

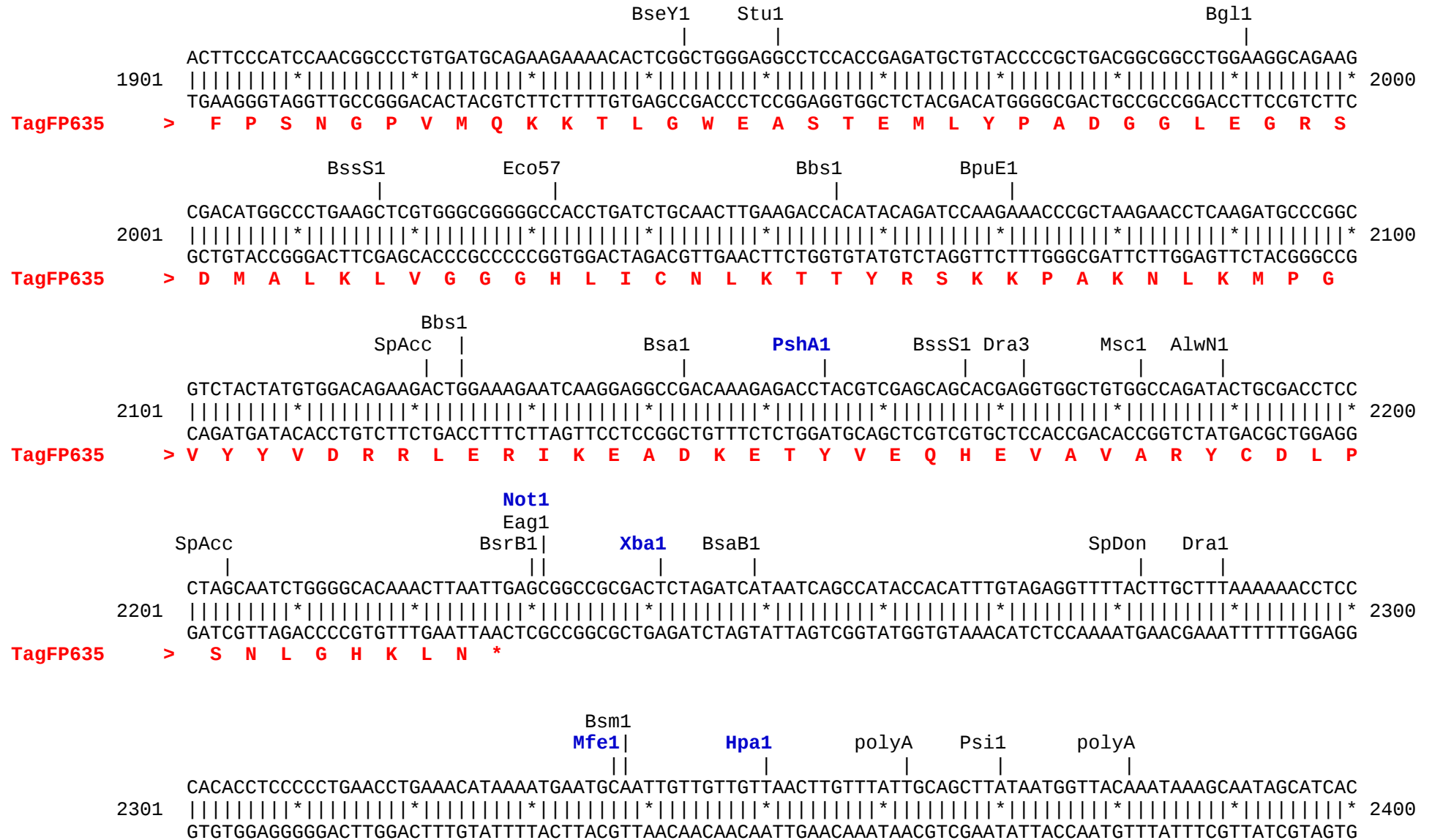
pTagFP635-EB3 vector restriction map

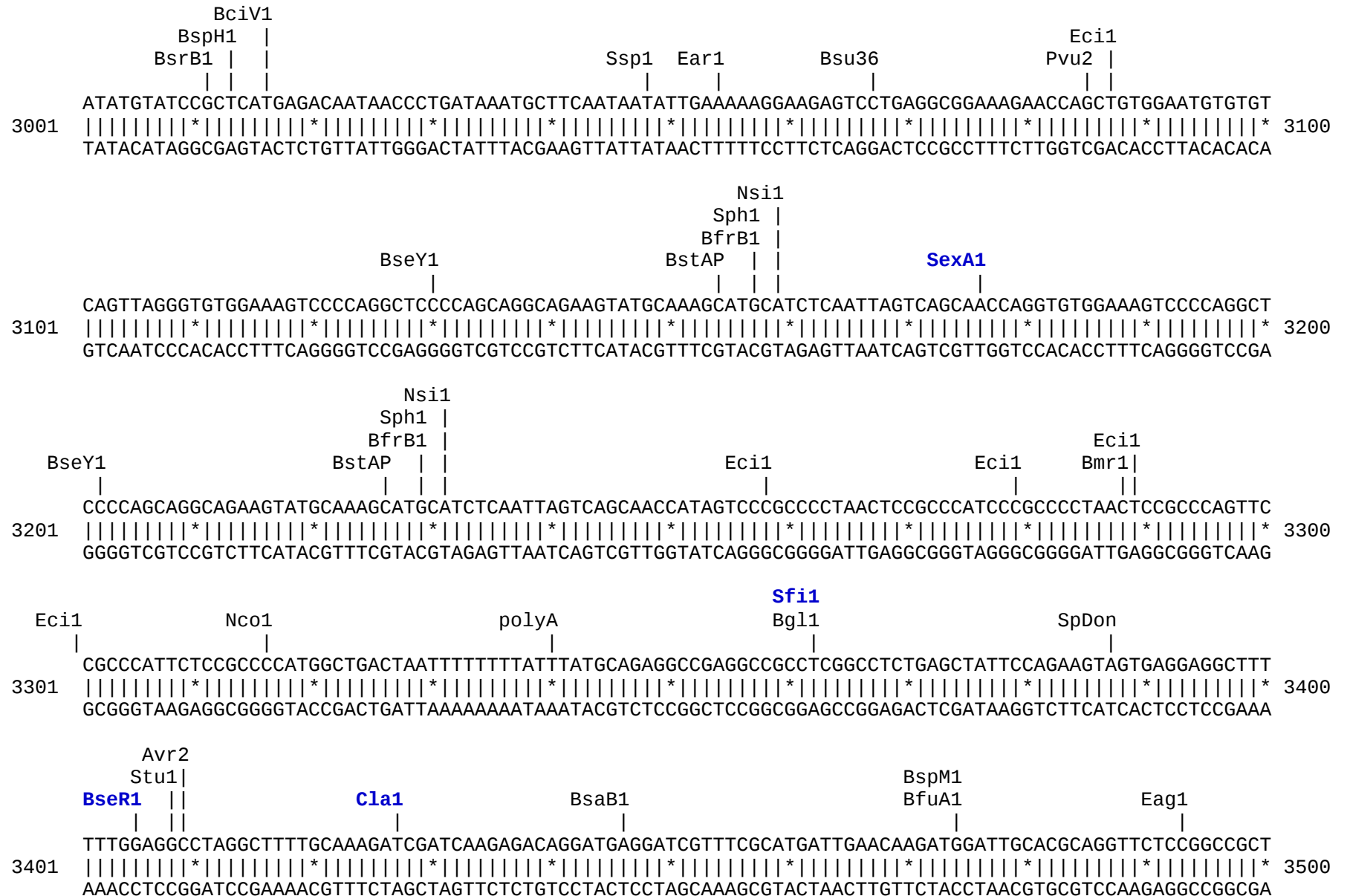
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 base pairs long are not included – for the more complete enzyme list please refer to the Table of restriction 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). TagFP635 amino acids are shown in red, EB3 amino acids are shown in green, linker amino acids are shown in black.



2





Bmr1

Nar1
Kas1

TGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGT CAGCGCAGGGGCGCCCGTTC TTT
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
ACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAA

Drd1 Msc1 Fsp1 Pvu2

TTGTCAAGACC GACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTT CCTTGCGCAGCTGTGCT
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
AACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGA

