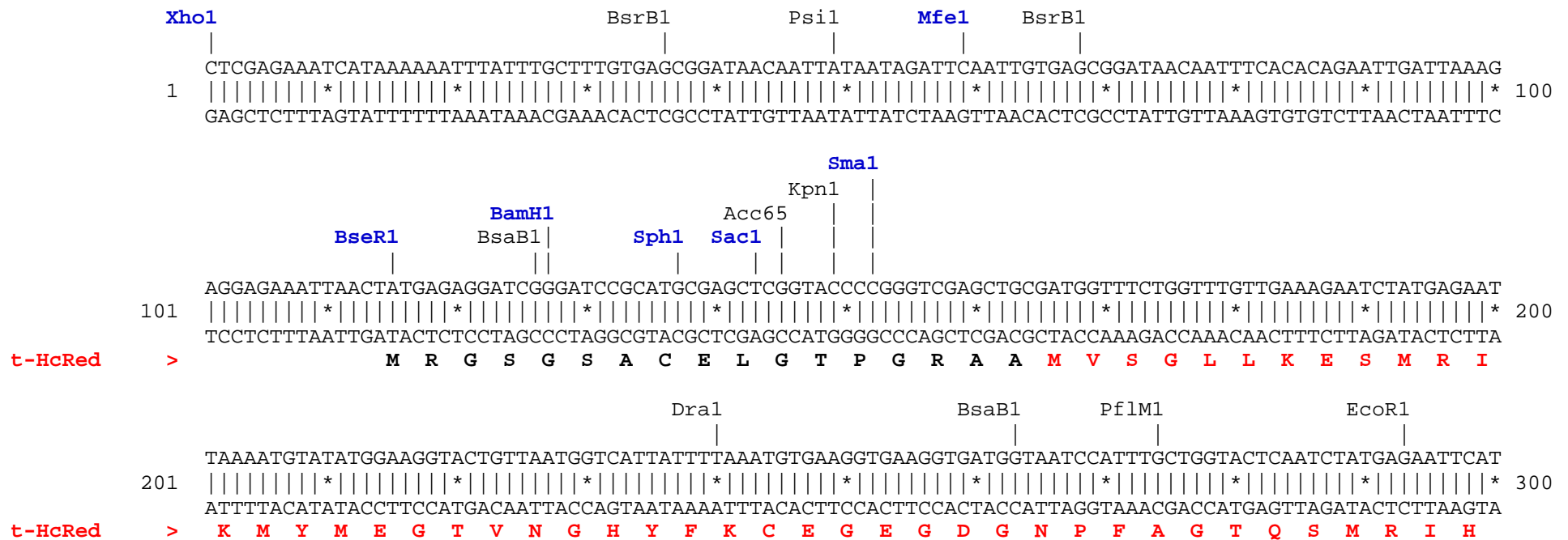


pHcRed-Tandem-YB vector restriction map

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 and amino acids coded by linker between two identical HcRed1 sequences are shown in black.




```
          BspE1
        Bsm1 |           BsrD1
        |   |           |
1901 TTGCCCGCCTGATGAATGCTCATCCGGAATTTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCCTTGTTACACCGTTTTTCCA 2000
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
    AACGGGCGGACTACTTACGAGTAGGCCTTAAAGCATAACCGTTACTTTCTGCCACTCGACCACTATAACCTATCACAAAGTGGGAACAATGTGGCAAAGGT

          Acl1           Bpm1
          |             |
2001 TGAGCAAACCTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAA 2100
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
    ACTCGTTTTGACTTTGCAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAAATGCCACTT

                                     BsmB1  PflM1
                                     |       |
2101 AACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTACCAGTTTTGATTTAAACGTGGCCAATA 2200
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
    TTGGACCGGATAAAGGGATTTCCCAAATAACTCTTATACA AAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAA AACTAAATTTGCACCGGTTAT

          Nco1           Ssp1
          |             |
2201 TGGACAACTTCTTCGCCCCGTTTTTCACCATGGGCAAATATTATACGCAAGGGCACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGTCTG 2300
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
    ACCTGTTGAAGAAGCGGGGGCAAAGTGGTACCCGTTTATAATATGCGTTCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGAC

                                     Bsm1           Scal
                                     |             |
2301 TGATGGCTTCCATGTCGGCAGAATGCTTAAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATTGGTGCCCT 2400
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
    ACTACCGAAGGTACAGCCGCTTACGAATTACTTAAATGTTGTCATGACGCTACTCACCGTCCCCGCCCGCATTA AAAAAAATTCGGTCAATAAACCACGGGA

                                               BpuE1           Bmr1
                                               |             |
2401 TAAACGCCTGGGGTAATGACTCTCTAGCTTGAGGCATCAAATAAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTTGTGGTGTG 2500
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
    ATTTGCGGACCCCATTA CTGAGAGATCGAACTCCG TAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGACCCGAAAGCAA AATAGACAACAAACAGCCAC
```



