**Katushka2S-B 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). Amino acids encoded by vector’s backbone sequence are shown in black.

```
            Xho1                                                         SpDon
          SpDon|                   polyA      BsrB1         Psi1      Mfe1   |BsrB1
              ||                       |          |            |         |   |    |
               CTCGAGAAATCATAAAAAATTTATTTGCTTTGTGAGCGGATAACAATTATAATAGATTCAATTGTGAGCGGATAACAATTTCACACAGAATTGATAAAGA
            1  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
               GAGCTCTTTAGTATTTTTTAAATAAACGAAACACTCGCCTATTGTTAATATTATCTAAGTTAACACTCGCCTATTGTTAAAGTGTGTCTTAACTATTTCT

                                                           BstX1
                        BseR1       BamH1                 Ale1 |
                     SpAcc  |      BsaB1|    Age1       Nco1 | |                Bcl1                      BsrG1
                         |  |          ||       |          | | |                   |                          |
               GGAGAAATTAACTATGAGAGGATCGGGATCCTTACCGGTCGCCACCATGGTGGGTGAGGATAGCGTGCTGATCACCGAGAACATGCACATGAAACTGTAC
          101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
               CCTCTTTAATTGATACTCTCCTAGCCCTAGGAATGGCCAGCGGTGGTACCACCCACTCCTATCGCACGACTAGTGGCTCTTGTACGTGTACTTTGACATG
Katushka2S    >             M  R  G  S  G  S  L  P  V  A  T  M  V  G  E  D  S  V  L  I  T  E  N  M  H  M  K  L  Y

                                           ApaL1                   SpAcc
                                               |                         |
               ATGGAGGGCACCGTGAACGACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAAGATCAAGGTGGTCGAGG
          201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
               TACCTCCCGTGGCACTTGCTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTTCTAGTTCCACCAGCTCC
Katushka2S   > M  E  G  T  V  N  D  H  H  F  K  C  T  S  E  G  E  G  K  P  Y  E  G  T  Q  T  M  K  I  K  V  V  E  G
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               GCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAACCTTTATCAACCACACCCAGGGCATCCCCGACTTCTTTAA
          301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
               CGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAAGTACATGCCGTCGTTTTGGAAATAGTTGGTGTGGGTCCCGTAGGGGCTGAAGAAATT
Katushka2S   >   G  P  L  P  F  A  F  D  I  L  A  T  S  F  M  Y  G  S  K  T  F  I  N  H  T  Q  G  I  P  D  F  F  K

                      Bsu36       SpDon                          Bbs1             Bpm1
                          |           |                             |                |
               GCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGGATCACCACATACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGAACGGCTGC
          401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
               CGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCCTAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCTTGCCGACG
Katushka2S   >  Q  S  F  P  E  G  F  T  W  E  R  I  T  T  Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  N  G  C

                                                                                    BseY1
                                                                                        |
               CTCATCTACAACGTCAAGATCAACGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAGCACCGAGATGCTGT
          501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
               GAGTAGATGTTGCAGTTCTAGTTGCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGTCGTGGCTCTACGACA
Katushka2S   > L  I  Y  N  V  K  I  N  G  V  N  F  P  S  N  G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  M  L  Y

                                 Sfi1                         Bsg1       Eco57
                                 Bgl1          Bgl1       BssS1  |       BpuE1 Bts1BspM1
                                    |             |           |  |           |    |    |
               ACCCCGCTGACAGCGGCCTGAGAGGCCATGCCCAGATGGCCCTGAAGCTCGTGGGCGGGGGCTACCTGCACTGCTCCCTCAAGACCACATACAGATCCAA
          601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
               TGGGGCGACTGTCGCCGGACTCTCCGGTACGGGTCTACCGGGACTTCGAGCACCCGCCCCCGATGGACGTGACGAGGGAGTTCTGGTGTATGTCTAGGTT
Katushka2S   >   P  A  D  S  G  L  R  G  H  A  Q  M  A  L  K  L  V  G  G  G  Y  L  H  C  S  L  K  T  T  Y  R  S  K

            BpuE1                                             SpAcc                  Bsa1       PshA1       BssS1
                |                                                 |                     |           |           |
               GAAACCCGCTAAGAACCTCAAGATGCCCGGCTTCTACTTCGTGGACCGGAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAC
          701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
               CTTTGGGCGATTCTTGGAGTTCTACGGGCCGAAGATGAAGCACCTGGCCTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTG
Katushka2S   >  K  P  A  K  N  L  K  M  P  G  F  Y  F  V  D  R  R  L  E  R  I  K  E  A  D  K  E  T  Y  V  E  Q  H
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                                                                   Not1
                                                                   Eag1
                                                                 BsrB1|
                                                              Blp1   ||
