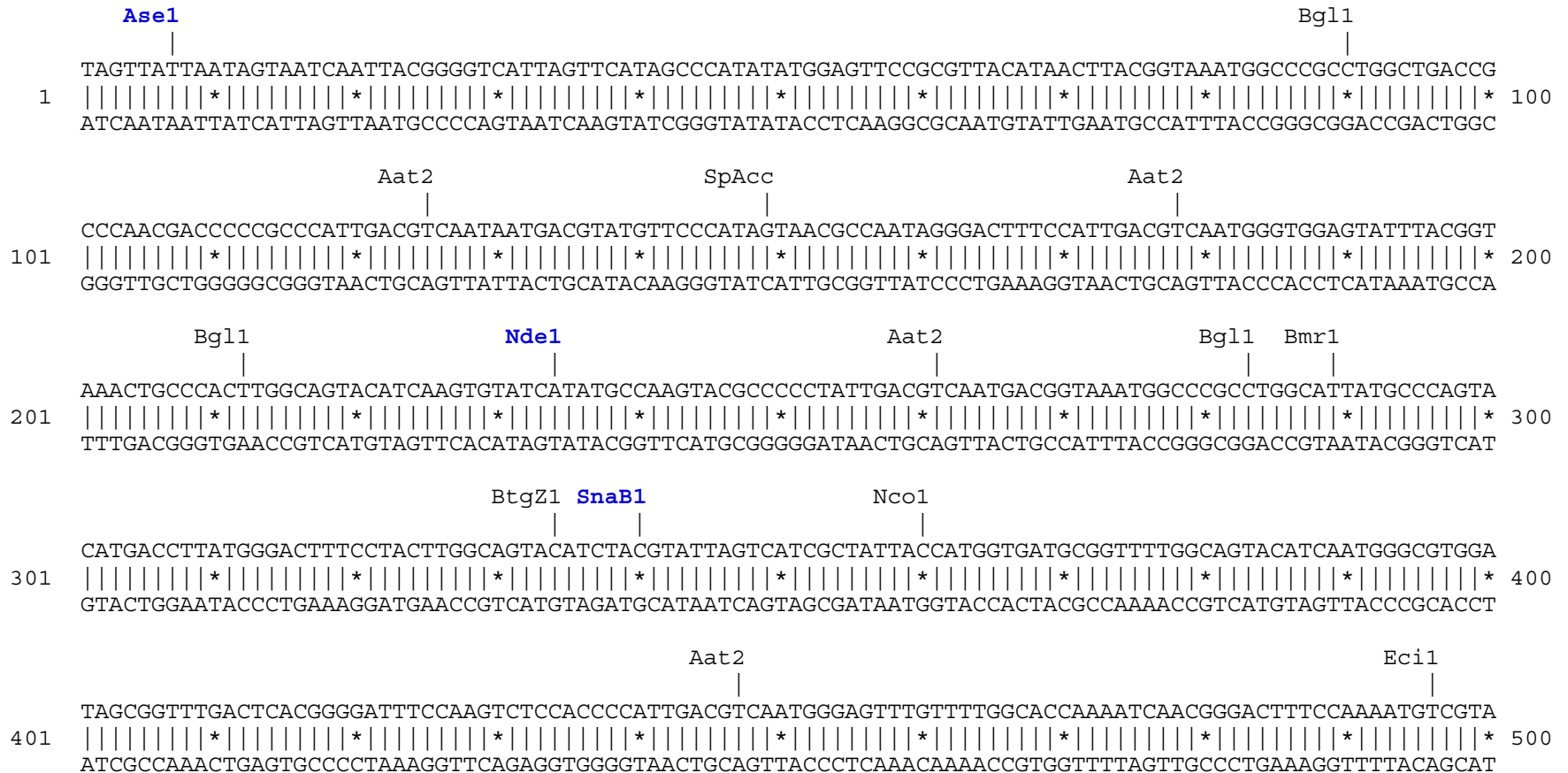


pTagCFP-actin vector restriction map

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). TagCFP amino acids are shown in dark-cyan, beta-actin amino acids are shown in orange, linker amino acids are shown in black.



