

pFusionRed-tubulin 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, tubulin amino acids are shown in green, linker amino acids are shown in black.



Bbs1 Bpm1 BseY1
TACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACCTTCCCAGCCA
901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
ATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTCCGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTTCGGT
FusionRed > Y E D G G V L T A T Q D T S L Q D G C L I Y N V K V R G V N F P A N

BsmB1 BseY1 StuI Bgl1
ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCT
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCGGACCTTCCGCGTACACTGTACCGGGA
FusionRed > G P V M Q K K T L G W E A S T E T M Y P A D G G L E G A C D M A L

BssS1 Eco57 Bsa1 BpuE1
GAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTG
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTTCGAGCACCCGCCCCGGTGGACTAGACGTTGGAACCTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGAGATGTTGCAC
FusionRed > K L V G G G H L I C N L E T T Y R S K K P A T N L K M P G V Y N V

SpAcc PflM1 Bsa1 PshA1 BssS1 Dra3 Msc1
GACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGTATG
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
CTGGTGTCTGACCTTTCTTAGTTCTCCTCCGGCTGCTACTCTGGATGCAGCTCGTCTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTAC
FusionRed > D H R L E R I K E A D D E T Y V E Q H E V A V A R Y S T G G A G D G

SpDon BspE1 BseR1 Bgl2 Eci1
GAGGTAAAGGTGGAGGAGGTTCCGGACTCAGATCTGGCAGCGGTGGAGGCAGCGCATCCGGCGGAAGCGGAAGCGTGCCTGAGTGCATCTCCATCCACGT
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
CTCCATTTCCACCTCCTCCAAGGCCTGAGTCTAGACCGTCGCCACCTCCGTCGCGTAGGCCGCTTCGCTTCGCACGCACTCACGTAGAGGTAGGTGCA
FusionRed > G K G G G G S G L R S G S G G S A S G G S G S V R E C I S I H V

BseY1
 BsrD1 | Sac1
 BstAP | Ecl2 |
 Msc1 | BstX1 | Msc1

1401 TGGCCAGGCTGGTGTCCAGATTGGCAATGCCTGCTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCCGATGGCCAGATGCCAAGTGACAAGACCATT 1500
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
 ACCGGTCCGACCACAGGTCTAACCGTTACGGACGACCCTCGAGATGACGGACCTTGTGCCGTAGGTCGGGCTACCGGTCTACGGTTCACGTGTTCTGGTAA
Tubulin > G Q A G V Q I G N A C W E L Y C L E H G I Q P D G Q M P S D K T I

SpAcc
 Eco57BseR1 | BsmB1 | Pml1 | Sma1

1501 GGGGGAGGAGATGACTCCTTCAACACCTTCTTCAGTGAGACGGGCGCTGGCAAGCACGTGCCCGGGCTGTGTTTGTAGACTTGGAACCCACAGTCATTG 1600
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 CCCCCCTCTACTGAGGAAGTTGTGGAAGAAGTCACTCTGCCCGGACCGTTTCGTGCACGGGGCCCGACACAAACATCTGAACCTTGGGTGTCAGTAAC
Tubulin > G G G D D S F N T F F S E T G A G K H V P R A V F V D L E P T V I D

Bpu10
 Sap1 |
 Ear1 |

1601 ATGAAGTTCGCACTGGCACCTACCGCCAGCTCTTCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTATGCCCGAGGGCACTACAC 1700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 TACTTCAAGCGTGACCGTGGATGGCGGTTCGAGAAGGTGGGACTCGTTCGAGTAGTGTCCGTTCTTCTACGACGGTTATTGATACGGGCTCCCGTGATGTG
Tubulin > E V R T G T Y R Q L F H P E Q L I T G K E D A A N N Y A R G H Y T

Age1
 Bbs1 | Xcm1
 EcoR1 | Eco57ApaL1 | BstX1 | SpAcc |

1701 CATTGGCAAGGAGATCATTGACCTTGTGTTGGACCGAATTCGCAAGCTGGCTGACCAAGTGCACCGGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGT 1800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 GTAACCGTTCCTCTAGTAACTGGAACACAACCTGGCTTAAGCGTTCGACCGACTGGTCACGTGGCCAGAAGTCCCGAAGAACCAAAAGGTGTCGAAACCA
Tubulin > I G K E I I D L V L D R I R K L A D Q C T G L Q G F L V F H S F G

