pHyPer-cyto 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).

```
            Ase1                                                                                  Bgl1
              |                                                                                     |
      TAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCG
    1 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 100
      ATCAATAATTATCATTAGTTAATGCCCCAGTAATCAAGTATCGGGTATATACCTCAAGGCGCAATGTATTGAATGCCATTTACCGGGCGGACCGACTGGC

                                Aat2                    SpAcc                         Aat2
                                  |                       |                             |
      CCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGT
  101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 200
      GGGTTGCTGGGGGCGGGTAACTGCAGTTATTACTGCATACAAGGGTATCATTGCGGTTATCCCTGAAAGGTAACTGCAGTTACCCACCTCATAAATGCCA

                Bgl1                  Nde1                        Aat2                  Bgl1  Bmr1
                  |                     |                           |                     |     |
      AAACTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTA
  201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 300
      TTTGACGGGTGAACCGTCATGTAGTTCACATAGTATACGGTTCATGCGGGGGATAACTGCAGTTACTGCCATTTACCGGGCGGACCGTAATACGGGTCAT

                                      BtgZ1 SnaB1                 Nco1
                                        |     |                     |
      CATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGTACATCAATGGGCGTGGA
  301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 400
      GTACTGGAATACCCTGAAAGGATGAACCGTCATGTAGATGCATAATCAGTAGCGATAATGGTACCACTACGCCAAAACCGTCATGTAGTTACCCGCACCT

                                                Aat2                                                Eci1
                                                  |                                                   |
      TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
  401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
      ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT
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                                                                                                                                Nhe1
                                                                                                                                  |
            ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCCA
        501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
            TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGGT

                                                Rsr2
                  BstX1                       BspE1  |                                                   Bsg1
                 Xcm1  |          Bgl1     PflF1   |  |                                              BspM1 |
              Nco1   |  |        BsmB1|    Bsg1 |   |  |                          SpAcc               BfuA1 |
                  |   |  |            ||       | |   |  |                                |                  | |
            CCATGGAGATGGCAAGCCAGCAGGGCGAGACGATGTCCGGACCGCTGCACATTGGTTTGATTCCCACAGTTGGACCGTACCTGCTACCGCATATTATCCC
        601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
            GGTACCTCTACCGTTCGGTCGTCCCGCTCTGCTACAGGCCTGGCGACGTGTAACCAAACTAAGGGTGTCAACCTGGCATGGACGATGGCGTATAATAGGG
HyPer         >  M  E  M  A  S  Q  Q  G  E  T  M  S  G  P  L  H  I  G  L  I  P  T  V  G  P  Y  L  L  P  H  I  I  P

                                                                  PflM1
                                                                  AlwN1
                                                                     |
            TATGCTGCACCAGACCTTTCCAAAGCTGGAAATGTATCTGCATGAAGCACAGACCCACCAGTTACTGGCGCAACTGGACAGCGGCAAACTCGATTGCGTG
        701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
            ATACGACGTGGTCTGGAAAGGTTTCGACCTTTACATAGACGTACTTCGTGTCTGGGTGGTCAATGACCGCGTTGACCTGTCGCCGTTTGAGCTAACGCAC
HyPer         >  M  L  H  Q  T  F  P  K  L  E  M  Y  L  H  E  A  Q  T  H  Q  L  L  A  Q  L  D  S  G  K  L  D  C  V

                     SpDon            Bsm1                                          SpAcc
                        |               |                                              |
            ATCCTCGCGCTGGTGAAAGAGAGCGAAGCATTCATTGAAGTGCCGTTGTTTGATGAGCCAATGTTGCTGGCTATCTATGAAGATCACCCGTGGGCGAACC
        801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
            TAGGAGCGCGACCACTTTCTCTCGCTTCGTAAGTAACTTCACGGCAACAAACTACTCGGTTACAACGACCGATAGATACTTCTAGTGGGCACCCGCTTGG
HyPer         > I  L  A  L  V  K  E  S  E  A  F  I  E  V  P  L  F  D  E  P  M  L  L  A  I  Y  E  D  H  P  W  A  N  R

                                                                                                      Nae1
                                                                                                   NgoM4 |
                 Bsm1           Bgl1                                                  Eci1      BsrD1 | |
                    |              |                                                     |          | | |
            GCGAATGCGTACCGATGGCCGATCTGGCAGGGGAAAAACTGCTGATGCTGGAAGATGGTCACTGTTTGCGCGATCAGGCAATGTCCGCCGGCTACAACAG
        901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1000
            CGCTTACGCATGGCTACCGGCTAGACCGTCCCCTTTTTGACGACTACGACCTTCTACCAGTGACAAACGCGCTAGTCCGTTACAGGCGGCCGATGTTGTC
HyPer         >  E  C  V  P  M  A  D  L  A  G  E  K  L  L  M  L  E  D  G  H  C  L  R  D  Q  A  M  S  A  G  Y  N  S
```