                                                             Pvu2|   ||
                        Msc1  AlwN1          BspM1          Bmr1||   ||  Hind3        Blp1
                           |      |              |             |||   ||      |           |
               GAGATGGCTGTGGCCAGATACTGCGACCTGCCTAGCAAACTGGGGCACAGCTGAGCGGCCGCAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGAT
          801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
               CTCTACCGACACCGGTCTATGACGCTGGACGGATCGTTTGACCCCGTGTCGACTCGCCGGCGTTCGAATTAATCGACTCGAACCTGAGGACAACTATCTA
Katushka2S   > E  M  A  V  A  R  Y  C  D  L  P  S  K  L  G  H  S  *

                                                                               polyA          Nhe1
                                                                                   |             |
               CCAGTAATGACCTCAGAACTCCATCTGGATTTGTTCAGAACGCTCGGTTGCCGCCGGGCGTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTT
          901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
               GGTCATTACTGGAGTCTTGAGGTAGACCTAAACAAGTCTTGCGAGCCAACGGCGGCCCGCAAAAAATAACCACTCTTAGGTTCGATCGAACCGCTCTAAA

                  Bpu10
                 SpAcc|
                     ||
               TCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAATCACTGGATATACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGAGGCATTTCAGT
         1001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
               AGTCCTCGATTCCTTCGATTTTACCTCTTTTTTTAGTGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTGTAAAACTCCGTAAAGTCA


                                              Pvu2                Dra1
                                                 |                   |
               CAGTTGCTCAATGTACCTATAACCAGACCGTTCAGCTGGATATTACGGCCTTTTTAAAGACCGTAAAGAAAAATAAGCACAAGTTTTATCCGGCCTTTAT
         1101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
               GTCAACGAGTTACATGGATATTGGTCTGGCAAGTCGACCTATAATGCCGGAAAAATTTCTGGCATTTCTTTTTATTCGTGTTCAAAATAGGCCGGAAATA

              SpDon                      BspE1
           polyA  |                    Bsm1  |                  BsrD1
               |  |                       |  |                      |
               TCACATTCTTGCCCGCCTGATGAATGCTCATCCGGAATTTCGTATGGCAATGAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCTTGTTACACC
         1201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
               AGTGTAAGAACGGGCGGACTACTTACGAGTAGGCCTTAAAGCATACCGTTACTTTCTGCCACTCGACCACTATACCCTATCACAAGTGGGAACAATGTGG
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               BtgZ1    Acl1                               Bpm1
                   |       |                                  |
      GTTTTCCATGAGCAAACTGAAACGTTTTCATCGCTCTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTCGCAAGATGTGGCGTGTT
1301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
      CAAAAGGTACTCGTTTGACTTTGCAAAAGTAGCGAGACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAA

                                       polyA                BsmB1   PflM1          SpDon        Dra1
                                           |                    |       |              |           |
      ACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTTATTGAGAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTTGATTTAAACGT
1401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
      TGCCACTTTTGGACCGGATAAAGGGATTTCCCAAATAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAAACTAAATTTGCA

                                     SpDon
    Msc1                              Nco1       Ssp1
       |                                 |          |
      GGCCAATATGGACAACTTCTTCGCCCCCGTTTTCACCATGGGCAAATATTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTCAGGTTCATCAT
1501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
      CCGGTTATACCTGTTGAAGAAGCGGGGGCAAAAGTGGTACCCGTTTATAATATGCGTTCCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTA

                                     Bsm1             Sca1              BtgZ1
                                        |                |                  |
      GCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCTTAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGGCGTAATTTTTTTAAGGCAGTTATT
1601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
      CGGCAGACACTACCGAAGGTACAGCCGTCTTACGAATTACTTAATGTTGTCATGACGCTACTCACCGTCCCGCCCCGCATTAAAAAAATTCCGTCAATAA

                                                polyA     BpuE1                       Bmr1T7Ter
                                                    |         |                          |    |
      GGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAGCTTGAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTCGTTTTATCTGTTGTT
1701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
      CCACGGGAATTTGCGGACCCCATTACTGAGAGATCGAACTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGACCCGGAAAGCAAAATAGACAACAA

                                          Xba1
                        Eci1           BsrB1 |                                                   BsmB1
                           |               | |                                                       |
      TGTCGGTGAACGCTCTCCTGAGTAGGACAAATCCGCCGCTCTAGAGCTGCCTCGCGCGTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCC
1801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
      ACAGCCACTTGCGAGAGGACTCATCCTGTTTAGGCGGCGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGG
```

