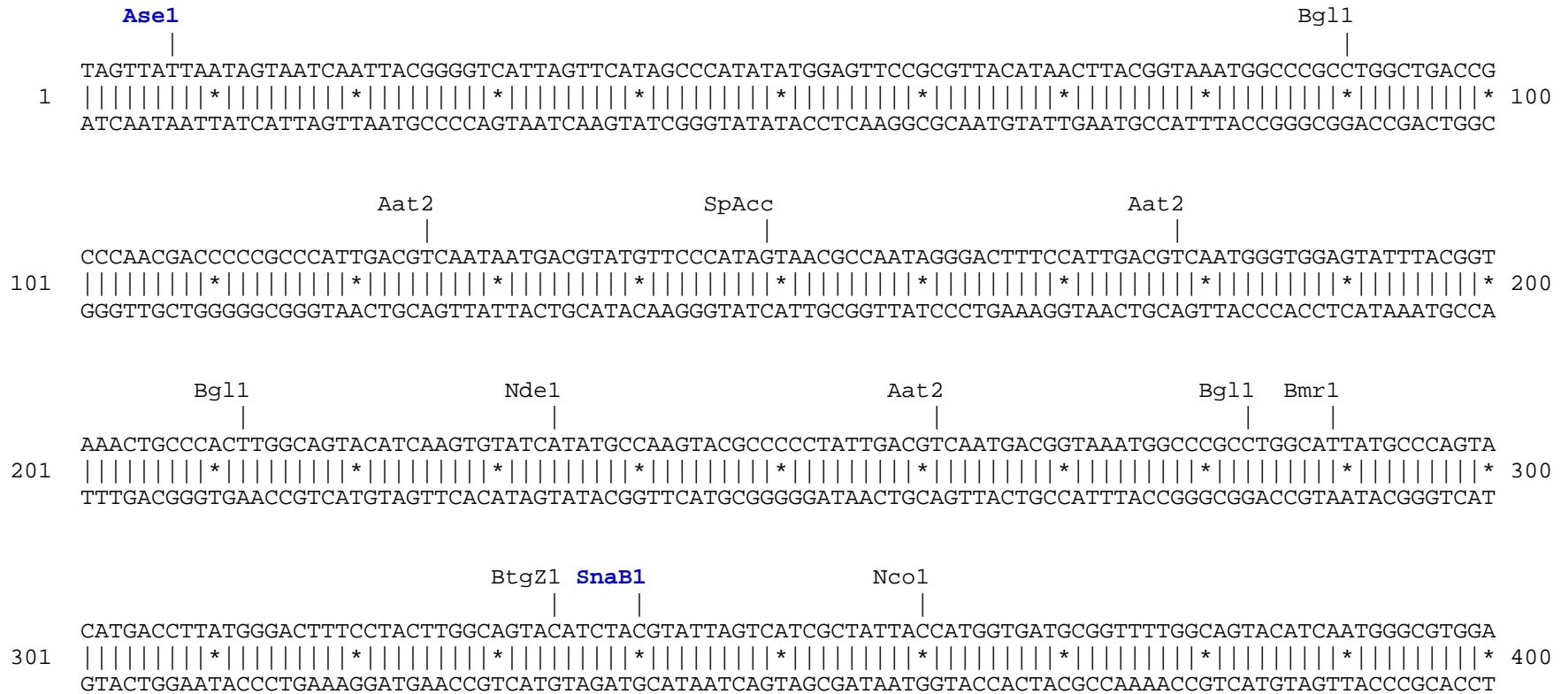


### pDendra2-Fibrillarlin vector restriction map

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). Dendra2 amino acids are shown in red, fibrillarlin amino acids are shown in green, linker amino acids are shown in black.





```

                                     SpAcc
                                     |
                                     |
    Bsg1                               Bgl1                               Bpm1 |
    |                                  |                                  |
    |                                  |                                  |
901  ACCATGACCTTCGAGGACAAGGGCATCTGCACCATCCGCAGCGACATCAGCCTGGAGGGCGACTGCTTCTTCCAGAACGTGCGCTTCAAGGGCACCAACT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
    TGGTACTGGAAGCTCCTGTTCCCGTAGACGTGGTAGGCGTCGCTGTAGTCGGACCTCCCGCTGACGAAGAAGGTCTTGCACGCGAAGTTCCCGTGGTTGA
Dendra2 > T M T F E D K G I C T I R S D I S L E G D C F F Q N V R F K G T N F

                                     Bbs1           Bsg1           Eco57           Pml1           _Chi
                                     |           |           |           |           |
1001  TCCCCCAACGGCCCCGTGATGCAGAAGAAGACCCTGAAGTGGGAGCCCAGCACCGAGAAGCTGCACGTGCGCGACGGCCTGCTGGTGGGCAACATCAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    AGGGGGGTTGCCGGGCACTACGTCTTCTTCTGGGACTTCACCCTCGGGTCGTGGCTCTTCGACGTGCACGCGCTGCCGGACGACCACCCGTTGTAGTT
Dendra2 > P P N G P V M Q K K T L K W E P S T E K L H V R D G L L V G N I N

                                     Bpm1           BstX1           Pvu2           PflM1
                                     |           |           |           |           |
1101  CATGGCCCTGCTGCTGGAGGGCGGGCCGCCCCTACCTGTGCGACTTCAAGACCACCTACAAGGCCAAGAAGGTGGTGCAGCTGCCCGACGCCACTTCGTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    GTACCGGGACGACGACTCCTCCCGCCCGGTGATGGACACGCTGAAGTTCTGGTGGATGTTCCGGTTCCTTCCACCACGTTCGACGGGCTGCGGGTGAAGCAC
Dendra2 > M A L L L E G G G H Y L C D F K T T Y K A K K V V Q L P D A H F V

                                     SpDon           Dra3           BseY1
