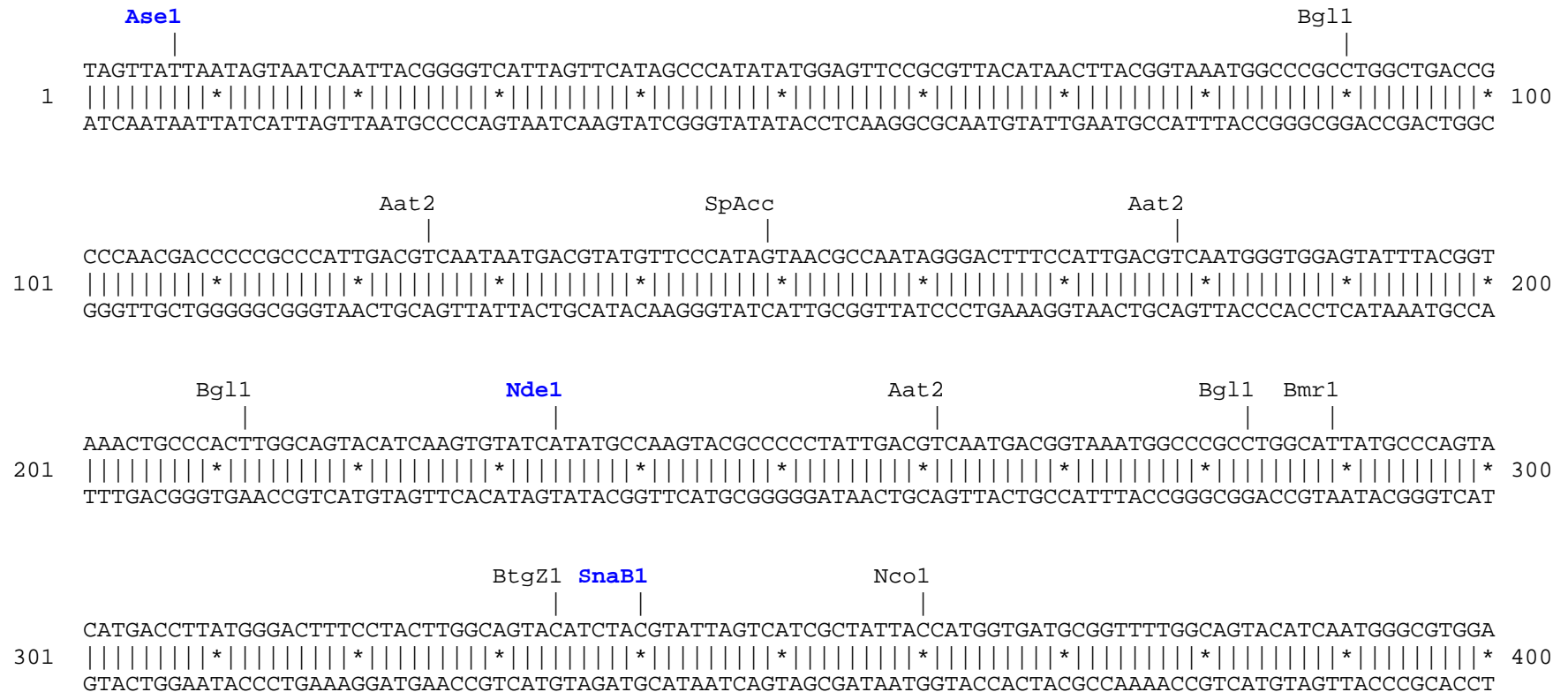


pPA-TagRFP-C vector restriction map

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.



