

pKillerRed-C 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 shown in black.



Aat2 Eci1

```
401 TAGCGGTTTGACTCACGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
```

Nhe1 Afel

```
501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
```

Age1 Nco1 SpDon

```
601 CCGGTCGCCACCATGGGTTTCAGAGGGCGGCCCGCCCTGTTCCAGAGCGACATGACCTTCAAATCTTCATCGACGGCGAGGTGAACGGCCAGAAGTTCA
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
GGCCAGCGGTGGTACCCAAGTCTCCCGCCGGGGCGGGACAAGGTCTCGCTGACTGGAAGTTTTAGAAGTAGCTGCCGCTCCACTTGCCGGTCTTCAAGT
```

KillerRed > M G S E G G P A L F Q S D M T F K I F I D G E V N G Q K F T

Ale1 SpDon ApaL1 Bsa1 Dra3 PflM1

```
701 CCATCGTGGCCGACGGCAGCAGCAAGTTCCCCACGGCGACTTCAACGTGCACGCCGTGTGCGAGACCGGCAAGCTGCCCATGAGCTGGAAGCCCATCTG
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
GGTAGCACCGGCTGCCGTCGTCGTTCAAGGGGGTGCCGCTGAAGTTGCACGTGCGGCACACGCTCTGGCCGTTTCGACGGGTACTCGACCTTCGGGTAGAC
```

KillerRed > I V A D G S S K F P H G D F N V H A V C E T G K L P M S W K P I C

Bpu10

```
801 CCACCTGATCCAGTACGGCGAGCCCTTCTTCGCCCCTACCCCGACGGCATCAGCCATTTTCGCCCAGGAGTGCTTCCCCGAGGGCCTGAGCATCGACCGC
| | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
GGTGGACTAGGTCATGCCGCTCGGGAAGAAGCGGGCGATGGGGCTGCCGTAGTCGGTAAAGCGGGTCTCACGAAGGGGCTCCCGGACTCGTAGCTGGCG
```

