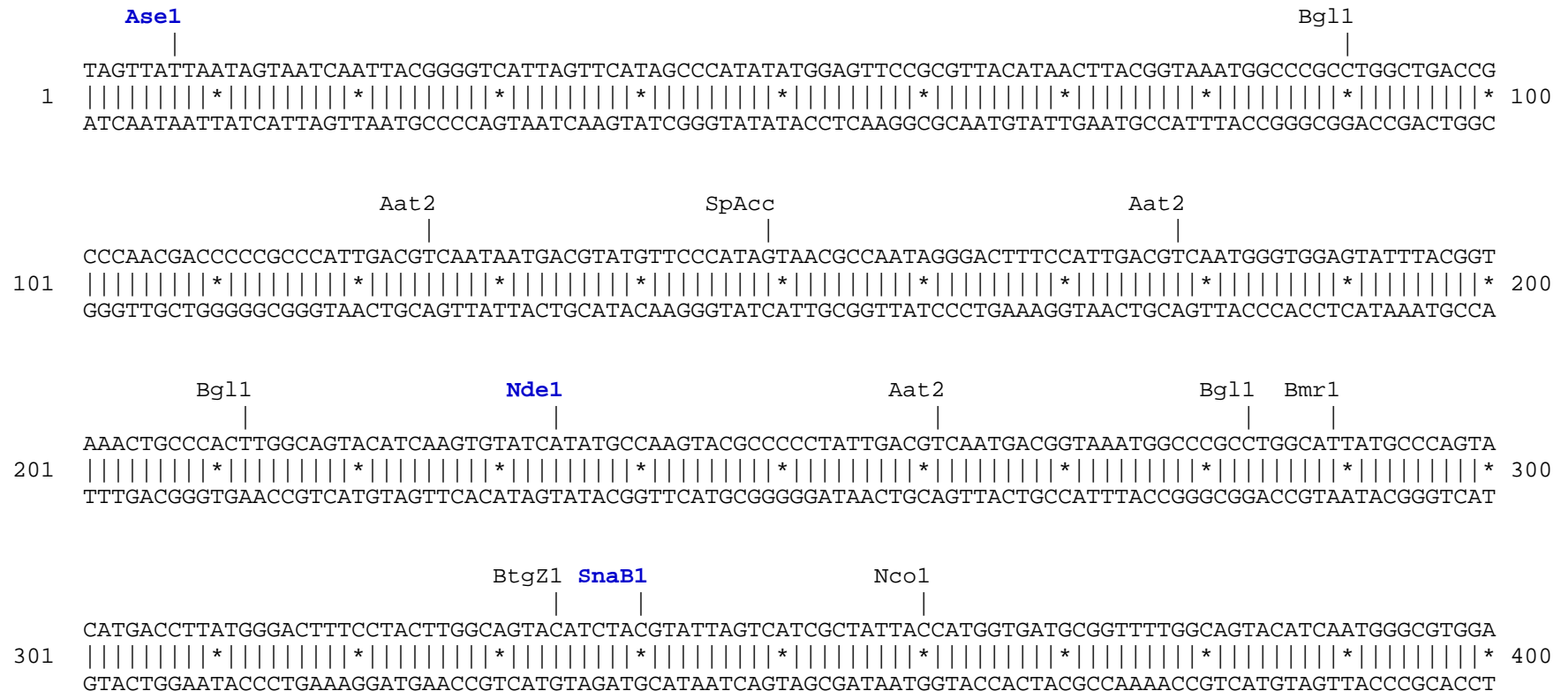


pTagRFP-EB3 vector restriction map

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). TagRFP amino acids are shown in red, EB3 amino acids are shown in green, linker amino acids are shown in black.




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                                SpAcc  SpAcc                                polyA
                                |      |                                |
AAGATGGGTGTTGACAAAATCATTCTGTAGAGAAAATTAGTGAAAGGAAAATTCCAAGATAATTTTGTAGTTTATTTCAGTGGTTTAAGAAATTCTTTGACG
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
TTCTACCCACAACACTGTTTTAGTAAGGACATCTCTTTAATCACTTTTCTTTAAGGTTCTATTAATAAACTCAAATAAGTCACCAAATTCTTTAAGAAACTGC
EB3  > K M G V D K I I P V E K L V K G K F Q D N F E F I Q W F K K F F D A

                                EcoN1  Bcl1  Bgl2
                                |      |      |
CAAACATATGATGGAAAAGGATTACAACCTCTGCTGGCGCGGCAGGGCCAGGACGTAGCGCCACCTCCTAACCAGGTGATCAGATCTTCAACAAATCCAA
1001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
GTTTGATACTACCTTTCTAATGTTGGGAGACGACCGCGCCGTCCCGGTCTGCATCGCGGTGGAGGATTGGGTCCACTAGTCTAGAAGTTGTTTAGGTT
EB3  > N Y D G K D Y N P L L A R Q G Q D V A P P P N P G D Q I F N K S K

