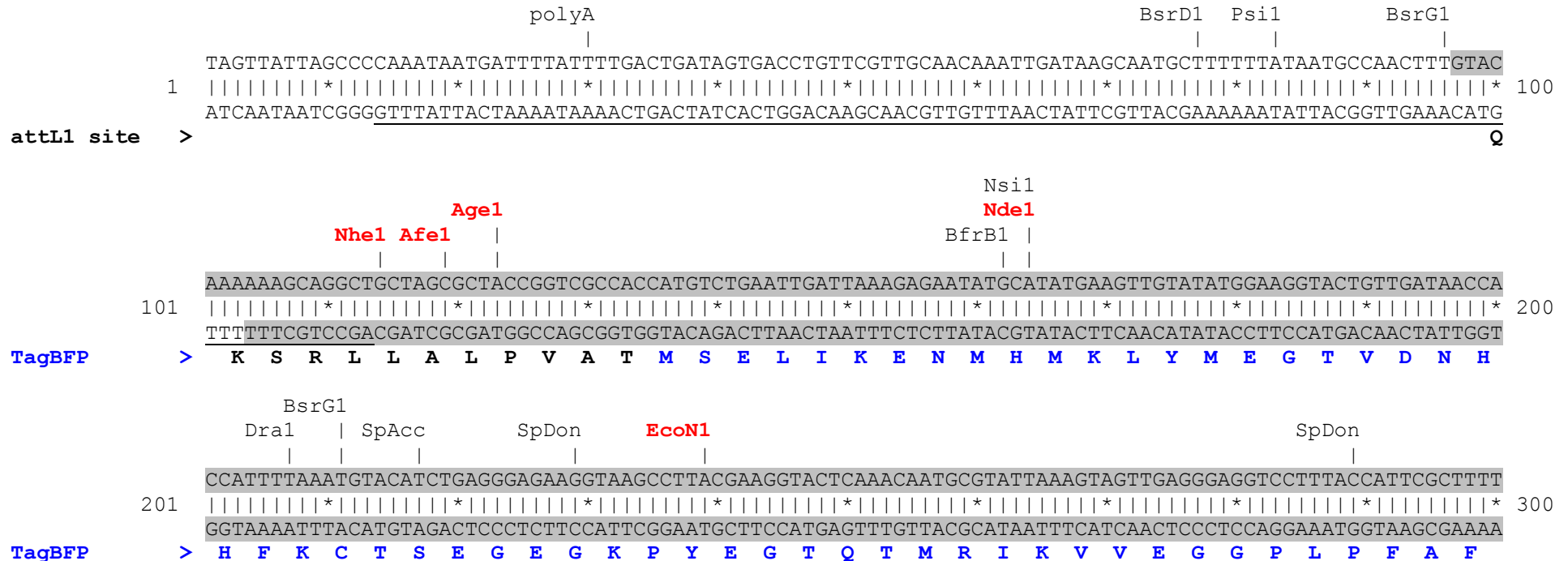
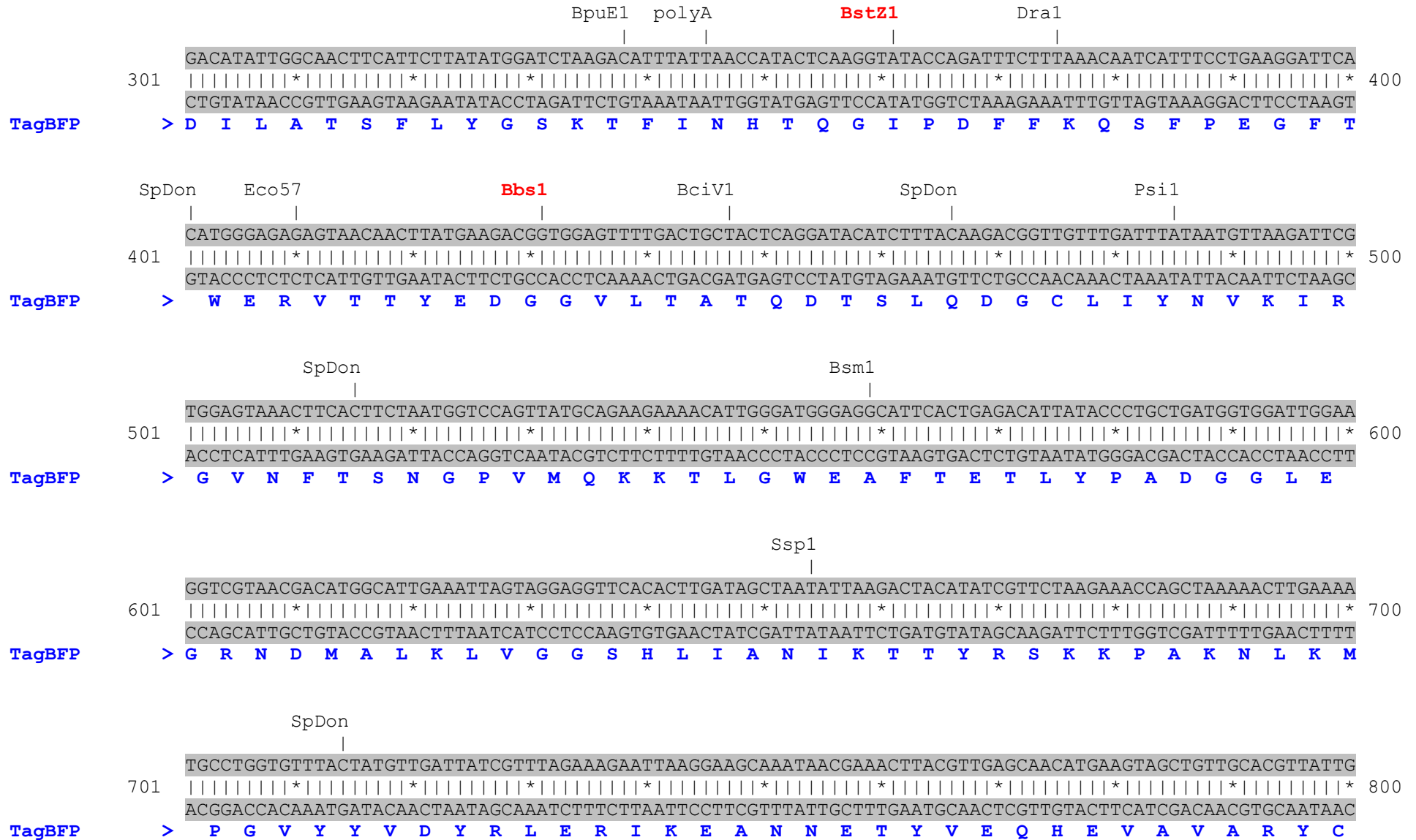


