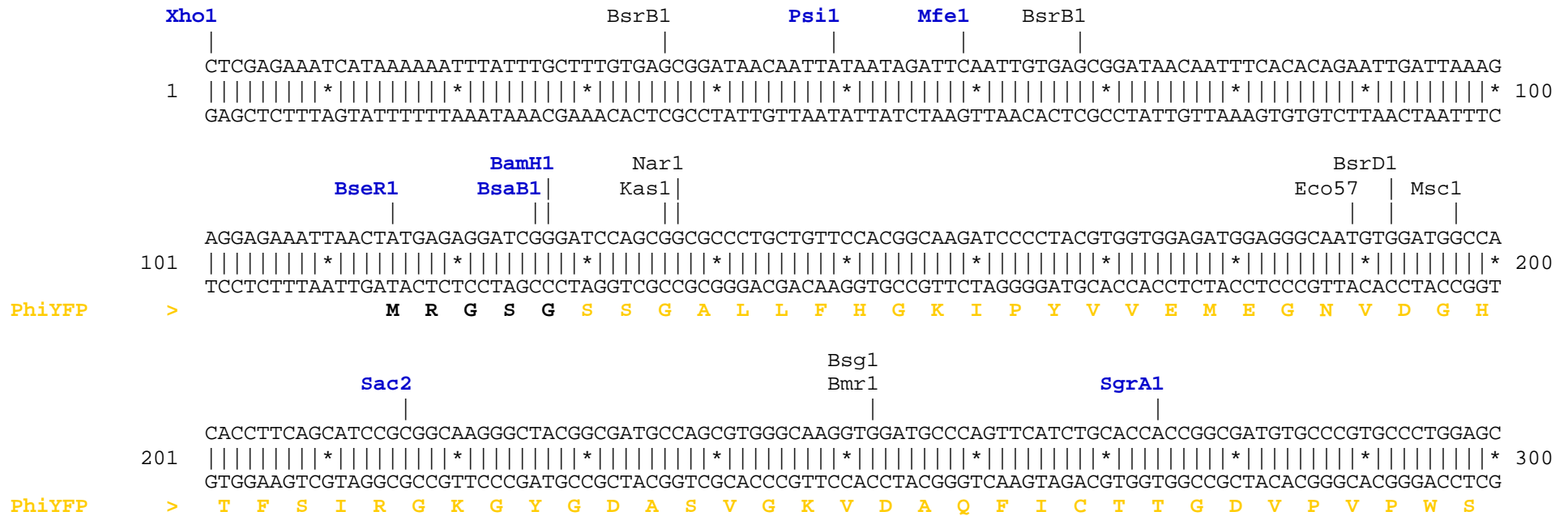


pPhi-Yellow-B vector restriction map

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.




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                                     BsmB1   PflM1                               Dra1   Msc1
1401  TTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACCTTCTTCGCCCCCGTTTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
      AAATAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAAACTAAATTTGCACCCGGTTATACCTGTTGAAGAAGCGGGGGCAA

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

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

                                     BpuE1                               Bmr1                               Eci1
1701  TAGCTTGAGGCATCAAATAAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTTTGTTCGGTGAACGCTCTCCTGAGTAGGACAAAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
      ATCGAACTCCGTAGTTTTATTTTCTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCTGTTTA

Xba1
BsrB1 | BsmB1
1801  CCGCCGCTCTAGAGCTGCCTCGCGCGTTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
      GGCGGCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAGTGTGCAACAGACATTGCGCTAC

Drd1      Bmr1 PflF1      BstZ1
1901  CCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTGGCGGGTGTGGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
      GGCCCTCGTCTGTTTCGGGCAGTCCCGCGCAGTCGCCCACAACCGCCACAGCCCCGCGTCCGTACTGGGTGAGTGCATCGCTATCGCCTCACATATGACC

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

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

CTTCAC
4101  ||||| 4106
GAAGTG

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Found:

Aat2	Acl1	Ahd1	Ale1	AlwN1	ApaL1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1	Bgl1	Bgl2
Blp1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BseR1	BseY1	Bsg1	Bsm1	BsmB1	BspE1	BspH1
BspLU	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstE2	BstZ1	Bts1	Dra1	Drd1	Ear1	Eci1
Eco57	EcoK	Fsp1	Hind3	Kas1	Mfe1	Msc1	Nar1	Nco1	Nde1	Nhe1	PflF1	PflM1	Pml1
Psi1	Pvu1	Pvu2	Sac2	Sap1	Sca1	SgrA1	Sph1	Ssp1	Xba1	Xho1	Xmn1		

Unique:

Aat2	Ahd1	Ale1	AlwN1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	Bgl1	Bgl2	Bpu10	BsaB1	BseR1
BspE1	BspLU	BssH2	BstAP	BstZ1	EcoK	Fsp1	Hind3	Mfe1	Nco1	Nde1	Nhe1	PflF1	Psi1
Pvu1	Pvu2	Sac2	SgrA1	Sph1	Xba1	Xho1							

Not found:

Aar1	Acc65	Afe1	Afl2	Age1	Apa1	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfrB1
BfuA1	BmgB1	BsaXa	BsaXb	BsiW1	BspM1	BstB1	BstX1	Bsu36	_Chi	Clal	Dra3	Eag1	EcoN1
EcoR1	EcoRV	ScFRT	Fse1	FspA1	Hpa1	I_Ceu	Kpn1	loxP	Mlu1	Nae1	NgoM4	Not1	Nrul
Nsil	Pac1	Pme1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sall	SanD1	Sbf1	SexA1	Sfi1	Sgf1
Sma1	SnaB1	Spe1	Srf1	Stu1	Swal	PISce	Xcm1						

Excluded by site complexity:

Acc1	Ac11	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	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													