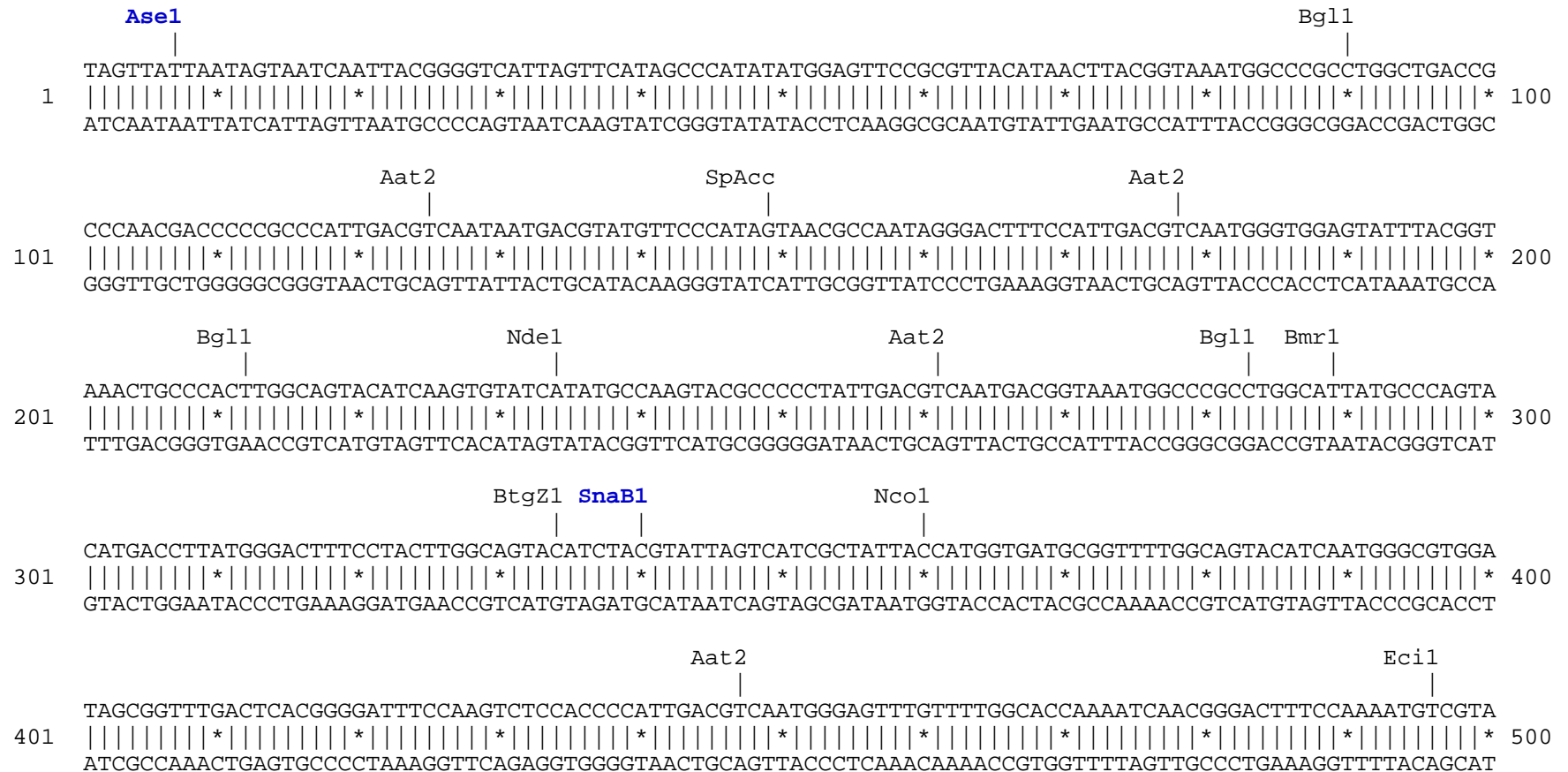


pTagRFP-tubulin vector restriction map

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). TagRFP amino acids are shown in red, tubulin amino acids are shown in green, linker amino acids are shown in black.



