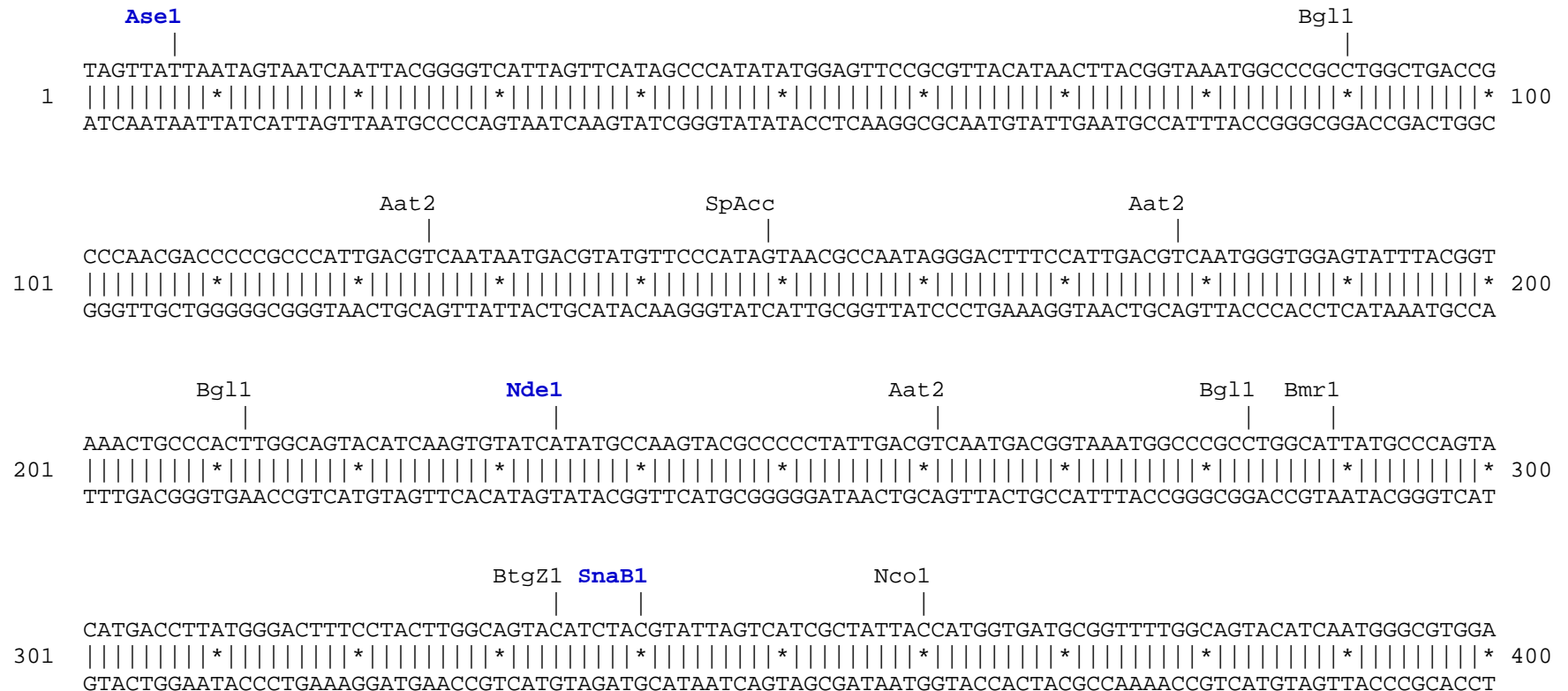


pTagRFP-keratin vector restriction map

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 base pairs 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). TagRFP amino acids are shown in red, Keratin amino acids are shown in green, linker amino acids are shown in black.



