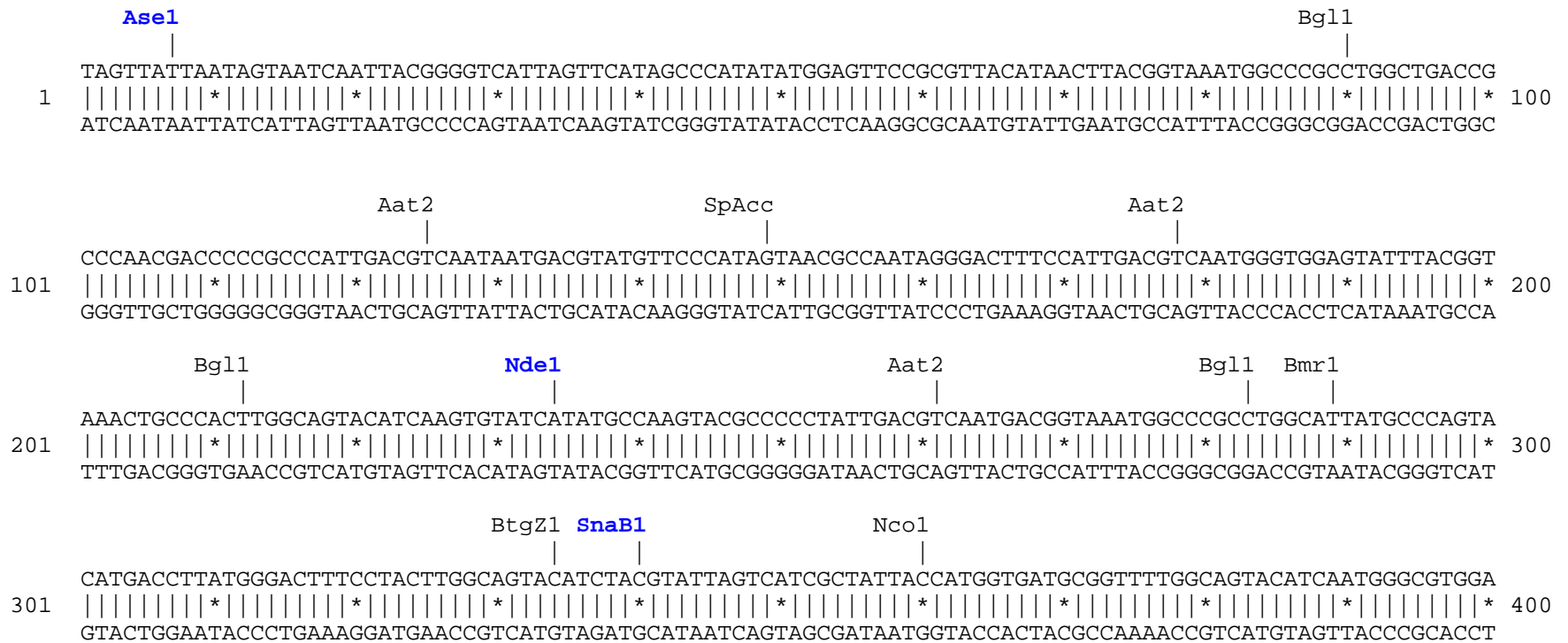


pFusionRed-myosin vector restriction map

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, mouse myosin light polypeptide 9 amino acids are shown in green, linker amino acids are shown in black.



```

                        Aat2                                  Eci1
                        |                                  |
401 TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTTGTTTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTA
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*|||* 500
    ATCGCCAAACTGAGTGCCCTAAAGGTTTACAGAGGTGGGGTAACTGCAGTTACCCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
                                             Nhe1 Afel
                                             |   |
501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*|||* 600
    TGTGTAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
                     SpDon
                   Ale1 |
                 Agel | Nco1 | |
601 CCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCCTGAACAACCACCACTTCAAGTGACATCCG
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*|||* 700
    GGCCAGCGGTGGTACCACTCGCTCGACTAATTCTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTCACGTGTAGGC
FusionRed >    M V S E L I K E N M P M K L Y M E G T V N N H H F K C T S E
                                                    BsrGI
                                                    |
                                                    SpDon
                                                    |
                                                    ApaL1
                                                    |
                                                    |
