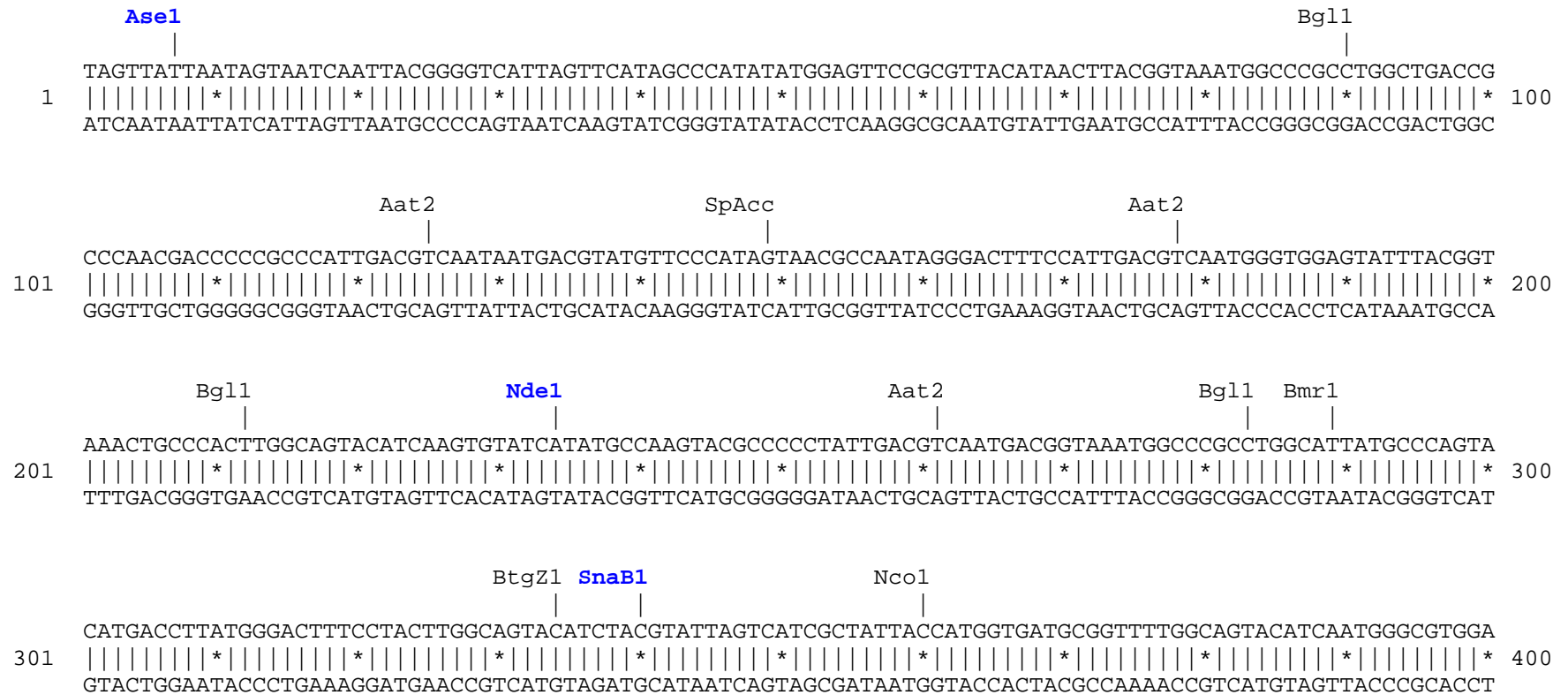


pFusionRed-talin vector restriction map

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).

