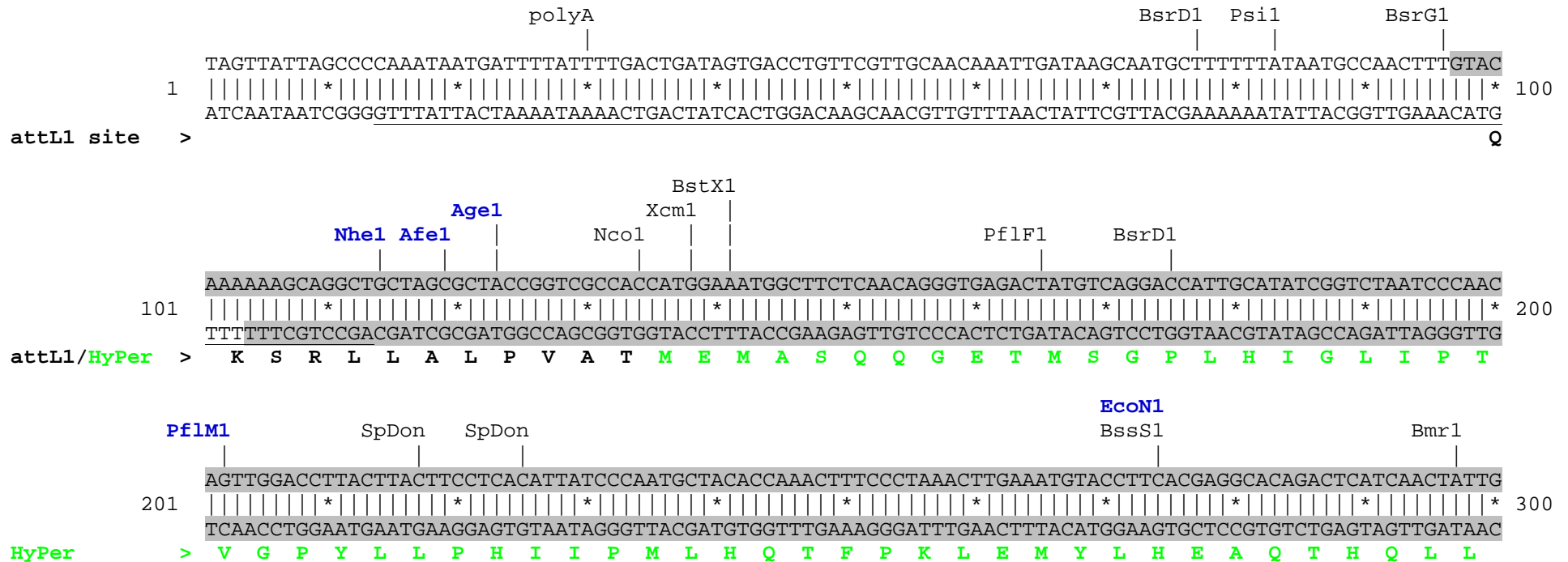


**Gateway® HyPer-AS entry clone** restriction map

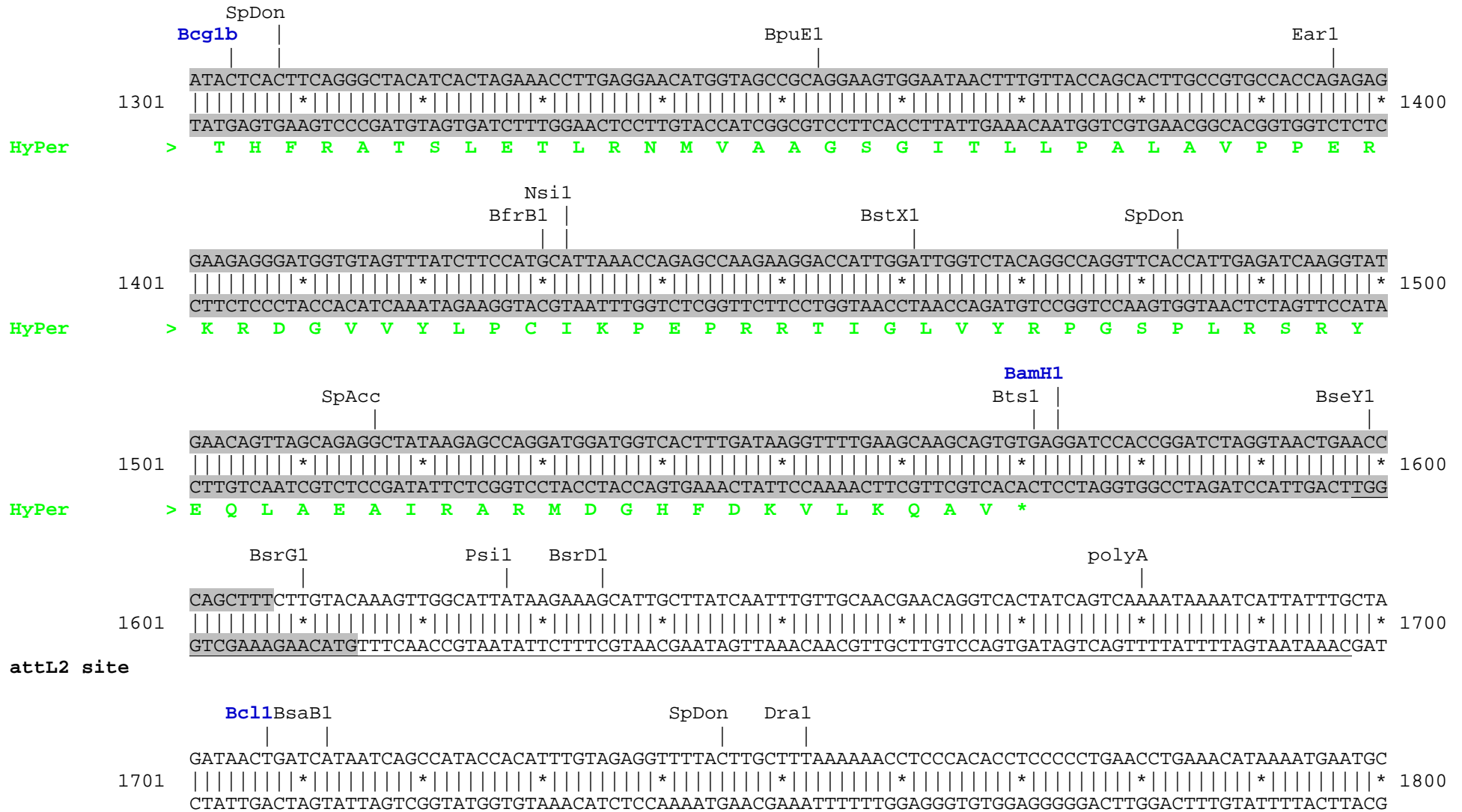
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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