701 AGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTCGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*|||* 800
    TCCCCTTCCTCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCACGAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAA
FusionRed >    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 T S F
                                                    Bsu36
                                                    |
                                                    SpDon
                                                    |
801 CATGTACGGCAGCAGAACCTTCATCAAGCACCCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCCTTCGAGGGCTTCACATGGGAGAGAGTACACCACA
    |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*|||* 900
    GTACATGCCGTCGTCTTGGAAGTAGTTCGTGGGAGGCCCGTAGGGGCTGAAGAAATTCGTGAGGAGGGACTCCCGAAGTGTACCCCTCTCTCAGTGGTGT
FusionRed >    M Y G S R T F I K H P P G I P D F F K Q S F P E G F T W E R V T T
```

Bbs1 Bpm1 BseY1
TACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCA
901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
ATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTTCGGT
FusionRed > 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 V R G V N F P A N

BsmB1 BseY1 StuI BglI
ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGGCGCATGTGACATGGCCCT
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGA
FusionRed > G P V M Q K K T L G W E A S T E T M Y P A D G G L E G A C D M A L

BssS1 Eco57 BsaI BpuE1 BpuE1
GAAGCTCGTGGGCGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACTCAAGATGCCCGGCGTCTACAACGTG
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTTCGAGACCCGCCCCGGTGGACTAGACGTTGGAACCTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGAGATGTTGCAC
FusionRed > K L V G G G H L I C N L E T T Y R S K K P A T N L K M P G V Y N V