FusionRed amino acids are shown in red, talin amino acids are shown in green, linker amino acids are shown in black.




```

                Ahd1      Eco57
                |        |
1901 TGGAGGACTCAGTGTCTCCAAAAAAGTCAACAGTCCTTCAGCAGCAGTACAACCGAGTGGGGAAAGTGGAGCACGGCTCTGTGGCTCTGCCAGCCATCAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
    ACCTCCTGAGTCACAGAGGGTTTTTCAGTTGTCAGGAAGTCGTCGTCATGTTGGCTCACCCCTTTTCACCTCGTGCCGAGACACCGAGACGGTCGGTAGTA
Talin > E D S V S P K K S T V L Q Q Q Y N R V G K V E H G S V A L P A I M

                BspM1
                Aar1
                Bpm1      Sph1      BseY1      Msc1      Eco57
                |        |        |        |        |
2001 GCGCTCTGGAGCCTCTGGTCCTGAGAATTTCCAGGTGGGGAGCATGCCACCTGCCCAGCAGCAGATCACAGTGGCCAGATGCACCGAGGACACATGCCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
    CGCGAGACCTCGGAGACCAGGACTCTTAAAGGTCCACCCCTCGTACGGTGGACGGGTCGTCGTCCTAGTGGTCACCGGTCTACGTGGCTCCTGTGTACGGT
Talin > R S G A S G P E N F Q V G S M P P A Q Q Q I T S G Q M H R G H M P

                BseY1 Bgl1      Bpm1      Sph1 BstAP      Bsg1
                |    |        |        |    |        |
2101 CCTCTGACTTCAGCCCAGCAGGCGCTCACTGGAACCATTAACCTCCAGCATGCAGGCTGTGCAGGCTGCCAGGCCACTCTGGATGACTTTGAGACTCTAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
    GGAGACTGAAGTCGGGTCGTCGCCGAGTGACCTTGGTAATTGAGGTCGTACGTCCGACACGTCCGACGGGTCCGGTGAGACCTACTGAAACTCTGAGATG
Talin > P L T S A Q Q A L T G T I N S S M Q A V Q A A Q A T L D D F E T L P

                PflM1
                Msc1      Hind3      Pvu2
                |        |        |
2201 CCCCTCTTGGCCAGGATGCTGCCTCCAAAGCTTGGCGTAAGAACAAGATGGATGAATCAAAGCATGAGATCCACTCCCAGGTAGATGCCATCACAGCTGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
    GGGGAGAACCGGTCCTACGACGGAGGTTTCGAACCGCATTCTTGTCTACCTACTTAGTTTCGTA CTCTAGGTGAGGGTCCATCTACGGTAGTGTGCGACC
Talin > P L G Q D A A S K A W R K N K M D E S K H E I H S Q V D A I T A G

                Bts1      SpDon      SpAcc Pst1      Bts1      Ear1
                |        |        |    |        |        |
2301 CACTGCCTCTGTGGTAAACCTGACAGCAGGAGATCCTGCAGAGACAGACTATAACAGCAGTGGGCTGTGCAGTCACCACCATCTCTTCCAACCTGACGGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
    GTGACGGAGACACCATTTGGACTGTCGTCCTCTAGGACGTCTCTGTCTGATATGTCGTCACCCGACACGTCAGTGGTGGTAGAGAAGGTTGGACTGCCTC
Talin > T A S V V N L T A G D P A E T D Y T A V G C A V T T I S S N L T E

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Ale1
SpDon | | BseY1 MscI SpAcc | | BstX1

2801 CCAAGGTGGTAGCACCTACAATCAGCTCACCTGTGTGCCAAGAACAGCTAGTCGAGGCTGGGCGACTGGTGGCCAAAGCTGTGGAGGGCTGTGTGTCTGC 2900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 GGTTCACCATCGTGGATGTTAGTCGAGTGGACACACGGTTCTTGTGTCGATCAGCTCCGACCCGCTGACCACCGGTTTCGACACCTCCCGACACACAGACG
Talin > K V V A P T I S S P V C Q E Q L V E A G R L V A K A V E G C V S A

SpAcc Pvu2 Pml1 Pst1 | |

2901 CTCGCAAGCAGCTACAGAAGATGGACAGCTGCTTCGAGGGGTAGGAGCAGCAGCCACGGCTGTCACCCAGGCCCTCAATGAGCTGCTGCAGCACGTGAAG 3000
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 GAGCGTTCGTCGATGTCTTCTACCTGTCGACGAAGCTCCCCATCCTCGTCGTCGGTGCCGACAGTGGGTCCGGGAGTTACTCGACGACGTTCGTGCACTTC
Talin > S Q A A T E D G Q L L R G V G A A A T A V T Q A L N E L L Q H V K

BseY1 Eco57 NcoI SpAcc BseY1

3001 GCCCACGCCACCGGAGCTGGGCCTGCCGGTTCGGTATGACCAAGCCACTGATACCATCCTCACCGTCACTGAAAACATCTTCAGCTCCATGGGTGATGCTG 3100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 CGGGTGCCGGTGGCCTCGACCCGGACGGCCAGCCATACTGGTTTCGGTACTATGGTAGGAGTGGCAGTGACTTTTTGTAGAAGTCGAGGTACCCACTACGAC
Talin > A H A T G A G P A G R Y D Q A T D T I L T V T E N I F S S M G D A G

PflF1 Bpu10 BbvC1 SpAcc Xba1
SexA1 | |
Xcm1 | |

3101 GGGAGATGGTGCGCCAGGCCCGCATCCTGGCCCAAGCCACCTCAGACCTGGTCAATGCTATCAAGGCCGATGCTGAGGGGGAGAGTGATCTGGGAACTC 3200
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 CCCTCTACCACGCGGTCCGGGCGTAGGACCGGGTTCGGTGGAGTCTGGACCAGTTACGATAGTTCCGGCTACGACTCCCCCTCTCACTAGACCTCTTGAG
Talin > E M V R Q A R I L A Q A T S D L V N A I K A D A E G E S D L E N S

Bpm1 Xcm1 BstX1

3201 TAGAAAGCTCCTGAGTGTGTGCCAAGATCCTCGCTGATGCCACCGCCAAGATGGTGGAGGCGGCCAAGGGAGCAGCCGCCACCCTGACAGTGAGGAACAG 3300
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*||
 ATCTTTCGAGGACTCACGACGGTTCTAGGAGCGACTACGGTGGCGGTTCTACCACCTCCGCCGGTTCCTCGTCGGCGGGTGGGACTGTCACTCCTTGTC
Talin > R K L L S A A K I L A D A T A K M V E A A K G A A A H P D S E E Q


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                                     MscI
                                     BsmBI
                                BtsI      Pvu2      BglI      BmgBI
                                |          |          |          |
CAGGTAGCTAAAGCAGTGACCCAAGCCCTGAACCGCTGTGTTCAGCTGCCTGCCTGGCCAAAGAGACGTGGATAATGCCCTACGAGCCGTTGGAGATGCCA
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
GTCCATCGATTTTCGTCACTGGGTTTCGGGACTTGGCGACACAGTCGACGGACGGACCGGTTTCTCTGCACCTATTACGGGATGCTCGGCAACCTCTACGGT
Talin > Q V A K A V T Q A L N R C V S C L P G Q R D V D N A L R A V G D A S

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                                     Pvu2
                                     BseYI
                                     PstI
                                     ||
GCAAGCGACTCCTGAGTGACTTGCCTTCCCAAGCACGGGGACATTTCAAGAAGCACAGAGCCGATTGAATGAAGCTGCAGCTGGGTTAAATCAGGCCGC
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
CGTTCGCTGAGGACTCACTGAACGAAGGAGTTTCGTGCCCTGTAAAGTTCTTCGTGTCTCGGCTAACTTACTTCGACGTCGACCCAATTTAGTCCGGCG
Talin > K R L L S D L L P P S T G T F Q E A Q S R L N E A A A G L N Q A A