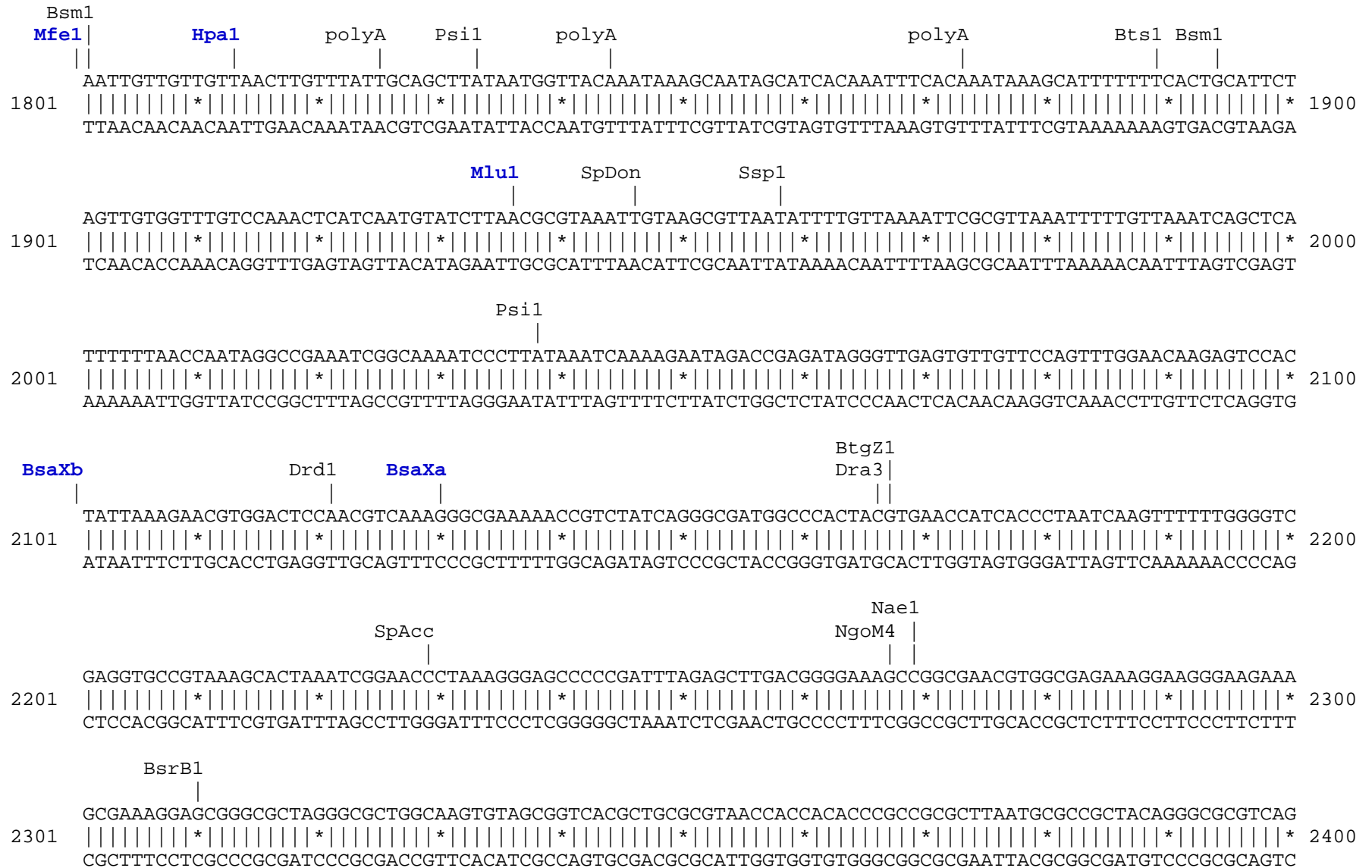
Unique sites are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). The attL sites are underlined. Shaded region corresponds to DNA sequence transferred from the entry clone into the destination vector following recombination. Non-HyPer amino acids are shown in black, HyPer amino acids are shown in green.

