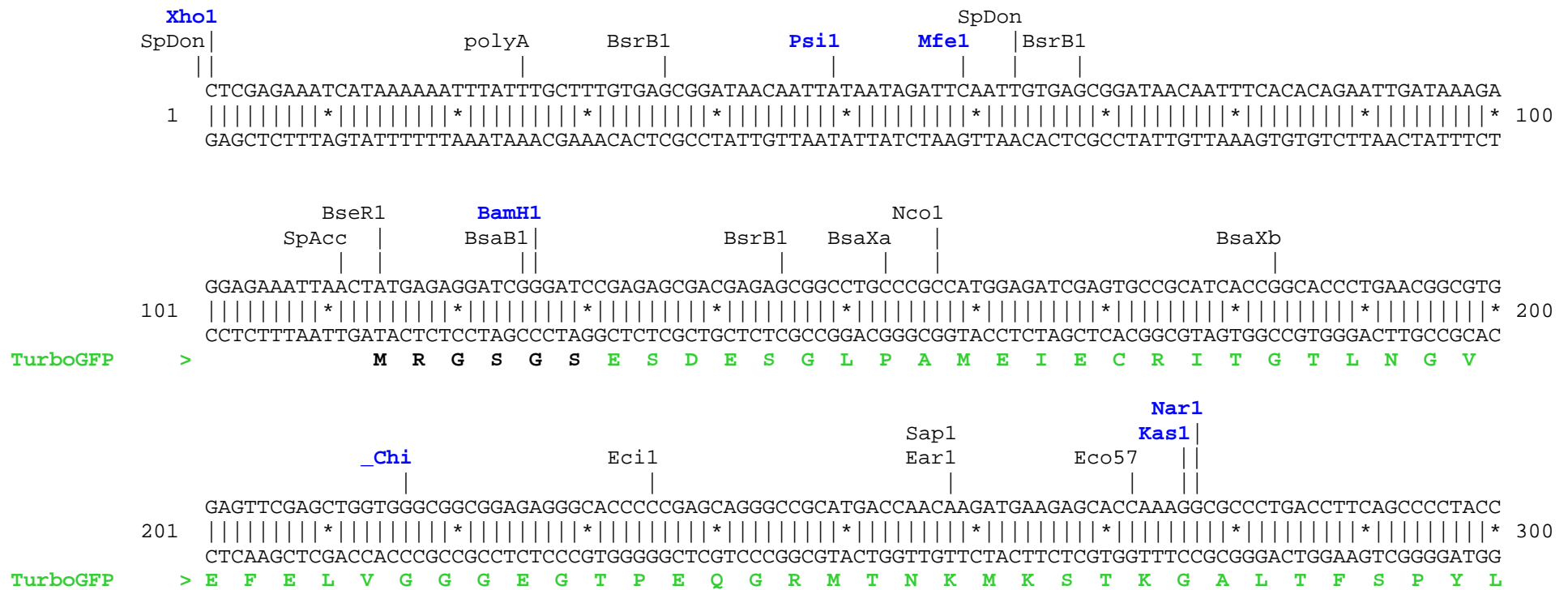


pTurboGFP-B vector restriction map

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 are shown in black.



```

          PflM1
        Pml1
      BspM1
    Blp1
  TGCTGAGCCACGTGATGGGCTACGGCTTCTACCACTTCGGCACCTACCCCAGCGGCTACGAGAACCCTTCTCTGCACGCCATCAACAACGGCGGCTACAC
301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 400
    ACGACTCGGTGCACTACCCGATGCCGAAGATGGTGAAGCCGTGGATGGGGTCGCCGATGCTCTTGGGGAAGGACGTGCCGGTAGTTGTTGCCGCCGATGTG
TurboGFP >  L S H V M G Y G F Y H F G T Y P S G Y E N P F L H A I N N G G Y T

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```

          FseI
        NaeI
        EagI
        NgoM4
      BsgI
    Eco57
  CAACACCCGCATCGAGAAGTACGAGGACGGCGGCGTGCTGCACGTGAGCTTTCAGCTACCGCTACGAGGCCGGCCCGCTGATCGGCGACTTCAAGGTGATG
401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
    GTTGTGGGCGTAGCTCTTCATGCTCCTGCCGCCGACGACGTGCACTCGAAGTGCATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCTACTAC
TurboGFP >  N T R I E K Y E D G G V L H V S F S Y R Y E A G R V I G D F K V M

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```

          NcoI
        BspM1
          AarI
          BsaB1
      BsgI
    GGCACCCGGCTTCCCCGAGGACAGCGTGATCTTCACCCGACAAGATCATCCGCAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGATCTGG
501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
    CCGTGGCCGAAGGGGCTCCTGTGCGCACTAGAAAGTGGCTGTTCTAGTAGGCGTTCGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCTAGACC
TurboGFP >  G T G F P E D S V I F T D K I I R S N A T V E H L H P M G D N D L D