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Dra1              Dra1
|                 |
3701 TTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGC
| | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * 3800
AAAATTTAATTTTTACTTCAAAATTTAGTTAGATTTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCC

              Ahd1              Bmr1              BsrD1
              |                 |                 |
3801 GATCTGTCTATTTTCGTTTCATCCATAGCTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATA
| | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * 3900
CTAGACAGATAAAGCAAGTAGGTATCGACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTACGACGTTACTAT

          Bpm1              Bgl1              Eci1
          |                 |                 |
3901 CCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGCAACTTTATCCGCCTCCA
| | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * 4000
GGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGT

              Acl1
              |
          Ase1              Fsp1              BsrD1
          |                 |                 |
4001 TCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCCGCAAGTTAATAGTTTTCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACAG
| | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * 4100
AGGTCAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGATGTCCGTAGCACCCACAGTGC

CTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGT
4101 | | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * 4200
GAGCAGCAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCA

          Pvul1              Bts1              Bts1
          |                 |                 |
4201 CCTCCGATCGTTGTGAGAAGTAAGTTGGCCGAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCT
| | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * | | | | * 4300
GGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGA

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          BssS1  Bbs1
          |      |
AGGCGTATCACGAGGCCCTTTTCGTCTTCAC
4801  |||||*|||*|||* 4830
TCCGCATAGTGCTCCGGGAAAGCAGAAGTG
    
```

Found:

Aat2	Acc65	Ac11	Ahd1	AlwN1	ApaL1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1	Bgl1	Bgl2
Blp1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BseR1	BseY1	Bsm1	BsmB1	BspE1	BspH1	BspLU
BsrB1	BsrD1	BssS1	BstAP	BstZ1	Bts1	Dra1	Drd1	Ear1	Eci1	Eco57	EcoK	EcoR1	Fsp1
Hind3	Kpn1	Mfe1	Msc1	Nco1	Nde1	Nhe1	PflF1	PflM1	Psi1	Pvu1	Pvu2	Sac1	Sac2
Sap1	Scal	Sma1	Sph1	Ssp1	Xba1	Xho1	Xmn1						

Unique:

Aat2	Ahd1	AlwN1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	Bgl1	Bgl2	Blp1	Bpu10	Bsa1	BseR1
BseY1	BspE1	BspLU	BstZ1	EcoK	Fsp1	Hind3	Mfe1	Msc1	Nco1	Nde1	Nhe1	PflF1	Pvu1
Pvu2	Sac1	Sac2	Sap1	Sma1	Sph1	Xho1	Xmn1						

Not found:

Aar1	Afe1	Afl2	Age1	Ale1	Apal	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfrB1
BfuA1	BmgB1	BsaXa	BsaXb	Bsg1	BsiW1	BspM1	BsrG1	BssH2	BstB1	BstE2	BstX1	Bsu36	_Chi
Clal	Dra3	Eag1	EcoN1	EcoRV	ScFRT	Fse1	FspA1	Hpa1	I_Ceu	Kas1	loxP	Mlu1	Nae1
Nar1	NgoM4	Not1	Nru1	Nsil	Pac1	Pme1	Pml1	PshA1	PspOM	Pst1	Rsr2	Sall	SanD1
Sbf1	SexA1	Sfil	Sgf1	SgrA1	SnaB1	Spe1	Srf1	Stu1	Swal	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													