

### pFusionRed-H2B 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 base pairs 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).

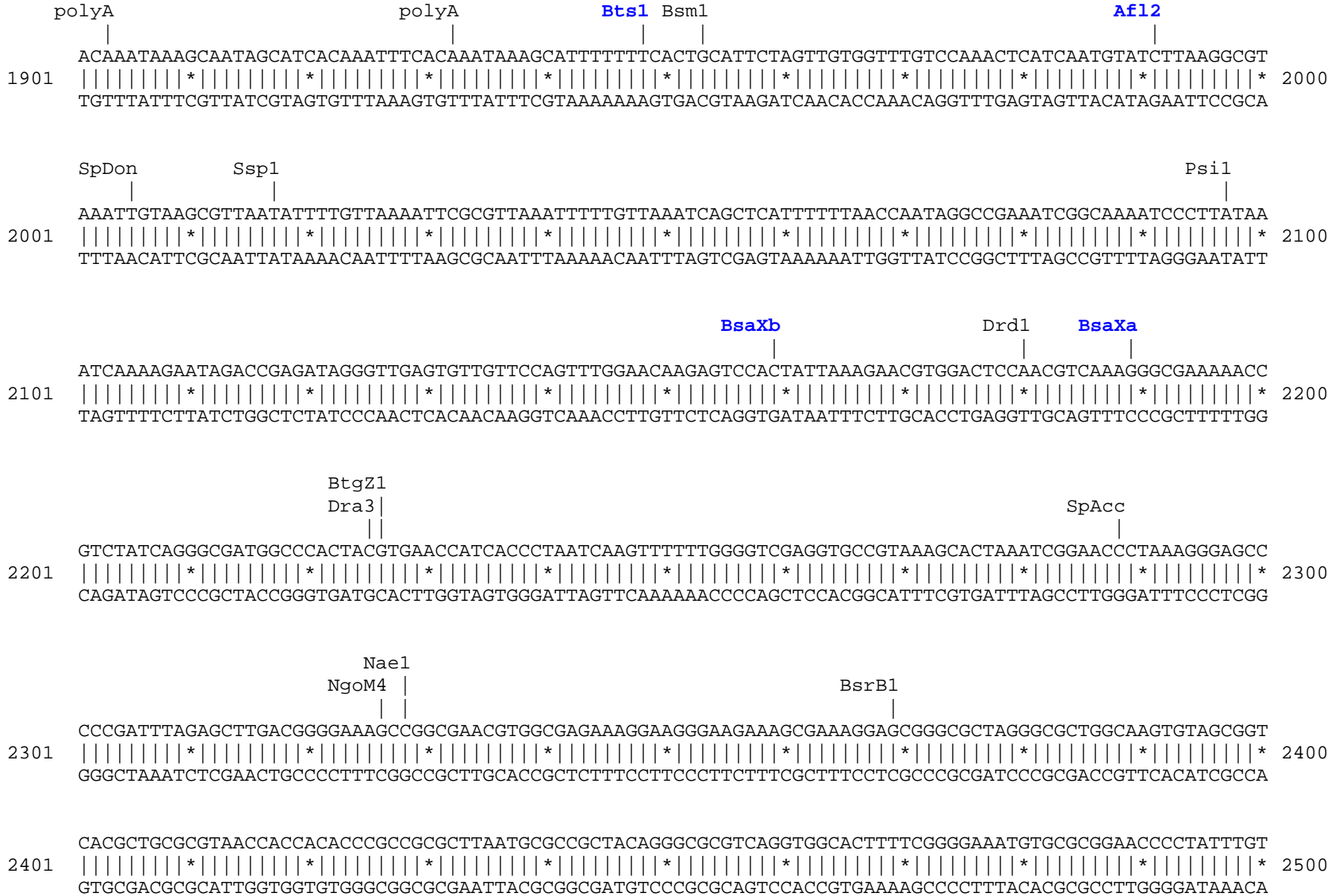
FusionRed amino acids are shown in red, H2B amino acids are shown in green, linker amino acids are shown in black.