```

```

    Eco57
  ATGGCAGCTTACCCGCACCTTTCAGCCTGCGGACGGCGGCTACTACAGCTCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCAGCAT
601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
    TACCGTCGAAGTGGGCGTGGAAGTCCGACGCGCTGCCGCCGATGATGTGAGGCACCACTGTCCGTGTACGTGAAGTTCGCGGTAGGTGGGGTCGTA
TurboGFP >  G S F T R T F S L R D G G Y Y S S V V D S H M H F K S A I H P S I

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              EciI
              |
        PstI  PspOM  Apal
              |   |   |
              |   |   |
    CCTGCAGAACGGGGGCCCATGTTTCGCCTTCCGCCGCGTGGAGGAGGATCACAGCAACACCGAGCTGGGCATCGTGAGTACCAGCACGCCTTCAAGACC
701  ||||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 800
    GGACGTCTTGCCCCGGGGTACAAGCGGAAGGCGGCGCACCTCCTCCTAGTGTGCGTTGTGGCTCGACCCGTAGCACCTCATGGTCTGTCGGAAGTTCTGG
TurboGFP > L Q N G G P M F A F R R V E E D H S N T E L G I V E Y Q H A F K T

              Hind3          BlnI
              |              |
              |              |
    CCGGATGCAGATGCCGGTGAAGAATGAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTTC
801  ||||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 900
    GGCCTACGTCTACGGCCACTTCTTACTTTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCTAAACAAG
TurboGFP > P D A D A G E E *

              polyA          NheI          BpuI0
              |              |              |
              |              |              |
    AGAACGCTCGGTTGCCGCGGGCGTTTTTTTATTTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAATC
901  ||||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1000
    TCTTGCGAGCCAACGGCGGGCCGCAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTAAAAGTCCTCGATTCTTCGATTTTACCTCTTTTTTTAG

                                                              Pvu2
                                                              |
    ACTGGATATACCACCGTTGATATATCCCAATGGC ATCGTAAAGAACATTTTGGAGGCATTTT CAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTTCAGC
1001 ||||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1100
    TGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTTG TAAAACCTCCGTAAAAGTCAGTCAACGAGTTACATGGATATTGGTCTGGCAAGTCG

              DraI          SpDon          BspE1
              |              |              |
              |              |              |
    TGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTTATT CACATTCTTGCCCGCCTGATGAATGCTCATCCGGA
1101 ||||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1200
    ACCTATAATGCCGAAAAATTTCTGGCATTTCTTTTTATTTCGTGTTCAAAATAGGCCGGAATAAGTGTAAAGAACGGGCGGACTACTTACGAGTAGGCCT