Nhe1 Afel

501 ACAACTCCGCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

ApaL1
BmgB1

Age1 BsrB1 BseR1

601 CCGGTCGCCACCATGAGCGGGGGCGAGGAGCTGTTTCGCTGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCCAGCGGTGGTACTCGCCCCGCTCCTCGACAAGCGACCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTCAGTTCGCACG

TagCFP > M S G G E E L F A G I V P V L I E L D G D V H G H K F S V R

BsaXb BstE2
Ale1

701 GCGGTGAGGGAGAGGGCGACGCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCAC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 CGCCACTCCCTCTCCCCTGCGGCTGATGCCGTTTCGACCTCTAGTTCGAAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGACCGGGTGGGACCACTGGTG

TagCFP > G E G E G D A D Y G K L E I K F I C T T G K L P V P W P T L V T T

BstAP Xmn1

801 CCTCGCTGGGGCATCCAGTGCTTCGCCGCTACCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 GGAGCGGACCCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGCTGAAGAAGTTCTCGCGGTACGGGCTCCCGATGTAGGTCCTCGCG

TagCFP > L A W G I Q C F A R Y P E H M K M N D F F K S A M P E G Y I Q E R

SpDon
Ale1

Sac2 SpDon

901 ACCATCCACTTCCAGGACGACGGCAAGTACAAGACCCGCGCGAGGTGAAGTTTCGAGGGCGACACCCTGGTGAACCGCGTCGAGCTGAAGGGCGAGGGCT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
 TGGTAGGTGAAGGTCTGCTGCCGTTTCATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGCAGCTCGACTTCCCCTCCCCT

TagCFP > T I H F Q D D G K Y K T R G E V K F E G D T L V N R V E L K G E G F


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                                Eco57                               Bmr1
                                |                               |
TCCTATGTGGGCGACGAGGCCAGAGCAAGAGAGGCATCCTCACCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGAAAA
1501 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 1600
AGGATACACCCGCTGCTCCGGGTCTCGTTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCTTTT
beta-actin > S Y V G D E A Q S K R G I L T L K Y P I E H G I V T N W D D M E K I

                                BseR1
                                Dra3
                                BstAP
                                |
TCTGGCACCACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGTCTGTGACCGAGGCCCCCTGAACCCCAAGGCCAACCGCGAGAA
1601 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 1700
AGACCGTGGTGTGGAAGATGTTACTCGACGCACACCGAGGGCTCCTCGTGGGGCACGACGACTGGCTCCGGGGGACTTGGGGTTCCGGTTGGCGCTCTT
beta-actin > W H H T F Y N E L R V A P E E H P V L L T E A P L N P K A N R E K

                                BsaI                               BseY1
                                |                               |
GATGACCCAGATCATGTTTGTGAGACCTTCAACACCCCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCAGC
1701 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 1800
CTACTGGGTCTAGTACAAACTCTGGAAGTTGTGGGGTCCGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCCGGCATGGTGGACCGTAG
beta-actin > M T Q I M F E T F N T P A M Y V A I Q A V L S L Y A S G R T T G I

                                BstE2                               Bcg1a                               Bcg1b                               Xcm1
                                PflF1 | Dra3 | SpAcc | Bcg1b | Xcm1 |
                                | | | | | | | | | |
GTGATGGACTCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACC
1801 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 1900
CACTACCTGAGGCCACTGCCCCAGTGGGTGTGACACGGGTAGATGCTCCCCATACGGGAGGGGGTACGGTAGGACGCAGACCTGGACCCGACCCGCCCTGG
beta-actin > V M D S G D G V T H T V P I Y E G Y A L P H A I L R L D L A G R D L