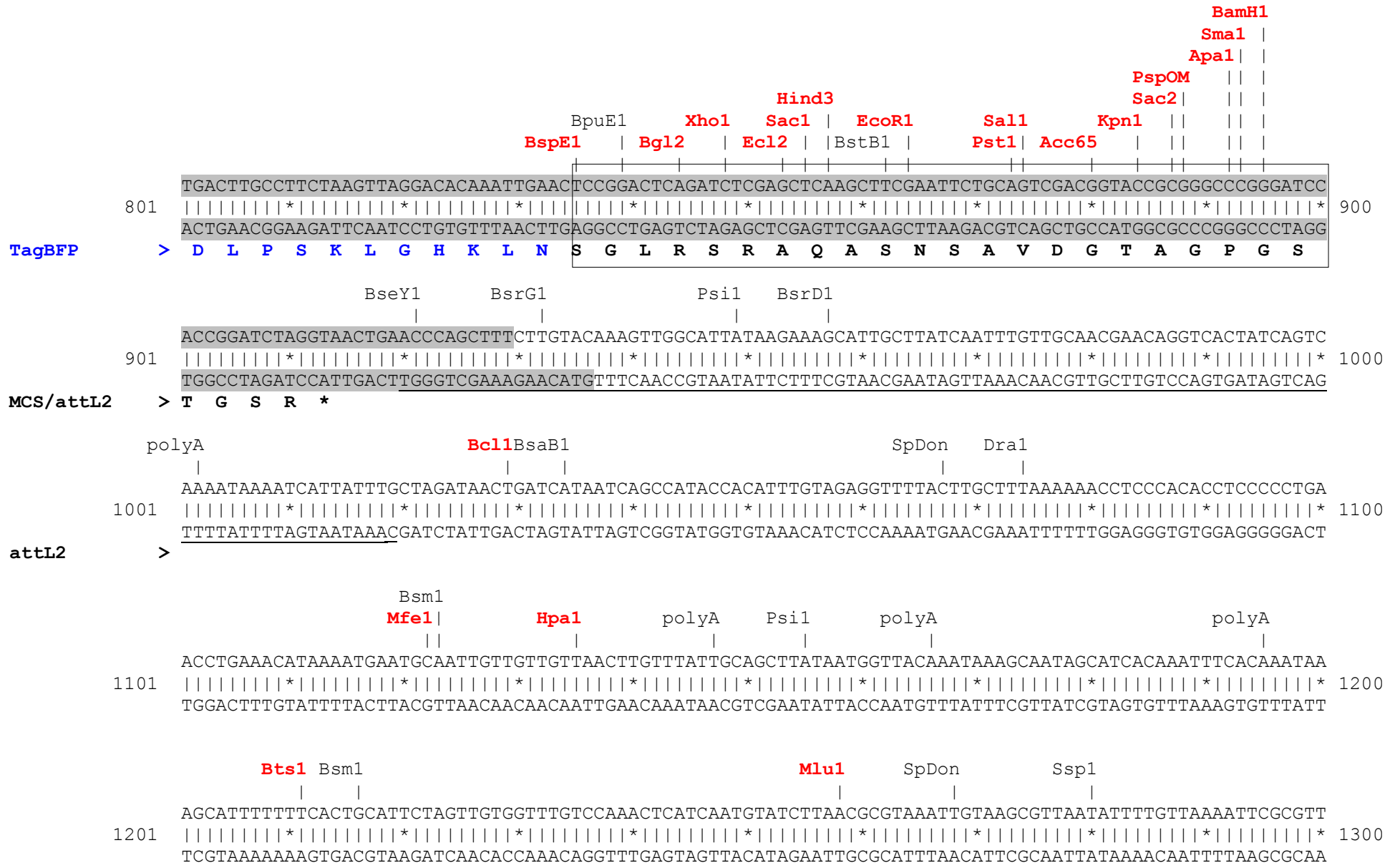
Gateway® TagBFP-AS-C entry clone restriction map