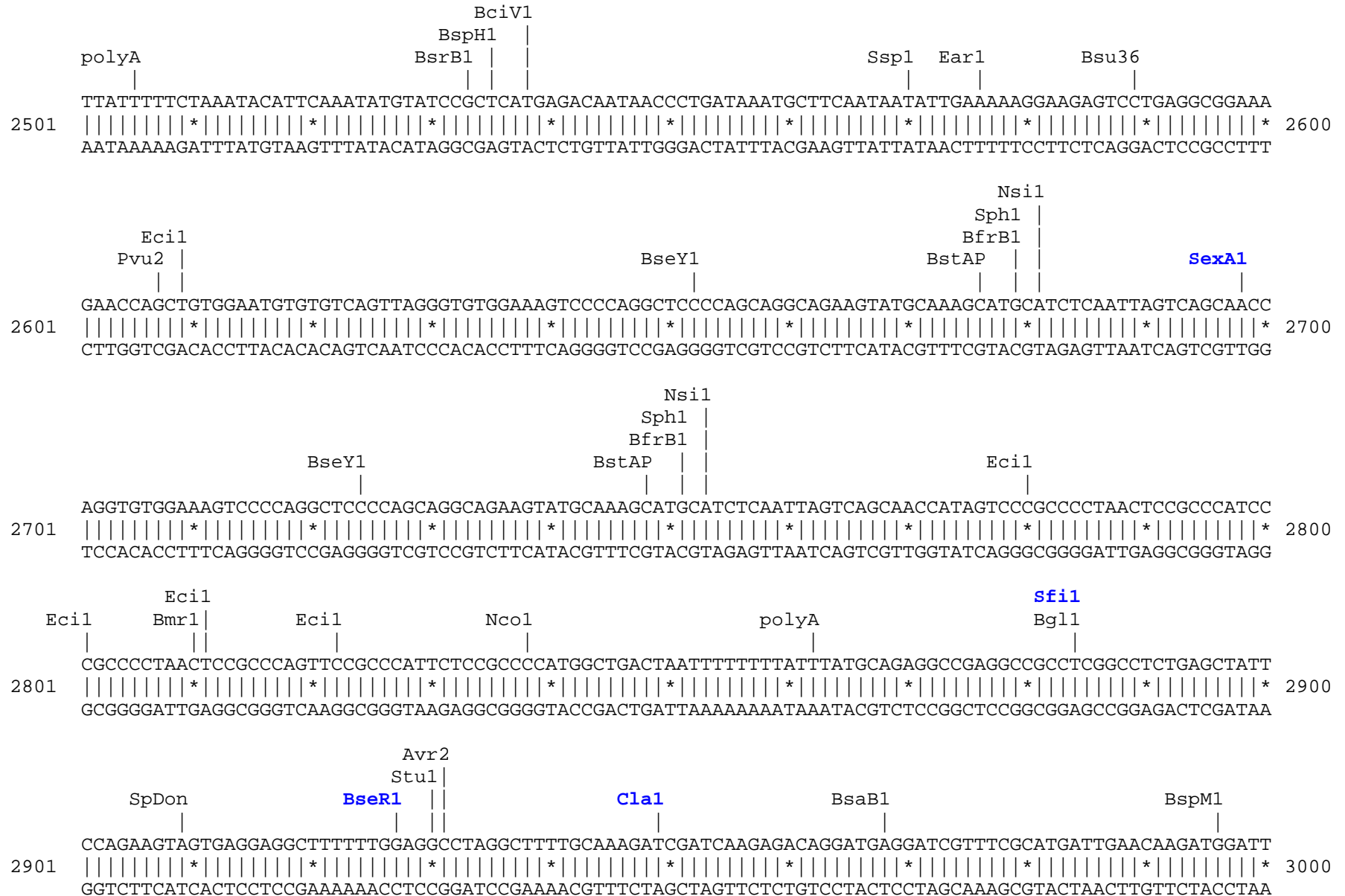












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                    EagI           BmrI
                    |               |
3001 GCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
CGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGT 3100

        NarI
        KasI |
            ||
                    DrdI
                    |
3101 GCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGG
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
CGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCC 3200

        Pvu2
        FspI |
            ||
                PflFI
                |
                    Eco57
                    |
                    SpDon
                    |
3201 GCGTTCCTTGGCGCAGCTGTGCTCGACGTTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTTCATCTCACCT
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
CGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCACGGCCCCGTCTCTAGAGGACAGTAGAGTGGA 3300

                    BciVI
                    |
                    BsrDI
                    |
                    BtgZI
                    BspMI |
                    |
3301 TGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGC
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
ACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTTCGCTTTGTAGCG 3400

                    SapI
                    EarI
                    |
                    BpuE1
                    |
3401 ATCGAGCGAGCACGTACTIONCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCCGCCAGGC
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
TAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTGGCTTGACAAGCGGTCCG 3500