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                PflF1                                       Eci1
                    |                                          |
                CGACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACGTCGAGGACGGCAGCGTGCAGCTCGCCGAC
        1001    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1100
                GCTGTTGCAGATATAGTACCGGCTGTTCGTCTTCTTGCCGTAGTTCCGGTTGAAGTTCTAGGCGGTGTTGCAGCTCCTGCCGTCGCACGTCGAGCGGCTG
HyPer         >  D  N  V  Y  I  M  A  D  K  Q  K  N  G  I  K  A  N  F  K  I  R  H  N  V  E  D  G  S  V  Q  L  A  D

                   Bsg1                                                 Bpu10            Bpu10
                      |                                                    |                |
                CACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCTTCCAGTCCGTCCTGAGCAAAGACCCCAACGAGA
        1101    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1200
                GTGATGGTCGTCTTGTGGGGGTAGCCGCTGCCGGGGCACGACGACGGGCTGTTGGTGATGGACTCGAAGGTCAGGCAGGACTCGTTTCTGGGGTTGCTCT
HyPer         > H  Y  Q  Q  N  T  P  I  G  D  G  P  V  L  L  P  D  N  H  Y  L  S  F  Q  S  V  L  S  K  D  P  N  E  K

                                                   Bpm1                    BsrG1
                                                      |                       |
                AGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAACGTGGATGGCGGTAGCGGTGGCACCGG
        1201    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1300
                TCGCGCTAGTGTACCAGGACGACCTCAAGCACTGGCGGCGGCCCTAGTGAGAGCCGTACCTGCTCGACATGTTGCACCTACCGCCATCGCCACCGTGGCC
HyPer         >   R  D  H  M  V  L  L  E  F  V  T  A  A  G  I  T  L  G  M  D  E  L  Y  N  V  D  G  G  S  G  G  T  G

                                     BseR1
                                      Ale1                                                          Bcg1a
                                         |                                                             |
                CAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG
        1301    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1400
                GTCGTTCCCGCTCCTCGACAAGTGGCCCCACCACGGGTAGGACCAGCTCGACCTGCCGCTGCATTTGCCGGTGTTCAAGTCGCACAGGCCGCTCCCGCTC
HyPer         >  S  K  G  E  E  L  F  T  G  V  V  P  I  L  V  E  L  D  G  D  V  N  G  H  K  F  S  V  S  G  E  G  E

