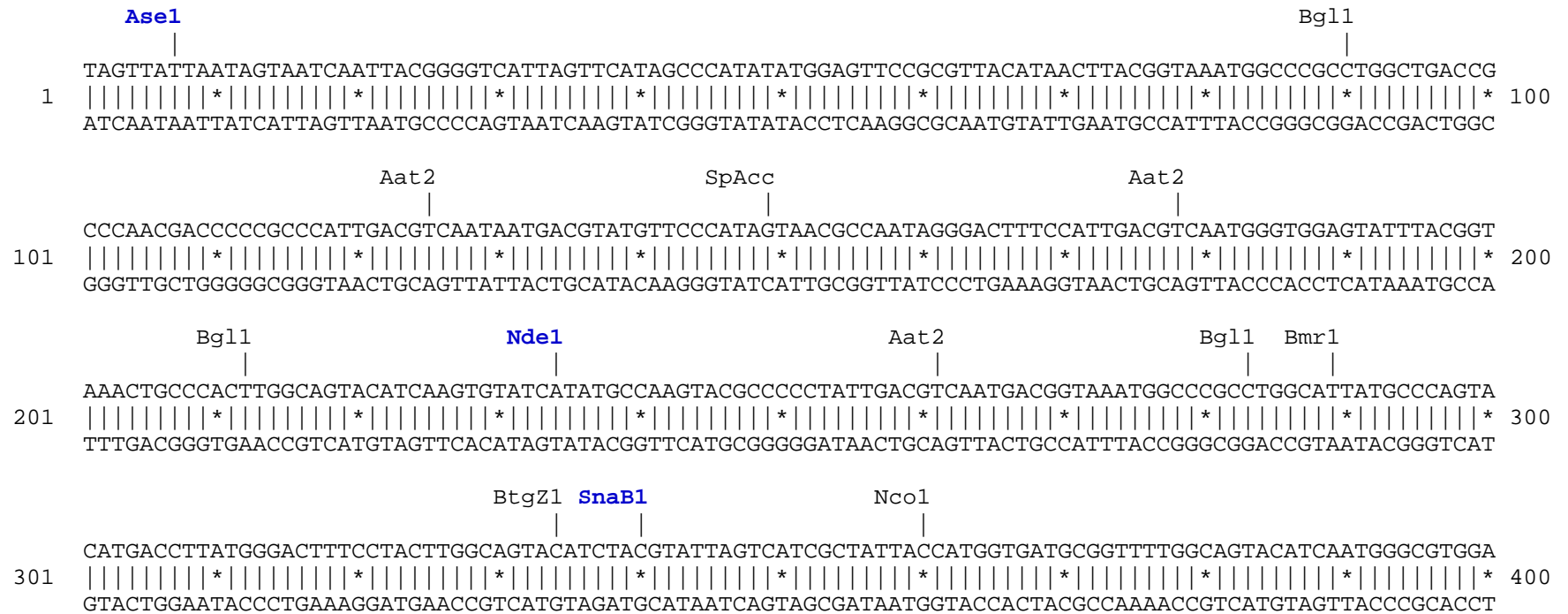
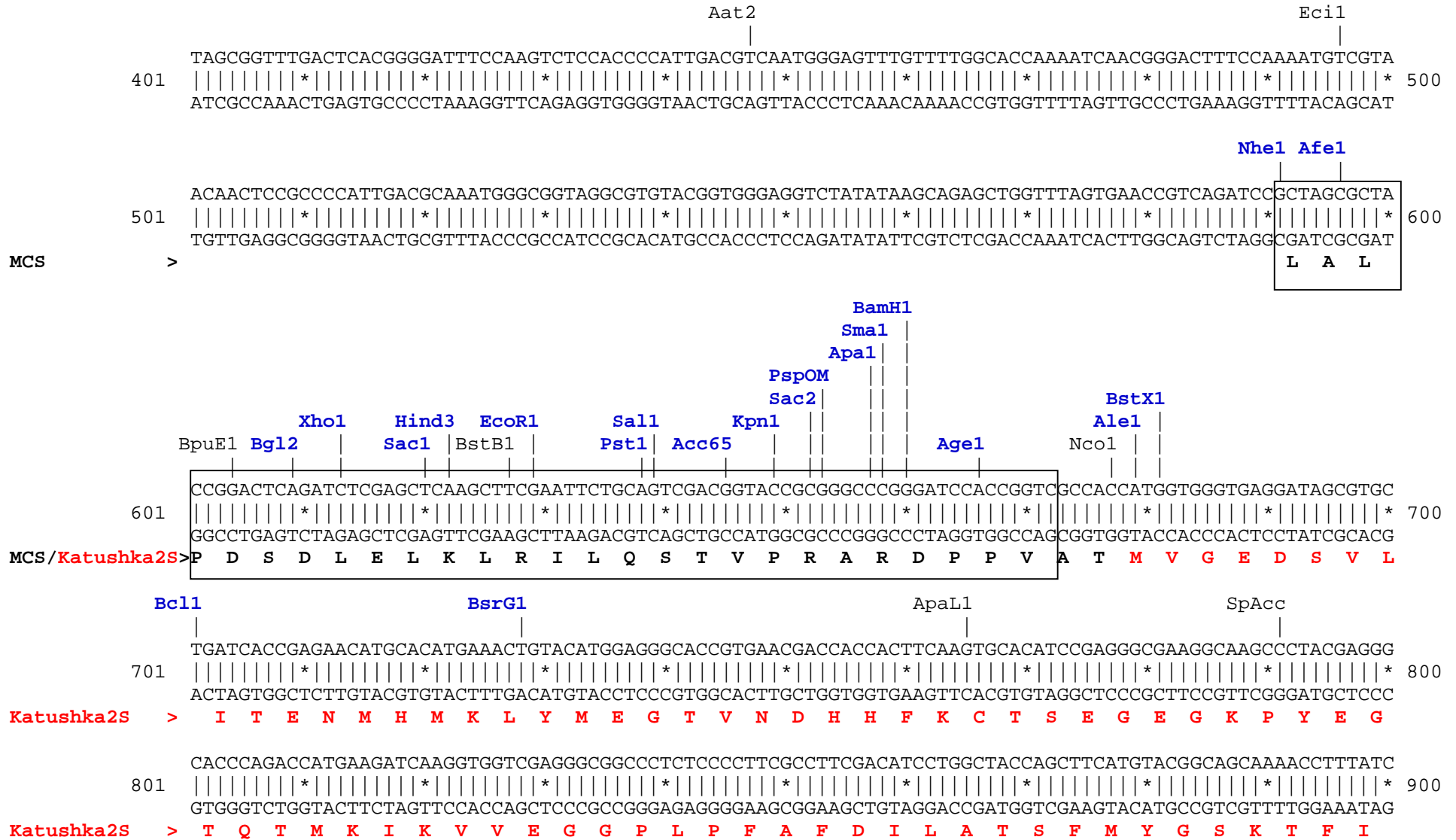


