

pTagFP635-vinculin 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 base pairs 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). TagFP635 amino acids are shown in red, Vinculin amino acids are shown in green, linker amino acids are shown in black.



SpAcc Hind3 Dra1 Xba1 SpAcc
AGTTCTCATTTCAGCTATGAAGATTTTTGTAACAACCTAAAACTCAAAAAACCAAGGCATAGAGGAAGCTTTAAAAAATCGCAATTTTACTCTAGAAAAA
2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
TCAAGAGTAAAGTCGATACTTCTAAAAACATTGTTGATTTTTGAGTTTTTTGGTTCCGTATCTCCTTCGAAATTTTTTAGCGTTAAAAATGAGATCTTTTT
Vinculin > V L I S A M K I F V T T K N S K N Q G I E E A L K N R N F T L E K

Ase1 SpDon Ear1
ATGAGTGCTGAAATTAATGAGATAATTCGTGTGTTACAACCTCACCTCTTGGGATGAAGATGCCTGGGCCAGCAAGGACACTGAAGCCATGAAGAGAGCAT
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
TACTCACGACTTTAATTACTCTATTAAGCACACAATGTTGAGTGGAGAACCCTACTTCTACGGACCCGGTCGTTCTGTGACTTCGGTACTTCTCTCGTA
Vinculin > M S A E I N E I I R V L Q L T S W D E D A W A S K D T E A M K R A L

Eco57 SpAcc PflM1 SpAcc SpDon Bgl2
TGGCCTCCATAGACTCCAAACTGAACCAGGCCAAAGGTTGGCTCCGTGACCCTAGTGCCTCCCCAGGGGATGCTGGTGAGCAGGCCATCAGACAGATCTT
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
ACCGGAGGTATCTGAGGTTTACTTGGTCCGGTTTCCAACCGAGGCACTGGGATCACGGAGGGGTCCCCTACGACCACTCGTCCGGTAGTCTGTCTAGAA
Vinculin > A S I D S K L N Q A K G W L R D P S A S P G D A G E Q A I R Q I L

SpAcc Bsg1 Bcl1
AGATGAAGCTGGAAAAGTTGGTGAACCTCTGTGCAGGCAAAGAACGCAGGGGAGATTCTGGGAACTTGCAAAATGCTAGGGCAGATGACTGATCAAGTGGCT
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
TCTACTTCGACCTTTTCAACCACTTGAGACACGTCCGTTTCTTGGCTCCCTCTAAGACCCTTGAACGTTTTACGATCCCGTCTACTGACTAGTTCCACCGA
Vinculin > D E A G K V G E L C A G K E R R E I L G T C K M L G Q M T D Q V A

BamH1 SgrA1 Msc1 BspM1 BfuA1 Blp1 AlwN1
GACCTCCGTGCCAGAGGACAAGGATCCTCACCGGTGGCCATGCAGAAAGCTCAGCAGGTATCTCAGGGTCTGGATGTGCTCACAGCAAAAGTGGAAAATG
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
CTGGAGGCACGGTCTCCTGTTTCTTAGGAGTGGCCACCGGTACGTCTTTTCGAGTCGTCCATAGAGTCCCAGACCTACACGAGTGTGTTTTACCTTTTAC
Vinculin > D L R A R G Q G S S P V A M Q K A Q Q V S Q G L D V L T A K V E N A

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                BsrD1                Cla1                PflM1
                |                    |                    |
CAGCTCGCAAGCTGGAAGCCATGACCAACTCAAAGCAGAGCATTGCAAAGAAGATCGATGCTGCTCAGAACTGGCTTGCAGATCCAAATGGTGGACCGGA
2501 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2600
GTCGAGCGTTCGACCTTCGGTACTGGTTGAGTTTCGTCTCGTAACGTTTCTTCTAGCTACGACGAGTCTTGACCGAACGTCTAGGTTTACCACCTGGCCT
Vinculin > A R K L E A M T N S K Q S I A K K I D A A Q N W L A D P N G G P E

Sap1
Ear1
                Eco57                SpAcc
                |                    |
AGGAGAAGAGCAGATTCGAGGTGCTTTGGCTGAAGCTCGGAAAATAGCAGAATTATGTGATGATCCTAAAGAAAGAGATGACATTCTACGTTCCCTTGGG
2601 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2700
TCCTCTTCTCGTCTAAGCTCCACGAAACCGACTTCGAGCCTTTTATCGTCTTAATACACTACTAGGATTTCTTTCTCTACTGTAAGATGCAAGGGAACCC
Vinculin > G E E Q I R G A L A E A R K I A E L C D D P K E R D D I L R S L G

