

pCasper3-GR 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 red. The location given specifies the 3' end of the cut DNA (the base to the left of the cut site). TagRFP amino acids are shown in blue, TagGFP amino acids are shown in green, Linker amino acids are shown in black.



Aat2 Eci1

| |

401 TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
 ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

Nhe1 Afel

| |

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

BamH1
 Sma1 |
 Apa1 | |
 PspOM | | |
 Sac2 | | |
 SpDon
 Ale1 |
 Xho1 Sac1 | EcoR1 Sal1 Kpn1 | | | |
 BpuE1 Bgl2 | Ecl2 | BstB1 | Pst1 | Acc65 | | | | | Agel Nco1 | |

601 CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCCGCCACCATGGTGAGCGAGCTGATTAAGG
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACTCGCTCGACTAATTCC
 TagRFP > M V S E L I K E

BsrG1 ApaL1 SpAcc

| | |

701 AGAACATGCACATGAAGCTGTACATGGAGGGCACCCTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCAGCCAGAC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 TCTTGACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTACAGTGTAGGCTCCCGCTTCCGTTCCGGATGCTCCCGTGGGTCTG
 TagRFP > N M H M K L Y M E G T V N N H H F K C T S E G E G K P Y E G T Q T

801 CATGAGAAATCAAGGTGGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 GTACTCTTAGTTCCACCAGCTCCCGCCGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCGTCTTGGAAGTAGTTGGTGTGG
 TagRFP > M R I K V V E G G P L P F A F D I L A T S F M Y G S R T F I N H T

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                                     Bsu36      SpDon      Bbs1      Bpm1
                                     |          |          |          |
          CAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGG
    901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
          GTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCC
TagRFP > Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G V L T A T Q D

                                     BseY1
                                     |
          ACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTG
    1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
          TGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGAC
TagRFP > T S L Q D G C L I Y N V K I R G V N F P S N G P V M Q K K T L G W

                                     Bgl1      BssS1      Eco57
                                     |          |          |
          GGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAAC
    1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
          CCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCCGCGGACCTTCCGTCTTCGCTGTACCGGGACTTTCGAGCACCCCGCCCCGGTGGACTAGACGTTG
TagRFP > E A N T E M L Y P A D G G L E G R S D M A L K L V G G G H L I C N

                                     BpuE1      SpAcc      PflM1      Bsa1
                                     |          |          |          |
          TTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACA
    1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
          AAGTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGGTGTCTGACCTTTCTTAGTTCCCTCCGGCTGT
TagRFP > F K T T Y R S K K P A K N L K M P G V Y Y V D H R L E R I K E A D K

                                     PshA1      BssS1      Dra3      Msc1      AlwN1      SpAcc      Bmr1      BseR1PflF1| |
                                     |          |          |          |          |          |          |          |
          AAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAGAGGAGGCAACAGCGGTGACGAGGTCGA
    1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
          TTCTCTGGATGCAGCTCGTCTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTCTCTCCGTTGTCGCCACTGCTCCAGCT
TagRFP/Linker> E T Y V E Q H E V A V A R Y C D L P S K L G H R G G N S G D E V D
    
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                Kpn1                Nae1                ApaL1
            Acc65 |                 NgoM4 |                 BmgB1 |
                |                 |                 |
 1401  CCGTACCTCAGTCGCCACCGGAAGCGGCGGGAGCTGTTCCGGCCTCGTGCACGAGCTGGACGGGCAGCTGCACGGCCACAAGTTCAGC
                |                 |                 |                 |                 |                 |
                *|                 *|                 *|                 *|                 *|                 *|
 1401  |          |          |          |          |          |          |          |          |          |          |
    G C C A T G G A G T C A G C G G T G G C C T T C G C C G C G C C T C G A C A A G C G G C C G T A G C A C G G G C A C G A C T A G C T C G A C C T G C C G C T G C A C G T G C C G G T G T T C A A G T C G
Linker/TagGFP>  G T S V A T G S G A E L F A G I V P V L I E L D G D V H G H K F S

                                BsaXb                BstE2
                BsaXa    Bsg1                Bpm1    |                Ale1 |
                                |                |                |                |
 1501  GTGCGCGGCGAGGGCGAGGGCGACCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCCCACCCTGGTGA
                                |                |                |                |                |
                                *|                 *|                 *|                 *|                 *|                 *|
 1501  |          |          |          |          |          |          |          |          |          |          |
    C A C G C G C C G C T C C C G C T C C C G C T G C G G C T G A T G C C G T T C G A C C T C T A G T T C A A G T A G A C G T G G T G G C C G T T C G A C G G G C A C G G G A C C G G T G G G A C C A C T
TagGFP          >  V R G E G E G D A D Y G K L E I K F I C T T G K L P V P W P T L V T

