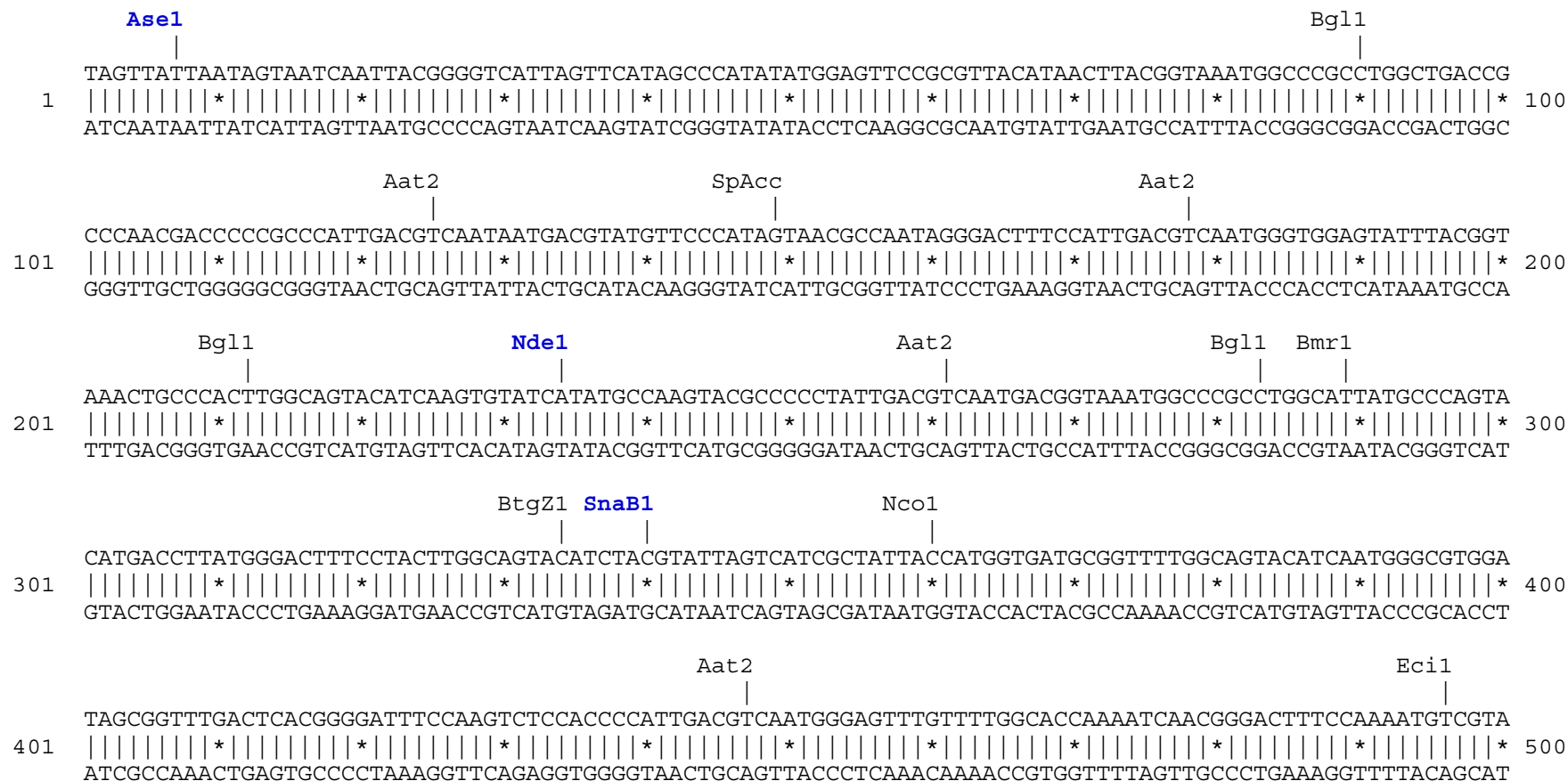