              BsrD1          BtgZ1          Acl1
              |              |              |
              |              |              |
    ATTTTCGTATGGCAAATGAAAGACGGGTGAGCTGGTGATATGGGATAGTGTTCACCC TTGTACACCGTTTTTCCATGAGCAAACCTGAAACGTTTTTCATCGCTC
1201 ||||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1300
    TAAAGCATACCGTTACTTTCTGCCACTCGACCACTATACCCTATCACAAAGTGGGAACAATGTGGCAAAAGGTACTCGTTTTGACTTTGCAAAAGTAGCGAG

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                Bpm1
                |
TGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTA
1301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1400
ACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCCGCACAATGCCACTTTTGGACCGGATAAAGGGATTTCCCAAAT

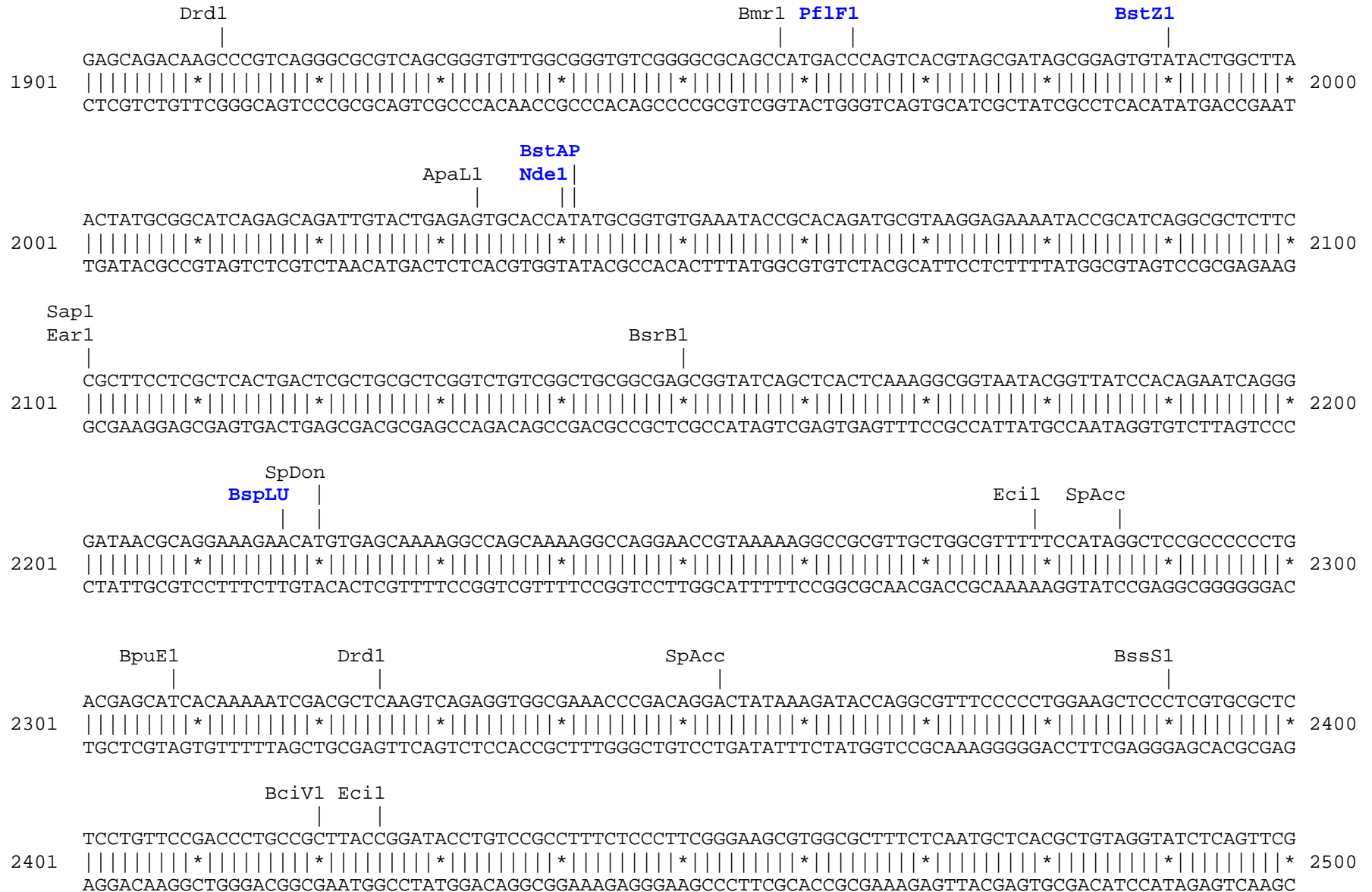
polyA          BsmB1    PflM1          SpDon          Dra1    MscI
|             |         |             |             |         |
TTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGTGGCCAATATGGACAACCTTCTTCGCCCCCGTTTTTCAC
1401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1500
AACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAACCTAAATTTGCACCGGTTATACCTGTTGAAGAAGCGGGGGCAAAGTG

SpDon
NcoI          SspI
|             |
CATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGCTCTGTGATGGCTTCCATGTTCGGCAGAATGCTT
1501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1600
GTACCCGTTTATAATATGCGTTCGGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGACACTACCGAAGGTACAGCCGTCTTACGAA

                Scal          BtgZ1
                |             |
AATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTTAAAGGCAGTTATTGGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAGC
1601 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1700
TTACTTAATGTTGTCATGACGCTACTCACCGTCCCGCCCGCATTAAAAAAATTCGTCATAAACCACGGGAATTTGCGGACCCCACTTACTGAGAGATCG

polyA          BpuE1          BmrI T7Ter          Ecil
|             |             |             |             |
TTGAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTTGTGTTGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGC
1701 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1800
AACTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAAACAGCCACTTGCGAGAGGACTCATCTGTGTTAGGCG

XbaI
BsrB1          BsmB1
|             |
CGCTCTAGAGCTGCCTCGCGGTTTTCCGGTGATGACGGTGAACCTCTGACACATGCAGTCCCAGGAGACGGTTCACAGCTTGTCTGTAAGCGGATGCCGG
1801 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1900
GCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAGTGTGCAACAGACATTGCGCTACGGCC
```



