pFusionRed-Rab5a 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).

FusionRed amino acids are shown in red, RAS-related protein Rab-5a amino acids are shown in green, linker amino acids are shown in black.

```
          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
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                                                  Aat2                                                  Eci1
                                                    |                                                     |
     TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 500
     ATCGCCAAACTGAGTGCCCCTAAAGGTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                                                                                Nhe1 Afe1
                                                                                                   |    |
     ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 600
     TGTTGAGGCGGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

                 SpDon
                Ale1 |
 Age1        Nco1 | |                                BsrG1                                ApaL1
    |           | | |                                   |                                    |
     CCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCG
601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 700
     GGCCAGCGGTGGTACCACTCGCTCGACTAATTCCTCTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTTGGTGGTGAAGTTCACGTGTAGGC
FusionRed    >            M  V  S  E  L  I  K  E  N  M  P  M  K  L  Y  M  E  G  T  V  N  N  H  H  F  K  C  T  S  E

                  SpAcc
                     |
     AGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTCGTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 800
     TCCCGCTTCCGTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTCGAA
FusionRed    >  G  E  G  K  P  Y  E  G  T  Q  T  M  R  I  K  V  V  E  G  G  P  L  P  F  A  F  D  I  L  A  T  S  F

                                                                                Bsu36       SpDon
                                                                                  |           |
     CATGTACGGCAGCAGAACCTTCATCAAGCACCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACA
801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 900
     GTACATGCCGTCGTCTTGGAAGTAGTTCGTGGGAGGCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGT
FusionRed    >  M  Y  G  S  R  T  F  I  K  H  P  P  G  I  P  D  F  F  K  Q  S  F  P  E  G  F  T  W  E  R  V  T  T
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                    Bbs1            Bpm1                                                        BseY1
                      |               |                                                           |
            TACGAAGACGGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCA
     901    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1000
            ATGCTTCTGCCCCCGCACGACTGGCGATGGGTCCTGTGGTCGGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTCGGT
FusionRed    > Y  E  D  G  G  V  L  T  A  T  Q  D  T  S  L  Q  D  G  C  L  I  Y  N  V  K  V  R  G  V  N  F  P  A  N

                                                BsmB1
                                BseY1    Stu1  |                                  Bgl1
                                    |        |  |                                   |
            ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCT
    1001    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1100
            TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGA
FusionRed    >   G  P  V  M  Q  K  K  T  L  G  W  E  A  S  T  E  T  M  Y  P  A  D  G  G  L  E  G  A  C  D  M  A  L

                                                                  BpuE1
            BssS1          Eco57        Bsa1                   BpuE1  |
                |              |           |                       |  |
            GAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTG
    1101    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1200
            CTTCGAGCACCCGCCCCCGGTGGACTAGACGTTGGAACTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGCAGATGTTGCAC
FusionRed    >  K  L  V  G  G  G  H  L  I  C  N  L  E  T  T  Y  R  S  K  K  P  A  T  N  L  K  M  P  G  V  Y  N  V

                SpAcc
                PflM1                   Bsa1       PshA1       BssS1 Dra3      Msc1
                    |                     |           |           |    |         |
            GACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGATG
    1201    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1300
            CTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGCTACTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTAC
FusionRed    > D  H  R  L  E  R  I  K  E  A  D  D  E  T  Y  V  E  Q  H  E  V  A  V  A  R  Y  S  T  G  G  A  G  D  G

                                      Xho1
                                 Bgl2   |
        SpDon              BspE1  BseR1 |   |  Nco1                                   PflM1polyA
            |                  |       | |   |     |                                     |    |
            GAGGTAAAGGTGGAGGAGGTTCCGGACTCAGATCTCGAGCCATGGCTAGTCGAGGCGCAACAAGACCCAACGGGCCAAATACTGGAAATAAAATATGCCA
    1301    |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 1400
            CTCCATTTCCACCTCCTCCAAGGCCTGAGTCTAGAGCTCGGTACCGATCAGCTCCGCGTTGTTCTGGGTTGCCCGGTTTATGACCTTTATTTTATACGGT
FusionRed/   >   G  K  G  G  G  G  S  G  L  R  S  R  A  M  A  S  R  G  A  T  R  P  N  G  P  N  T  G  N  K  I  C  Q
      Rab5a
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                    SpAcc
          Spe1 Sca1   |                                                    BspH1
                |    |    |                                                    |
        GTTCAAACTAGTACTTCTGGGAGAGTCTGCTGTTGGCAAATCAAGCCTAGTGCTTCGTTTTGTGAAGGGCCAATTTCATGAATTTCAAGAGAGTACCATA
1401    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1500