PflF1 Eco57 SpDon

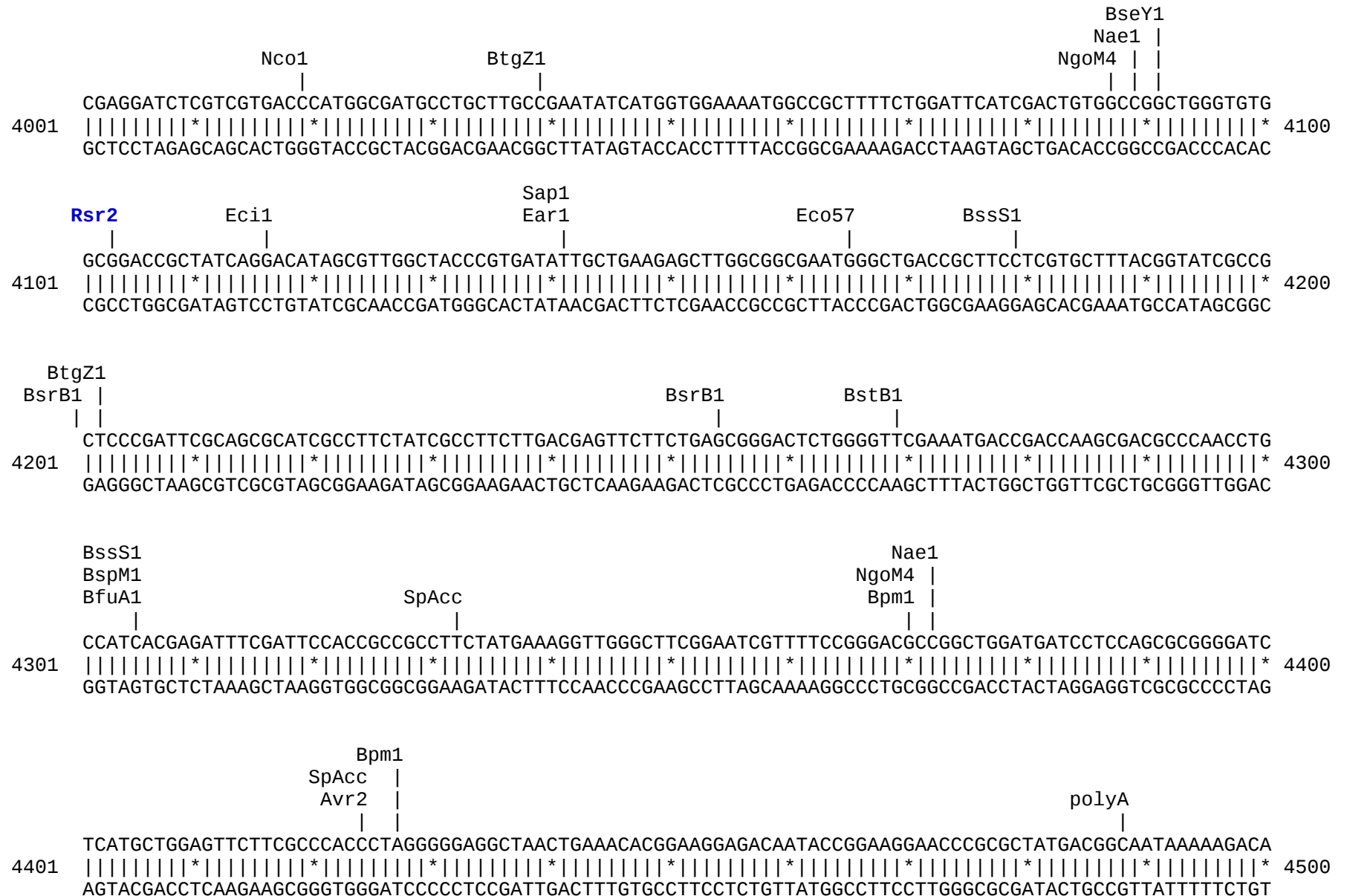
CGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGT CATCTCACCTTGCTCCTGCCGAGAAAGTATCC
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
GCTGCAACAGTGACTTCGCCCTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGG

BtgZ1 BspM1 BfuA1 BciV1 BsrD1

ATCATGGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
TAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCT

Sap1 Ear1 BpuE1 Sph1

TGGAAGCCGGTCTTGT CGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGA AACTGTT CGCCAGGCTCAAGGCGAGCATGCCCGACGG
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
ACCTTCGGCCAGAACAGCTAGTCTCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTGCGCTTGACAAGCGGTCCGAGTTCGCTCGTACGGGCTGCC



BpuE1
 |
 TGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCACACAG
 5101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
 ACGGTCACCGCTATTACGACACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTC

BseY1
 |
 CCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATC
 5201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
 GGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAG

BciV1
 Eci1 |
 |
 CGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTTCGCCACCTCTGACT
 5301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
 GCCATTCGCCGTCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGA

BssS1
 |
 SpAcc
 |
 TGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTT
 5401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
 ACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAA

Drd1
 |
 BpuE1
 |
 SpAcc
 |
 Eci1
 |
 GCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
 5501 |||||*|||||*|||||*|||||*|||||*|||||*|||||* 5563
 CGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

SpDon
 BspLU
 ||
 Nsi1
 BfrB1
 |
 |

Found:

Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1	BfrB1
BfuA1	Bgl1	Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1
Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
_Chi	Cla1	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoK	EcoN1	EcoR1	Fsp1	Hind3
Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	PflM1
polyA	PshA1	Psi1	Pst1	Pvu2	Rsr2	Sac1	Sal1	Sap1	SexA1	Sfi1	SnaB1	SpAcc	SpDon
Sph1	Ssp1	Stu1	Xba1	Xho1									

Unique:

Afe1	Afl2	Age1	Ase1	BamH1	Bcl1	Blp1	BsaXa	BsaXb	BseR1	Bsg1	BspE1	BspLU	BsrG1
Bts1	_Chi	Cla1	EcoK	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1
Not1	PflF1	PshA1	Pst1	Rsr2	Sal1	SexA1	Sfi1	SnaB1	Xba1	Xho1			

Not found:

Aar1	Acc65	Acl1	Ahd1	Apa1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Bcg1a	Bcg1b	BmgB1	Bpu10
BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1
I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL	R4atP	R4atR
Sac2	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce
Xcm1	Xmn1												

Excluded by site complexity:

Acc1	Aci1	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													