

pTagGFP2-actin 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). TagGFP2 amino acids are shown in green, beta-actin amino acids are shown in red, linker amino acids are shown in black.



```
                                Aat2                                Eci1
                                |                                |
401 TAGCGGTTTGACTCACGGGGATTTC AAGTCTCCACCCATTGACGTCAATGGGAGTTTGTTTTGGCACC AAAATCAACGGGACTTTCCAAAATGTGCGTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
    ATCGCCAAACTGAGTGCCCTAAAGGTTCA GAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGTTTTACAGCAT

                                                                                               Nhe1
                                                                                               |
501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGGTC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
    TGTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGCTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCCAG

                BseR1
                Nae1|
                BsrB1          NgoM4  ||                      ApaL1          BmgB1|
                |              |||                               ||
601 GCCACCATGAGCGGGGGCGAGGAGCTGTTTCGCCGGCATCGTGCCCGTGCTGATCGAGCTGGACGGCGACGTGCACGGCCACAAGTTCAGCGTGCGCGGCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
    CGGTGGTACTCGCCCCGCTCCTCGACAAGCGGCCGTAGCACGGGCACGACTAGCTCGACCTGCCGCTGCACGTGCCGGTGTTC AAGTCGCACGCGCCGC
TagGFP2   >      M S G G E E L F A G I V P V L I E L D G D V H G H K F S V R G E

                BsaXb
                BsaXa  Bsp1                Bpm1  |                BstE2
                |      |                    |    |                |    |
701 AGGGCGAGGGCGACCCGACTACGGCAAGCTGGAGATCAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTGGTGACCACCCTCTG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
    TCCCCTGCCGCTGCGGCTGATGCCGTTTCGACCTCTAGTTCAAGTAGACGTGGTGGCCGTTTCGACGGGCACGGGACCGGGTGGGACCCTGGTGGGAGAC
TagGFP2   >      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 T L C

                BstAP                                Xmn1                                EcoK
                |                                |                                |
801 CTACGGCATCCAGTGCTTCGCCCCTACCCCGAGCACATGAAGATGAACGACTTCTTCAAGAGCGCCATGCCCGAGGGCTACATCCAGGAGCGCACCATC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
    GATGCCGTAGGTCACGAAGCGGGCGATGGGGCTCGTGTACTTCTACTTGTGAAGAAGTTCTCGCGGTACGGGCTCCC GATGTAGGTCCTCGCGTGGTAG
TagGFP2   >      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 R T I
```

Sac2 SpDon Ale1 SpDon

```

CAGTTCAGGACGACGGCAAGTACAAGACCCGCGGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAAGGACTTCAAGG
901 ||||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
GTCAAGGTCTGCTGCCGTTTATGTTCTGGGCGCCGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTTTCTGAAGTTCC
TagGFP2 > Q 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 D F K E

```

Eco57 PflM1 Bpm1 Ecil Dra3 BsrG1 Xcm1

```

AGGACGGCAACATCCTGGGCCACAAGCTGGAGTACAGCTTCAACAGCCACAACGTGTACATCCGCCCCGACAAGGCCAACAACGGCCTGGAGGCTAACTT
1001 ||||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
TCCTGCCGTTGTAGGACCCGGTGTTCGACCTCATGTCSGAAGTTGTCGGTGTTCACATGTAGGCGGGGCTGTTCCGGTGTTCGCGGACCTCCGATTGAA
TagGFP2 > D G N I L G H K L E Y S F N S H N V Y I R P D K A N N G L E A N F

```

Bpm1 Pvu2 Bsg1 Xcm1 BsaB1

```

CAAGACCCGCCACAACATCGAGGGCGGCGGTGCAGCTGGCCGACCACTACCAGACCAACGTGCCCTGGGCGACGGCCCCGTGCTGATCCCCATCAAC
1101 ||||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
GTTCTGGGCGGTGTGTAGCTCCCGCCCGCACGTCGACCGGCTGGTGTGCTGGTTGCACGGGGACCCGCTGCCGGGGCACACTAGGGGTAGTTG
TagGFP2 > K T R H N I E G G G V Q L A D H Y Q T N V P L G D G P V L I P I N

