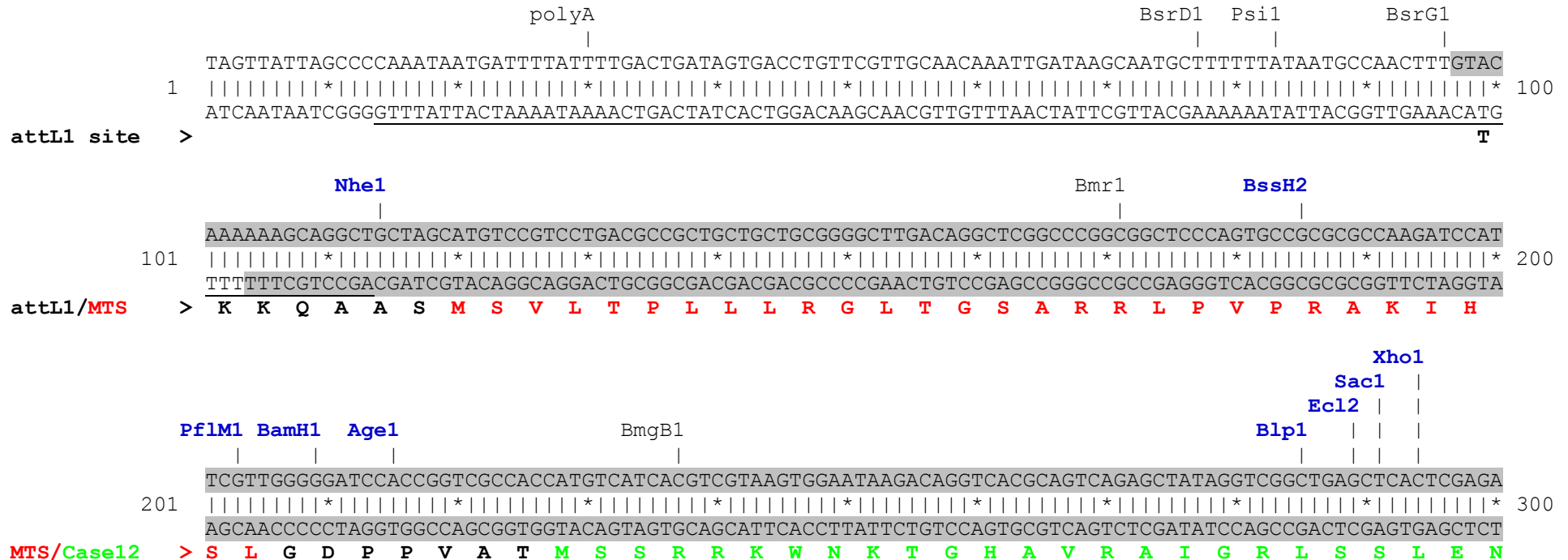


Gateway® Case12-mito entry clone restriction map

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). MCS sequence is shown in frame, the attL sites are underlined. Shaded regions correspond to DNA sequences transferred from the entry clone into the destination vector following recombination. Non-Case12 amino acids coded by those DNA sequences are shown in black, mitochondrial targeting sequence (MTS) amino acids are shown in red, Case12 amino acids are shown in green.



Eci1
|

301
ACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGACCACTA
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 400
TGCAGATATAGTACCGGCTGTTTCGTCTTCTTGCCGTAGTTCGGTTGAAGTTCTAGGCGGTGTTGCAGCTCCTGCCGTCGCACGTCGAGCGGCTGGTGAT
Case12 > V Y I M A D K Q K N G I K A N F K I R H N V E D G S V Q L A D H Y

Bsg1 | Bpu10 | Bpu10 |

401
CCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTTCCAGTCCGTCTTGAGCAAAGACCCCAACGAGAAGCGC
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 500
GGTCGTCTTGTGGGGGTAGCCGCTGCCGGGACACGACACGGGCTGTTGGTGATGGACTCGAAGGTCAGGCAGGACTCGTTTTCTGGGGTTGCTCTTCGCG
Case12 > Q Q N T P I G D G P V L L P D N H Y L S F Q S V L S K D P N E K R