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                                                  Drd1                                          Bmr1
                                                     |                                             |
      GGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCGGGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCGCAGCCATGACC
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      CCTCTGCCAGTGTCGAACAGACATTCGCCTACGGCCCTCGTCTGTTCGGGCAGTCCCGCGCAGTCGCCCACAACCGCCCACAGCCCCGCGTCGGTACTGG

                                                                              BstAP
 PflF1                     BstZ1                                      ApaL1   Nde1|
     |                         |                                          |      ||
      CAGTCACGTAGCGATAGCGGAGTGTATACTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGTGCACCATATGCGGTGTGAAATACCGCACAG
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      GTCAGTGCATCGCTATCGCCTCACATATGACCGAATTGATACGCCGTAGTCTCGTCTAACATGACTCTCACGTGGTATACGCCACACTTTATGGCGTGTC

                                       Sap1
                                       Ear1                                            BsrB1
                                          |                                               |
      ATGCGTAAGGAGAAAATACCGCATCAGGCGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTCTGTCGGCTGCGGCGAGCGGTATCAGCTCAC
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      TACGCATTCCTCTTTTATGGCGTAGTCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGACAGCCGACGCCGCTCGCCATAGTCGAGTG

                                                         SpDon
                                                      BspLU  |
                                                          |  |
      TCAAAGGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAGGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCG
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      AGTTTCCGCCATTATGCCAATAGGTGTCTTAGTCCCCTATTGCGTCCTTTCTTGTACACTCGTTTTCCGGTCGTTTTCCGGTCCTTGGCATTTTTCCGGC

                 Eci1  SpAcc                 BpuE1             Drd1                       SpAcc
                    |      |                     |                |                           |
      CGTTGCTGGCGTTTTTCCATAGGCTCCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATA
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      GCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATATTTCTAT


                           BssS1                     BciV1 Eci1
                               |                         |    |
      CCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTCTCCTGTTCCGACCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCG
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      GGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGAGAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGC
```

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                                                          BseY1     ApaL1
                                                              |         |
      CTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTCAGCCCGACCGCTGCG
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      GAAAGAGTTACGAGTGCGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGC

                                           BpuE1                      AlwN1
                                               |                          |
      CCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGT
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      GGAATAGGCCATTGATAGCAGAACTCAGGTTGGGCCATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCATACA

                                                SpAcc
                                                    |
      AGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGA
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      TCCGCCACGATGTCTCAAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCCTGTCATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCT

  Eco57                                                                             BpuE1
      |                                                                                 |
      AAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCAGATTACGCGCAGAAAAAAAGGATCTC
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      TTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTGGTGGCGACCATCGCCACCAAAAAAACAAACGTTCGTCGTCTAATGCGCGTCTTTTTTTCCTAGAG

                                                                          BspH1
                                                                              |
      AAGAAGATCCTTTGATCTTTTCTACGGGGTCTGACGCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCAC
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      TTCTTCTAGGAAACTAGAAAAGATGCCCCAGACTGCGAGTCACCTTGCTTTTGAGTGCAATTCCCTAAAACCAGTACTCTAATAGTTTTTCCTAGAAGTG

              Dra1               Dra1
                 |                  |
      CTAGATCCTTTTAAATTAAAAATGAAGTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCT
3001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
      GATCTAGGAAAATTTAATTTTTACTTCAAAATTTAGTTAGATTTCATATATACTCATTTGAACCAGACTGTCAATGGTTACGAATTAGTCACTCCGTGGA
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                                                                                        Bmr1
                                                Ahd1                               SpDon   |
                                                   |                                   |   |
      ATCTCAGCGATCTGTCTATTTCGTTCATCCATAGCTGCCTGACTCCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTG
3101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
      TAGAGTCGCTAGACAGATAAAGCAAGTAGGTATCGACGGACTGAGGGGCAGCACATCTATTGATGCTATGCCCTCCCGAATGGTAGACCGGGGTCACGAC


        BsrD1
         Bsa1     Bpm1                         polyA                Bgl1                   Eci1
            |        |                             |                   |                      |
      CAATGATACCGCGAGACCCACGCTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATC
3201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
      GTTACTATGGCGCTCTGGGTGCGAGTGGCCGAGGTCTAAATAGTCGTTATTTGGTCGGTCGGCCTTCCCGGCTCGCGTCTTCACCAGGACGTTGAAATAG
                                                                          Acl1
                    Ase1                                              Fsp1   |    BsrD1
                       |                                                 |   |        |
      CGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGTAAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTG
3301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
      GCGGAGGTAGGTCAGATAATTAACAACGGCCCTTCGATCTCATTCATCAAGCGGTCAATTATCAAACGCGTTGCAACAACGGTAACGATGTCCGTAGCAC


      GTGTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCT
3401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
      CACAGTGCGAGCAGCAAACCATACCGAAGTAAGTCGAGGCCAAGGGTTGCTAGTTCCGCTCAATGTACTAGGGGGTACAACACGTTTTTTCGCCAATCGA


                  Pvu1      SpDon               Bts1                Bts1
                     |          |                  |                   |
      CCTTCGGTCCTCCGATCGTTGTCAGAAGTAAGTTGGCCGCAGTGTTATCACTCATGGTTATGGCAGCACTGCATAATTCTCTTACTGTCATGCCATCCGT
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      GGAAGCCAGGAGGCTAGCAACAGTCTTCATTCAACCGGCGTCACAATAGTGAGTACCAATACCGTCGTGACGTATTAAGAGAATGACAGTACGGTAGGCA

                     SpDon  Sca1                    Bcg1a                             Bcg1b
                         |     |                        |                                 |
      AAGATGCTTTTCTGTGACTGGTGAGTACTCAACCAAGTCATTCTGAGAATAGTGTATGCGGCGACCGAGTTGCTCTTGCCCGGCGTCAATACGGGATAAT
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      TTCTACGAAAAGACACTGACCACTCATGAGTTGGTTCAGTAAGACTCTTATCACATACGCCGCTGGCTCAACGAGAACGGGCCGCAGTTATGCCCTATTA
```

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                                               Xmn1
                         Dra1                  Acl1 BpuE1
                            |                     |     |
      ACCGCGCCACATAGCAGAACTTTAAAAGTGCTCATCATTGGAAAACGTTCTTCGGGGCGAAAACTCTCAAGGATCTTACCGCTGTTGAGATCCAGTTCGA
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      TGGCGCGGTGTATCGTCTTGAAATTTTCACGAGTAGTAACCTTTTGCAAGAAGCCCCGCTTTTGAGAGTTCCTAGAATGGCGACAACTCTAGGTCAAGCT