KillerRed > H L I Q Y G E P F F A R Y P D G I S H F A Q E C F P E G L S I D R

```

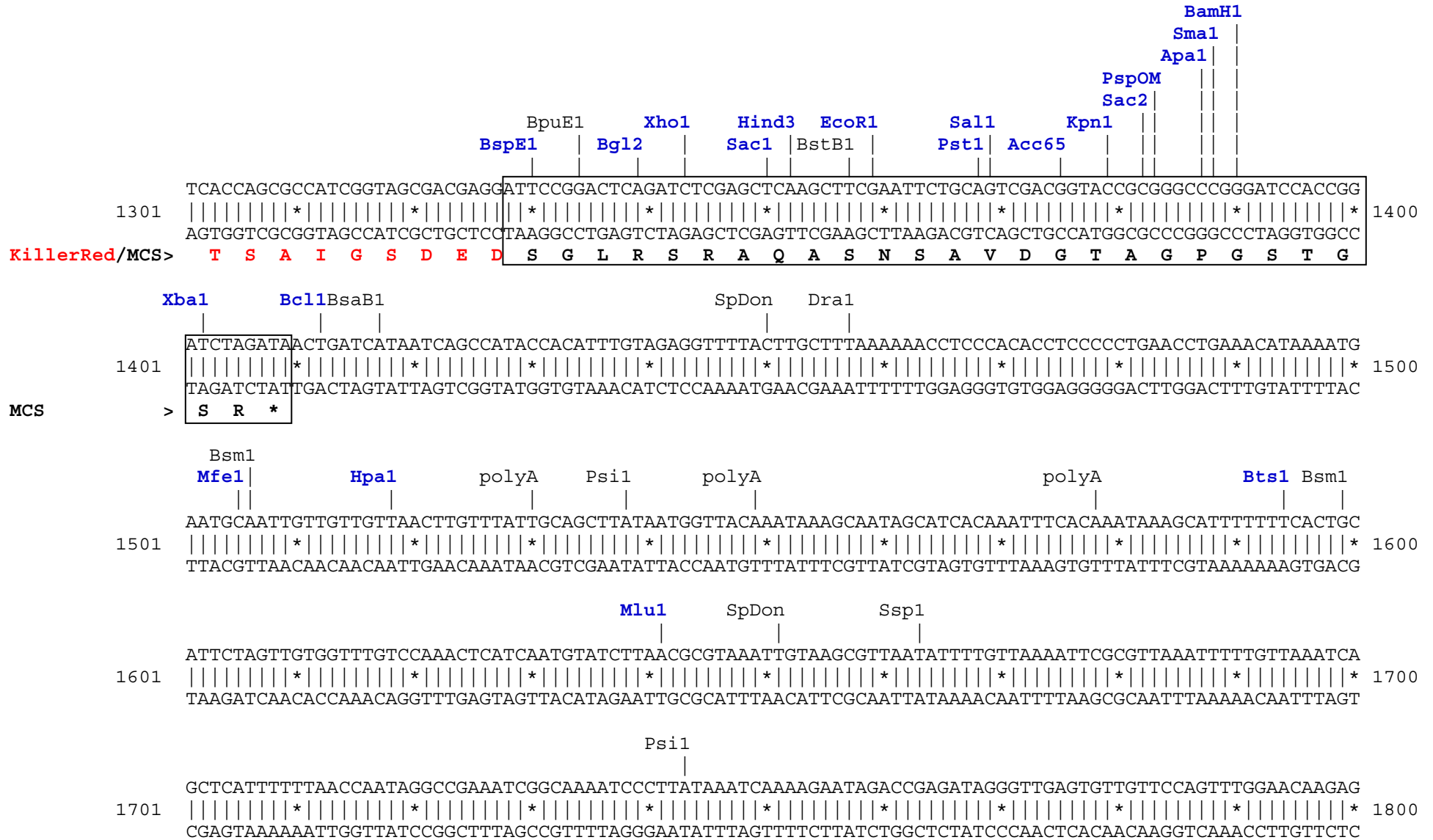
                                                                 BspM1
                                                                 BfuA1
                                                                 Aar1
                                                                 Ale1SpDon
                                                                 |
                                                                 |
1001 ACCGTGCGCTTCGAGAACGACGGCACCATGACCAGCCACcACACCTACGAGCTGGACGACACCTGCGTGGTGTGAGCCGCATCACCGTGAACCTGCGACGGCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
    TGGCACGCGAAGCTCTTGCTGCCGTGGTACTGGTTCGGTgTGTGGATGCTCGACCTGCTGTGGACGCACCACTCGGGCGTAGTGGCACTTGACGCTGCCGA
KillerRed > T V R F E N D G T M T S H H T Y E L D D T C V V S R I T V N C D G F

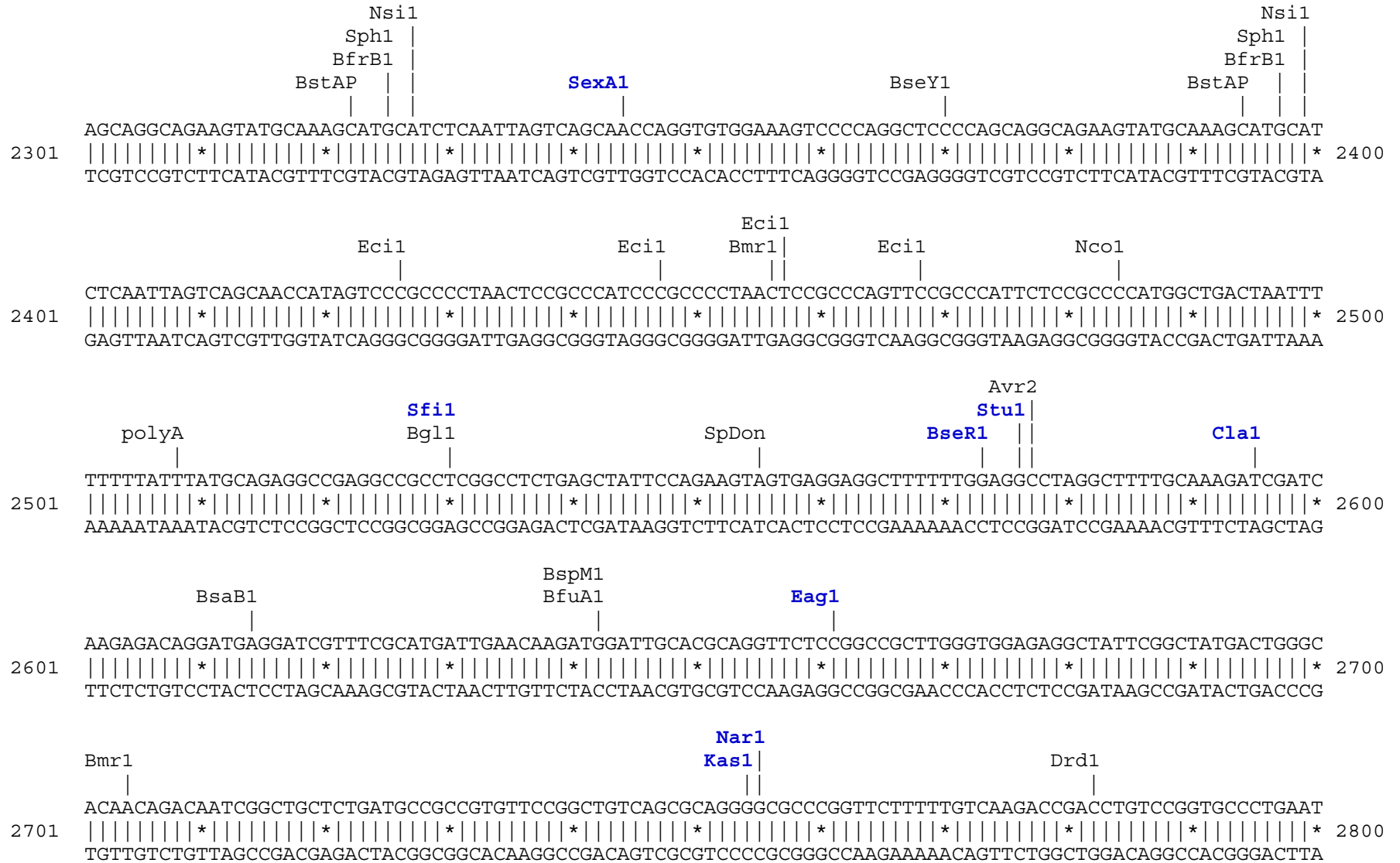
                                                                 _Chi
                                                                 PflM1
                                                                 Pvu2
                                                                 Bsa1
                                                                 BspLU
                                                                 Pvu2
1001 TCCAGCCCGACGGCCCCATCATGCGCGACCAGCTGGTGGACATCCTGCCAACGAGACCCACATGTTCCCCCACGGCCCCAACGCCGTGCGCCAGCTGGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    AGGTCGGGCTGCCGGGGTAGTACGCGCTGGTTCGACCACCTGTAGGACGGGTTGCTCTGGGTGTACAAGGGGGTGCCGGGGTTGCGGCACGCGGTTCGACCG
KillerRed > Q P D G P I M R D Q L V D I L P N E T H M F P H G P N A V R Q L A

                                                                 SpDon
                                                                 |
1101 CTTTCATCGGCTTCACCACCGCCGACGGCGGCCTGATGATGGGCCACTTCGACAGCAAGATGACCTTCAACGGCAGCCGCGCCATCGAGATCCCCGGCCCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    GAAGTAGCCGAAGTGGTGGCGGCTGCCGCCGACTACTACCCGGTGAAGCTGTGCTTCTACTGGAAGTTGCCGTCCGGCGCGGTAGCTCTAGGGGCGGGT
KillerRed > F I G F T T A D G G L M M G H F D S K M T F N G S R A I E I P G P

                                                                 Dra3
                                                                 Pml1
                                                                 Dra3
1201 CACTTCGTGACCATCATCACCAAGCAGATGAGGGACACCAGCGACAAGCGCGACCACGTGTGCCAGCGCGAGGTGGCCTACGCCCACAGCGTGCCCCGCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    GTGAAGCACTGGTAGTAGTGGTTTCGTCTACTCCCTGTGGTTCGCTGTTTCGCGCTGGTGCACACGGTTCGCGCTCCACCGGATGCGGGTGTTCGCACGGGGCGT
KillerRed > H F V T I I T K Q M R D T S D K R D H V C Q R E V A Y A H S V P R I

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          SapI      Eco57      BssS1      BtgZ1