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                BseY1      ApaL1
                |         |
2501  GTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
      CACATCCAGCAAGCGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCC

      BpuE1              AlwN1
      |                 |
2601  TAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
      ATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGATT

                SpAcc              Eco57
                |                 |
2701  CTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
      GATGCCGATGTGATCTTCCTGTCATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGG

                                BpuE1
                                |
2801  ACCGCTGGTAGCGGTGGTTTTTTTTGTTTGC AAGCAGCAGATTACGCGCAGAAAAAAGGATCTCAAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
      TGGCGACCATCGCCACCAAAAAACAAACGTTTCGTGCTAATGCGCGTCTTTTTTTTCTAGAGTTCTTCTAGGAACTAGAAAAGATGCCCCAGACTGC

                                BspH1              DraI              DraI
                                |                 |                 |
2901  CTCAGTGAACGAAAACCTCACGTTAAGGGATTTTGGTTCATGAGATTATCAAAAAGGATCTTACCTAGATCCTTTTAAATTA AAAATGAAGTTTTAAATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
      GAGTACCTTGCTTTTGAGTGCAATTCCTAAAACAGTACTCTAATAGTTTTTCTAGAAAGTGATCTAGGAAAATTTAATTTTTACTTCAAAAATTTAG

      AATCTAAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTTCGTTTCATCCATAGCT
3001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
      TTAGATTTTATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGATAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCGA

      Ahd1              Bmr1              BsrD1              Bpm1
      |                 |                 |                 |
3101  GCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAGACCCACGCTCACCGGCTCCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      CGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGACGTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTC
```

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polyA      Bgl1      Eci1      Ase1
|          |          |          |
ATTTATCAGCAATAAACCCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCTCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGC
3201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
TAAATAGTCGTTATTTGGTCGGTCGGCCTTCCC GGCTCGCGTCTTCACCAGGACGTTGAAATAGGCGGAGGTAGGT CAGATAATTAACAACGGCCCTTCG

      Acl1      BsrD1
      |          |
      Fsp1
      |
TAGAGTAAGTAGTTCGCCAGTTAATAGTTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGT CACGCTCGTCGTTTGGTATGGCTTCATT CAGC
3301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
ATCTCATTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGATGTCCGTAGCACCACAGTGC GAGCAGCAAACCATAACCGAAGTAAGTCG

      Pvu1      SpDon
      |          |
TCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCTCCGATCGTTGT CAGAAGTAAGTTGG
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
AGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTTCGCCAATCGAGGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACC

      Bts1      Bts1      SpDon      Scal
      |          |          |          |
CCGCAGTGT TATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGT CATGCCATCCGTAAGATGCTTTTCTGTGACTGGT GAGTACTCAACCAA
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
GGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCATTCTACGAAAAGACACTGACCACTCATGAGTTGGTT

      Bcg1a      Bcg1b      Dra1
      |          |          |
GTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTTGCCCGGCGTCAATACGGGATAATACCGCGCCACATAGCAGA ACTTTAAAAGTGCTCATC
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCCGAGTTATGCCCTATTATGGCGCGGTGTATCGTCTTGAAATTTT CACGAGTAG

      EcoK
      |
      Eco57
      |
      ApaL1
      |
      BssS1
      |
      Xmn1      Acl1      BpuE1
      |          |          |
      ATTTGAAAAACGTTCTTCGGGGCGAAAAC TCTCAAGGATCTTACCCTGTTGAGATCCAGTTTCGATGTAACCCACTCGTGCACCCA ACTGATCTTCAGCAT
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
TAACCTTTTGAAGAAGCCCCGCTTTTGGAGAGTTCC TAGAATGGCGACAAC TCTAGGTCAAGCTACATTGGGTGAGCACGTGGGTTGACTAGAAAGTCGTA
```


Unique:

Aar1	Aat2	Ahd1	AlwN1	Apa1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	Bgl1	Bpu10	Bsa1	BspE1
BspLU	BstAP	BstZ1	_Chi	Eag1	EcoK	Fse1	Fsp1	Hind3	Kas1	Mfe1	Msc1	Nae1	Nar1
Nde1	NgOM4	Nhe1	PflF1	Psi1	PspOM	Pst1	Pvu1	Pvu2	T7Ter	Xba1	Xho1		

Not found:

Acc65	Afe1	Afl2	Age1	Ale1	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfrB1	Bgl2
BmgB1	BsiW1	BsrG1	BssH2	BstB1	BstE2	BstX1	Bsu36	BxatB	BxatL	BxatR	BxatP	Clal	Dra3
Ecl2	EcoN1	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	FspA1	Hpa1	I_Ceu	Kpn1	loxP
Mlu1	Not1	Nru1	Nsi1	Pac1	Pme1	PshA1	R4atB	R4atL	R4atP	R4atR	Rsr2	Sac1	Sac2
Sall	SanD1	Sbf1	SexA1	Sfi1	Sgf1	SgrA1	Sma1	SnaB1	Spe1	Sph1	Srf1	Stu1	Swal
T3RNA	T7RNA	PISce	Xcm1										

Excluded by site complexity:

Acc1	Ac1	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													