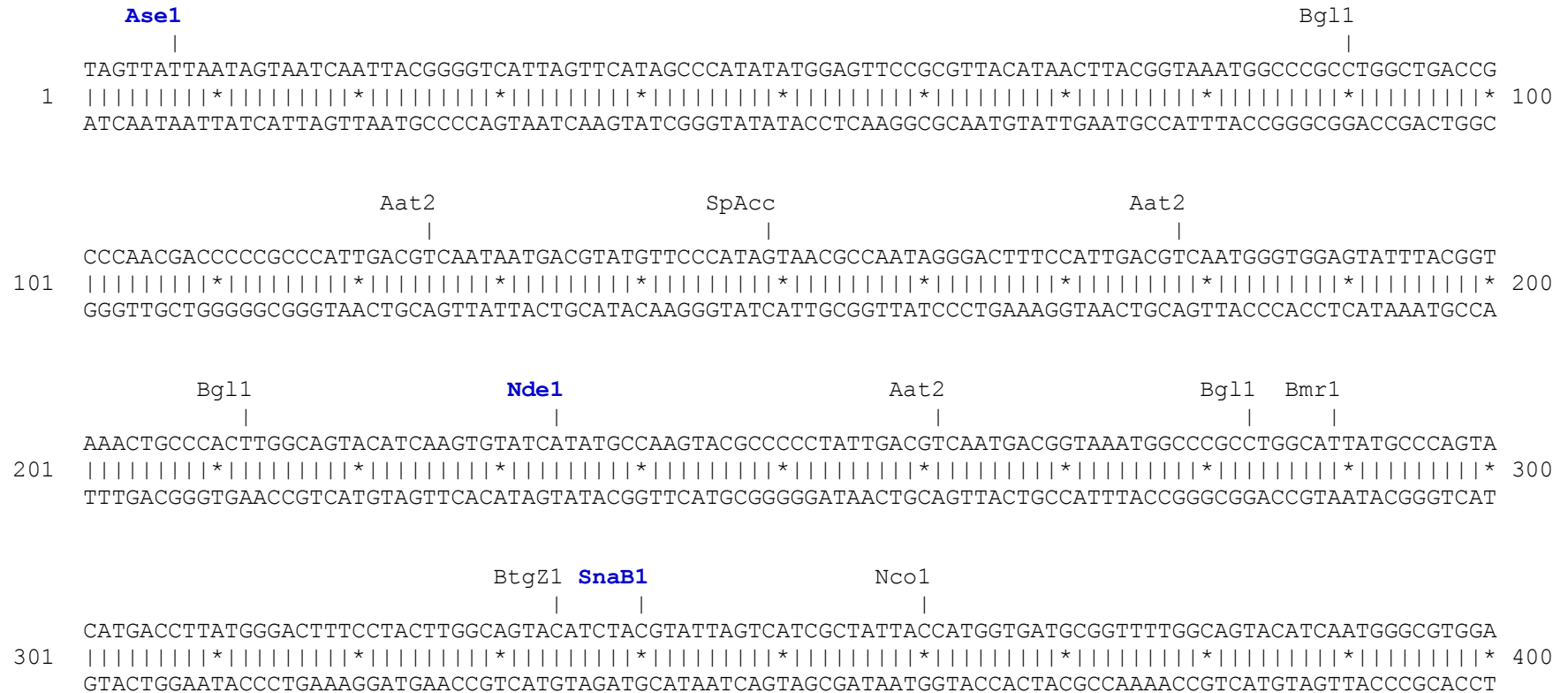


pmKate2-profilin vector restriction map

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). mKate2 amino acids are shown in red, profilin amino acids are shown in green, linker amino acids are shown in black.