Nhe1 Afel

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Age1 Ale1 Sap1
 Nco1 | Ear1 BsrG1 ApaL1

601 CCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACCTTCAAGT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCCAGCGGTGGTACCACAGATTCCCGCTTCTCGACTAATTCCTCTTGTACGTGTACTTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTCA
TagRFP > M V S K G E E L I K E N M H M K L Y M E G T V N N H H F K C

SpAcc

701 GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCTTCGCTTCGACATCCTGGC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 CGTGTAGGCTCCCGCTTCCGTTCCGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCG
TagRFP > T S E G E G K P Y E G T Q T M R I K V V E G G P L P F A F D I L A

Bsu36 SpDon

801 TACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 ATGGTCGAAGTACATGCCGTCGTCTTGAAGTAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
TagRFP > T S F M Y G S R T F I N H T Q G I P D F F K Q S F P E G F T W E R

Bbs1 Bpm1 SpDon

901 GTCACCACATACGAAGACGGGGCGTGTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
 CAGTGGTGTATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
TagRFP > V T T Y E D G G V L T A T Q D T S L Q D G C L I Y N V K I R G V N F

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            BseY1                               Bgl1
            |                                   |
1001   TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
   |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| *
TagRFP > P S N G P V M Q K K T L G W E A N T E M L Y P A D G G L E G R S D

            BssS1       Eco57                               BpuE1
            |           |                                   |
1101   CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC
   |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| *
TagRFP > M A L K L V G G G H L I C N F K T T Y R S K K P A K N L K M P G V

            SpAcc
            PflM1                Bsa1                PshA1                BssS1 Dra3                Msc1                AlwN1
            |                   |                   |                   |                   |                   |
1201   TACTATGTGGACCACAGACTGGAAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
   |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| *
TagRFP > Y Y V D H 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

            SpAcc                Bmr1                BspE1                Bgl12                Xho1                Msc1                BsrD1
            |                   |                   |                   |                   |                   |                   |
1301   GCAAAC TGGGGC ACAAAC TTAATTCCGGACTCAGATCTCGAGTGCCTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTG
   |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| *
TagRFP/Tubulin > K L G H K L N S G L R S R V R E C I S I H V G Q A G V Q I G N A C

            BseY1                Sac1                BstX1                Msc1                Eco57BseR1                BsmB1
            |                   |                   |                   |                   |                   |
1401   CTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCAGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTTC
   |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| *
Tubulin > W E L Y C L E H G I Q P D G Q M P S D K T I G G G D D S F N T F F

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SpAcc Pml1 Sma1

1501 AGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTTGGAACCCACAGTCATTGATGAAGTTTCGCACTGGCACCTACCGCCAGCTCT 1600

Tubulin > S E T G A G K H V P R A V F V D L E P T V I D E V R T G T Y R Q L F

Bpu10 Sap1 Ear1

1601 TCCACCCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTATGCCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGTGTTGGA 1700

Tubulin > H P E Q L I T G K E D A A N N Y A R G H Y T I G K E I I D L V L D

EcoR1 Eco57ApaL1 Age1 Bbs1 Xcm1 BstX1 SpAcc Xmn1 SpDon

1701 CCGAATTTCGCAAGCTGGCTGACCAGTGCACCGGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTACCTCCCTGCTC 1800

Tubulin > R I R K L A D Q C T G L Q G F L V F H S F G G G T G S G F T S L L

BsmB1 Bpm1 BseY1 SpAcc Pvu2

1801 ATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTGGAGTTCTCCATTTACCCAGCACCCCAGGTTTCCACAGCTGTAGTTGAGCCCTACAAC 1900

Tubulin > M E R L S V D Y G K K S K L E F S I Y P A P Q V S T A V V E P Y N S

SpDon Bpm1 PshA1 EcoRV

1901 CCATCCTCACCACCCACACCACCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTTCGTAGAAACCTCGATATCGA 2000

Tubulin > I L T T H T T L E H S D C A F M V D N E A I Y D I C R R N L D I E

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                                Bts1
                                |
GCGCCCAACCTACTACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCTCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTGACA
2001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2100
CGCGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACCTGGACTGT
Tubulin > R P T Y T N L N R L I S Q I V S S I T A S L R F D G A L N V D L T

EcoR1           SexA1           MscI Nde1           SpAcc
|               |               |     |               |
GAATTCCAGACCAACCTGGTGCCCTACCCCCGCATCCACTTCCCTCTGGCCACATATGCCCTGTGCATCTCTGCTGAGAAAGCCTACCATGAACAGCTTT
2101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2200
CTTAAGGTCTGGTTGGACCACGGGATGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGTAGAGACGACTCTTTTCGGATGGTACTTGTTCGAAA
Tubulin > E F Q T N L V P Y P R I H F P L A T Y A P V I S A E K A Y H E Q L S