```

```

                                     Eco57
                                BstXI      BseR1      Bsu36      AlwNI      EagI
                                |          |          |          |          |
CACAGAACTGGTGCAAGCCTCCCGAGGAACTCCTCAGGACCTGGCTCGGGCCTCCGGCCGATTTGGACAGGACTTCAGCACCTTCTGGAAGCTGGTGTG
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
GTGTCTTGACCACGTTTCGGAGGGCTCCTTGAGGAGTCCTGGACCGAGCCCGGAGGCCGGCTAAACCTGTCTGAAGTCGTGGAAGGACCTTCGACCACAC
Talin > T E L V Q A S R G T P Q D L A R A S G R F G Q D F S T F L E A G V

```

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                                SfiI
                                BglI
                                |
GAGATGGCCGGACAGGCCCCGAGCCAGGAGGACCCAGCCAGGTGGTGTCCAACCTGAAGGGCATATCCATGTCTTCAAGCAAACCTTCTCCTTGCCGCTA
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
CTCTACCGGCCTGTCCGGGGCTCGGTCCTCCTGGCTCGGGTCCACCACAGGTTGGACTTCCCGTATAGGTACAGAAGTTTCGTTTGAAGAGGAACGGCGAT
Talin > E M A G Q A P S Q E D R A Q V V S N L K G I S M S S S K L L L A A K

