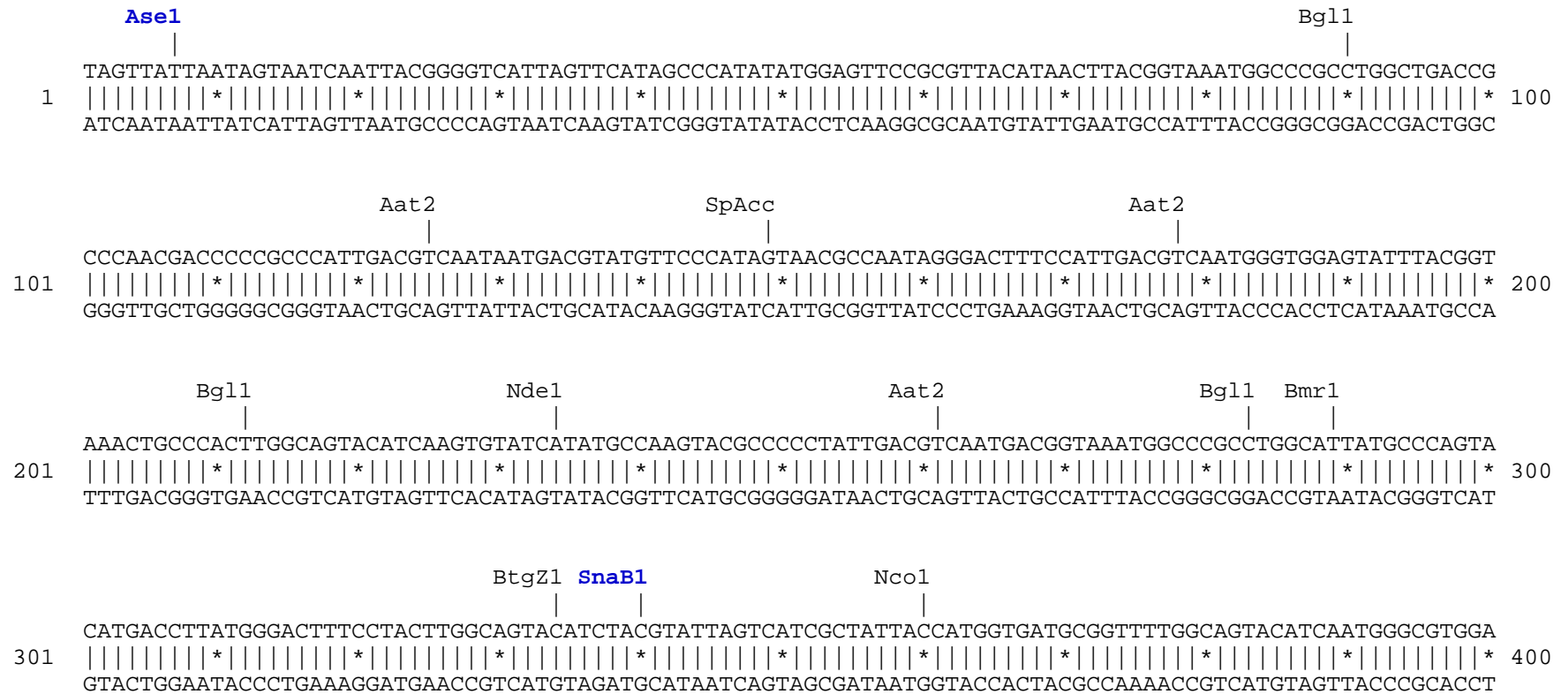


pTagFP635-tubulin vector restriction map

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). TagFP635 amino acids are shown in red, Tubulin amino acids are shown in green, linker amino acids are shown in black.



