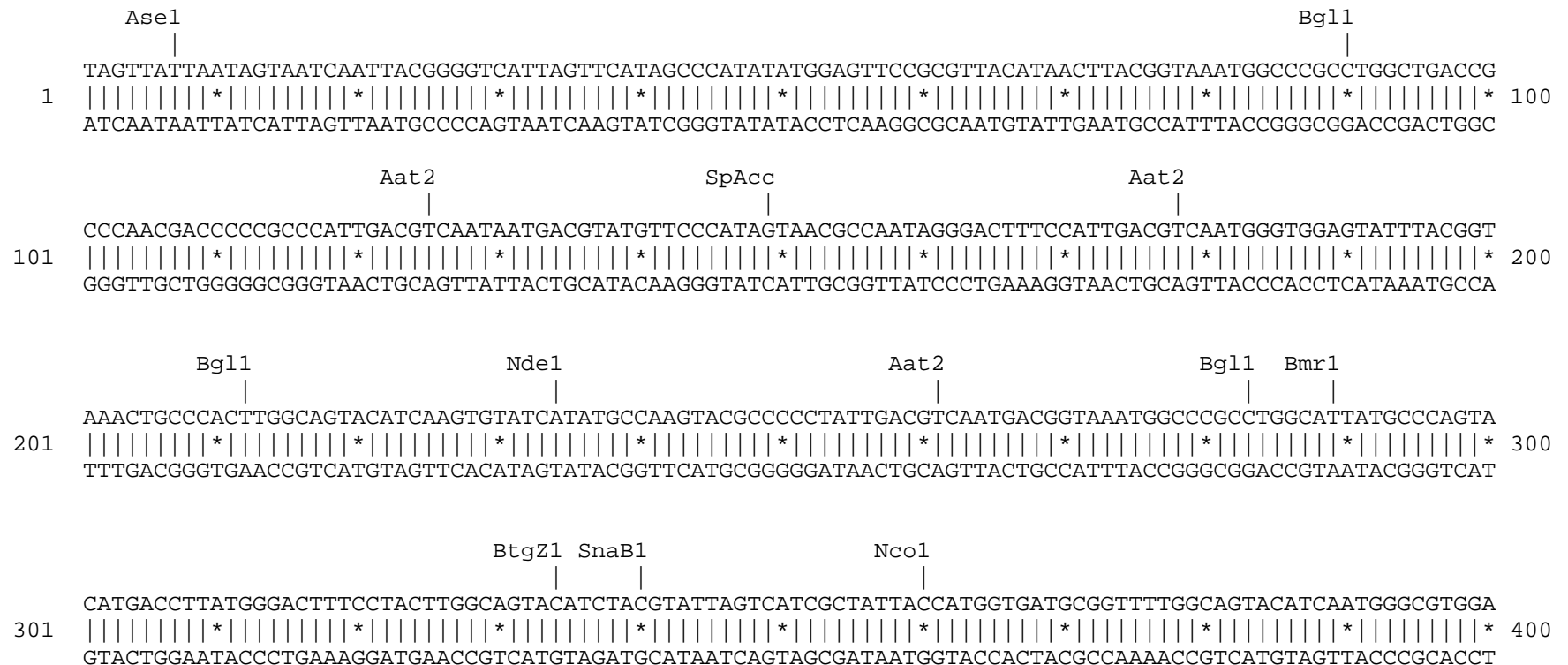


pTagRFP-integrin vector restriction map

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). TagRFP amino acids are shown in red, α -V-Integrin amino acids are shown in green, linker amino acids are shown in black.