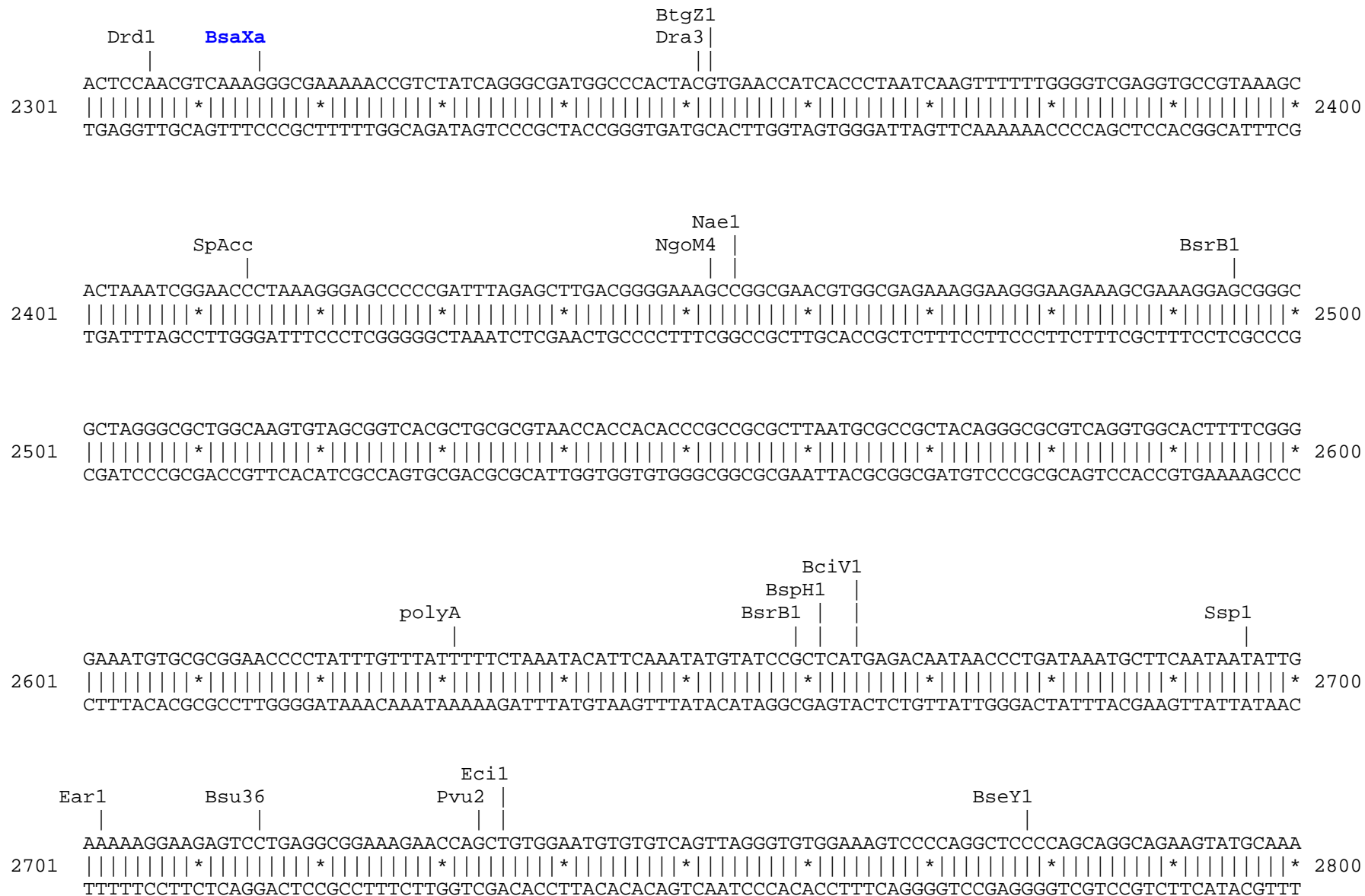
SpAcc PflM1 BsaI PshA1 BssS1 Dra3 MscI
GACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGTATG
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
CTGGTGTCTGACCTTTCTTAGTTCTCCGGCTGCTACTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCACCCTAC
FusionRed > D H R L E R I K E A D D E T Y V E Q H E V A V A R Y S T G G A G D G

