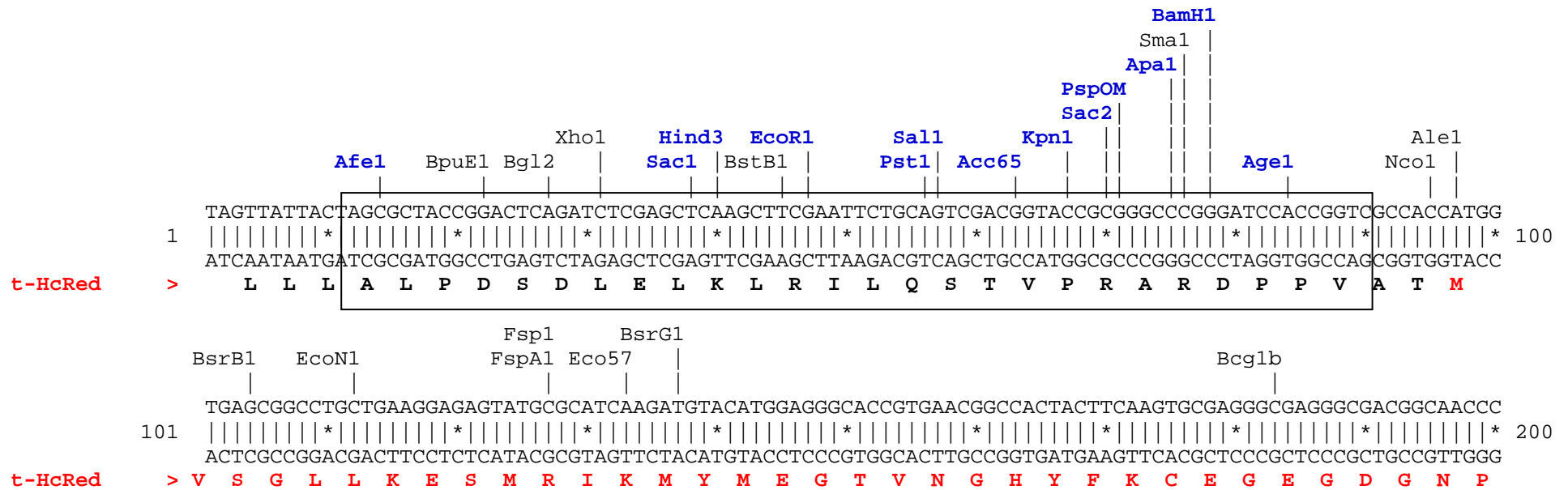


pHcRed-Tandem-PRL vector restriction map

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.



```

      NaeI      NarI
      NcoM4 |   BclI      PmlI      KasI      BclIb
      |     |           |           |           |
201  CTTTCGCCGGCACCCAGAGCATGAGAATCCACGTGACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 300
    GAAGCGCCCGTGGGTCTCGTACTCTTAGGTGCACTGGCTCCCCGCGGGGGGACGGGAAGCGGAAGCTGTAGGACCGGGGGACGACGCTCATGCCGTTCGTCC
t-HcRed > F A G T Q S 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

      ApaI      BclI
      |         |
301  ACCTTCGTGCACCACACCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACTGGGAGAGAACCACCACCTACGAGGACGGCGGCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 400
    TGAAGCACGTGGTGTGGCGGCTCTAGGGGCTGAAGAAGTTCGTCTCGAAGGGGCTCCCGAAGTGGACCCTCTCTTGGTGGTGGATGCTCCTGCCGCCGT
t-HcRed > T F V H H T 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

      BglI      BpmI      ApaI
      |         |         |
401  TCCTGACCGCCCACCAGGACACCAGCCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCGCGACGGCCCCGTGATGAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
    AGGACTGGCGGGTGGTCTGTGGTTCGGACCTCCCCGTTGACGGACTAGATGTTCCACTTCCACGTGCCGTGGTTGAAGGGGGCGGCTGCCGGGGCACTACTT
t-HcRed > I L T A H Q 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

      AleI
      BsrB1 BseY1 BseY1 XcmI |           EagI
      |     |     |     |     |           |
501  GAACAAGAGCGGCGGCTGGGAGCCCAGCACCGAGGTGGTGTACCCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATGGCCCTGAAGGTGGGCGACCGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
    CTTGTTCTCGCCCGGACCTCGGGTTCGTGGCTCCACCACATGGGGCTCTTGCCGCACGACACGCCGGCCTTGCCTACTCCGGGACTTCCACCCGCTGGCC
t-HcRed > N K S G G W E P S T E V V Y P E N G V L C G R N V M A L K V G D R

      Eco57      BssH2      BpmI      AlwNI
      |         |         |         |
601  CACCTGATCTGCCACCACTACACCAGCTACCGGAGCAAGAAGGCCGTGCGCGCCCTGACCATGCCCGGCTTCACTTACCGACATCCGGCTCCAGATGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
    GTGGACTAGACGGTGGTGTGGTTCGATGGCCTCGTTCTTCCGGCACGCGCGGGACTGGTACGGGCCGAAGGTGAAGTGGCTGTAGGCCGAGGTCTACG
t-HcRed > 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 D I R L Q M

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                                     SfiI      BspM1
                                     BglI      BfuA1      Bgl2      SmaI
          TCGGGAAGAAGAAGGACGAGTACTTTCGAGCTGTACGAGGCCAGCGTGGCCCGGTACAGCGACCTGCCCGAGAAGGCCAACAGATCTCCCGGGATGGTGAG