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SpAcc Pst1                               BstE2
|                                           |
CTGCAGGAGTCGTTGGCGGCATGGTGGACTCTATCACTCAGGCCATCAACCAGCTAGATGAAGGACCTATGGGTGACCCAGAAGGCTCATTTCGTAGATTA
6101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6200
GACGTCCTCAGCAACCGCCGTACCACCTGAGATAGTGAGTCCGGTAGTTGGTTCGATCTACTTCTGGATACCCACTGGGTCTTCCGAGTAAGCATCTAAT
Talin > A G V V G G M V D S I T Q A I N Q L D E G P M G D P E G S F V D Y

SpDon                                     BsrD1                               BstE2                               Sap1
Nco1 |                                     |                                     |                                     |
|     |     |                             |     |                             |     |                             |     |
CCAGACAACCATGGTGAGGACAGCCAAGGCCATTGCTGTCACTGTTTCCAGGAGATGGTAACCAAGTCAAACACCAGCCCTGAAGAGCTAGGCCCTCTTGCC
6201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6300
GGTCTGTTGGTACCACTCCTGTTCGGTTCCGGTAACGACAGTGACAAGTCTCTACCATTGGTTTTCAGTTTGTGGTTCGGGACTTCTCGATCCGGGAGAACGG
Talin > Q T T M V R T A K A I A V T V Q E M V T K S N T S P E E L G P L A

Pvu2                                     SpDon                               Pst1                               Ear1                               SpDon
|                                     |                                     |     |                             |     |                             |     |
AACCAGCTGACCAGTGACTATGGCCGACTGGCCTCAACAAGCCAAGCCTGCAGCTGTGGCTGCTGAAAATGAAGAGATAGGCGCTCACATCAAACACCGAG
6301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6400
TTGGTTCGACTGGTCACTGATAACCGGCTGACCGGAGTGTTCCGGTTCGGACGTCGACACCGACGACTTTTACTTCTCTATCCGCGAGTGATGTTTGTGGCTC
Talin > N Q L T S D Y G R L A S Q A K P A A V A A E N E E I G A H I K H R V

BspM1                                     BseY1                               Aar1                               Bts1                               Sac1
|                                     |     |                             |     |                             |     |                             |     |
|     |     |                             |     |                             |     |                             |     |
TACAGGAGCTGGGCCATGGCTGCTCTGCTCTGGTTCACCAAGGCAGGTGCCTTGCAGTGTAGCCCCAGTGATGTCTACACCAAGAAGGAGCTCATAGAGTG
6401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6500
ATGTCCTCGACCCGGTACCGACGAGACGAGACCAGTGGTTCCGTCCACGGAACGTCACATCGGGGTCACTACAGATGTGGTTCTTCTCGAGTATCTCAC
Talin > Q E L G H G C S A L V T K A G A L Q C S P S D V Y T K K E L I E C

Bpm1                                     Bsa1                               Bsg1                               PflM1                               BseY1                               Kpn1                               Stu1                               BstAP
|                                     |     |                             |     |                             |     |                             |     |                             |     |
|     |     |                             |     |                             |     |                             |     |
TGCCCCGAGAGTGTTCAGAGAAGGTCTCCCATGTTCTGGCTGCACTCCAGGCTGGGAATCGTGGTACCCAGGCCTGCATTACAGCAGCCAGTGCTGTGTCT
6501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6600
ACGGGCGTCTCACAGTCTCTTCCAGAGGGTACAAGACCGACGTGAGGTCCGACCCTTAGCACCATGGGTCCGGACGTAATGTCGTCGGTCACGACACAGA
Talin > A R R V S E K V S H V L A A L Q A G N R G T Q A C I T A A S A V S

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BsrD1
|
GGTATCATTGCTGACCTCGACACCACCATCATGTTTCGCTACTGCTGGCACACTTAACCGTGAGGGTGTCTGAAACTTTTTGCTGACCACCGGGAGGGTATCT
6601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6700
CCATAGTAACGACTGGAGCTGTGGTGGTAGTACAAGCGATGACGACCGTGTGAATTGGCACTCCCACGACTTTGAAAACGACTGGTGGCCCTCCCATAGA
Talin > G I I A D L D T T I M F A T A G T L N R E G A E T F A D H R E G I L

