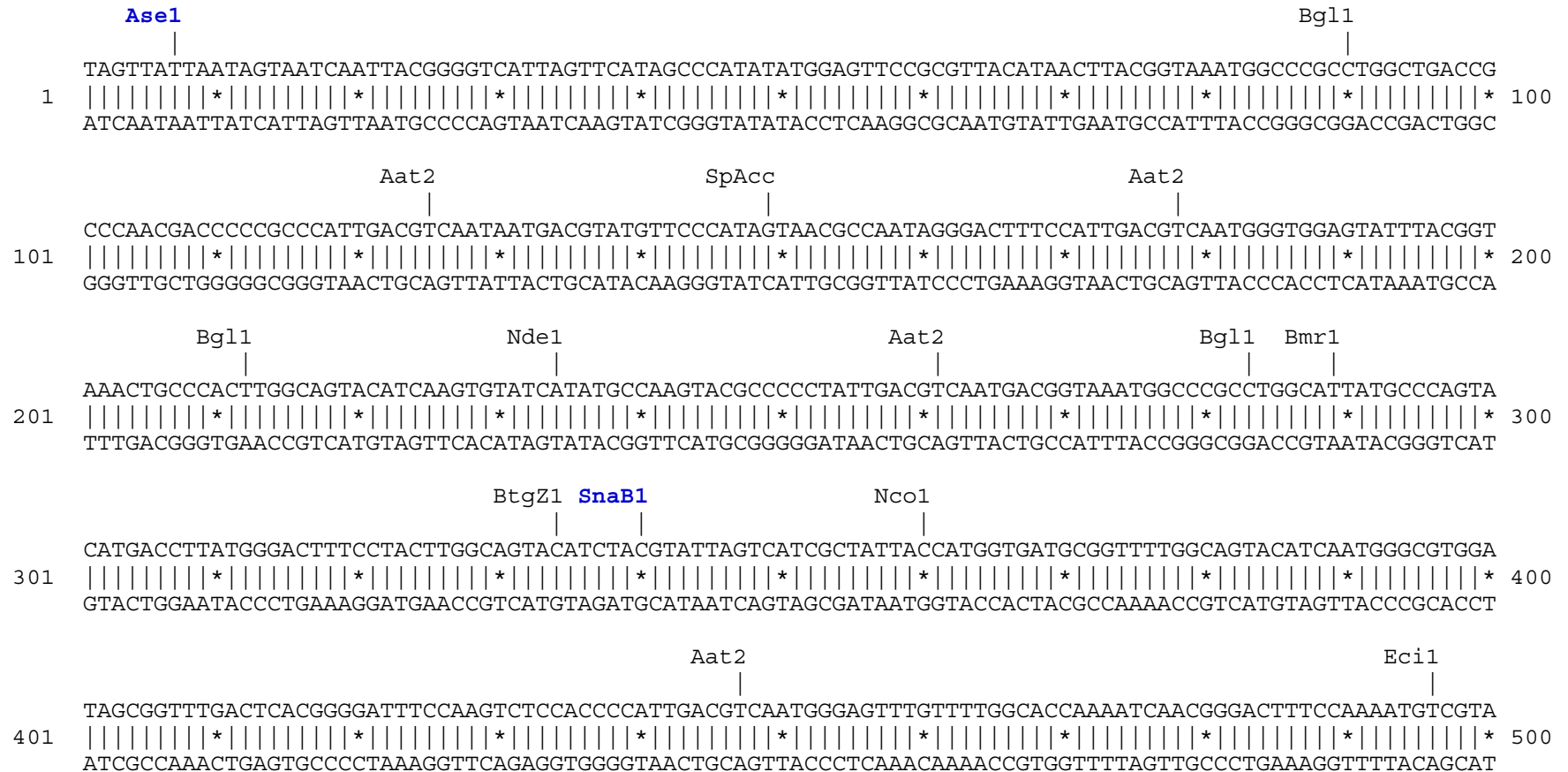
