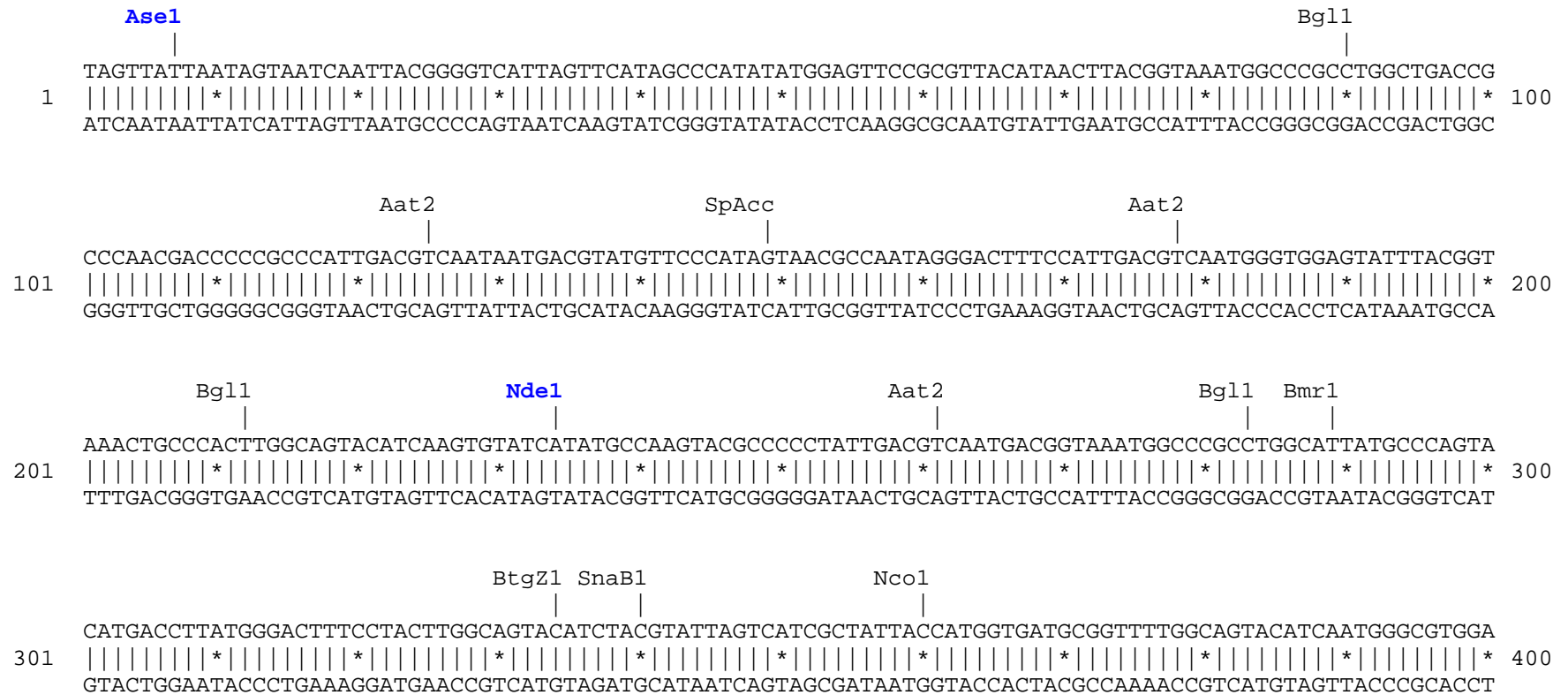


pFusionRed-paxillin vector restriction map

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 base pairs 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, paxillin amino acids are shown in green, linker amino acids are shown in black.