                                Bln1
                                |
GAAACTCATTGGCACAGCAGTTCCACAGAGGACGTCCCCCACAGGCCCAAAAAACATGCAGACCTCTGGCCGGCTGAGCAATGTGGCCCCCCCCCTGCATT
1101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTTTGAGTAACCGTGTCTGTCAGAGTGTCTCCTGCAGGGGGTGTCCGGGTTTTTTGTACGTCTGGAGACCGGCCGACTCGTTACACCGGGGGGGGACGTAA
EB3  > K L I G T A V P Q R T S P T G P K N M Q T S G R L S N V A P P C I

                                Aat2  SpAcc                                Nae1  NgoM4  BsrD1  Bsm1
                                |      |                                |      |      |      |
GAAACTCATTGGCACAGCAGTTCCACAGAGGACGTCCCCCACAGGCCCAAAAAACATGCAGACCTCTGGCCGGCTGAGCAATGTGGCCCCCCCCCTGCATT
1101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTTTGAGTAACCGTGTCTGTCAGAGTGTCTCCTGCAGGGGGTGTCCGGGTTTTTTGTACGTCTGGAGACCGGCCGACTCGTTACACCGGGGGGGGACGTAA
EB3  > K L I G T A V P Q R T S P T G P K N M Q T S G R L S N V A P P C I

                                BspE1                                Pvu2  PflM1  _Chi
                                |                                |      |      |
CTCCGGAAGAATCCTCCATCAGCCCGAAATGGCGGCCATGAGACTGATGCCCAAATTTCTTGAACCTCAACCAACAGCTGGTGGACTTGAAGCTGACAGTGG
1201  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GAGGCCTTCTTAGGAGGTAGTCGGGCTTTACCGCCGGTACTCTGACTACGGGTTTAAGAACTTGAGTTGGTTGTGCGACCACCTGAACTTCGACTGTCACC
EB3  > L R K N P P S A R N G G H E T D A Q I L E L N Q Q L V D L K L T V D

                                SpAcc  Eco57  Bpm1                                Sac1  SpDon
                                |      |      |                                |      |
ATGGGCTGGAGAAGGAACGTGACTTCTACTTCAGCAAACCTTCGTGACATCGAGCTCATCTGCCAGGAGCATGAAAGTGAAAACAGCCCTGTTATCTCAGG
1301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
TACCCGACCTCTTCTTGCAGTGAAGATGAAGTCGTTTGAAGCACTGTAGCTCGAGTAGACGGTCTCTCGTACTTTCACTTTTGTGCGGGACAATAGAGTCC
EB3  > G L E K E R D F Y F S K L R D I E L I C Q E H E S E N S P V I S G

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                                     BseY1                                     Bgl1
ACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAG
1901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
TGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCGGACCTTCCGTCTTC
TagRFP > F P S N G P V M Q K K T L G W E A N T E M L Y P A D G G L E G R S