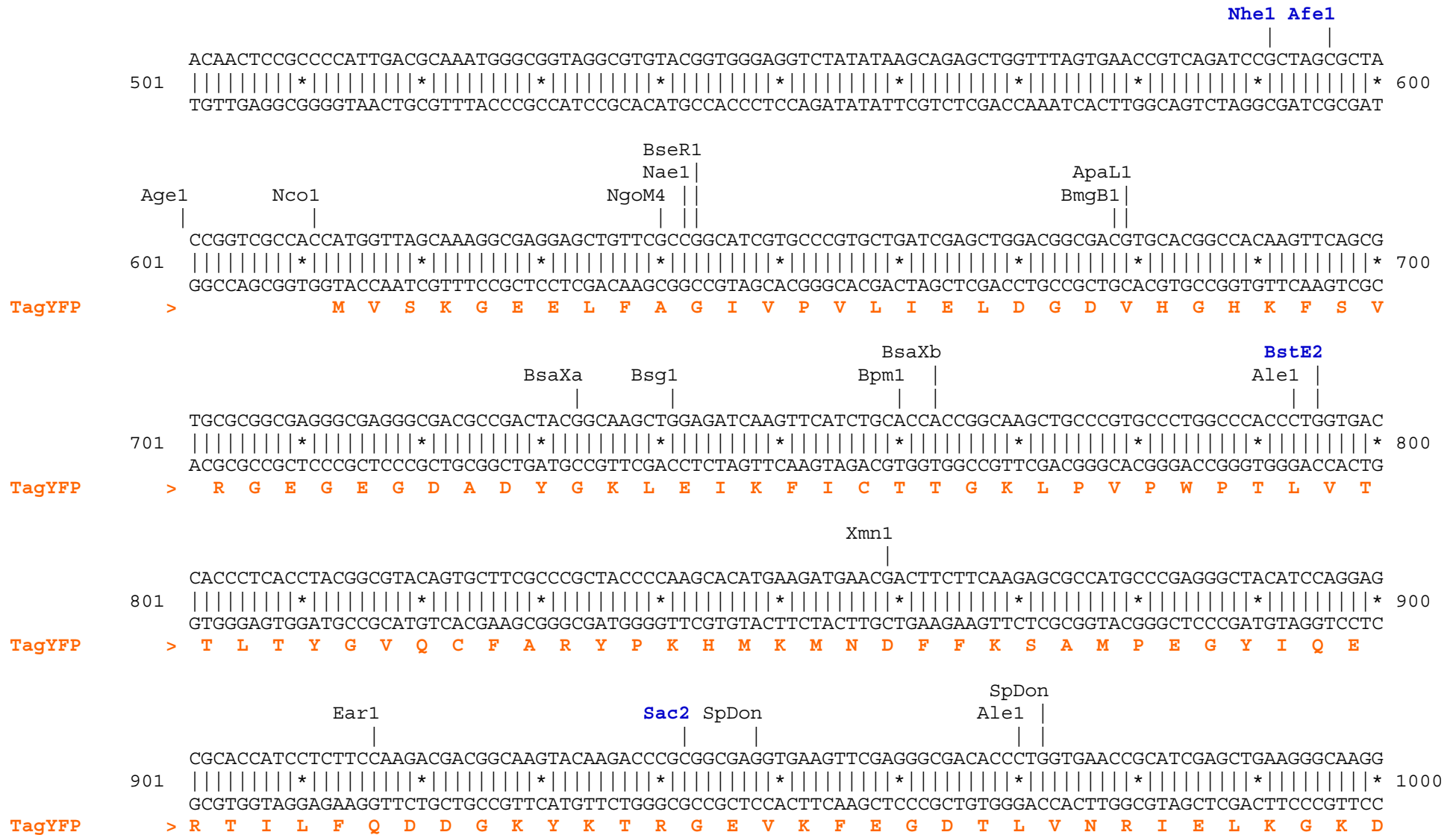


