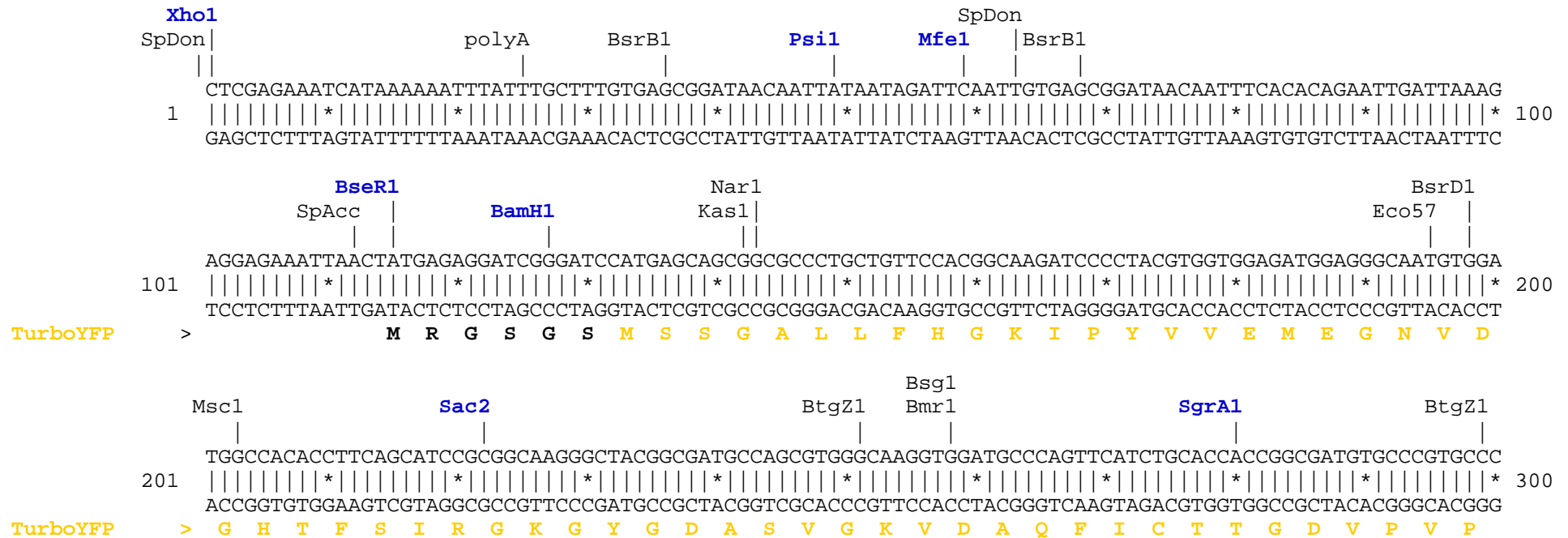
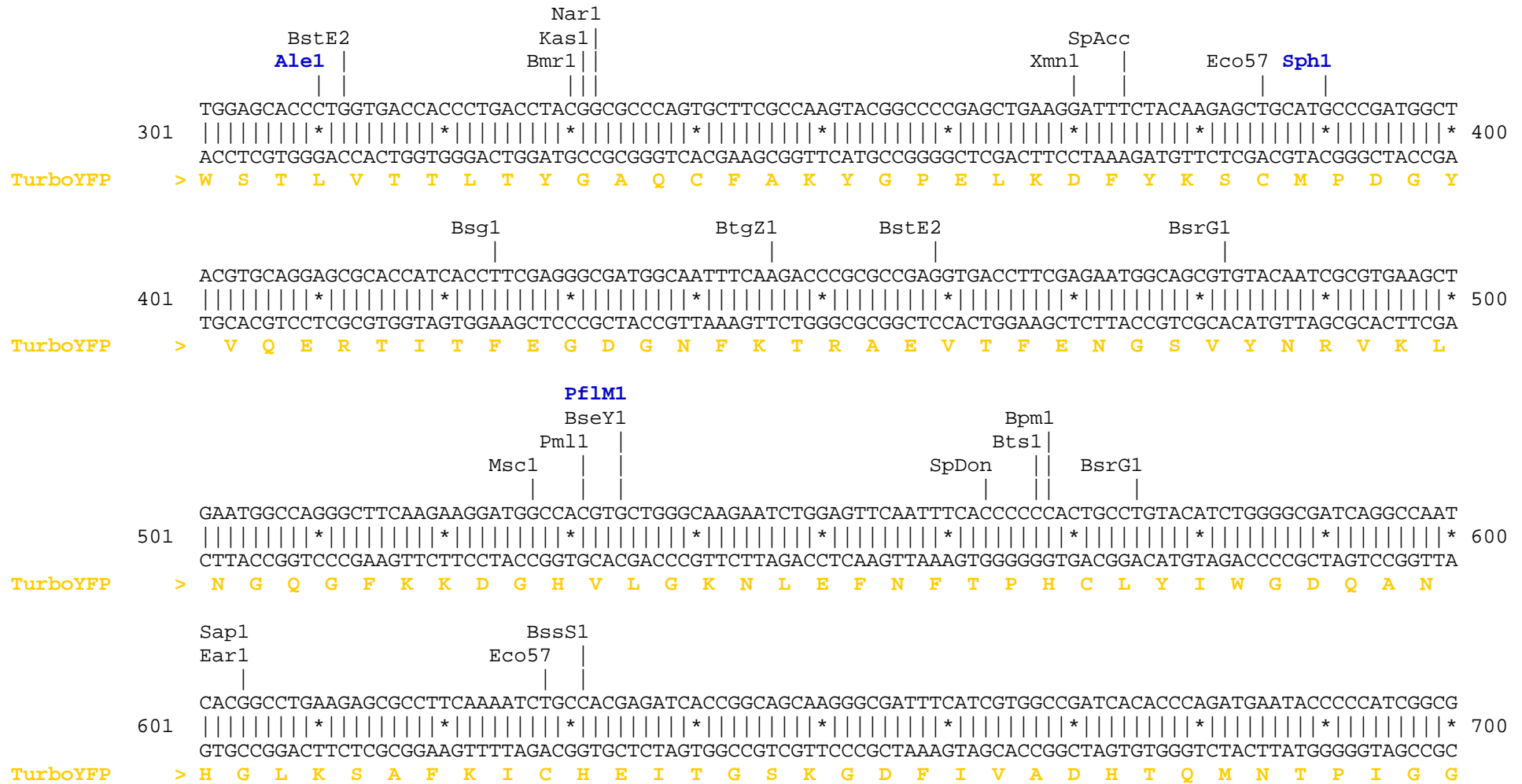