                                     |           |           |
1201  GACCACCGCATCGAGATCCTGGGCAACGACAGCGACTACAACAAGGTGAAGCTGTACGAGCACGCCGTGGCCCGCTACAGCCCCCTGCCAGCCAGGTGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    CTGGTGGCGTAGCTCTAGGACCCGTTGCTGTCGCTGATGTTGTTCCACTTCGACATGCTCGTTCGGCACCAGGGGCGATGTCGGGGGACGGGTTCGGTCCACA
Dendra2 > D H R I E I L G N D S D Y N K V K L Y E H A V A R Y S P L P S Q V W

                                     BsrG1           Xho1           Eag1           Bgl1           BstE2
                                     |           |           |           |           |
1301  GGTCCGGCGACAGCGGCGTGTACAAGACTCGAGCCATGAAGCCAGGATTTCAGTCCCCGTGGGGGTGGCTTTGGCCGGCCGAGGGGGCTTTGGTGACCGTGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    CCAGGCCGCTGTCGCCGCACATGTTCTGAGCTCGGTACTTCGGTCCCTAAGTCAGGGGCACCCCCACCGAAACCGCCGGCTCCCCCGAAACCACTGGCACC
Fibrillarlin > S G D S G V Y K T R A M K P G F S P R G G G F G G R G G F G G D R G

```

```

                                Bgl1                Ecil                BseR1
                                |                |                |
                                |                |                |
1401 TGGTCGTGGAGGCCGAGGGGGCTTTGGCGGGGGCCGAGGTCGAGGCCGAGGCTTTAGAGGTCGTGGACGAGGAGGAGGTGGAGGCCGGCCGGCCGGTGGA
    |||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||* 1500
    ACCAGCACCTCCGGCTCCCCGAAACCGCCCCGGCTCCAGCTCCGCCTCCGAAATCTCCAGCACCTGCTCCTCCTCCACCTCCGCCGCCGCCGCCACCT
Fibrillarlin > G R G G R G G F G G R G R G G G F R G R G R G G G G G G G G G

```

```

                                BseR1
                                |
                                |
Ear1  BseR1  |           BstX1
|       |       |           |
1501 GGAGGAGGAAGAGGTGGTGGAGGCTTCCATTCTGGTGGCAACCGGGGTCGTGGTGGGGAGGAAAAAGAGGAAACAGTCGGGGAAGAATGTGATGGTGG
    |||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||* 1600
    CCTCCTCCTTCTCCACCACCTCCGAAGGTAAGACCACCGTTGGCCCCAGCACCAGCCCCTCCTTTTTCTCCTTTGGTCAGCCCCTTCTTACACTACCACC
Fibrillarlin > G G G R G G G G F H S G G N R G R G R G G K R G N Q S G K N V M V E