pTagYFP-tubulin vector restriction map

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). TagYFP amino acids are shown in orange, tubulin amino acids are shown in green, linker amino acids are shown in black.





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          Eco57              PflM1              Bpm1              Xcm1
          |                  |                  |                  |
1001  ACTTCAAGGAGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTCTACATCACCCCGACAAGGCCAACACGGCCTGGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
      TGAAGTTCTCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCTGAAGTTGTCGGTGTTCAGATGTAGTGGGGGCTGTTCCGGTTGTTGCCGGACCT
TagYFP >  F K E D G N I L G H K L E Y S F N S H N V Y I T P D K A N N G L E

          SpDon              Bpm1              Pvu2              Bsg1              Xcm1
          |                  |                  |                  |                  |
1101  GGTGAACCTTCAAGACCCGCCACAACATCGAGGGCGGGCGGCGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCCCTGGGCGACGGCCCCGTGCTGATC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
      CCACTTGAAGTTCTGGGCGGTGTTGTAGCTCCCGCCGCCGACGTCGACCCGGCTGGTGTGGTCTGGTTGCACGGGGACCCGCTGCCGGGGCACGACTAG
TagYFP >  V N F K T R H N I E G G G V Q L A D H Y Q T N V P L G D G P V L I

          BsaB1              Bpu10              Dra3              AlwN1 Bpm1 Pst1
          |                  |                  |                  |                  |
1201  CCCATCAACCACTACCTGAGCTACCAGACCCGACATCAGCAAGGACCCGCAACGAGGCCCGCGACCACATGGTGCTCCTGGAGTCCGTGAGCGCCTGCAGCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
      GGGTAGTTGGTGTATGGACTCGATGGTCTGGCTGTAGTTCCTGGCGTTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGCAGTCGCGGACGTTCGG
TagYFP >  P I N H Y L S Y Q T D I S K D R N E A R D H M V L L E S V S A C S H

          PflM1              BspE1              Xho1              BsrB1              Bgl2              Msc1
          |                  |                  |                  |                  |
1301  ACACCCACGGCATGGACGAGCTGTACCGCTCCGGACTCAGATCTCGAGTGCCTGAGTGCATCTCCATCCACGTTGGCCAGGCTGGTGTCCAGATTGGCAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
      TGTGGGTGCCGTACCTGCTCGACATGGCGAGGCCCTGAGTCTAGAGCTCACGCACTCACGTAGAGGTAGGTGCAACCGGTCCGACCACAGGTCTAACCGTT
TagYFP/tubulin T H G M D E L Y R S G L R S R V R E C I S I H V G Q A G V Q I G N

          BseY1              BsrD1              BstAP              Sac1              BstX1              Msc1              Eco57BseR1
          |                  |                  |                  |                  |
1401  TGCTGCTGGGAGCTCTACTGCCTGGAACACGGCATCCAGCCCGATGGCCAGATGCCAAGTGACAAGACCATTGGGGGAGGAGATGACTCCTTCAACACC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
      ACGGACGACCTCGAGATGACGGACCTTGTGCCGTAGGTCTGGGCTACCGGTCTACGGTTCACTGTTCTGGTAACCCCTCCTCTACTGAGGAAGTTGTGG
tubulin >  A C 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

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BsmB1 | SpAcc | Pml1 | Sma1 |
 TTCTTCAGTGAGACGGGCGCTGGCAAGCACGTGCCCCGGGCTGTGTTTGTAGACTTGGAAACCCACAGTCATTGATGAAGTTCGCACTGGCACCTACCGCC
 1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 AAGAAGTCACTCTGCCCGACCGTTCGTGCACGGGGCCCCGACACAAACATCTGAACCTTGGGTGTGAGTAAGTCAAGCGTGACCGTGGATGGCGG
 tubulin > F F 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

Bpu10 | Sap1 | Ear1 |
 AGCTCTTCCACCTGAGCAGCTCATCACAGGCAAGGAAGATGCTGCCAATAACTATGCCCCGAGGGCACTACACCATTGGCAAGGAGATCATTGACCTTGT
 1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 TCGAGAAGGTGGGACTCGTCGAGTAGTGTCCGTTCTTCTACGACGGTTATTGATACGGGCTCCCGTGATGTGGTAACCGTTCCTCTAGTAACTGGAACA
 tubulin > L F 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

EcoR1 | Bbs1 | Age1 | Xcm1 | BstX1 | SpAcc | Xmn1 | SpDon |
 GTTGGACCGAATTCGCAAGCTGGCTGACCAGTGCACCGGTCTTCAGGGCTTCTTGGTTTTCCACAGCTTTGGTGGGGGAACTGGTTCTGGGTTACCTCC
 1701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 CAACCTGGCTTAAGCGTTCGACCGACTGGTACGTTGCCAGAAGTCCCAGAAGAACAAAAGGTGTGAAACCACCCCTTGACCAAGACCCAAGTGGAGG
 tubulin > L D 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

BsmB1 | Bpm1 | BseY1 | SpAcc | Pvu2 |
 CTGCTCATGGAACGTCTCTCAGTTGATTATGGCAAGAAGTCCAAGCTGGAGTTCTCCATTTACCCAGCACCCAGGTTTCCACAGCTGTAGTTGAGCCCT
 1801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
 GACGAGTACCTTGCAGAGAGTCAACTAATACCGTTCTTCAGGTTTCGACCTCAAGAGGTAAATGGGTTCGTTGGGGTCCAAAGGTGTGACATCAACTCGGGA
 tubulin > L L 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