          EarI      |          |          |          |
          |          |          |          |          |
3301  CCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      GGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCG

          BssS1
          BspM1
          BfuA1
          BsrB1      BstB1      |
          |          |          |
3401  CTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
      GAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAA

          NaeI      Bpm1
          NgoM4    |          |
          Bpm1    |          |
          |          |          |
3501  CTATGAAAAGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
      GATACTTTCCAACCCGAAGCCTTAGCAAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCC

          polyA      polyA
          |          |
          |          |
3601  AGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCTTTGTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
      TCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTTGCGTGCCACAACCCAGCAAACAAG

          BsaI
          |
3701  ATAAACGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCCGCTTTCTTCTTTTCCCCACCCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
      TATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGT
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                                     BstAP
                                     AlwN1
                                     Bsu36
                                     Dra1
3801  CCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTA
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3900
      GGGGGTTCAAGCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAAT

                                     Dra1
                                     BspH1
3901  AAAC TTCATTTTAAATTTAAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAG
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4000
      TTTGAAGTAAAAATTAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTC

                                     BpuE1
4001  ACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACCCTACCAGCGGTGGTTTTG
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4100
      TGGGCATCTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTGCACCACCAAAC

                                     Eco57
                                     SpAcc
4101  TTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGC
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4200
      AAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCG

                                     AlwN1
                                     BpuE1
4201  CACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGT
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4300
      GTGGTGAAGTCTTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACCGACGACGGTCAACCGCTATTGAGCAGAGAATGGCCCA

                                     ApaL1
                                     BseY1
4301  TGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACT
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4400
      ACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTGCAACCTCGCTTGCTGGATGTGGCTTGA
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                                     BciV1
                                     Eci1
                                     |
          SpAcc
          |
4401  GAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCCGGAACAGGAGAGCGC
      |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
      CTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTGCGCCGTCCCAGCCTTGTCTCTCGCG

BssS1
|
          SpAcc
          |
          Drd1
          |
          BpuE1
          |
4501  ACGAGGGGAGCTTCCAGGGGGAAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGG
      |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      TGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCC

                                     SpDon
                                     BspLU
                                     ||
          SpAcc
          |
          Eci1
          |
4601  GGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTTACGGTTCCTGGCCTTTTTGCTGGCCTTTTGTCTCACATGTTCTTTCCTGCGTTATCCCCTGA
      |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      CCGCCTCGGATACCTTTTTGCGGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACT

                                     NsiI
          BfrB1
          |
          |
4701  TTCTGTGGATAACCGTATTACCGCCATGCAT
      |||||||||*|||||||||*|||||||||*| 4731
      AAGACACCTATTGGCATAATGGCGGTACGTA
  
```

Found:

Aar1	Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	_Chi
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1
Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1	Pml1	polyA
Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc
SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1								

Unique:

Aar1	Acc65	Afe1	Age1	Apa1	Ase1	BamH1	Bcl1	Bgl2	Bpu10	BsaXa	BsaXb	BseR1	BspE1
BsrD1	Bts1	_Chi	Clal	Eag1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Msc1
Nar1	Nde1	Nhe1	PflF1	Pml1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SexA1	Sfi1	Sma1
SnaB1	Stu1	Xba1	Xho1										

Not found:

Acl1	Afl2	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bcg1a	Bcg1b	Blp1	BmgB1	Bsg1
BsiW1	BsmB1	BsrG1	BssH2	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu
loxP	Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1
Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1	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													