

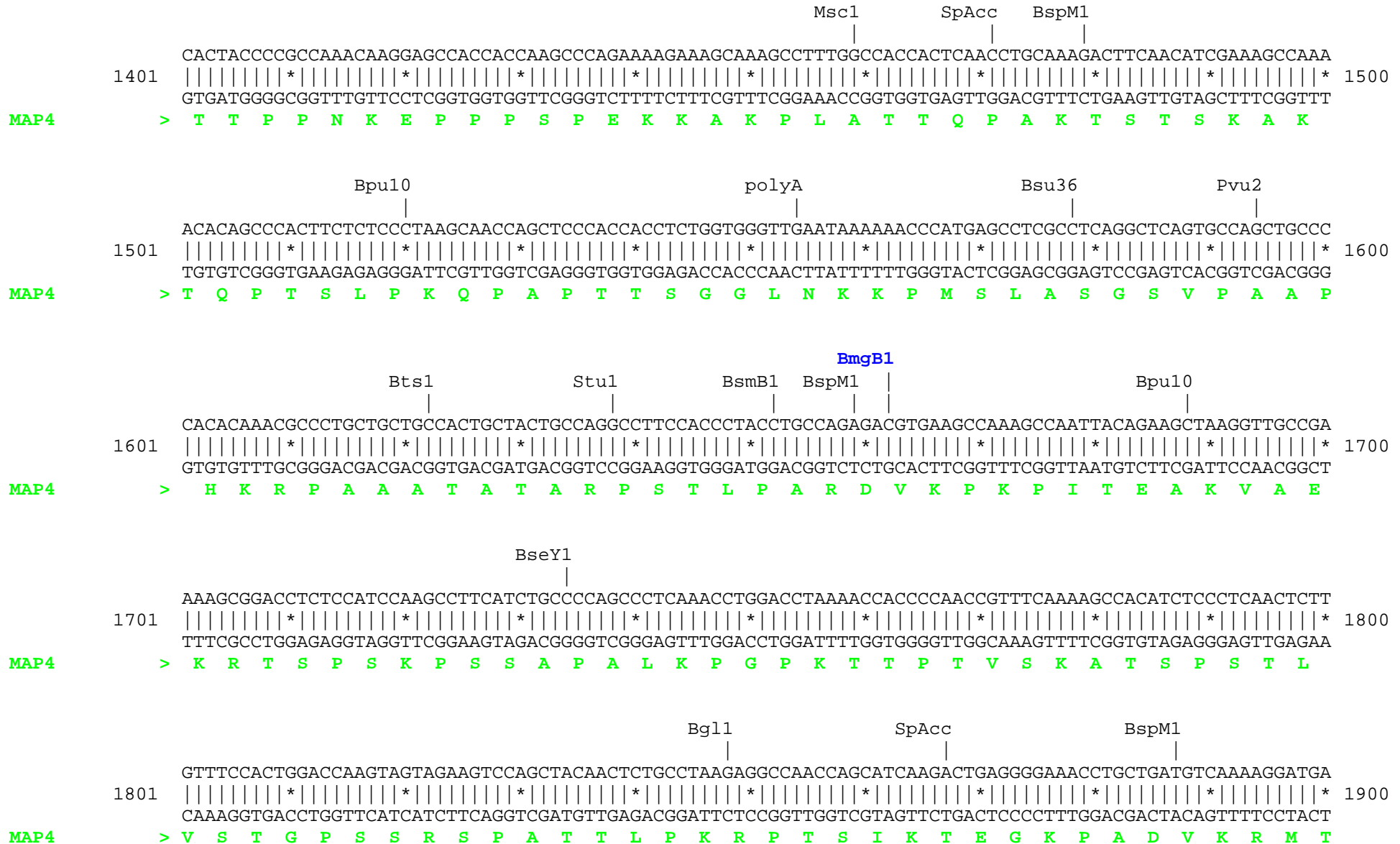
pFusionRed-MAP4 vector restriction map

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 are shown in bold blue. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site).

FusionRed amino acids are shown in red, microtubule binding domain of microtubule-associated protein 4 (MAP4) amino acids are shown in green, linker amino acids are shown in black.