NaeI
NcoM4 | PflM1

1401 GATGAGCTGATGGCGTCCCTCTCTGACTTTTAAAGTTTCATGGCACAGGGGAAAGCCGGCGGCAGCAGCTCCCCACCATCCACCACCCCAAAAGCCTGGCAGTC 1500
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
 CTACTCGACTACCGCAGGGAGAGACTGAAATTC AAGTACCGTGTCCCTTTTCGGCCGCCGTTCGTCGAGGGGTGGTAGGTGGTGGGGTTTCGGACCGTCAG
 paxillin > D E L M A S L S D F K F M A Q G K A G G S S S P P S T T P K P G S Q

Pvu2 BseY1 Pst1 Bmr1 SpAcc BspM1 BseY1

1501 AGCTGGACACCATGCTGGGAAGTCTGCAGTCTGACCTGAACAAACTGGGGGTAGCGACGGTGC CCAAGGGTGTGTGCGGAGCCTGCAAGAAGCCGATTGC 1600
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
 TCGACCTGTGGTACGACCCTTCAGACGTCAGACTGGACTTGTGTTTGACCCCCATCGCTGCCAGCGGTTCCACACACGCCTCGGACGTTCTTCGGCTAACG
 paxillin > L D T M L G S L Q S D L N K L G V A T V A K G V C G A C K K P I A

Bpu10 BstAP
NcoI BbsI Bsp1 Bts1 XcmI BseR1 BsrB1

1601 TGGGCAGGTAGTTACAGCCATGGGGAAGACCTGGCACCCCTGAGCACTTCGTCTGCACCCACTGCCAGGAGGAGATTGGATCACGGAACCTTCTTTGAGCGG 1700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
 ACCCGTCCATCAATGTCGGTACCCCTTCTGGACCGTGGGACTCGTGAAGCAGACGTTGGGTGACGGTCTCCTCTAACCTAGTGCCTTGAAGAACTCGCC
 paxillin > G Q V V T A M G K T W H P E H F V C T H C Q E E I G S R N F F E R

SpAcc BseR1 Ear1 BsrD1

1701 GATGGGCAGCCCTACTGTGAGAAGGACTATCACAACCTCTTCTCTCCTCGCTGCTACTACTGCAATGGGCCAATCCTTGATAAAGTGGTGACGGCTTTGG 1800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
 CTACCCGTCGGGATGACACTCTTCTGATAGTGTGGAGAAGAGAGAGCGACGATGATGACGTTACCCGGTTAGGAACTATTTACCACCTGCCGAAACC
 paxillin > D G Q P Y C E K D Y H N L F S P R C Y Y C N G P I L D K V V T A L D

BmgB1 Bmr1 Xmn1 Eco57 BspH1

1801 ACAGGACGTGGCACCCCTGAACACTTTTTCTGTGCCAGTGTGGAGTTTTCTTTGGACCTGAAGGATTTTCATGAGAAGGATGGCAAAGCCTATTGCCGCAA 1900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1900
 TGTCTGCACCGTGGGACTTGTGAAAAAGACACGGGTCACACCTCAAAGAAACCTGGACTTCTTAAAGTACTCTTCTACCGTTTTCGGATAACGGCGTT
 paxillin > R T W H P E H F F C A Q C G V F F G P E G F H E K D G K A Y C R K

Restriction enzyme sites: Sma1, BamH1, Apal, PspOM, Sac2, SpDon, Ale1, Nco1, Age1, BsrG1, Sall, Kpn1, Acc65, Pst1.

2301 CAGTCGACGGTACCGCGGGCCCCGGGATCCACCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCG * * * * * 2400
GTCAGCTGCCATGGCGCCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACTCGCTCGACTAATTCTTGTACGGGTACTTCGACATGTACCTCCCGTGGC
Fusionred > Q S T V P R A R D P P V A T M V S E L I K E N M P M K L Y M E G T V

Restriction enzyme sites: SpAcc, ApaL1.

