

pFusionRed-PCNA 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).

FusionRed amino acids are shown in red, human proliferating cell nuclear antigen (PCNA) amino acids are shown in green, linker amino acids are shown in black.



		BseR1	Xmn1	Baela				
1901	TTGGAAATGGAAACATTTAAATTGTCACAGACAAGTAATGTCGATAAAGAGGAGGAAGCTGTTACCATAGAGATGAATGAACCAGTTCAACTAACTTTTTC				2000			
	* * * * * * * * * * *							
PCNA	> G N G N I K L S Q T S N V D K E E E A V T I E M N E P V Q L T F A							
		Acc65	Kpn1	Baelb	Ear1	Pst1		
2001	ACTGAGGTACCTGAACTTCTTTACAAAAGCCACTCCACTCTCTTCAACGGTGACTCAGTATGTCTGCAGATGTACCCCTTGTGTAGAGTATAAAAATT							
	* * * * * * * * * *							
PCNA	> L R Y L N F F T K A T P L S S T V T L S M S A D V P L V V E Y K I							
					BamH1	Xba1	Bcl1	BsaB1
2101	GCGGATATGGGACACTTAAAATACTACTTTGGCTCCCAAGATCGAGGATGAAGAAGGATCTTAGGGATCCACCGGATCTAGATAACTGATCATAATCAGCC							
	* * * * * * * * * *							
PCNA	> A D M G H L K Y Y L A P K I E D E E G S *							
		SpDon	Dra1		Bsm1	Mfe1	Hpa1	
2201	ATACCACATTTGTAGAGGTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGGT							
	* * * * * * * * * *							
	TATGGTGTAAACATCTCCAAAATGAACGAAATTTTTGGAGGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTAAACAACAACAATTGAACAA							
		polyA	PsiI	polyA				
2301	TATTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTCACAAATAAAGCATTCTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTC							
	* * * * * * * * *							
	ATAACGTCGAATATTACCAATGTTTATTTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGGAG							
		Mlu1	SpDon	Ssp1				
2401	ATCAATGTATCTTAAACGCGTAAATTGTAAGCGTAAATATTTTGTAAATTCGCGTAAATTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAA							
	* * * * * * * * *							
	TAGTTACATAGAATTGCGCATTAAACATTTCGCAATTATAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTT							
2500								

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                Psil                                BsaXb
                |                                  |
2501 ATCGGCAAAATCCCTTATAAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGGACTCCA 2600
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      TAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGACCTGAGGT

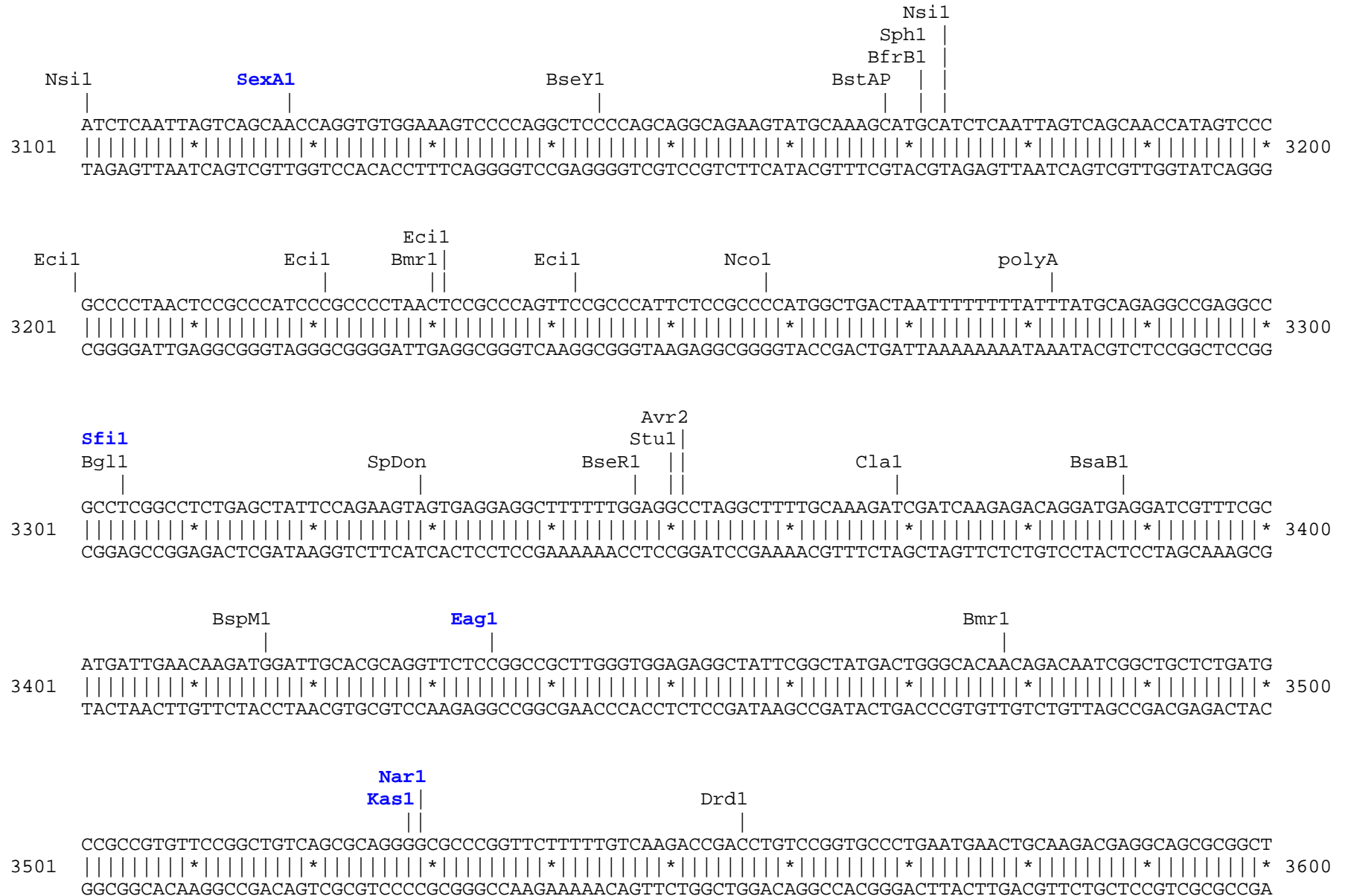
                BtgZ1
                |
                Dra3
                ||
Drd1   BsaXa
|       |
2601 ACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAA 2700
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      TGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCAGCTCCACGGCATTTCGTGATTT