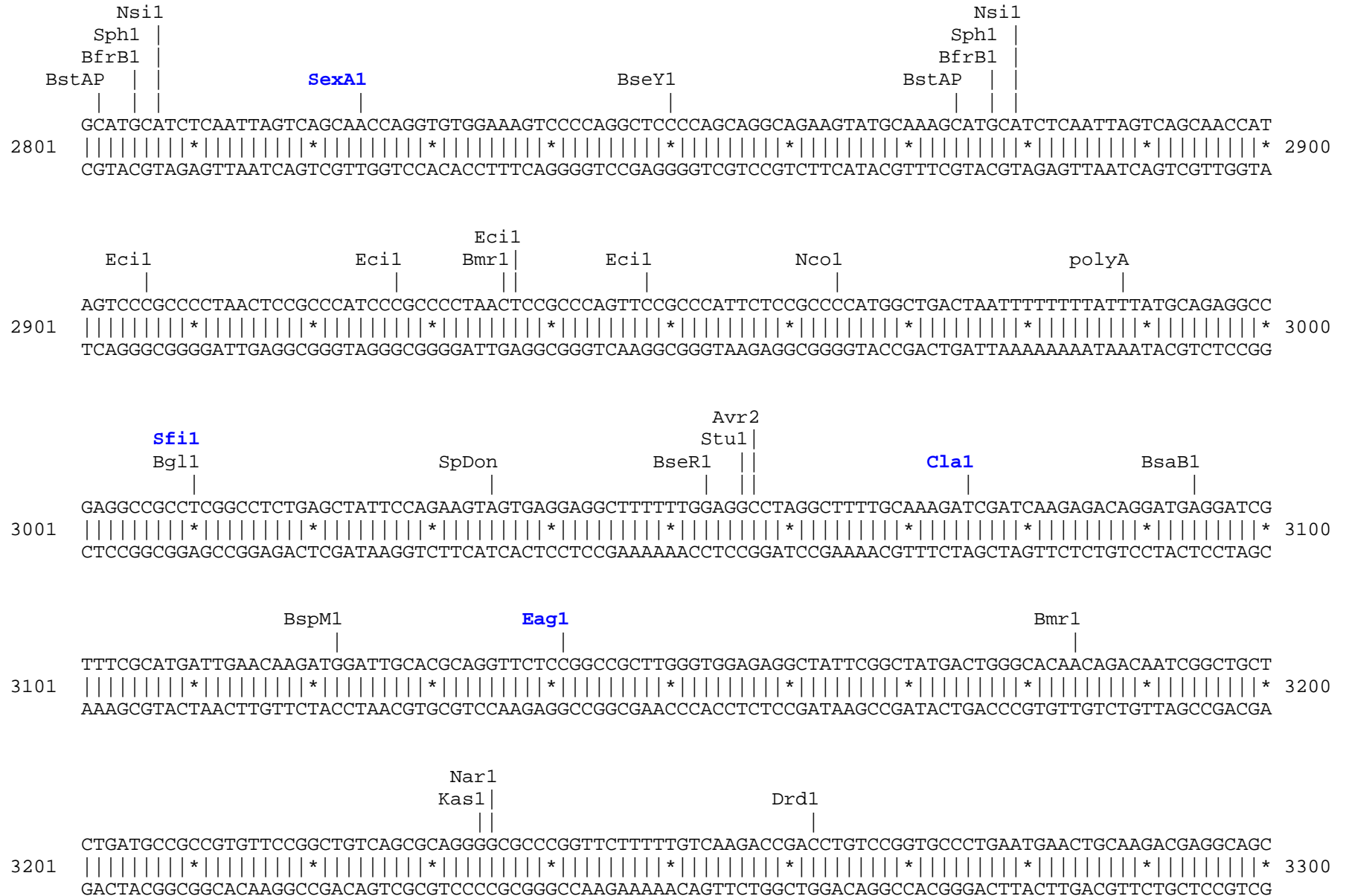
```
                                Xho1  
                               Bgl12  
                              BseR1  
                             BpuE1  
                            BspE1  
                           SpDon  
                          GAGGTAAAGGTGGAGGAGGTTCCGGACTCAGATCTCGAGCTCAAGCTTCGATGTCGAGCAAGAGAGCCAAGGCCAAGACCACCAAGAAGAGGCCCCAGAG  
1301 |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * 1400  
CTCCATTTCCACCTCCTCCAAGGCCTGAGTCTAGAGCTCGAGTTTCGAAGCTACAGCTCGTTTCTCTCGGTTCCGGTTCTGGTGGTTCTTTCTCCGGGGTCTC  
FusionRed/ > G K G G G S G L R S R A Q A S M S S K R A K A K T T K K R P Q R  
Myosin
```

