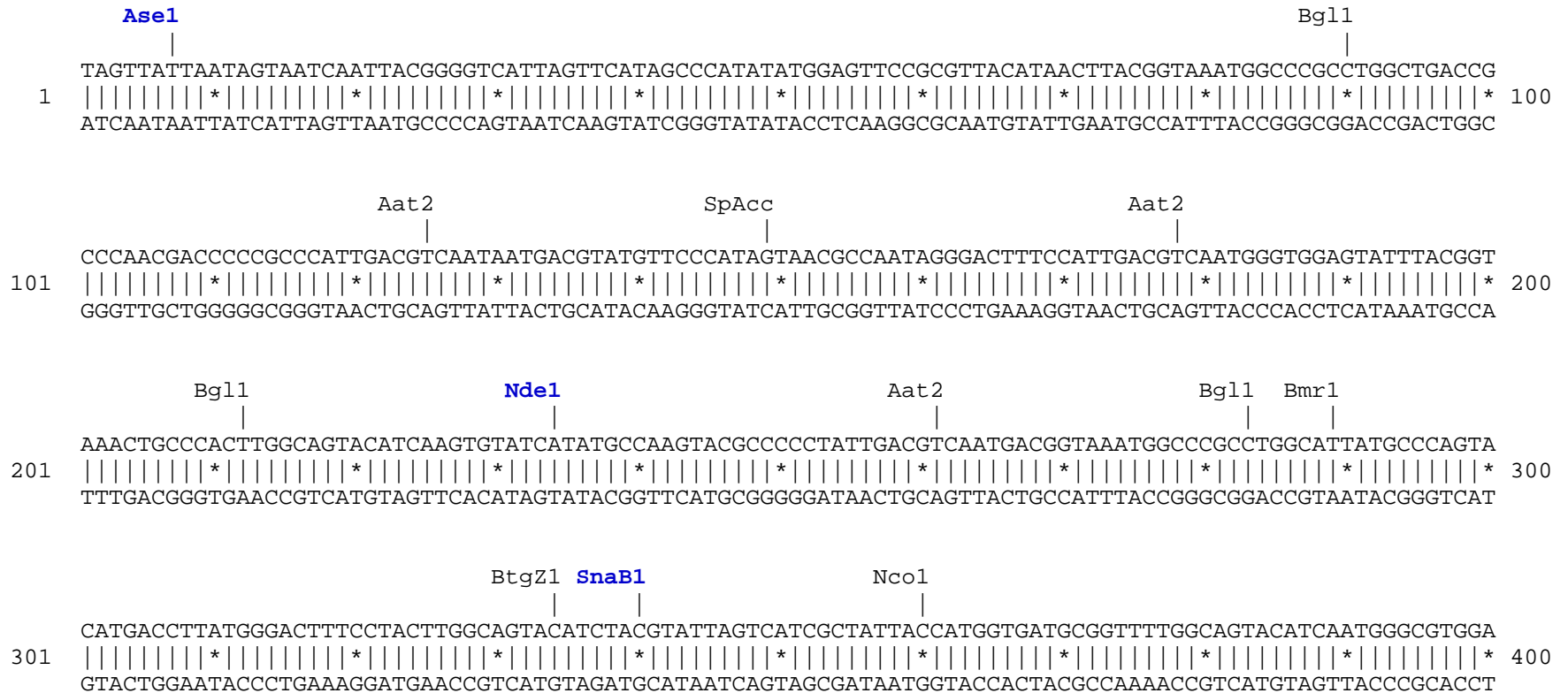


pTagFP635-actin vector restriction map

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).

TagFP635 amino acids are shown in red, beta-actin amino acids are shown in green, linker amino acids are shown in black.