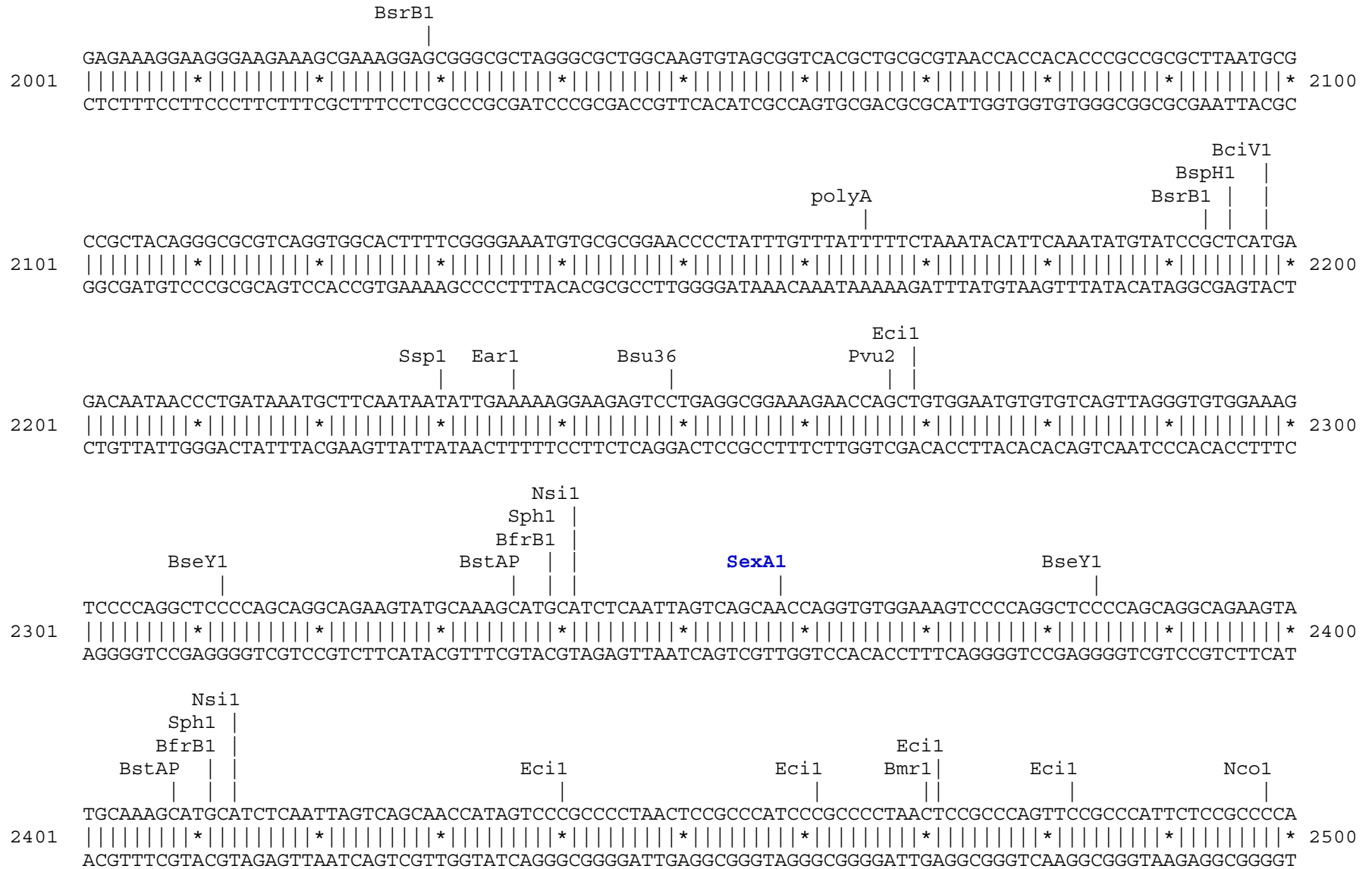