```

                                     Aat2
                                     |
TACGGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                               Eci1
                                               |
ACAAC TCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGGTG
501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
TGTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAC

      Ale1
      |
MscI  NcoI  SapI
|      |      |      |
601 GCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACCTTCAAGTGCACAT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
CGGTGGTACCACAGATTCCCCTTCTCGACTAATTCCTCCTTGTACGTGTACTTTCGACATGTACCTCCCCTGGCACTTGTTGGTGGTGAAGTTCACGTGTA

PA-TagRFP > M V S K G E E L I K E N M H M K L Y M E G T V N N H H F K C T S

      BsrGI
      |
      SpAcc
      |
CCGAGGGCGAAGGCAAGCCCTACGAGGGCAGCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAG
701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
GGCTCCCGCTTCCGTTCCGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTC

PA-TagRFP > E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S

                                     Bsu36
                                     |
CTTCATGTACGGCAGCAGCACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTGGAAGCAGTCCTTCCCCTGAGGGCTTCACATGGGAGAGAGTCAACC
801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
GAAGTACATGCCGTCGTCGTGGAAGTAGTTGGTGTGGGTCCCCTAGGGGCTGAAGACCTTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGG

PA-TagRFP > F M Y G S S T F I N H T Q G I P D F W K Q S F P E G F T W E R V T

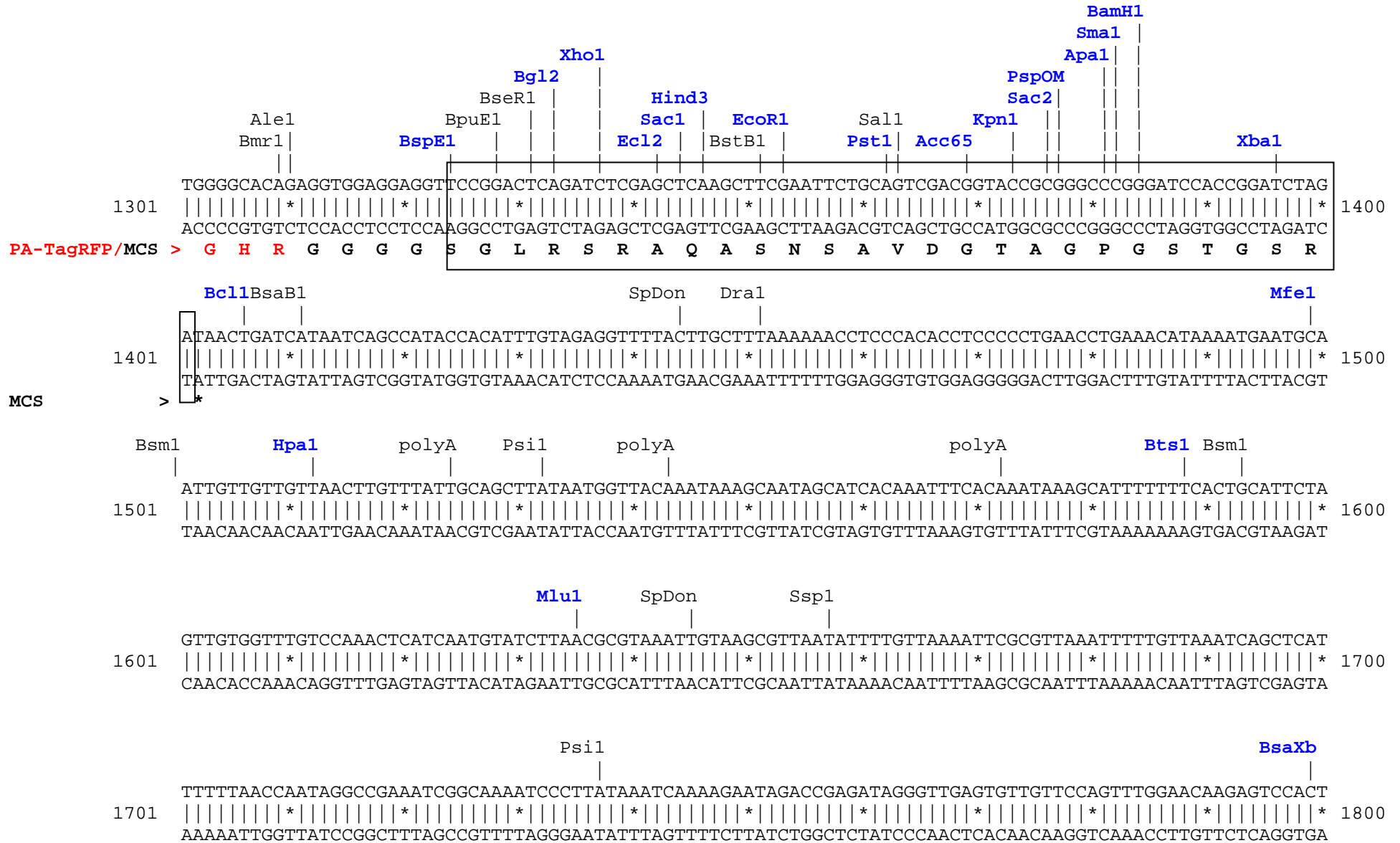
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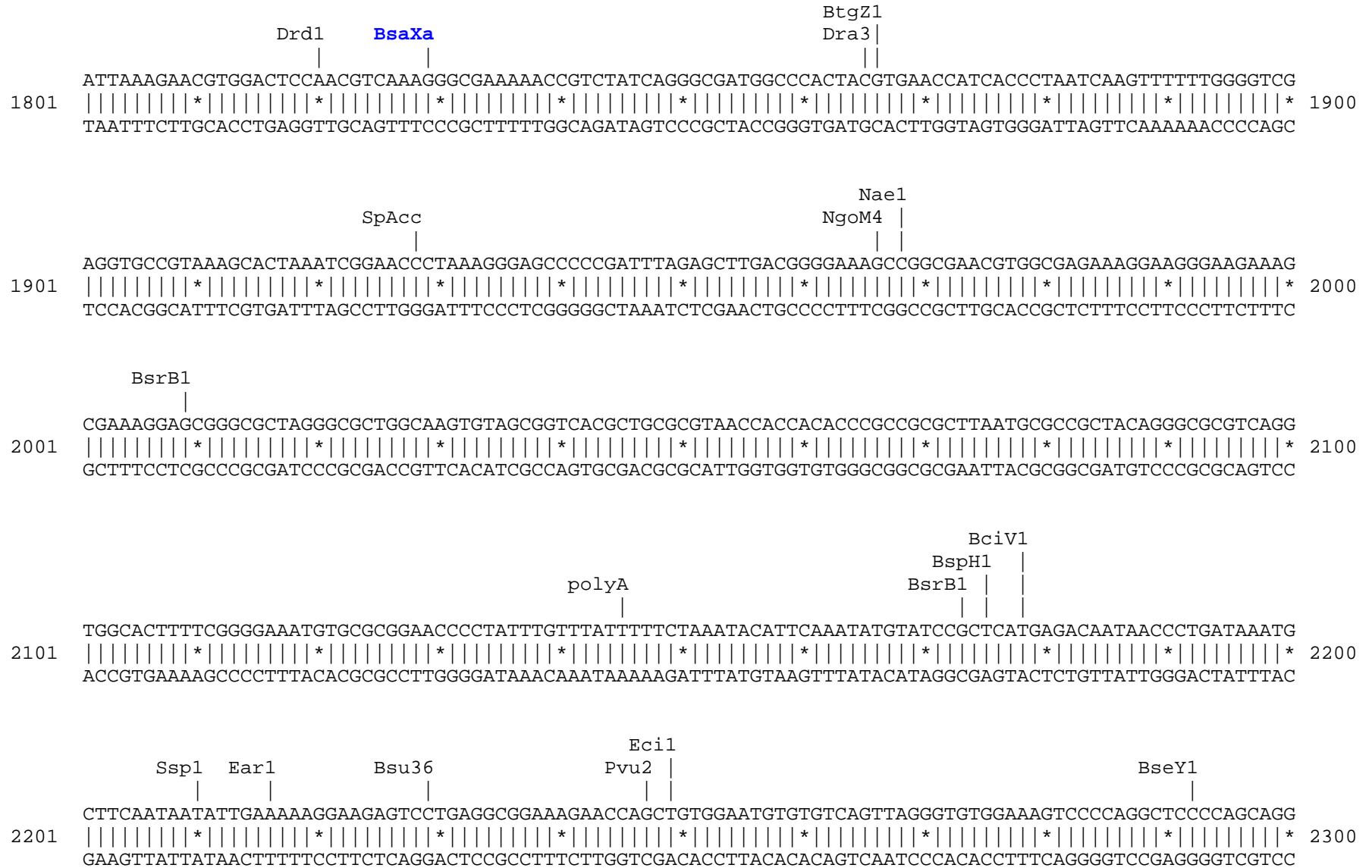
Bbs1 Bpm1
ACATACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCAT
901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
TGTATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTCGGAGGTCTCGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTA
PA-TagRFP > T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F P S

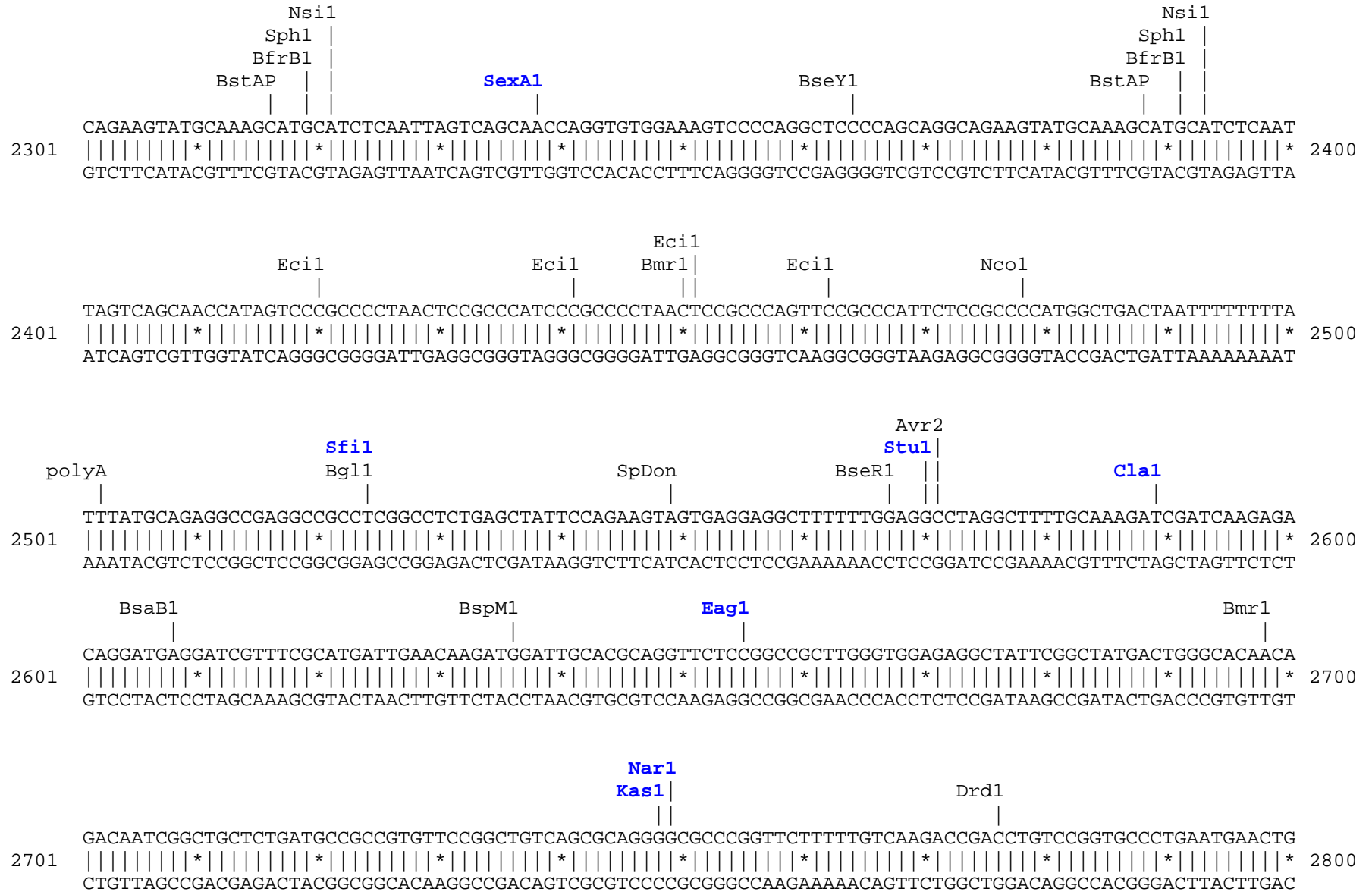
BseY1 Bgl1 Sall
CCAACGGCCCTGTGATGAAGAAGAAAACACTCGGCTGGGAACCGAGCACCCGAGAAACTGAAACCCGCTGACGGCGGCCTGGAAGGCAGGGTTCGACATGGC
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
GGTTGCCGGGACACTACTTCTTCTTTGTGAGCCGACCCTTGGCTCGTGGCTCTTTGACTTTGGGCGACTGCCGCCGGACCTTCCGTCCCAGCTGTACCG
PA-TagRFP > N G P V M K K K T L G W E P S T E K L K P A D G G L E G R V D M A

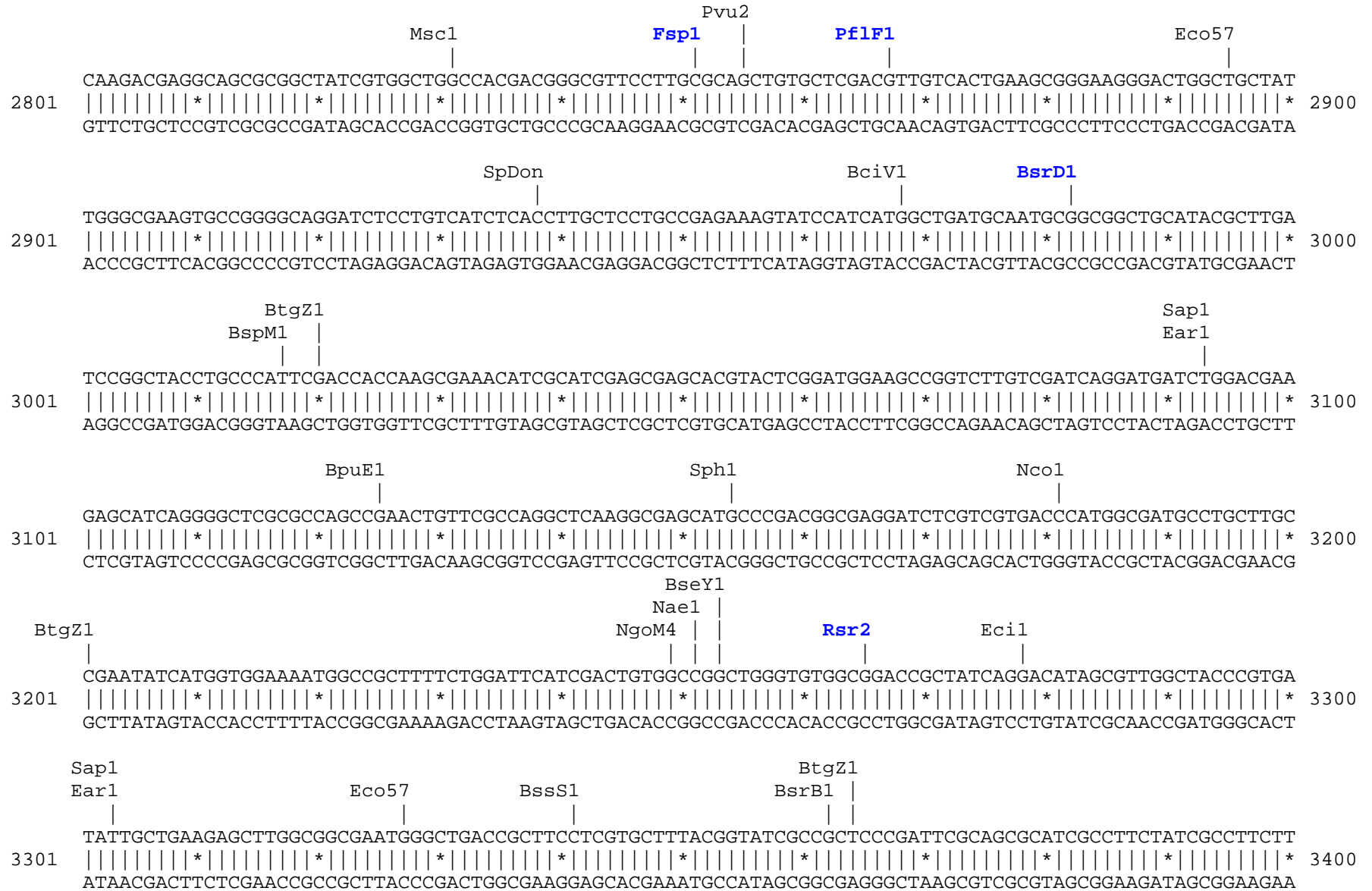
BssS1 Eco57 BpuE1
CCTGAAGCTCGTGGGCGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTAT
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
GGACTTCGAGCACCCGCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATA
PA-TagRFP > L K L V G G G H L I C N F K T T Y R S K K P A K N L K M P G V Y Y

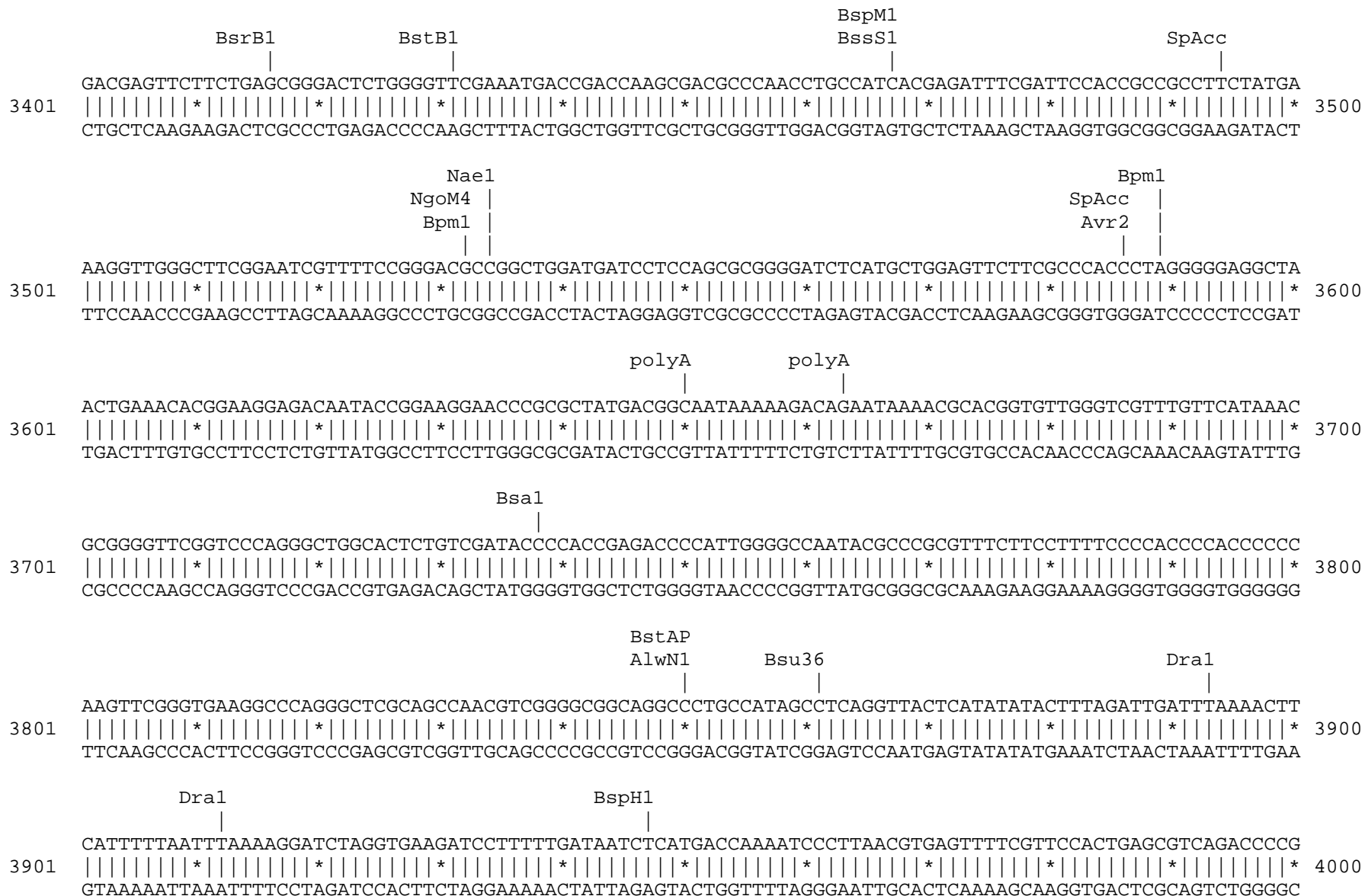
Bsa1 BssS1 Bmr1 Dra3 Msc1 SpAcc
GTGGACCGCAGACTGGAAATCATCAAGGAGGCCGACAAAGAGACCTACTGGGAGCAGCACGAGGTGGCTGTGGCCAGATACTCCGACCTCCCTAGCAAAC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
CACCTGGCGTCTGACCTTTAGTAGTTCCTCCGGCTGTTTCTCTGGATGACCCTCGTTCGTGCTCCACCGACACCGGTCTATGAGGCTGGAGGGATCGTTTG
PA-TagRFP > V D R R L E I I K E A D K E T Y W E Q H E V A V A R Y S D L P S K L

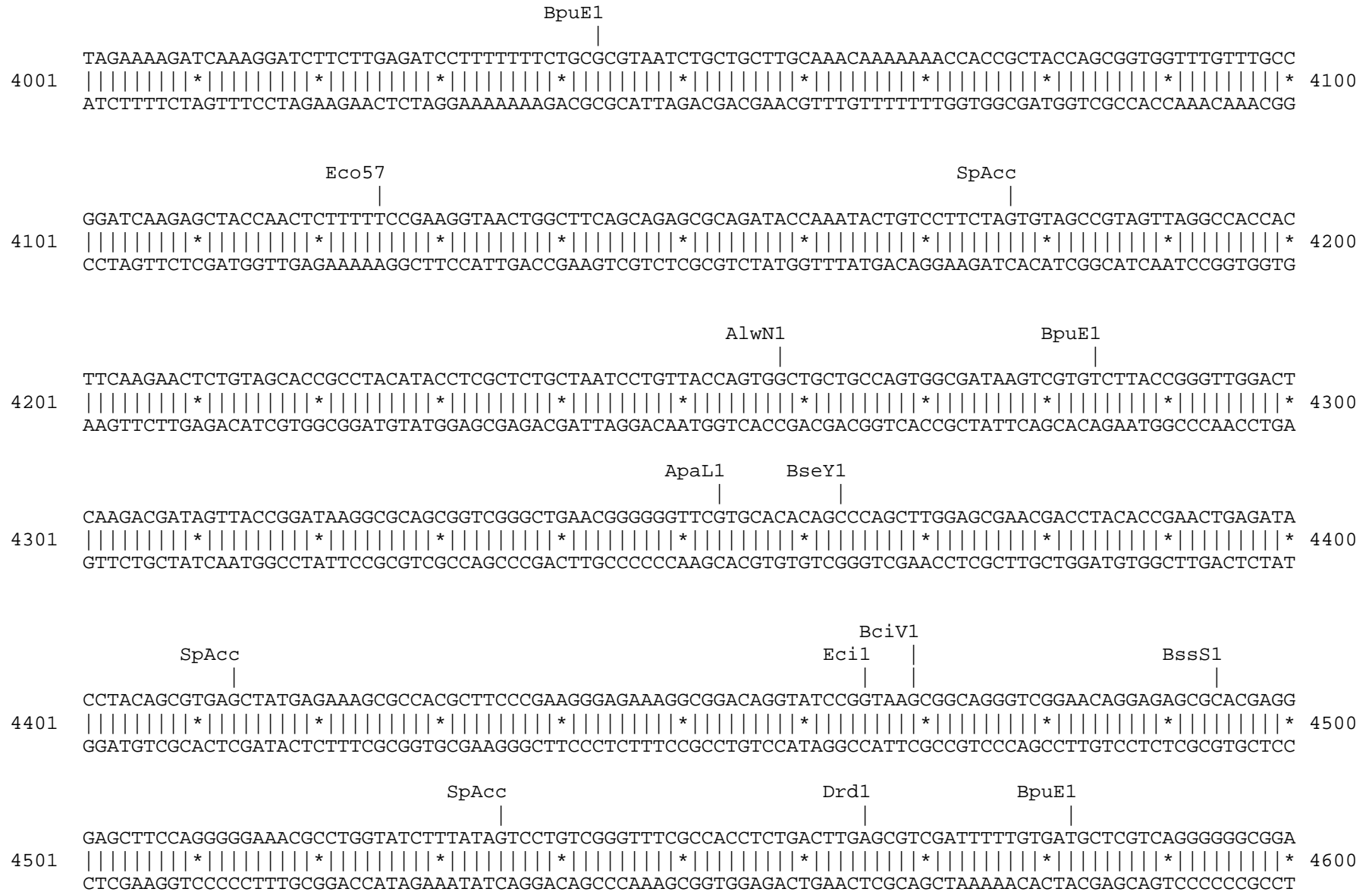