                                         Bsg1
                                Bcg1b     |                                                  BssS1
                            BtgZ1  |      |                       Eco57                       Ale1
                                |  |      |                          |                          |
                GGCGATGCCACCTACGGCAAGCTGACCCTGAAGCTGATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTCGGCTACGGCC
        1401    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
                CCGCTACGGTGGATGCCGTTCGACTGGGACTTCGACTAGACGTGGTGGCCGTTCGACGGGCACGGGACCGGGTGGGAGCACTGGTGGGAGCCGATGCCGG
HyPer         > G  D  A  T  Y  G  K  L  T  L  K  L  I  C  T  T  G  K  L  P  V  P  W  P  T  L  V  T  T  L  G  Y  G  L
```

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                Xmn1          Eco57                   Eci1
                  |             |                       |
           TGAAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAA
      1501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
           ACTTCACGAAGCGGGCGATGGGGCTGGTGTACTTCGTCGTGCTGAAGAAGTTCAGGCGGTACGGGCTTCCGATGCAGGTCCTCGCGTGGTAGAAGAAGTT
HyPer      >  K  C  F  A  R  Y  P  D  H  M  K  Q  H  D  F  F  K  S  A  M  P  E  G  Y  V  Q  E  R  T  I  F  F  K

                                                                 SpDon
                                          SpDon                 Ale1 |                                Eco57
                                              |                     | |                                  |
           GGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGGCTTCAAGGAGGACGGC
      1601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
           CCTGCTGCCGTTGATGTTCTGGGCGCGGCTCCACTTCAAGCTCCCGCTGTGGGACCACTTGGCGTAGCTCGACTTCCCGTAGCCGAAGTTCCTCCTGCCG
HyPer      >  D  D  G  N  Y  K  T  R  A  E  V  K  F  E  G  D  T  L  V  N  R  I  E  L  K  G  I  G  F  K  E  D  G

                                          Age1  Bpm1                            Eci1
                                            |     |                               |
           AACATCCTGGGGCACAAGCTGGAGTACAACGGCACCGGTTTCTGTTTTGAAGCCGGGGCGGATGAAGATACACACTTCCGCGCGACCAGCCTGGAAACTC
      1701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
           TTGTAGGACCCCGTGTTCGACCTCATGTTGCCGTGGCCAAAGACAAAACTTCGGCCCCGCCTACTTCTATGTGTGAAGGCGCGCTGGTCGGACCTTTGAG
HyPer      > N  I  L  G  H  K  L  E  Y  N  G  T  G  F  C  F  E  A  G  A  D  E  D  T  H  F  R  A  T  S  L  E  T  L

                 BspM1
             Fsp1 BfuA1                                Afe1                                      BtgZ1
                |     |                                  |                                         |
           TGCGCAACATGGTGGCGGCAGGTAGCGGGATCACTTTACTGCCAGCGCTGGCTGTGCCGCCGGAGCGCAAACGCGATGGGGTTGTTTATCTGCCGTGCAT
      1801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
           ACGCGTTGTACCACCGCCGTCCATCGCCCTAGTGAAATGACGGTCGCGACCGACACGGCGGCCTCGCGTTTGCGCTACCCCAACAAATAGACGGCACGTA
HyPer      >  R  N  M  V  A  A  G  S  G  I  T  L  L  P  A  L  A  V  P  P  E  R  K  R  D  G  V  V  Y  L  P  C  I

                                                                  Fsp1            Pvu2
                                                                    |               |
           TAAGCCGGAACCACGCCGCACTATTGGCCTGGTTTATCGTCCTGGCTCACCGCTGCGCAGCCGCTATGAGCAGCTGGCAGAGGCCATCCGCGCAAGAATG
      1901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
           ATTCGGCCTTGGTGCGGCGTGATAACCGGACCAAATAGCAGGACCGAGTGGCGACGCGTCGGCGATACTCGTCGACCGTCTCCGGTAGGCGCGTTCTTAC
HyPer      >  K  P  E  P  R  R  T  I  G  L  V  Y  R  P  G  S  P  L  R  S  R  Y  E  Q  L  A  E  A  I  R  A  R  M
```

```
                                                                                                BamH1
                                                                                               Sma1 |
                                                                                              Apa1| |
                                                                                         PspOM   || |
                                                                                         Sac2|   || |
                                                  Hind3  EcoR1      Sal1      Kpn1  ||   || |
                 Msc1              Dra1          Dra1  |BstB1 |     Pst1| Acc65   |  ||   || |        Xba1
                    |                |            |  |    | |        ||      |   |  ||   || |           |
            GATGGCCATTTCGATAAAGTTTTAAAACAGGCGGTTTAAAAGCTTCGAATTCTGCAGTCGACGGTACCGCGGGCCCGGGATCCACCGGATCTAGATAACT
      2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
            CTACCGGTAAAGCTATTTCAAAATTTTGTCCGCCAAATTTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCTAGATCTATTGA
HyPer         > D  G  H  F  D  K  V  L  K  Q  A  V  *

                                                                                                          Bsm1
          Bcl1BsaB1                                SpDon   Dra1                                         Mfe1|
             |    |                                   |      |                                              ||
            GATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTT
      2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
            CTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAA

              Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
                  |          |       |          |                           |                |    |
            GTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTG
      2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
            CAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACGTAAGATCAACAC

                                     Mlu1     SpDon        Ssp1
                                        |         |           |
            GTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTA
      2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
            CAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAAT

                                      Psi1                                                          BsaXb
                                        |                                                             |
            ACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAGTCCACTATTAAA
      2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
            TGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTT
```