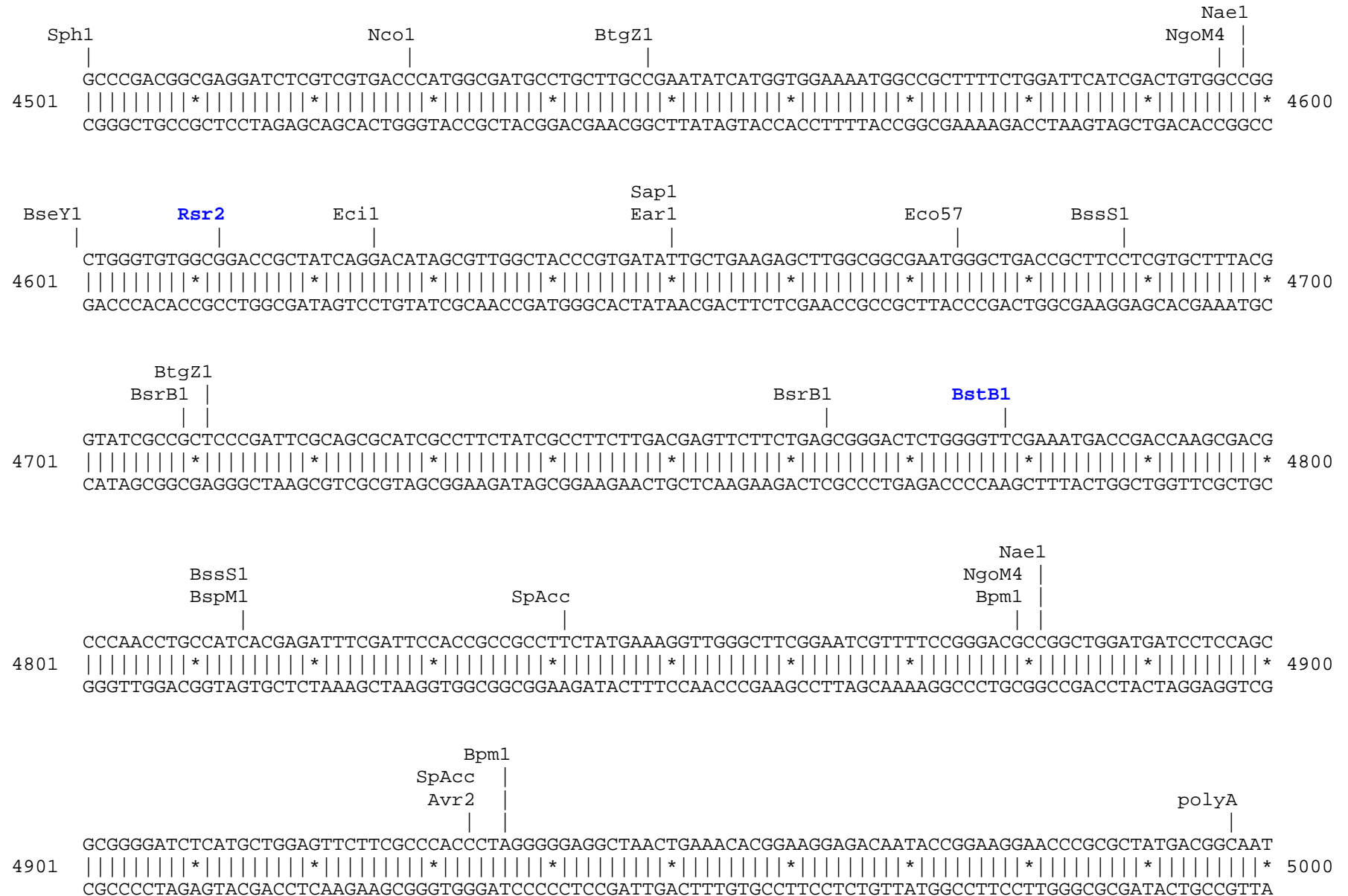
Xmn1 SpDon BsmB1 BseY1 Bpm1
GGGGAACTGGTTCTGGGTTACCTCCCTGCTCATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTGGAGTTCTCCATTTACCCAGCACCCC
1801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
CCCCCTTGACCAAGACCCAAGTGGAGGGACGAGTACCTTGCAGAGAGTCAACTAATACCGTTCTTCAGGTTTCGACCTCAAGAGGTAATGGGTCTGTTGGG
Tubulin > G G T G S G F T S L L M E R L S V D Y G K K S K L E F S I Y P A P Q