pTurboYFP-B vector restriction map

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.





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                                     Bsa1
                                     SpAcc |
          ApaL1 Pml1                    Pml1  Blp1
          |     |                       |     |
701  GCGGCCCGTGCACGTGCCCCGAGTACCACCACATGAGCTACCACGTGAAGCTGAGCAAGGATGTGACCGATCACCGCGATAATATGAGCCTGAAGGAGAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
    CGCCGGGGCACGTGCACGGGCTCATGGTGGTGTACTCGATGGTGCACCTTCGACTCGTTCCTACACTGGCTAGTGGCGCTATTATACTCGGACTTCTCTG
TurboYFP >  G P V H V P E Y H H M S Y H V K L S K D V T D H R D N M S L K E T

          BssH2 Eco57                    BspE1          Hind3          Blp1
          |     |                       |               |           |
801  CGTGCGCGCCGTGGATTGCCGCAAGACCTACGACTTCGACGCCGGTTCCGGAGATACAAGCTGAAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
    GCACGCGCGGCACCTAACGGCGTCTGGATGCTGAAGCTGCGCCAAGGCCTCTATGTTTCGACTTTTCGAATTAATCGACTCGAACCTGAGGACAACCTATC
TurboYFP >  V R A V D C R K T Y D F D A G S G D T S *

                                     polyA          Nhe1
                                     |               |
901  ATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTTTCAGAACGCTCGGTTGCCGCCGGGCGTTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
    TAGGTCATTACTIONTGGAGTCTTGAGGTAGACCTAAACAAGTCTTGCGAGCCAACGGCGGCCCGCAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTA

          Bpu10
          SpAcc |
          |     |
1001 TTTCCAGGAGCTAAGGAAGCTAAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGGAGGCATTTCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    AAAGTCCTCGATTCCTTCGATTTTACCTCTTTTTTTTAGTGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTGTA AAACTCCGTAAAGT