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                Pvu2
          Drd1  Bpu10  BbvC1  PshA1  BpuE1  SpAcc  Ear1  Bmr1  BseY1
1901  CTGCTAAGTCTGCCTCAGCTGACTTGAGTCGCTCAAAGACCACCTCTGCCAGTTCTGTGAAGAGAAACACCCTCCCACTGGGGCAGCACCCCCAGCAGG 2000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
MAP4  >  A K S A S A D L S R S K T T S A S S V K R N T T P T G A A P P A G
                Bsg1  Xho1  BsrB1  Sap1  Ear1  BseR1
2001  GATGACTTCCACTCGAGTCAAGCCCATGTCTGCACCTAGCCGCTCTTCTGGGGCTCTTTCTGTGGACAAGAAGCCCACTTCCACTAAGCCTAGCTCCTCT 2100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
MAP4  >  M T S T R V K P M S A P S R S S G A L S V D K K P T S T K P S S S
                Msc1  Ear1  Eco57  SpAcc  SpAcc
2101  GCTCCCAGGGTGAGCCGCTGGCCACAACCTGTTTCTGCCCTGACCTGAAGAGTGTTTCGCTCCAAGGTCGGCTCTACAGAAAACATCAAACACCAGCCTG 2200
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
MAP4  >  A P R V S R L A T T V S A P D L K S V R S K V G S T E N I K H Q P G
          EcoN1  Bpm1  BseR1  Pvu2  BseY1  Nae1  NgoM4  BsrD1
2201  GAGGAGGCCGGGCCAAGGTAGAGAAAAAACAGAGGCAGCTACCACAGCTGGGAAGCCTGAACCTAATGCAGTCACTAAAGCAGCCGGCTCCATTGCGAG 2300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
MAP4  >  G G R A K V E K K T E A A T T A G K P E P N A V T K A A G S I A S
          ApaL1  SpAcc  BseY1  SpDon  BciV1  Ssp1
2301  TGCACAGAAACCGCCTGCTGGGAAAGTCCAGATAGTATCCAAAAAGTGAGCTACAGTCATATTCAATCCAAGTGTGTTTCCAAGGACAATATTAAGCAT 2400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
MAP4  >  A Q K P P A G K V Q I V S K K V S Y S H I Q S K C V S K D N I K H

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BtgZ1

Drd1 BsaXa Dra3

3001 GGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAA
 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3100
 CCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGTTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATT

Nae1

SpAcc NgoM4 BsrB1

3101 GCACTAAATCGGAACCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAAGCGAAAGGAGCGG
 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3200
 CGTGATTTAGCCTTGGGATTTCCCTCGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCC

3201 GCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCG
 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3300
 CGCGATCCCGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGC

BciV1

BspH1 BsrB1 Ssp1

polyA

3301 GGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT
 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3400
 CCTTTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATA

Ear1 Bsu36 Pvu2 Ecil BseY1

3401 TGAAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCA
 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3500
 ACTTTTTCCTTCTCAGGACTCCGCCTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGT

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           NsiI                      NsiI
            SphI                      SphI
            BfrB1                    BfrB1
           BstAP                      BstAP
                   SexA1                      BseY1
AAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACC
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
TTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGG
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           EciI                      EciI
            EciI                      Bmr1
            EciI                      EciI
            NcoI                      polyA
ATAGTCCC GCCCTAACTCCGCCATCCCGCCCCTAACTCCGCCAGTTCCGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGG
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
TATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGTACCGACTGATTAATAAATAAATAACGTCTCC
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           sfiI                      Avr2
            BglI                      StuI
            SpDon                      BseR1
            ClaI                      BsaB1
CCGAGGCCGCTCGGCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGAT
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
GGCTCCGGCGGAGCCGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAACCTCCGGATCCGAAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTA
```

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           BspM1                      Eag1
            Bmr1
CGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTG
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
GCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGAC
```

```
           NarI
            KasI                      Drd1
CTCTGATGCCCGGTGTTCCGGCTGTACAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCA
3901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
GAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGT
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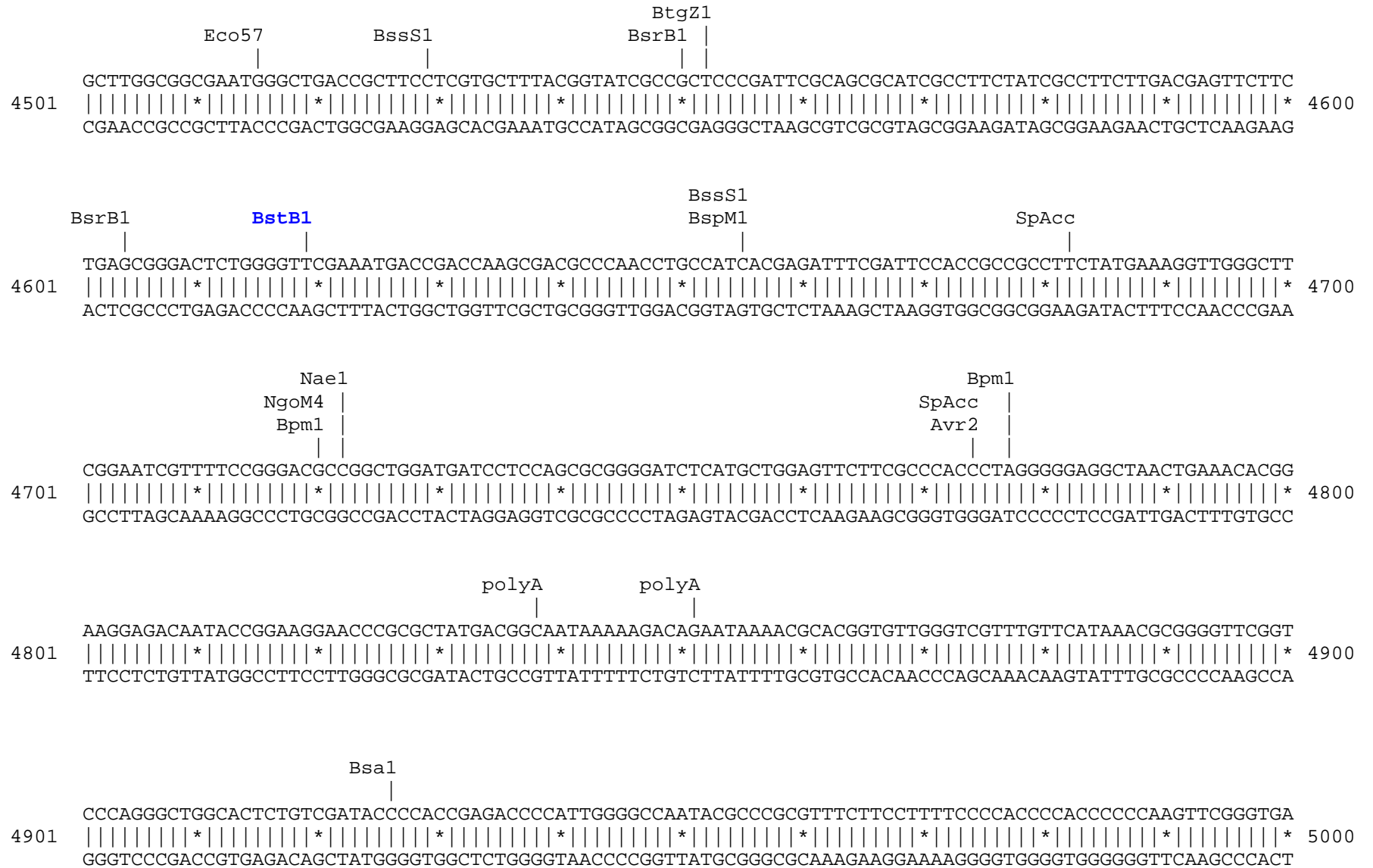

MscI | **FspI** | **Pvu2** | **PflF1** | **Eco57**
 4001 | GCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGC | 4100
 ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| *
 CGCGCCGATAGCACCGACCGGTGCTGCCCAGGAACGCGTTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACG

SpDon | **BciV1** | **BsrD1**
 4101 | CGGGGACAGGATCTCCTGTCATCTCACCTTGGCTCCTGCCCAGAAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCGGCTACCTG | 4200
 ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| *
 GCCCCGTCCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCCGGACGATGCGAACTAGGCCGATGGAC

BtgZ1 | **Sap1**
BspM1 | **Ear1**
 4201 | CCCATTCGACCACCAAGCGAAAACATCGCATCGAGCGAGCACGTAAGCTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGG | 4300
 ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| *
 GGGTAAGCTGGTGGTTGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTAGTCCCC

BpuE1 | **Sph1** | **Nco1** | **BtgZ1**
 4301 | CTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGAGCATGCCCCAGGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGG | 4400
 ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| *
 GAGCGCGTTCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACC

BseY1 | **Sap1**
Nae1 | **Ear1**
NgoM4 | **Rsr2** | **Eci1**
 4401 | TGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGA | 4500
 ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| * ||||| *
 ACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTGTATCGCAACCGATGGGCACTATAACGACTTCT




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                    BciV1
                    Eci1
SpAcc
|
GCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGG
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
CGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCC

                    SpAcc
                    Drd1
                    BpuE1
                    SpAcc
                    Eci1
GGAAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGGAAAA
5701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
CCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTT

                    SpDon
                    BspLU
                    ||
ACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTAT
5801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5900
TGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATA

                    NsiI
                    BfrB1
                    |
                    |
TACCGCCATGCAT
5901 |||||*||| 5913
ATGGCGGTACGTA

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Found:

Aat2	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BbvC1	BciV1	Bcl1	BfrB1
Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1
Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1
Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoN1	Fsp1	Hpa1	Kas1	Mfe1
Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1	polyA	PshA1	Psi1
Pvu2	Rsr2	Sap1	SexA1	Sfi1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1	

Unique:

Afe1	Age1	Ale1	Ase1	Bbs1	BbvC1	Bcl1	Bgl2	BmgB1	Bsg1	BspE1	BspLU	BsrG1	BstB1
Clal	Eag1	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nde1	Nhe1	PflF1	PflM1	Rsr2	SexA1
Sfi1	SnaB1	Xba1	Xho1										

Not found:

Aar1	Acc65	Ac11	Afl2	Ahd1	Apal	Asc1	AsiS1	Baela	Baelb	Bcgl1a	Bcgl1b	Blp1	BsiW1
BssH2	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	EcoR1	EcoRV	FCatB
FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1
Pml1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	Sall	SanD1	Sbf1	Scal
Sgfl	SgrA1	Sma1	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													