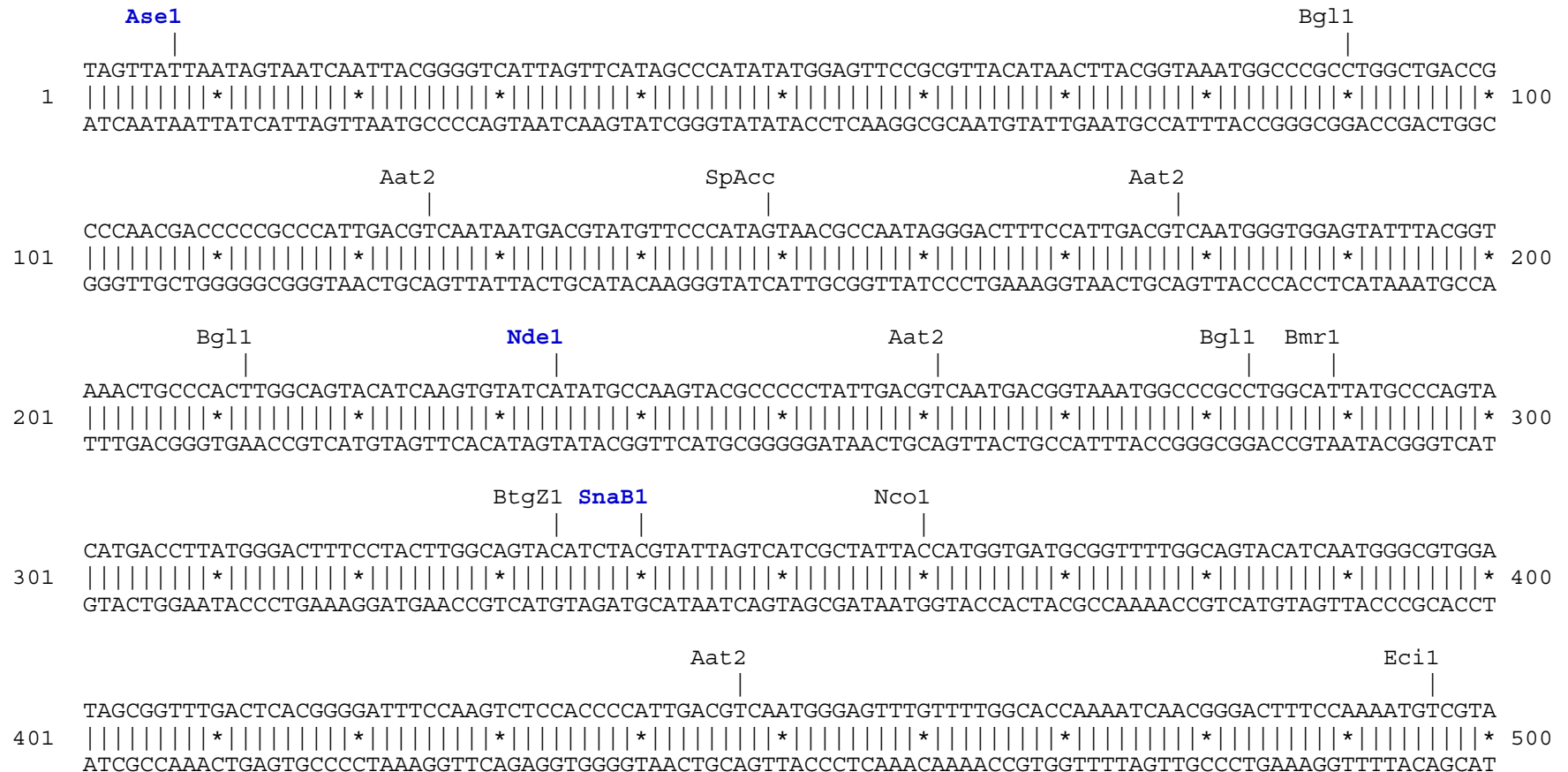


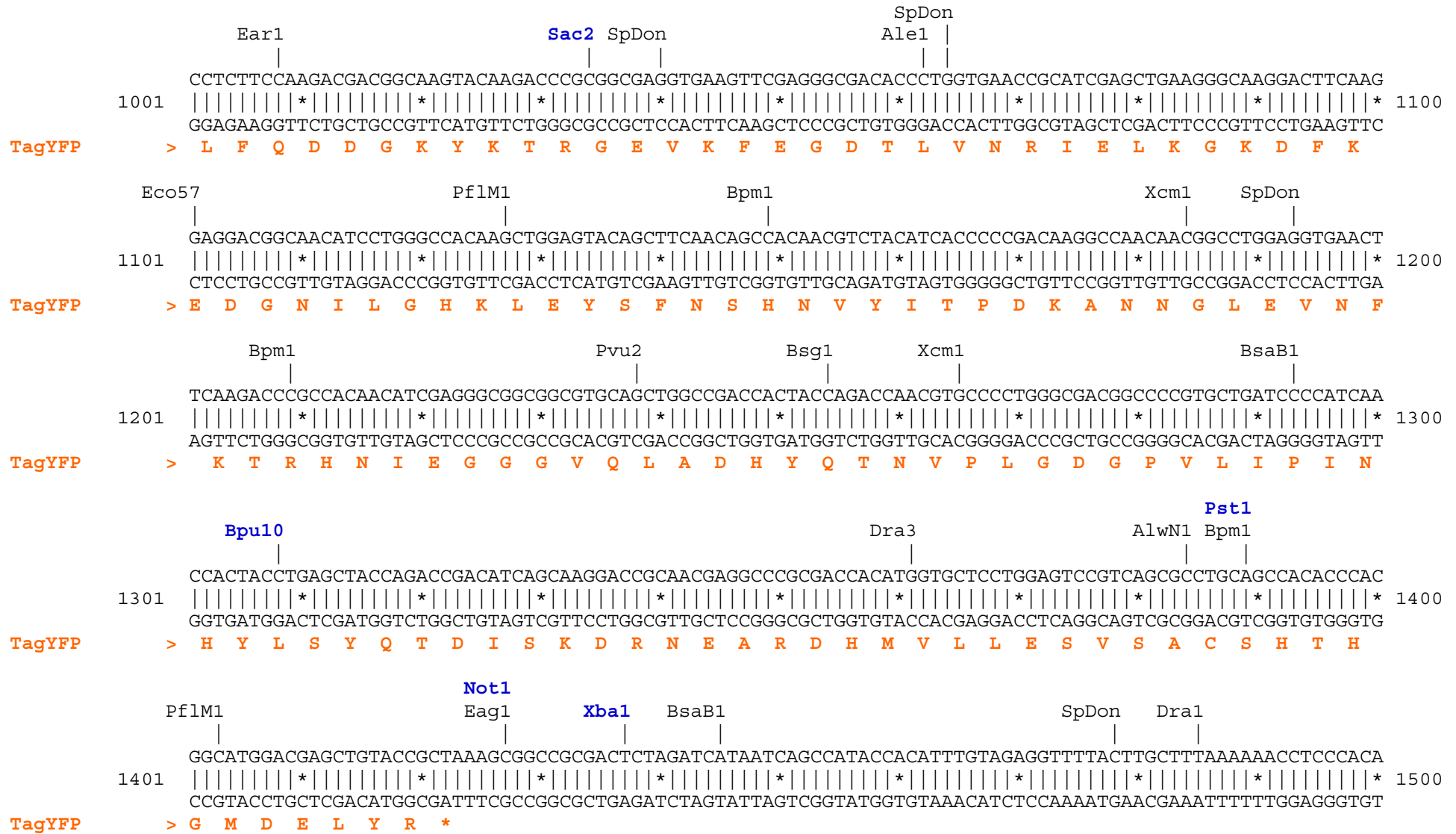
pTagYFP-mito vector restriction map

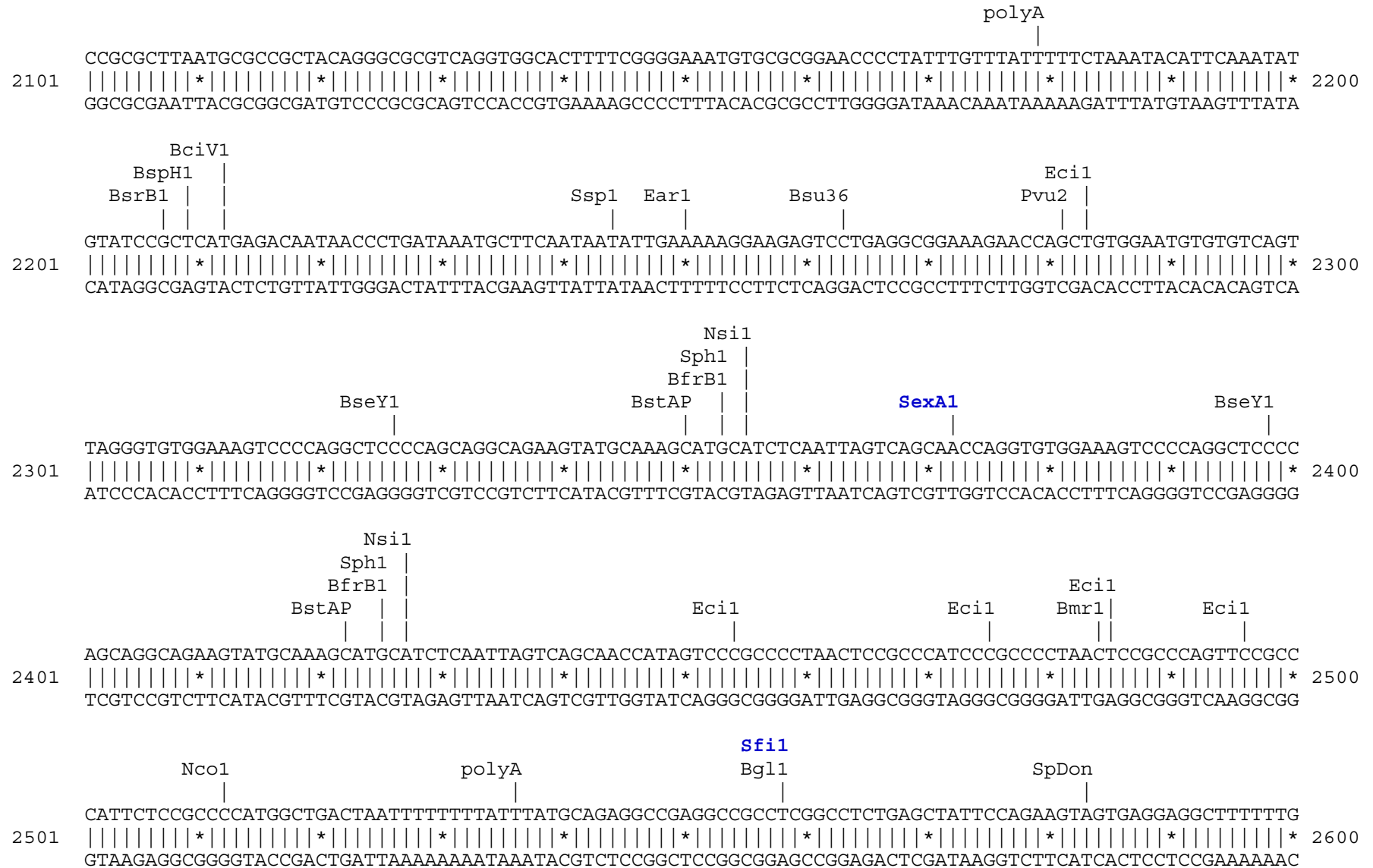
The data has not been verified by restriction digestion with each enzyme listed and does not take into account possible methylation sites. Enzymes that recognize unambiguous sequences less than 6 basepairs long are not included – for the more complete enzyme list please refer to the Table of restriction 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).

Mitochondrial targeting sequence (MTS) is shown in bold black.