SpDon | Bpm1 | PshA1 |
 ACAACTCCATCCTCACCACCCACACCACCTGGAGCACTCTGATTGTGCCTTCATGGTAGACAATGAGGCCATCTATGACATCTGTGCGTAGAAAACCTCGA
 1901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
 TGTTGAGGTAGGAGTGGTGGGTGTGGTGGGACCTCGTGAGACTAACACGGAAGTACCATCTGTTACTCCGGTAGATACTGTAGACAGCATCTTTGGAGCT
 tubulin > N S 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

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EcoRV                                     Bts1
|                                         |
2001  TATCGAGCGCCCAACCTACACTAACCTTAACCGCCTTATTAGCCAGATTGTGTCTCCATCACTGCTTCCCTGAGATTTGATGGAGCCCTGAATGTTGAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
      ATAGCTCGCGGGTTGGATGTGATTGGAATTGGCGGAATAATCGGTCTAACACAGGAGGTAGTGACGAAGGGACTCTAAACTACCTCGGGACTTACAACCTG
tubulin > I E 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

      EcoR1      SexA1      Msc1 Nde1      SpAcc
      |         |         |   |   |         |
2101  CTGACAGAATTCAGACCAACCTGGTGCCTTACCCCGCATCCACTTCCCTCTGGCCACATATGCCCTGTGCATCTCTGCTGAGAAAGCCTACCATGAAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
      GACTGTCTTAAGGTCTGGTTGGACCACGGGATGGGGCGTAGGTGAAGGGAGACCGGTGTATACGGGGACAGTAGAGACGACTCTTTTCGGATGGTACTTG
tubulin > L T 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

      SpAcc      SpDon      SpDon
      |         |   |   |         |   |
2201  AGCTTTCTGTAGCAGAGATCACCAATGCTTGCTTTGAGCCAGCCAACCAGATGGTGAAATGTGACCCTCGCCATGGTAAATACATGGCTTGCTGCCTGTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
      TCGAAAAGACATCGTCTCTAGTGGTTACGAACGAAACTCGGTTCGGTTGGTCTACCCTTTACACTGGGAGCGGTACCATTTATGTACCGAACGACGGACAA
tubulin > L S 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

      BmgB1      BsrD1      PflM1      Bgl1
      |         |         |         |
2301  GTACCGTGGTGACGTGGTTCCCAAAGATGTCAATGCTGCCATTGCCACCATCAAAAACCAAGCGCAGCATCCAGTTTGTGGATTGGTGCCCCACTGGCTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      CATGGCACCCTGCACCAAGGGTTTCTACAGTTACGACGGTAACGGTGGTAGTTTTTGGTTTCGCGTCGTAGGTCAAACACCTAACCACGGGGTGACCGAAG
tubulin > Y R 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

      Ale1      Bsa1      Msc1      Bsp1      BsrD1
      |         |         |         |         |
2401  AAGGTTGGCATCAACTACCAGCCTCCCCTGTTGGTGCCTGGTGGAGACCTGGCCAAGGTACAGAGAGCTGTGTGCATGCTGAGCAACACCACAGCCATTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
      TTCCAACCGTAGTTGATGGTTCGGAGGGTGACACCACGGACCCTCTGGACCGGTTCCATGTCTCTCGACACACGTACGACTCGTTGTGGTGTTCGGTAAC
tubulin > K V 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

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Bpu10
BbvC1  Stu1                                Baelb                                Baela
|      |                                  |                                  |
CTGAGGCCCTGGGCTCGCCTGGACCACAAGTTTGACCTGATGTATGCCAAGCGTGCCTTTTGTTCACTGGTACGTGGGTGAGGGGATGGAGGAAGGCCGAGTT
2501 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*||| 2600
GACTCCGGACCCGAGCGGACCTGGTGTTCAAACTGGACTACATACGGTTCGCACGGAAACAAGTGACCATGCACCCACTCCCCTACCTCCTTCCGCTCAA
tubulin >  E A 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

EcoN1      BpuE1      BseR1      SpDon
|          |          |          |
TTCAGAGGCCCGTGAAGATATGGCTGCCCTTGAGAAGGATTATGAGGAGGTTGGTGTGGATTCTGTTGAAGGAGAGGGTGAGGAAGAAGGAGAGGAATAC
2601 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*||| 2700
AAGTCTCCGGCACTTCTATAACCGACGGAACTCTTCCTAATACTCCTCCAACCACACCTAAGACAACCTTCTCTCCCACTCCTTCTCCTCCTTATG
tubulin >  S E 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