SpAcc Pvu2 SpDon Bpm1
AGGTTTCCACAGCTGTAGTTGAGCCCTACAACCTCCATCCTCACCACCCACACCACCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCAT
1901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
TCCAAAGGTGTCGACATCAACTCGGGATGTTGAGGTAGGAGTGGTGGGTGTGGTGGGACCTCGTGAGACTAACACGGAAGTACCATCTGTTACTCCGGTA
Tubulin > V S T A V V E P Y N S I L T T H T T L E H S D C A F M V D N E A I

PshA1 EcoRV Bts1
CTATGACATCTGTCTAGAAAACCTCGATATCGAGCGCCCAACCTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCTCCATCACTGCTTCCCTG
2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
GATACTGTAGACAGCATCTTTGGAGCTATAGCTCGCGGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGAC
Tubulin > Y D I C R R N L D I E R P T Y T N L N R L I S Q I V S S I T A S L

EcoR1 SexA1 MscI NdeI
AGATTTGATGGAGCCCTGAATGTTGACCTGACAGAATTCCAGACCAACCTGGTGCCTTACCCCGCATCCACTTCCCTCTGGCCACATATGCCCTGTCA
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
TCTAAACTACCTCGGGACTTACAACCTGGACTGTCTTAAGGTCTGGTTGGACCACGGGATGGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGT
Tubulin > R F D G A L N V D L T E F Q T N L V P Y P R I H F P L A T Y A P V I

SpAcc SpAcc SpDon BstX1 NcoI
TCTCTGCTGAGAAAACCTACCATGAACAGCTTTTCTGTAGCAGAGATCACCAATGCTTGTCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCA
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
AGAGACGACTCTTTCGGATGGTACTTGTTCGAAAGACATCGTCTCTAGTGGTTACGAACGAAACTCGGTTCGGTTGGTCTACCACCTTACTGGGAGCGGT
Tubulin > S A E K A Y H E Q L S V A E I T N A C F E P A N Q M V K C D P R H



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polyA                                     Bsa1
|                                         |
AAAAAAGACAGAATAAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACCGCGGGTTTCGGTCCCAGGGCTGGCACTCTGTGCGATACCCACCGAGACCCCAT
5001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5100
TTTTTCTGTCTTATTTTTCGCTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTA

                                     BstAP
                                     AlwN1
                                     |
TGGGGCCAATACGCCCAGTTTCTTCCTTTTCCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTG
5101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5200
ACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTCCGGGAC

Bsu36                                     DraI                                     DraI                                     BspH1
|                                         |                                         |                                         |
CCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGAC
5201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5300
GGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTG

                                     BpuE1
                                     |
CAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGC
5301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5400
GTTTLAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATTAGACG

                                     Eco57
                                     |
TGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGC
5401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5500
ACGAACGTTTGTTTTTTGGTGGCGATGGTTCGCCACCAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAGGCTTCCATTGACCGAAGTCGTCTCGCG

SpAcc
|
AGATACCAAATACTGTCCCTTCTAGTGTAGCCGTAGTTAGGCCACCCTTCAAGAAGTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACC
5501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5600
TCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTCTTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGG
```


Found:

Aat2	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	Baela	Baelb	BamH1	Bbs1	BbvC1	BciV1
Bcl1	BfrB1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb
BseR1	BseY1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1
BstX1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoN1
EcoR1	EcoRV	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1
Nsi1	PflF1	PflM1	Pml1	polyA	PshA1	Psi1	Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfi1	Sma1
SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xmn1					

Unique:

Afe1	Ase1	Baela	Baelb	BamH1	BbvC1	Bcl1	Bgl2	Blp1	BmgB1	BsaXa	BsaXb	BspE1	BspLU
BsrG1	BstB1	Clal	Eag1	Ecl2	EcoRV	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nhe1	PflF1
Pml1	Rsr2	Sac1	Sfi1	Sma1	SnaB1	Xba1	Xcm1	Xmn1					

Not found:

Aar1	Acc65	Acc1	Afl2	Ahd1	Apa1	Asc1	AsiS1	BcglA	Bcglb	Bsg1	BsiW1	BssH2	BstE2
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1
Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP
R4atR	Sac2	Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter
PISce	Xho1												

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	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													