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                                BseY1   Stul1                                 Bgl1
1001 | TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA | 1100
      | |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
      | AGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCGCGGACCTTCCGTCTTTCGCT
TagFP635 > P S N G P V M Q K K T L G W E A S T E M L Y P A D G G L E G R S D

                                BssS1   Eco57                                 Bbs1   BpuE1
1101 | CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGGCGTC | 1200
      | |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
      | GTACCGGGACTTCGAGCACCCGCCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCAG
TagFP635 > M A L K L V G G G H L I C N L K T T Y R S K K P A K N L K M P G V

                                Bbs1
                                SpAcc | |                               Bsa1   PshA1   BssS1   Dra3   Msc1   AlwN1
1201 | TACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA | 1300
      | |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
      | ATGATACACTGTCTTCTGACCTTCTTAGTTCTCCGGCTGTTTCTCTGGATGCAGCTCGTCTGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
TagFP635 > Y Y V D R R L E R I K E A D K E T Y V E Q H E V A V A R Y C D L P S

                                Xho1
SpAcc | |                               Bmr1   BspE1   Bgl12 | |                               EcoRV   BsaXb   Sal1 | |                               NgoM4
1301 | GCAAACCTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGCTATGGATGATGATATCGCCCGCCTCGTCTGCGACAACGGCTCCGGCATGTGCAAGGC | 1400
      | |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      | CGTTTGACCCCGTGTGTTGAATTAAGGCCTGAGTCTAGAGCTCGATACTACTACTATAGCGGCGGAGCAGCAGCTGTTGCCGAGGCCGTACACGTTCCG
beta-actin > K L G H K L N S G L R S R A M D D D I A A L V V D N G S G M C K A

                                Smal
Nael | |                               Bgl1 | |                               Nar1
                                Bbs1 | |                               Kas1 | |
1401 | CGGCTTCGCGGGCGACGATGCCCCCGGGCCGTCCTTCCCCTCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTGAGAAGGATTCC | 1500
      | |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
      | GCCGAAGCGCCCGCTGCTACGGGGGGCCCCGGCAGAAGGGGAGGTAGCACCCCGGGGTCCGTGGTCCCGCACTACCACCCGTACCCAGTCTTCCTAAGG
beta-actin > G F A G D D A P R A V F P S I V G R P R H Q G V M V G M G Q K D S

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                                     Eco57                               Bmr1
TATGTGGGCGACGAGGCCAGAGCAAGAGAGGCATCCTCACCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGAAAATCT
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
ATACACCCGCTGCTCCGGGTCTCGTTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCTTTTAGA
beta-actin > 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 W

                                     BseR1
                                     Dra3
                                     BstAP
GGCACCACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGCTGCTGACCGAGGCCCCCTGAACCCCAAGGCCAACCGCGAGAAGAT
1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
CCGTGGTGTGGAAGATGTTACTCGACGCACACCGAGGGCTCCTCGTGGGGCACGACGACTGGCTCCGGGGGACTTGGGGTTCCGGTTGGCGCTCTTCTA
beta-actin > 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 M

                                     Bsa1                               BseY1
GACCAGATCATGTTTGGAGACCTTCAACACCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCATCGTG
1701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
CTGGGTCTAGTACAAACTCTGGAAGTTGTGGGGTCCGGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCGGCATGGTGACCGTAGCAC
beta-actin > 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 V

                                     BstE2                               Bcg1a
                                     PflF1 |                               Dra3 |                               SpAcc
                                     |                               |                               |
ATGGACTCCGGTGACGGGGTCACCCACACTGTGCCCATCTACGAGGGGTATGCCCTCCCCCATGCCATCCTGCGTCTGGACCTGGCTGGCCGGGACCTGA
1801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
TACCTGAGGCCACTGCCCCAGTGGGTGTGACACGGGTAGATGCTCCCCATACGGGAGGGGGTACGGTAGGACGCAGACCTGGACCGACCGGCCCTGGACT
beta-actin > 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 T

