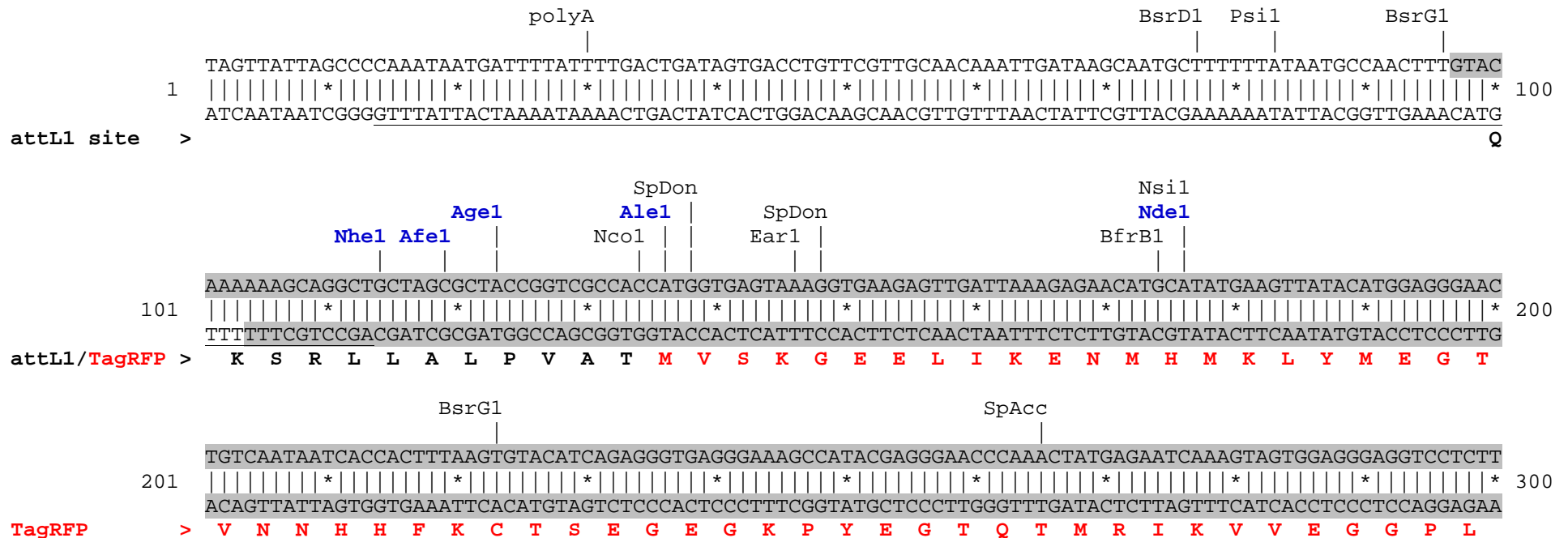
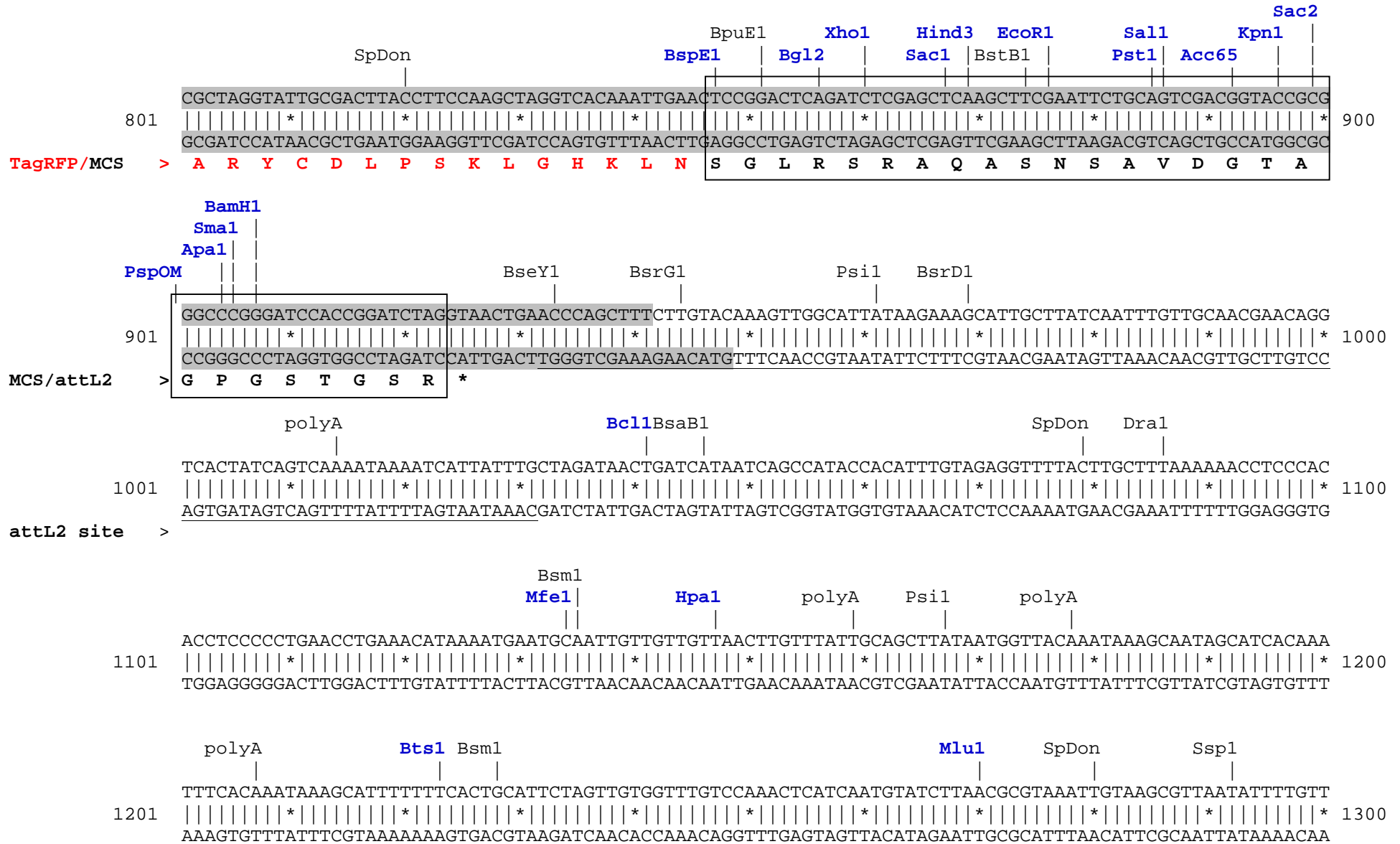