701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
          ACGCCTTCTTCTTCTCCTGCTCATGAAGCTCGACATGCTCCGGTTCGCACCGGGCCATGTCGCTGGACGGGCTCTTCCGGTTGTCTAGAGGGCCCTACCACTC
t-HcRed  > 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 R S P G M V S

                                     FspI      BsrGI
          BsrBI      EcoNI      FspAI      Eco57      BcgIb
          CGGCCTGTGTAAGGAGAGTATGCGCATCAAGATGTACATGGAGGGCACCCTGAACGGCCACTACTTCAAGTGGCAGGGGCGAGGGCGACGGCAACCCCTTC
801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
          GCCGGACGACTTCTCCTCATACGCGTAGTTCTACATGTACCTCCCGTGGCACTTGCCGGTGTATGAAGTTCACGCTCCCCTCCCGCTGCCGTTGGGGAAG
t-HcRed  > G L L K 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

          NaeI      NarI
          NgoM4      BcgIa      PmlI      KasI      BcgIb
          GCCGGCACCCAGAGCATGAGAATCCACGTGACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACCT
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
          CGGCCGTGGGTCTCGTACTCTTAGGTGCACTGGCTCCCGCGGGGGGACGGGAAGCGGAAGCTGTAGGACCGGGGGACGACGCTCATGCCGTGCTCCTGGA
t-HcRed  > A G T Q S 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

          ApaI      BcgIa
          TCGTGCACCACACCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAGAGAACCACCACCTACGAGGACGGCGGCATCCT
1001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
          AGCACGTGGTGTGGCGGCTCTAGGGGCTGAAGAAGTTCGTCTCGAAGGGGCTCCCGAAGTGGACCTCTCTTGGTGGTGGATGCTCCTGCCGCCGTAGGA
t-HcRed  > F V H H T 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

                                     BglI      BpmI      ApaI
          GACCGCCACCAGGACACCAGCCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAAC
1101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
          CTGGCGGGTGGTCTGTGGTTCGGACCTCCCGTTGACGGACTAGATGTTCCACTTCCACGTGCCGTGGTTGAAGGGGCGGCTGCCGGGGCACTACTTCTTG
t-HcRed  > T A H Q 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

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              Ale1
      BsrB1  BseY1  BseY1  Xcm1 |                               Eag1
1201  AAGAGCGGCGGCTGGGAGCCCAGCACCGAGGTGGTGTACCCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATGGCCCTGAAGGTGGGCGACCCGGCACC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
      TTCTCGCCCGCGACCCCTCGGGTCGTGGCTCCACCACATGGGGCTCTTGCCGCACGACACGCCGGCCTTGCACTACCGGGACTTCCACCCGCTGGCCGTGG
t-HcRed  >  K S G G W E P S T E V V Y P E N G V L C G R N V M A L K V G D R H