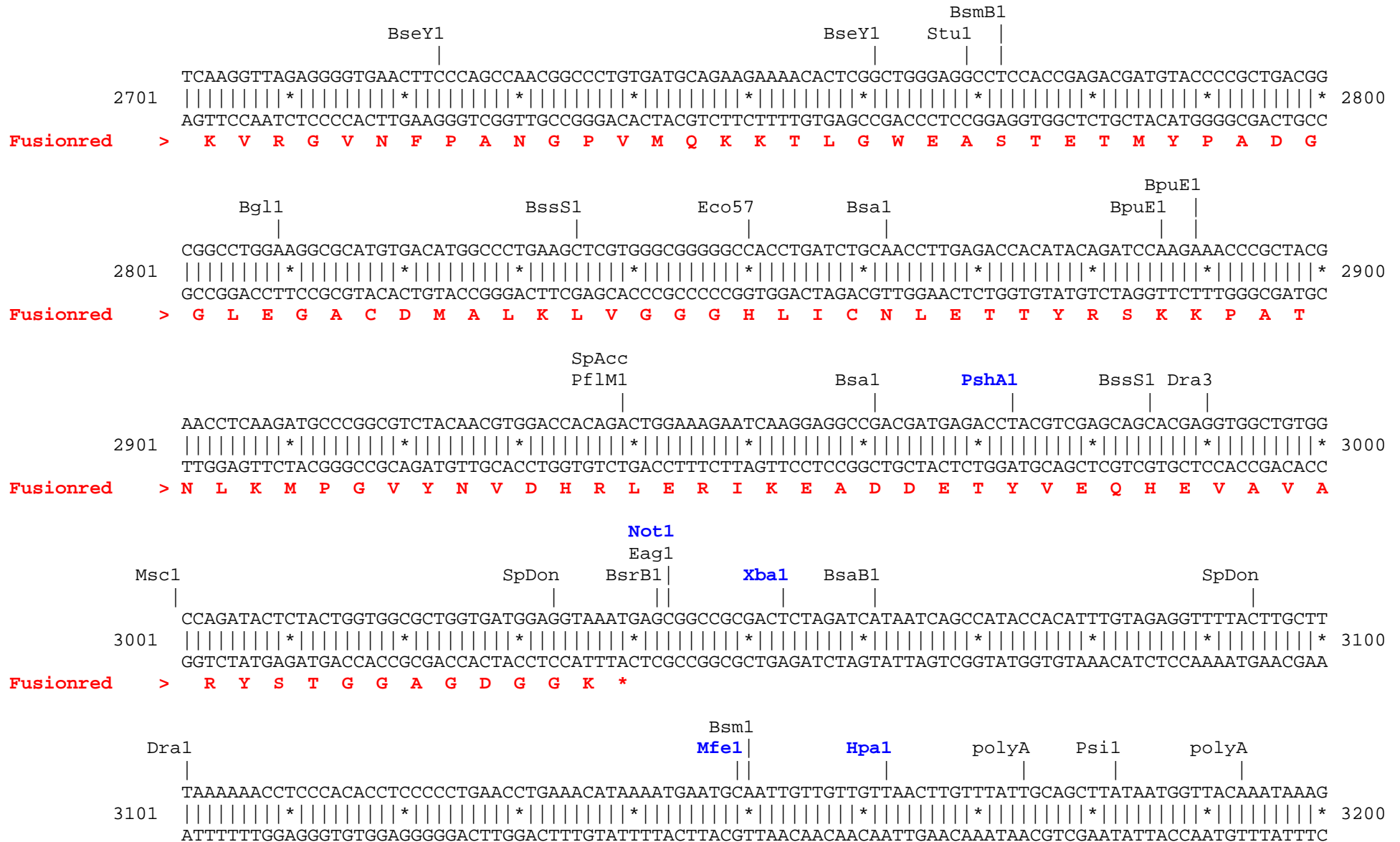
2401 TGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCAGACCATGAGAATCAAGGTCGTCGAGGGCGGCCCTCTCCC * * * * * 2500
ACTTGTGGTGGTGAAGTTACAGTGTAGGCTCCCCGCTTCCGTTCCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCCCCGGGAGAGGG
Fusionred > N N H H F K C T S E G E G K P Y E G T Q T M R I K V V E G G P L P