                                BstAP                Xmn1
                |                |
 1601  CCACCCCTCTGCTACGGCATCCAGTGCTTCGCCCCTACCCCAGGACACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCCGAGGGCTACATCCAGGA
                                |                |
                                *|                 *|                 *|                 *|                 *|                 *|
 1601  |          |          |          |          |          |          |          |          |          |          |
    G G T G G G A G A C G A T G C C G T A G G T C A C G A A G C G G G C G A T G G G G C T C G T G T A C T T C T A C T T G C T G A A G A A G T T C T C G C G G T A C G G G C T C C C G A T G T A G G T C C T
TagGFP          >  T L C Y G I Q C F A R Y P E H M K M N D F F K S A M P E G Y I Q E

                SpAcc
                Earl |
                EcoN1 | |
                | |
 1701  GCGCACCATCCTCTTCCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTTCGAGGGCGACACCCTGGTGAACCCGCATCGAGCTGAAGGGCAAG
                | |                 | |                 | |                 | |                 | |                 | |
                *|                 *|                 *|                 *|                 *|                 *|                 *|                 *|
 1701  |          |          |          |          |          |          |          |          |          |          |
    C G C G T G G T A G G A G A A G G T C C T G C T G C C G T T C A T G T T C T G G G C G C C G C T C C A C T T C A A G C T C C C G C T G T G G G A C C A C T T G G C G T A G C T C G A C T T C C C G T T C
TagGFP          >  R T I L F Q D D G K Y K T R G E V K F E G D T L V N R I E L K G K

                                BsrG1
                Eco57                PflM1                Bpm1 Dra3 |                Xcm1
                |                 |                 |                |                |                |
 1801  GACTTCAAGGAGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTGTACATCATGCCCCGACAAGGCCAACAACGGCCTGG
                |                 |                 |                |                |                |
                *|                 *|                 *|                 *|                 *|                 *|                 *|                 *|
 1801  |          |          |          |          |          |          |          |          |          |          |
    C T G A A G T T C C T C C T G C C G T T G T A G G A C C C G G T G T T C G A C C T C A T G T C G A A G T T G T C G G T G T T G C A C A T G T A G T A C G G G C T G T T C C G G T T G T T G C C G G A C C
TagGFP          >  D F K E D G N I L G H K L E Y S F N S H N V Y I M P D K A N N G L E

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                                Psil
                                |
2401 TTTTGTAAAATTCGCGTTAAATTTTGTAAAATCAGCTCATTTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAAATCAAAAGAATAGACCGA
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 2500
    AAAACAATTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCT

                                BsaXb           Drd1           BsaXa
                                |               |               |
2501 GATAGGGTTGAGTGTGTTCCAGTTTGGAACAAGAGTCCACTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGC
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 2600
    CTATCCCAACTCACAACAAGGTCAAACCTTGTTCAGGTGATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCG

    BtgZ1
    Dra3 |
    ||
2601 CCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGAC
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 2700
    GGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTG

    NaeI
    NgoM4 |
    ||
2701 GGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCAC
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 2800
    CCCCTTTCGGCCGCTTGCACCGCTTTTCTTCCTTCTTCGCTTTCCTCGCCCGCATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTG

                                                                polyA
                                                                |
2801 CACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACAT
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 2900
    GTGTGGGCGGGCGGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCCTTTACACGCGCCTTGGGGATAAAACAAAATAAAAAGATTTATGTA

                                BciV1
                                BspH1 |
                                BsrB1 | |
                                ||
2901 TCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGT
    | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * 3000
    AGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACA
  
```

Nsi1
Sph1 |
BfrB1 |
BseY1 BstAP | | SexA1
| | | |

```
3001 GTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCA
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      CACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGT 3100
```

Nsi1
Sph1 |
BfrB1 |
BseY1 BstAP | | Eci1 Eci1 Eci1 Bmr1 |
| | | | |