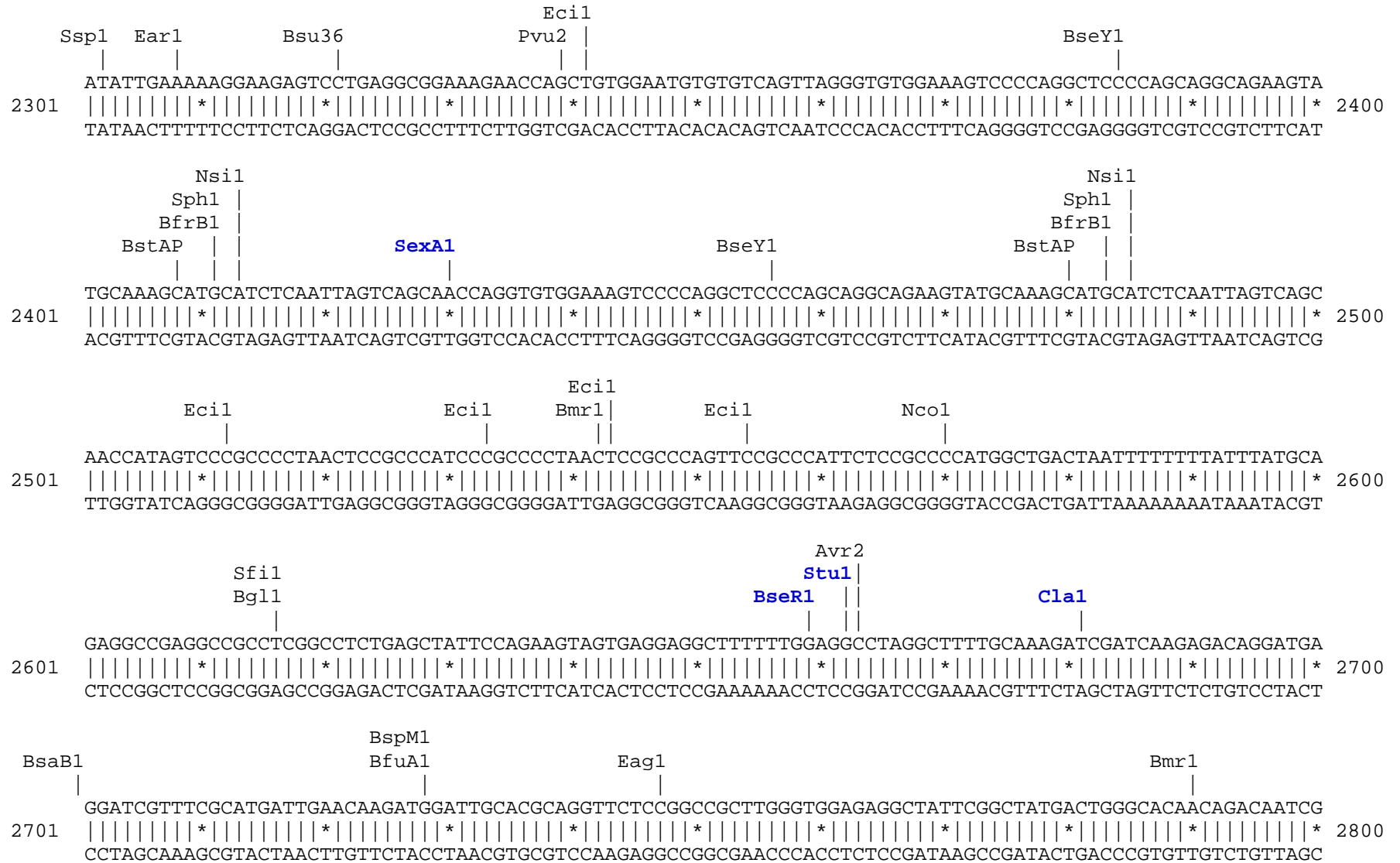
      Eco57              BssH2              Bpm1              AlwN1
1301  TGATCTGCCACCACTACACCAGCTACCGGAGCAAGAAGGCCGTGCGCGCCCTGACCATGCCCGGCTTCCACTTCACCGACATCCGGCTCCAGATGCTGCG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      ACTAGACGGTGGTGATGTGGTCGATGGCCTCGTTCTTCCGGCACGCGCGGGACTGGTACGGGCCGAAGGTGAAGTGGCTGTAGGCCGAGGTCTACGACGC
t-HcRed  >  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 D I R L Q M L R

              Sfi1              BspM1              Xho1              Xba1
      Sca1              Bgl1              BfuA1
1401  GAAGAAGAAGGACGAGTACTTTCGAGCTGTACGAGGCCAGCGTGGCCCCGGTACAGCGACCTGCCCGAGAAGGCCAACAGAACTCGAGGCCGCGACTCTAGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
      CTTCTTCTTCTCCTGCTCATGAAGCTCGACATGCTCCGGTCGCACCGGGCCATGTCGCTGGACGGGCTCTTCCGGTTGTCTTGAGCTCCGGCGCTGAGATCT
t-HcRed  >  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 R T R G R D S R

              Dra1              Bsm1
      BsaB1              Mfe1
1501  TCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
      AGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACA
t-HcRed  >  S *

      Hpa1              Pst1              Bts1  Bsm1
1601  TGTAACTTGTATTGTCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
      ACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTATTTTCGTAAAAAAGTGACGTAAGATCAACACCA

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DraI       BspH1
  |         |
4001 ATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAAATCCCTTAAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAG
  |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|* 4100
TAAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTC

      BpuE1
          |
4101 ATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAG
  |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|* 4200
TAGTTTTCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAAACAAACGGCCTAGTTC

          Eco57
             |
4201 AGCTACCAACTCTTTTTCCGAAGGTAAC TGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAA
  |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|* 4300
TCGATGGTTGAGAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTT

          AlwN1       BpuE1
             |         |
4301 CTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
  |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|* 4400
GAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTGAGCACAGAATGGCCCAACCTGAGTTCTGCT