```

```

                                BstX1
                                ||
                                ||
                                |
Bgl1  Bbs1                BstE2  SexA1                Ear1
|       |                |         |                 |
1601 AGCCGCATCGGCATGAGGGTGTCTTCATTTGTCGAGGAAAAGAAAGATGCACTGGTCACCAAGAACCTGGTCCCTGGGGAATCAGTTTATGGAGAGAAGAG
    |||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||* 1700
    TCGGCGTAGCCGTACTIONTCCACAGAAGTAAACAGCTCCTTTTCTTCTACGTGACCAGTGGTTCTTGGACCAGGGACCCCTTAGTCAAATACCTCTCTTCTC
Fibrillarlin > P H R H E G V F I C R G K E D A L V T K N L V P G E S V Y G E K R

```

```

                                Xmn1  BsrB1  Nhe1
                                |       |       |
                                |       |       |
1701 AGTCTCGATTTTCGGAAGGAGATGACAAAATTGAGTACCGAGCCTGGAACCCCTTCCGCTCCAAGCTAGCAGCAGCAATCCTGGGTGGTGTGGACCAGATC
    |||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||* 1800
    TCAGAGCTAAAGCCTTCTCTACTGTTTTAACTCATGGCTCGGACCTTGGGGAAGGCGAGGTTTCGATCGTTCGTTAGGACCCACCACACCTGGTCTAG
Fibrillarlin > V S I S E G D D K I E Y R A W N P F R S K L A A A I L G G V D Q I

```

```

BsaB1                Bpu10                Bsa1                BspE1
|                   |                   |                   |
1801 CACATCAAACCGGGGCTAAGGTTCTCTACCTCGGGGCTGCCTCGGGCACCACGGTCTCCCATGTCTCTGACATCGTTGGTCCGGATGGTCTAGTCTATG
    |||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||*||||* 1900
    GTGTAGTTTGGCCCCGATTCCAAGAGATGGAGCCCCGACGGAGCCCCTGGTGCCAGAGGGTACAGAGACTGTAGCAACCAGGCCTACCAGATCAGATAC
Fibrillarlin > H I K P G A K V L Y L G A A S G T T V S H V S D I V G P D G L V Y A