        SphI
        |
                    NcoI
                    |
                    BtgZI
                    |
3501 TCAAGCGAGCATGCCCGACGGCGAGGATCTCGTCTGTGACCCATGGCGATGCCTGCTTGC CGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCAT
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
AGTTCGCTCGTACGGGCTGCCGCTCTCTAGAGCAGCACTGGGTACCCTACGGACGAACGGCTTATAGTACCACCTTTTACGGGCGAAAAGACCTAAGTA 3600

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BseY1  
 NaeI  
 NgoM4 | | | | |

Rsr2  
 | |

EciI  
 |

SapI  
 EarI  
 | |

Eco57  
 |

3601 CGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCCGAATGGGCTGACCGCTTC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3700  
 GCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAG

BssS1  
 |

BtgZ1  
 BsrB1 | |

BsrB1  
 |

BstB1  
 |

3701 CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGAC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3800  
 GAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAAGTCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTG

BssS1  
 BspM1 |

SpAcc  
 |

Bpm1  
 NgoM4 |  
 Bpm1 |

3801 CGACCAAGCGACGCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGG  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 3900  
 GCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACC

Bpm1  
 SpAcc |  
 Avr2 |

3901 ATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCG  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4000  
 TACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTTGGGCGC

polyA  
 |

polyA  
 |

Bsa1  
 |

4001 CTATGACGGCAATAAAAAGACAGAATAAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACCGGGGTTGCGTCCAGGGCTGGCACTCTGTTCGATACCCC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4100  
 GATACTGCCGTTATTTTTCTGTCTTATTTTGCCTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGG





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          ApaL1      BseY1                               SpAcc
          |         |                                   |
AACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAA
4701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
TTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTT

          BciV1      Eci1      BssS1                               SpAcc
          |         |         |                                   |
GGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTG
4801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
CCCTCTTTCGCTGTCCATAGGCCATTTCGCCGTCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGAC

          Drd1      BpuE1      SpAcc      Eci1
          |         |         |         |
TCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTT
4901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
AGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTTCGGTTCGTTGCGCCGGAAAAATGCCAA

          SpDon      BspLU      Nsil      BfrB1
          |         |         |         |
CCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5085
GGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

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Found:

<b>Aar1</b>	Aat2	<b>Acc65</b>	Afe1	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	<b>Bbs1</b>	BciV1
BfrB1	Bgl1	<b>Bgl2</b>	Bmr1	Bpm1	<b>Bpu10</b>	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	BseY1	Bsm1
<b>BsmB1</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	<b>BsrD1</b>	BsrG1	BssS1	BstAP	BstB1	<b>BstX1</b>	Bsu36	BtgZ1	<b>Bts1</b>
<b>Clal</b>	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	<b>Ecl2</b>	Eco57	EcoR1	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>
<b>Kpn1</b>	<b>Mfe1</b>	Msc1	Nae1	<b>Nar1</b>	Nco1	<b>Nde1</b>	NgoM4	<b>Nhe1</b>	<b>Not1</b>	Nsi1	<b>PflF1</b>	<b>PflM1</b>	polyA
<b>PshA1</b>	Psi1	<b>Pst1</b>	Pvu2	<b>Rsr2</b>	<b>Sac1</b>	<b>Sall</b>	Sap1	<b>SexA1</b>	<b>Sfi1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1
Ssp1	Stu1	<b>Xba1</b>	<b>Xho1</b>										

Unique:

<b>Aar1</b>	<b>Acc65</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>Bbs1</b>	<b>Bgl2</b>	<b>Bpu10</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	<b>BsmB1</b>
<b>BspLU</b>	<b>BsrD1</b>	<b>BstX1</b>	<b>Bts1</b>	<b>Clal</b>	<b>Ecl2</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kas1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>Nar1</b>	<b>Nde1</b>
<b>Nhe1</b>	<b>Not1</b>	<b>PflF1</b>	<b>PflM1</b>	<b>PshA1</b>	<b>Pst1</b>	<b>Rsr2</b>	<b>Sac1</b>	<b>Sall</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>SnaB1</b>	<b>Xba1</b>	<b>Xho1</b>

Not found:

Acl1	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	BcglA	Bcglb	Bcl1	Blp1	BmgB1	Bsg1
BsiW1	BspE1	BssH2	BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV	FCatB
FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PspOM
Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Sma1	Spe1	Srf1
Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1							

Excluded by site complexity:

Acc1	Acil	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	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													