        CAAGTTTGATCATGAAGACCCTCTCAGACGACAACCGTTTAGTTCGGATCACGAAGCAAAACACTTCCCGGTTAAAGTACTTAAAGTTCTCTCATGGTAT
Rab5a     >  F  K  L  V  L  L  G  E  S  A  V  G  K  S  S  L  V  L  R  F  V  K  G  Q  F  H  E  F  Q  E  S  T  I

                                 Bae1b                       BciV1Bae1a    Pvu2                   Blp1
                                    |                           |    |       |                      |
        GGGGCTGCTTTTCTAACCCAAACTGTGTGTCTTGATGATACAACAGTAAAGTTTGAAATATGGGATACAGCTGGTCAAGAACGATACCATAGCTTAGCAC
1501    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1600
        CCCCGACGAAAAGATTGGGTTTGACACACAGAACTACTATGTTGTCATTTCAAACTTTATACCCTATGTCGACCAGTTCTTGCTATGGTATCGAATCGTG
Rab5a     > G  A  A  F  L  T  Q  T  V  C  L  D  D  T  T  V  K  F  E  I  W  D  T  A  G  Q  E  R  Y  H  S  L  A  P

                                                                                   PflM1
          SpAcc                BseR1          EcoRV                    BseR1    Eco57|      Bmr1
             |                    |              |                        |        ||         |
        CAATGTACTACAGAGGAGCACAAGCAGCCATAGTTGTATATGATATCACAAATGAGGAGTCCTTTGCCAGAGCCAAAAACTGGGTTAAAGAACTTCAGAG
1601    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1700
        GTTACATGATGTCTCCTCGTGTTCGTCGGTATCAACATATACTATAGTGTTTACTCCTCAGGAAACGGTCTCGGTTTTTGACCCAATTTCTTGAAGTCTC
Rab5a     >   M  Y  Y  R  G  A  Q  A  A  I  V  V  Y  D  I  T  N  E  E  S  F  A  R  A  K  N  W  V  K  E  L  Q  R

                                                                  polyA
                                                                    |
        GCAAGCCAGTCCTAACATTGTAATAGCTTTATCAGGAAACAAGGCTGATCTTGCAAATAAAAGAGCTGTCGATTTCCAGGAAGCACAGTCCTATGCAGAT
1701    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1800
        CGTTCGGTCAGGATTGTAACATTATCGAAATAGTCCTTTGTTCCGACTAGAACGTTTATTTTCTCGACAGCTAAAGGTCCTTCGTGTCAGGATACGTCTA
Rab5a     >  Q  A  S  P  N  I  V  I  A  L  S  G  N  K  A  D  L  A  N  K  R  A  V  D  F  Q  E  A  Q  S  Y  A  D

                  polyA                       Cla1   SpDon       Ssp1
                     |                           |       |           |
        GACAACAGTTTATTATTCATGGAGACATCAGCTAAAACATCGATGAATGTAAATGAAATATTCATGGCAATAGCTAAAAAGTTGCCAAAGAACGAACCAC
1801    |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 1900
        CTGTTGTCAAATAATAAGTACCTCTGTAGTCGATTTTGTAGCTACTTACATTTACTTTATAAGTACCGTTATCGATTTTTCAACGGTTTCTTGCTTGGTG
Rab5a     > D  N  S  L  L  F  M  E  T  S  A  K  T  S  M  N  V  N  E  I  F  M  A  I  A  K  K  L  P  K  N  E  P  Q
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                        BstAP Ear1                  BseR1                                      BamH1
                           |    |                      |                                          |
      AGAATCCAGGAGCAAATTCTGCCAGAGGAAGAGGAGTAGACCTTACTGAACCCACGCAGCCAACCAGGAATCAGTGTTGTAGTAACTAAGGATCCACCGG
1901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2000
      TCTTAGGTCCTCGTTTAAGACGGTCTCCTTCTCCTCATCTGGAATGACTTGGGTGCGTCGGTTGGTCCTTAGTCACAACATCATTGATTCCTAGGTGGCC
Rab5a     >   N  P  G  A  N  S  A  R  G  R  G  V  D  L  T  E  P  T  Q  P  T  R  N  Q  C  C  S  N  *

      Xba1      Bcl1BsaB1                           SpDon   Dra1
        |         |    |                                |      |
      ATCTAGATAACTGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATG
2001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2100
      TAGATCTATTGACTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTAC

        Bsm1
       Mfe1|        Hpa1       polyA    Psi1      polyA                        polyA            Bts1 Bsm1
          ||           |           |       |          |                            |               |    |
      AATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGC
2101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2200
      TTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTCGTTATCGTAGTGTTTAAAGTGTTTATTTCGTAAAAAAAGTGACG

                                          Mlu1     SpDon        Ssp1
                                             |         |           |
      ATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCA
2201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2300
      TAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATTCGCAATTATAAAACAATTTTAAGCGCAATTTAAAAACAATTTAGT

                                           Psi1
                                             |
      GCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAACAAGAG
2301  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2400
      CGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTC

                                                                  BtgZ1
      BsaXb                  Drd1    BsaXa                      Dra3|
          |                     |        |                         ||
      TCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTG
2401  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 2500
      AGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAAC
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                                                                   Nae1
                                SpAcc                            NgoM4 |
                                   |                                 | |
     GGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGA
2501 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2600
     CCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCT

              BsrB1
                 |
     AGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGC
2601 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2700
     TCTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCCGCG

                                                                                   BciV1
                                                                                BspH1  |
                                                   polyA                      BsrB1 |  |
