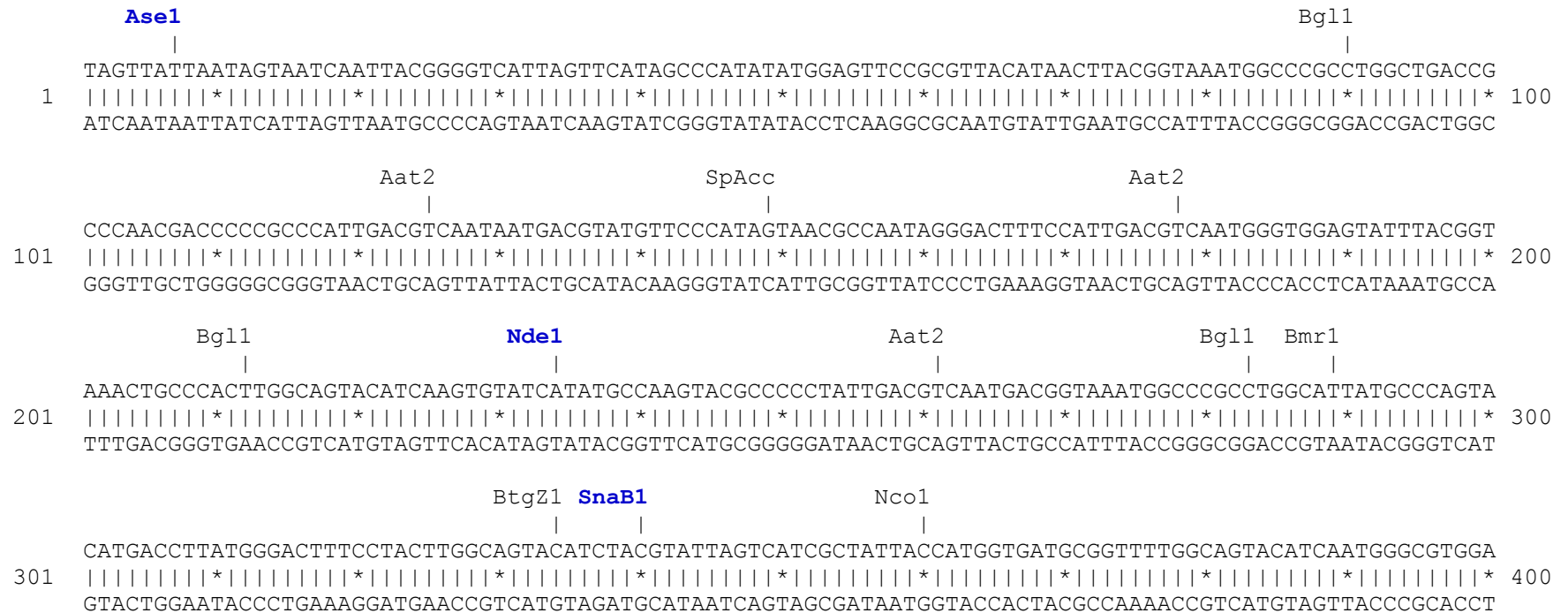
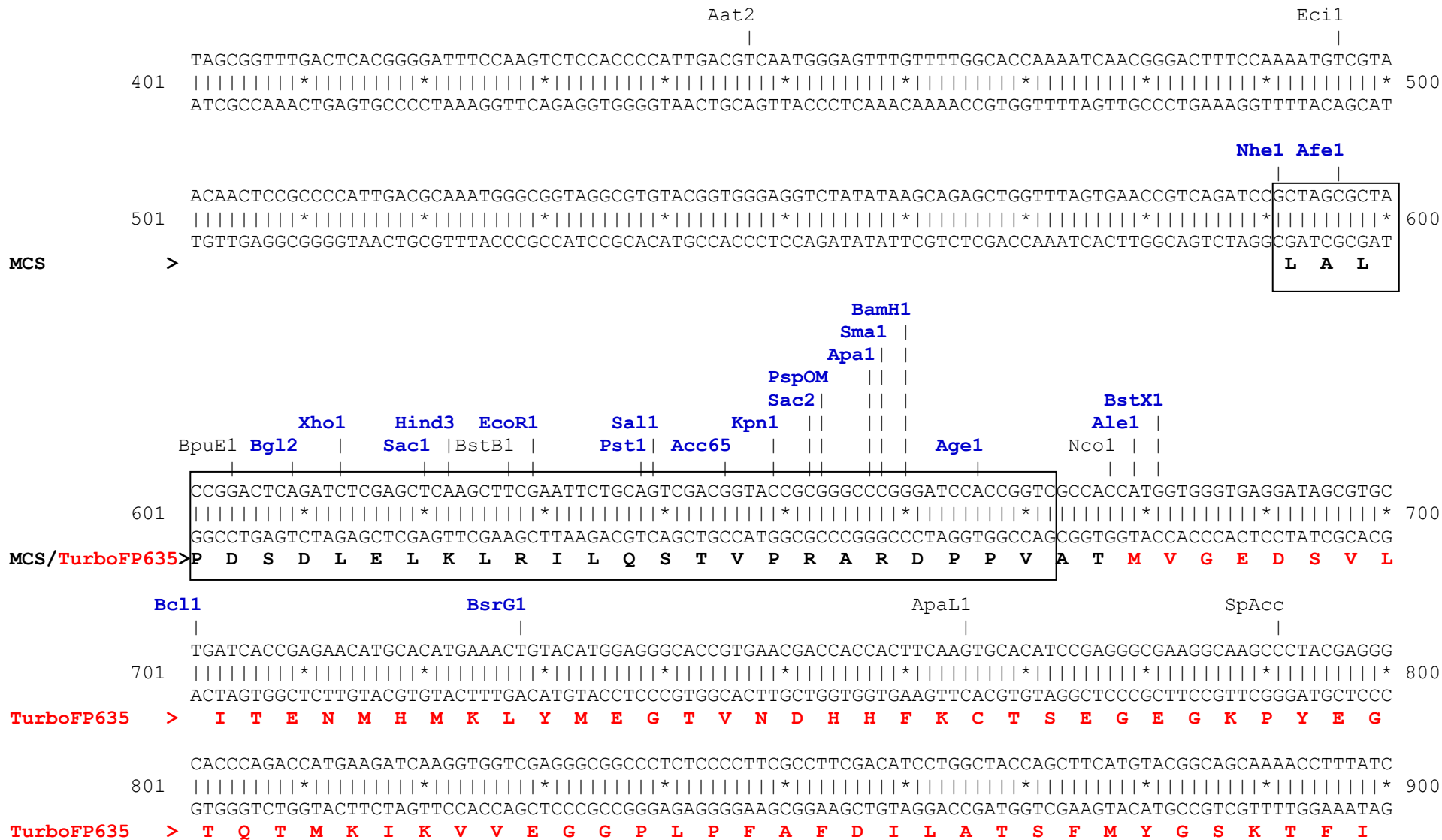