Pvu2
BseY1
|
Drd1 | Bsm1 | Bsg1 | Bmr1 | Msc1
| | | | |
TAAAGACAGCAAAGGTTCTTGTGGAGGACACCAAGGTCCTAGTGCAGAATGCAGCTGGGAGCCAGGAGAAGTTGGCACAAGCCGCCAGTCTCCGTGGC
6701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6800
ATTTCTGTCGTTTCCAAGAACACCTCCTGTGGTTCAGGATCACGTCTTACGTCGACCCTCGGTCTCTTCAACCGTGTTCGGCGGGTCAGGAGGCACCG
Talin > K T A K V L V E D T K V L V Q N A A G S Q E K L A Q A A Q S S V A

Avr2 | Bsg1 | Bbs1 | Bcl1
| | | |
CACCATTACCCGCTCGCTGATGTGGTCAAGCTCGGTGCAGCCAGCCTAGGAGCCGAAGACCCTGAAACTCAGGTGGTGTGATCAATGCAGTAAAGGAC
6801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6900
GTGGTAATGGGCGGAGCGACTACACCAGTTCGAGCCACGTCCGGTCCGATCCTCGGCTTCTGGGACTTTGAGTCCACCACGACTAGTTACGTCATTTCTCG
Talin > T I T R L A D V V K L G A A S L G A E D P E T Q V V L I N A V K D

BstE2 | SpAcc
| |
BstX1 | Afel | Pst1 | BpuE1 | Pst1 | Bts1
| | | | |
GTAGCCAAGGCCCTGGGTGACCTCATCAGCGCTACGAAGGCTGCAGCGGGCAAAGTTGGGGATGACCCTGCAGTGTGGCAGCTCAAGAACTCTGCCAAGG
6901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7000
CATCGGTTCCGGGACCCACTGGAGTAGTCGCGATGCTTCCGACGTCGCCCCGTTTCAACCCCTACTGGGACGTACACCGTTCGAGTTCTTGAGACGGTTCC
Talin > V A K A L G D L I S A T K A A A G K V G D D P A V W Q L K N S A K V