                                                      |                          | |  |
     GTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGA
2701 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2800
     CAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACT

                                                   Eci1
                Ssp1  Ear1        Bsu36            Pvu2 |                                      BseY1
                   |     |            |                | |                                         |
     TAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCC
2801 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 2900
     ATTTACGAAGTTATTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGG

                          Nsi1                                                                     Nsi1
                        Sph1 |                                                                   Sph1 |
                       BfrB1 |                                                                  BfrB1 |
                    BstAP  | |            SexA1                      BseY1                    BstAP  | |
                        |  | |                |                        |                        |  | |
     AGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCAT
2901 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 3000
     TCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTA
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                                                   Eci1
                        Eci1                 Eci1     Bmr1|       Eci1            Nco1
                          |                    |        ||          |               |
     CTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTT
3001 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3100
     GAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAA

                                                                                  Avr2
                                Sfi1                                              Stu1|
        polyA                   Bgl1                        SpDon             BseR1  ||              Cla1
          |                       |                           |                  |  ||                |
     TTTTTATTTATGCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGCAAAGATCGATC
3101 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3200
     AAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAG

              BsaB1                        BspM1                Eag1
                |                            |                    |
     AAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGC
3201 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3300
     TTCTCTGTCCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCG

                                                      Nar1
     Bmr1                                             Kas1|                        Drd1
        |                                               ||                           |
     ACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAAT
3301 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3400
     TGTTGTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTA

                                                         Pvu2
                                     Msc1                Fsp1   |        PflF1
                                        |                   |   |            |
     GAACTGCAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGC
3401 |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3500
     CTTGACGTTCTGCTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGCAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCG
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  Eco57                                   SpDon                        BciV1         BsrD1
      |                                       |                            |             |
      TGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATAC
3501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3600
      ACGATAACCCGCTTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATG

                          BtgZ1                                                                   Sap1
                        BspM1  |                                                                  Ear1
                               |  |                                                                  |
      GCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTG
3601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3700
      CGAACTAGGCCGATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGAC

                                BpuE1                        Sph1                        Nco1
                                   |                           |                           |
      GACGAAGAGCATCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCT
3701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3800
      CTGCTTCTCGTAGTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGA

                                                      BseY1
                                                     Nae1 |
        BtgZ1                                      NgoM4 | |        Rsr2         Eci1
            |                                          | | |           |            |
      GCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTAC
3801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 3900
      CGAACGGCTTATAGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATG

           Sap1                                                   BtgZ1
           Ear1                   Eco57         BssS1                BsrB1 |
              |                       |             |                    | |
      CCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGC
3901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4000
      GGCACTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCG
```