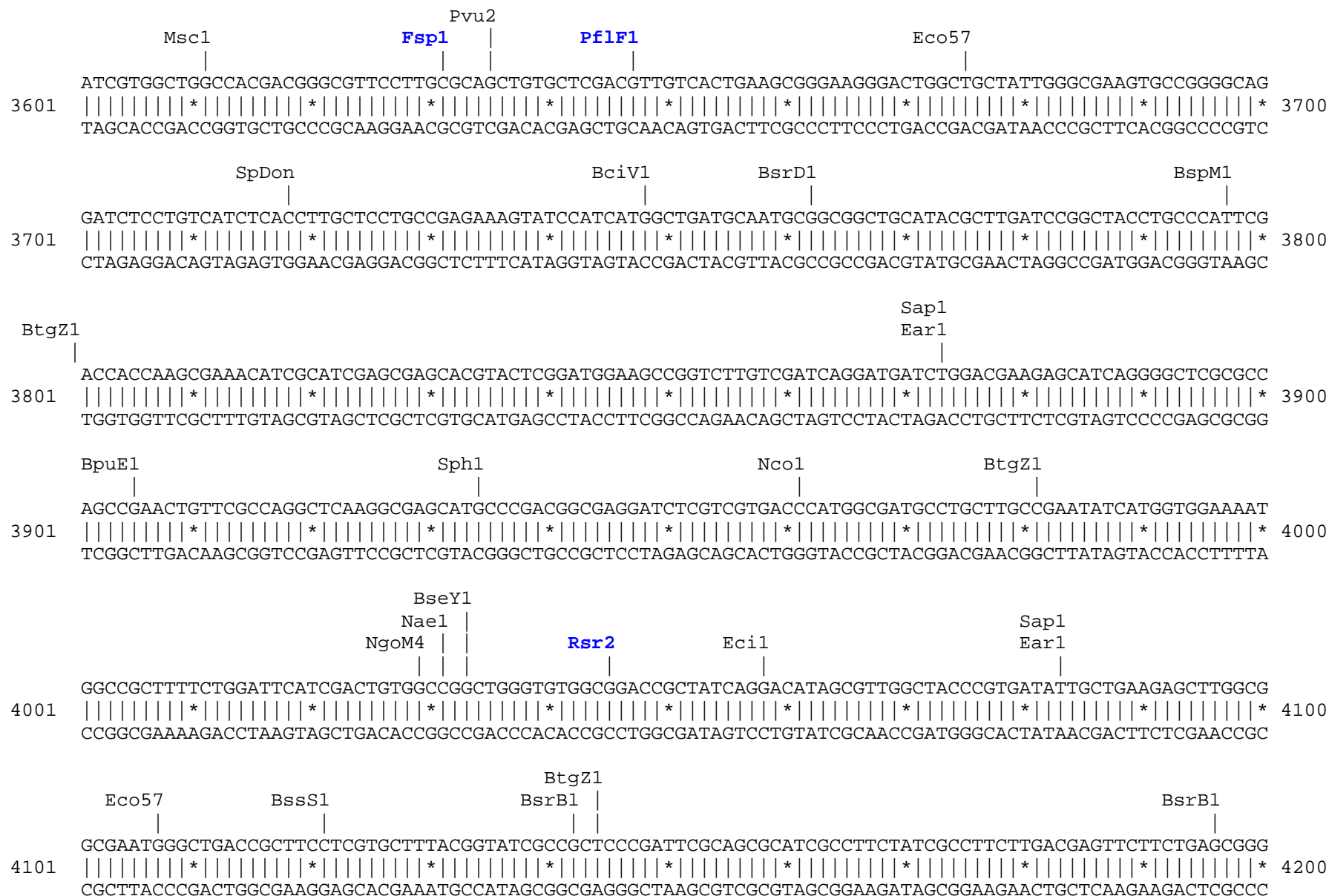
                NaeI
                |
                NgoM4
                ||
                BsrB1
                |
2701 TCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGG 2800
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      AGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCTTCCCTTCTTTTCGCTTTTCTCGCCCGCGATCC