```

```

                BstX1                MscI                BtgZ1
                BsrB1 |                Ear1                Bcg1b |
                |                |                |
1901 CAGTCGAGTTCTCCACCGCTCTGGCCGTGACCTCATTAACCTGGCCAAGAAGAGGACCAACATCATTCTGTGATCGAGGATGCTCGACACCCACACAA 2000
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
    GTCAGCTCAAGAGGGTGGCGAGACCGGCACTGGAGTAATTGAACCGGTTCTTCTCCTGGTTGTAGTAAGGACTAGCTCCTACGAGCTGTGGGTGTGTT
Fibrillarín > V E F S H R S G R D L I N L A K K R T N I I P V I E D A R H P H K

                Sph1                BsrD1|Bcg1a                BseY1                Bsm1
                |                |                |                |
2001 ATACCGCATGCTCATCGCAATGGTGGATGTGATCTTTGCTGATGTGGCCCAGCCAGACCAGACCCGGATTGTGGCCCTGAATGCCACACCTTCCTGCGT 2100
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
    TATGGCGTACGAGTAGCGTTACCACCTACACTAGAAAACGACTACACCGGGTCTGGTCTGGGCCTAACACCGGGACTTACGGGTGTGGAAGGACGCA
Fibrillarín > Y R M L I A M V D V I F A D V A Q P D Q T R I V A L N A H T F L R

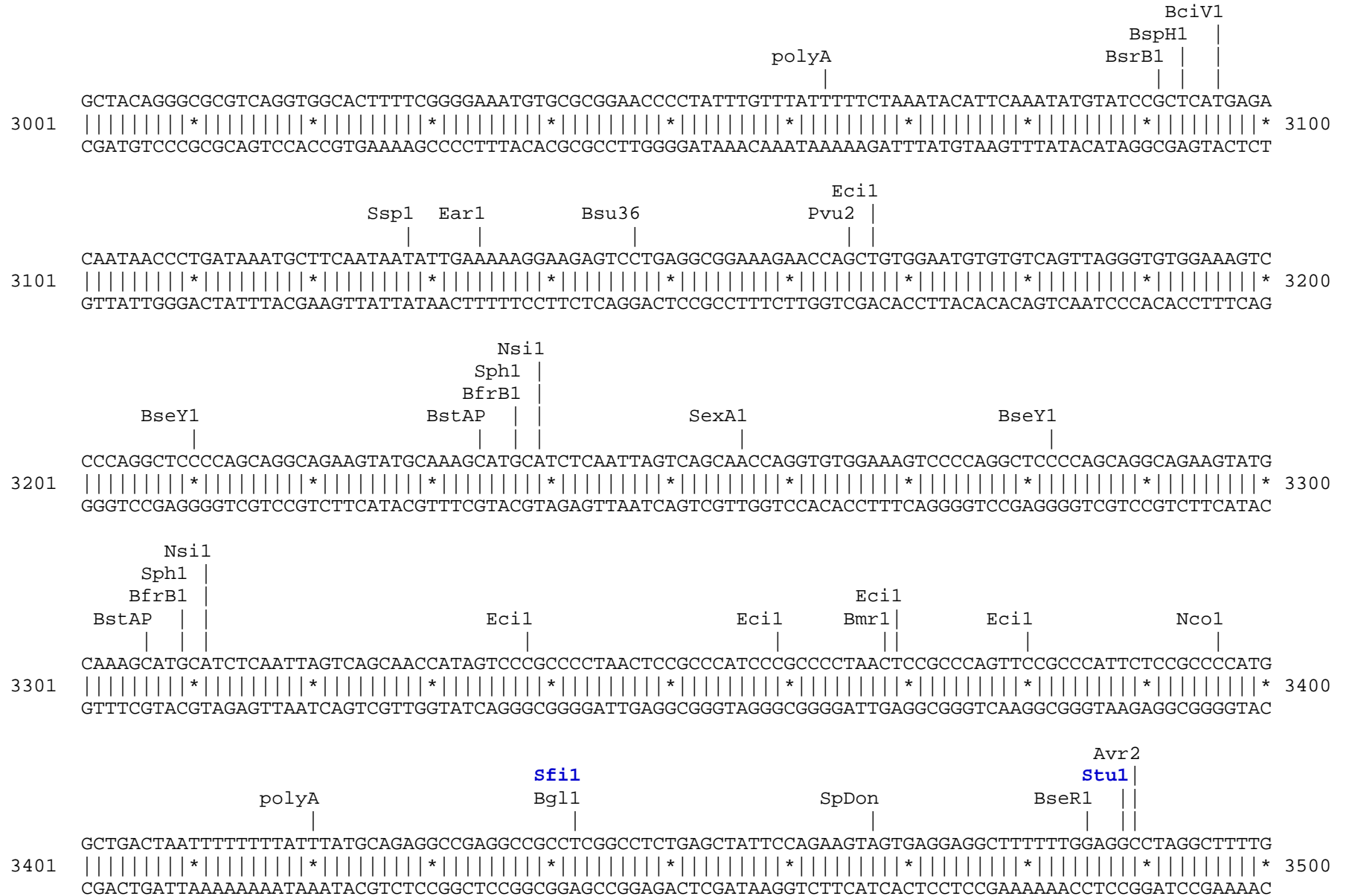
                Dra3                Bpu10                SpDon
                |                BbvC1 |                |
2101 AATGGAGGACACTTTGTGATTTCCATTAAGGCCAACTGCATTGACTCCACAGCCTCAGCCGAGGCCGTGTTTGCCTCCGAAGTGAAAAAGATGCAACAGG 2200