                SpAcc                Bbs1                Msc1
                Bgl2                Bpm1                Xho1                Msc1                BstX1
                |                |                |                |                |
GAAATATCTGCTCTGACTTCTAAATTAGCAGATCTACGAAGACAGGGGAAAAGGAGATTCTCCAGAGGCTCGAGCCTTGGCCAAACAGGTGGCCACGGCCC
2701 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2800
CTTTATAGACGAGACTGAAGATTTAATCGTCTAGATGCTTCTGTCCCTTTTCTCTAAGAGGTCTCCGAGCTCGGAACCGGTTTGTCCACCGGTGCCGGG
Vinculin > E I S A L T S K L A D L R R Q G K G D S P E A R A L A K Q V A T A L

                BstAP                BspM1
                AlwN1                BfuA1
                Pst1                Pst1                Xcm1                Msc1                BsrG1                Pvu2                BpuE1                Ale1
                |                |                |                |                |                |                |                |
TGCAGAACCTGCAGACCAAAACCAACCGGGCTGTGGCCAACAGCAGACCGGCCAAAGCAGCTGTACACCTTGAGGGCAAGATTGAGCAAGCACAGCGGTG
2801 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2900
ACGTCTTGGACGTCTGGTTTTGGTTGGCCCCGACACCGGTTGTCTGTGGCCGGTTTTCGTGCAGATGTGGAACCTCCCGTTCTAACTCGTTTCGTGTGCCAC
Vinculin > Q N L Q T K T N R A V A N S R P A K A A V H L E G K I E Q A Q R W

                Drd1
                |
GATTGATAATCCCACAGTGGATGACCGTGGAGTCGGTCAGGCTGCCATCCGGGGGCTTGTGGCCGAAGGGCATCGTCTGGCTAATGTTATGATGGGGCCT
2901 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 3000
CTAACTATTAGGGTGTACCTACTGGCACCTCAGCCAGTCCGACGGTAGGCCCCCGAACACCGGCTTCCCGTAGCAGACCGATTACAATACTACCCCGGA
Vinculin > I D N P T V D D R G V G Q A A I R G L V A E G H R L A N V M M G P

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                                     Bgl1
                                     Pvu2  BseY1  Pvu2  Bgl1
Bgl1  Bgl2                                     Bsu36  BssS1
|      |                                     |         |
TATCGGCAAGATCTTCTCGCCAAGTGTGACCGAGTGGACCAGCTGACAGCCCAGCTGGCTGACCTGGCTGCCAGAGGGGAAGGGGAGAGTCTCTCAGGCAC
3001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
ATAGCCGTTCTAGAAGAGCGGTTACACTGGCTCACCTGGTTCGACTGTCTGGGTCGACCGACTGGACCGACGGTCTCCCCTTCCCCTCTCAGGAGTCCGTG
Vinculin  > Y R Q D L L A K C D R V D Q L T A Q L A D L A A R G E G E S P Q A R

                                     BsaXb
GAGCACTTGCATCTCAGCTCCAAGACTCCTTAAAGGATCTAAAAGCTCGGATGCAGGAGGCCATGACTCAGGAAGTGTGAGATGTTTTTCAGCGATAACCAC
3101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
CTCGTGAACGTAGAGTCGAGGTTCTGAGGAATTTCTAGATTTTCGAGCCTACGTCCTCCGGTACTGAGTCCTTCACAGTCTACAAAAGTCGCTATGGTG
Vinculin  > A L A S Q L Q D S L K D L K A R M Q E A M T Q E V S D V F S D T T

                BsaXa                Nar1                Ear1
                Xcm1  BsaXb  Bts1  Kas1                BsaXa
                |    |    |    |    |                |    |
AACTCCCATCAAGCTGTTGGCAGTGGCAGCCACGGCGCCTCTCTGATGCGCCTAACAGGGGAAGAGGTATTTGATGAGAGGGCAGCTAACTTTGAAAACCAT
3201  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
TTGAGGGTAGTTTCGACAACCGTCAACCGTCCGGTCCCGCGGAGGACTACGCGGATTGTCCCTTCTCCATAAACTACTCTCCCGTCGATTGAAACTTTTGGTA
Vinculin  > T P I K L L A V A A T A P P D A P N R E E V F D E R A A N F E N H

                Hind3                Eag1  Bgl1                polyA                Xmn1  Stu1                Bbs1
                |          |          |          |                |          |          |          |
TCAGGAAAGCTTGGTGCTACGGCCGAGAAGGCGGCTGCGGTTGGTACTGCTAATAAATCAACAGTGGGAAGGCATTCAGGCCTCAGTGAAGACGGCCCGAG
3301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
AGTCCTTTTCGAACCACGATGCCGGCTCTTCCGCGGACGCCAACCATGACGATTATTTAGTTGTCACCTTCCGTAAGTCCGGAGTCACTTCTGCCGGGCTC
Vinculin  > S G K L G A T A E K A A A V G T A N K S T V E G I Q A S V K T A R E