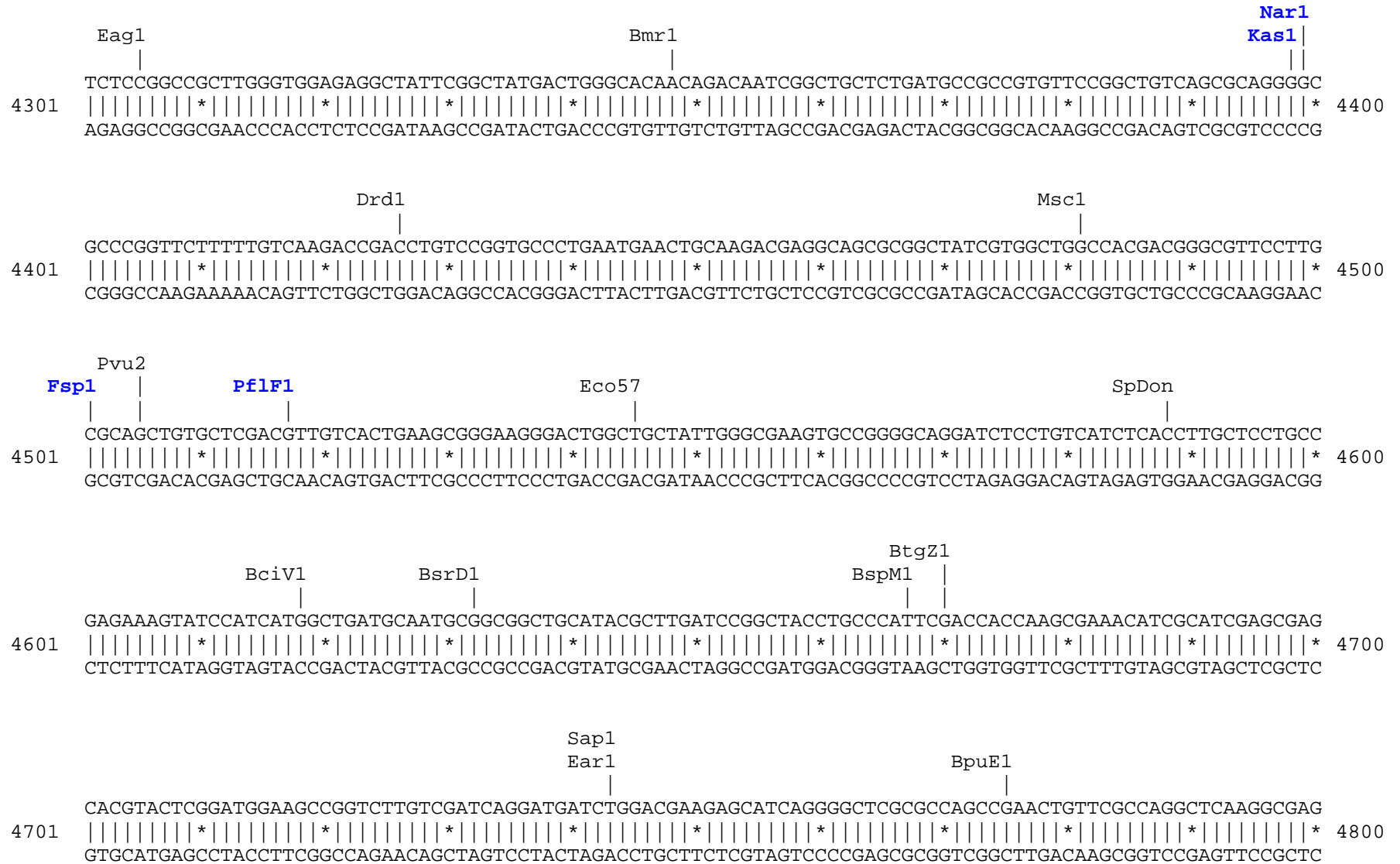
Restriction enzyme sites: Bsu36.