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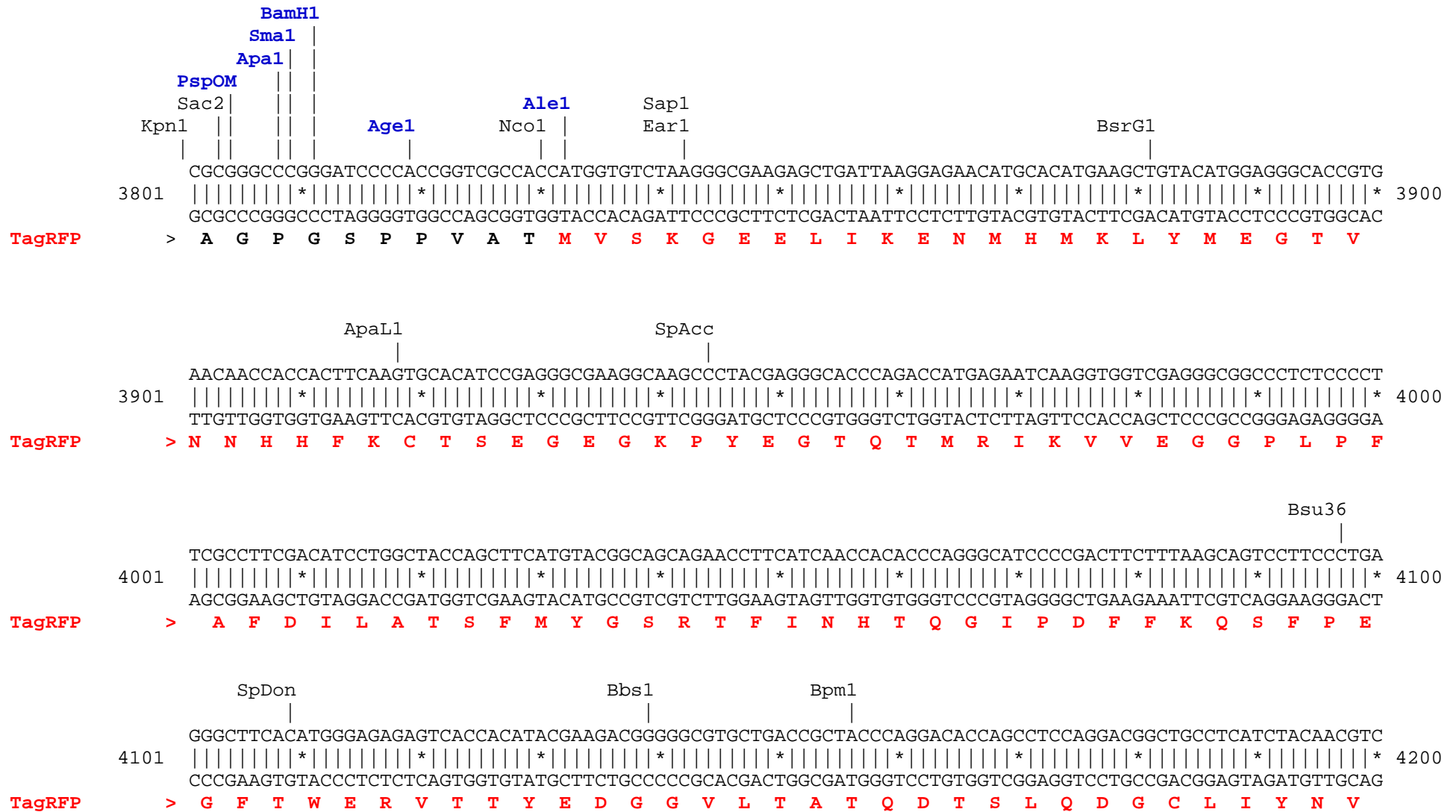
                                polyA                                Eco57
                                |                                |
AGTCATTACTGTGGACTGAGACTTTTTATGAATAAAGAAAATCAGAATCATTTCCTATTCTCTGAAGTCGTCTGCTTCATTTAATGTCATAGAGTTTCCTTA
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
TCAGTAATGACACCTGACTCTGAAAATACTTATTTCTTTTAGTCTTAGTAAGGATAAGAGACTTCAGCAGACGAAGTAAATTACAGTATCTCAAAGGAAT
Integrin > S L L W T E T F M N K E N Q N H S Y S L K S S A S F N V I E F P Y

PsiI      MfeI      EcoRV      XcmI  BstE2      BsmI      BclI
|         |         |         |         |         |         |
TAAGAATCTTCCAATTGAGGATATCACCAACTCCACATTGGTTACCACTAATGTCACCTGGGGCATTTCAGCCAGCGCCCATGCCTGTGCCTGTGTGGGTG
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
ATTCTTAGAAGGTAACTCCTATAGTGGTTGAGGTGTAACCAATGGTGATTACAGTGGACCCCGTAAGTCGGTCGCGGGTACGGACACGGACACACCCAC
Integrin > K N L P I E D I T N S T L V T T N V T W G I Q P A P M P V P V W V