```

                SpAcc                               AlwN1
                |                                   |
TGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCC
4201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4300
ACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGG

                BpuE1                               ApaL1   BseY1
                |                                   |         |
AGTGGCGATAAGTTCGTGCTTACCAGGTTGGACTCAAGACGATAGTTACCAGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCA
4301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4400
TCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGT

                                SpAcc                               Eci1
                                |                                   |
GCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCAGAGGGAGAAAGGCGGACAGGTATCCGGT
4401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4500
CGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCA

BciV1                               BssS1                               SpAcc                               Drd1
|                                   |                                   |                                   |
AAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAG
4501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4600
TTCGCCGTCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTC

                BpuE1                               SpAcc   Eci1
                |                                   |         |
CGTCGATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTC
4601 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4700
GCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTGCTTGCGCCGAAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAG

SpDon                               Nsi1
BspLU |                               BfrB1 |
||                                       ||
ACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
4701 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4759
TGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

| | | | | | | | | | | | | | |
|-------------|--------------|--------------|--------------|--------------|-------------|--------------|--------------|--------------|-------------|-------------|-------------|-------|--------------|
| Aat2 | Afl2 | Age1 | Ale1 | AlwN1 | ApaL1 | Ase1 | Avr2 | BamH1 | BciV1 | BfrB1 | BfuA1 | Bgl1 | BmgB1 |
| Bmr1 | Bpm1 | Bpu10 | BpuE1 | Bsa1 | BsaB1 | BsaXa | BsaXb | BseR1 | BseY1 | Bsg1 | Bsm1 | BspH1 | BspLU |
| BspM1 | BsrB1 | BsrD1 | BssH2 | BssS1 | BstAP | BstB1 | BstE2 | Bsu36 | BtgZ1 | Bts1 | Cla1 | Dra1 | Dra3 |
| Drd1 | Eag1 | Ear1 | Eci1 | Eco57 | Fsp1 | Hpa1 | Kas1 | Mfe1 | Msc1 | Nae1 | Nar1 | Nco1 | Nde1 |
| NgoM4 | Nhe1 | Not1 | Nsi1 | PflF1 | PflM1 | polyA | Psi1 | Pst1 | Pvu2 | Rsr2 | Sac2 | Sap1 | SexA1 |
| Sfi1 | SnaB1 | SpAcc | SpDon | Sph1 | Ssp1 | Stu1 | Xba1 | Xcm1 | Xmn1 | | | | |

Unique:

| | | | | | | | | | | | | | |
|-------------|--------------|-------------|--------------|--------------|--------------|-------------|--------------|--------------|--------------|--------------|--------------|-------------|--------------|
| Afl2 | Age1 | Ase1 | BamH1 | BmgB1 | Bpu10 | Bsa1 | BspLU | BsrD1 | BssH2 | BstB1 | BstE2 | Bts1 | Cla1 |
| Fsp1 | Hpa1 | Kas1 | Mfe1 | Msc1 | Nar1 | Nde1 | Nhe1 | Not1 | PflF1 | Pst1 | Rsr2 | Sac2 | SexA1 |
| Sfi1 | SnaB1 | Stu1 | Xba1 | Xmn1 | | | | | | | | | |

Not found:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|------|-------|-------|-------|
| Aar1 | Acc65 | Acl1 | Afe1 | Ahd1 | Apa1 | Asc1 | AsiS1 | Bae1a | Bae1b | Bbs1 | BbvC1 | Bcg1a | Bcg1b |
| Bcl1 | Bgl2 | Blp1 | BsiW1 | BsmB1 | BspE1 | BsrG1 | BstX1 | BstZ1 | _Chi | EcoK | EcoN1 | EcoR1 | EcoRV |
| ScFRT | Fse1 | FspA1 | Hind3 | I_Ceu | Kpn1 | loxP | Mlu1 | Nru1 | Pac1 | Pme1 | Pml1 | PshA1 | PspOM |
| Pvu1 | Sac1 | Sal1 | SanD1 | Sbf1 | Sca1 | Sgf1 | SgrA1 | Sma1 | Spe1 | Srf1 | Swa1 | T3RNA | T7RNA |
| T7Ter | PISce | Xho1 | | | | | | | | | | | |

Excluded by site complexity:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Acc1 | Ac1 | 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 | | | | | | | | | | | | | |