

### pHcRed-Tandem-N2 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).

MCS sequence shown in frame, amino acids coded by MCS and by a linker between two HcRed1 coding sequences (see vector description) shown in black.







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                Sfi1
                Bgl1
                BspM1
                BfuA1
                Bgl2
                Sma1
                BsrB1
                EcoN1
                |
                |
                |
1301  GACGAGTACTTTCGAGCTGTACGAGGCCAGCGTGGCCCCGGTACAGCGACCTGCCCGAGAAGGCCAACAGATCTCCCGGGATGGTGAGCGGCCTGCTGAAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    CTGCTCATGAAGCTCGACATGCTCCGGTTCGCACCGGGCCATGTCGCTGGACGGGCTCTTCCGGTTGTCTAGAGGGCCCTACCACTCGCCGGACGACTTCC
t-HcRed > D E Y F E L Y E A S V A R Y S D L P E K A N R S P G M V S G L L K

                Fsp1
                BsrG1
                FspA1
                Eco57
                Bcg1b
                Nae1
                NgoM4
                Bcg1a
                |
                |
                |
1401  AGAGTATGCGCATCAAGATGTACATGGAGGGCACCGTGAACGGCCACTACTTCAAGTGCAGGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
    TCTCATACGCGTAGTTCTACATGTACCTCCCGTGGCACTTGCCGGTGATGAAGTTCACGCTCCCCTCCCGCTGCCGTTGGGGAAGCGGCCGTGGGTCTC
t-HcRed > E S M R I K M Y M E G T V N G H Y F K C E G E G D G N P F A G T Q S

                Nar1
                Pml1
                Kas1
                Bcg1b
                ApaL1
                |
                |
                |
1501  CATGAGAATCCACGTGACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACCTTCGTGCACCACACC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
    GTACTCTTAGGTGCACTGGCTCCCGCGGGGGGACGGGAAGCGGAAGCTGTAGGACCGGGGGACGACGCTCATGCCGTGCTCCTGGAAGCACGTGGTGTGG
t-HcRed > M R I H V T E G A P L P F A F D I L A P C C E Y G S R T F V H H T

                Bcg1a
                |
                |
                |
1601  GCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTACCTGGGAGAGAACCACCACCTACGAGGACGGCGGCATCCTGACCGCCCACCAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
    CGGCTCTAGGGGCTGAAGAAGTTCGTCTCGAAGGGGCTCCCGAAGTGGACCTCTCTTGGTGGTGGATGCTCCTGCCGCCGTAGGACTGGCGGGTGGTCC
t-HcRed > A E I P D F F K Q S F P E G F T W E R T T T Y E D G G I L T A H Q

                Bgl1
                Bpm1
                ApaL1
                BsrB1
                BseY1
                |
                |
                |
1701  ACACCAGCCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCCGACGGCCCCGTGATGAAGAACAAGAGCGGGCGGCTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
    TGTGGTCGGACCTCCCGTTGACGGACTAGATGTTCCACTTCCACGTGCCGTGGTTGAAGGGGCGGCTGCCGGGGCACTACTTCTTGTTCCTCGCCGCCGAC
t-HcRed > D T S L E G N C L I Y K V K V H G T N F P A D G P V M K N K S G G W