```

                                     Aat2                                     Eci1
                                     |                                     |
TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTTCGTA
401 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 500
ATCGCCAAACTGAGTGCCCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTTACAGCAT

                                     Nhe1 Afe1
                                     |     |
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 600
TGTTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCTGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Age1       Ale1       Sap1       BsrG1       ApaL1
|         |     |     |         |           |           |
CCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACACCACCACTTCAAGT
601 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 700
GGCCAGCGGTGGTACCACAGATTCCCCTTCTCGACTAATTCCCTCTTGTACGTGTACTTTCGACATGTACCTCCCCTGGGCACTTGTTGGTGTTGAAGTTCA
TagFP635 >      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
                                     |
GCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGC
701 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 800
CGTGTAGGCTCCCGCTTCCGTTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCCTGGGAGAGGGGAAGCGGAAGCTGTAGGACCG
TagFP635 >  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
                                     |           |
TACCAGCTTCATGTACGGCAGCAAAAACCTTCATCAACCACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGA
801 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 900
ATGGTCAAGTACATGCCGTTCGTTTTGGAAGTAGTTGGTGTGGGTCCCCTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCT
TagFP635 >  T S F M Y G S K 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
                                     |           |
GTCACCACATACGAAGACGGGGCGTGTCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAAGT
901 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 1000
CAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGA
TagFP635 >  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   Stul1                               Bgl1
                                |         |                               |
TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA
1001 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1100
AGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
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

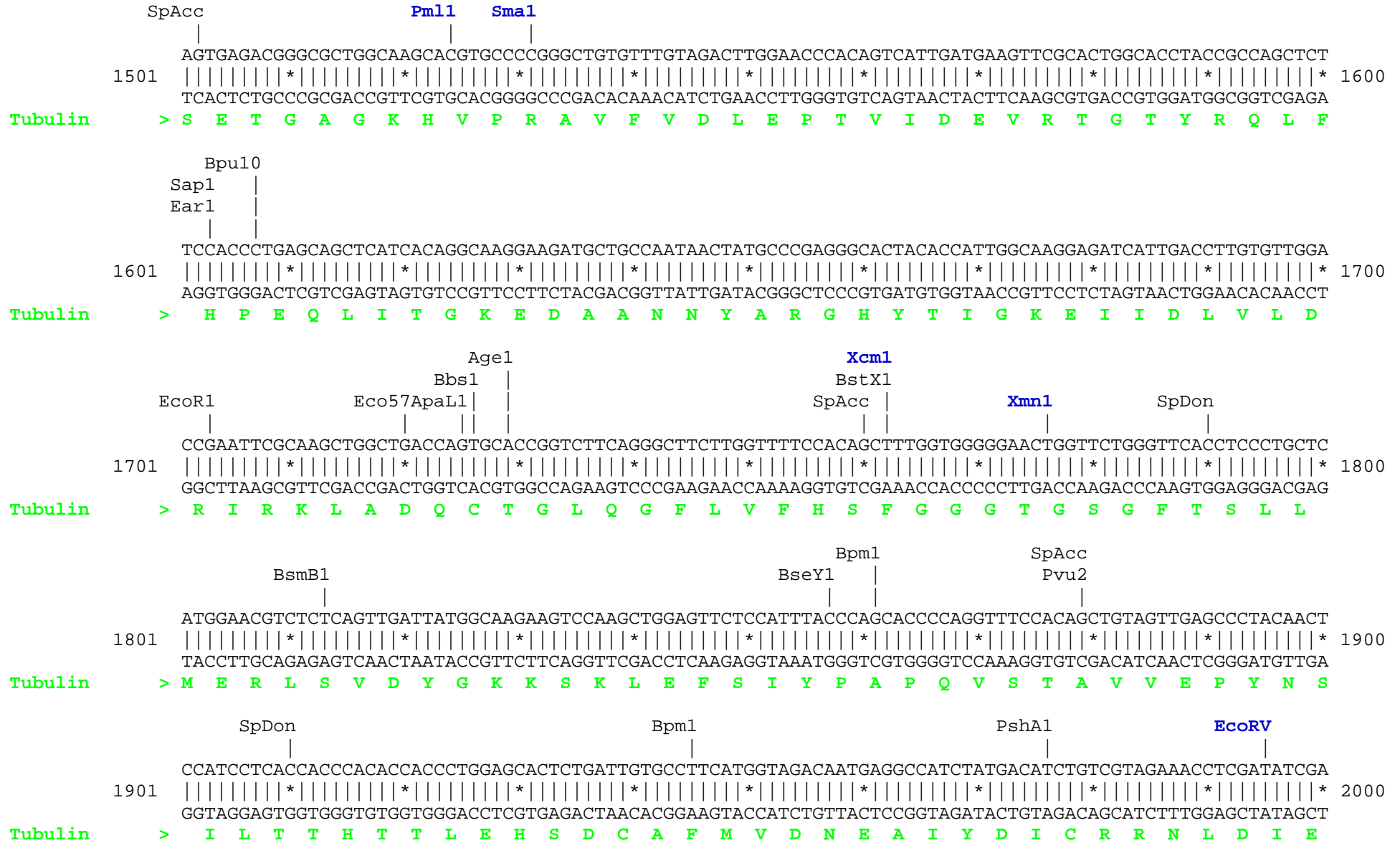
                                BssS1   Eco57                               Bbs1   BpuE1
                                |         |                               |         |
CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGGCGTC
1101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 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 |
                                |         |
TACTATGTGGACAGAAGACTGGAAAAGAAATCAAGGAGGCCGACAAAGAGACCTACGTTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA
1201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1300
ATGATACACCTGTCTTCTGACCTTTCTTAGTTCTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
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 |
                                |         |
                                Bgl2 |
                                |         |
                                Msc1 |
                                |         |
                                BsrD1 |
                                |         |
                                BstAP |
                                |         |
GCAAACCTGGGGCACAAACTTAATTCCGGACTCAGATCTCGAGTGCCTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAATGCCTG
1301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1400
CGTTTGACCCCGTGTTTGAATTAAGGCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGGTCCGACCACAGGTCTAACCGTTACGGAC
FP635/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