          ApaL1       BseY1
             |         |
4401 TAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGC
  |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|* 4500
ATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCSCCCCCAAGCACGTGTGTGCGGGTTCGAACCTCGCTTGTCTGGATGTGGCTTGGACTCTATGGATGTGCG

          BciV1       BssS1
             |         |
4501 GTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCC
  |*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|*|* 4600
CACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTCGCCGTCCAGCCTTGTCTCTCGCGTGTCTCCCTCGAAGG
```

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                                Drd1                BpuE1
                                |                    |
AGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGG
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
TCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATAACC

Eci1                                BspLU
|                                    |
AAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTCTGGCCTTTTGTCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACC
4701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
TTTTTTCGGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGG

                NsiI
                BfrB1 |
                |     |
GTATTACCGCCATGCAT
4801 |||||*||||| 4817
CATAATGGCGGTACGTA

```

Found:

Acc65	AfeI	Afl2	AgeI	AleI	AlwNI	ApaI	ApaLI	Avr2	BamHI	BcgIa	BcgIb	BciVI	BfrB1
BfuAI	BglI	Bgl2	BmrI	BpmI	BpuE1	BsaI	BsaBI	BsaXa	BsaXb	BseR1	BseY1	BsmI	BspHI
BspLU	BspMI	BsrBI	BsrDI	BsrGI	BssH2	BssSI	BstAP	BstBI	Bsu36	Bts1	ClaI	DraI	Dra3
Drd1	EagI	EarI	EciI	Eco57	EcoNI	EcoRI	FspAI	FspI	Hind3	HpaI	KasI	KpnI	MfeI
MscI	NaeI	NarI	NcoI	NgOM4	NsiI	PflFI	PmlI	PsiI	PspOM	PstI	Pvu2	Rsr2	SacI
Sac2	SalI	SapI	Scal	SexA1	SfiI	SmaI	SphI	SspI	StuI	XbaI	XcmI	XhoI	

Unique:

Acc65	Afe1	Afl2	Age1	Apa1	BamH1	Bsa1	BsaXa	BsaXb	BseR1	BspLU	BsrD1	Bts1	Clal
Dra3	EcoR1	Hind3	Hpa1	Kpn1	Mfe1	Msc1	PflF1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall
SexA1	Stu1	Xba1											

Not found:

Aar1	Aat2	Acl1	Ahd1	Asc1	Ase1	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	Nde1	Nhe1	Not1	Nru1	Pac1	PflM1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sgf1
SgrA1	SnaB1	Spe1	Srf1	Swal	PISce	Xmn1							

Excluded by site complexity:

Acc1	Acil	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	Faul	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													