                  EcoK
              Eco57  |
              ApaL1  |
           BssS1  |  |                      SpDon SpDon
               |  |  |                          |     |
      TGTAACCCACTCGTGCACCCAACTGATCTTCAGCATCTTTTACTTTCACCAGCGTTTCTGGGTGAGCAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGG
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      ACATTGGGTGAGCACGTGGGTTGACTAGAAGTCGTAGAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTGTCCTTCCGTTTTACGGCGTTTTTTCCC

                                                                                        BsrB1
                                                                                    BciV1   |
                                           Ear1     Ssp1                          BspH1 |   |
                                              |        |                              | |   |
      AATAAGGGCGACACGGAAATGTTGAATACTCATACTCTTCCTTTTTCAATATTATTGAAGCATTTATCAGGGTTATTGTCTCATGAGCGGATACATATTT
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      TTATTCCCGCTGTGCCTTTACAACTTATGAGTATGAGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAA

                polyA                                                 Aat2             BspH1       SpAcc
                    |                                                    |                 |           |
      GAATGTATTTAGAAAAATAAACAAATAGGGGTTCCGCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCT
4001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
      CTTACATAAATCTTTTTATTTGTTTATCCCCAAGGCGCGTGTAAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGA

                  BssS1   Bbs1
                      |      |
      ATAAAAATAGGCGTATCACGAGGCCCTTTCGTCTTCAC
4101  |||||||||*|||||||||*|||||||||*|||||||| 4138
      TATTTTTATCCGCATAGTGCTCCGGGAAAGCAGAAGTG
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Found:

    Aat2    Acl1    Age1    Ahd1    Ale1   AlwN1   ApaL1    Ase1   BamH1    Bbs1   Bcg1a   Bcg1b   BciV1    Bcl1
    Bgl1    Blp1    Bmr1    Bpm1   Bpu10   BpuE1    Bsa1   BsaB1   BseR1   BseY1    Bsg1    Bsm1   BsmB1   BspE1
   BspH1   BspLU   BspM1   BsrB1   BsrD1   BsrG1   BssS1   BstAP   BstX1   BstZ1   Bsu36   BtgZ1    Bts1    Dra1
    Drd1    Eag1    Ear1    Eci1   Eco57    EcoK    Fsp1   Hind3    Mfe1    Msc1    Nco1    Nde1    Nhe1    Not1
   PflF1   PflM1   polyA   PshA1    Psi1    Pvu1    Pvu2    Sap1    Sca1    Sfi1   SpAcc   SpDon    Ssp1   T7Ter
    Xba1    Xho1    Xmn1


Unique:

    Aat2    Age1    Ahd1    Ale1    Ase1   BamH1   Bcg1a   Bcg1b    Bcl1   Bpu10   BsaB1   BseR1    Bsg1   BspE1
   BspLU   BsrG1   BstAP   BstX1   BstZ1   Bsu36    Eag1    EcoK    Fsp1   Hind3    Mfe1    Nde1    Nhe1    Not1
   PflF1   PflM1   PshA1    Psi1    Pvu1    Sap1    Sfi1   T7Ter    Xba1    Xho1    Xmn1


Not found:

    Aar1   Acc65    Afe1    Afl2    Apa1    Asc1   AsiS1    Avr2   Bae1a   Bae1b   BbvC1   BfrB1    Bgl2   BmgB1
   BsaXa   BsaXb   BsiW1   BssH2   BstB1   BstE2   BxatB   BxatL   BxatR   BxatP    _Chi    Cla1    Dra3    Ecl2
   EcoN1   EcoR1   EcoRV   FCatB   FCatL   FCatR   FCatP   ScFRT    Fse1   FspA1    Hpa1   I_Ceu    Kas1    Kpn1
    loxP    Mlu1    Nae1    Nar1   NgoM4    Nru1    Nsi1    Pac1    Pme1    Pml1   PspOM    Pst1   R4atB   R4atL
   R4atP   R4atR    Rsr2    Sac1    Sac2    Sal1   SanD1    Sbf1   SexA1    Sgf1   SgrA1    Sma1   SnaB1    Spe1
    Sph1    Srf1    Stu1    Swa1   T3RNA   T7RNA   PISce    Xcm1

Excluded by site complexity:

    Acc1    Aci1    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
```