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 red. 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, the attL sites are underlined. Shaded region corresponds to DNA sequence transferred from the entry clone into the destination vector following recombination. Non-TagBFP amino acids are shown in black, TagBFP amino acids are shown in bold blue.








```

                                                                 BstAP
                                                                 AlwN1       Bsu36
                                                                 |           |
3401 TCCTTTTCCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
   AGGAAAAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATAT

                Dra1           Dra1           BspH1
                |             |             |
3501 TACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
   ATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAG

                                                                 BpuE1
                                                                 |
3601 GTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACACCG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
   CAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGC

                                                                 Eco57
                                                                 |
3701 CTACCAGCGGTGGTTTGGTTGCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
   GATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATC

SpAcc                                                                 AlwN1
|                                                                 |
3801 TGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCAGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
   ACATCGGCATCAATCCGGTGGTGAAGTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATT

                BpuE1           ApaI1           BseY1
                |             |             |
3901 GTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
   CAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGCTTGCCCCCAAGCACGTGTGTGCGGGTCGAACCTCGCT
```


Found:

Acc65	Afe1	Age1	AlwN1	Apa1	ApaL1	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	BstZ1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3
Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1
Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	polyA	Psi1	PspOM	Pst1
Pvu2	Rsr2	Sac1	Sac2	Sall1	Sap1	SexA1	Sfi1	Sma1	SpAcc	SpDon	Sph1	Ssp1	Stu1
Xho1													

Unique:

Acc65	Afe1	Age1	Apa1	ApaL1	BamH1	Bbs1	Bcl1	Bgl1	Bgl2	Bsa1	BsaXa	BsaXb	BseR1
BspE1	BspLU	BstZ1	Bts1	Clal	Dra3	Eag1	Ecl2	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Kpn1	Mfe1	Mlu1	Msc1	Nar1	Nde1	Nhe1	PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall1
SexA1	Sfi1	Sma1	Stu1	Xho1									

Not found:

Aar1	Aat2	Acl1	Afl2	Ahd1	Ale1	Asc1	Ase1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b
Blp1	BmgB1	Bpu10	Bsg1	BsiW1	BsmB1	BssH2	BstE2	BstX1	BxatB	BxatL	BxatR	BxatP	_Chi
EcoK	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Not1	Nru1	Pac1
PflM1	Pme1	Pml1	PshA1	Pvu1	R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Sca1	Sgf1	SgrA1
SnaB1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xba1	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	Bs11	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													