                Bsa1                Bsa1
                |          |
AACTCACACCCCAGGTGGTCTCGGCTGCTCGTATCTTACTTAGGAACCTTGAAATCAAGCTGCTTATGAACATTTTGAGACCATGAAGAACCAGTGGAT
3401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
TTGAGTGTGGGGTCCACCAGAGCCGACGAGCATAGAATGAATCCTTGGGACCTTTAGTTTCGACGAATACTTGTAATACTCTGGTACTTCTTGGTCACTTA
Vinculin  > L T P Q V V S A A R I L L R N P G N Q A A Y E H F E T M K N Q W I

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          Eco57      Stu1
          Avr2      |
          |          |
          |          |          Ear1          Bpu10
          |          |          |          |
4001  TCCCTCCACCTAGGCCCTCCACCACCAGAGGAAAAGGATGAAGAGTTCCCTGAGCAGAAGGCCGGGGAGGTGATTAACCAGCCAATGATGATGGCTGCCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
      AGGGAGGTGGATCCGGAGGTGGTGGTCTCCTTTTCTACTTCTCAAGGGACTCGTCTTCCGGCCCCCTCCACTAATTGGTCGGTTACTACTACCGACGGTC
Vinculin > P P P R P P P P E E K D E E F P E Q K A G E V I N Q P M M M A A R
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          BsrD1
          BsrD1 |          BstX1
          |     |          |
          |     |          |
4101  ACAGCTCCATGATGAAGCTCGCAAATGGTCCAGCAAGGGCAATGACATCATTGCAGCAGCCAAGCGCATGGCTCTGCTGATGGCTGAGATGTCTCGGCTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
      TGTTCGAGGTACTACTTCGAGCGTTTACCAGGTCGTTCCCGTTACTGTAGTAACGTCGTCGTTCCGCTACCGAGACGACTACCGACTCTACAGAGCCGAC
Vinculin > Q L H D E A R K W S S K G N D I I A A A K R M A L L M A E M S R L
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          Kpn1
          Bts1 |
          |   |
          |   |          BtgZ1          Stu1          Msc1
          |   |          |          |          |
4201  GTAAGAGGGGGCAGTGGTACCAAGCGGGCACTCATTTCAGTGTGCCAAGGACATCGCCAAGGCCTCAGATGAGGTGACTCGGTTGGCCAAGGAGGTTGCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
      CATTCTCCCCGTCACCATGGTTTCGCCCCTGAGTAAGTCACACGGTTTCTGTAGCGGTTCCGGAGTCTACTCCACTGAGCCAACCGGTTTCTCCAACGGT
Vinculin > V R G G S G T K R A L I Q C A K D I A K A S D E V T R L A K E V A K
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          Bts1
          ApaL1 |
          |     |
          |     |          EcoN1SpAcc          BseY1
          |     |          |          |
4301  AGCAGTGCACAGATAAACGGATTAGAACCAACCTCTTACAGGTATGTGAGCGAATCCCAACCATAAGCACCCAGCTCAAAAATCCTGTCCACAGTGAAGGC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
      TCGTCACGTGTCTATTTGCCTAATCTTGGTTGGAGAATGTCCATACACTCGCTTAGGGTTGGTATTCGTGGGTCGAGTTTTAGGACAGGTGTCACTTCCG
Vinculin > Q C T D K R I R T N L L Q V C E R I P T I S T Q L K I L S T V K A
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                                     Psil
                                     |
4901 ATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAAACAAGAGTCCA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
TAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCCTCAGGT

                                     BtgZ1
                                     |
BsaXb          Drd1          BsaXa          Dra3
|              |              |              |
5001 CTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
GATAATTTCTTGACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAACCCCA

                                     NaeI
                                     |
                                     NgoM4
                                     |
5101 CGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGGAAGAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
GCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCTTCCCTTCTT

BsrB1
|
5201 AGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
TCGCTTTCCTCGCCCGGATCCCGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGGGCGATGTCCCGCGCAGT

                                     BciV1
                                     |
                                     BspH1
                                     |
                                     BsrB1
                                     |
                                     |
polyA
|
5301 GGTGGCACTTTTCGGGGAAAATGTGCGCGGAACCCCTATTTGTTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
CCACCGTGAAAAGCCCCCTTACACGCGCCTTGGGGATAAACAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTT

                                     Ecil
                                     |
Ssp1          Ear1          Bsu36          Pvu2          BseY1
|              |              |              |              |
5401 TGCTTCAATAATATTGAAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
ACGAAGTTATTATAACTTTTCTTCTCAGGACTCCGCCTTTCTTGGTTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTTCGT
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                NsiI
                SphI
                BfrB1
                BstAP
                SexA1
                BseY1
                NsiI
                SphI
                BfrB1
                BstAP
5501  GGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
      CCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGT

                EciI
                EciI
                Bmr1
                EciI
                NcoI
5601  ATTAGTCAGCAACCATAGTCCC GCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCAGTTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
      TAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAAAAAAA

                polyA
                sfiI
                Bgl1
                SpDon
                Avr2
                StuI
                BseR1
                ClaI
5701  TATTTATGCAGAGGCCGAGGCCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCCTAGGCTTTTGCAAAGATCGATCAAGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
      ATAAATACGTCTCCGGCTCCGGCGGAGCCGAGACTCGATAAGGTCTTCATCACTCCTCCGAAAAACCTCCGGATCCGAAAACGTTTCTAGCTAGTTCT

                BsaB1
                BspM1
                BfuA1
                Eag1
5801  GACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCCGGCTATGACTGGGCACAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5900
      CTGTCTACTCCTAGCAAAGCGTACTAACTTGTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTT

                Bmr1
                Kas1
                Nar1
                Drd1
5901  CAGACAATCGGCTGCTCTGATGCCCGGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6000
      GTCTGTTAGCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTG

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      SapI      BtgZ1
      EarI      Eco57      BssS1      BsrB1
GATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTC
6501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6600
CTATAACGACTTCTCGAACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAG

      BssS1
      BspM1
      BfuA1      SpAcc
      BsrB1      BstB1
TTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTAT
6601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6700
AACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATA

      NaeI      Bpm1
      NgoM4      SpAcc
      Bpm1      Avr2
GAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCTAGGGGGAGGC
6701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6800
CTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTGCGGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCG

      polyA      polyA
TAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTCGTTTGTTCATAA
6801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6900
ATTGACTTTGTGCCCTTCTCTGTTATGGCCTTCTTGGGCGCGATACTGCCGTTATTTTCTGTCTTATTTTTCGCTGCCACAACCCAGCAAACAAGTATT

      BsaI
ACGCGGGGTTCCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTCTTCTTTTCCCCACCCACCCC
6901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7000
TGCGCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGG

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                                BstAP
                                AlwN1
                                Bsu36
                                Dra1
7001  CCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7100
      GGTTC AAGCCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTG

                                Dra1
                                BspH1
7101  TTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7200
      AAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGG

                                BpuE1
7201  CGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCGGTGGTTTGTGTTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7300
      GCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTGCACCACCAAACAAAC

                                Eco57
                                SpAcc
7301  CCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7400
      GGCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGG

                                AlwN1
                                BpuE1
7401  ACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTTCGTGTCTTACCGGGTTGGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7500
      TGAAGTCTTGGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCAACCGCTATTGAGCAGAGAATGGCCCAACT

                                ApaL1
                                BseY1
7501  CTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAAGTGGAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7600
      GAGTTCGTATCAATGGCTATTCCGCGTCGCCAGCCCCGACTTGCCCCCAAGCACGTGTGTGGGTGGAACCTCGCTTGCTGGATGTGGCTTGACTCT
```


Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BbvC1	BciV1	Bcl1
BfrB1	BfuA1	Bgl1	Bgl2	Blp1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsg1	Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1
Bsu36	BtgZ1	Bts1	_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoN1	EcoR1
EcoRV	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4
Nhe1	Not1	Nsi1	PflF1	PflM1	polyA	PshA1	Psi1	Pst1	Pvu1	Pvu2	Rsr2	Sac1	Sap1
SexA1	Sfi1	SgrA1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	T7Ter	Xba1	Xcm1	Xho1	Xmn1

Unique:

Afe1	BbvC1	Bcl1	Blp1	BspE1	BspLU	EcoN1	EcoR1	EcoRV	Fsp1	Hpa1	Mfe1	Mlu1	Nde1
Nhe1	Not1	PflF1	PshA1	Pvu1	Rsr2	Sfi1	SgrA1	SnaB1					

Not found:

Aar1	Acl1	Afl2	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	Bcgl1a	Bcgl1b	BmgB1	BsiW1	BsmB1
BssH2	BstE2	BstZ1	EcoK	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Nru1
Pac1	Pme1	Pml1	PspOM	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1	Scal	Sgf1
Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA	PISce							

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	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	Styl	Taq1	Tat1	Tfil	Tse1	Tsp45	Tsp50
TspR1													