Found:

Aat2	Acc65	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1	BfrB1	Bgl1
Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1	BspE1	BsrD1	BsrG1
BssS1	BstAP	BstB1	BspH1	BspLU	BspM1	BsrB1	Bsu36	BtgZ1	Bts1	Cla1	Dra1	Dra3	Drd1
Eag1	Ear1	Ecil	Ecl2	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Msc1
Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	polyA	Psi1	PspOM	Pst1	Pvu2	Rsr2
Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1
Xho1													

Unique:

Acc65	Apa1	Ase1	BamH1	Bbs1	Bcl1	Bgl2	BsaXa	BsaXb	BspE1	BsrD1	BsrG1	BspLU	Bts1
Cla1	Eag1	Ecl2	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Nar1	Nde1	Nhe1
PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	SexA1	Sfi1	Sma1	SnaB1	Stu1	Xba1	Xho1	

Not found:

Aar1	Acl1	Afe1	Afl2	Age1	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Blp1
BmgB1	Bpu10	Bsg1	BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi
EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Not1	Nru1
Pac1	PflM1	Pme1	Pml1	PshA1	Pvu1	R4atB	R4atL	R4atP	R4atR	SanD1	Sbf1	Sca1	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	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bsl1	BsmA1	BsmF1	Bsp12	BspCa	BspCb	BsrF1
BssK1	BstF5	BstN1	BstU1	BstY1	Bsr1	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													