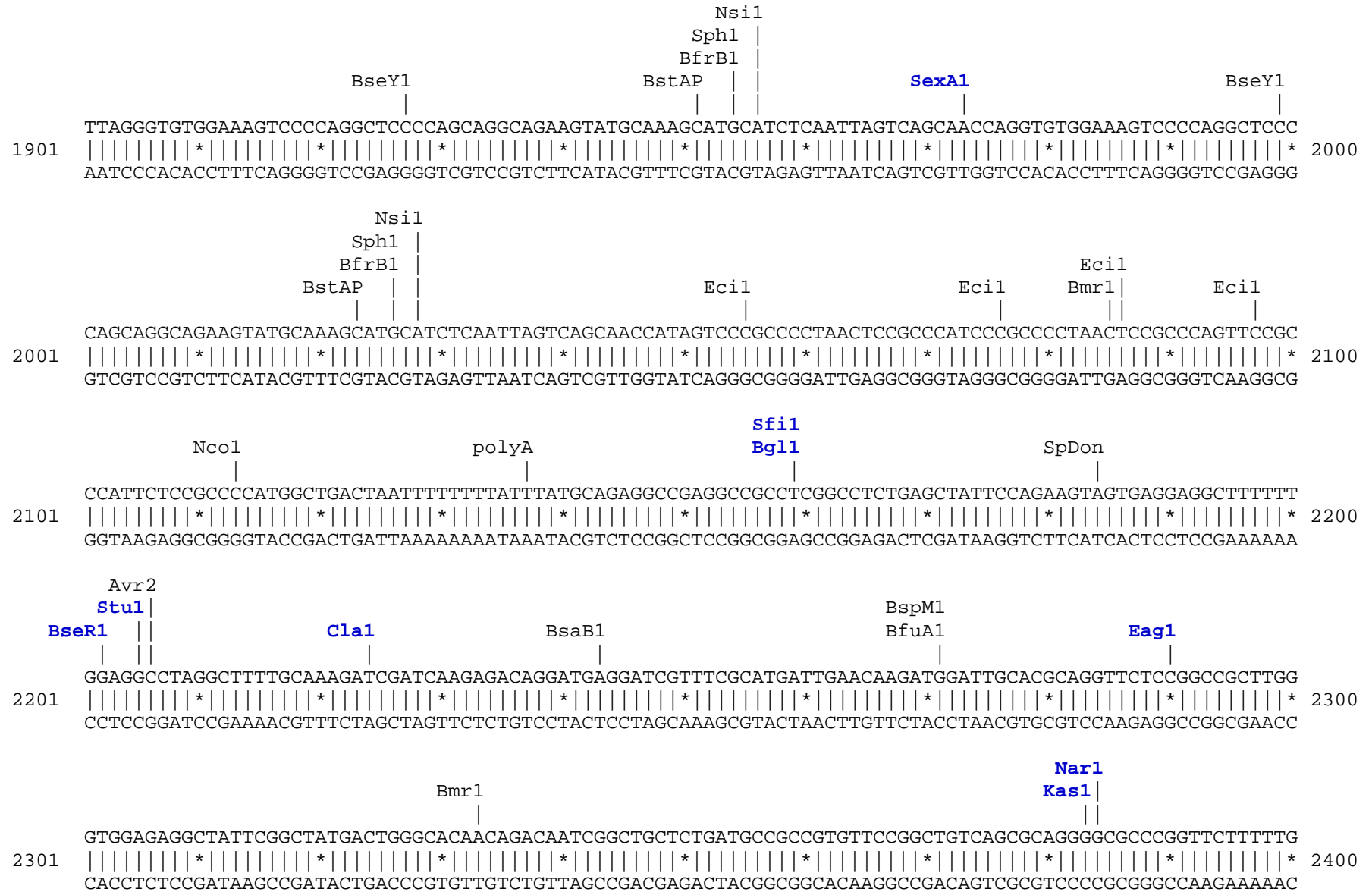
Gateway® TagRFP-AS-C entry clone restriction map