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                                                                BssS1
                    BsrB1          BstB1                        BspM1
                        |              |                            |
     CTTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTCGATTCCACCGCCGCCTT
4001 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4100
     GAAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAA

                                        Nae1                                                   Bpm1
                                     NgoM4 |                                              SpAcc  |
 SpAcc                                Bpm1 |                                               Avr2  |
     |                                    | |                                                   |  |
     CTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGG
4101 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4200
     GATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCC

                                                        polyA        polyA
                                                           |            |
     AGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTC
4201 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4300
     TCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCGTGCCACAACCCAGCAAACAAG

                                            Bsa1
                                              |
     ATAAACGCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCCCGCGTTTCTTCCTTTTCCCCACCCCA
4301 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4400
     TATTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGT

                                                        BstAP
                                                        AlwN1      Bsu36                          Dra1
                                                           |          |                              |
     CCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTA
4401 |||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||*||||||||||* 4500
     GGGGGGTTCAAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAAT
```

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                 Dra1                                BspH1
                   |                                   |
      AAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAG
4501  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4600
      TTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTC

                                                BpuE1
                                                  |
      ACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTG
4601  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4700
      TGGGGCATCTTTTCTAGTTTCCTAGAAGAACTCTAGGAAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAAC

                            Eco57                                                 SpAcc
                              |                                                     |
      TTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGC
4701  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4800
      AAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCG

                                                                  AlwN1                     BpuE1
                                                                    |                         |
      CACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGT
4801  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 4900
      GTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCA

                                                            ApaL1     BseY1
                                                              |         |
      TGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACT
4901  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5000
      ACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGA

                                                                        BciV1
                 SpAcc                                                Eci1   |
                   |                                                    |   |
      GAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGC
5001  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5100
      CTCTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTCCTCTCGCG
```

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 BssS1                                   SpAcc                          Drd1            BpuE1
     |                                       |                              |                |
      ACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGG
5101  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5200
      TGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCC


                                                                                  SpDon
         SpAcc     Eci1                                                          BspLU|
             |        |                                                              ||
      GGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGA
5201  |||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||*|||||||||* 5300
      CCGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACT


                                 Nsi1
                              BfrB1 |
                                    | |
      TTCTGTGGATAACCGTATTACCGCCATGCAT
5301  |||||||||*|||||||||*|||||||||*| 5331
      AAGACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	**Afe1**	**Age1**	**Ale1**	AlwN1	ApaL1	**Ase1**	Avr2	**Bae1a**	**Bae1b**	**BamH1**	**Bbs1**	BciV1	**Bcl1**
BfrB1	Bgl1	**Bgl2**	**Blp1**	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	**BsaXa**	**BsaXb**	BseR1	BseY1	Bsm1
BsmB1	**BspE1**	BspH1	**BspLU**	BspM1	BsrB1	**BsrD1**	**BsrG1**	BssS1	BstAP	**BstB1**	Bsu36	BtgZ1	**Bts1**
Cla1	Dra1	Dra3	Drd1	**Eag1**	Ear1	Eci1	Eco57	**EcoRV**	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Mlu1**
Msc1	Nae1	**Nar1**	Nco1	**Nde1**	NgoM4	**Nhe1**	Nsi1	**PflF1**	PflM1	polyA	**PshA1**	Psi1	Pvu2
Rsr2	Sap1	**Sca1**	**SexA1**	**Sfi1**	**SnaB1**	SpAcc	SpDon	**Spe1**	Sph1	Ssp1	Stu1	**Xba1**	**Xho1**

Unique:

Afe1	**Age1**	**Ale1**	**Ase1**	**Bae1a**	**Bae1b**	**BamH1**	**Bbs1**	**Bcl1**	**Bgl2**	**Blp1**	**BsaXa**	**BsaXb**	**BsmB1**
BspE1	**BspLU**	**BsrD1**	**BsrG1**	**BstB1**	**Bts1**	**Eag1**	**EcoRV**	**Fsp1**	**Hpa1**	**Kas1**	**Mfe1**	**Mlu1**	**Nar1**
Nde1	**Nhe1**	**PflF1**	**PshA1**	**Rsr2**	**Sca1**	**SexA1**	**Sfi1**	**SnaB1**	**Spe1**	**Xba1**	**Xho1**		

Not found:

Aar1	Acc65	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	BbvC1	Bcg1a	Bcg1b	BmgB1	Bpu10	Bsg1
BsiW1	BssH2	BstE2	BstX1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	Ecl2	EcoK	EcoN1	EcoR1
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Not1	Nru1	Pac1
Pme1	Pml1	PspOM	Pst1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1	Sac2	Sal1	SanD1	Sbf1
Sgf1	SgrA1	Sma1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xmn1			

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													