAAAGCCCCCTTTACACGCGCCTTGGGGATAAACAATAAAAAGATTTATGTAA

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                                         Nco1
                                         |
CGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGT
2701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
GCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCA

                                         Sap1
                                         |
                                         Ear1
                                         |
                                         Eco57
                                         |
                                         BssS1
                                         |
GTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCG
2801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
CACCGCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGC

BsrB1
|
                                         BsrB1
                                         |
                                         BstB1
                                         |
2901 CCGCTCCCATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAAATGACCGACCAAGCGACGCCAAC
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
GGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAAGTCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTG

                                         BssS1
                                         |
                                         BspM1
                                         |
                                         BfuA1
                                         |
                                         Nae1
                                         |
                                         NgoM4
                                         |
                                         Bpm1
                                         |
3001 CTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
GACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCC

                                         Bpm1
                                         |
                                         Avr2
                                         |
                                         |
3101 ATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
TAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTGGGCGGATACTGCCGTTATTTTTTC
```



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                                     BpuE1                                     ApaL1
                                     |                                     |
3801  TGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTTCGTGCACA 3900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      ACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGT

BseY1
      |
3901  CAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGT 4000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GTCGGGTGCAACCTCGCTTGCTGGATGTGGCTTACTCTATGGATGTGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCTGTCCA

      BciV1
      Eci1      |      BssS1
      |      |      |
4001  ATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTG 4100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGAC

      Drd1      BpuE1      Eci1
      |      |      |
4101  ACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGGCCTTTTTACGGTTCCTGGCCTTTTGTGGCCT 4200
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TGAACTCGCAGCTAAAAACTACGAGCAGTCCCCCGCTCGGATACCTTTTTTGCGGTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGA

                                     NsiI
      BspLU      |      BfrB1
      |      |      |
4201  TTTGCTCACATGTTCTTTCTCGGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4266
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      AAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Acc65	Afe1	Afl2	Age1	AlwN1	Apa1	ApaL1	Avr2	BamH1	BciV1	BfrB1	BfuA1	Bgl1
Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1
BspLU	BspM1	BsrB1	BsrD1	BssS1	BstAP	BstB1	Bsu36	Bts1	_Chi	Clal	Dra1	Dra3	Drd1
Eag1	Ear1	Eci1	Eco57	EcoR1	EcoRV	Fse1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1
Nae1	Nar1	Nco1	NgoM4	Nsi1	PflF1	PflM1	Pml1	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1
Sac2	Sal1	Sap1	SexA1	Sfi1	SgrA1	Sma1	Sph1	Ssp1	Stu1	Xba1	Xho1	Xmn1	

Unique:

Aar1	Acc65	Afe1	Afl2	Age1	ApaL1	BamH1	Bgl1	Blp1	Bsa1	BspLU	BsrD1	Bts1	_Chi
Clal	Dra3	EcoR1	EcoRV	Fse1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Msc1	PflF1	PflM1	Rsr2
Sac1	Sac2	Sal1	SexA1	Sfi1	SgrA1	Sma1	Stu1	Xba1	Xmn1				

Not found:

Aat2	Ac11	Ahd1	Ale1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1
BmgB1	Bpu10	BsiW1	BsmB1	BspE1	BsrG1	BssH2	BstE2	BstX1	BstZ1	EcoK	EcoN1	ScFRT	FspA1
I_Ceu	loxP	Mlu1	Nde1	Nhe1	Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Scal
Sgf1	SnaB1	Spe1	Srf1	Swal	PISce	Xcm1							

Excluded by site complexity:

Acc1	Ac11	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													