Aat2 Eci1

| |

401 TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
 ATCGCCAAACTGAGTGCCCTAAAGGTTTACAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGTTTTACAGCAT

Nhe1 Afel

| |

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTGAGGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

SpDon

Ale1 |

Age1 Nco1 | | BsrG1 ApaL1

| | | | |

601 CCGGTAGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCCTGAACAACCACCACTTCAAGTGCACATCCG
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCCATCGGTGGTACCACTCGCTCGACTAATTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTACAGTGTAGGC

mKate2 > M V S E L I K E N M H M K L Y M E G T V N N H H F K C T S E

SpAcc

|

701 AGGGCGAAGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGCGGTGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 TCCCGCTTCCGTTCCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCGCCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAA

mKate2 > G E G K P Y E G T Q T M R I K A V E G G P L P F A F D I L A T S F

Bsu36 SpDon

| |

801 CATGTACGGCAGCAAAACCTTCATCAACCACACCAGGGCATCCCCGACTTCTTTAAGCAGTCCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 GTACATGCCGTCGTTTTGGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGT

mKate2 > M Y G S K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T

1401
CGCGGCCATCGTAGGCTACAAGGACTCGCCCTCCGTCTGGGCGCCCGTCCCGGGAAGACCTTCGTTAGCATTACGCCAGCTGAGGTTGGTGTCTGGTA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
GCGCCGGTAGCATCCGATGTTCTTGAGCGGGAGGCAGACCCGGCGGCAGGGGCCCCTTCTGGAAGCAATCGTAATGCGGTTCGACTCCAACCACAGGACCAT
profilin > **A A I V G Y K D S P S V W A A V P G K T F V S I T P A E V G V L V**

1501
GGCAAAGACCGGTCAAGTTTTTTCGTCAATGGGCTGACACTTGGGGCCAGAAATGTTCTGTGATCCGGGACTCACTGCTGCAAGACGGGGAATTTACAA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
CCGTTTCTGGCCAGTTCAAAAAGCAGTTACCCGACTGTGAACCCCGGTCTTTACAAGACACTAGGCCCTGAGTGACGACGTTCTGCCCCTTAAATGTT
profilin > **G K D R S S F F V N G L T L G G Q K C S V I R D S L L Q D G E F T M**

1601
TGGATCTTCGTACCAAGAGCACCGGAGGAGCCCCACCTTCAATGTCACTGTCAACCATGACTGCCAAGACGCTAGTCTCTGCTGATGGGCAAAGAAGGTGT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
ACCTAGAAGCATGGTTCTCGTGGCCTCCTCGGGGGTGGAAATTACAGTGACAGTGGTACTGACGGTTCTGCGATCAGGACGACTACCCGTTTCTTCCACA
profilin > **D L R T K S T G G A P T F N V T V T M T A K T L V L L M G K E G V**

1701
CCACGGTGGTTTGATCAACAAGAAATGTTATGAAATGGCCTCTCACCTGCGGCGTTCAGTACTAAGGATCCACCGGATCTAGATAACTGATCATAATC
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
GGTGCCACCAACTAGTGTCTTTACAATACTTTACCCGGAGAGTGGACGCCGCAAGGGTCATGATTCTAGGTGGCCTAGATCTATTGACTAGTATTAG
profilin > **H G G L I N K K C Y E M A S H L R R S Q Y ***

1801
AGCCATACCACATTTGTAGAGGTTTTACTTTGCTTTAAAAACCTCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTGTTAACT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
TCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTGGAGGGTGTGGAGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGA

Restriction enzymes shown: SpAcc, BsaXb, BsaXa, Sma1, Xmn1, Bbs1, Bpu10, BbvC1, Pvu2, Age1, Bts1, SpDon, BseR1, PshA1, BspM1, BfuA1, Aar1, Bcl1, SpDon, Bmr1, Scal, BamH1, Xba1, Bcl1BsaB1, SpDon, Dra1, Bsm1, Mfe1, Hpa1.