                                     Pvu2          Dra1
                                     |               |
1101 GTCAGTTGCTCAATGTACCTATAACCAGACCGTTTCAGCTGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    CAGTCAACGAGTTACATGGATATTGGTCTGGCAAGTCGACCTATAATGCCGAAAAATTTCTGGCATTCTTTTTTATTTCGTGTTCAAAAATAGGCCGGAAA

          SpDon          BspE1          Bsm1          BsrD1          SpDon
          |     |     |     |           |           |           |           |
1201 ATTCACATTCCTTGCCCGCCTGATGAATGCTCATCCGGAATTTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCCACCTTGTTACA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    TAAGTGTAAGAACGGGCGGACTACTTACGAGTAGGCCTTAAAGCATACCGTTACTTTCTGCCACTCGACCACTATACCCTATCACAAGTGGGAACAATGT

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                BtgZ1   Acl1           SpDon           Bpm1
1301  CCGTTTTCCATGAGCAAACCTGAAACGTTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTGCAAGATGTGGCGTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      GGCAAAAGGTACTCGTTTGACTTTGCAAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCAC

                polyA           BsmB1           SpDon           Dra1
1401  TTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
      AATGCCACTTTTGACC GGATAAAGGGATTTCCCAAATAACTCTTATACAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAACTAAATTTG

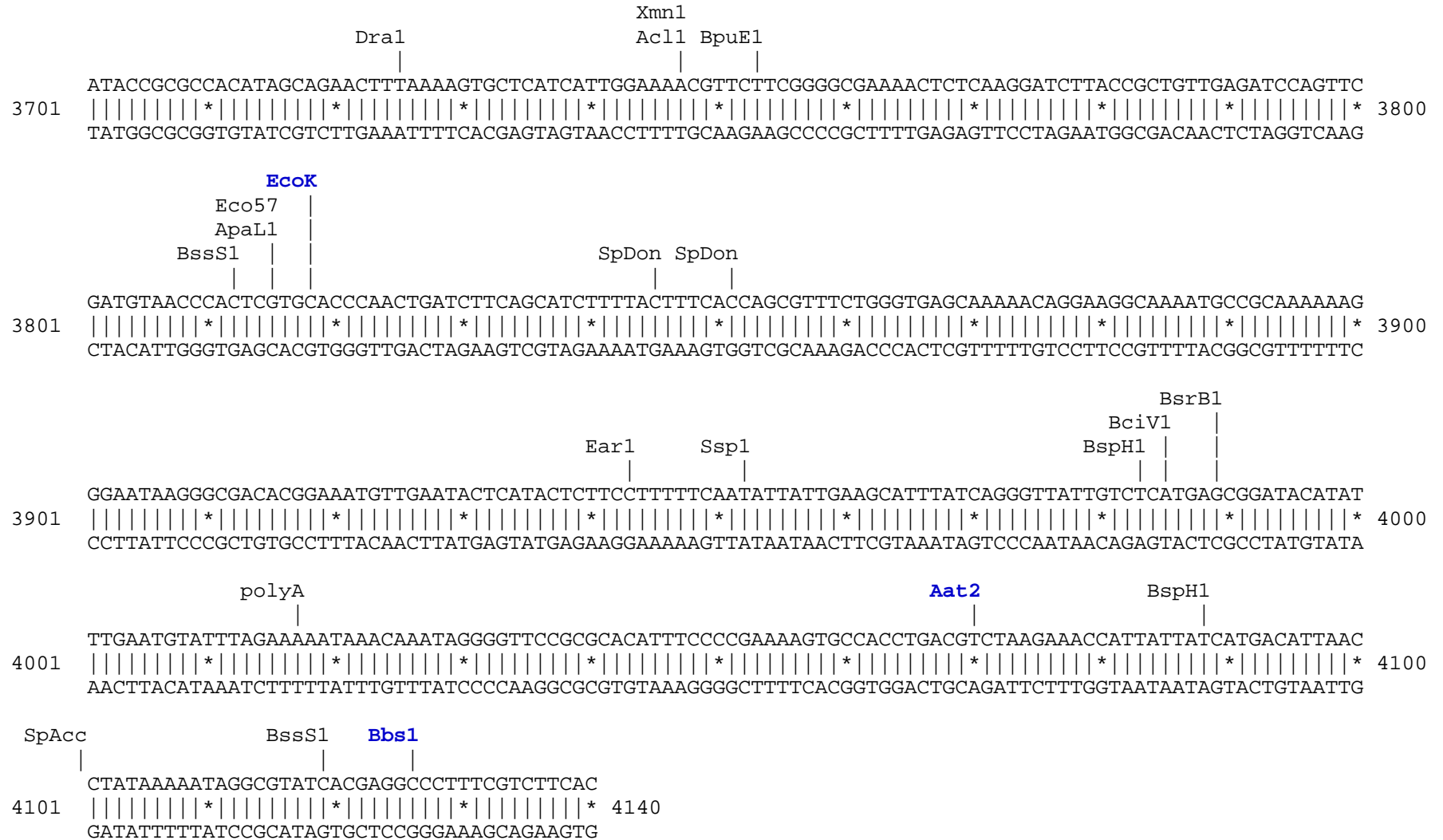
                Msc1           SpDon           Nco1           Ssp1
1501  GTGGCCAATATGGACAACCTTCTTCGCCCCCGTTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
      CACCGGTTATACCTGTTGAAGAAGCGGGGGCAAAAGTGGTACCCGTTTATAATATGCGTTCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAG

                Bsm1           Scal           BtgZ1
1601  ATGCCGCTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
      TACGGCAGACACTACCGAAGGTACAGCCGCTTTACGAATTACTTAATGTTGTCATGACGCTACTCACCGTCCCGCCCCGCATTAAAAAAATTCCGTCAAT

                polyA           BpuE1           Bmr1 T7Ter
1701  TTGGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAGCTTGAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
      AACACGGGAATTTGCGGACCCATTACTGAGAGATCGAACTCCGTAGTTTATTTTGTCTTCCGAGTCAGCTTTCTGACCCGAAAGCAAAATAGACAAC

                Eci1           BsrB1           Xba1           BsmB1
1801  TTTGTCCGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGCTCTAGAGCTGCCTCGCGCTTTCCGGTGATGACGGTGAACCTCTGACACATGCAGCTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
      AAACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCGGCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAG

```

Found:

Aat2	AcI1	Ahd1	Ale1	AlwN1	ApaL1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1	Bgl1	Blp1
Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BseR1	BseY1	Bsg1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BsrB1
BsrD1	BsrG1	BssH2	BssS1	BstAP	BstE2	BstZ1	BtgZ1	Bts1	Dra1	Drd1	Ear1	Ecil	Eco57
EcoK	Fsp1	Hind3	Kas1	Mfe1	Msc1	Nar1	Nco1	Nde1	Nhe1	PflF1	PflM1	Pml1	polyA
Psi1	Pvu1	Pvu2	Sac2	Sap1	Sca1	SgrA1	SpAcc	SpDon	Sph1	Ssp1	T7Ter	Xba1	Xho1
Xmn1													

Unique:

Aat2	Ahd1	Ale1	AlwN1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	Bgl1	Bpu10	BseR1	BspLU	BssH2
BstAP	BstZ1	EcoK	Fsp1	Hind3	Mfe1	Nco1	Nde1	Nhe1	PflF1	PflM1	Psi1	Pvu1	Pvu2
Sac2	SgrA1	Sph1	T7Ter	Xba1	Xho1								

Not found:

Aar1	Acc65	Afe1	Afl2	Age1	Apal	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfrB1
BfuA1	Bgl2	BmgB1	BsaB1	BsaXa	BsaXb	BsiW1	BspM1	BstB1	BstX1	Bsu36	_Chi	Clal	Dra3
Eag1	EcoN1	EcoR1	EcoRV	ScFRT	Fse1	FspA1	Hpa1	I_Ceu	Kpn1	loxP	Mlu1	Nae1	NgoM4
Not1	Nru1	Nsi1	Pac1	Pme1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sall1	SanD1	Sbf1	SexA1
Sfil	Sgfl	Sma1	SnaB1	Spe1	Srf1	Stu1	Swal	T3RNA	T7RNA	PISce	Xcm1		

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apol	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfal	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bs11	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	Styl	Taq1	Tat1	Tfil	Tse1	Tsp45	Tsp50
TspR1													