Bpm1 | BsrG1 |

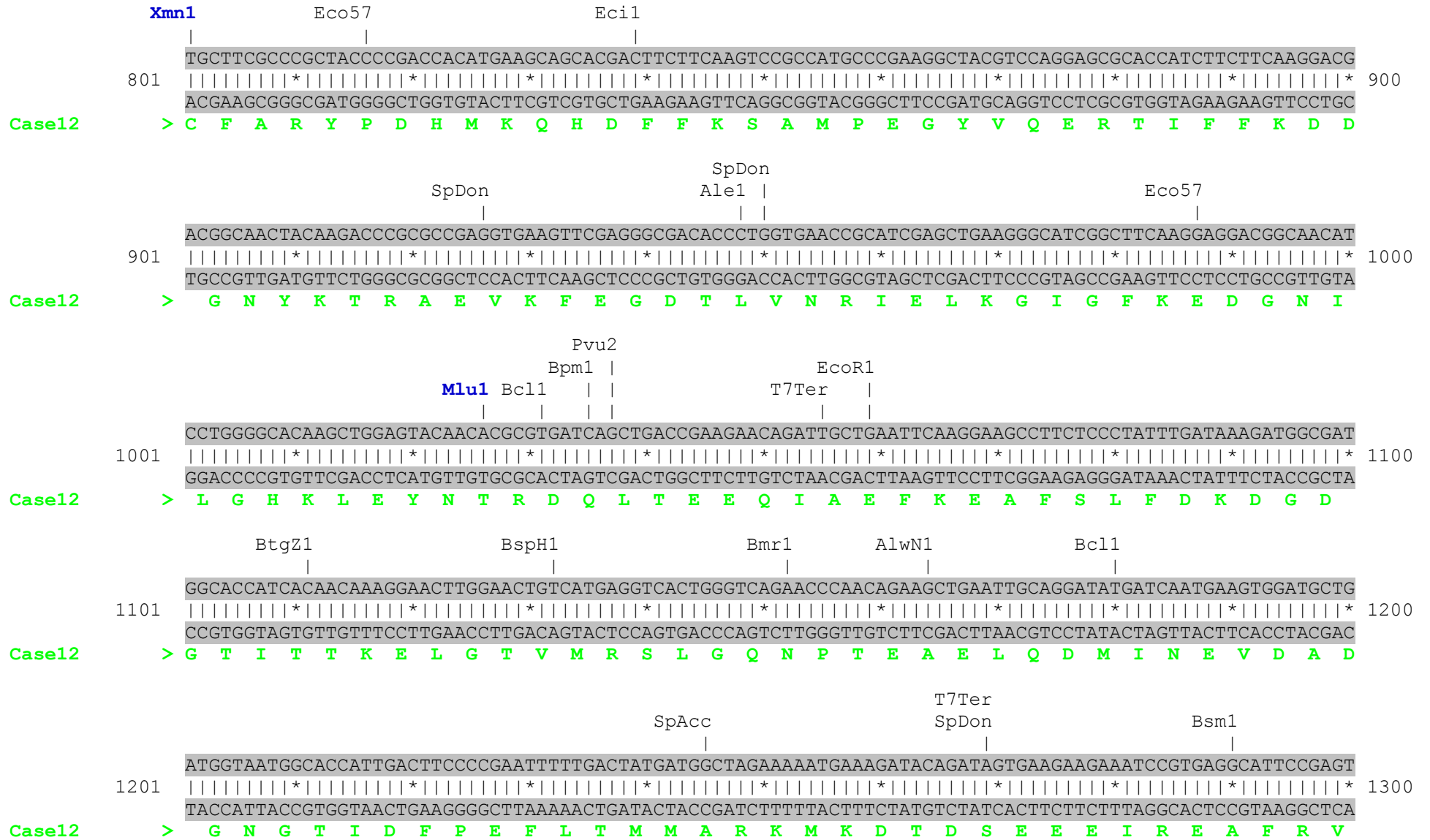
501
GATCACATGGTCCTGCTGGAGTTCGTGACC GCCCGGGATCACTCTCGGCATGGACGAGCTGTACAACGTGGATGGCGGTAGCGGTGGCACC GGCCAGCA
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 600
CTAGTGTACCAGGACGACCTCAAGCACTGGCGGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTGCACCTACCGCCATCGCCACCGTGGCCGTCGT
Case12 > D H M V L L E F V T A A G I T L G M D E L Y N V D G G S G G T G S K

BseR1 | Ale1 | Bcg1a |

601
AGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 700
TCCCCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTC AAGTTCGCACAGGCCGCTCCCCTCCCCT
Case12 > G E E L F T G V V P I L V E L D G D V N G H K F S V S G E G E G D

Bsg1 | Bcg1b | BssS1 | Ale1 | Eco57 | BtgZ1 |

701
TGCCACCTACGGCAAGCTGACCCCTGAAGCTGATCTGCACCACCGGAAGCTGCCCGTGCCCTGGCCCCACCTCGTGACCACCCTCGGCTACGGCCTGAAG
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 800
ACGGTGGATGCCGTTGCACTGGGACTTCGACTAGACGTGGTGGCCGTTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGAGCCGATGCCGGACTTC
Case12 > A T Y G K L T L K L I C T T G K L P V P W P T L V T T L G Y G L K