                                BspH1                               SpDon                               Eag1                               BsrB1                               BsaXa
                                |                               |                               |                               |                               |
TGACTGACTACCTCATGAAGATCCTCACCGAGCGGGCTACAGCTTACCACCACGGCCGAGCGGAAATCGTGCCTGACATTAAGGAGAAGCTGTGCTA
1901 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 2000
ACTGACTGATGGAGTACTTCTAGGAGTGGCTCGCGCCGATGTCTGAAGTGGTGGTGGCCGGCTCGCCCTTTAGCACGCACTGTAATTCCTCTTCGACACGAT
beta-actin > T D Y L M K I L T E R G Y S F T T T A E R E I V R D I K E K L C Y
```

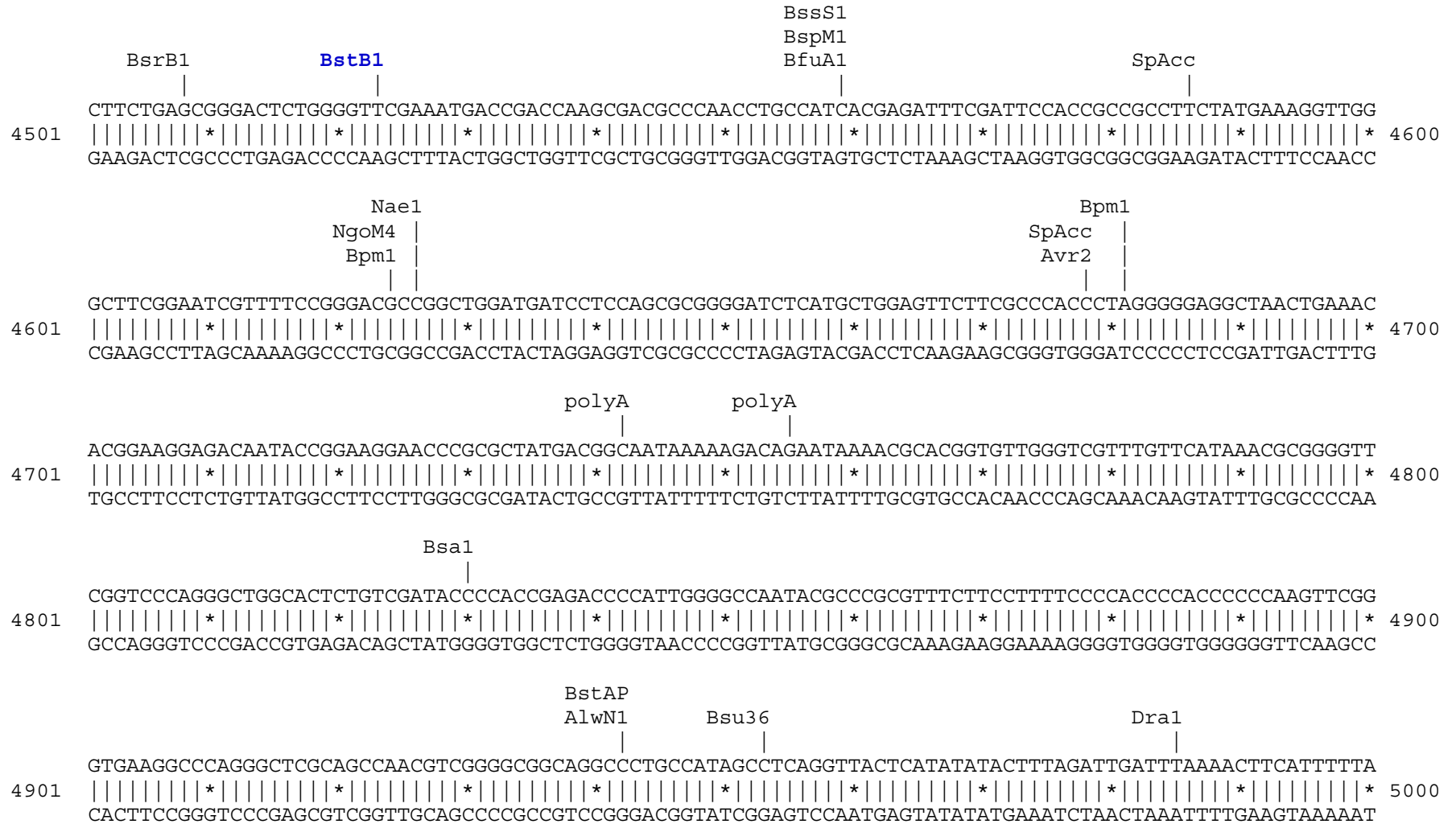
```