                                BsrG1      BpuE1      DraI
                                |         |         |
ATCATTTTAGCAGTTCTAGCAGGATTGTTGCTACTGGCTGTTTTGGTATTTGTAATGTACAGGATGGGCTTTTTTAAACGGGTCCGGCCACCTCAAGAAG
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
TAGTAAAAATCGTCAAGATCGTCCTAACCAACGATGACCGACAAAACCATAAACATTACATGTCCTACCCGAAAAAATTTGCCAGGCCGGTGGAGTTCTTC
Integrin > I I L A V L A G L L L L A V L V F V M Y R M G F F K R V R P P Q E E

                                BspH1      SpDon      BpuE1      Xho1      Hind3  EcoR1      Sall
                                |         |         |         |         |         |         |
AACAAAGAAAGGGAGCAGCTTCAACCTCATGAAAATGGTGAAGGAAAACCTCAGAAACTCCGGGATCTCGAGCTCAAGCTTTCGAATTCTGCAGTTCGACGGTAC
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
TTGTTCTTTCCCTCGTCAAGTTGGAGTACTTTTACCACTTCCCTTTGAGTCTTTGAGGCCCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATG
Integrin > Q E R E Q L Q P H E N G E G N S E T P G S R A Q A S N S A V D G T

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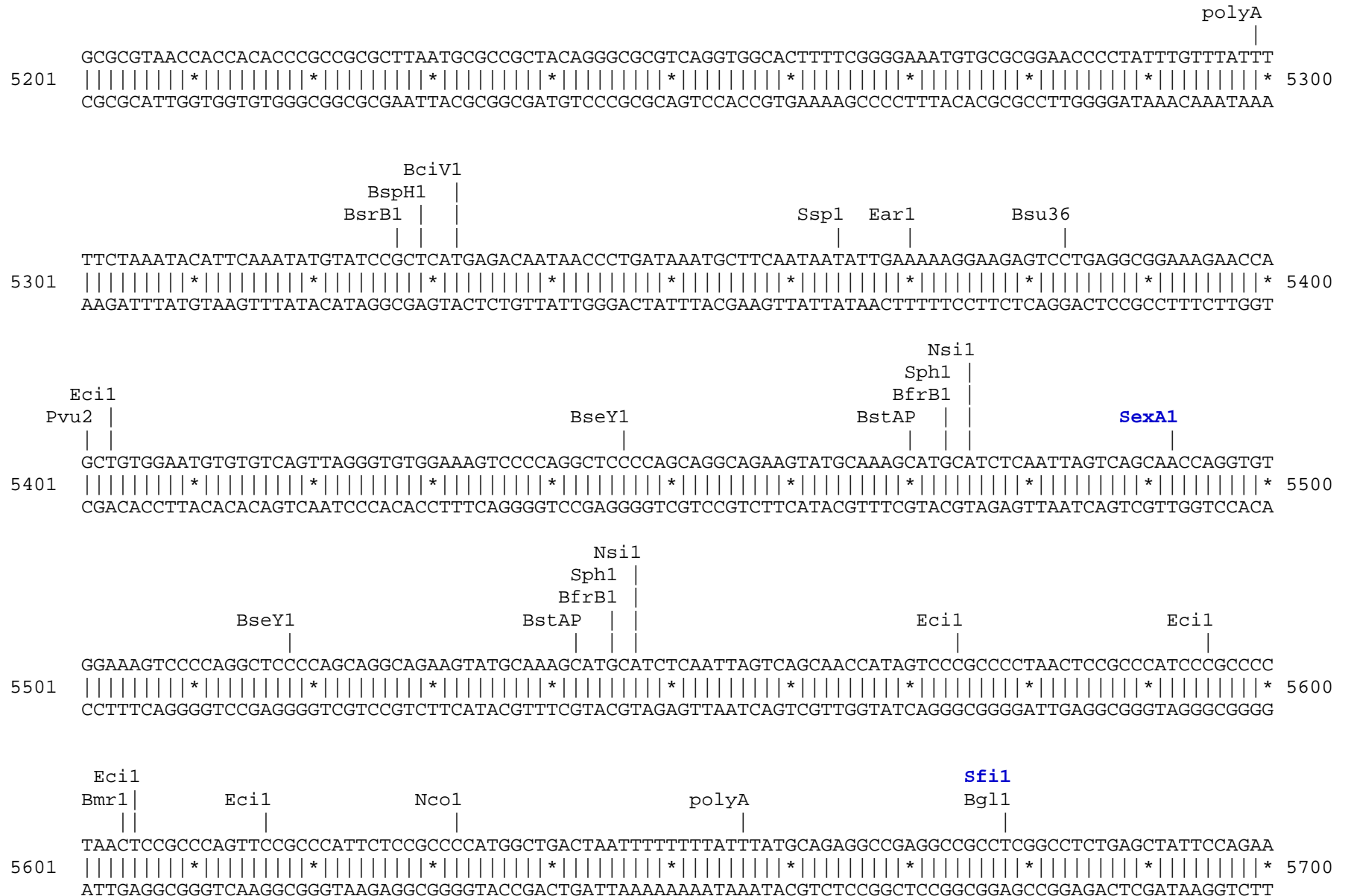
                                polyA          Bts1 Bsm1          Af12          SpDon
                                |              |   |              |              |
4701 AAAGCAATAGCATCACAAATTTACAAATAAAGCATTCTTTTCTACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
    TTTTCGTTATCGTAGTGTAAAGTGTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCGCATTTAAC

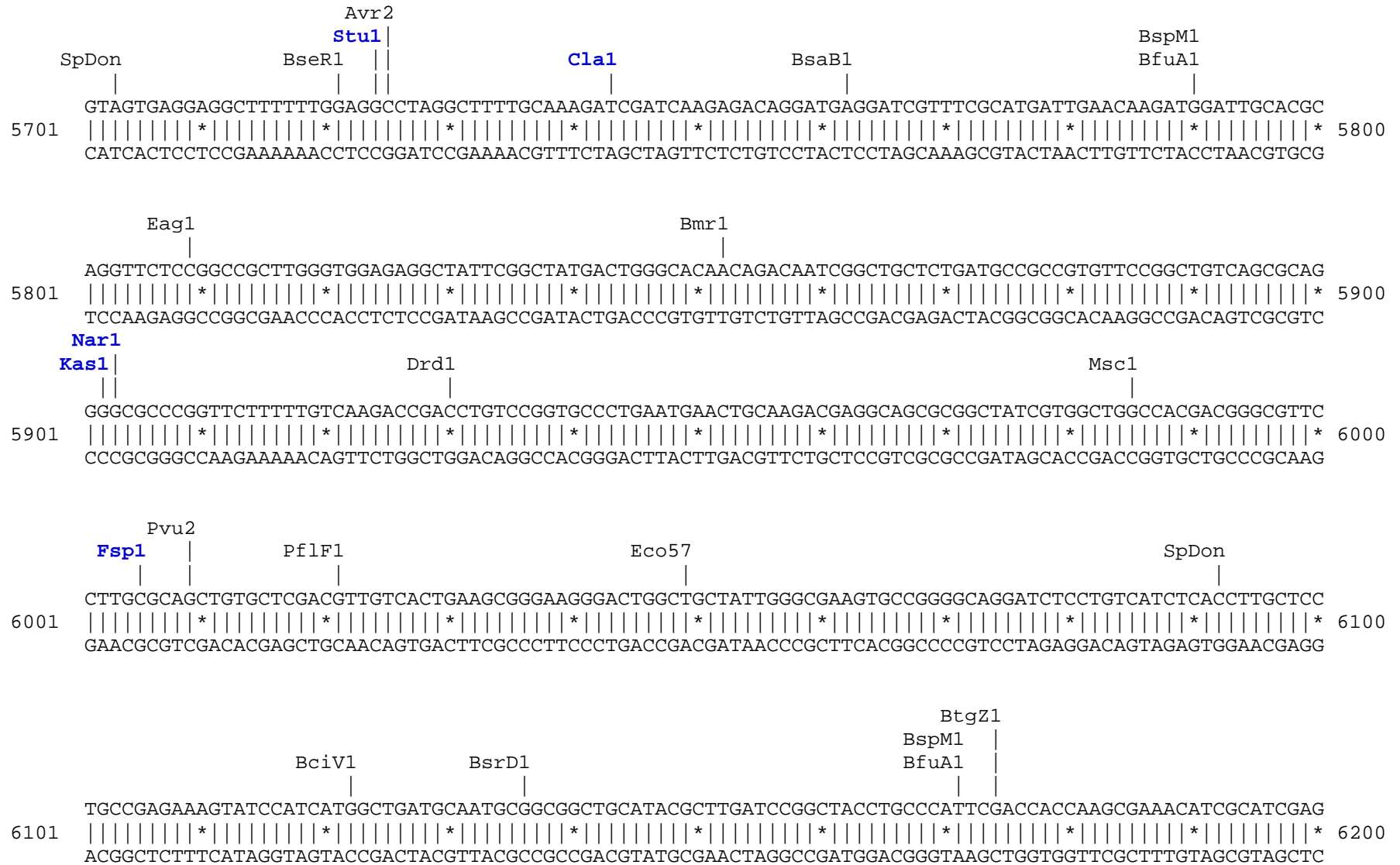
                                Ssp1          Psil
                                |              |
4801 TAAGCGTTAATATTTTGTAAAATTCGCGTTAAAATTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
    ATTTCGCAATTATAAAACAATTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTT

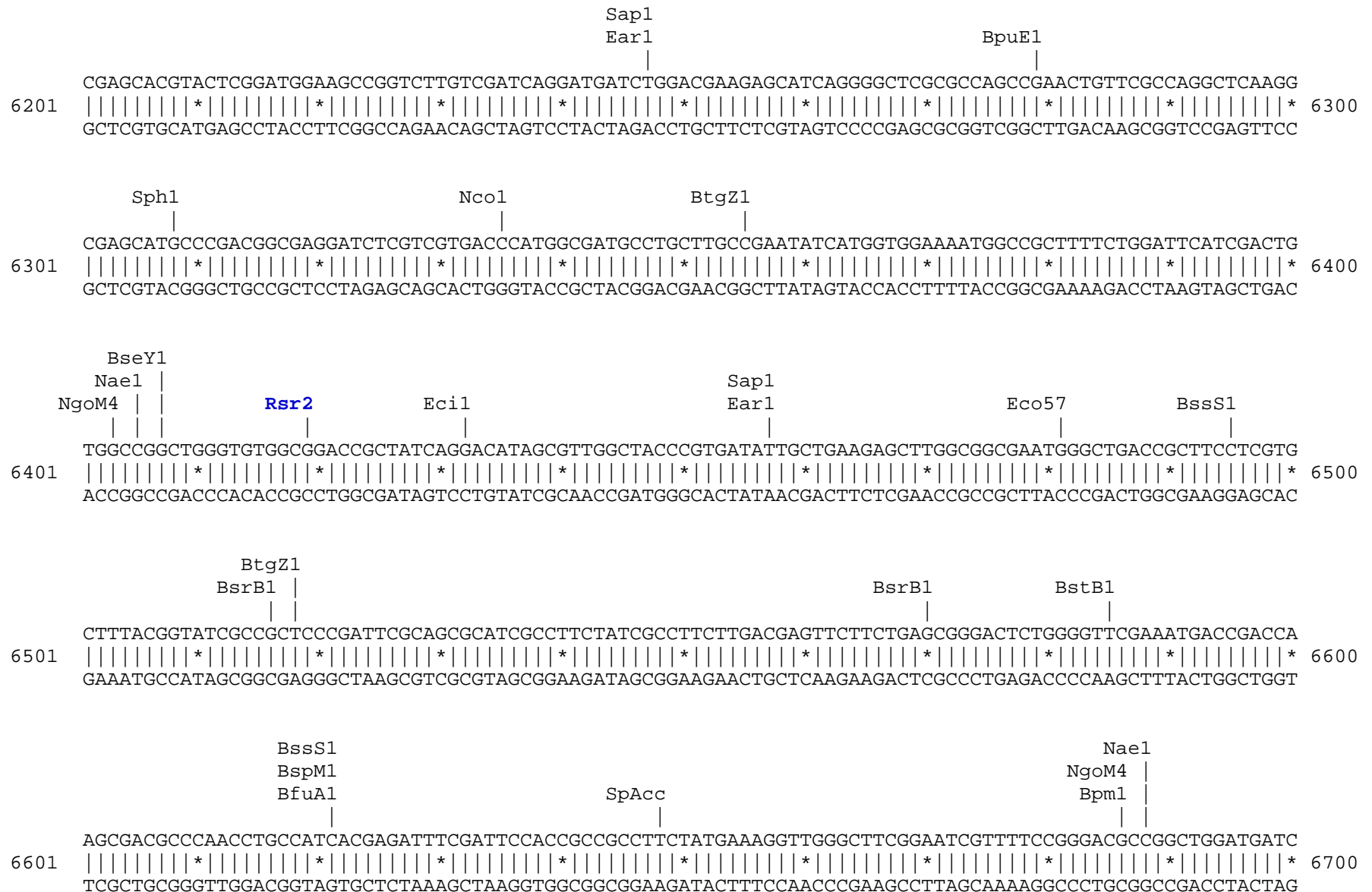
                                BsaXb          Drd1          BsaXa
                                |              |   |              |
4901 AGAATAGACCGAGATAGGGTTGAGTGTGTTCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
    TCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATA

                                BtgZ1          Dra3          SpAcc
                                |   |              |              |
5001 CAGGGCGATGGCCCACTACGTGAACCATCACCCATAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCGAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
    GTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTA

                                Nae1          NgoM4          BsrB1
                                |   |              |              |
5101 TTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    AATCTCGAACTGCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGGATCCCGCGACCGTTCACATCGCCAGTGCGA
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                                     Bpm1
                                     SpAcc
                                     Avr2
                                     |
                                     |
6701 CTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCCACCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6800
    GAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTATGGCCTTCTTTGGGCGCGATACT

polyA      polyA
|          |
6801 CGGCAATAAAAAGACAGAATAAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTTCGATACCCCCACCGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6900
    GCCGTTATTTTCTGTCTTATTTTTCGCGTCCACAACCCAGCAAACAAGTATTTTCGCCCCAACCCAGGGTCCCAGCGTGGAGACAGCTATGGGGTGGCTC
6901 ACCCCATTGGGGCCAATACGCCCGGTTTCTTCTTTTCCCCACCCCACCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7000
    TGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCAGCGTCGTTTGCAGCCCCGCCGT

BstAP
AlwN1      Bsu36
|          |
7001 GGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7100
    CCGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAG

BspH1
|
7101 TCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7200
    AGTACTGGTTTTAGGGAATTGCACTCAAAAAGCAAGGTGACTCGCAGTCTGGGGCATTTTTCTAGTTTCTAGAAGAACTCTAGGAAAAAAGACGCGCA

                                     Eco57
                                     |
7201 AATCTGCTGCTTGCAAACAAAAAACCCACCGCTACCAGCGGTGGTTTTGTTTGC CGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7300
    TTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCG
```

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                                SpAcc
                                |
7301 AGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7400
    TCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGG

                AlwN1                    BpuE1
                |                        |
7401 TGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7500
    ACAATGGTCAACCGACGACGGTCACCGCTATTACAGCACAGAATGGCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCC

        ApaL1      BseY1                                SpAcc
        |          |                                    |
7501 GGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGGAGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7600
    CCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCT

                    BciV1
                    |
                    Eci1      BssS1                                SpAcc
                    |          |                                    |
7601 AAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTGGGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7700
    TTCCGCTGTCCATAGGCCATTCGCCGTCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCA

                Drd1                    BpuE1                    SpAcc      Eci1
                |                        |                        |          |
7701 TTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7800
    AAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACTTTTTGCGGTGCTTGCGCCGGAAAAATGCCAAGGACCG

                                SpDon
                                |
                                BspLU|
                                ||
7801 CTTTTGCTGGCCTTTTGTCTACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7879
    GAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
  
```


Found:

Aat2	Acc65	Afl2	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	Baela	Baelb	BamH1	Bbs1
BciV1	Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1
BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP
BstB1	BstE2	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoR1
EcoRV	Fsp1	Hind3	Hpal	Kas1	Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Not1
Nsi1	PflF1	PflM1	polyA	PshA1	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1
Sca1	SexA1	Sfi1	SgrA1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xho1

Unique:

Afl2	Age1	Ale1	Apal	Baela	Baelb	BamH1	Blp1	BmgB1	Bpu10	BstE2	Clal	EcoR1	Fsp1
Hpal	Kas1	Nar1	Not1	PshA1	PspOM	Rsr2	SexA1	Sfi1	SgrA1	Sma1	Stu1	Xba1	

Not found:

Aar1	Acl1	Afe1	Ahd1	Asc1	AsiS1	BbvC1	BcglA	Bcglb	BsiW1	BsmB1	BspE1	BssH2	BstX1
BstZ1	_Chi	EcoK	EcoN1	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1
Nhe1	Nru1	Pac1	Pme1	Pml1	Pvu1	R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Sgf1	Spe1
Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	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	Bs11	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													