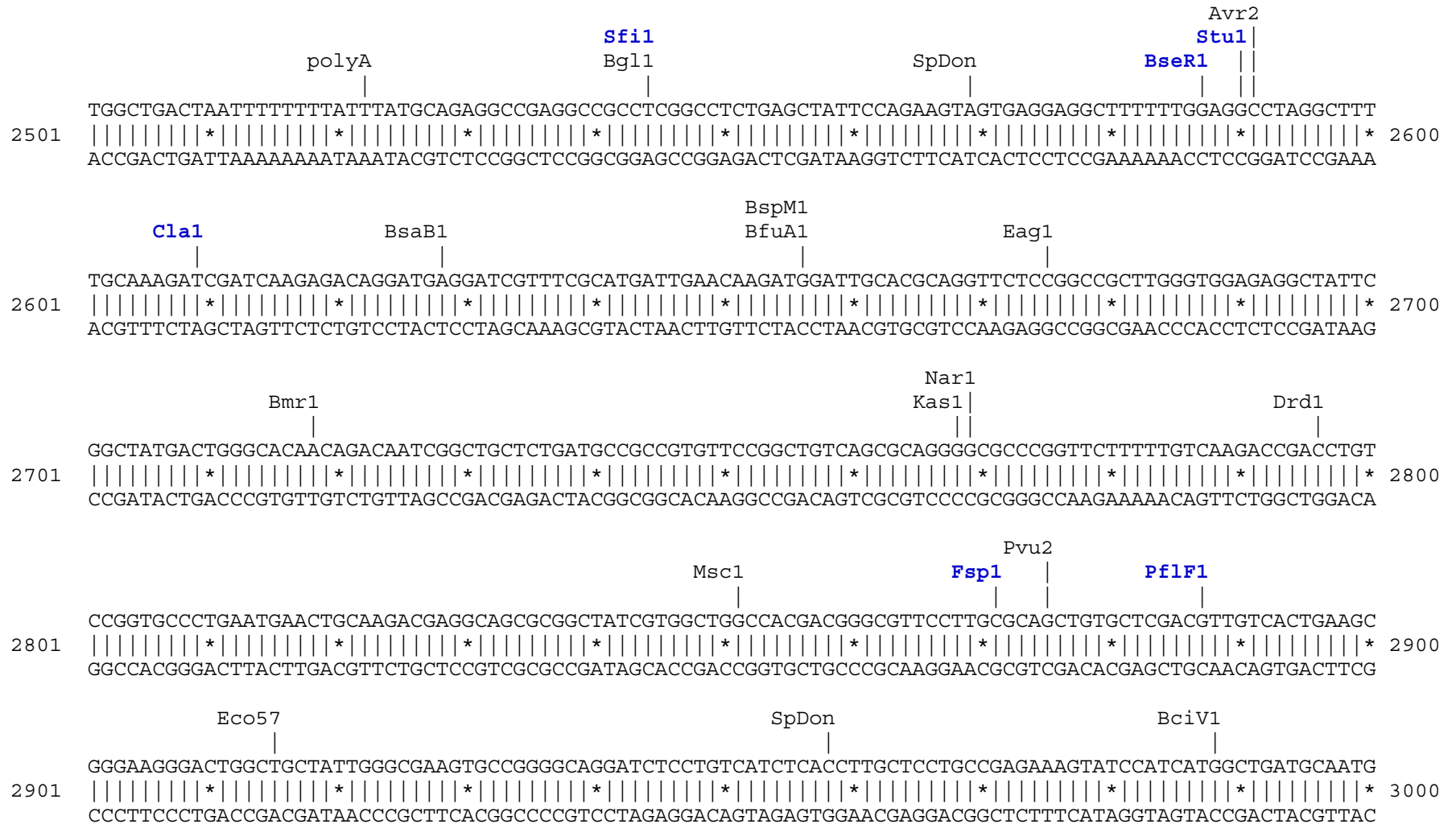
pTurboYFP-N vector restriction map

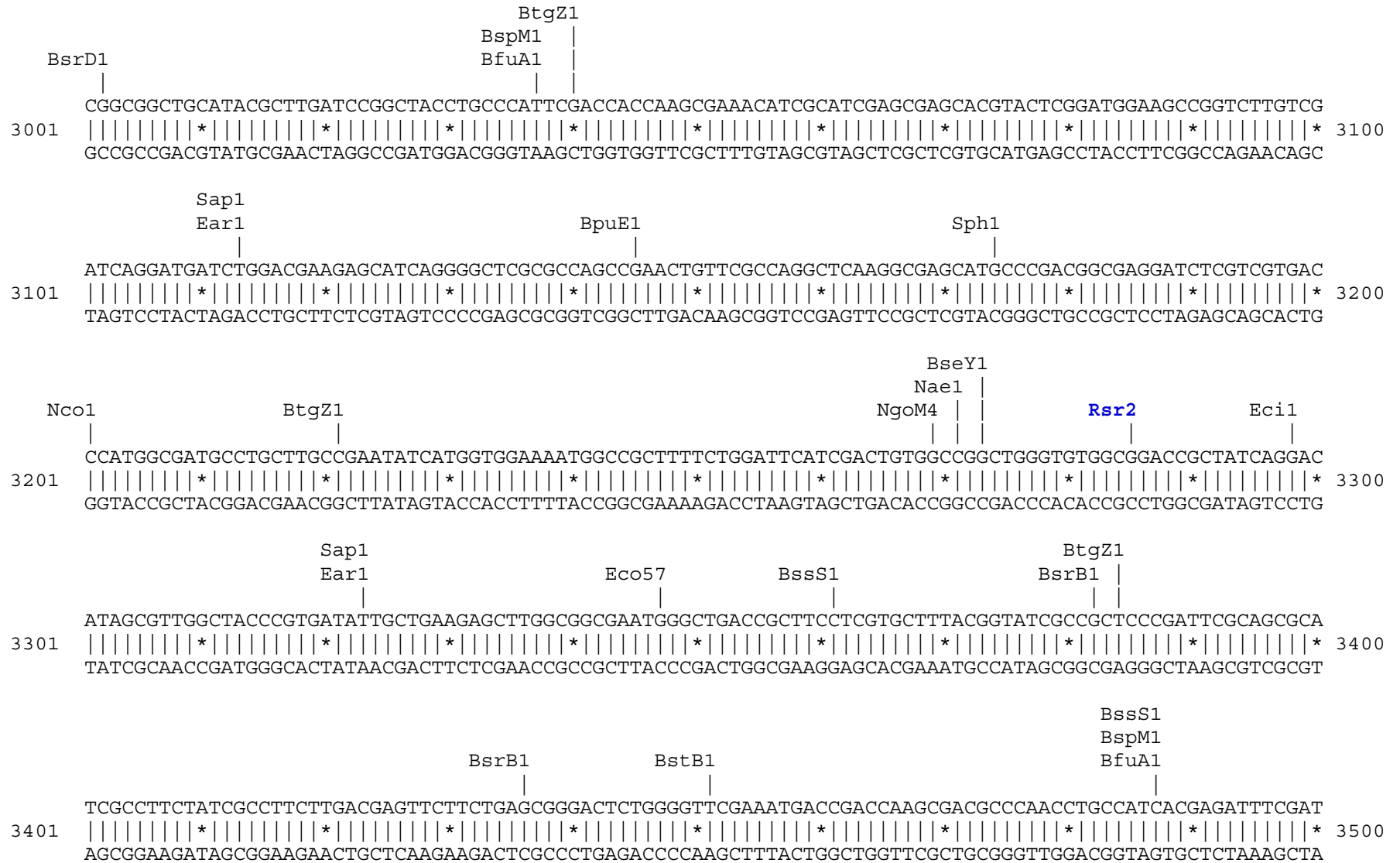
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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









Eco57 | SpAcc |
4101 CCAGCGGTGGTTTGTGGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGT * 4200
GGTCGCCACCAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACA

AlwN1 |
4201 AGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTC * 4300
TCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTACCGGACGACGGTACCGCTATTGAG

BpuE1 | ApaL1 | BseY1 |
4301 GTGCTTACCGGGTTGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACCGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACG * 4400
CACAGAATGGCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTTCGGGTGCAACCTCGCTTGC

SpAcc | BciV1 | Eci1 |
4401 ACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCG * 4500
TGGATGTGGCTTGACTCTATGGATGTGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTGCGCGTCCCAGC

BssS1 | SpAcc | Drd1 |
4501 GAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTG * 4600
CTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACAC

BpuE1 | SpAcc | Eci1 | SpDon | **BspLU** |
4601 ATGCTCGTCAGGGGGCGGAGCCTATGGAACAAACGCGCCAGCAACGCGGCTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTTGTGCTCACATGTTCTTTCT * 4700
TACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTCGTTCGCGCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGA

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                                NsiI
                                BfrB1 |
                                | |
4701  GCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 4745
      |||||*|||||*|||||*|||||*|||||
      CGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

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Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	BamH1	BciV1	BfrB1
BfuA1	Bgl1	Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1
Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	BstE2	Bsu36
BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1
Kas1	Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	PflM1
Pml1	polyA	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	SgrA1
Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1	Xmn1				

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apal	Ase1	BamH1	Bgl2	Blp1	BsaXa	BsaXb	BseR1	BspE1
BspLU	BssH2	Clal	Dra3	EcoR1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Nde1	Nhe1	Not1	PflF1
PflM1	PspOM	Pst1	Rsr2	Sac1	Sall	SexA1	Sfi1	SgrA1	Sma1	SnaB1	Stu1	Xba1	Xho1
Xmn1													

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1	BmgB1	Bpu10
BsiW1	BsmB1	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1
Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	Spe1	Srf1	Swa1	T3RNA	T7RNA
T7Ter	PISce	Xcm1											

Excluded by site complexity:

Acc1	Ac11	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													