```
3101 GGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCA
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      CCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTATGGGCGGGGATTGAGGCGGGT 3200
```

Eci1 Nco1 polyA Sfi1 Bgl1 SpDon
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

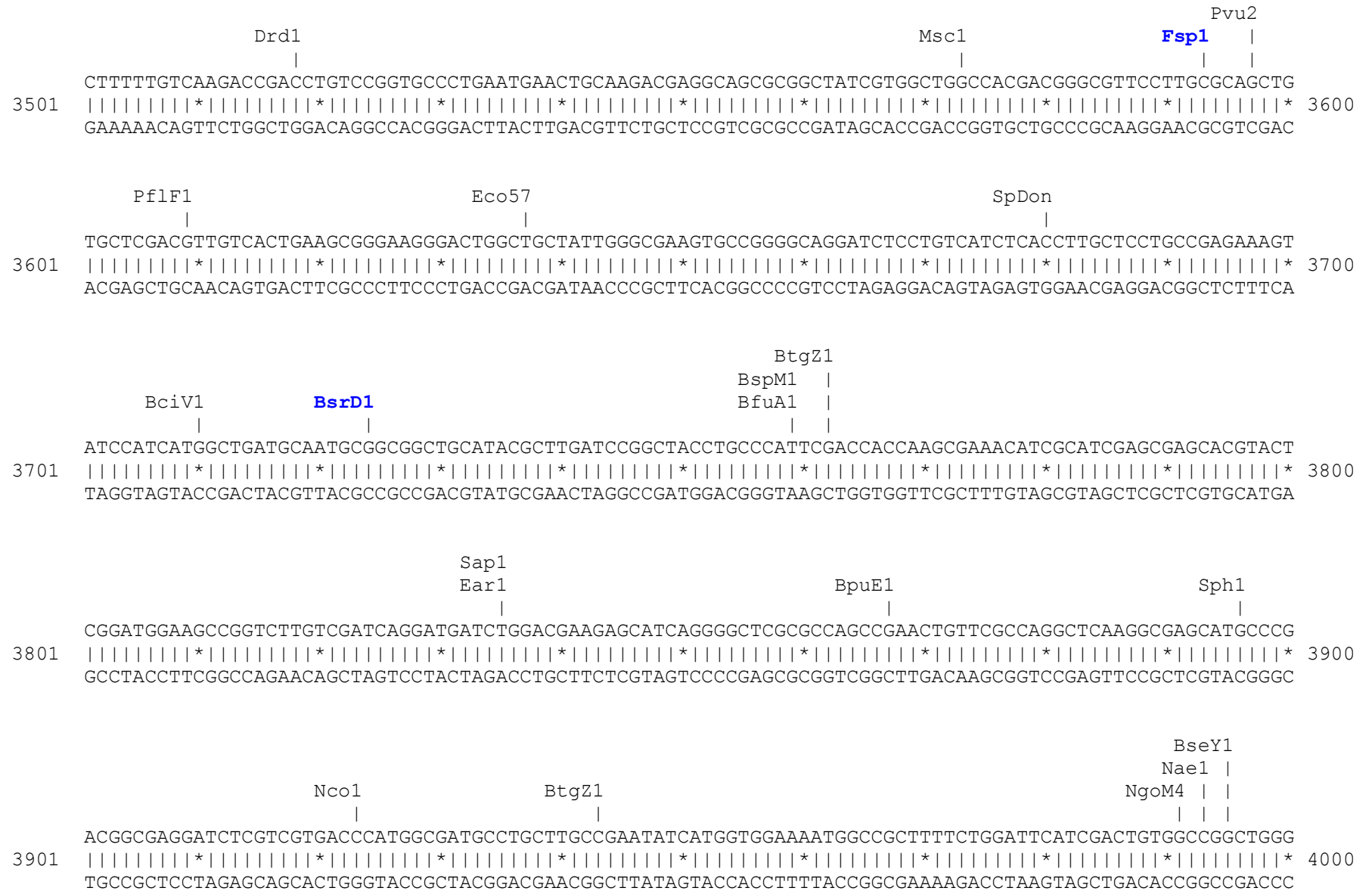
```
3201 GTTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGG
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      CAAGGCGGGTAAAGAGCGGGGTACCGACTGATTAATAAAAAATAAATACGTCTCCGGCTCCGGCGAGCCGAGACTCGATAAGGTCTTCATCACTCCTCC 3300
```

Avr2
Stu1 |
BseR1 | | Cla1 BsaB1 BspM1 BfuA1 Eag1
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```
3301 CTTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGC
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      GAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCG 3400
```

Bmr1 Nar1 Kas1
| |
| |

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3401 CGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTT
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
      GCGAACCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAA 3500
```




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           BseY1                   SpAcc
           |                       |
ACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGG
5101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
TGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCGACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCCTGTCC

           BciV1                   BssS1                   SpAcc
           |   |                   |                       |
TATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTTCGGGTTTCGCCACCTCT
5201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
ATAGGCCATTTCGCCGTCAGCCTTGTCTTCTCGCGTGCTCCCTCGAAGGTCCCCTTTGCGGACCATAGAAATATCAGGACAGCCAAAGCGGTGGAGA

           Drd1                   BpuE1                   SpAcc                   Eci1
           |                   |                   |                   |
GACTTGAGCGTCGATTTTTGTGATGCTTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTTACGGTTCTTGCCCTTTTGTGGCC
5301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
CTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTCGTTGCGCCGAAAAATGCCAAGGACCGAAAAACGACCGG

           SpDon                   BspLU|                   Nsi1                   BfrB1|
           |                   |                   |                   |
TTTTGCTCACATGTTCTTTCTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
5401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5467
AAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	Baela	Baelb	BamH1
Bbs1	BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1
BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP
BstB1	BstE2	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57
EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4
Nhe1	Not1	Nsi1	PflF1	PflM1	polyA	PshA1	Psi1	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2
Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1	Xho1
Xmn1													

Unique:

Afe1	Afl2	Age1	Apa1	Ase1	Baela	Baelb	BamH1	Bbs1	Bgl2	Blp1	BmgB1	Bpu10	BspLU
BsrD1	BstE2	Bts1	Clal	Ecl2	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Nar1	Nde1
Nhe1	Not1	PshA1	PspOM	Pst1	Rsr2	Sac1	SexA1	Sfi1	Sma1	SnaB1	Stu1	Xba1	Xho1
Xmn1													

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	BbvC1	Bcgl1a	Bcgl1b	Bcl1	BsiW1	BsmB1	BspE1	BssH2	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1	R4atB	R4atL	R4atP	R4atR	SanD1
Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swa1	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	Bs11	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													