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 bold blue. 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-TagRFP amino acids are shown in black, TagRFP amino acids are shown in red.







SpAcc
|
AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGG
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
TCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCC

BciV1
Eci1 | BssS1 | SpAcc |
TAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGA
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
ATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTCGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACT

Drd1 | BpuE1 | SpAcc | Eci1 |
GCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCT
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTTCGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGA

SpDon
BspLU | Nsi1
BfrB1 |
CACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4360
GTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

Found:

Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	Apal1	Avr2	BamH1	BciV1	Bcl1	BfrB1	BfuA1
Bgl1	Bgl2	Bmr1	Bpml	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	BspE1	BspH1
BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstE2	Bsu36	BtgZ1	Bts1	Clal	Dra1
Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1
Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsil	PflF1	polyA	Psi1	PspOM	Pst1	Pvu2
Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfil	Sma1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xho1

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	Apal1	BamH1	Bcl1	Bgl1	Bgl2	Bsa1	BsaXa	BsaXb
BseR1	BspE1	BspLU	BstE2	Bts1	Clal	Dra3	Eag1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1
Mfe1	Mlu1	Msc1	Nar1	Nde1	Nhe1	PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SexA1
Sfil	Sma1	Stu1	Xho1										

Not found:

Aar1	Aat2	Ac11	Ahd1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcgl1a	Bcgl1b	Blp1
BmgB1	Bpu10	Bsg1	BsiW1	BsmB1	BssH2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK
EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Not1	Nrul	Pac1
PflM1	Pme1	Pml1	PshA1	Pvu1	R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Scal	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	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													