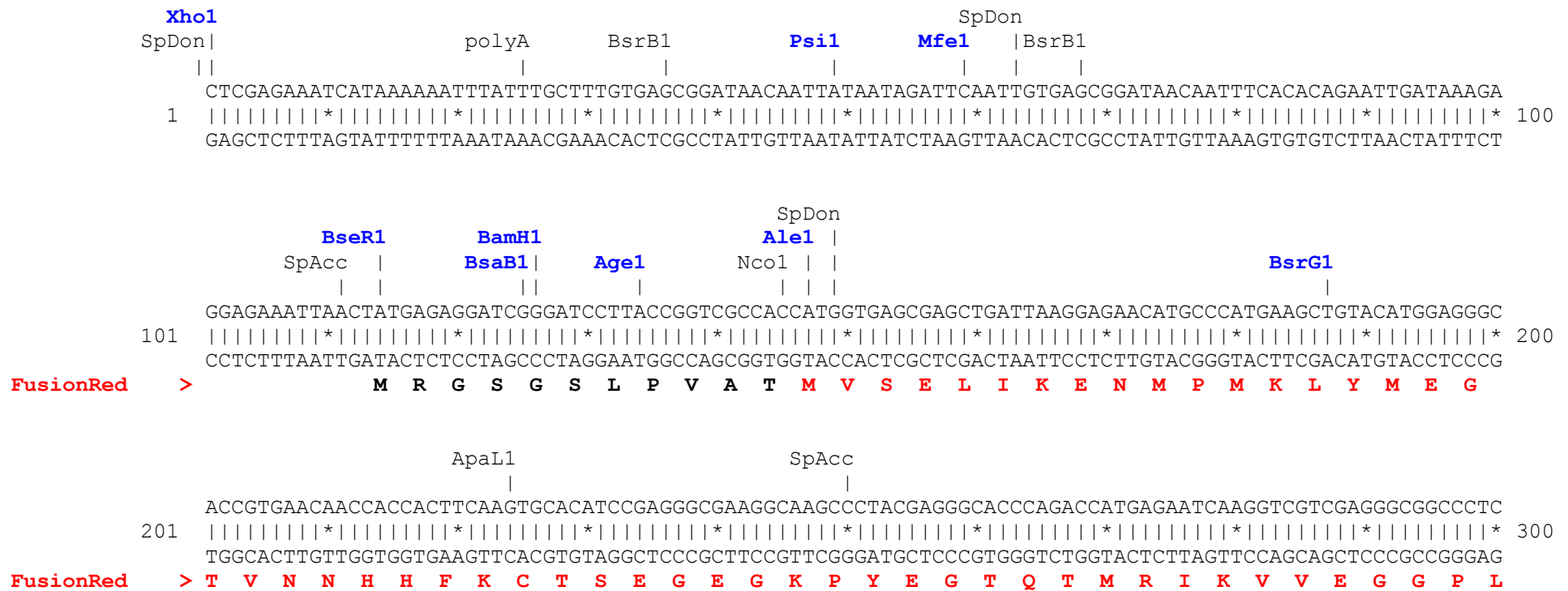


pFusionRed-B vector restriction map

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.




```

                                     Not1
                                     Eag1
MscI          SpDon    BsrB1 | Hind3          Bln1
|             |         ||          |           |
GTGGCCAGATACTCTACTGGTGGCGCTGGTGATGGAGGTAAATGAGCGGCCGCAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATG
801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
CACCGTCTATGAGATGACCACCGCGACCACTACCTCCATTTACTCGCCGGCGTTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTAC
FusionRed > V A R Y S T G G A G D G G K *

                                     polyA          Nhe1          Bpu10
                                     |             |             SpAcc|
ACCTCAGAACTCCATCTGGATTTGTTTCAGAACGCTCGGTTGCCGCCGGCGTTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCT
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
TGGAGTCTTGAGGTAGACCTAAACAAGTCTTGCGAGCCAACGGCGGCCCGCAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTAAAAGTCCTCGA

AAGGAAGCTAAAAATGGAGAAAAAATCACTGGATATAACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTC
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
TTCTTCGATTTTACCTCTTTTTTTAGTGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTGTAAAACTCCGTAAAGTCAGTCAACGAG

                                     SpDon
                                     polyA |
AATGTACCTATAACCAGACCGTTTCAGCTGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTTATTCACATTCT
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
TTACATGGATATTGGTCTGGCAAGTCGACCTATAATGCCGGAAAAATTTCTGGCATTTCCTTTTTTATTCGTGTTCAAATAGGCCGGAAATAAGTGTAAGA

                                     BspE1
Bsm1 |         BsrD1
|     |         |
TGCCCGCTGATGAATGCTCATCCGGAATTTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTACCCCTTGTTACACCGTTTTCCAT
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
ACGGGCGGACTACTTACGAGTAGGCCTTAAAGCATACCGTTACTTTCTGCCACTCGACCACTATACCCTATCACAAGTGGGAACAATGTGGCAAAAGGTA

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BtgZ1    Acl1                                Bpm1
|        |                                 |
GAGCAAAC TGAACG TTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAA
1301 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1400
CTCGTTTGACTTTGCAAAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAAATGCCACTTT

                polyA                BsmB1    PflM1                SpDon                Dra1    Msc1
                |                |        |                |                |        |
ACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAAGTTTGGATTTAAACGTGGCCAATAT
1401 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1500
TGGACCGGATAAAAGGGATTTCCCAAATAACTCTTATACAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAACCTAAATTTGCACCGGTTATA

                SpDon
                Nco1        Ssp1
                |        |
GGACAACCTTCTTCGCCCCCGTTTTTCACCATGGGCAAATATATACGCAAGGCCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGTCTGT
1501 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1600
CCTGTTGAAGAAGCGGGGGCAAAAAGTGGTACCCGTTTATAATATGCGTTCCGCTGTTCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGACA

                Bsm1                Scal                BtgZ1
                |                |                |
GATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATTGGTGCCCTT
1601 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1700
CTACCGAAGGTACAGCCGCTTACGAATTACTTAATGTTGTCATGACGCTACTCACCGTCCC GCCCCGCATTA AAAAAAATTC CGTCAATAACCACGGGAA

                polyA    BpuE1                Bmr1 T7Ter
                |        |                |        |
AAACGCCTGGGGTAATGACTCTCTAGCTTGAGGCATCAAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTCTGGTGA
1701 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1800
TTTGCGGACCCCATTA CTGAGAGATCGAACTCCGTAGTTTATTTTGCTTTCGGAGTCAGCTTTCTGACCCGAAAGCAA AATAGACAACAAACAGCCACT

                Xba1
                Eci1        BsrB1 |                BsmB1
                |        |        |                |
ACGCTCTCCTGAGTAGGACAAAATCCGCCGCTCTAGAGCTGCCTCGCGGTTTTCCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGT
1801 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1900
TGC GAGAGGACTCATCCTGTTTAGCGGGCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGAGACTGTGTACGTTCGAGGGCCTCTGCCA

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Found:

Aat2	Ac11	Age1	Ahd1	Ale1	AlwN1	ApaL1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1	Bgl1
Blp1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BseR1	BseY1	Bsm1	BsmB1	BspE1	BspH1	BspLU
BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstZ1	Bsu36	BtgZ1	Bts1	Dra1	Dra3	Drd1	Eag1	Ear1
Eci1	Eco57	EcoK	Fsp1	Hind3	Mfe1	Msc1	Nco1	Nde1	Nhe1	Not1	PflF1	PflM1	polyA
PshA1	Psi1	Pvu1	Pvu2	Sap1	Sca1	SpAcc	SpDon	Ssp1	Stu1	T7Ter	Xba1	Xho1	Xmn1

Unique:

Aat2	Age1	Ahd1	Ale1	AlwN1	Ase1	BamH1	Bcg1a	Bcg1b	Blp1	Bpu10	BsaB1	BseR1	BspE1
BspLU	BsrG1	BstAP	BstZ1	Bsu36	Dra3	Eag1	EcoK	Fsp1	Hind3	Mfe1	Nde1	Nhe1	Not1
PflF1	PshA1	Psi1	Pvu1	Pvu2	Sap1	Stu1	T7Ter	Xba1	Xho1	Xmn1			

Not found:

Aar1	Acc65	Afe1	Afl2	Apa1	Asc1	AsiS1	Avr2	Bae1a	Bae1b	BbvC1	Bcl1	BfrB1	Bgl2
BmgB1	BsaXa	BsaXb	Bsg1	BsiW1	BspM1	BssH2	BstB1	BstE2	BstX1	BxatB	BxatL	BxatR	BxatP
_Chi	Clal	Ecl2	EcoN1	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hpa1
I_Ceu	Kas1	Kpn1	loxP	Mlu1	Nae1	Nar1	NgoM4	Nru1	Nsi1	Pac1	Pme1	Pml1	PspOM
Pst1	R4atB	R4atL	R4atP	R4atR	Rsr2	Sac1	Sac2	Sall	SanD1	Sbf1	SexA1	Sfi1	Sgf1
SgrA1	Sma1	SnaB1	Spe1	Sph1	Srf1	Swa1	T3RNA	T7RNA	PISce	Xcm1			

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	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													