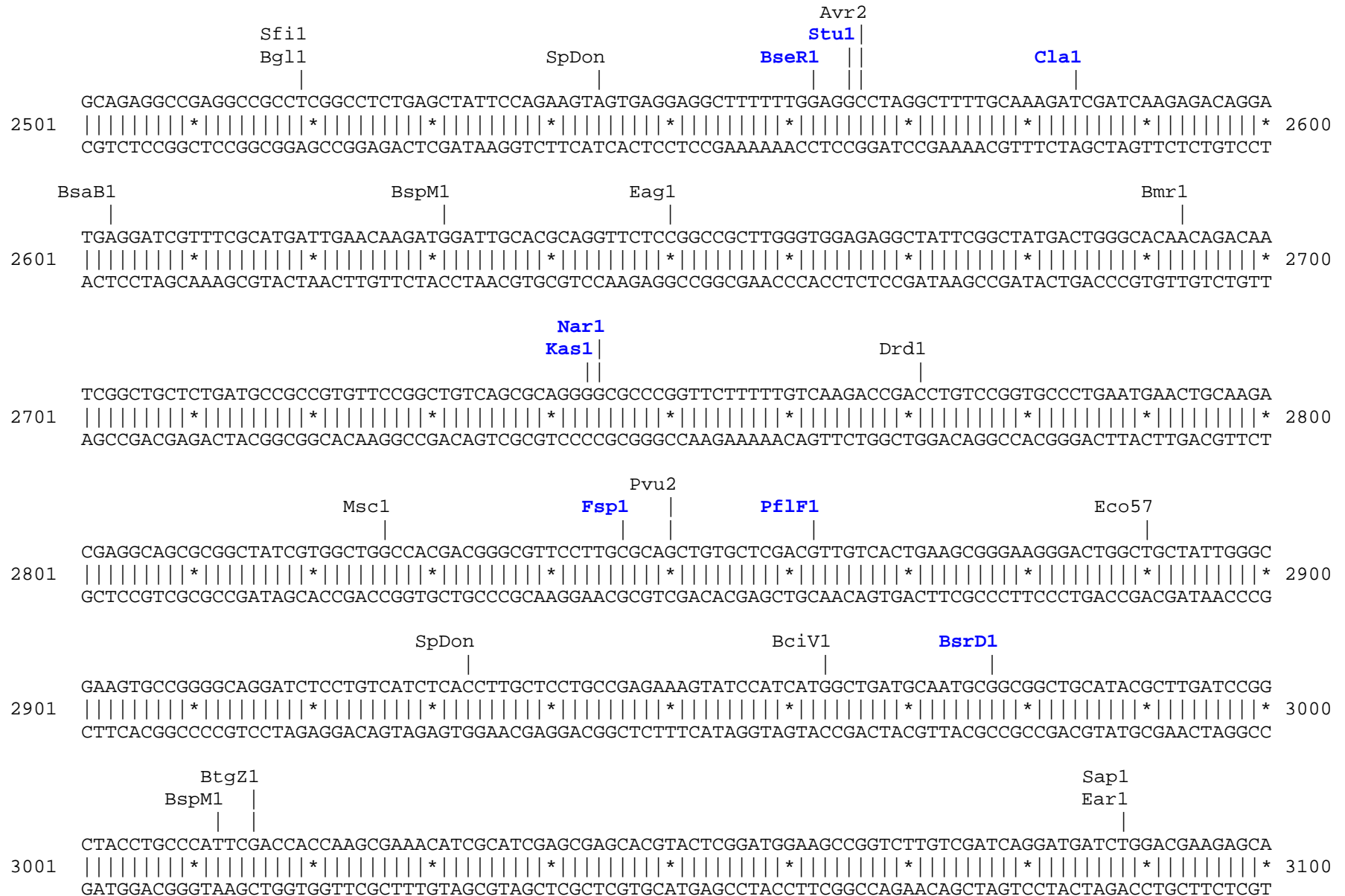
pKatushka2S-N vector restriction map

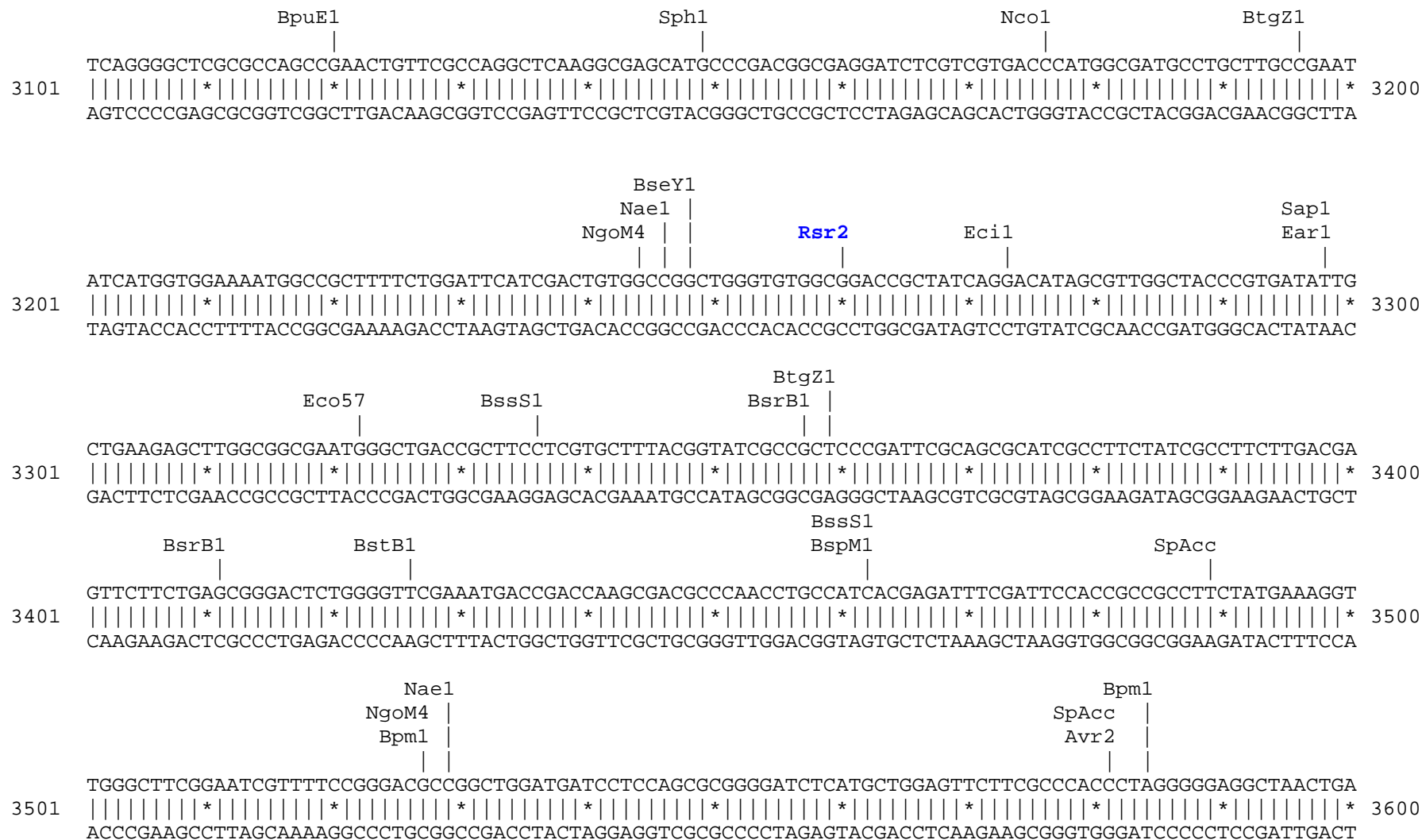
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction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