BspH1
Bsg1
BsrD1 BmgB1 T7Ter Bcl1

1301 CTTTGACAAGGATGGCAATGGTTATATCAGTGCAGCAGAACTACGTACCGTCATGACAAACTTAGGAGAAAACTAACAGATGAAGAAGTAGATGAAATG 1400
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
 GAAACTGTTCCCTACCGTTACCAATATAGTCACGTCGTCTTGATGCAGTGCAGTACTGTTTGAATCCTCTTTTTGATTGTCTACTTCTTCATCTACTTTAC
Case12 > F D K D G N G Y I S A A E L R H V M T N L G E K L T D E E V D E M

BsmB1 Drd1 SpAcc EcoR1 T7Ter polyA Not1
Eag1 BseY1

1401 ATCAGAGAAGCAGATATTGATGGAGACGGACAAGTCAACTATGAAGAATTCGTACAGATGATGACTGCAAAAATAAAGCGGCCGCGACTCTAGGACCCAGC 1500
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
 TAGTCTCTTCGTCTATAACTACCTCTGCCTGTTTCAGTTGATACTTCTTAAGCATGTCTACTACTGACGTTTTATTTTCGCCGGCGCTGAGATCCTGGGTCTG
Case12 > I R E A D I D G D G Q V N Y E E F V Q M M T A K *

BsrG1 Psi1 BsrD1 polyA

1501 TTTCTTGTACAAAGTTGGCATTATAAGAAAACATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAAATAAAATCATTATTTGCTAGATC 1600
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 AAAGAACATGTTTCAACCGTAATATTCTTTTCGTAACGAATAGTTAAACAACGTTGCTTGTCCAGTGATAGTCAGTTTTATTTTAGTAATAAACGATCTAG

attL2 site

BsaB1 SpDon Dra1 Bsm1
Mfe1

1601 ATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTG 1700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 TATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAAC

Hpa1 polyA Psi1 polyA polyA Bts1 Bsm1

1701 TTAACTTGTATTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTT 1800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 AATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAA


```

                                Nar1
                                Kas1 |
                                ||
                                Drd1
                                |
2901 TGCTCTGATGCCGCGTGTTCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
    ACGAGACTACGGCGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCC

                                Pvu2
                                Msc1 |
                                Fsp1 |
                                PflF1 |
                                Eco57
                                |
3001 CAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
    GTCGCGCCGATAGCACCGACCGGTGCTGCCCGAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGCTTCA

                                SpDon
                                |
                                BciV1
                                |
                                BsrD1
                                |
3101 GCCGGGGCAGGATCTCCTGTTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
    CGGCCCCGTCTTAGAGGACAGTAGAGTGGAAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGG

                                BtgZ1
                                BspM1 |
                                BfuA1 |
                                |
                                Sap1
                                |
                                Ear1
                                |
3201 TGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
    ACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCC

                                BpuE1
                                |
                                Sph1
                                |
                                Nco1
                                |
                                BtgZ1
                                |
3301 GGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
    CCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTA

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Found:

Afl2	Age1	Ale1	AlwN1	ApaL1	Avr2	BamH1	Bcg1a	Bcg1b	BciV1	Bcl1	BfrB1	BfuA1	Bgl1
Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1
BsmB1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoR1	Fsp1	Hpa1	Kas1	Mfe1
Mlu1	Msc1	Nae1	Nar1	Nco1	NgoM4	Nhe1	Not1	Nsi1	PflF1	PflM1	polyA	Psi1	Pvu2
Rsr2	Sac1	Sap1	SexA1	Sfi1	SpAcc	SpDon	Sph1	Ssp1	Stu1	T7Ter	Xho1	Xmn1	

Unique:

Afl2	Age1	ApaL1	BamH1	Bcg1a	Bcg1b	Bgl1	Blp1	Bsa1	BsaXa	BsaXb	BsmB1	BspLU	BssH2
BstB1	Bts1	Clal	Dra3	Ecl2	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Msc1	Nar1	Nhe1	Not1
PflF1	PflM1	Rsr2	Sac1	SexA1	Sfi1	Stu1	Xho1	Xmn1					

Not found:

Aar1	Aat2	Acc65	Acl1	Afe1	Ahd1	Apal	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1
Bgl2	BsiW1	BspE1	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Nde1	Nru1	Pac1
Pme1	Pml1	PshA1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1
Sca1	Sgf1	SgrA1	Sma1	SnaB1	Spe1	Srf1	Swal	T3RNA	T7RNA	PISce	Xba1	Xcm1	

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	Bs11	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													