```

                                     Aat2                                     Eci1
                                     |                                     |
TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAAATCAACGGGACTTTCCAAAATGTCGTA
401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                     Nhe1
                                     |
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCACCA
501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
TGTTGAGGCGGGGTAACCTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTGGT

Keratin >
                                     BseY1
                                     Nar1 | Nar1
                                     Kas1 | Kas1 | Eag1
                                     | | |
TGAGCTTCACCACTCGCTCCACCTTCTCCACCAACTACCGGTCCCTGGGCTCTGTCCAGGCGCCAGCTACGGCGCCCGGCCGGTCAGCAGCGCGGCCAG
601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
ACTCGAAGTGGTGAGCGAGGTGGAAGAGGTGGTTGATGGCCAGGGACCCGAGACAGGTCCGCGGGTTCGATGCCGCGGGCCGGCCAGTCGTGCGCGCCGGTC

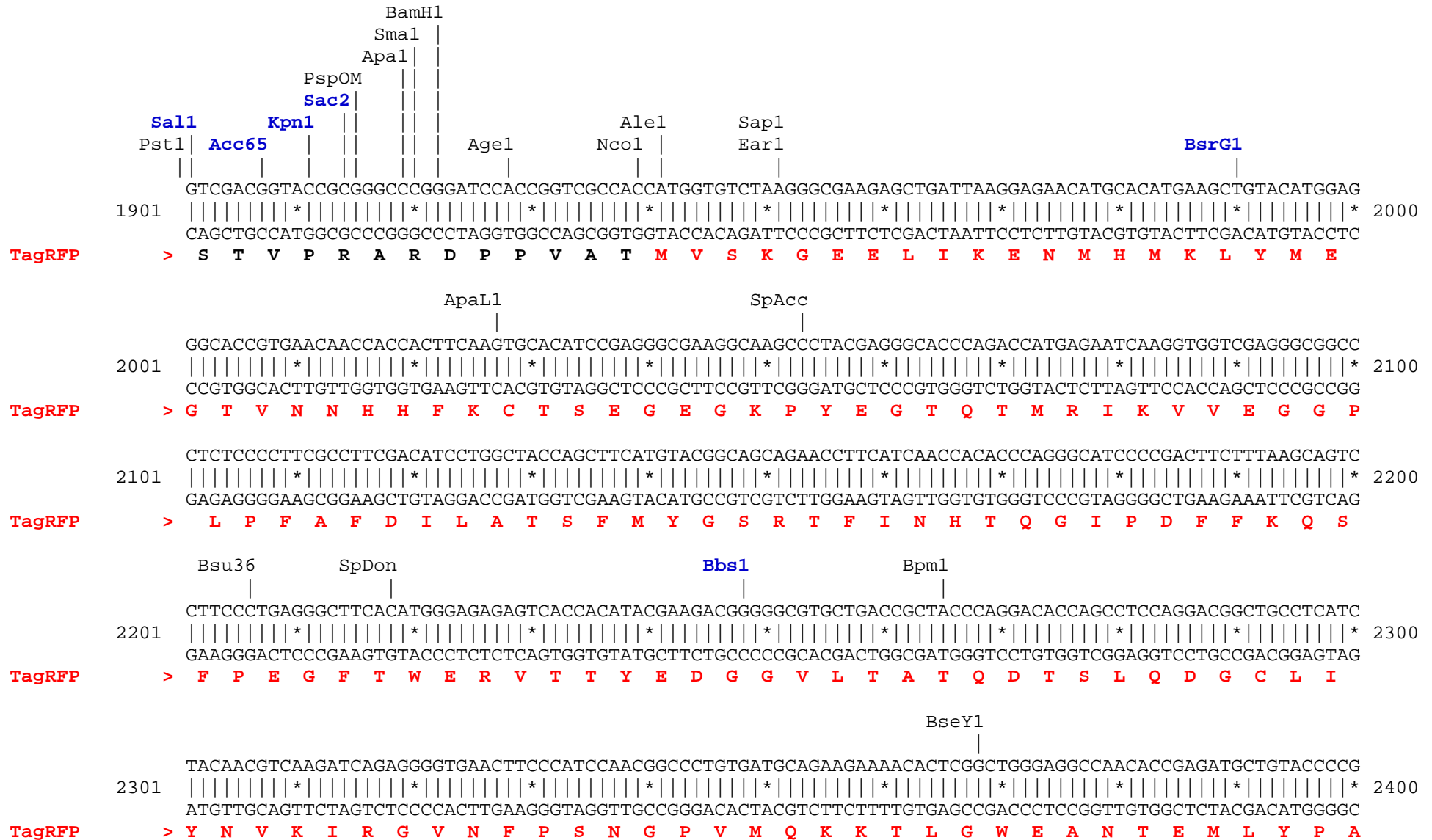
Keratin > S F T T R S T F S T N Y R S L G S V Q A P S Y G A R P V S S A A S

                                     BseY1           _Chi
                                     AlwN1           Eco57BsrB1 | Msc1
                                     |           | |           |
CGTCTATGCAGGCGCTGGGGGCTCTGGTTCCCGGATCTCCGTGTCCCGCTCCACCAGCTTCAGGGGCGGCATGGGGTCCGGGGGCTGGCCACCGGGATA
701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
GCAGATACGTCCGCGACCCCGAGACCAAGGGCCTAGAGGCACAGGGCGAGGTGGTTCGAAGTCCCGCCGTACCCCGAGGCCCCCGGACCGGTGGCCCTAT

Keratin > V Y A G A G G S G S R I S V S R S T S F R G G M G S G G L A T G I

                                     Bsa1           SpDon           Bsa1
                                     |           |           |
GCCGGGGTCTGGCAGGAATGGGAGGCATCCAGAACGAGAAGGAGACCATGCAAAGCCTGAACGACCGCCTGGCCTCTTACCTGGACAGAGTGAGGAGCC
801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
CGGCCCCCAGACCGTCCCTTACCCTCCGTAGGTCTTGTCTCTTCTCTGGTACGTTTCGGACTTGCTGGCGGACCGGAGAATGGACCTGTCTCACTCCTCGG

Keratin > A G G L A G M G G I Q N E K E T M Q S L N D R L A S Y L D R V R S L
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                Bgl1              BssS1              Eco57              BpuE1
                |                |                |                |
2401  CTGACGGCGGCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACC 2500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GACTGCCGCCGGACCTTCCGTCTTCGCTGTACCGGGACTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGG
TagRFP >  D G G L E G R S D M A L K L V G G G H L I C N F K T T Y R S K K P

                SpAcc              PflM1              Bsa1              PshA1              BssS1              Dra3
                |                |                |                |                |                |