                                     BspH1                               SpDon                               Eag1                               BsrB1                               BsaXa
CTGACTACCTCATGAAGATCCTCACCGAGCGGGCTACAGCTTACCACCACGGCCGAGCGGGAAATCGTGCGTGACATTAAGGAGAAGCTGTGCTACGT
1901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
GACTGATGGAGTACTTCTAGGAGTGGCTCGCGCCGATGTCTGAAGTGGTGGTGCCGGCTCGCCCTTTAGCACGCACTGTAATTCCTCTTCGACACGATGCA
beta-actin > 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 V
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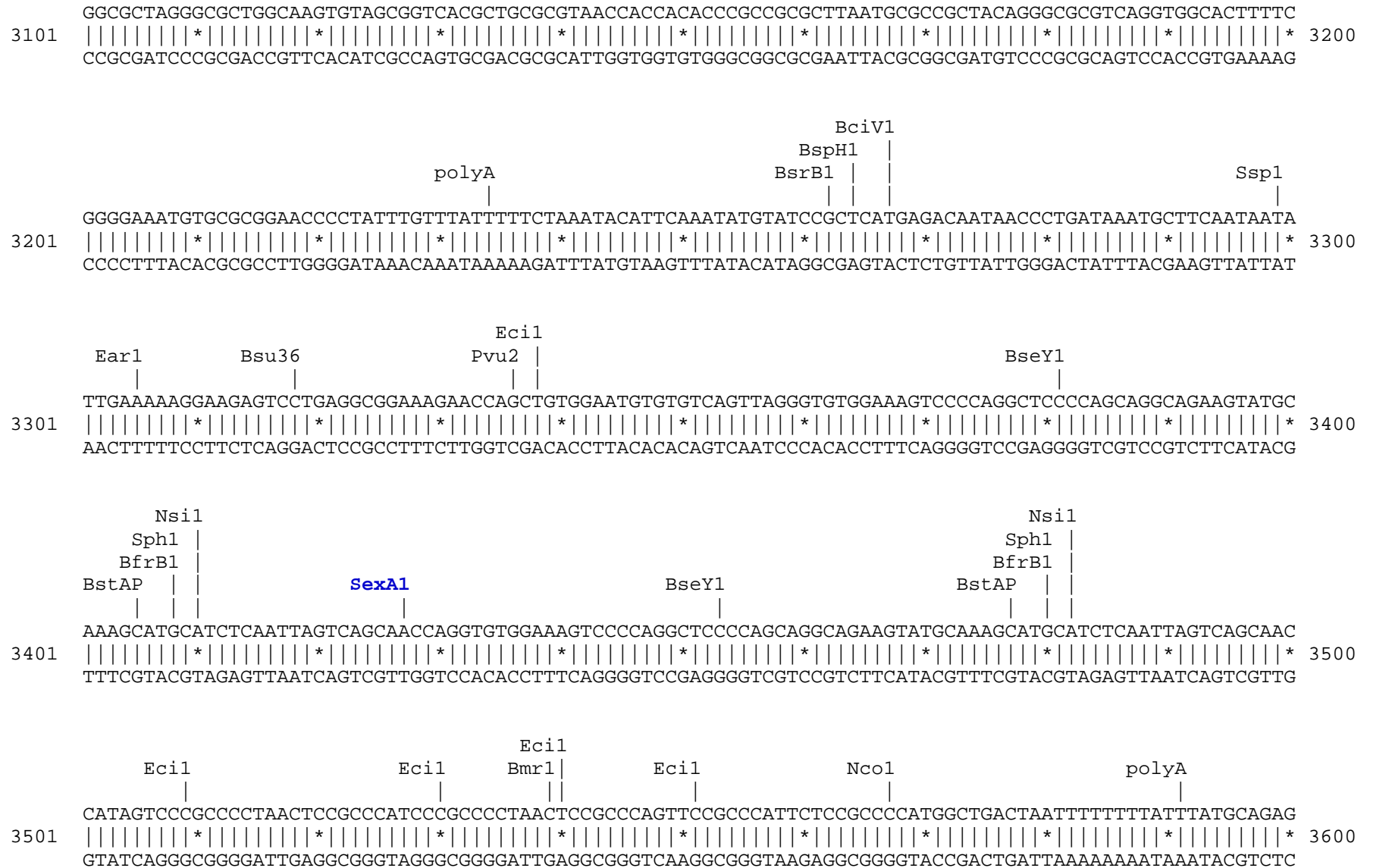
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2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
GCGGGACCTGAAGCTCGTTCTTCTACCAGTCCGACGAAGGTCGAGGAGGGACCTCTTCTCGATGCTCGACGGACTGCCGGTCCAGTAGTGTTAACCGTTA
beta-actin > A L D F E Q E M A T A A S S S S L E K S Y E L P D G Q V I T I G N