BamH1      Xba1      Bcl1  BsaB1      SpDon      Dra1
|          |          |          |          |          |
TAAGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATAACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACTCCCCCTGAACC
2701 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*||| 2800
ATTCTAGGTGGCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGG
tubulin > *

Bsm1
Mfe1      Hpa1      polyA      Psi1      polyA      polyA
|          |          |          |          |          |
TGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGC
2801 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*||| 2900
ACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTATTTTCG

Bts1  Bsm1                                Mlu1      SpDon      Ssp1
|     |                                  |          |          |
ATTTTTTTTCACTGCATTCTAGTTGTTGGTTTTGTCCAAACTCATCAATGTATCTTAACCGTAAATTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAA
2901 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*||| 3000
TAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTTCGAATTATAAAACAATTTTAAGCGCAATTT

Psi1
|
TTTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGGATAGGGTTGAGTGTTGTTCCA
3001 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*||| 3100
AAAAACAATTTAGTCGAGTAAAAAATTTGGTTATCCGGCTTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAAACAAGGT

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                                     BsaXb          Drd1          BsaXa          BtgZ1
                                     |              |              |              |
                                     |              |              |              |
3101  GTTTGGAAACAAGAGTCCACTATTTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      CAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGA

                                     SpAcc          NaeI
                                     |              |
                                     |              |
3201  AATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCTTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
      TTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCG

                                     BsrB1
                                     |
                                     |
3301  GAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      CTCTTTCCTTCCCTTCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGGAATTACGC

                                     polyA          BciV1
                                     |              |
                                     |              |
3401  CCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
      GGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCTTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACT

                                     Ssp1  Ear1          Bsu36          Eci1          Pvu2
                                     |    |              |              |    |
                                     |    |              |              |    |
3501  GACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCTTGAGGCGGAAAGAACAGCTGTGGAATGTGTGTGTCAGTTAGGGTGTGGAAAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
      CTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTC
```

NsiI
SphI
BfrB1
BseY1 BstAP SexA1 BseY1

3601 TCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTA 3700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
 AGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCAT

NsiI
SphI
BfrB1
BstAP EciI EciI Bmr1 EciI NcoI

3701 TGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCC GCCCTAACTCCGCCATCCC GCCCTAACTCCGCCAGTTCCGCCATTCTCCGCCCA 3800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
 ACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGT

polyA SfiI BglI SpDon BseR1 Avr2
StuI

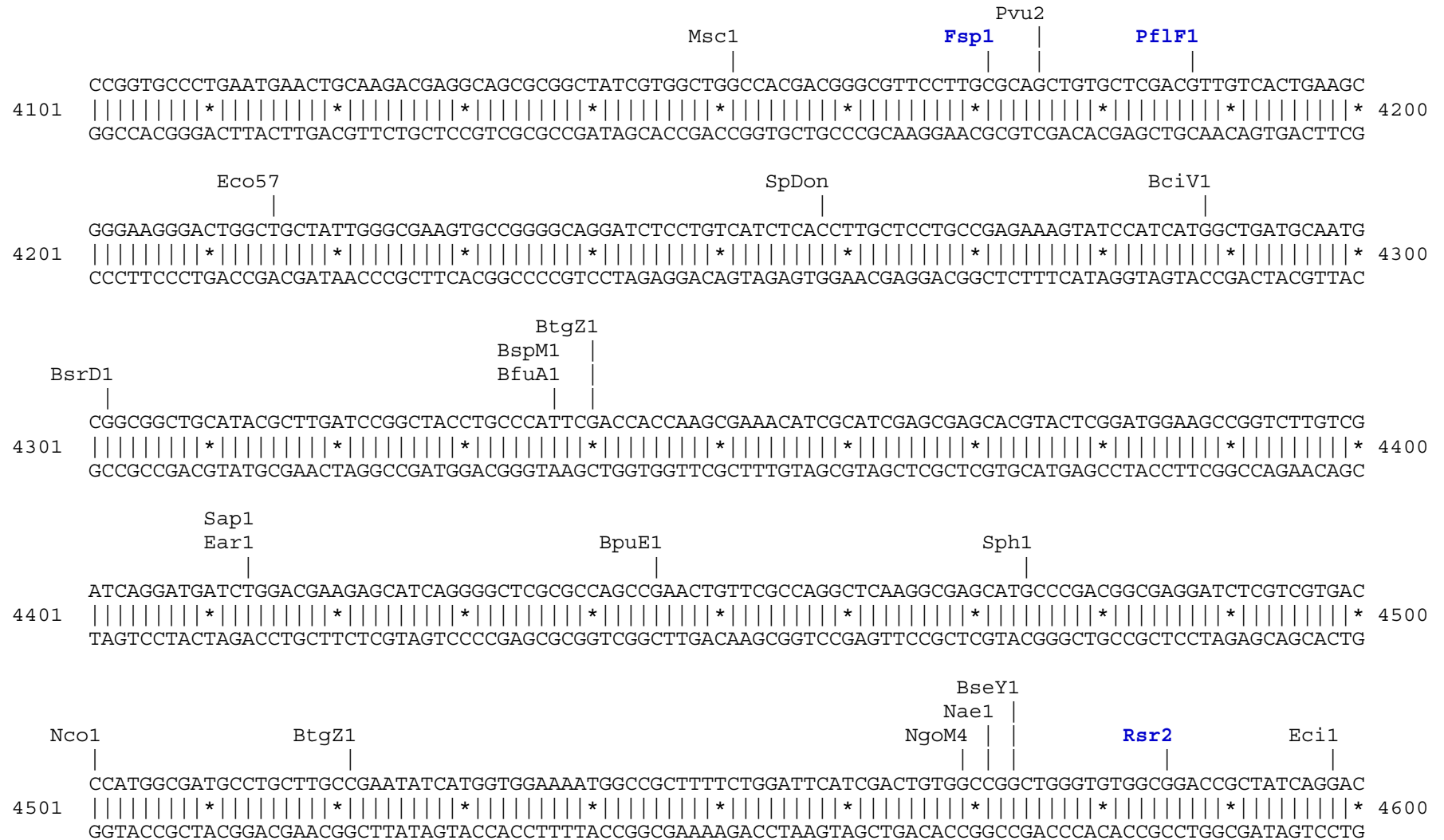
3801 TGGCTGACTAATTTTTTTTATTTATG CAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTT 3900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
 ACCGACTGATTAATAAATAAATACGTCTCCGGCTCCGGCGGAGCCGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAACCTCCGGATCCGAAA

ClaI BsaB1 BspM1 BfuA1 EagI

3901 TGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 4000
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
 ACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTA ACTTGTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAG

Bmr1 NarI KasI Drd1

4001 GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTG CAGCGCAGGGCGCCCGGTTCTTTTTGTCAAGACCGACTGT 4100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
 CCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACA




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                                     SpDon          BstAP          AlwN1          Bsu36
                                     |              |              |              |
5101 TTTTCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    AAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATG

          DraI          DraI          BspH1
          |            |            |
5201 TTTAGATTGATTTAAAACTTCATTTTTAATTTAAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    AAATCTAACTAAATTTTGAAGTAAAAATTAATTTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAA

                                     BpuE1
                                     |
5301 CCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCCCGCTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    GGTGACTCGCAGTCTGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGAT

                                     Eco57                                     SpAcc
                                     |                                     |
5401 CCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
    GGTGCGCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCTCTATGGTTTATGACAGGAAGATCACA

                                     AlwN1
                                     |
5501 AGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
    TCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGGAGACGATTAGGACAATGGTTCACCGACGACGGTCACCGCTATTTCAG

BpuE1          ApaL1          BseY1
|              |              |
5601 GTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
    CACAGAATGGCCAACTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTGGGTGCAACCTCGCTTGC

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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	Bsg1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BssS1	BstAP
BstB1	BstE2	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	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sap1
SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xho1	Xmn1	

Unique:

Afe1	Ase1	Baela	Baelb	BamH1	Bbs1	BbvC1	Bcl1	Bgl2	Blp1	BspE1	BspLU	BstB1	BstE2
Clal	Eag1	EcoRV	Fsp1	Hpa1	Kas1	Mfe1	Mlu1	Nar1	Nhe1	PflF1	Pml1	PshA1	Pst1
Rsr2	Sac1	Sac2	Sfi1	Sma1	SnaB1	Xba1	Xho1						

Not found:

Aar1	Acc65	Acc1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Bcg1a	Bcg1b	BsiW1	BsrG1	BssH2	BstZ1
_Chi	EcoK	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	PspOM
Pvu1	Sal1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce

Excluded by site complexity:

Acc1	Aci1	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													