2501  CGCTAAGAACCTCAAGATGCCCCGGCTCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTG 2600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGGTGTCTGACCTTTCTTAGTTCTCCGGCTGTTTCTCTGGATGCAGCTCGTCTGTGCTCCAC
TagRFP >  A K N L K M P G V Y Y V D H R L E R I K E A D K E T Y V E Q H E V

                Not1
                Eag1
                Msc1  AlwN1              SpAcc              Bmr1              BsrB1              Xba1              BsaB1
                |    |                |                |                |                |                |
2601  GCTGTGGCCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAAACTTAATTGAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAG 2700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTGTTGAATTAACCTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTC
TagRFP >  A V A R Y C D L P S K L G H K L N *

                Bsm1
                SpDon  Dra1              MfeI              Hpa1              polyA              PsiI
                |    |                |                |                |                |                |
2701  GTTTTACTTGGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATG 2800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTAC

                polyA              polyA              Bts1  Bsm1              Afl2
                |                |                |    |                |                |
2801  GTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGG 2900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGGAGTAGTTACATAGAATTCC

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      SpDon      Ssp1
      |          |
CGTAAATTGTAAGCGTTAATATTTTGTAAAAATTCGCGTTAAATTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGC AAAATCCCTTA
2901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3000
GCATTTAACATTTCGCAATTATAAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAAT

      PstI
      |
TAAATCAAAAAG AATAGACCGAGATAGGGTTGAGTGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAA
3001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3100
ATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCCTTTT

      BtgZ1      Dra3
      |         |
ACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCC TAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGA
3101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3200
TGGCAGATAGTCCCCTACCGGGTGATGCACCTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCT

      NaeI      NgoM4      BsrB1
      |         |         |
GCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGC
3201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3300
CGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTTCGCTTTCCTCGCCCGGATCCC CGGACCGTTTACATCG

GGTCACGCTGCGCGTAACCACCACACCCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATT
3301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3400
CCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGCGATGTCCC CGCAGTCCACCGTGAAAAGCCCTTTTACACGCGCCTTGGGGATAA

      BciV1      BspH1      BsrB1      polyA
      |         |         |         |
TGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCC TGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCCTGAGGCGG
3401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3500
ACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCC

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NsiI

SphI

BfrB1

BstAP

EciI

Pvu2

BseY1

3501 AAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
 TTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGT

NsiI

SphI

BfrB1

BstAP

EciI

BseY1

SexA1

3601 ACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCCGCCCTAACTCCGCCCA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
 TGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGT

sfiI

BglI

polyA

NcoI

EciI

BmrI

EciI

3701 TCCCCGCCCTAACTCCGCCAGTTCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCCTCGGCCTCTGAGCT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
 AGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGTACCGACTGATTAATAAATAAATAACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGA

BspM1

BfuA1

BsaB1

clal

BseR1

StuI

Avr2

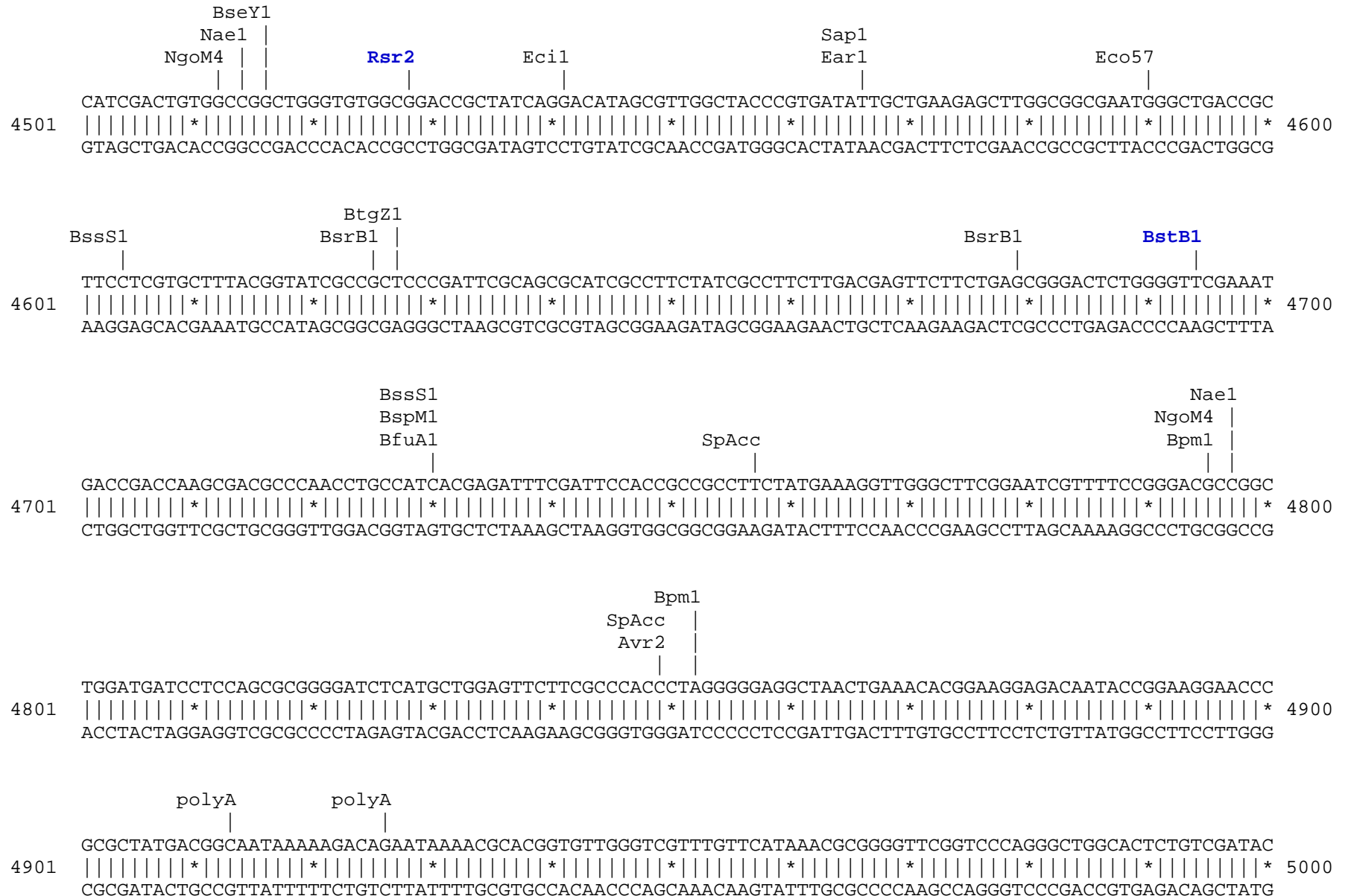
SpDon

3801 ATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGC AAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGG
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
 TAAGGTCTTCATCACTCCTCCGAAAAAACCCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAACTTGTCTACC

Bmr1

EagI

3901 ATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTG
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
 TAACGTGCGTCCAAGAGGCCGGCGAACCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGAC



Found:

Aat2	Acc65	Afl2	Age1	Ahd1	Ale1	AlwN1	Apa1	Apal1	Ase1	Avr2	BamH1	Bbs1	BbvC1
BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsg1	Bsm1	BsmB1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1
Bsu36	BtgZ1	Bts1	_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoN1	EcoR1
Fsp1	Hpa1	Kas1	Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1
PflF1	PflM1	polyA	PshA1	Psil	PspOM	Pst1	Pvu2	Rsr2	Sac2	Sall	Sand1	Sap1	Scal
SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stul	T7Ter	Xba1			

Unique:

Acc65	Afl2	Ase1	Bbs1	BbvC1	Bgl2	Bpu10	Bsg1	BspLU	BsrD1	BsrG1	BstB1	BstX1	Bts1
_Chi	Clal	EcoN1	EcoR1	Fsp1	Hpa1	Kpn1	Mfe1	Nde1	Nhe1	Not1	PflF1	PshA1	Rsr2
Sac2	Sall	Sand1	Scal	SexA1	Sfi1	SnaB1	T7Ter	Xba1					

Not found:

Aar1	Acl1	Afe1	Asc1	AsiS1	Baela	Baelb	Bcgl1a	Bcgl1b	Bcl1	Blp1	BmgB1	BsiW1	BspE1
BssH2	BstE2	BstZ1	EcoK	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu
loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sbf1	Sgf1
SgrA1	Spe1	Srf1	Swa1	T3RNA	T7RNA	PISce	Xcm1	Xho1	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	Faul	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													