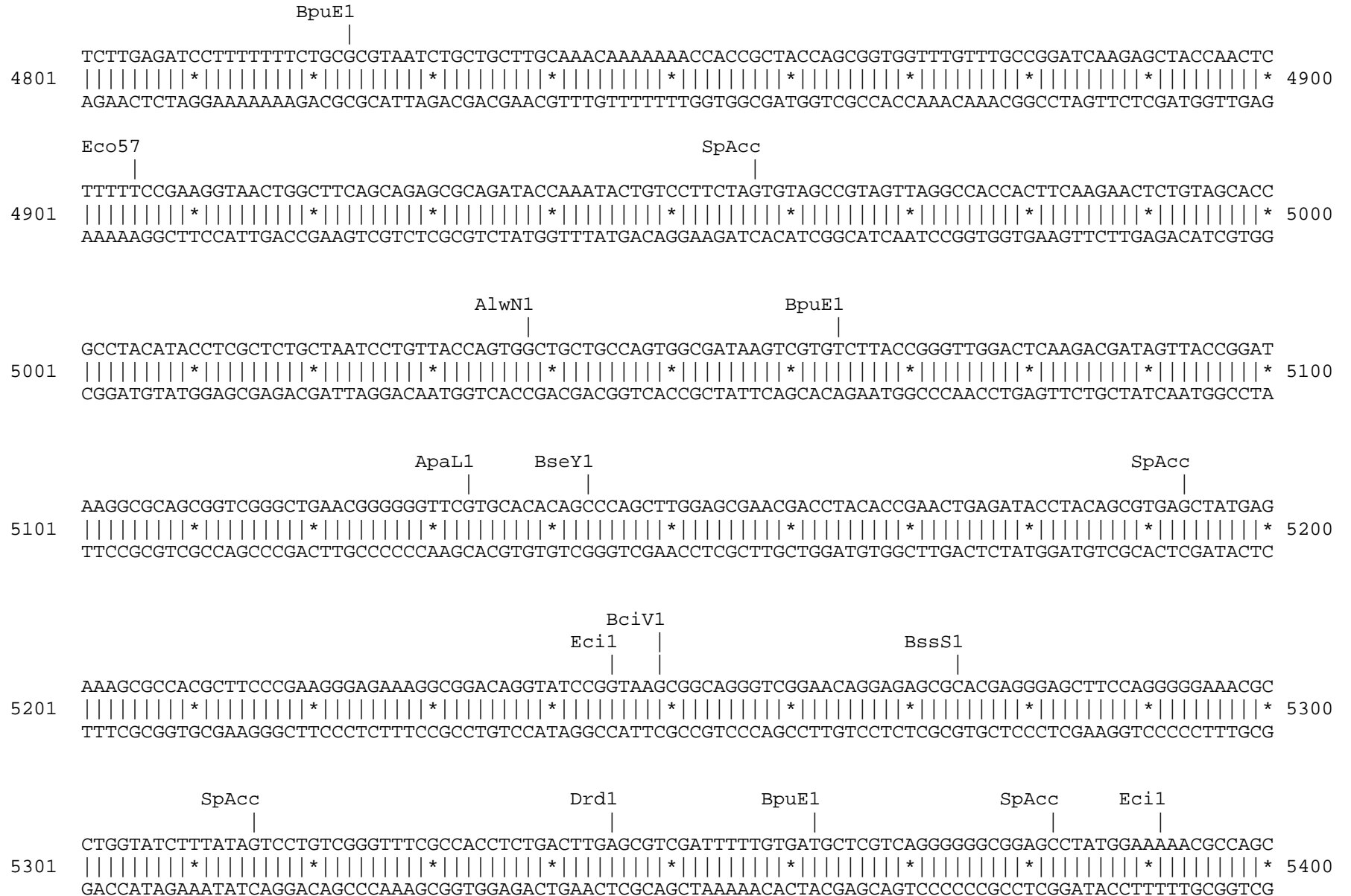
2801 GCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATG 2900
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      CGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCCTTTAC

                BciV1
                |
                BspH1
                |
                BsrB1
                ||
                SspI
                |
                EarI
                |
2901 TGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAG 3000
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      ACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTTC

                SphI
                |
                BfrB1
                |
                BstAP
                |
                Bsu36
                |
                Pvu2
                |
                EciI
                |
                BseY1
                |
3001 GAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGC 3100
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      CTTCTCAGGACTCCGCTTTCTTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTTTCGTACG
```







Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	ApaL1	Asc1	Ase1	Avr2	Baela	Baelb	BamH1	Bbs1
BciV1	Bcl1	BfrB1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsg1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP
BstB1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoN1	EcoR1
EcoRV	Fsp1	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1
Nsil	PflF1	PflM1	polyA	PshA1	Psil	Pst1	Pvu2	Rsr2	Sac2	Sap1	SexA1	Sfi1	SnaB1
SpAcc	SpDon	Sph1	Ssp1	Stul	Xba1	Xmn1							

Unique:

Acc65	Afe1	Age1	Ale1	Asc1	Ase1	Baela	Baelb	BamH1	Bbs1	Bcl1	Bgl2	BmgB1	Bsg1
BspE1	BspLU	BsrG1	BssH2	BstB1	Bts1	Eag1	EcoR1	EcoRV	Fsp1	Hpa1	Kas1	Kpn1	Mfe1
Nar1	Nde1	Nhe1	PflF1	PflM1	PshA1	Rsr2	Sac2	SexA1	Sfi1	SnaB1	Xba1	Xmn1	

Not found:

Aar1	Acl1	Afl2	Ahd1	Apa1	AsiS1	BbvC1	BcglA	Bcglb	Blp1	Bpu10	BsiW1	BstE2	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	Hind3	I_Ceu	loxP	Not1	Nru1	Pac1	Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL	R4atP
R4atR	Sac1	Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA
T7Ter	PISce	Xcm1	Xho1										

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	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													