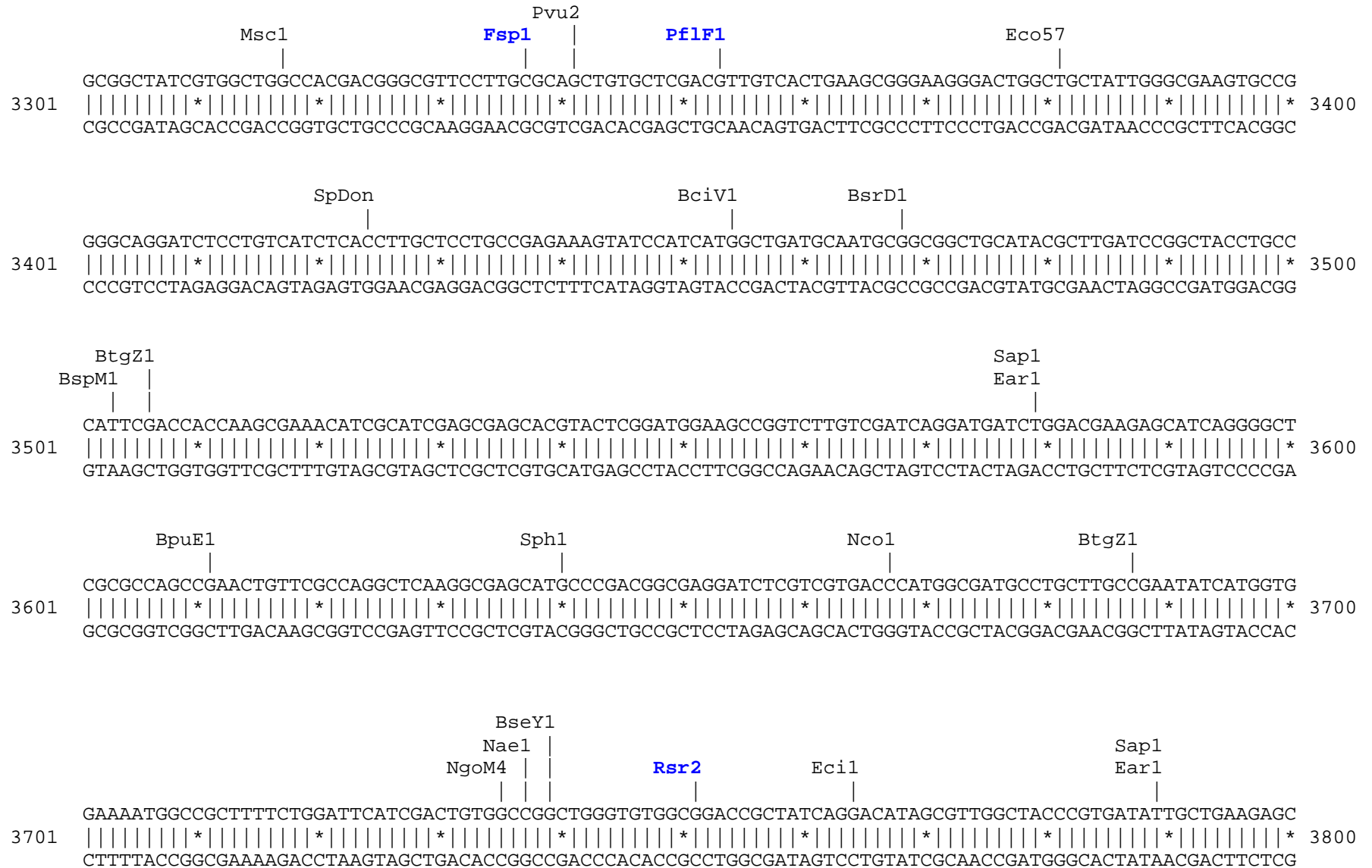
```
                                Bbs1  
                                Stu1  
                               Bcl1  
                               Bsg1  
                               BtgZ1  
                             GGCTACGTCCAATGCTTCGCCATGTTTGACCAGTCCCAGATCCAGGAGTTTAAAGGAGGCCCTTCAACATGATTGATCAGAACCGCGATGGCTTCATTGAT  
1401 |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * 1500  
CCGATGCAGGTTACAGAAGCGGTACAAACTGGTCAAGGCTTAGGTCCTCAAATTCCTCCGGAAGTTGTAATACTAGTCTTTGGCGCTACCGAAGTAACCTA  
Myosin > A T S N V F A M F D Q S Q I Q E F K E A F N M I D Q N R D G F I D
```

```
                                BspM1  
                                BspLU  
                                SpAcc  
                                Nar1  
                                Bpm1  
                                Kas1  
                                PspOM  
                                Apa1  
                             AAGGAGGACCTGCACGACATGTTGGCCTCTCTGGGGGAAGAACCCACAGACGAGTACCTGGAGGGCATGATGAACGAGGCGCCAGGGGCCATCAACTTCA  
1501 |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * 1600  
TTCTCCTGGACGTGCTGTACAACCGGAGAGACCCCTTCTTGGGGTGTCTGCTCATGGACCTCCCGTACTACTTGTCTCCGCGGTCCCGGGTAGTTGAAGT  
Myosin > K E D L H D M L A S L G K N P T D E Y L E G M M N E A P G P I N F T
```

```
                                SpDon  
                                SpDon  
                                BsrD1  
                                Bsu36  
                                Stu1  
                                BseR1  
                             CCATGTTCTCACAATGTTTGGGGAGAAGCTGAACGGCACAGACCCCGAGGATGTGATCCGCAATGCCTTTGCCTGCTTTGATGAGGAGGCCCTCAGGCTT  
1601 |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * |||||||| * 1700  
GGTACAAGGAGTGTACAACCCCTCTTCGACTTGCCGTGTCTGGGGCTCCTACACTAGGCGTTACGGAAACGGACGAAACTACTCCTCCGGAGTCCGAA  
Myosin > M F L T M F G E K L N G T D P E D V I R N A F A C F D E E A S G F
```






```

                                     BspH1
                                     |
4401 AAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
   TTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTT

                                     BpuE1
                                     |
4501 GGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
   CCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTGCACCACAAACAAACGGCCTAGTTCTCGATG

      Eco57                                     SpAcc
      |                                     |
4601 CAACTCTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATAACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
   GTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACA

                                     AlwN1                                     BpuE1