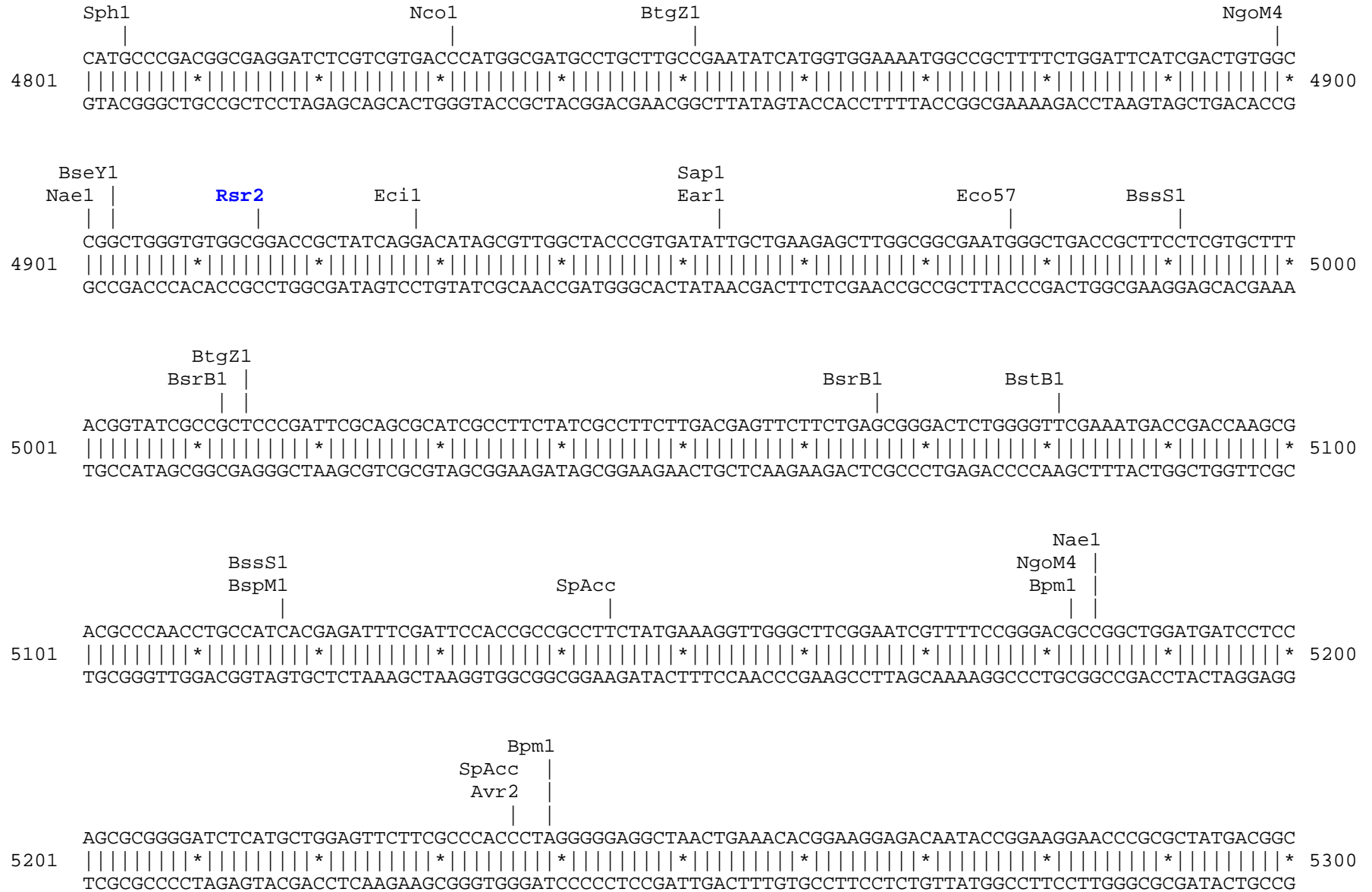
2501 CTTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAAGCACCCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCT * * * * * 2600
GAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTGCTTGGAAAGTAGTTTCGTGGGAGGCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGA
Fusionred > F A F D I L A T S F M Y G S R T F I K H P P G I P D F F K Q S F P

Restriction enzyme sites: SpDon, Bbs1, Bpm1.

2601 GAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACG * * * * * 2700
CTCCCGAAGTGTACCCCTCTCAGTGGTGTATGCTTCTGCCCGGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCCTGCCGACGGAGTAGATGTTGC
Fusionred > E G F T W E R 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







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polyA          polyA                              Bsa1
|              |                                   |
AATAAAAAAGACAGAATAAAACGCACGGTGTGGGTGCGTTTGTTCATAAACCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTTCGATACCCCACCGAGACCC
5301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
TTATTTTTCTGTCTTATTTTTCGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGG

CATTGGGGCCAATACGCCCGCGTTTCTTCTTTTCCCCACCCCAACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCC
5401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
GTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTCCGG

BstAP
AlwN1          Bsu36                Dra1          Dra1          BspH1
|              |                    |              |              |
CTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTTCATTTTTAATTTAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCAT
5501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
GACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTA

GACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATC
5601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
CTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTTCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAG

TGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTCCGAAGGTAAGTGGCTTCAGCAGAG
5701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
ACGACGAACGTTTTGTTTTTTGGTGGCGATGGTTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTC

CGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCCTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTT
5801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5900
GCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAA

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          AlwNI          BpuEI
          |              |
5901 ACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGA C TCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGT
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 6000
      TGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCGCGCTCGCCAGCCCGACTTGCCCCCA

          ApaLI          BseYI          SpAcc
          |              |              |
6001 TCGTGACACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGG
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 6100
      AGCACGTGTGTCGGGTGCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCACTCGATACTCTTTGCGGGTGCGAAGGGCTTCCTCTTTTC

          BciVI          EciI          BssSI          SpAcc
          |              |              |              |
6101 CGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTTCGGTTTTTCG
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 6200
      GCCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAAATATCAGGACAGCCCAAAGC

          DrdI          BpuEI          SpAcc          EciI
          |              |              |              |
6201 CCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTTACGGTTCCTGGCCTTT
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 6300
      GGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAA

          SpDon          BspLU          NsiI          BfrBI
          |              |              |              |
6301 TGCTGGCCTTTTTGCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
      ||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||*||||||||* 6375
      ACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

| | | | | | | | | | | | | | |
|--------------|--------------|--------------|-------------|--------------|-------|--------------|--------------|-------------|-------------|--------------|--------------|--------------|-------------|
| Aat2 | Acc65 | Afl2 | Age1 | Ale1 | AlwN1 | Apa1 | ApaL1 | Ase1 | Avr2 | BamH1 | Bbs1 | Bcg1a | Bcg1b |
| BciV1 | BfrB1 | Bgl1 | Blp1 | BmgB1 | Bmr1 | Bpm1 | Bpu10 | BpuE1 | Bsa1 | BsaB1 | BsaXa | BsaXb | BseR1 |
| BseY1 | Bsg1 | Bsm1 | BsmB1 | BspH1 | BspLU | BspM1 | BsrB1 | BsrD1 | BsrG1 | BssS1 | BstAP | BstB1 | Bsu36 |
| BtgZ1 | Bts1 | _Chi | Clal | Dra1 | Dra3 | Drd1 | Eag1 | Ear1 | Ecil | Ecl2 | Eco57 | EcoR1 | 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 | Sac2 | Sall | Sap1 |
| SexA1 | Sfi1 | SgrA1 | Sma1 | SnaB1 | SpAcc | SpDon | Sph1 | Srf1 | Ssp1 | Stu1 | Xba1 | Xcm1 | Xho1 |
| Xmn1 | | | | | | | | | | | | | |

Unique:

| | | | | | | | | | | | | | |
|--------------|--------------|--------------|-------------|--------------|--------------|-------------|--------------|--------------|--------------|--------------|-------------|--------------|--------------|
| Acc65 | Afl2 | Ale1 | Apa1 | Ase1 | BamH1 | Blp1 | BmgB1 | Bpu10 | BsaXa | BsaXb | _Chi | Clal | EcoR1 |
| Fsp1 | Hind3 | Hpa1 | Kas1 | Kpn1 | Mfe1 | Nar1 | Nde1 | Nhe1 | Not1 | PflF1 | Pml1 | PshA1 | PspOM |
| Rsr2 | Sall | SexA1 | Sfi1 | SgrA1 | Srf1 | Xba1 | Xho1 | Xmn1 | | | | | |

Not found:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Aar1 | Acl1 | Afe1 | Ahd1 | Asc1 | AsiS1 | Baela | Baelb | BbvC1 | Bcl1 | Bgl2 | BsiW1 | BspE1 | BssH2 |
| BstE2 | BstX1 | BstZ1 | BxatB | BxatL | BxatR | BxatP | EcoK | EcoN1 | EcoRV | FCatB | FCatL | FCatR | FCatP |
| ScFRT | Fse1 | FspA1 | I_Ceu | loxP | Mlu1 | Nru1 | Pac1 | Pme1 | Pvu1 | R4atB | R4atL | R4atP | R4atR |
| SanD1 | Sbf1 | Sca1 | Sgf1 | 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 | 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 | | | | | | | | | | | | | |