BstE2 | SpAcc | Bgl1
| | |
BstX1 | BpuE1 | BsrD1 | SpAcc | PspOM | Apa1 | Bgl1
| | | | | | |
TGATGGTGACCAATGTGACATCATTGCTCAAGACAGTGAAGGCTGTGGAAGATGAGGCCACCAAAGGCACACGGGCCCTAGAGGCAACCACAGAGCACAT
7001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7100
ACTACCACTGGTTACTACTGTAGTAACGAGTTCTGTCACTTCCGACACCTTCTACTCCGGTGGTTTCCGTGTGCCCGGGATCTCCGTTGGTGTCTCGTGTA
Talin > M V T N V T S L L K T V K A V E D E A T K G T R A L E A T T E H I

```


BstX1 Pvu2 Bpm1 Eco57 Eci1 BtgZ1
 CCAAGAAGCTGGAGCAGCTGAAGCCCAGGGCCAAACCCAAGGAGGCGGATGAGTCCTTGAACCTTTGAGGAACAAATCCTAGAAGCTGCCAAGTCCATCGC
 7601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7700
 GGTTCCTTCGACCTCGTCGACTTCGGGTCCCAGTTTGGGTTCCCTCCGCCTACTCAGGAACTTGAAACTCCTTGTTTAGGATCTTCGACGGTTCAGGTAGCG
Talin > K K L E Q L K P R A K P K E A D E S L N F E E Q I L E A A K S I A

SpDon
 BstX1
 Pst1 Xcm1 BpuE1 _Chi Nar1 Kas1 BstX1
 TGCAGCCACCAGTGCCTGAAAGGCTGCGTCAGCAGCCAGAGGGAGCTGGTGGCTCAAGGAGAGGTGGGCGCCATTCCAGCCAATGCCTGGATGAT
 7701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7800
 ACGTCGGTGGTCACGTGACCATTTCCGACGCAGTCGTCGGGTCTCCCTCGACCACCGAGTTCCCTCTCCACCCGCGGTAAGGTCGGTTACGTGACCTACTA
Talin > A A T S A L V K A A S A A Q R E L V A Q G E V G A I P A N A L D D

Bts1 Pvu2 Nhe1
 GGGCAGTGGTCGAGGGCCTCATTTCGCTGCCCCTATGGTGGCTGCGGCCACCAACAATCTGTGTGAAGCAGCTAACGCAGCTGTCCAGGGCCATGCTA
 7801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7900
 CCCGTCACCAGCGTCCCGGAGTAAAGGCGACGGGCATACCACCGACCCGGTGGTTGTTAGACACACTTCGTCGATTGCGTCGACAGGTCCCAGGTACGAT
Talin > G Q W S Q G L I S A A R M V A A A T N N L C E A A N A A V Q G H A S

SpAcc
 Bpu10 BbvC1 Blp1 SpAcc AlwN1 Bpm1
 GCCAGGAGAACTCATTTCCTCAGCCAAGTAGCTGCCTCCACAGCTCAGCTCCTGGTAGCTTGAAGGTCAAAGCAGATCAGGACTCTGAGGCAAT
 7901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 8000
 CGGTCTCTTTGAGTAAAGGAGTCGGTTCGTTTCATCGACGGAGGTGTCGAGTCGAGGACCATCGAACGTTCCAGTTTCGTCTAGTCCTGAGACTCCGTTA
Talin > Q E K L I S S A K Q V A A S T A Q L L V A C K V K A D Q D S E A M

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                                EcoN1
                                SpDon
                                BsmB1
BsrD1      BstX1      BsrD1      Ear1      Bts1      SexA1      Pst1BstB1      Bbs1
|          |          |          |          |          |          |          |
8001  GAAACGGCTCCAGGCTGCTGGCAATGCAGTGAAGAGGGCCCTCAGATAACCTGGTAAAGGCGGCCCCAGAAAGCTGCAGCCTTCGAAGACCAGGAGAATGAG 8100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 8100
      CTTTGCCGAGGTCCGACGACCGTTACGTCACCTTCTCCCGGAGTCTATTGGACCATTTCCGCCGGGTCTTTTCGACGTTCGGAAGCTTCTGGTCCTCTTACTC
Talin  > K R L Q A A G N A V K R A S D N L V K A A Q K A A A F E D Q E N E

                                SpAcc
                                Ear1
SpDon      BsrD1      Ear1
|          |          |
8101  ACGGTGGTGGTGAAGGAGAAAATGGTTGGGGGCATTGCCCAGATTATCGCAGCACAGGAAGAGATGCTTCGGAAGGAACGAGAGCTGGAAGAGGCTCGGA 8200
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 8200
      TGCCACCACCACTTCTCTTTTACCAACCCCGTAACGGGTCTAATAGCGTTCGTGTCTTCTCTACGAAGCCTTCCTTGCTCTCGACCTTCTCCGAGCCT
Talin  > T V V V K E K M V G G I A Q I I A A Q E E M L R K E R E L E E A R K

                                Eco57      BsmB1      BseY1
                                |          |          |
8201  AAAAGCTCGCCCAGATCCGGCAGCAGCAGTACAAGTTCTTGCCTTCAGAGCTTCGAGACGAGCACGGCGCTGGGTCCGGGTCCGGGCAAGGGTCCGGCGC 8300
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 8300
      TTTTCGAGCGGGTCTAGGCCGTCGTCGTCATGTTCAAGAACGGAAGTCTCGAAGCTCTGCTCGTGCCGCGACCCAGGCCAGGCCCGTTCCAGGCCGCG
Talin  > K L A Q I R Q Q Q Y K F L P S E L R D E H G A G S G S G Q G S G A

                                SpDon
                                Ale1      Nco1      BsrG1
                                |          |          |          |
8301  AGGCTCCGCGTCCCAGATCACCGGTCGCCACCATGGTGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCGTGAACAACCAC 8400
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 8400
      TCCGAGGCGCAGGGCTAGTGGCCAGCGGTGGTACCACCTCGCTCGACTAATTCCCTCTTGTACGGGTACTTTCGACATGTACCTCCCGTGGCACTTGTGGTG
FusionRed  > G S A S R S P V A T M V S E L I K E N M P M K L Y M E G T V N N H

                                ApaL1      SpAcc
                                |          |
8401  CACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTCGTTCGAGGGCGGCCCTCTCCCTTCGCCTTCG 8500
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 8500
      GTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGC
FusionRed  > H F K C 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

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Not1
Eag1
SpDon BsrB1 Xba1 BsaB1 SpDon Dra1

9001 ACTGGTGGCGCTGGTGATGGAGGTAAATGAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTC 9100
TGACCACCGCGACCACTACCTCCATTTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAACATCTCCAAAATGAACGAAATTTTTTGGAG
FusionRed > T G G A G D G G K *

Bsm1 MfeI HpaI polyA PstI polyA

9101 CCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCA 9200
GGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTGCAATATTACCAATGTTTATTTTCGTTATCGTAGT

polyA BtsI Bsm1 AflII SpDon SspI

9201 CAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTT 9300
GTTTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGTAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAA

PstI

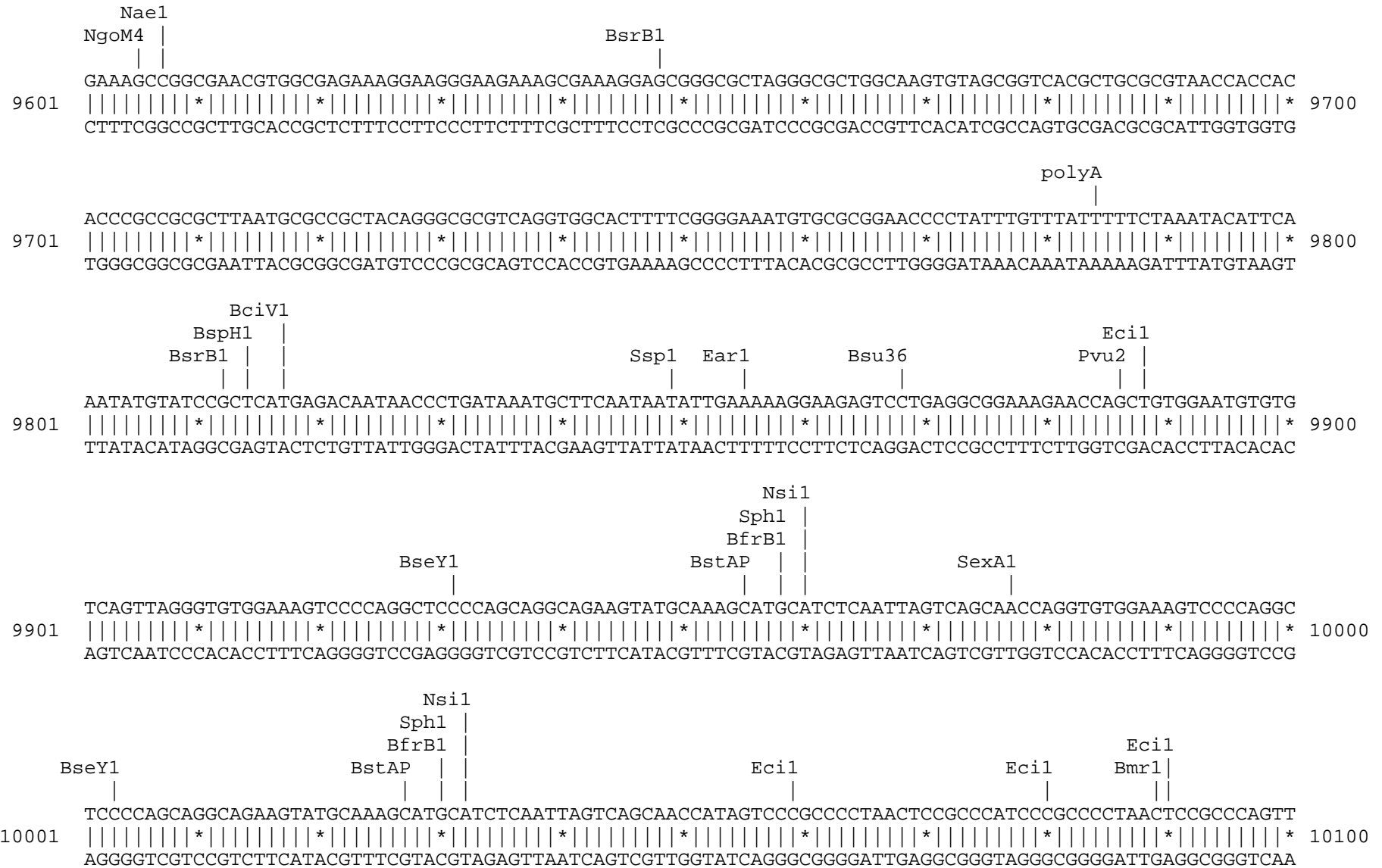
9301 TGTTAAATTCGCGTTAAATTTTTGTAAATCAGCTCATTTTTTAAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGAT 9400
ACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTA

BsaXb DrdI BsaXa

9401 AGGGTTGAGTGTGTTCCAGTTTTGGAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCA 9500
TCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTTTTGGCAGATAGTCCCGCTACCGGGT

BtgZ1 Dra3 SpAcc

9501 CTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCTAAAGGGAGCCCCCGATTAGAGCTTGACGGG 9600
GATGCACCTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCC




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                                     NaeI
                                     |
BssS1                               SpAcc                               NgoM4 |
BspM1                               |                               Bpm1 |
|                                   |                               |
11101 GCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 11200
      CGGTAGTGCTCTAAAGCTAAGGTGGCGGC GGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTA

                                     Bpm1
                                     |
                                     SpAcc
                                     |
                                     Avr2
                                     |
11201 CTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATAACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 11300
      GAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTG

polyA                               BsaI
|                                   |
11301 AGAATAAAACGCACGGTGTGGGTTCGTTTGTTCATAAACCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGATAACCCACCGAGACCCCATTTGGGGCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 11400
      TCTTATTTTTCGCTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGT

                                     BstAP
                                     |
                                     AlwN1
                                     |
11401 ATACGCCCCGCTTTCTTCCTTTTCCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 11500
      TATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGG

Bsu36                               DraI                               DraI                               BspH1
|                                   |                                   |                                   |
11501 TCAGGTTACTCATATATACTTTAGATTGATTTTAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 11600
      AGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGG

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                                            BpuE1
                                                |
11601  CTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCA
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      GAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGT 11700

                                            Eco57
                                                |
11701  AACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCA
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      TTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAACGGCCTAGTTCTCGATGGTTGAGAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGT 11800

      SpAcc
      |
11801  AATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACC GCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTG
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      TTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGACAATGGTCACCGAC 11900

                                            BpuE1
                                                |
                                            ApaL1
                                                |
11901  CTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGCGGGCTGAACGGGGGGTTCGTGCACACA
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      GACGGTCAACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGACTTGCCCCCAAGCACGTGTGT 12000

BseY1
|
12001  GCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTAT
      |||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*
      CGGGTCGAACCTCGCTTGCTGGATGTGGCTTACTCTATGGATGTGCGACTCGATACTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCGTGTCCATA 12100
    
```

```
          BciV1
          Eci1  |
          |
          |          BssS1
          |          |
          |          |          SpAcc
          |          |          |
12101  CCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGAC
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 12200
      GGCCATTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTG
```

```
          Drd1          BpuE1          SpAcc          Eci1
          |          |          |          |
          |          |          |          |
12201  TTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTT
      | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 12300
      AACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTGCGGTTCGTTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAA
```