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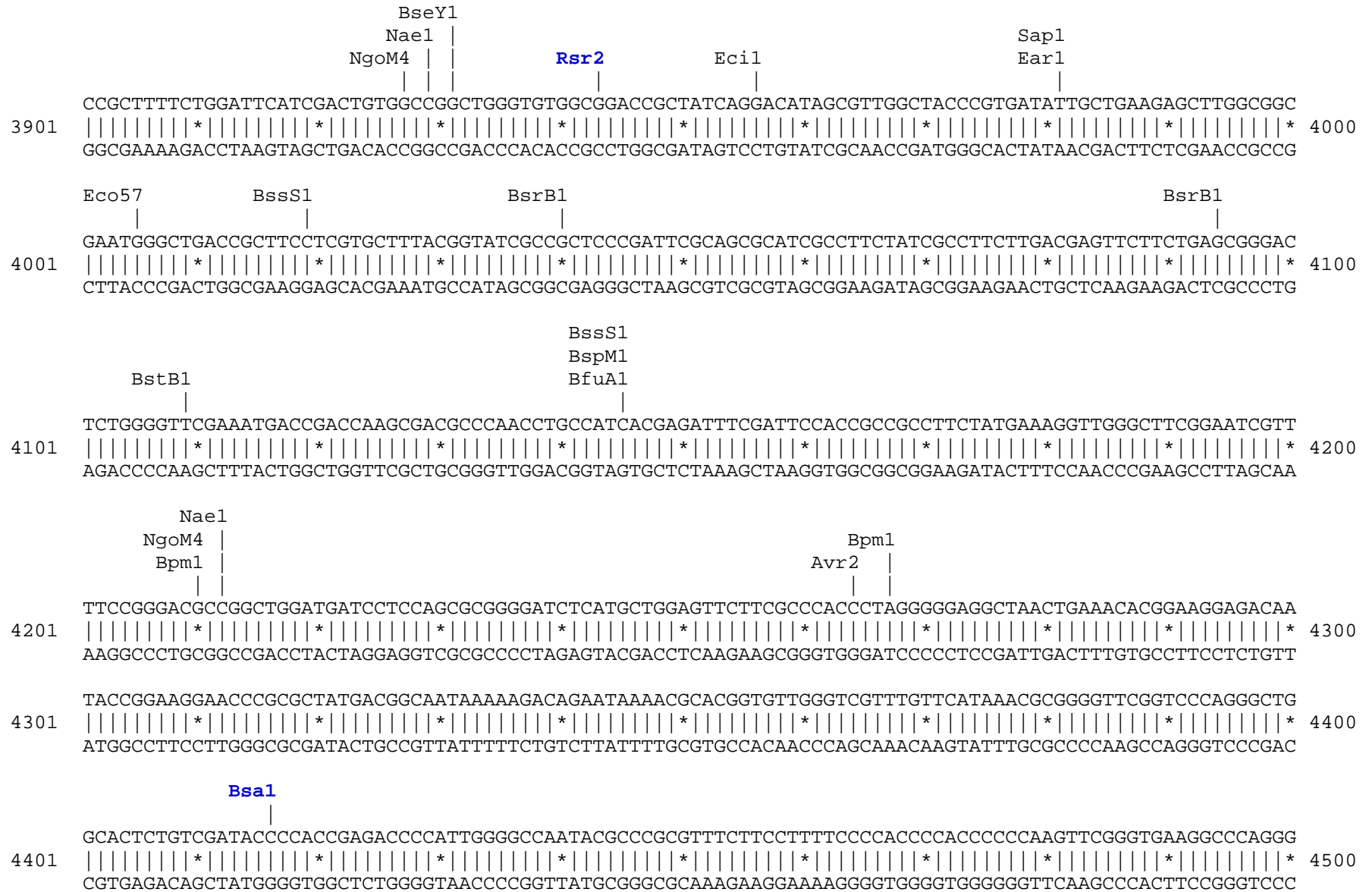












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          BstAP
          AlwN1      Bsu36
          DraI      DraI
4501  CTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTTAATTTAAAAGGATCT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
      GAGCGTCGGTTGCAGCCCCGCCGTCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCCTAGA

          BspH1
4601  AAGTGAAGATCCTTTTTGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
      TCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCCTAGAAG

          BpuE1
4701  TTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
      AACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAA

Eco57
4801  TTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
      AAAGGCTTCCATTGACCGAAGTCGTCTCGGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCG

          AlwN1      BpuE1
4901  CTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
      GATGTATGGAGCGAGACGATTAGGACAATGGTCAACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATT

          ApaL1      BseY1
5001  GGCGCAGCGGTCGGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
      CCGGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTCGAACCTCGCTTGTGATGTGGCTTACTCTATGGATGTGCACTCGATACTCTT
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Found:

Aat2	<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	Ale1	AlwN1	<b>Apa1</b>	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	BcglA	Bcglb	BciV1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	<b>Bsa1</b>	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	BseY1	Bsm1
BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	<b>Bts1</b>	<b>Cla1</b>	Dra1
<b>Dra3</b>	Drd1	Eag1	Ear1	Eci1	Eco57	EcoN1	<b>EcoR1</b>	FspA1	Fsp1	<b>Hind3</b>	<b>Hpa1</b>	Kas1	<b>Kpn1</b>
<b>Mfe1</b>	<b>Msc1</b>	Nae1	Nar1	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	Nsi1	<b>PflF1</b>	Pml1	Psi1	<b>PspOM</b>	<b>Pst1</b>
Pvu2	<b>Rsr2</b>	<b>Sac1</b>	<b>Sac2</b>	<b>Sall</b>	Sap1	Sca1	<b>SexA1</b>	Sfi1	Sma1	<b>SnaB1</b>	Sph1	Ssp1	<b>Stu1</b>
<b>Xba1</b>	Xcm1	Xho1											

Unique:

<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Apa1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bsa1</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	<b>BspLU</b>	<b>BsrD1</b>	<b>Bts1</b>	<b>Cla1</b>
<b>Dra3</b>	<b>EcoR1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Msc1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>PflF1</b>	<b>PspOM</b>	<b>Pst1</b>	<b>Rsr2</b>	<b>Sac1</b>
<b>Sac2</b>	<b>Sall</b>	<b>SexA1</b>	<b>SnaB1</b>	<b>Stu1</b>	<b>Xba1</b>								

Not found:

Aar1	Acl1	Age1	Ahd1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcl1	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BspE1	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoRV	ScFRT	Fse1	I_Ceu	loxP
Mlu1	Not1	Nru1	Pac1	PflM1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sgf1	SgrA1	Spe1	Srf1
Swal	PISce	Xmn1											

Excluded by site complexity:

Acc1	Ac11	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													