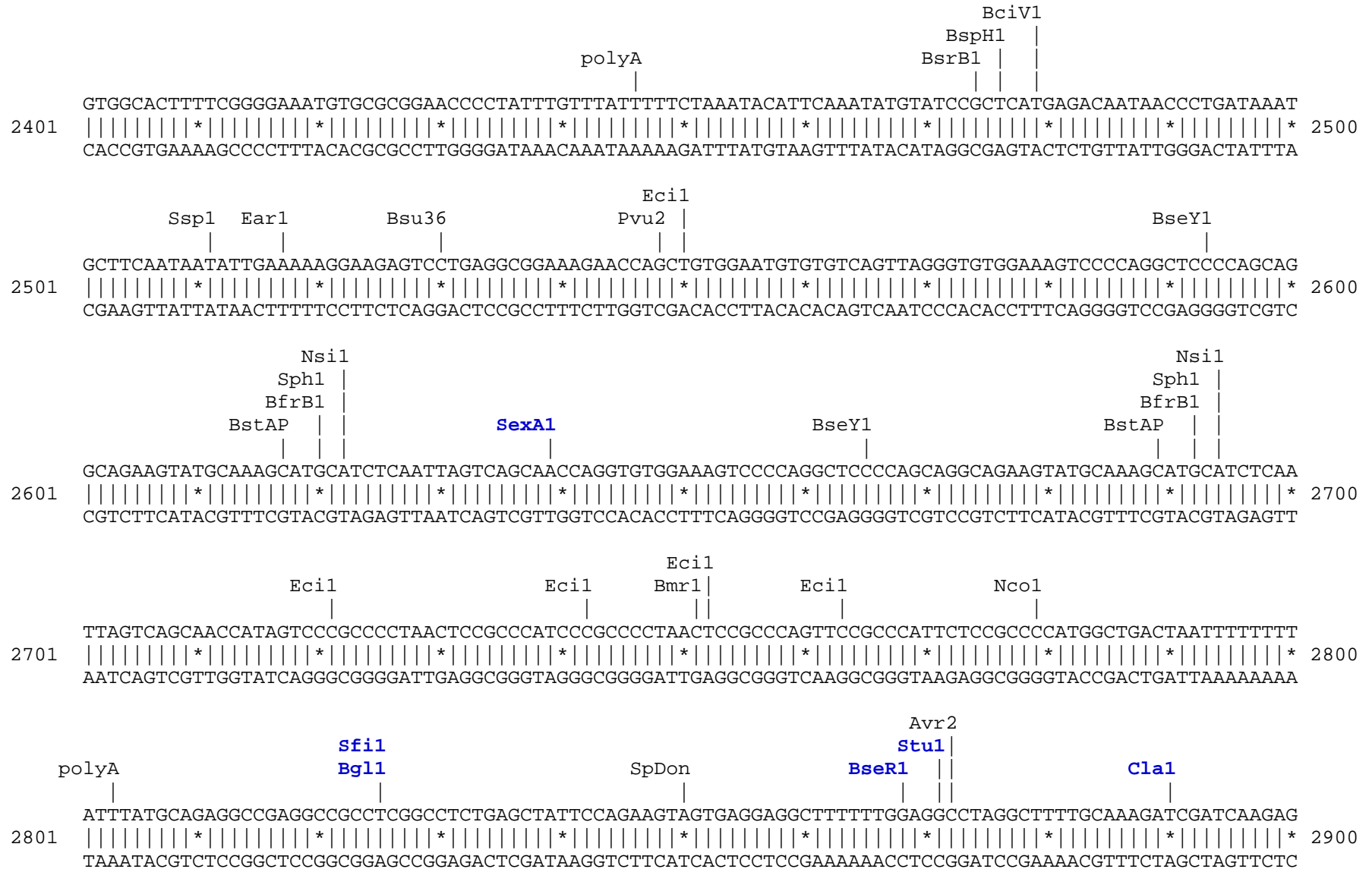






















Found:

<b>Afe1</b>	<b>Age1</b>	AlwN1	<b>ApaL1</b>	<b>Ase1</b>	Avr2	<b>Baela</b>	<b>Baelb</b>	<b>BamH1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	BciV1	<b>Bcl11</b>	BfrB1
BfuA1	<b>Bgl1</b>	<b>BmgB1</b>	Bmr1	Bpm1	BpuE1	<b>Bsa1</b>	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	BseY1	Bsm1	<b>BspE1</b>
BspH1	<b>BspLU</b>	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1	Bts1	<b>Clal</b>
Dra1	Dra3	Drd1	<b>Eag1</b>	Ear1	Ecil	Eco57	<b>EcoN1</b>	<b>EcoRV</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Mlu1</b>
Msc1	Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	Nsi1	PflF1	<b>PflM1</b>	polyA	Psi1	Pvu2	<b>Rsr2</b>
Sap1	<b>SexA1</b>	<b>Sfil</b>	SpAcc	SpDon	Sph1	Ssp1	<b>Stul</b>	<b>T7Ter</b>	Xcm1	<b>Xmn1</b>			

Unique:

<b>Afe1</b>	<b>Age1</b>	<b>ApaL1</b>	<b>Ase1</b>	<b>Baela</b>	<b>Baelb</b>	<b>BamH1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	<b>Bcl11</b>	<b>Bgl1</b>	<b>BmgB1</b>	<b>Bsa1</b>	<b>BsaXa</b>
<b>BsaXb</b>	<b>BseR1</b>	<b>BspE1</b>	<b>BspLU</b>	<b>Clal</b>	<b>Eag1</b>	<b>EcoN1</b>	<b>EcoRV</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Mfe1</b>	<b>Mlu1</b>	<b>Nar1</b>
<b>Nde1</b>	<b>Nhe1</b>	<b>PflM1</b>	<b>Rsr2</b>	<b>SexA1</b>	<b>Sfil</b>	<b>Stul</b>	<b>T7Ter</b>	<b>Xmn1</b>					

Not found:

Aar1	Aat2	Acc65	Ac11	Afl2	Ahd1	Ale1	Apal	Asc1	AsiS1	Bbs1	BbvC1	Bgl2	Blp1
Bpu10	Bsg1	BsiW1	BsmB1	BssH2	BstE2	BstZ1	_Chi	EcoK	EcoR1	FCatB	FCatL	FCatR	FCatP
ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	Pml1	PshA1	PspOM
Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	Sall	SanD1	Sbf1	Scal	Sgf1	SgrA1
Sma1	SnaB1	Spe1	Srf1	Swa1	T3RNA	T7RNA	PISce	Xba1	Xho1				

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	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													