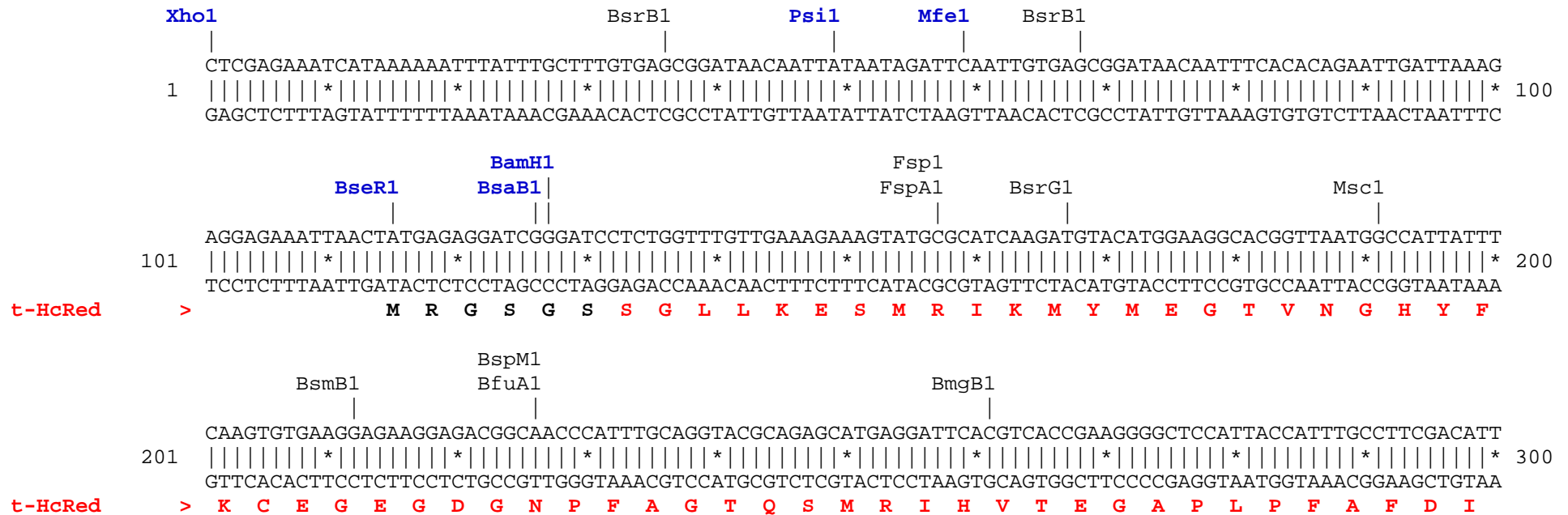


**pHcRed-Tandem-B vector** restriction map

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







```

                                                                                               BstAP
                                                                                               |
                                                                                               Eco57
                                                                                               |
                                                                                               EciI
                                                                                               |
1301  CCCTTAAAGTCGGTGATCGTCATTTGATCTGCCATCACTATACTTCTTACAGGTCCAAGAAAGCAGTCCGTGCCTTGACAATGCCAGGATTTTCATTTTAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      GGAATTTTCAGCCACTAGCAGTAAACTAGACGGTAGTGATATGAAGAATGTCCAGGTTCTTTTCGTCAGGCACGGAAGTGTACGGTCTTAAAGTAAAATG
t-HcRed >  L K V G D R H L I C H H Y T S Y R S K K A V R A L T M P G F H F T

                Bpu10
                BbvC1
                AlwN1 |
                |
                ScaI
                |
1401  AGACATCCGCCTTCAGATGCTGAGGAAAAAGAAAGACGAGTACTTTGAACTGTACGAAGCATCTGTGGCTAGGTACAGTGATCTTCCTGAAAAAGCAAAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
      TCTGTAGGCGGAAGTCTACGACTCCTTTTTCTTTCTGCTCATGAAACTTGACATGCTTCGTAGACACCGATCCATGTCACTAGAAGGACTTTTTTCGTTTA
t-HcRed >  D I R L Q M L R K K K D E Y F E L Y E A S V A R Y S D L P E K A N

Hind3          BlnI
|              |
1501  TAGAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTTCAGAACGCTCGGTTGCCGCCGGGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
      ATCTTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCTAAACAAGTCTTGCGAGCCAACGGCGGCCCG
t-HcRed > *

                NheI
                |
                Bpu10
                |
1601  GTTTTTTATTGGTGAGAAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATCACTGGATATAACCACCGTTGATAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
      CAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTAAAAGTCTTCGATTCTTTTCGATTTTACCTCTTTTTTTTAGTGACCTATATGGTGGCAACTATA

                                                                                               Pvu2
                                                                                               |
                                                                                               DraI
                                                                                               |
1701  ATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTTCAGCTGGATATTACGGCCTTTTTTAAAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
      TAGGTTACCGTAGCATTTCTTGTA AAACTCCGTAAAGTCAGTCAACGAGTTACATGGATATTGGTCTGGCAAGTCGACCTATAATGCCGAAAAATTC
```



```
              Bmr1                             Eci1                                Xba1  
              |                                |                                |  
GGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGCTCTAGAGCTGCCTCGCGCGT  
2401 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2500  
CCGAGTCAGCTTTCTGACCCGAAAGCAAAATAGACAACAACAGCCACTTGCAGAGAGGACTCATCCTGTTTGTAGCGGCGAGATCTCGACGGAGCGCGCA  
      BsmB1                                       Drd1  