                                     Sap1
                                     Ear1
                                     SpAcc
          BsaXb           Msc1      BseR1           Xcm1           Bpm1           Drd1
          |               |         |               |             |             |
2001  CGTCGCCCTGGACTTCGAGCAAGAGATGGCCACGGCTGCTTCCAGCTCCTCCCTGGAGAAGAGCTACGAGCTGCCTGACGGCCAGGTCATCACCATTGGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
      GCAGCGGGACCTGAAGCTCGTTCTCTACCGGTGCCGACGAAGGTCGAGGAGGGACCTCTTCTCGATGCTCGACGGACTGCCGGTCCAGTAGTGGTAACCG
beta-actin > V A L D F E Q E M A T A A S S S S L E K S Y E L P D G Q V I T I G

          BsrD1           Bsu36           SpAcc           BspH1
          BsrB1           |         Ear1           |
          |               |         |             |
2101  AATGAGCGGTTCGCTGCCCTGAGGCACTCTTCCAGCCTTCTTCTGGGCATGGAGTCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
      TTACTCGCCAAGGCGACGGGACTCCGTGAGAAGGTCGGAAGGAAGGACCCGTACCTCAGGACACCGTAGGTGCTTTGATGGAAGTTGAGGTAGTACTTCA
beta-actin > N E R F R C P E A L F Q P S F L G M E S C G I H E T T F N S I M K C

          BmgB1           BsrD1           Bts1
          |               |             |
2201  GTGACGTGGACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
      CACTGCACCTGTAGGCGTTTCTGGACATGCGGTTGTGTACGACAGACCGCCGTGGTGGTACATGGGACCGTAACGGCTGTCCTACGTCTTCTCTAGTG
beta-actin > D V D I R K D L Y A N T V L S G G T T M Y P G I A D R M Q K E I T

          BseY1           BseR1           Bpu10           Scal
          |               |         |             |
2301  TGCCCTGGCACCCAGCACAAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAAGTACTCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      ACGGGACCGTGGGTCTGTTACTTCTAGTTCTAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCGGAGCGACAGGTGG
beta-actin > A L A P S T M K I K I I A P P E R K Y S V W I G G S I L A S L S T
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                SpAcc                Drd1                BpuE1                SpAcc
                |                    |                    |                    |
AGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGG
5601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
TCCCCCTTTCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATAACC

                SpDon
                BspLU|
Eci1          |
AAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTTCTGCGTTATCCCCTGATTCTGTGGATAACC
5701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
TTTTTTCGGTTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGG

                Nsi1
                BfrB1 |
                |
GTATTACCGCCATGCAT
5801  |||||*||||| 5817
CATAATGGCGGTACGTA

```

Found:

Aat2	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsg1	Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstE2
Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoRV	Fsp1	Hpa1
Kas1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1	polyA
Psi1	Pvu2	Rsr2	Sac2	Sall	Sap1	Scal	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1
Ssp1	Stu1	Xba1	Xcm1	Xho1	Xmn1								

Unique:

Afe1 Age1 Ase1 BamHI Bbs1 BcgIa BcgIb Bcl1 Bgl2 BspEI BspLU BsrGI BstBI Cla1
EcoRV FspI HpaI MfeI MluI NdeI NheI Rsr2 Sac2 Sall Scal SexAI SfiI SmaI
SnaBI StuI XbaI XhoI XmnI

Not found:

AarI Acc65 AclI Afl2 AhdI ApaI AscI AsiSI BaeIa BaeIb BbvCI BlpI BsiWI BsmBI
BssH2 BstXI BstZI _Chi EcoK EcoNI EcoRI ScFRT FseI FspAI Hind3 I_Ceu KpnI loxP
NotI NruI PacI PmeI PmlI PshAI PspOM PstI PvuI SacI SanDI SbfI SgfI SgrAI
SpeI SrfI SwaI T3RNA T7RNA T7Ter PISce

Excluded by site complexity:

AccI AcI1 Afl3 AluI AlwI ApoI Ava1 Ava2 Ban1 Ban2 Bbv1 BceAI Bfa1 Bme15
BsaAI BsaHI BsaJI BsaWI BseM2 BsiE1 BsiH1 Bsl1 BsmAI BsmF1 Bsp12 BspCa BspCb Bsr1
BsrF1 BssK1 BstF5 BstNI BstUI 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 MspAI Mwo1 Nci1 Nla3 Nla4 Nsp1 Ple1
PpuM1 RsaI Sau3A Sau96 SfaNI SfcI Sml1 Sty1 Taq1 Tat1 Tfi1 Tse1 Tsp45 Tsp50
TspR1