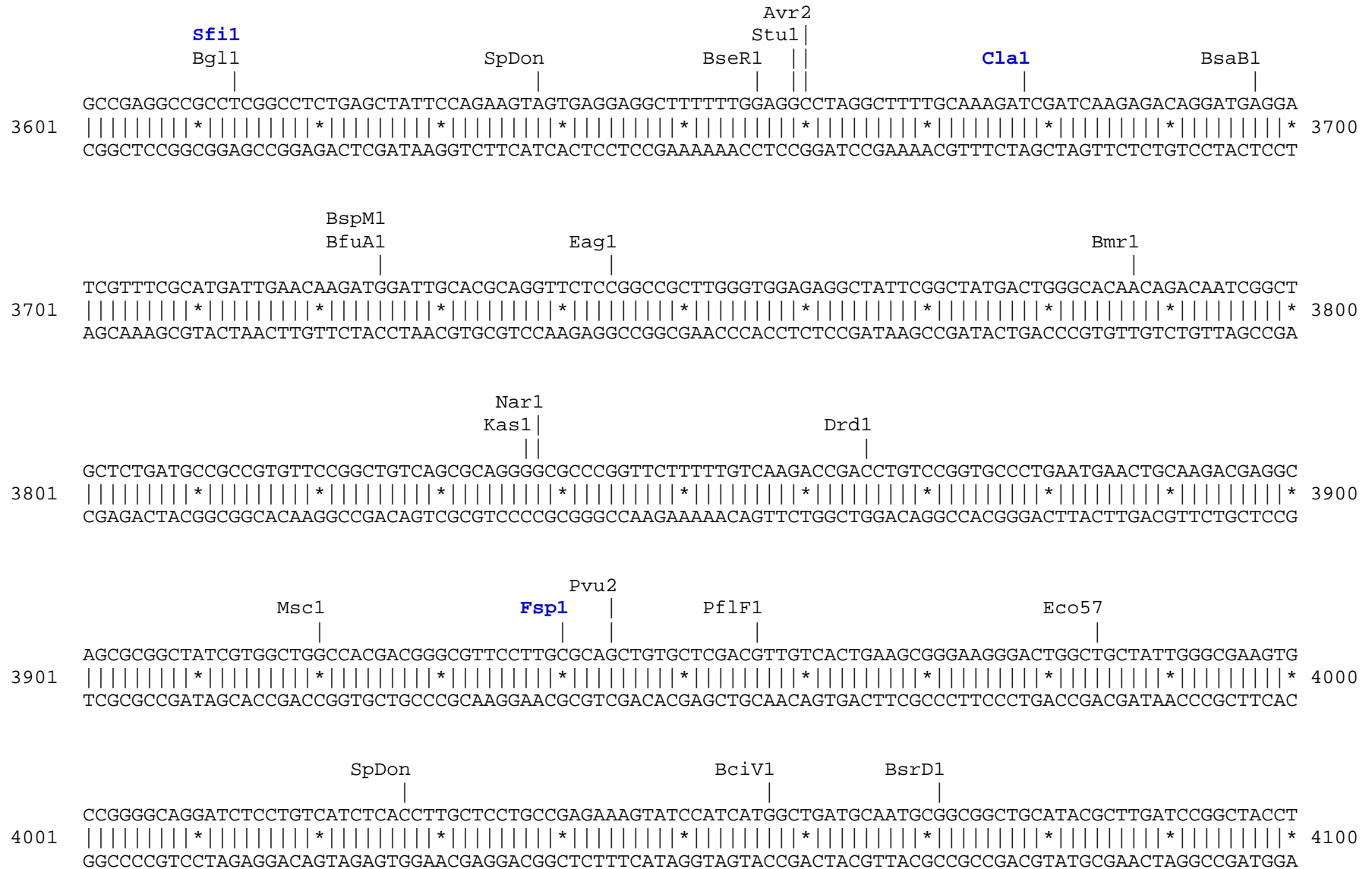
GAGCGGTTCCGCTGCCCTGAGGCACTCTTCCAGCCTTCCTTCCCTGGGCATGGAGTCCTGTGGCATCCACGAAACTACCTTCAACTCCATCATGAAGTGTG
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
CTCGCCAAGGCGACGGGACTCCCGTGAGAAGGTCGGAAGGAAGGACCCGTACCTCAGGACACCGTAGGTGCTTTGATGGAAGTTGAGGTAGTACTTCACAC
beta-actin > 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 D