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                                polyA      polyA
                                |           |
AACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGTTTTGTTTCATAAACGCGGG
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
TTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTTCGTGCCACAACCCAGCAAACAAGTATTTGCGCCC

                                Bsa1
                                |
GTTCGGTCCCAGGGCTGGCACTCTGTGCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCAGTTTCTTCCTTTTCCCAACCCACCCCAAGTT
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
CAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAA

                                BstAP      AlwN1      Bsu36      Dra1
                                |           |           |           |
CGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTT
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
GCCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAA

                                Dra1      BspH1
                                |           |
TTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA
3901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
AATTAAATTTTCCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTT

                                BpuE1
                                |
AAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTGTGGCCGGATC
4001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
TTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTTCGCCACCAAACAAACGGCCTAG

                                Eco57      SpAcc
                                |           |
AAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAA
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
TTCTCGATGGTTGAGAAAAAGGCTTCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTT

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                                     AlwN1                               BpuE1
                                     |                               |
GAACTCTGTAGCACCGCCTACATACCTCGTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGA
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCT

                                     ApaL1           BseY1
                                     |               |
CGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTAC
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
GCTATCAATGGCCTATTCCGCGTGCAGCCGACTTGCCCCCAAGCACGTGTGTGCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATG

                                     BciV1
                                     |   |
      SpAcc                               Eci1                               BssS1
      |                                   |   |                               |
AGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCT
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
TCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGA

                                     SpAcc                               Drd1           BpuE1           SpAcc
                                     |                                   |   |               |                               |
TCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTA
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
AGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGAT

                                     Eci1
                                     |
TGGAAAAACGCCAGCAACGCGGCCTTTTTTACGGTTTCTGGCCTTTTGTGCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATA
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
ACCTTTTTTTCGGTTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTAT

                                     NsiI
                                     |
      BfrB1 |
      |   |
ACCGTATTACCGCCATGCAT
4701 |||||*|||||* 4720
TGGCATAATGGCGGTACGTA
```

Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	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	polyA	PshA1
Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall1	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc
SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1								

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	Ase1	BamH1	Bbs1	Bcl1	Bgl2	BsaXa	BsaXb	BseR1
Bsg1	BspLU	BsrD1	BsrG1	BstX1	Clal	Dra3	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1
Nar1	Nde1	Nhe1	Not1	PflF1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall1	SexA1	Sma1
SnaB1	Stu1	Xba1	Xho1										

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Blp1	BmgB1	Bpu10	BsiW1
BsmB1	BspE1	BssH2	BstE2	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP
Mlu1	Nru1	Pac1	PflM1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Scal	Sgf1	SgrA1	Spe1	Srf1
Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1							

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfal	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													