```

Bpu10 Eco57 Dra3 AlwN1 Bpm1

```

CACTACCTGAGCACTCAGACCAAGATCAGCAAGGACCGCAACGAGGCCCGGACACATGGTGTCTCTGGAGTCTTCAGCGCTGCTGCCACACCCACG
1201 ||||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
GTGATGGACTCGTGAGTCTGGTCTTAGTCGTTCTGCGGCTGCTCCGGGCGCTGGTGTACCACGAGGACCTCAGGAAGTCGCGGACGACGGTGTGGGTGC
TagGFP2 > H Y L S T Q T K I S K D R N E A R D H M V L L E S F S A C C H T H G

```

Restriction enzymes: PflM1, BsrG1, **BspE1**, **Bgl2**, **Xho1**, **EcoRV**, BsaXb, **Sall**, BsaXa, NgoM4, NaeI

```
1301 GCATGGACGAGCTGTACAGGTCCGGACTCAGATCTCGAGCTATGGATGATGATATCGCCGCGCTCGTCGTTCGACAACGGCTCCGGCATGTGCAAGGCCGG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
CGTACCTGCTCGACATGTCCAGGCCTGAGTCTAGAGCTCGATACTACTACTATAGCGGCGCGAGCAGCAGCTGTTGCCGAGGCCGTACACGTTCCGGCC
TagGFP2/actin > M D E L Y R S G L R S R A M D D D I A A L V V D N G S G M C K A G
```

Restriction enzymes: **Sma1**, Bgl1, Nar1, **Bbs1**, Kas1

```
1401 CTTTCGGGGCAGCATGCCCGCCGCGTCTTCCCTCCATCGTGGGGCGCCCCAGGCACCAGGGCGTGATGGTGGGCATGGGTCAGAAGGATTCCTAT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
GAAGCGCCGCTGCTACGGGGGCCCGGCAGAAGGGGAGGTAGCACCCCGCGGGTCCGTGGTCCC GCACTACCACCCGTACCCAGTCTTCTTAAGGATA
Actin > F A G D D A P R A V F P S I V G R P R H Q G V M V G M G Q K D S Y
```

Restriction enzymes: Eco57, Bmr1

```
1501 GTGGGCGACGAGGCCCAGAGCAAGAGAGGCATCCTCACCTGAAGTACCCCATCGAGCACGGCATCGTCACCAACTGGGACGACATGGAGAAAATCTGGC
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
CACCCGCTGCTCCGGGCTCGTCTCTCCGTAGGAGTGGGACTTCATGGGGTAGCTCGTGCCGTAGCAGTGGTTGACCCTGCTGTACCTCTTTTAGACCG
Actin > V G D E A Q S K R G I L T L K Y P I E H G I V T N W D D M E K I W H
```

Restriction enzymes: BseR1, Dra3, BstAP

```
1601 ACCACACCTTCTACAATGAGCTGCGTGTGGCTCCCGAGGAGCACCCCGTGTCTGCTGACCGAGGCCCCCTGAACCCCAAGGCCAACC GCGAGAAGATGAC
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
TGGTGTGGAAGATGTTACTCGACGCACACCGAGGGCTCCTCGTGGGGCAGCAGACTGGCTCCGGGGGGACTTGGGGTTCCGGTTGGCGCTCTTCTACTG
Actin > H T F Y N E L R V A P E E H P V L L T E A P L N P K A N R E K M T
```

Restriction enzymes: Bsa1, BseY1

```
1701 CCAGATCATGTTTGAGACCTTCAACACCCAGCCATGTACGTTGCTATCCAGGCTGTGCTATCCCTGTACGCCTCTGGCCGTACCACTGGCATCGTGTATG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
GGTCTAGTACAAACTCTGGAAGTTGTGGGGTCGGTACATGCAACGATAGGTCCGACACGATAGGGACATGCGGAGACCGGCATGGTGTACCGTAGCACTAC
Actin > Q I M F E T F N T P A M Y V A I Q A V L S L Y A S G R T T G I V M
```



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                BsrD1
                BseR1 |
                BseY1   BsaB1| |             Bpu10   ScaI
                |         || |             |         |
                GGCACCCAGCACAAATGAAGATCAAGATCATTGCTCCTCCTGAGCGCAAGTACTCCGTGTGGATCGGCGGGCTCCATCCTGGCCTCGCTGTCCACCTTCCAG
2301 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2400
                CCGTGGGTTCGTGTTACTTCTAGTTCTAGTAACGAGGAGGACTCGCGTTCATGAGGCACACCTAGCCGCCGAGGTAGGACCCGGAGCGACAGGTGGAAGGTC
Actin >  A P S T M K I K I I A P P E R K Y S V W I G G S I L A S L S T F Q