      |                                       |  
TTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTACACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCG  
2501 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2600  
AAGCCACTACTGCCACTTTTGAGACTGTGTACGTGAGGGCCTCTGCCAGTGTGCAACAGACATTGCGCTACGGCCCTCGTCTGTTCGGGCAGTCCCAGC  
      Bmr1 PflF1                              BstZ1  
      |    |                                  |  
CGTCAGCGGGTGTGGCGGGTGTGCGGGCGCAGCCATGACCCAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATT  
2601 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2700  
GCAGTCGCCACAAACCGCCCACAGCCCCGCGTCCGTAAGTGGTGTGATGATGCGCTCACATATGACCGAATTGATACGCCGTAAGTCTCTGCTCTAA  
      ApaL1  BstAP  Nde1                                     Sap1  
      |    |    |    |                                       |  
GTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAGATGCGTAAGGAGAAAATACCGCATCAGGCCTCTTCCGCTTCCCTCGCTCACTGACTCGC  
2701 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2800  
CATGACTCTCACGTGTTATACGCCACACTTTATGGCGTGTCTACGCATTCCCTCTTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCGAGTACTGAGCG  
      BsrB1                                     BspLU  
      |                                       |  
TGCGCTCGGTCTGTGCGGTGCGGCGAGCGGTATCAGCTCACTCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTG  
2801 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2900  
ACGCGAGCCAGACAGCCGACCCGCTCGCCATAGTCGAGTGAGTTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTTCTGTACAC  
      Eci1                                     BpuE1  
      |                                       |  
AGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCGACGC  
2901 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 3000  
TCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTCCTCCGGCGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGACTGCTCGTAGTGTTCCTTTAGCTGCG
```

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Drdl                               BssS1                               BciV1
|                                   |                                   |
TCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTA
3001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3100
AGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAAT

Eci1                               BseY1
|                                   |
CCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTGCTTCGCTCCAAGCT
3101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3200
GGCCTATGGACAGGCGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTTACGAGTGCACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTTCCA

ApaL1                               BpuE1
|                                   |
GGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTG
3201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3300
CCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAAGTTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGAC

AlwN1
|
GCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAG
3301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3400
CGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTCTGTC

Eco57
|
TATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTT
3401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3500
ATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAAGTTCAGGCGGTTTGGTTGGTGGCGACCATCGCCACCAAAAAA