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                                                        BtgZ1
                 Drd1    BsaXa                          Dra3|
                    |        |                             ||
      GAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGC
2501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2600
      CTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACG

                                                           Nae1
                       SpAcc                            NgoM4 |
                          |                                 | |
      CGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAG
2601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2700
      GCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTCGCTTTC

    BsrB1
       |
      GAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCAC
2701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2800
      CTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTG

                                                                   BciV1
                                                             BspH1  |
                                         polyA                BsrB1 |  |
                                            |                    | |  |
      TTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAA
2801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2900
      AAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTT

                                            Eci1
      Ssp1  Ear1        Bsu36             Pvu2 |                                      BseY1
         |     |            |                | |                                         |
      TAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAG
2901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3000
      ATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTC
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                 Nsi1                                                                  Nsi1
               Sph1 |                                                               Sph1 |
              BfrB1 |                                                              BfrB1 |
         BstAP  | |            SexA1                     BseY1                   BstAP  | |
              |  | |                |                       |                       |  | |
     TATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCA
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     ATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGT

                                                Eci1
                Eci1                  Eci1     Bmr1|       Eci1            Nco1                    polyA
                   |                    |        ||          |               |                       |
     GCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATG
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     CGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAAATAAATAC

                                                                    Avr2
                  Sfi1                                             Stu1|
                  Bgl1                      SpDon             BseR1  ||              Cla1
                    |                         |                  |  ||                |
     CAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGAT
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     GTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCCTA

                              BspM1
   BsaB1                      BfuA1               Eag1                                      Bmr1
     |                          |                   |                                         |
     GAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAAT
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     CTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTA

                                          Nar1
                                         Kas1|                        Drd1
                                            ||                          |
     CGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGAC
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     GCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTG
```

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                                                Pvu2
                         Msc1                Fsp1   |       PflF1                       Eco57
                            |                   |   |           |                           |
     GAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCG
3501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
     CTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGC

                                SpDon                         BciV1         BsrD1
                                   |                            |             |
     AAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGC
3601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
     TTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCG

              BtgZ1
           BspM1  |                                                                  Sap1
           BfuA1  |                                                                  Ear1
               |  |                                                                     |
     TACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCAT
3701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
     ATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTA

                   BpuE1                        Sph1                       Nco1                BtgZ1
                       |                           |                          |                   |
     CAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATA
3801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
     GTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTAT

                                          BseY1
                                         Nae1 |                                          Sap1
                                       NgoM4 | |        Rsr2         Eci1                Ear1
                                           | | |           |            |                     |
     TCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGC
3901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
     AGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACG
```

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                                                   BtgZ1
                   Eco57         BssS1                BsrB1 |
                       |             |                    | |
     TGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAG
4001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4100
     ACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTC

                                                       BssS1
                                                       BspM1
          BsrB1          BstB1                        BfuA1                      SpAcc
              |              |                            |                          |
     TTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTT
4101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4200
     AAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAA

                            Nae1                                                   Bpm1
                         NgoM4 |                                             SpAcc  |
                          Bpm1 |                                              Avr2  |
                             | |                                                  |  |
     GGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGCTAACTGAA
4201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4300
     CCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTT