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
    TTACCTCCTGTGAAACACTAAAAGTAATTCCGGTTGACGTAAGGTGTGCGGAGTCGGCTCCGGCACAAAACGGAGGCTTCACTTTTTCTACGTTGTCC
Fibrillarín > N G G H F V I S I K A N C I D S T A S A E A V F A S E V K K M Q Q E

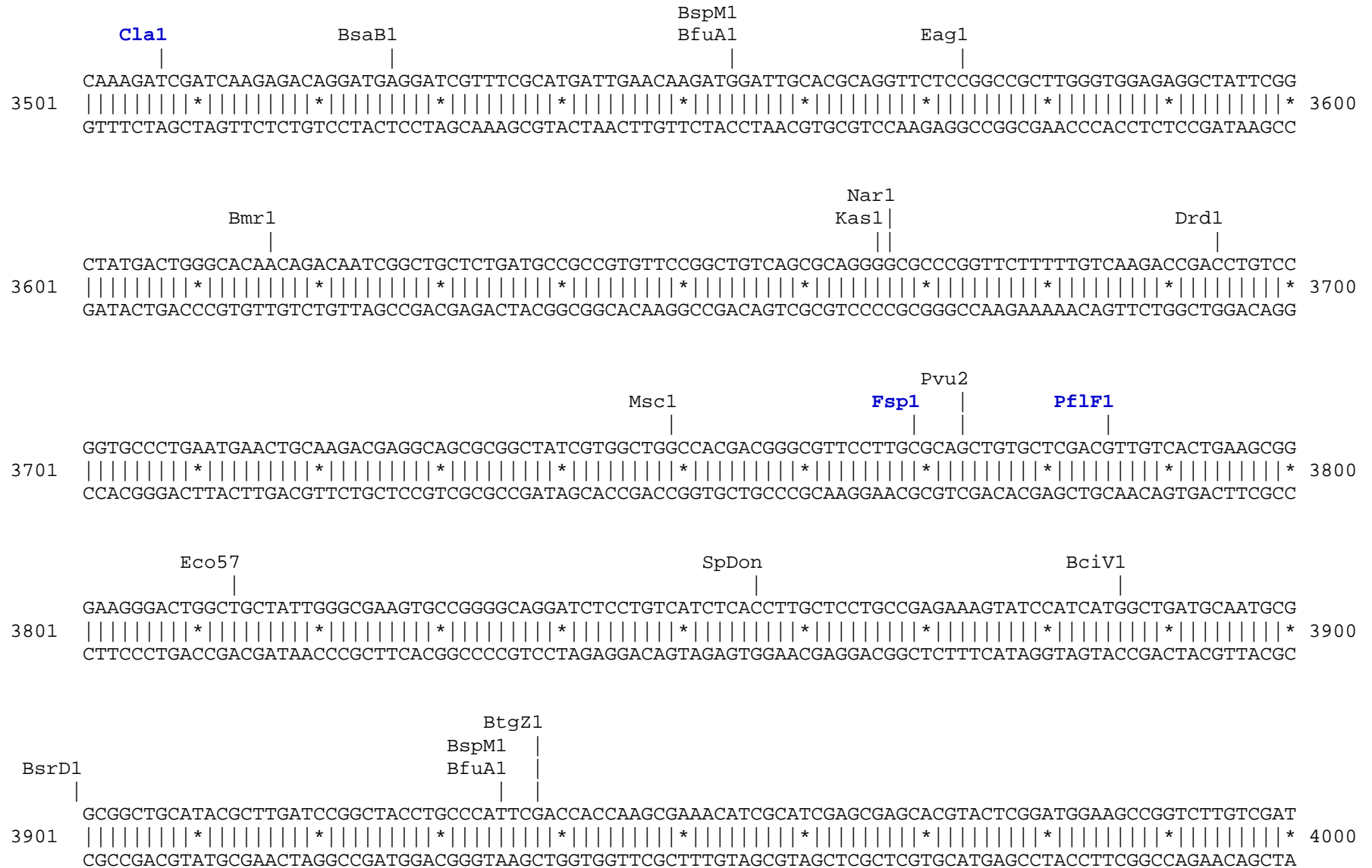
                Bsa1                BpuE1PflM1                BsrG1                SpDon
                Nde1 |                |                |                |
2201 AGAACATGAAGCCGCAGGAGCAGTTGACCCTTGAGCCATATGAAAGAGACCATGCCGTGGTTCGTGGGAGTGTACAGGCCACCCCAAGGTGAAGAAGCTG 2300
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
    TCTTGTAAGTTCGGCGTCTCGTCAACTGGGAAGTTCGGTATACTTTCTCTGGTACGGCACCAAGCACCCTCACATGTCCGGTGGGGGGTTCCACTTCTTGAC
Fibrillarín > N M K P Q E Q L T L E P Y E R D H A V V V G V Y R P P P K V K N *

    BamH1                Xba1                Bcl1|BsaB1                SpDon                Dra1
    |                |                |                |                |
2301 AGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATAACACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTG 2400
    |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
    TCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTGGAGGGTGTGGAGGGGGACTTGGAC