                                Msc1
                                |
                                BseY1 |
                                |         |
                                Sac1 |
                                |         |
                                BstX1 |
                                |         |
                                Eco57 |
                                |         |
                                BseR1 |
                                |         |
                                BsmB1 |
                                |         |
CTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACCTTCTTC
1401 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 1500
GACCTCGAGATGACGGACCTTGTGCCGTAGGTTCGGGCTACCGGTCTACGGTTCCTGTTCTGGTAACCCCTCCTCTACTGAGGAAGTTGTGGAAGAAG
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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                                     Bts1
                                     |
GCGCCCAACCTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGACCTGACA
2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
CGCGGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACCTGGACTGT
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 NdeI      SpAcc
|          |          |   |   |          |
GAATTCCAGACCAACCTGGTGCCTTACCCCGCATCCACTTCCCTCTGGCCACATATGCCCTGTTCATCTCTGCTGAGAAAGCCTACCATGAACAGCTTT
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
                                     |          |
CTGTAGCAGAGATCACCAATGCTTGTCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGTGCCTGTTGTACCG
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
GACATCGTCTCTAGTGGTTACGAACGAAACTCGGTTCGGTTGGTCTACCCTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAACATGGC
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

BmgB1      BsrD1      PflM1      Bgl1
|          |          |          |
TGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTCAAGGTT
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
ACCACTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTGGTTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAGTTCCAA
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      Blp1      Bpu10
                                     |          |          |
GGCATCAACTACCAGCCTCCCCTGTTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTGCTGAGG
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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StuI
|
CCTGGGCTCGCCTGGACCACAAGTTTGGACCTGATGTATGCCAAGCGTGCCTTTTGTTCCTACTGGTACGTGGGTGAGGGGATGGAGGAAGGCGAGTTTTTCAGA
2501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
GGACCCGAGCGGACCTGGTGTTCAAACTGGACTACATACGGTTCGCACGGAAACAAGTGACCATGCACCCACTCCCCTACCTCCTTCCGCTCAAAAAGTCT
Tubulin > W A R L D H K F D L M Y A K R A F V H W Y V G E G M E E G E F S E

EcoNI BpuEI BseRI BamHI
| | | |
GGCCCGTGAAGATATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATACTAAGGA
2601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
CCGGGCACTTCTATACCGACGGGAACCTTCTTAATACTCCTCCAACCACACCTAAGACAACCTTCTCTCCACTCCTTCTTCTCCTTATGATTCTCT
Tubulin > A R E D M A A L E K D Y E E V G V D S V E G E G E E E G E E Y *

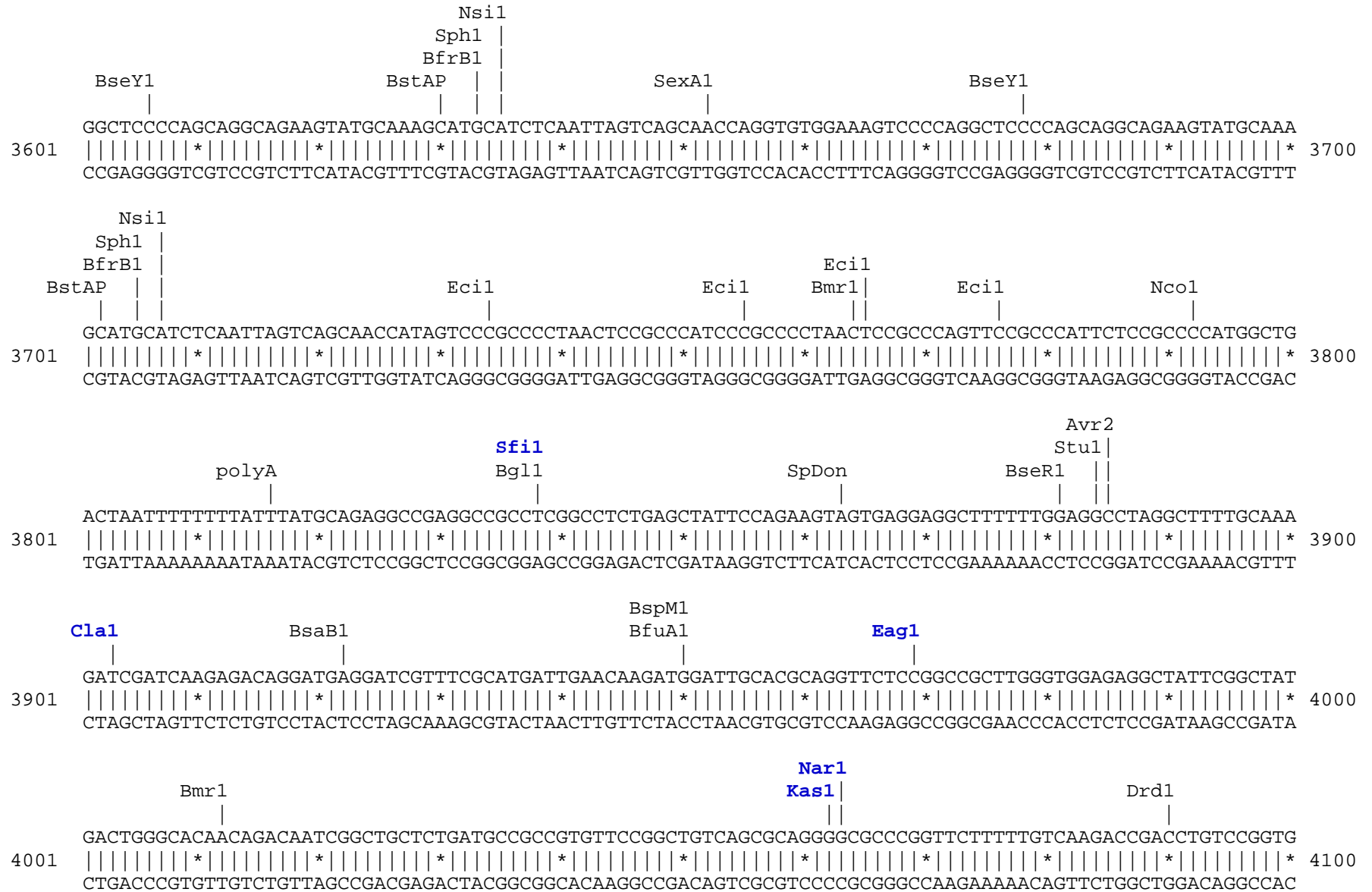
XbaI BclI BsaBI SpDon DraI
| | | | |
TCCACCGGATCTAGATAACTGATCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCTGAACCTGAAAC
2701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
AGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTG

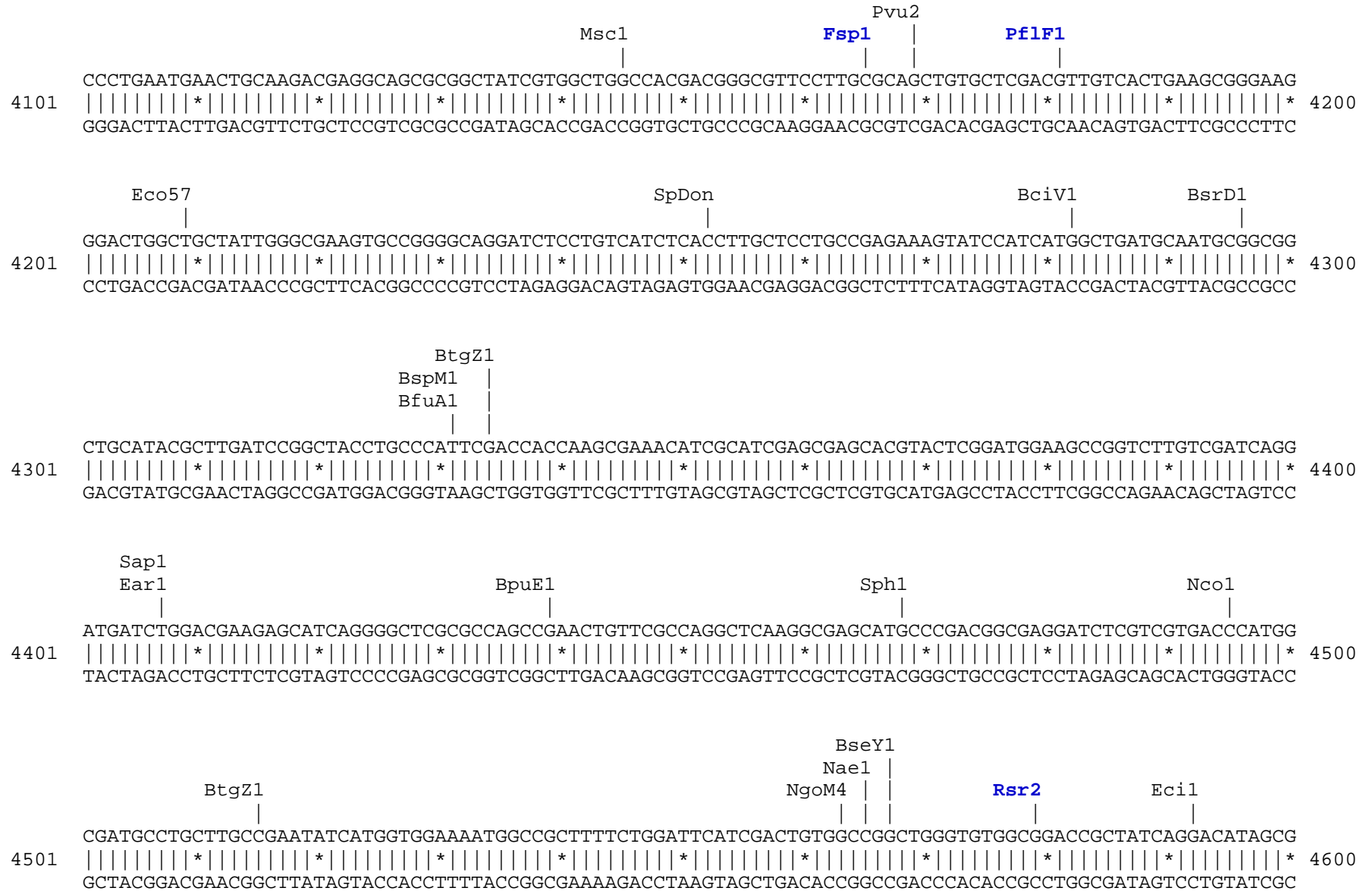
BsmI MfeI HpaI polyA PsiI polyA polyA
| | | | | | |
ATAAAATGAATGCAATTGTTGTTGTTAACTTGTATTATGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTT
2801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
TATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTATTTTCGTAAAAA

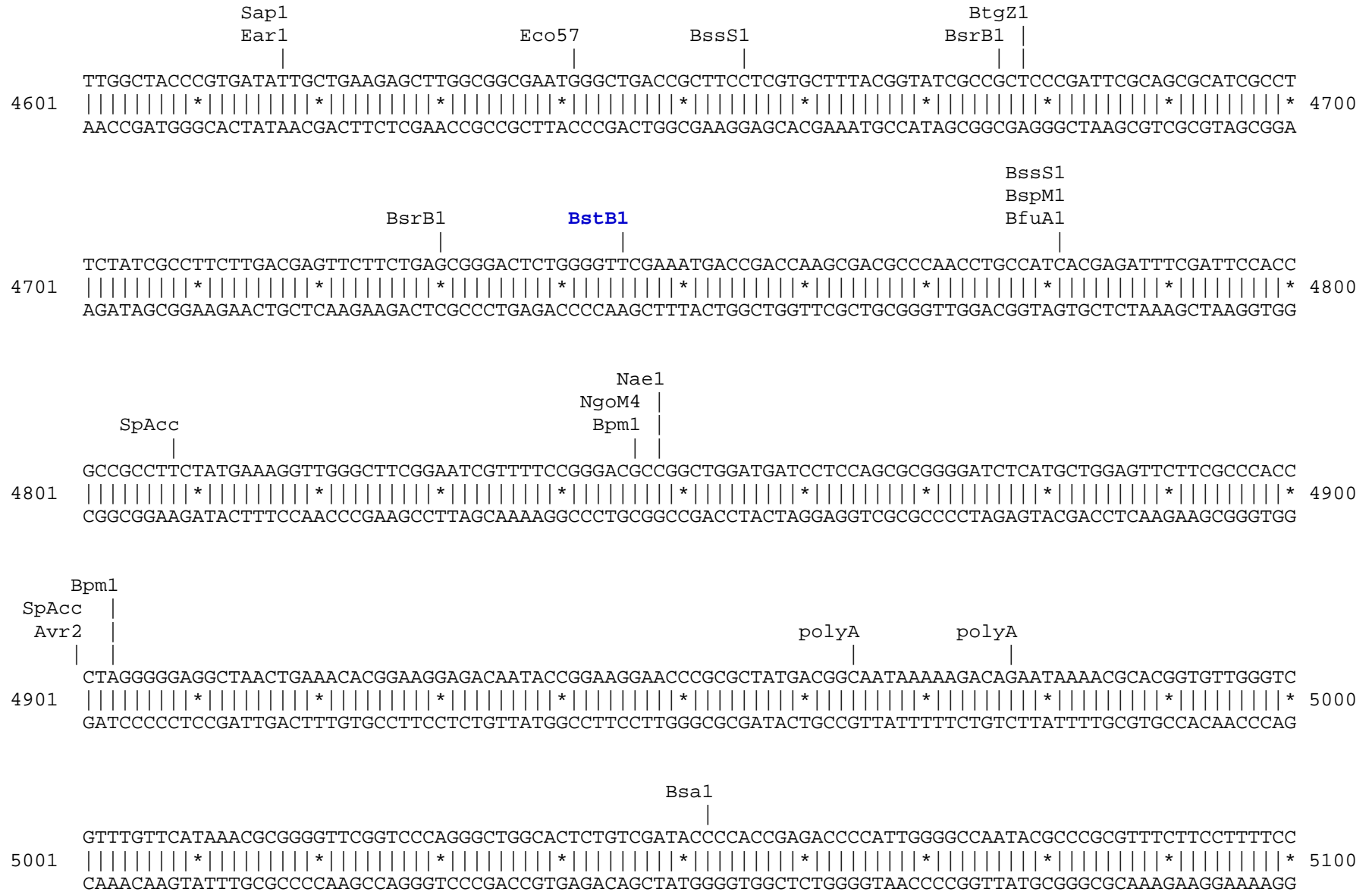
BtsI BsmI MluI SpDon SspI
| | | | |
TTCCTGCACTTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAACCGGTAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTG
2901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
AAGTGACGTAAGATCAACACCAACAGGTTTGGAGTAGTTACATAGAATTGCGCATTAAACATTTCGAATTATAAAACAATTTAAGCGCAATTTAAAAAC

PsiI
|
TTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGG
3001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
AATTTAGTCGAGTAAAAAATGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACC

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                                     BstAP
                                     AlwN1
                                     Bsu36
5101 CCACCCACCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
GGTGGGTGGGGGTTC AAGCCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCT

      DraI          DraI          BspH1
      |             |             |
5201 TTGATTTAAAACTTCATTTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
AACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGAC

                                     BpuE1
                                     |
5301 AGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACCCTACCAGCG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
TCGCAGTCTGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTTCGC

                                     Eco57
                                     |
5401 GTGGTTTGTGGCCGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
CACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCA

                                     AlwN1
                                     BpuE1
5501 AGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
TCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCACCGCTATTGAGCAGAGA

                                     ApaI1
                                     BseY1
5601 TACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGAGAGCGAACGACCTAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
ATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTGCGGGTCGAACCTCGCTTGTGATG
```

5701
 ACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCCGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAG
 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5800
 TGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCT

5801
 GAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTC
 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 5900
 CTCTCGCGTGCTCCCTCGAAGGTCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACTACTAGAG

5901
 GTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTTGGCCTTTTGCTGGCCTTTTGTCTCACATGTTCTTTCCTGCGTTA
 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 6000
 CAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTGGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAAT

6001
 TCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
 |||||*|||*|||*|||*|||*|||*|||*|||* 6039
 AGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

Restriction enzymes shown above the sequences:
 - SpAcc (above 5701-5801)
 - BciV1 (above 5701)
 - Ecil (above 5701)
 - BssS1 (above 5801)
 - SpAcc (above 5801)
 - Drd1 (above 5801)
 - BpuE1 (above 5801)
 - SpAcc (above 5901)
 - Ecil (above 5901)
 - SpDon (above 5901)
 - BspLU (above 5901)
 - Nsi1 (above 6001)
 - BfrB1 (above 6001)

Found:

Aat2	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	Baela	Baelb	BamH1	Bbs1	BbvC1	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	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	Psi1	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	PflM1
Pml1	Rsr2	Sac1	Sfi1	Sma1	SnaB1	Xba1	Xcm1	Xho1	Xmn1				

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bcgl1a	Bcgl1b	Bsg1	BsiW1	BssH2	BstE2
BstZ1	_Chi	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP
Not1	Nru1	Pac1	Pme1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1
Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce			

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	Bs11	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													