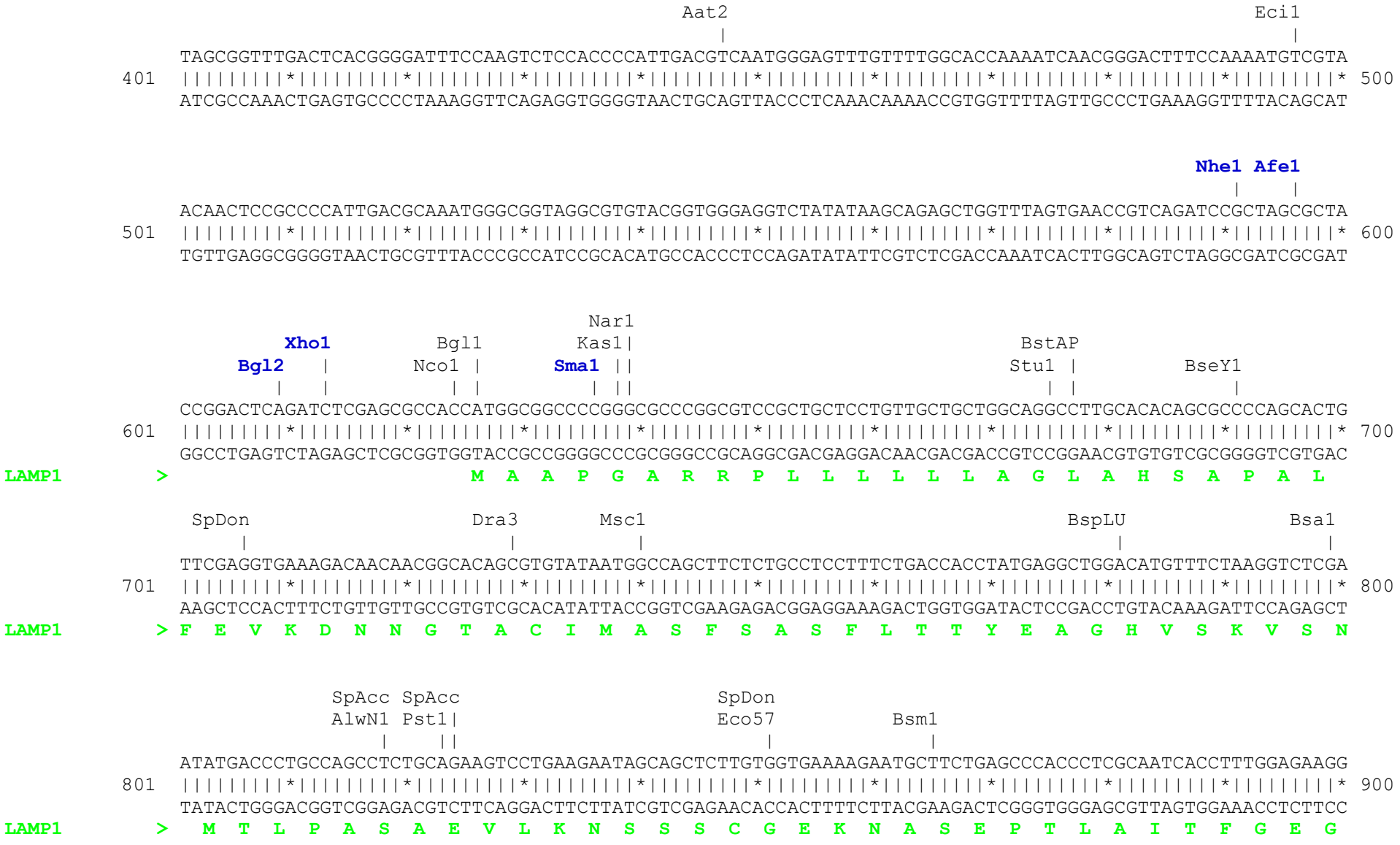
pmKate2-lyso vector restriction map

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). mKate2 amino acids are shown in red, Lysosomal Associated Membrane Protein 1 (LAMP1) amino acids are shown in green, linker amino acids are shown in black.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Msc1
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AlwN1 Pst1
SpDon
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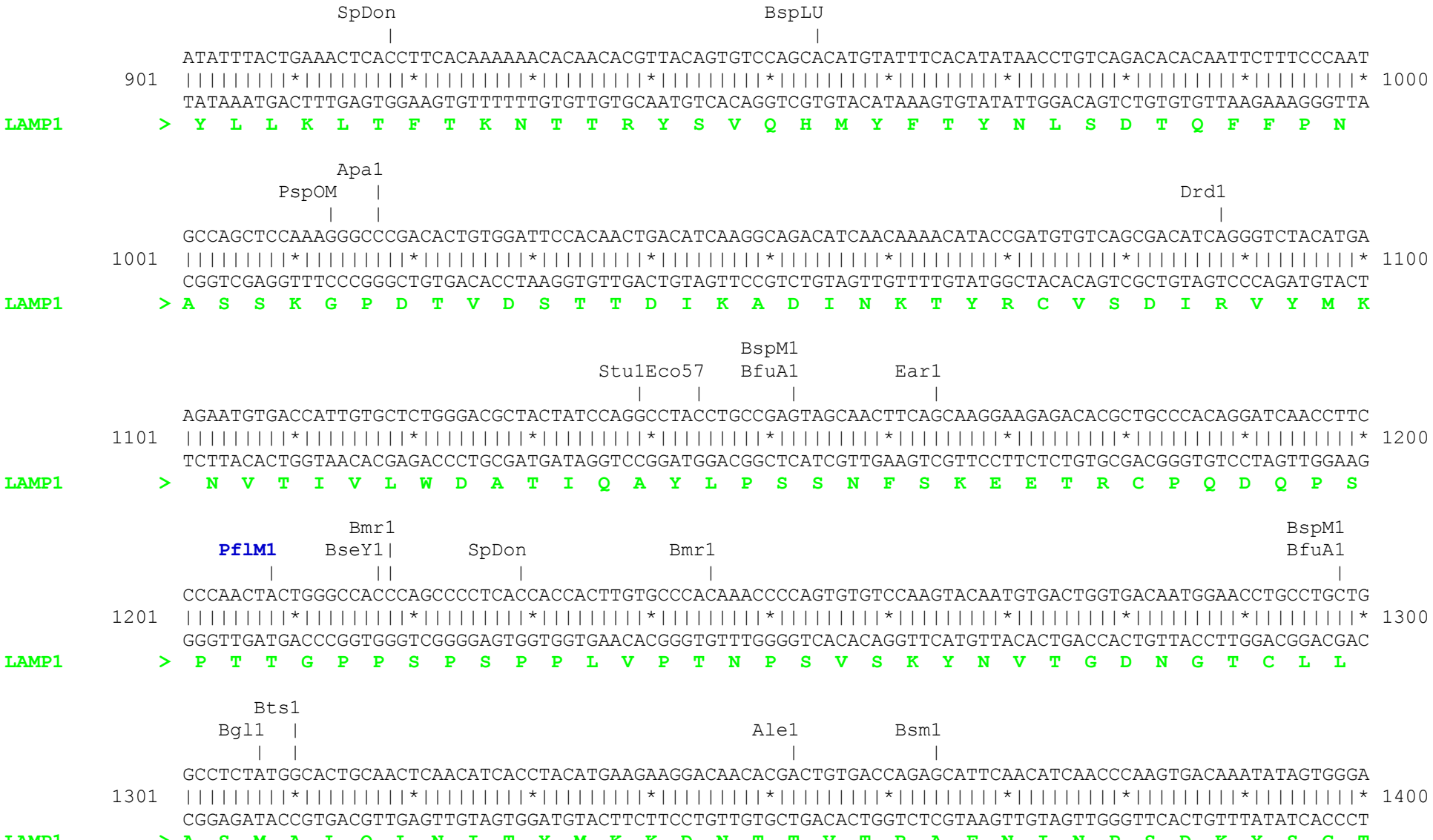