pTurboFP635-N vector restriction map

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). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.






```
          BtgZ1
      BspM1 |
      BfuA1 |
          | |
3001 GCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
    CGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCG

          BpuE1          Sph1          Nco1          BtgZ1
          |             |             |             |
3101 ATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCTGTGACCCATGGCGATGCCTGCTTGCCGAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
    TAGTCCCGAGCGCGGTTCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTT

          BseY1
          Nae1 |
          NgoM4 | |
          | | |
3201 TATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCCGGACCCTATCAGGACATAGCGTTGGCTACCCGTGATATT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
    ATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCTGGCGATAGTCTGTATCGCAACCGATGGGCACTATAA

          BtgZ1
          Eco57          BssS1          BsrB1 |
          |             |             | |
3301 GCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
    CGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAAGTGC

          BssS1
          BspM1
          BfuA1
          BsrB1          BstB1          SpAcc
          |             |             |             |
3401 AGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTGATTCCACCGCCGCTTCTATGAAAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
    TCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCC
```

```
                  NaeI                      BpmI
                  NgoM4 |                  SpAcc |
                  BpmI |                  Avr2 |
                   | |                      | |
3501 TTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTG
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3600
      AACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGAC

                      polyA              polyA
                      |                   |
3601 AAACACGGAAGGAGACAATAACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAACGCACGGTGTTGGGTGCTTTGTTTCATAAACGCGG
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3700
      TTTGTGCTTCTCTGTTATGGCCTTCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTTCGTGCCACAACCCAGCAAACAAGTATTTGCGCC

                               BsaI
                               |
3701 GGTTTCGGTCCCAGGGCTGGCACTCTGTTCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCGCGTTTCTTCTTTTCCCCACCCCAACCCCAAGT
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3800
      CCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTC

                               BstAP
    SpDon                      AlwN1         Bsu36                      DraI
    |                          |             |                          |
3801 TCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATT
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3900
      AGCCCACTTCGGGTCCCAGCGTCGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAA

      DraI                          BspH1
      |                              |
3901 TTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGA
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4000
      AAATTAATTTTCTTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCT

                               BpuE1
                               |
4001 AAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTTGCTTGCAAACAAAAAACACCCGCTACCAGCGGTGGTTTTGTTTGCCGGAT
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 4100
      TTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTGCACCACAAACAAACGGCCTA
```



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                Eco57                        SpAcc
                |                            |
4101  CAAGAGCTACCAACTCTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTCTTAGTGTAGCCGTAGTTAGGCCACCACTTCA
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4200
      GTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGT

                                AlwN1                        BpuE1
                                |                            |
4201  AGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGAACAAG
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4300
      TCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCAACCGCTATTACAGCACAAGAATGGCCAACTGAGTTC

                                ApaL1      BseY1
                                |          |
4301  ACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAAACGGGGGTTTCGTGCACACAGCCAGCTTGAGGAGCGAACGACCTACACCGAACTGAGATACCTA
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4400
      TGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGAT

                                BciV1
                                |
                                Eci1 |           BssS1
                                |     |           |
4401  CAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGC
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4500
      GTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCG

                SpAcc                                Drd1                BpuE1                SpAcc
                |                                |                |                |
4501  TTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCT
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4600
      AAGGTCCCCCTTTGCGGACCATAGAAAATATCAGGACAGCCCCAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGA

                                SpDon
                                |
                                BspLU|
                                ||
4601  ATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTTGCCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGAT
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 4700
      TACCTTTTTCGCGTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTA

```

```

                NsiI
                BfrB1 |
                | |
AACC GTATTACCGCCATGCAT
4701  |||*|||*|||  4721
                TTGGCATAATGGCGGTACGTA
    
```

Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsg1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1
Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	polyA	PshA1
Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc
SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1								

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apal	Ase1	BamH1	Bbs1	Bcl1	Bgl2	BsaXa	BsaXb	BseR1
Bsg1	BspLU	BsrD1	BsrG1	BstX1	Clal	Dra3	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1
Nar1	Nde1	Nhe1	Not1	PflF1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SexA1	Sma1
SnaB1	Stu1	Xba1	Xho1										

Not found:

Aar1	Ac11	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Blp1	BmgB1	Bpu10	BsiW1
BsmB1	BspE1	BssH2	BstE2	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP
Mlu1	Nru1	Pac1	PflM1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1
Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1							

Excluded by site complexity:

Acc1	Ac11	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													