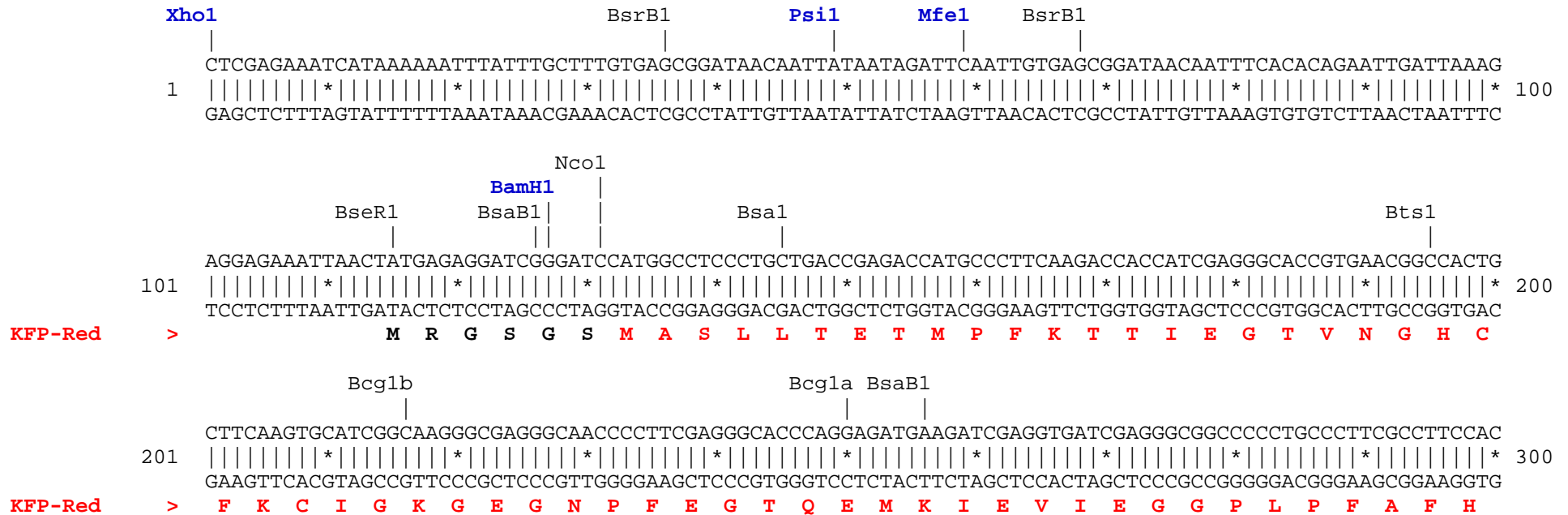


pKindling-Red-B vector restriction map

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 shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). Amino acids coded by vector's backbone sequence are shown in black.




```

                                     BsmB1   PflM1
                                     |       |
1401 TTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTTAAACGTGGCCAATATGGACAACCTTCTTCGCCCCCGTTTT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
AAATAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAAACTAAATTTGCACCGGTTATACCTGTTGAAGAAGCGGGGGCAA

Nco1       Ssp1
  |         |
1501 TCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
AGTGGTACCCGTTTATAATATGCGTTCGGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGACACTACCGAAGGTACAGCCGTCTTA

Bsm1       Scal
  |         |
1601 GCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATTGGTGCCCTTAAACGCCTGGGGTAATGACTCTC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
CGAATTACTTAATGTTGTCATGACGCTACTCACCGTCCCGCCCCGCATTAATAAATTCCGTCAATAACCACGGGAATTTGCGGACCCATTACTGAGAG

                                     BpuE1       Bmr1       Eci1
                                     |           |           |
1701 TAGCTTGAGGCATCAAATAAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
ATCGAACTCCGTAGTTTATTTTGCCTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCTGTTTA

Xba1
BsrB1 | BsmB1
  |   | |
1801 CCGCCGCTCTAGAGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
GGCGGCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGGAGACTGTGTACGTCGAGGGCCTCTGCCAGTGTGCAACAGACATTGCGCTAC

Drd1       Bmr1 PflF1       BstZ1
  |         |       |       |
1901 CCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGCGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
GGCCCTCGTCTGTTGCGGCAGTCCCGCGCAGTCGCCCACAACCGCCACAGCCCCGCGTCCGTACTGGGTGAGTGCATCGCTATCGCCTCACATATGACC

```



```

                                     BsrB1
                               BciV1
                               BspH1
Ear1   Ssp1
|       |
TACTCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGT
3901  |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4000
ATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCA

                                     Aat2
                                     BspH1
                                     BssS1
                                     Bbs1
TCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGT
4001  |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4100
AGGCGCGTGTAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCA

CTTCAC
4101  ||||||| 4106
GAAGTG

```

Found:

- [Aar1](#) [Aat2](#) [Acl1](#) [Ahd1](#) [AlwN1](#) [ApaL1](#) [Ase1](#) [BamH1](#) [Bbs1](#) [Bcg1a](#) [Bcg1b](#) [BciV1](#) [BfuA1](#) [Bgl1](#)
- [Blp1](#) [Bmr1](#) [Bpm1](#) [Bpu10](#) [BpuE1](#) [Bsa1](#) [BsaB1](#) [BseR1](#) [BseY1](#) [Bsg1](#) [Bsm1](#) [BsmB1](#) [BspE1](#) [BspH1](#)
- [BspLU](#) [BspM1](#) [BsrB1](#) [BsrD1](#) [BsrG1](#) [BssS1](#) [BstAP](#) [BstZ1](#) [Bts1](#) [Dra1](#) [Drd1](#) [Eag1](#) [Ear1](#) [Eci1](#)
- [Eco57](#) [EcoK](#) [Fsp1](#) [Hind3](#) [Mfe1](#) [Msc1](#) [Nae1](#) [Nco1](#) [Nde1](#) [Ngom4](#) [Nhe1](#) [PflF1](#) [PflM1](#) [Psi1](#)
- [Pvu1](#) [Pvu2](#) [Sap1](#) [Sca1](#) [Ssp1](#) [Xba1](#) [Xho1](#) [Xmn1](#)

Unique:

Aar1	Aat2	Ahd1	Ase1	BamH1	Bbs1	Blp1	Bpu10	Bsg1	BspE1	BspLU	BsrG1	BstAP	BstZ1
EcoK	Fsp1	Hind3	Mfe1	Msc1	Nae1	Nde1	Ngom4	Nhe1	PflF1	PflM1	Psi1	Pvu1	Pvu2
Sap1	Xba1	Xho1	Xmn1										

Not found:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfrB1
Bgl2	BmgB1	BsaXa	BsaXb	BsiW1	BssH2	BstB1	BstE2	BstX1	Bsu36	_Chi	Clal	Dra3	EcoN1
EcoR1	EcoRV	ScFRT	Fse1	FspA1	Hpa1	I_Ceu	Kas1	Kpn1	loxP	Mlu1	Nar1	Not1	Nru1
Nsi1	Pac1	Pme1	Pml1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sal1	SanD1	Sbf1	SexA1
Sfi1	Sgf1	SgrA1	Sma1	SnaB1	Spe1	Sph1	Srf1	Stu1	Swal	PISce	Xcm1		

Excluded by site complexity:

Acc1	Ac1	Afl3	Alu1	Alw1	Ap01	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													