```









SapI  
 EarI  
 BpuE1  
 SphI  
 NcoI

4001  
 CAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCCGAAGCTGTTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTTCGTGACCC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4100  
 GTCCCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGG

BseY1  
 NaeI  
 NgoM4  
 BtgZ1  
 Rsr2  
 EciI

4101  
 ATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACAT  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4200  
 TACCCTACGGACGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCTCTGTA

SapI  
 EarI  
 Eco57  
 BssS1  
 BtgZ1  
 BsrB1

4201  
 AGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4300  
 TCGCAACCGATGGGCACCTATAACGACTTCTCGAACCGCGCTTACCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTTCGCGTAG

BssS1  
 BspM1  
 BfuA1  
 BsrB1  
 BstB1

4301  
 GCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4400  
 CGGAAGATAGCGGAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAG

NaeI  
 NgoM4  
 Bpm1  
 SpAcc

4401  
 CACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 4500  
 GTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAAGGCCCTGCGGCCGACCTACTAGGAGGTTCGCGCCCCTAGAGTACGACCTCAAGAAGCGG

```
      Bpm1
    SpAcc  |
    Avr2   |
  CACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTG
4501 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 4600
    GTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTTGCGTGCCACAAC

           Bsa1
             |
    GGTCGTTTGTTTCATAAACGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGCGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCCGCGTTTTCTTCCTT
4601 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 4700
    CCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAA

           BstAP
          AlwN1        Bsu36
             |             |
    TTCCCCACCCCAACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTT
4701 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 4800
    AAGGGGTGGGGTGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAA

           Dra1      Dra1      BspH1
             |      |             |
    TAGATTGATTTAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCC
4801 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 4900
    ATCTAACTAAATTTTGAAGTAAAAATTAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGG

                                 BpuE1
                                   |
    ACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACC
4901 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 5000
    TGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGG

                                 Eco57
                                   |
    AGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAG
5001 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 5100
    TCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTTATGACAGGAAGATCACATC
```

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                                     AlwN1
                                     |
CCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGT
5101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
GGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCA

BpuE1                                     ApaL1       BseY1
|                                     |               |
GTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGAC
5201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
CAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTTCGAACCTCGCTTGCTG

                                     SpAcc
                                     |
CTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGA
5301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
GATGTGGCTTGACTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCAGCCT

BssS1                                     SpAcc                                     Drd1
|                                     |                                     |
ACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGAT
5401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
TGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACTA

                                     SpDon
                                     BspLU|
BpuE1                                     SpAcc       Ecil
|                                     |               |
GCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTCTTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTTCTGC
5501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
CGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTGCTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACG

                                     NsiI
                                     BfrB1
                                     |
GTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5643
CAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	<b>Afe1</b>	<b>Age1</b>	<b>Ale1</b>	AlwN1	ApaL1	<b>Ase1</b>	Avr2	<b>BamH1</b>	Bbs1	<b>BbvC1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	BseR1	BseY1
Bsg1	Bsm1	<b>BspE1</b>	BspH1	<b>BspLU</b>	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	<b>BstB1</b>	BstE2	BstX1
Bsu36	BtgZ1	<b>Bts1</b>	<b>_Chi</b>	<b>Clal</b>	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	<b>EcoN1</b>	<b>Fsp1</b>
<b>Hpa1</b>	Kas1	<b>Mfe1</b>	<b>Mlu1</b>	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsil	<b>PflF1</b>	PflM1
<b>Pml1</b>	polyA	Psil	Pvu2	<b>Rsr2</b>	Sap1	SexA1	<b>Sfi1</b>	<b>Sma1</b>	<b>SnaB1</b>	SpAcc	SpDon	Sph1	Ssp1
<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>										

Unique:

<b>Afe1</b>	<b>Age1</b>	<b>Ale1</b>	<b>Ase1</b>	<b>BamH1</b>	<b>BbvC1</b>	<b>Bcg1a</b>	<b>Bcg1b</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BspE1</b>	<b>BspLU</b>	<b>BstB1</b>	<b>Bts1</b>
<b>_Chi</b>	<b>Clal</b>	<b>EcoN1</b>	<b>Fsp1</b>	<b>Hpa1</b>	<b>Mfe1</b>	<b>Mlu1</b>	<b>PflF1</b>	<b>Pml1</b>	<b>Rsr2</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>SnaB1</b>	<b>Stu1</b>
<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>											

Not found:

Aar1	Acc65	Ac11	Afl2	Ahd1	Apal	Asc1	AsiS1	Baela	Baelb	Bgl2	Blp1	BmgB1	BsiW1
BsmB1	BssH2	BstZ1	EcoK	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fsel	FspA1	Hind3
I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1	Pme1	PshA1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP
R4atR	Sac1	Sac2	Sall	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA
T7Ter	PISce	Xcm1											

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	Tfil	Tse1	Tsp45	Tsp50
TspR1													