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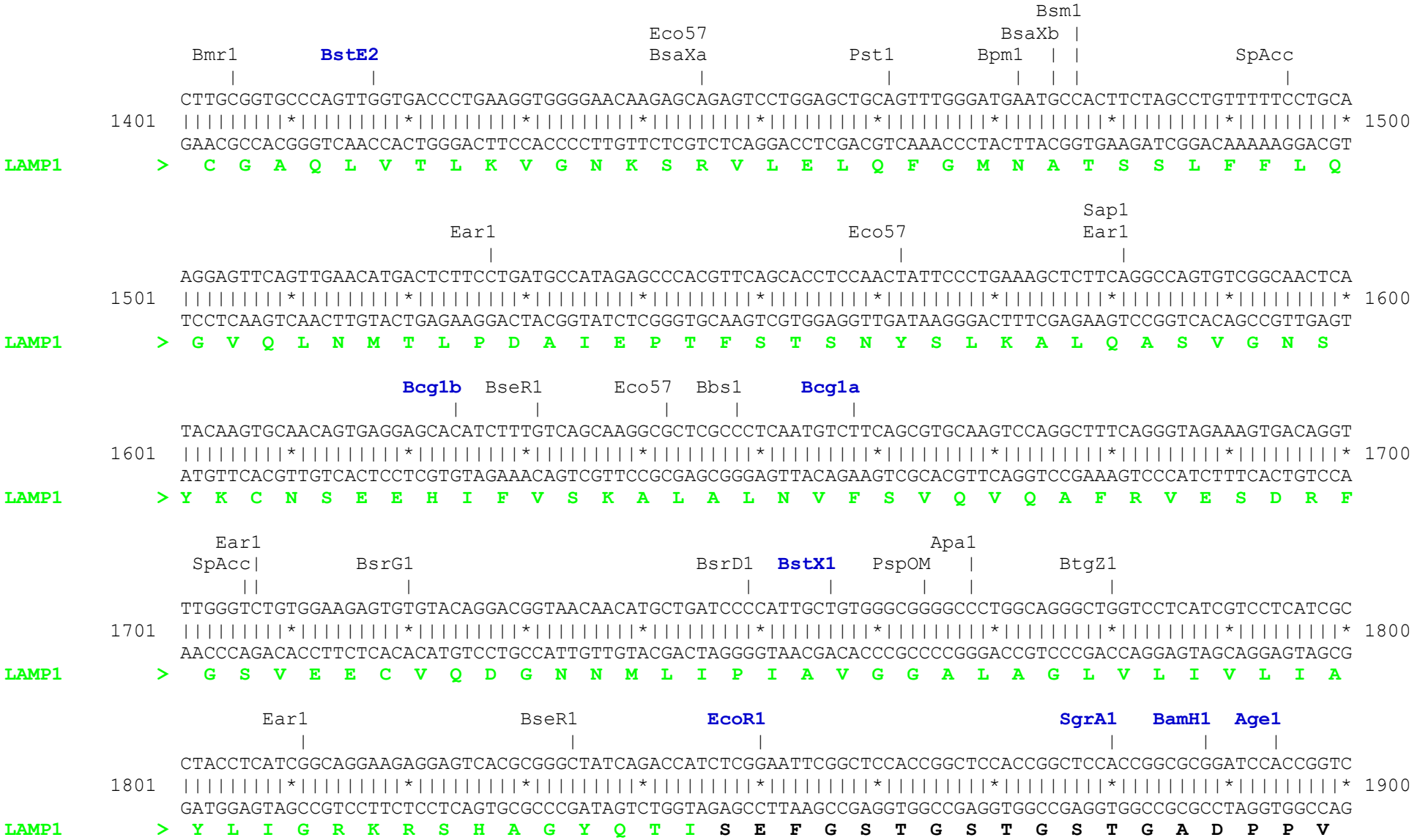
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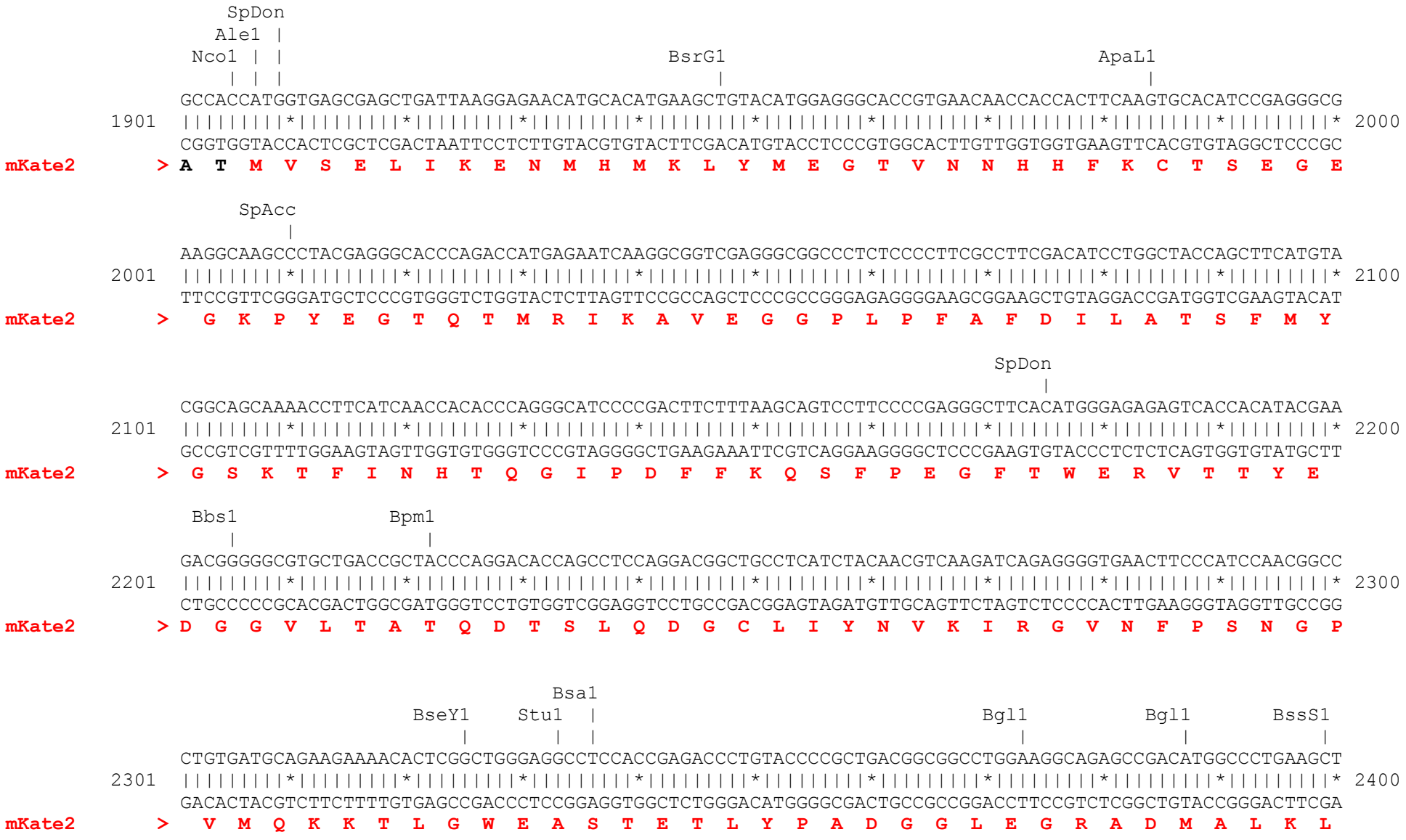
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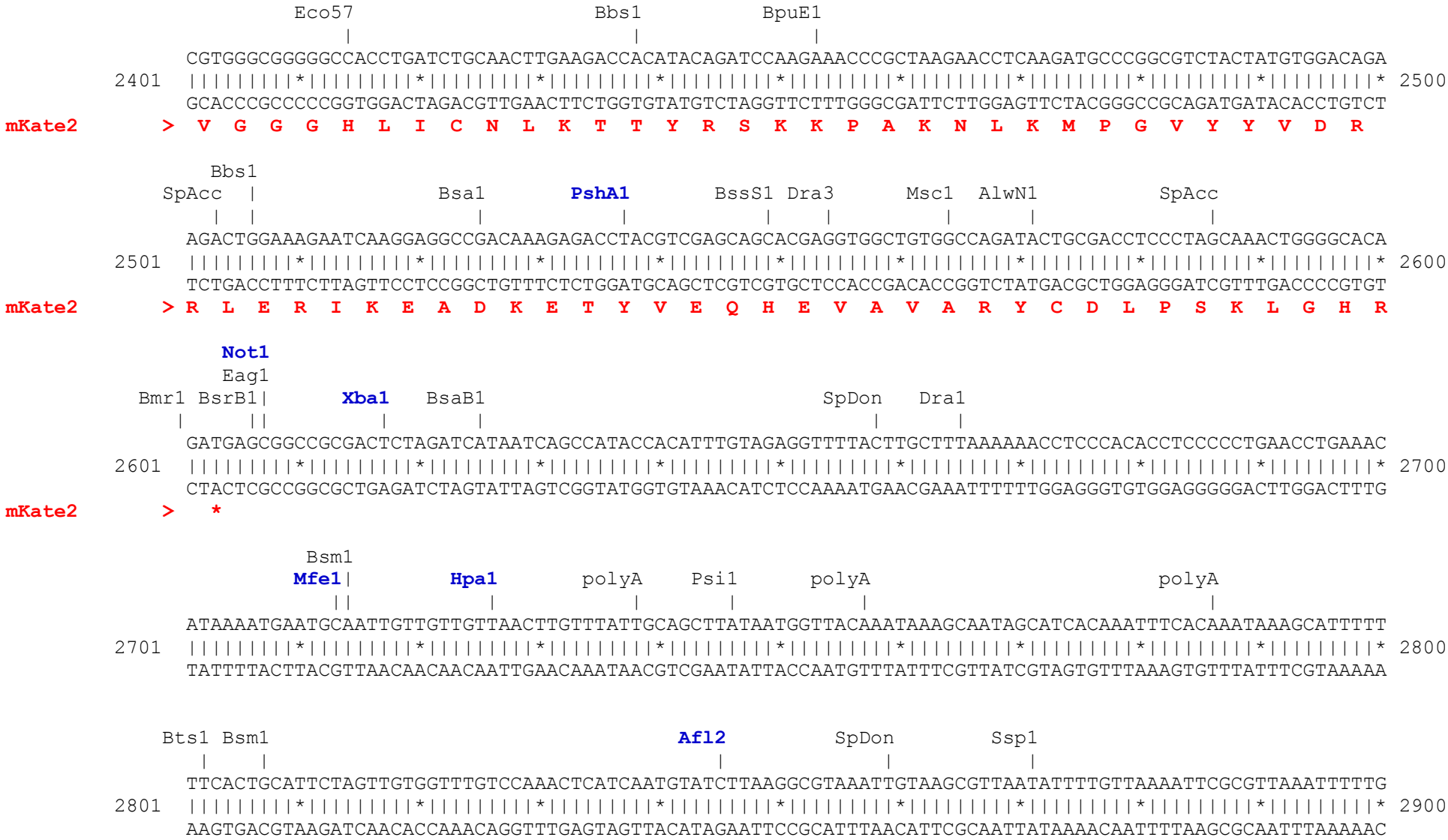
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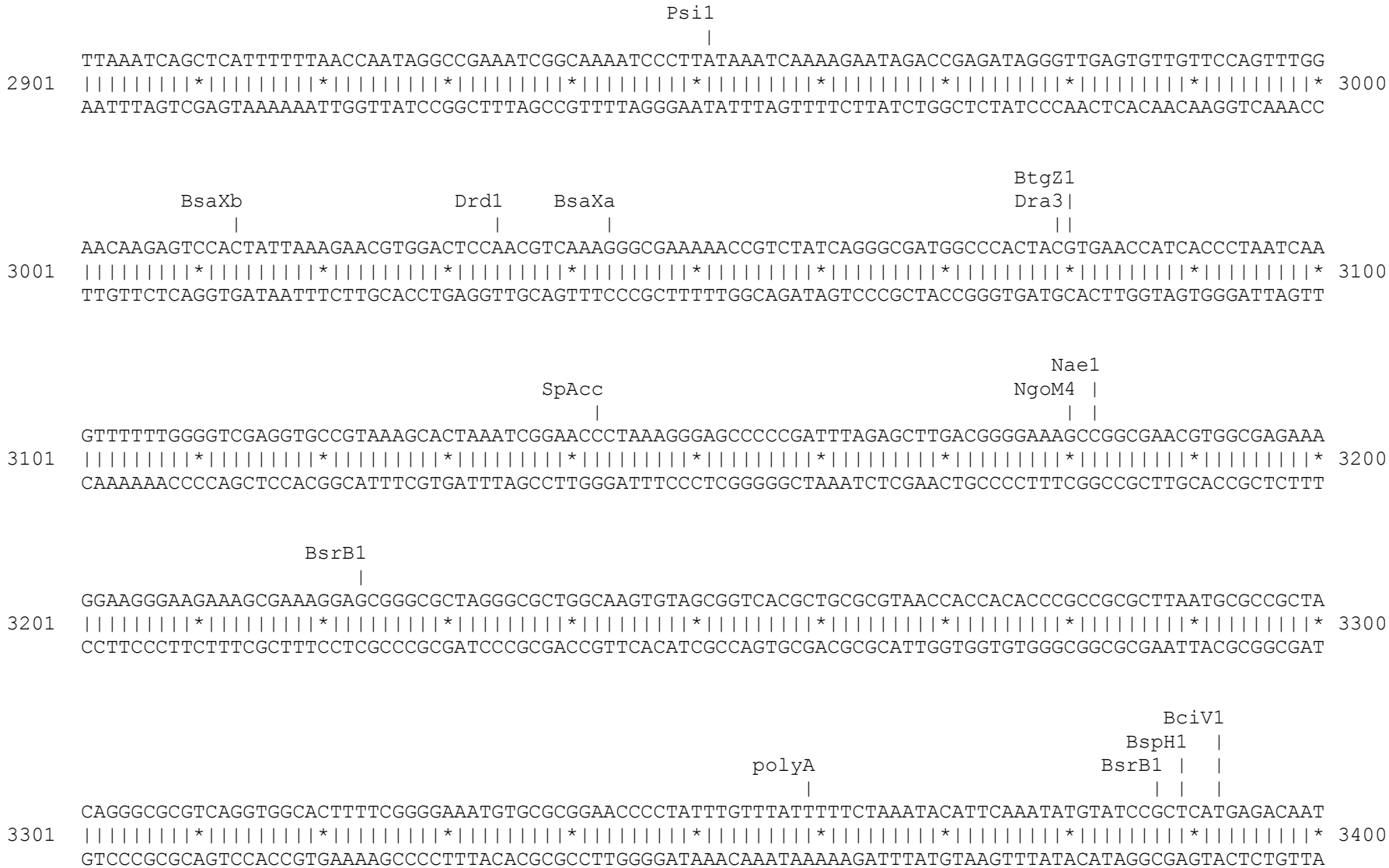
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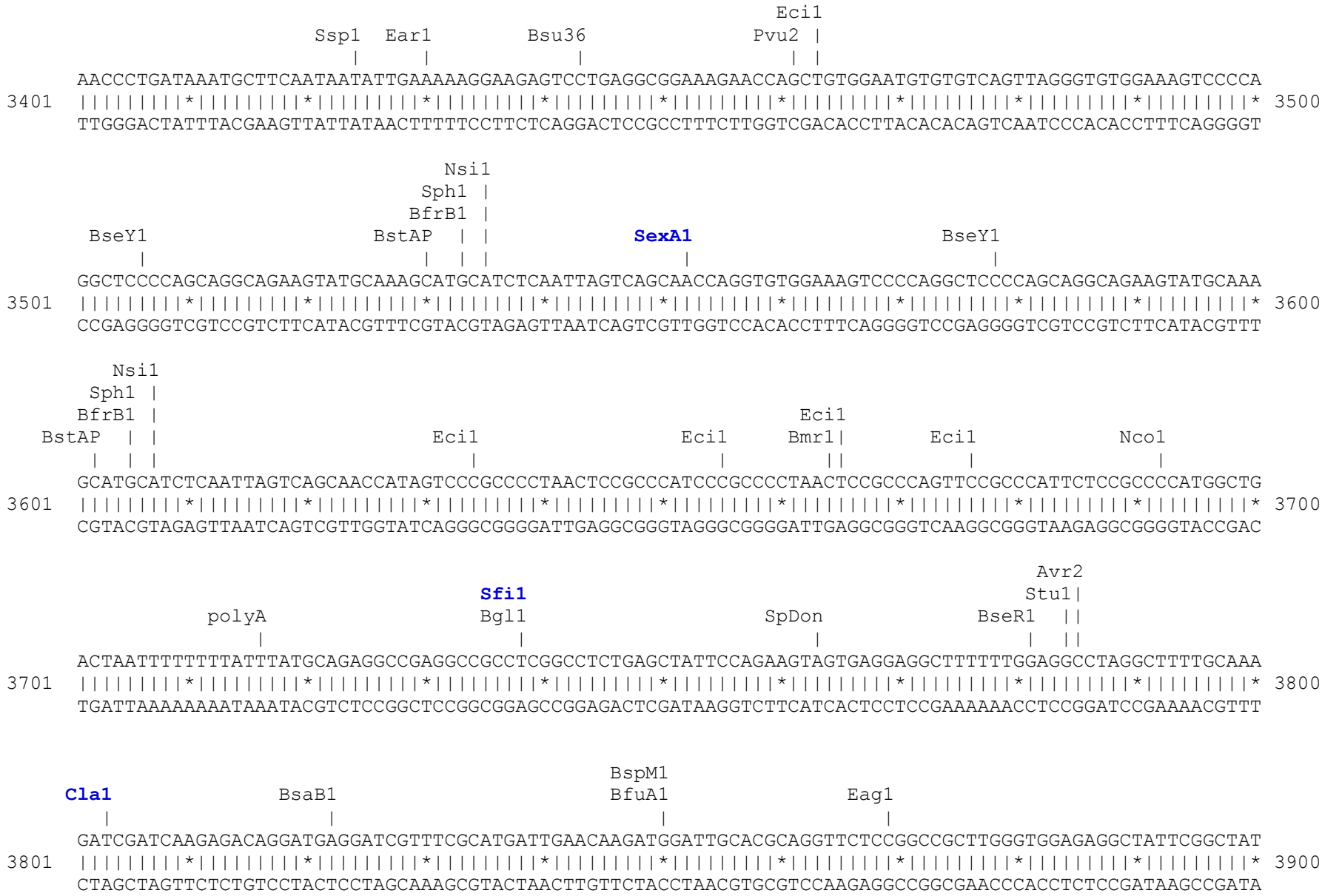