                               SpDon           SpDon
                               |               |
CTGTAGCAGAGATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTGTTGTACCG
2201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2300
GACATCGTCTCTAGTGGTTACGAACGAAACTCGGTCGGTGGTCTACCCTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAACATGGC
Tubulin > V A E I T N A C F E P A N Q M V K C D P R H G K Y M A C C L L Y R

SpAcc           BstX1           NcoI           SpDon
|               |               |               |
TGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGTT
2301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2400
ACCACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTTGGTTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTCCAA
Tubulin > G D V V P K D V N A A I A T I K T K R S I Q F V D W C P T G F K V

BmgBI           BsrD1           PflM1           Bgl1
|               |               |               |
TGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGTT
2301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2400
ACCACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTTGGTTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTCCAA
Tubulin > G D V V P K D V N A A I A T I K T K R S I Q F V D W C P T G F K V

                               MscI           Bsp1
                               |               |
GGCATCAACTACCAGCCTCCCCTACTGTGGTGCCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGG
2401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2500
CCGTAGTTGATGGTTCGGAGGGTGACACCACGGACCACCTCTGGACCGGTTCCATGTCTCTCGACACACGTACGACTCGTTGTGGTGTTCGGTAACGACTCC
Tubulin > G I N Y Q P P T V V P G G D L A K V Q R A V C M L S N T T A I A E A

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                                     BsaXb          Drd1          BsaXa          BtgZ1          Dra3
          |          |          |          |          |          |
3101   AACAAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAA
       |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 3200
       TTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTT

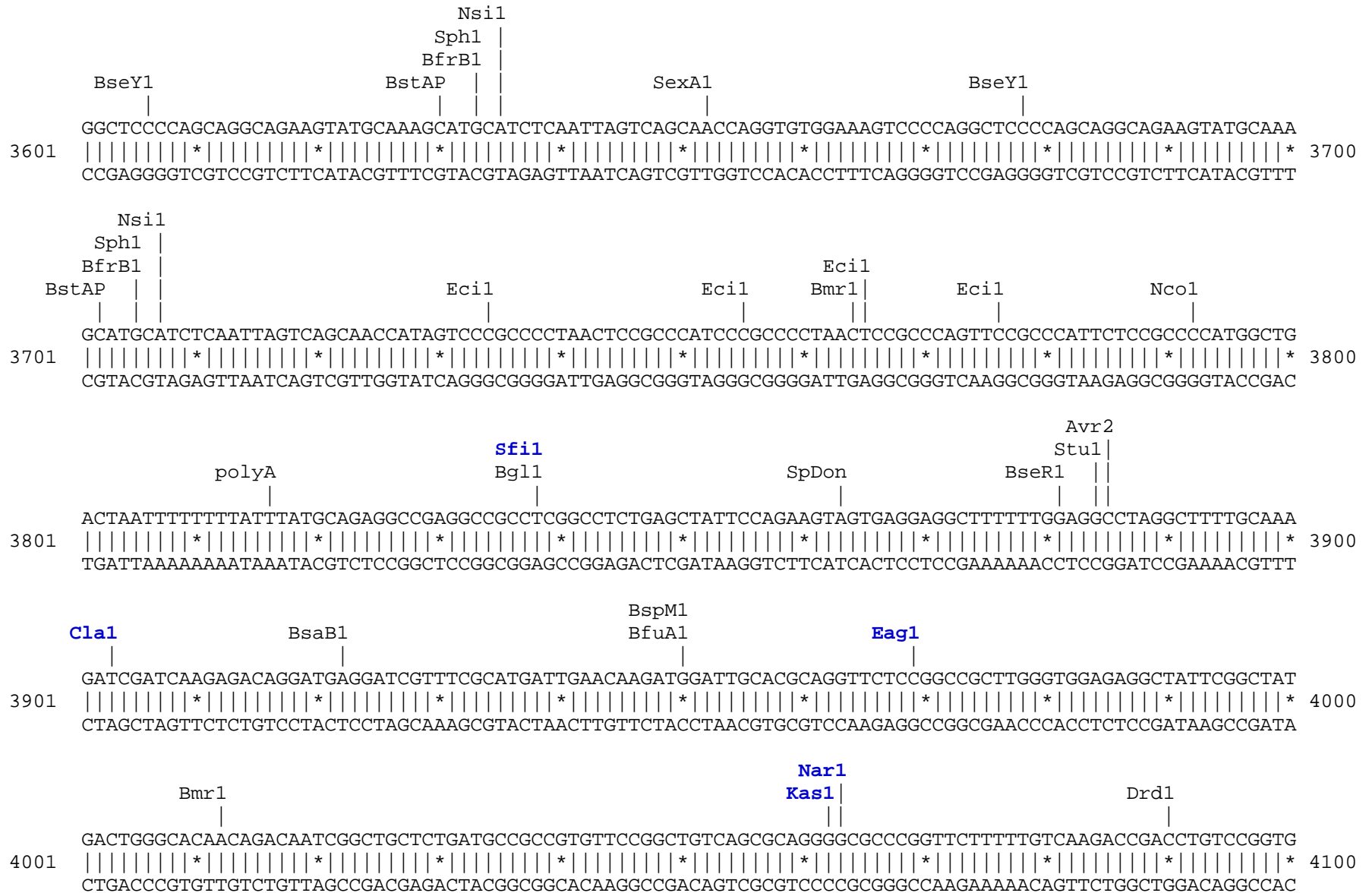
                                     SpAcc          Nae1          NgoM4
          |          |          |
3201   GTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAA
       |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 3300
       CAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTT

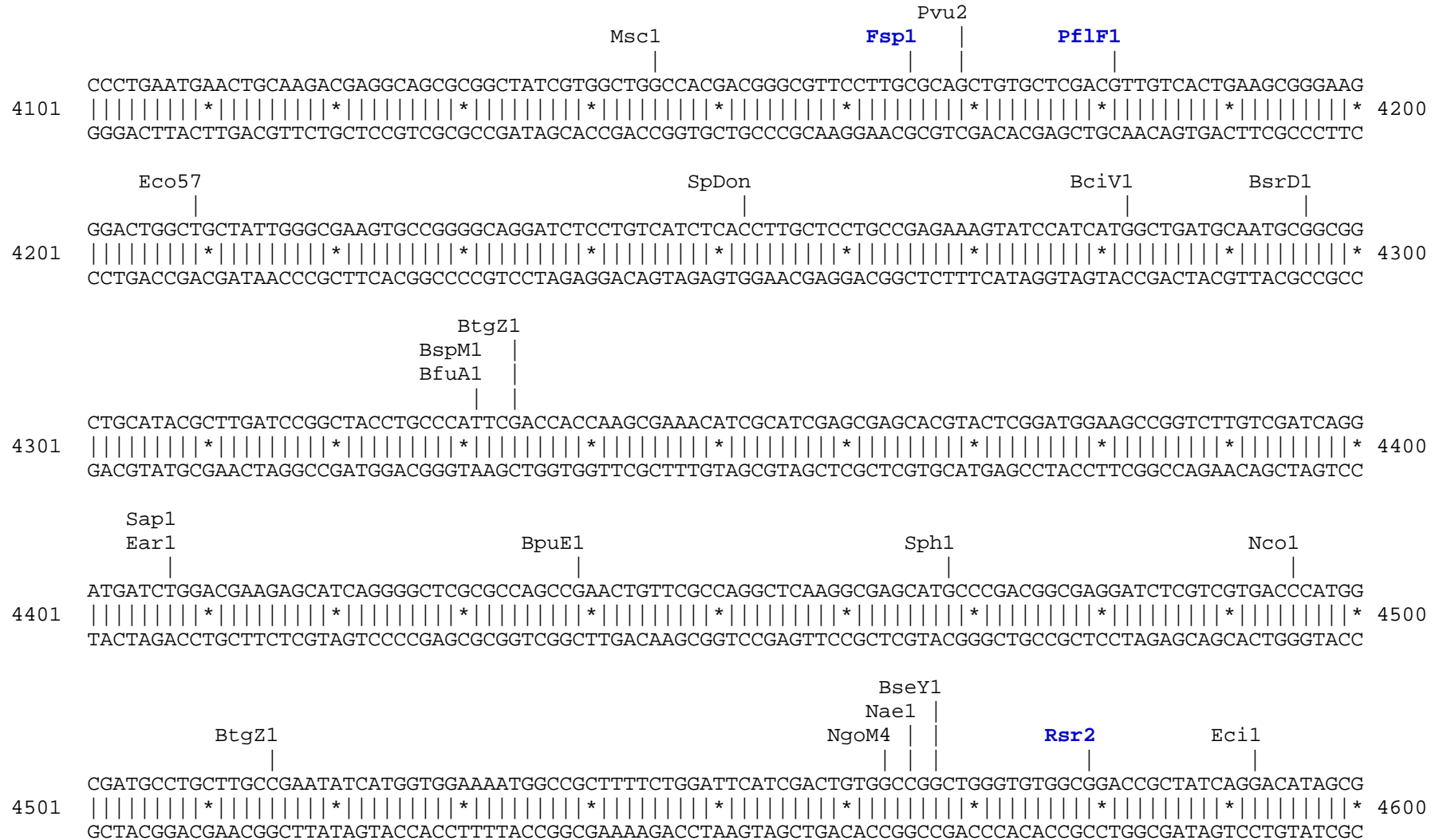
                                     BsrB1
          |
3301   GGAAGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTA
       |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 3400
       CCTTCCCTTCTTTCGCTTTCCTCGCCCCGCGATCCC CGGACCGTTTACATCGCCAGTGCAGCGCATTTGGTGGTGTGGGCGGGCGGAATTACGCGGCGAT