                BsaB1                                     BamH1      Xba1      Bcl1 BsaB1
                |                                         |              |         |         |
                CAGATGTGGATCAGCAAGCAGGAGTATGACGAGTCCGGCCCCCTCCATCGTCCACCGCAAATGCTTCTAGGGATCCACCGGATCTAGATAACTGATCATAA
2401 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2500
                GTCTACACCTAGTCGTTCGTCCCTCATACTGCTCAGGCCGGGAGGTAGCAGGTGGCGTTTACGAAGATCCCTAGGTGGCCTAGATCTATTGACTAGTATT
Actin >  Q M W I S K Q E Y D E S G P S I V H R K C F *

                                SpDon   Dra1
                                |         |
                TCAGCCATACCACATTTGTAGAGGTTTTACTTTGCTTTAAAAAACCTCCACACCTCCCCCTGAACTGAAACATAAAATGAATGCAATTGTTGTTGTTAA
2501 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2600
                AGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAACAACAATT

                                polyA   Psil   polyA                                polyA          Bts1 Bsm1
                                |         |           |                                         |               |         |
                CTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTACAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGTTTGTCC
2601 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2700
                GAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGG

                                Mlu1   SpDon   Ssp1
                                |         |           |
                AAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAG
2701 | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * | | | | | | * 2800
                TTTGAGTAGTTACATAGAATTGCGCATTTAACATTTCGCAATTATAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATC

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                                Psil                      BsaXb
                                |                          |
GCCGAAATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAGAACGTGG
2801 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2900
CGGCTTTAGCCGTTTLAGGAATATTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGACC

                                BtgZ1
                                Dra3|
                                ||
Drd1      BsaXa
|          |
ACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGGGTTCGAGGTGCCGTAAAGC
2901 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3000
TGAGGTTGCAGTTTCCCGCTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCAGCTCCACGGCATTTCG

                                NaeI
                                NgoM4 |
                                ||
SpAcc
|
ACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAGGAGCGGGC
3001 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3100
TGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTTCGCTTTTCCTCGCCCG

GCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGG
3101 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3200
CGATCCCGGACCGTTCACATCGCCAGTGCAGCGCATTTGGTGGTGTGGGCGGCGCAATTACGCGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCC

                                BciV1
                                BspH1 |
                                BsrB1 | |
                                Ssp1
                                |
GAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTG
3201 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3300
CTTTACACGCGCCTTGGGGATAAACAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAAC

                                Ecil
Earl      Bsu36      Pvu2 |
|         |         |
AAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAA
3301 |||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3400
TTTTTCCTTCTCAGGACTCCGCCTTTCCTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCGGAGGGGTCCGTCCGTCTTCATACGTTT

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          NsiI                      NsiI
          SphI |                      SphI |
          BfrB1 |                      BfrB1 |
          BstAP | |                      BstAP | |
          | | |                          | | |
          |                               |
          SexA1                          BseY1
          |                               |
          GCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAT
3401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
          CGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTA

          EciI                      EciI      Bmr1 |                      EciI                      NcoI                      polyA
          |                          |          ||                      |                          |                      |
          AGTCCC GCCCTAACTCCGCCATCCCGCCCTAACTCCGCCAGTTCCGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCC
3501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
          TCAGGGCGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAATAAATAACGTCTCCGG

          Avr2
          SfiI                      StuI |                      ClaI                      BsaB1
          BglI                      SpDon                      BseR1 ||                      |                      |
          |                          |                          |          ||                      |                      |
          GAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCG
3601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
          CTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGC

          BspM1                      EagI                      Bmr1
          BfuA1                      |                          |
          |                          |                          |
          TTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAACAGACAATCGGCTGCT
3701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
          AAAGCGTACTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGA

          NarI                      Drd1
          KasI |                      |
          ||                          |
          CTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGC
3801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
          GACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTCG

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                                     BtgZ1
                               Eco57   BssS1   BsrB1 |
                               |         |         |
4401 TTGGCGGCGAATGGGCTGACCGCTTCCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
   AACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAAGTCTCAAGAAGAC

                                     BssS1
                                     BspM1
                                     BfuA1
                               BsrB1   BstB1   |         |         SpAcc
                               |         |         |         |
4501 AGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
   TCGCCCTGAGACCCCAAGCTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGC

                                     Nae1
                                     NgoM4 |
                                     Epm1 |
                                     |     |
4601 GAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAAACACGGAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
   CTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTT

                                     polyA   polyA
                                     |         |
4701 GGAGACAATAACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTCGTTTGTTCATAAACCGGGGTTTCGGTCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
   CCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCCTGCCACAACCCAGCAAACAAGTATTTGCGCCCCAAGCCAGG

                                     Bsa1
                                     |
4801 CAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGCGTTTCTTCTTTTCCCCACCCCAACCCCAAGTTTCGGGTGAAG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
   GTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAGCCCACTTC

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Found:

| | | | | | | | | | | | | | |
|-------------|--------------|-------------|--------------|-------------|-------------|--------------|-------------|--------------|--------------|--------------|-------------|-------------|-------|
| Aat2 | Ale1 | AlwN1 | ApaL1 | Ase1 | Avr2 | BamH1 | Bbs1 | Bcg1a | Bcg1b | BciV1 | Bcl1 | BfrB1 | BfuA1 |
| Bgl1 | Bgl2 | BmgB1 | Bmr1 | Bpm1 | Bpu10 | BpuE1 | Bsa1 | BsaB1 | BsaXa | BsaXb | BseR1 | BseY1 | Bsg1 |
| Bsm1 | BspE1 | BspH1 | BspLU | BspM1 | BsrB1 | BsrD1 | BsrG1 | BssS1 | BstAP | BstB1 | BstE2 | Bsu36 | BtgZ1 |
| Bts1 | Cla1 | Dra1 | Dra3 | Drd1 | Eag1 | Ear1 | Eci1 | Eco57 | EcoK | EcoRV | Fsp1 | Hpa1 | Kas1 |
| Mfe1 | Mlu1 | Msc1 | Nae1 | Nar1 | Nco1 | Nde1 | NgoM4 | Nhe1 | Nsi1 | PflF1 | PflM1 | polyA | Psi1 |
| Pvu2 | Rsr2 | Sac2 | Sall | Sap1 | Sca1 | SexA1 | Sfi1 | Sma1 | SnaB1 | SpAcc | SpDon | Sph1 | Ssp1 |
| Stu1 | Xba1 | Xcm1 | Xho1 | Xmn1 | | | | | | | | | |

Unique:

| | | | | | | | | | | | | | |
|-------------|--------------|-------------|--------------|--------------|-------------|-------------|--------------|--------------|--------------|-------------|-------------|--------------|-------------|
| Ase1 | BamH1 | Bbs1 | Bcg1a | Bcg1b | Bcl1 | Bgl2 | BspE1 | BspLU | BstB1 | Cla1 | EcoK | EcoRV | Fsp1 |
| Hpa1 | Mfe1 | Mlu1 | Nde1 | Nhe1 | Rsr2 | Sac2 | Sall | Sca1 | SexA1 | Sfi1 | Sma1 | SnaB1 | Stu1 |
| Xba1 | Xho1 | Xmn1 | | | | | | | | | | | |

Not found:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Aar1 | Acc65 | Ac11 | Afe1 | Afl2 | Age1 | Ahd1 | Apa1 | Asc1 | AsiS1 | Bae1a | Bae1b | BbvC1 | Blp1 |
| BsiW1 | BsmB1 | BssH2 | BstX1 | BstZ1 | BxatB | BxatL | BxatR | BxatP | _Chi | Ecl2 | EcoN1 | EcoR1 | FCatB |
| FCatL | FCatR | FCatP | ScFRT | Fse1 | FspA1 | Hind3 | I_Ceu | Kpn1 | loxP | Not1 | Nru1 | Pac1 | Pme1 |
| Pml1 | PshA1 | PspOM | Pst1 | Pvu1 | R4atB | R4atL | R4atP | R4atR | Sac1 | SanD1 | Sbf1 | Sgf1 | SgrA1 |
| Spe1 | Srf1 | Swa1 | T3RNA | T7RNA | T7Ter | PISce | | | | | | | |

Excluded by site complexity:

| | | | | | | | | | | | | | |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Acc1 | Ac11 | 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 | | | | | | | | | | | | | |