BciV1
BspH1 |
BsrB1 | |
Ssp1 |

polyA
|

```

AATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAA
2501 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 2600
TTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTT

```

Eci1
|

Ear1
|

Bsu36
|

Pvu2 |

BseY1
|

```

AAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGC
2601 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 2700
TTTCCTTCTCAGGACTCCGCCTTCTTGGTCGACACCTTACACACAGTCAATCCACACCTTTCAGGGGTCCGAGGGGTTCGCCTTTCATACGTTTTCG

```

Nsil
Sph1 |
BfrB1 |
BstAP | |

SexA1
|

BseY1
|

Nsil
Sph1 |
BfrB1 |
BstAP | |

```

ATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAG
2701 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 2800
TACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGCCTTTCATACGTTTTCGTACGTAGAGTTAATCAGTCGTTGGTATC

```

Eci1
|

Eci1
|

Eci1
|

Bmr1 |

Eci1
|

Nco1
|

polyA
|

```

TCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCCAGTTCGCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTTTATTTATGCAGAGGCCGA
2801 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 2900
AGGGCGGGGAT TGAGGCGGGT AGGGCGGGGATTGAGGCGGGT CAAGGCGGGT AAAGGCGGGT ACCGACTGAT TAAAAAATAAATACGTCTCCGGCT

```

Avr2
Stu1 |

Sfi1
Bgll |

SpDon
|

BseR1 | |

Cla1
|

BsaB1
|

```

GGCCGCCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCC TAGGCTTTTGC AAAGATCGATCAAGAGACAGGATGAGGATCGTT
2901 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 3000
CCGGCGGAGCCGGAGACTCGATAAAGTCTTCATCACTCCTCCGAAAAAACC TCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAA

```



```

          Bsa1
          |
4101 GGGCTGGCACTCTGTCGATACCCACCGAGACCCATTGGGGCCAATACGCCCGGTTTCTTCCTTTTCCCACCCACCCCCAAGTTCGGGTGAAGGC 4200
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCG

          BstAP          Bsu36          Dra1          Dra1
          |              |              |              |
4201 CCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAA 4300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGTCCCAGCGTCGGTTGCAGCCCCGCCGTCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAAATTTT

          BspH1
          |
4301 GGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGG 4400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCC

          BpuE1
          |
4401 ATCTTCTTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCA 4500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGT

          Eco57          SpAcc
          |              |
4501 ACTCTTTTTCGAAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAG 4600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATC

          AlwN1          BpuE1
          |              |
4601 CACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTACCGGGTTGGACTCAAGACGATAGTTACC 4700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGG

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                ApaL1      BseY1      SpAcc
                |          |          |
GGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTA
4701 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 4800
CCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTCTGGGTCTCGAACCTCGCTTGTGATGTGGCTTGGACTCTATGGATGTCTGCACTCGAT

                        BciV1
                        Eci1      |      BssS1
                        |          |          |
TGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCTGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAA
4801 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 4900
ACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTT

                SpAcc      Drd1      BpuE1      SpAcc      Eci1
                |          |          |          |          |
ACGCCTGGTATCTTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGC
4901 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 5000
TGCGGACCATAGAAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACTTTTTTGCG

                               SpDon
                               BspLU|
                               ||
CAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACC
5001 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 5100
GTCGTTGCCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGG

                Nsi1
                BfrB1 |
                |  |
GCCATGCAT
5101 | | | | | | | 5109
CGGTACGTA
```

Found:

Aar1	Aat2	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BbvC1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	Fsp1	Hind3	Hpa1	Kas1	Mfe1
Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	polyA	PshA1	Psi1	Pvu2
Rsr2	Sac1	Sap1	Sca1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1
Xho1	Xmn1												

Unique:

Aar1	Afe1	Ale1	Ase1	BamH1	BbvC1	Bgl2	Bpu10	BspE1	BspLU	BsrD1	BsrG1	BstB1	Clal
Eag1	Ecl2	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nde1	Nhe1	PflF1	Rsr2	Sac1
Sca1	SexA1	Sfi1	Sma1	SnaB1	Xba1	Xho1	Xmn1						

Not found:

Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	Bcgl1a	Bcgl1b	Blp1	BmgB1	Bsg1
BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoR1
EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1
PflM1	Pme1	Pml1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1
Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce	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													