BpuE1
|
TGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAAACGAAAACCTCACGT
3501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3600
ACAAACGTTTCGTGCTAATGCGCGTCTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTTGCTTTTGGAGTGCA
```

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          BspH1                      DraI          DraI
          |                          |              |
3601 TAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAGATCCTTTTAAATTTAAAAATGAAGTTTTTAAATCAATCTAAAGTATATATGAGTAAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
      ATTCCTAAAACCAGTACTCTAATAGTTTTTCTAGAAAGTGGATCTAGGAAAATTTAATTTTTACTTCAAAAATTTAGTTAGATTTTCATATATACTCATT

                                          AhdI
                                          |
3701 CTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGCTGCCTGACTCCCCGTCGTGTAGAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
      GAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCGACGGACTGAGGGGCAGCACATCTA

          BsrD1          BmrI          BsaI          BpmI
          |              |              |              |
3801 AACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
      TTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGT

          BglI          EciI          AseI
          |              |              |
3901 GCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGTAAGTAGTTCGCCAGTTA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
      CGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGTGAGATAATTAACAACGGCCCTTCGATCTCATTTCATCAAGCGGTCAAT

          AclI          FspI          BsrD1
          |              |              |
4001 ATAGTTTTCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTACAGCTCGTTCGTTTGGTATGGCTTCATTTCAGCTCCGGTTCCTCAACGATCAAGGCG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
      TATCAAACGCGTTGCAACAACGGTAACGATGTCCGTAGCACACAGTGCAGCAGCAAACCATAACGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCGCG

                                          PvuI          BtsI
                                          |              |
4101 AGTTACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCCGTCCGATCGTTGTCAGAAGTAAGTTGGCCGAGTGTATCACTCATGGTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
      TCAATGTACTAGGGGTACAACACGTTTTTTTCGCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAA

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          Bts1                      Scal                      Bcg1a
          |                          |                          |
4201 ATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGTAAGATGCTTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGC 4300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTTTCAGTAAGACTCTTATCACATACG

          Bcg1b                      Dra1                      Xmn1
          |                          |                          |
4301 GCGGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCG 4400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCGCTGGCTCAACGAGAACGGGCCGAGTTATGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTTACGAGTAGTAACCTTTTGCAAGAAGCCCCGC

          EcoK
          |
          Eco57
          |
          ApaL1
          |
          BssS1
          |
4401 AAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGATGTAACCCACTCGTGCACCCAAGTATCTTTCAGCATCTTTTACTTTTACCAGCGTTTCT 4500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TTTTGAGAGTTCTTAGAATGGCGACAACCTTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTTCGCAAAGA

          Ear1                      Ssp1
          |                          |
4501 GGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAA 4600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCCACTCGTTTTTGTCTTCCGTTTTTACGGCGTTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTATGAGTATGAGAAGGAAAAAGTTATAATAACTT

          BsrB1
          |
          BciV1
          |
          BspH1
          |
4601 GCATTTATCAGGGTTATTGTCTCATGAGCGGATAACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCC 4700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAAGGGGCTTTTCACGG
    
```

```

          Aat2          BspH1          BssS1  Bbs1
          |             |             |       |
ACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTTCAC
4701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4779
TGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTG

```

Found:

<b>Aat2</b>	Acc65	AcI1	<b>Ahd1</b>	Ale1	AlwN1	ApaL1	<b>Ase1</b>	<b>BamH1</b>	<b>Bbs1</b>	BbvC1	<b>Bcg1a</b>	<b>Bcg1b</b>	BciV1
BfuA1	<b>Bgl1</b>	<b>Bgl2</b>	<b>Blp1</b>	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	<b>Bsa1</b>	<b>BsaB1</b>	<b>BseR1</b>	<b>BseY1</b>	Bsm1
BsmB1	<b>BspE1</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	<b>BstZ1</b>	Bts1	Dra1	Drd1
Ear1	Eci1	Eco57	<b>EcoK</b>	FspA1	Fsp1	<b>Hind3</b>	Kpn1	<b>Mfe1</b>	Msc1	Nco1	<b>Nde1</b>	<b>Nhe1</b>	<b>PflF1</b>
PflM1	PshA1	<b>Psi1</b>	<b>Pvu1</b>	<b>Pvu2</b>	<b>Sap1</b>	Sca1	<b>Sma1</b>	Ssp1	<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>		

Unique:

<b>Aat2</b>	<b>Ahd1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bbs1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	<b>Bgl1</b>	<b>Bgl2</b>	<b>Blp1</b>	<b>Bsa1</b>	<b>BsaB1</b>	<b>BseR1</b>	<b>BseY1</b>
<b>BspE1</b>	<b>BspLU</b>	<b>BstZ1</b>	<b>EcoK</b>	<b>Hind3</b>	<b>Mfe1</b>	<b>Nde1</b>	<b>Nhe1</b>	<b>PflF1</b>	<b>Psi1</b>	<b>Pvu1</b>	<b>Pvu2</b>	<b>Sap1</b>	<b>Sma1</b>
<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>											

Not found:

Aar1	Afe1	Afl2	Age1	Apa1	Asc1	AsiS1	Avr2	Baela	Baelb	Bcl1	BfrB1	BsaXa	BsaXb
Bsg1	BsiW1	BssH2	BstB1	BstE2	BstX1	Bsu36	_Chi	Clal	Dra3	Eag1	EcoN1	EcoR1	EcoRV
ScFRT	Fse1	Hpa1	I_Ceu	Kas1	loxP	Mlu1	Nae1	Nar1	NgoM4	Not1	Nrul	Nsil	Pac1
Pme1	Pml1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SanD1	Sbf1	SexA1	Sfil	Sgf1	SgrA1
SnaB1	Spe1	Sph1	Srf1	Stu1	Swal	PISce	Xcm1						

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													