                                          polyA        polyA
                                             |            |
     ACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGG
4301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4400
     TGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCC

                                 Bsa1
                                   |
     TTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTC
4401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4500
     AAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGGTTCAAG
```

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                                        BstAP
                                        AlwN1      Bsu36                           Dra1
                                            |          |                               |
     GGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTT
4501 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
     CCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAA

       Dra1                              BspH1
          |                                 |
     TAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAA
4601 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
     ATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTT

                                    BpuE1
                                       |
     AGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCA
4701 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
     TCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGT

                  Eco57                                                 SpAcc
                     |                                                     |
     AGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAG
4801 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
     TCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTC

                                                      AlwN1                     BpuE1
                                                         |                          |
     AACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGAC
4901 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
     TTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTG

                                                 ApaL1      BseY1
                                                    |          |
     GATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACA
5001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
     CTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGT
```

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                                                          BciV1
        SpAcc                                           Eci1   |                    BssS1
            |                                              |   |                       |
     GCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTT
5101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
     CGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAA

                            SpAcc                         Drd1            BpuE1               SpAcc
                                |                            |                |                     |
     CCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTAT
5201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
     GGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCCGCCTCGGATA

                                                          SpDon
      Eci1                                               BspLU|
          |                                                  ||
     GGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAA
5301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5400
     CCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATT

                  Nsi1
               BfrB1 |
                   | |
     CCGTATTACCGCCATGCAT
5401 |||||||||*||||||||| 5419
     GGCATAATGGCGGTACGTA
```

Found:

Aat2	**Acc65**	**Afe1**	**Age1**	Ale1	AlwN1	**Apa1**	**ApaL1**	**Ase1**	Avr2	**BamH1**	**Bcg1a**	**Bcg1b**	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bmr1	Bpm1	Bpu10	BpuE1	**Bsa1**	BsaB1	**BsaXa**	**BsaXb**	BseR1	BseY1
Bsg1	Bsm1	**BsmB1**	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	BsrD1	**BsrG1**	BssS1	BstAP	BstB1	**BstX1**
Bsu36	BtgZ1	**Bts1**	**Cla1**	Dra1	**Dra3**	Drd1	**Eag1**	Ear1	Eci1	Eco57	**EcoR1**	Fsp1	**Hind3**
Hpa1	**Kas1**	**Kpn1**	**Mfe1**	**Mlu1**	Msc1	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	Nsi1	PflF1
PflM1	polyA	Psi1	**PspOM**	**Pst1**	Pvu2	Rsr2	**Sac2**	**Sal1**	Sap1	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**
SpAcc	SpDon	Sph1	Ssp1	**Stu1**	**Xba1**	**Xcm1**	**Xmn1**						

Unique:

Acc65	**Afe1**	**Age1**	**Apa1**	**ApaL1**	**Ase1**	**BamH1**	**Bcg1a**	**Bcg1b**	**Bcl1**	**Bsa1**	**BsaXa**	**BsaXb**	**BsmB1**
BspE1	**BspLU**	**BsrG1**	**BstX1**	**Bts1**	**Cla1**	**Dra3**	**Eag1**	**EcoR1**	**Hind3**	**Hpa1**	**Kas1**	**Kpn1**	**Mfe1**
Mlu1	**Nar1**	**Nde1**	**Nhe1**	**PflM1**	**PspOM**	**Pst1**	**Sac2**	**Sal1**	**SexA1**	**Sfi1**	**Sma1**	**SnaB1**	**Stu1**
Xba1	**Xcm1**	**Xmn1**											

Not found:

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Bae1a	Bae1b	Bbs1	BbvC1	Bgl2	Blp1	BmgB1	BsiW1
BssH2	BstE2	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	loxP	Not1	Nru1
Pac1	Pme1	Pml1	PshA1	Pvu1	Sac1	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swa1
T3RNA	T7RNA	T7Ter	PISce	Xho1									

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													