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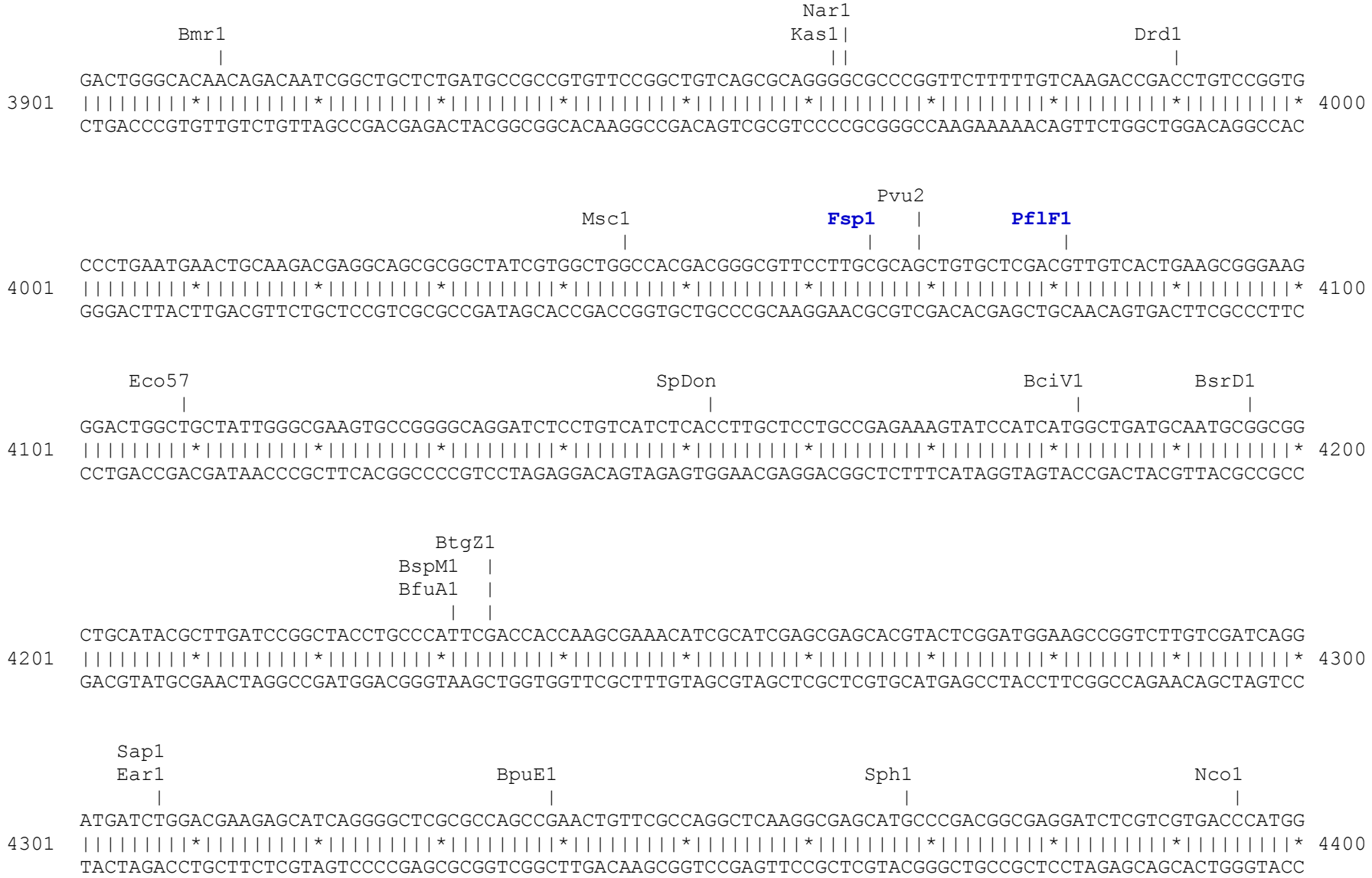
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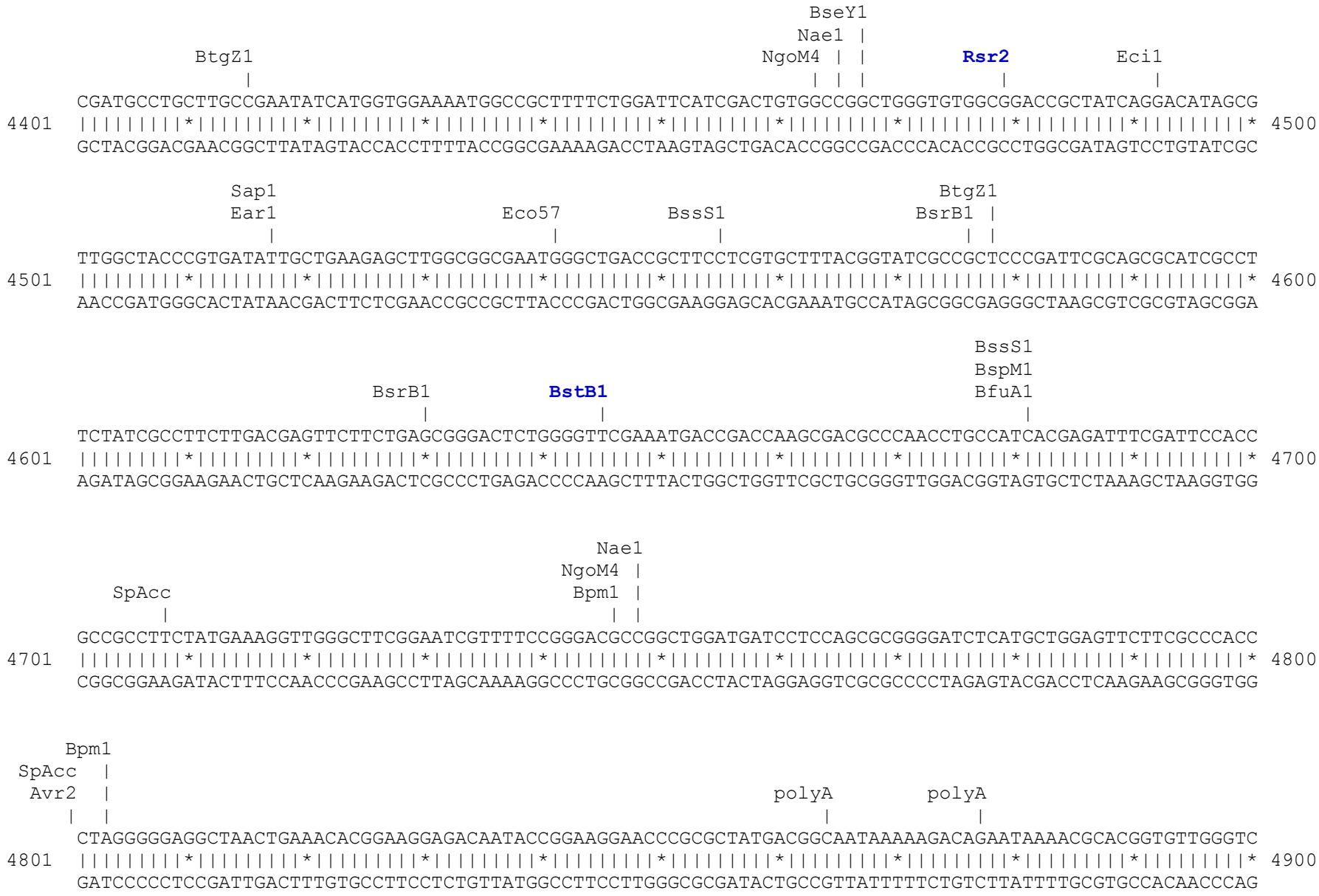
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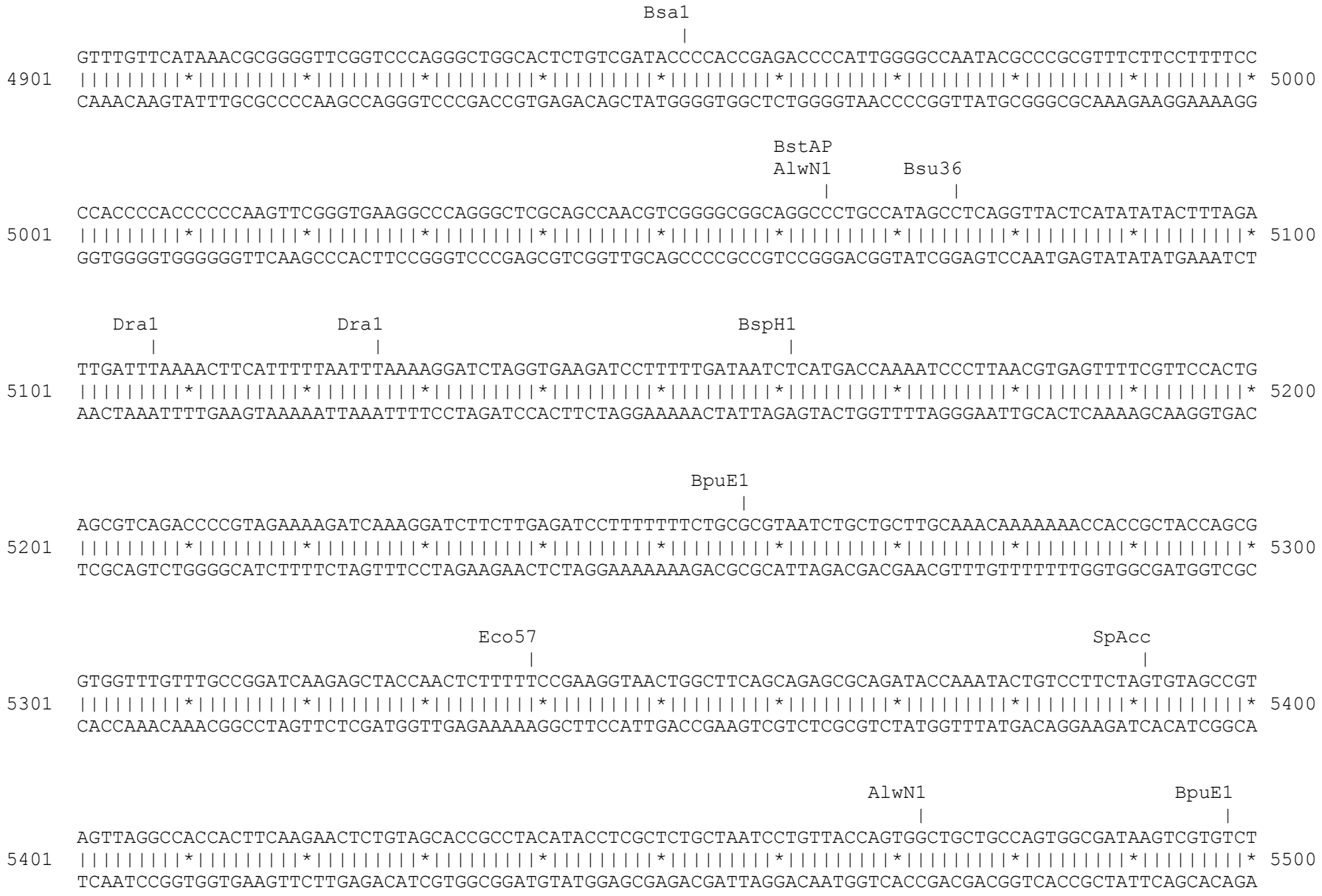
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AACTAAATTTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGAC
BpuE1
AGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCG
5201 * 5300
TCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGC
Eco57
SpAcc
GTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGT
5301 * 5400
CACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCA
AlwN1
BpuE1
AGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCT
5401 * 5500
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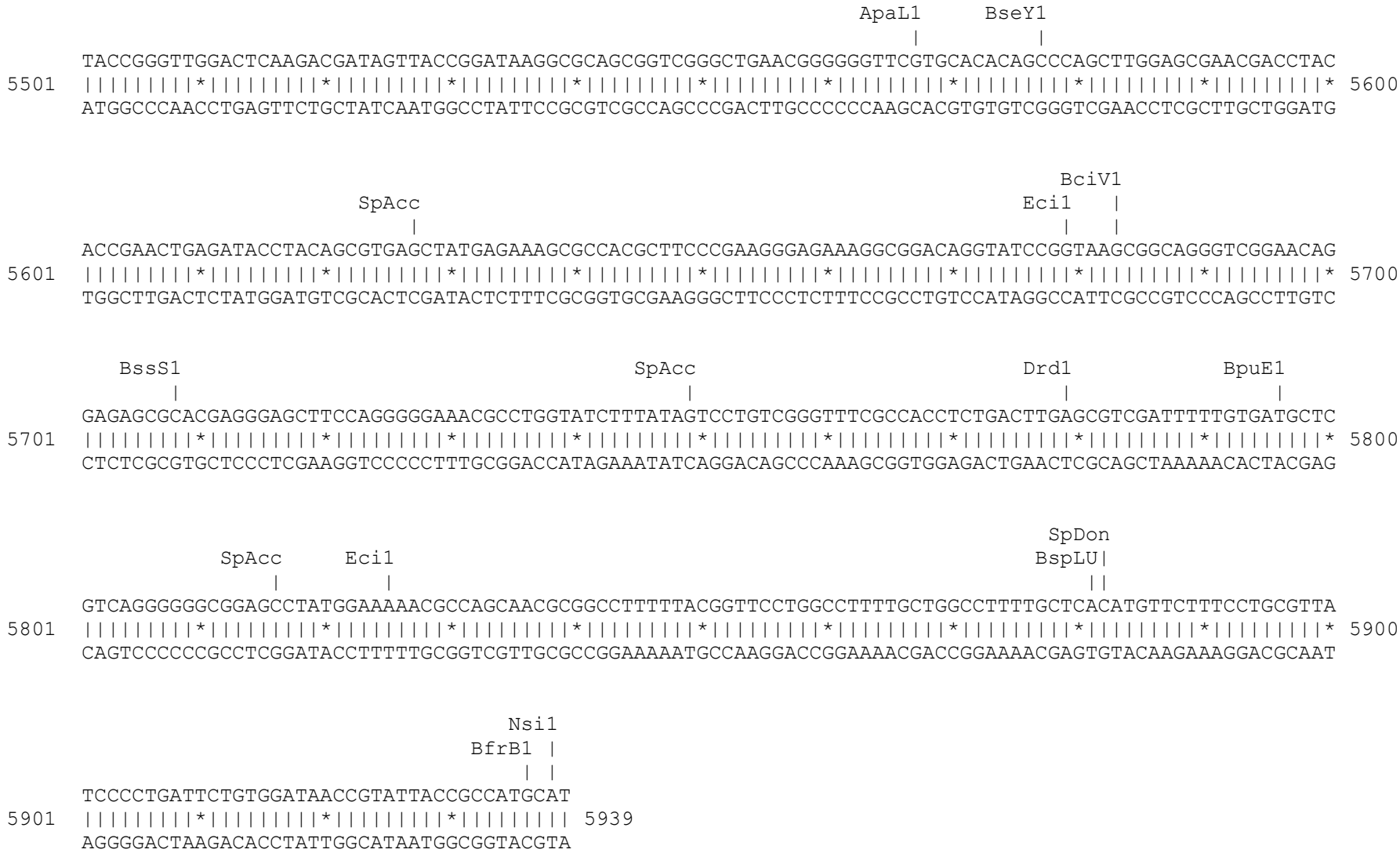
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BseY1