                                     BciV1          BspH1          BsrB1          polyA
          |          |          |          |          |
3401   CAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAAT
       |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 3500
       GTCCCGCGCAGTCCACCGTGAAAAGCCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTA

                                     Ssp1          Ear1          Bsu36          Ecil          Pvu2
          |          |          |          |          |
3501   AACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCTTGAGGGCGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCA
       |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 3600
       TTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGT

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                                         BstAP
                                         AlwN1     Bsu36
          SpDon
          |
          |
CCACCCACCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGA
5101 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5200
GGTGGGTGGGGGTTC AAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCT

          Dra1           Dra1           BspH1
          |             |             |
          |             |             |
TTGATTTAAAACTTCATTTTTAATTTAAAAAGGATCTAGGTGAAGATCCTTTTTTGTATAATCTCATGACCAAAAATCCCTTAAACGTGAGTTTTTCGTTCCACTG
5201 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5300
AACTAAATTTTGAAGTAAAAATTTAAATTTTCTAGATCCACTTCTAGGAAAACCTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGAC

                                         BpuE1
                                         |
                                         |
AGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGC AAACAAAAAACACCGCTACCAGCG
5301 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5400
TCGCAGTCTGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGCGAACGTTTGTTTTTTGGTGCGATGGTTCGC

          Eco57
          |
          |
GTGGTTTGTGTGCCGGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATAACAAATACTGTCTTCTAGTGTAGCCGT
5401 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5500
CACC AAACAAACGGCCTAGTTCGATGGTTGAGAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCA

                                         AlwN1           BpuE1
                                         |             |
                                         |             |
AGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCCTACATACTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTTCGTGTCT
5501 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5600
TCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGGACGATTAGGACAATGGTTCACCGACGACGGTCAACCGCTATTTCAGCACAGA

          ApaL1     BseY1
          |       |
          |       |
TACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTAC
5601 |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5700
ATGCCCCAACCTGAGTTCGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGTGGATG

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                                     BciV1
                                     Eci1
                                     |
                                     |
          SpAcc
          |
ACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAG
5701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
TGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGGCCTGTCCATAGGCCATTGCGCCGTCCCAGCCTTGTC

          BssS1
          |
          SpAcc
          |
          Drd1
          |
          BpuE1
          |
GAGAGCGCACGAGGGGAGCTTCCAGGGGGAAAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTC
5801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5900
CTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAG

          SpAcc
          |
          Eci1
          |
          SpDon
          |
          BspLU
          |
GTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTTACGGTTCTTGGCCTTTTGGCTGGCCTTTTGGCTCACATGTTCTTTCCTGCGTTA
5901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6000
CAGTCCCCCGCCTCGGATACCTTTTTGCGGTCTGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAAT

          NsiI
          |
          BfrB1
          |
          |
TCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6039
AGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	Baela	Baelb	BamH1	Bbs1	BbvC1	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpml	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa
BsaXb	BseR1	BseY1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP
BstB1	BstX1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoN1
EcoR1	EcoRV	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1
Nsi1	PflF1	PflM1	Pml1	polyA	PshA1	Psil	Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfi1	Sma1
SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xho1	Xmn1				

Unique:

Afe1	Ase1	Baela	Baelb	BamH1	BbvC1	Bcl1	Bgl2	Blp1	BmgB1	BsaXa	BsaXb	BspE1	BspLU
BsrG1	BstB1	Clal	Eag1	EcoRV	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nhe1	PflF1	Pml1
Rsr2	Sac1	Sfi1	Sma1	SnaB1	Xba1	Xcm1	Xho1	Xmn1					

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apal	Asc1	AsiS1	Bcgl1a	Bcgl1b	Bsg1	BsiW1	BssH2	BstE2
BstZ1	_Chi	EcoK	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1
PspOM	Pst1	Pvu1	Sac2	Sall	SanD1	Sbf1	Scal	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA
T7RNA	T7Ter	PISce											

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apol	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfal	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													