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          SpDon          Nsil
          BspLU |          BfrB1 |
          |          |
          |          |
12301  TGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
      | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 12364
      ACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aar1	Aat2	Acc65	Acl1	Afe1	Afl2	Age1	Ahd1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2
Baela	Baelb	BamH1	Bbs1	BbvC1	Bcg1a	Bcg1b	BciV1	Bcl1	BfrB1	Bgl1	Bgl2	Blp1	BmgB1
Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BsmB1	BspH1
BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstE2	BstX1	Bsu36	BtgZ1	Bts1	_Chi
Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoN1	EcoR1	EcoRV	Fse1	Fsp1
Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1
PflF1	PflM1	Pml1	polyA	PshA1	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sall	SanD1	Sap1
Sca1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Srf1	Ssp1	Stu1	Xba1	Xcm1	Xho1
Xmn1													

Unique:

Acc65	Acl1	Age1	Ahd1	Ase1	Baela	Baelb	BamH1	Bcg1a	Bcg1b	Bcl1	BmgB1	Clal	EcoR1
EcoRV	Fse1	Hpa1	Kpn1	Mfe1	Nde1	Not1	Rsr2	Sall	Sca1	Sma1	SnaB1	Srf1	

Not found:

Asc1	AsiS1	BsiW1	BspE1	BssH2	BstZ1	BxatB	BxatL	BxatR	BxatP	EcoK	FCatB	FCatL	FCatR
FCatP	ScFRT	FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pvu1	R4atB	R4atL	R4atP	R4atR
Sac2	Sbf1	Sgf1	SgrA1	Spe1	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	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	Hinfl	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													