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5501
5600
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BciV1
SpAcc
Eci1
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5601
5700
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BssS1
SpAcc
Drd1
BpuE1
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5701
5800
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SpDon
SpAcc
Eci1
BspLU|
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5801
5900
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Nsi1
BfrB1
TCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5901
5939
AGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

Found:

Aat2	**Afe1**	**Afl2**	**Age1**	Ale1	AlwN1	Apa1	ApaL1	**Ase1**	Avr2	**BamH1**	Bbs1	**Bcg1a**	**Bcg1b**
BciV1	BfrB1	BfuA1	Bgl1	**Bgl2**	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	**BstB1**	**BstE2**	**BstX1**	Bsu36	BtgZ1
Bts1	**Cla1**	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	**EcoR1**	**Fsp1**	**Hpa1**	Kas1	**Mfe1**
Msc1	Nae1	Nar1	Nco1	**Nde1**	NgoM4	**Nhe1**	**Not1**	Nsi1	**PflF1**	**PflM1**	polyA	**PshA1**	Psi1
PspOM	Pst1	Pvu2	**Rsr2**	Sap1	**SexA1**	**Sfi1**	**SgrA1**	**Sma1**	**SnaB1**	SpAcc	SpDon	Sph1	Ssp1
Stu1	**Xba1**	**Xho1**											

Unique:

Afe1	**Afl2**	**Age1**	**Ase1**	**BamH1**	**Bcg1a**	**Bcg1b**	**Bgl2**	**BstB1**	**BstE2**	**BstX1**	**Cla1**	**EcoR1**	**Fsp1**
Hpa1	**Mfe1**	**Nde1**	**Nhe1**	**Not1**	**PflF1**	**PflM1**	**PshA1**	**Rsr2**	**SexA1**	**Sfi1**	**SgrA1**	**Sma1**	**SnaB1**
Xba1	**Xho1**												

Not found:

Aar1	Acc65	Acl1	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	BbvC1	Bcl1	Blp1	BmgB1	Bpu10	Bsg1
BsiW1	BsmB1	BspE1	BssH2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	EcoN1	EcoRV
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1
Pme1	Pml1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	Sal1	SanD1	Sbf1	Sca1	Sgf1
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													