                                     |                                     |
4701 AGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
   TCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAAT

                                     ApaL1       BseY1                                     SpAcc
                                     |         |                                     |
4801 CCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
   GGCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTTCGAACCTCGCTTGTGGATGTGGCTTACTCTATGGATGTGCACTCG

                                     BciV1
                                     |         |
4901 TATGAGAAAGCGCCACGCTTCCCGAAGGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
   ATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCC
```

```
                SpAcc                Drd1                BpuE1                SpAcc                Eci1
                |                    |                    |                    |                    |
5001 AAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
   TTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTG
```

```
                SpDon
                BspLU|
                ||
5101 GCCAGCAACGCGGCCTTTTTTACGGTTCCTGGCCTTTTGGCTGGCCTTTTGGCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
   CGGTCGTTGCGCCGAAAAATGCCAAGGACCGAAAAACGACCGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAAT
```

```
                Nsi1
                BfrB1 |
                ||
5201 CCGCCATGCAT
   |||||*| 5211
   GGCGGTACGTA
```

Found:

Aat2	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1	BfrB1
Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BsmB1
BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal
Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Ecl2	Eco57	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Mlu1
Msc1	Nae1	Nar1	Nco1	Nde1	Ngom4	Nhe1	Nsi1	PflF1	PflM1	polyA	PshA1	Psi1	PspOM
Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfi1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1

Unique:

Afe1	Age1	Ale1	Apa1	Ase1	BamH1	Bgl2	BsaXa	BsaXb	Bsg1	BsmB1	BspE1	BsrG1	BstB1
Bts1	Clal	Eag1	Ecl2	Fsp1	Hind3	Hpa1	Mfe1	Mlu1	Nde1	Nhe1	PflF1	PflM1	PshA1
PspOM	Rsr2	Sac1	SexA1	Sfi1	SnaB1	Xba1	Xho1						

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	BcglA	Bcglb	Blp1	BmgB1
Bpu10	BsiW1	BssH2	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoR1
EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1
Pme1	Pml1	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1	Sca1	Sgf1
SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1			

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	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													