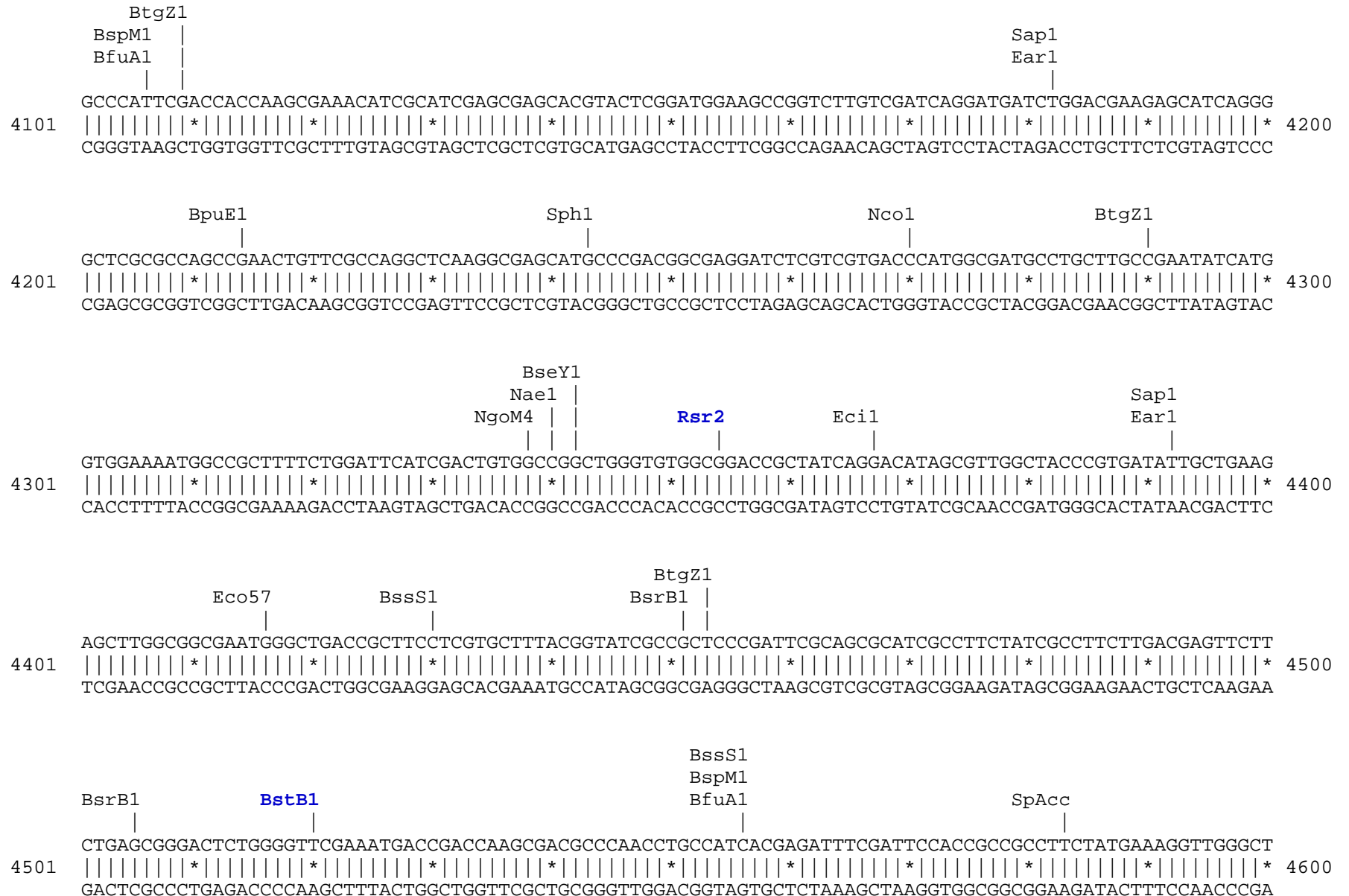
ACGTGGACATCCGCAAAGACCTGTACGCCAACACAGTGCTGTCTGGCGGCACCACCATGTACCCTGGCATTGCCGACAGGATGCAGAAGGAGATCACTGC
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
TGCACCTGTAGGCGTTTCTGGACATGCGGTTGTGTACAGACAGACCCTGGTGGTACATGGGACCGTAACGGCTGTCTCTACGTCTTCTCTAGTGACG
beta-actin > 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 A

CCTGGCACCCAGCACAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCCGTGTGGATCGGCGGCTCCATCCTGGCCTCGCTGTCCACCTTC
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
GGACCGTGGGTCGTGTTACTTCTAGTTCTAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCGGAGCGACAGGTGGAAG
beta-actin > 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 F

CAGCAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCCTCCATCGTCCACCGCAAATGCTTCTAGGGATCCACCGGATCTAGATAACTGATCA
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
GTCGTCTACACCTAGTCGTTTCGTCCTCATACTGCTCAGGCCGGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTGACTAGT
beta-actin > Q Q M W I S K Q E Y D E S G P S I V H R K C F *







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          NaeI
      NgoM4 |
      BpmI  |
          |
TCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACG
4601 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4700
AGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGC

          polyA      polyA
          |           |
GAAGGAGACAATAACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACGCGGGGTTCGG
4701 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4800
CTTCCTCTGTTATGGCCTTCCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTTCGCGTCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCC

          BsaI
          |
TCCCAGGGCTGGCACTCTGTTCGATACCCACCCAGACCCCATTTGGGGCCAATACGCCCGCGTTTTCTTCTTTTCCCACCCCACCCCCAAGTTCGGGTG
4801 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4900
AGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCAC

          BstAP
          AlwNI      Bsu36
          |           |
AAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTTAATT
4901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5000
TTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAA

          DraI
          |
TAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATC
5001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5100
ATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAG

          BpuE1
          |
AAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACCCAGCTACCAGCGGTGGTTTTGTTTCCGGATCAAGAGC
5101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5200
TTTCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTCCACCAAACAAACGGCCTAGTTCTCG

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          Eco57                               SpAcc
          |                                   |
5201 TACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATAACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAATC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    ATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAG

          AlwN1                               BpuE1
          |                                   |
5301 TGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    ACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATC

          ApaL1   BseY1
          |       |
5401 TTACCGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
    AATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCTGGGTGCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCGCAC

          BciV1
          |
          SpAcc   Eci1   BssS1
          |       |       |
5501 AGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
    TCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCC

          SpAcc   Drd1   BpuE1   SpAcc
          |       |       |       |
5601 GGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
    CCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTT

          Eci1   SpDon
          |       |
          BspLU
          |
5701 AACGCCAGCAACGCGGCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
    TTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCAT

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          NsiI
        BfrB1 |
          |   |
    TTACCGCCATGCAT
5801  |||||*||||| 5814
    AATGGCGGTACGTA

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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	Bsm1
BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstE2	Bsu36	BtgZ1	Bts1	Clal
Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoRV	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Msc1	Nae1
Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	polyA	PshA1	Psi1	Pvu2	Rsr2	Sall1	Sap1	Scal
SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xho1			

Unique:

Afe1	Age1	Ale1	Ase1	BamH1	Bcg1a	Bcg1b	Bcl1	Bgl2	BmgB1	Bpu10	BspE1	BspLU	BsrG1	BstB1
BstE2	Clal	EcoRV	Fsp1	Hpa1	Mfe1	Mlu1	Nde1	Nhe1	PshA1	Rsr2	Sall1	Scal	SexA1	Sfi1
Sma1	SnaB1	Xba1	Xho1											

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	Blp1	Bsg1	BsiW1	BsmB1
BssH2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoR1	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3
I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	PflM1	Pme1	Pml1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP
R4atR	Sac1	Sac2	SanD1	Sbf1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce	Xmn1

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	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					