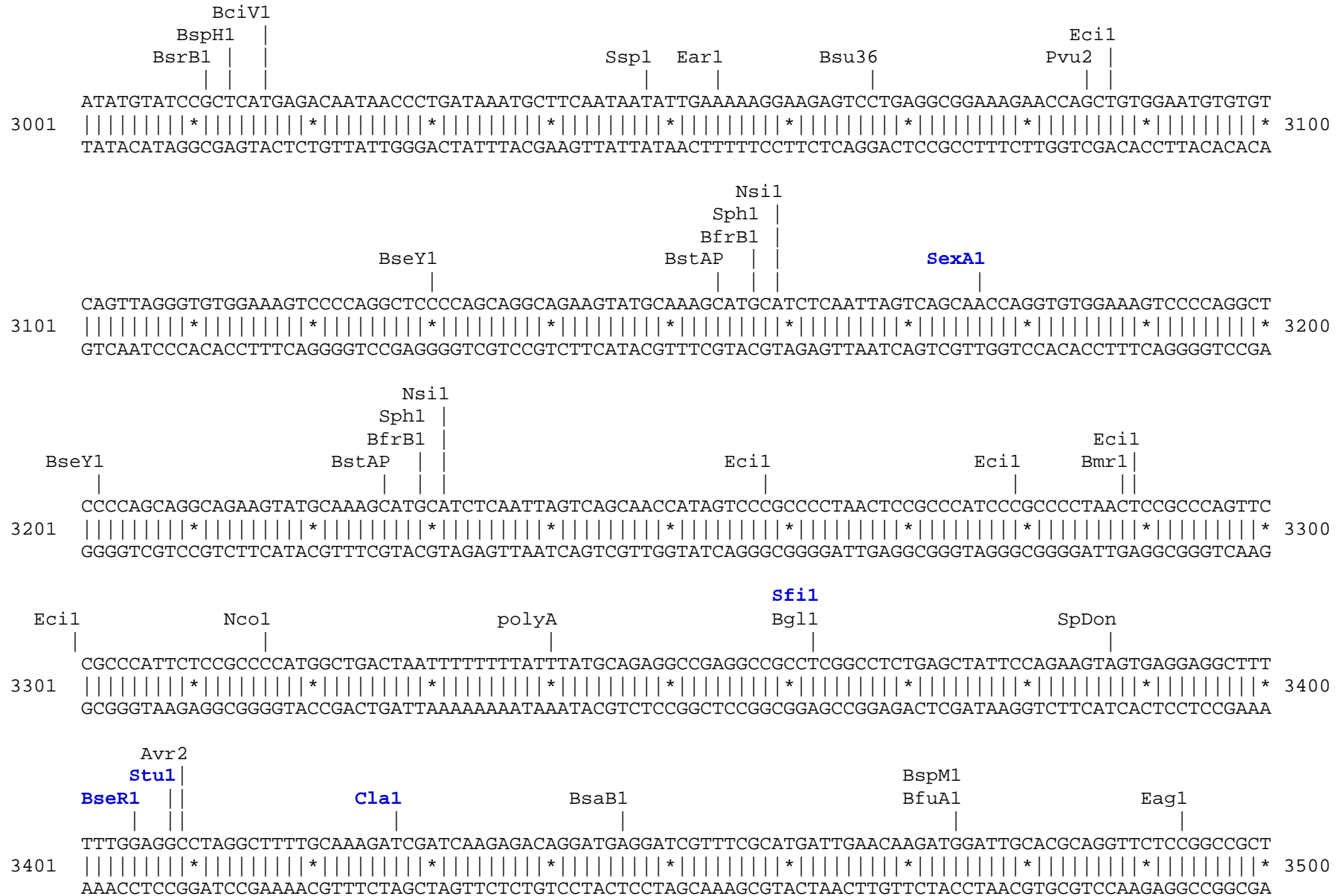
                                     BssS1       Eco57                                     BpuE1
CGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAAACCCGCTAAGAACCTCAAGATGCCCGGC
2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
GCTGTACCGGGACTTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCG
TagRFP > D M A L K L V G G G H L I C N F K T T Y R S K K P A K N L K M P G

                                     SpAcc
                                     PflM1                                     Bsa1       PshA1       BssS1 Dra3       Msc1 AlwN1
GTCTACTATGTGGACCACAGACTGGAAAAGAAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTGCGACCTCC
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
CAGATGATACACCTGGTGTCTGACCTTTCTTAGTTTCTCCGGCTGTTTCTCTGGATGCAGCTCGTTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGG
TagRFP > V Y Y V D H R L E R I K E A D K E T Y V E Q H E V A V A R Y C D L P

                                     Not1
                                     Eag1
SpAcc       Bmr1       BsrB1 |       Xba1       BsaB1                                     SpDon       Dra1
CTAGCAAACCTGGGGCACAAACTTAATTGAGCGGCCGCGACTCTAGATCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCC
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
GATCGTTTGACCCCGTGTGTTGAATTAACCTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGG
TagRFP > S K L G H K L N *

                                     Bsm1
                                     Mfe1 |       Hpa1       polyA       Pst1       polyA
CACACCTCCCCCTGAACCTGAAACATAAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCAC
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
GTGTGGAGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTG

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                BpuE1                                     ApaL1
                |                                         |
5101  TGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCACACAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    ACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTC

BseY1                                     SpAcc
|                                         |
5201  CCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    GGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAG

                BciV1
    Eci1 |                                     BssS1 |                                     SpAcc |
5301  CGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    GCCATTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAAATATCAGGACAGCCCAAAGCGGTGGAGACTGA

Drd1 |                                     BpuE1 |                                     SpAcc |                                     Eci1 |
5401  TGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
    ACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTCGTTGCGCCGAAAAAATGCCAAGGACCGGAAAAACGACCGGAAAA

                SpDon
    BspLU |
5501  GCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5563
    CGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

                Nsi1
                BfrB1 |

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Found:

Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1	BfrB1
BfuA1	Bgl1	Bgl2	Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1
Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoK	EcoN1	EcoR1	Fsp1	Hind3
Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	PflM1
polyA	PshA1	Psi1	Pst1	Pvu2	Rsr2	Sac1	Sall	Sap1	SexA1	Sfil	SnaB1	SpAcc	SpDon
Sph1	Ssp1	Stu1	Xba1	Xho1									

Unique:

Afe1	Afl2	Age1	Ase1	BamH1	Bcl1	Blp1	BsaXa	BsaXb	BseR1	Bsg1	BspE1	BspLU	BsrG1
Bts1	_Chi	Clal	EcoK	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1
Not1	PflF1	PshA1	Pst1	Rsr2	Sall	SexA1	Sfil	SnaB1	Stu1	Xba1	Xho1		

Not found:

Aar1	Acc65	Ac11	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	BmgB1	Bpu10
BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1
I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL	R4atP	R4atR
Sac2	SanD1	Sbf1	Scal	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													