

pmKate2-vimentin 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). mKate2 amino acids are shown in red, vimentin amino acids are shown in green, linker amino acids are shown in black.



Aat2Eci1

TAGCGGTTTGACTCACGGGATTTCCAAGTCTCCACCCATTGACGTCAATGGGAGTTTGTGTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
 401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
 ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGTTTTTACAGCAT

Nhe1 Afel

ACAACCTCCGCCCATTTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Hind3

Xho1 Sac1 | EcoR1Srf1 Bpm1

BpuE1 Bgl2 | Ecl2 | BstB1 | SexA1Bcg1b EcoN1Sma1 Bcg1a |

CCGACTCAGATCTCGAGCTCAAGCTTCGAATTTCCCATGTCCACCAGGTCCGTGTCTCCTCGTCCTCCTACCGCAGGATGTTTCGGCGGGCCCGGGCACCCGGA
 601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCTGAGTCTAGAGCTCGAGTTTCGAAGCTTAAGGGTACAGGTGGTCCAGGCACAGGAGCAGGAGGATGGCGTCTACAAGCCCGCCGGGGCCCGTGGCGCT

vimentin > M S T R S V S S S S Y R R M F G G P G T A S

Nae1
 Eag1 Sac1
 NgoM4 | Ecl2 | PflF1BssH2 BseY1

GCCGGCCGAGCTCCAGCCGAGCTACGTGACTACGTCCACCCGCACCTACAGCCTGGGCAGCGCGCTGCGCCCCAGCACCAGCCGCAGCCTCTACGCCTC
 701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 CGGCCGGCTCGAGGTCGGCTCGATGCACTGATGCAGGTGGGCGTGGATGTCGGACCCGTCGCGCGACGCGGGGTTCGTGGTTCGGCGTTCGGAGATGCGGAG

vimentin > R P S S S R S Y V T T S T R T Y S L G S A L R P S T S R S L Y A S

SpAcc
 Sbf1 |
 Pst1 |

Sma1 BseR1Sma1Pst1

GTCCCCGGGCGGCGTGTATGCCACGCGCTCCTCTGCCGTGCGCCTGCGGAGCAGCGTGCCCCGGGGTTCGGGCTCCTGCAGGACTCGGTGGACTTCTCGCTG
 801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 CAGGGGCCCGCCGCACATACGTTGCGCGAGGAGACGGCACGCGGACGCCTCGTTCGCACGGGCCCCACGCCGAGGACGTCCTGAGCCACCTGAAGAGCGAC

vimentin > S P G G V Y A T R S S A V R L R S S V P G V R L L Q D S V D F S L

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                                     AlwN1
                                     |
                               Xcm1  SpAcc Pst1  |
                               |      |      |
GCGGACGCCATCAACACCGAGTTCAAGAACACCCGCACCAACGAGAAGGTGGAGCTGCAGGAGCTGAATGACCGCTTCGCCAACTACATCGACAAGGTGC
101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
CGGCTGCGGTAGTTGTGGCTCAAGTTCTTGTGGGCGTGGTTGCTCTTCCACCTCGACGTCCTCGACTTACTGGCGAAGCGGTTGATGTAGCTGTTCCACG
vimentin > A D A I N T E F K N T R T N E K V E L Q E L N D R F A N Y I D K V R

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                                     Sac1
                                     |
                               Xho1|
                               |    |
                               Bpm1 BpuE1 Ecl2||
                               |    |    |
GCTTCTGGAGCAGCAGAATAAGATCCTGCTGGCCGAGCTCGAGCAGCTCAAGGGCCAAGGCAAGTCGCGCCTGGGGGACCTCTACGAGGAGGAGATGCG
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CGAAGACCTCGTCGTCCTTATTCTAGGACGACCGGCTCGAGCTCGTCGAGTTCCCGGTTCCGTTTCAGCGCGGACCCCTGGAGATGCTCCTCCTCTACGC
vimentin > F L E Q Q N K I L L A E L E Q L K G Q G K S R L G D L Y E E E M R

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                                     Nae1
                                     |
                               NgoM4 |
                               |    |
                               BseR1 |    |
                               BspM1 |    |
                               BfuA1 |    |
                               Aar1  |    |
                               BseR1 ||    |
                               |    |    |
                               |    |    |
GGAGCTGCGCCGGCAGGTGGACCAGCTAACCAACGACAAAGCCCCGCGTCGAGGTGGAGCGCGACAACCTGGCCGAGGACATCATGCGCCTCCGGGAGAAA
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CCTCGACGCGGCCGTCCACCTGGTCGATTGGTTGCTGTTTTCGGGCGCAGCTCCACCTCGCGCTGTTGGACCGGCTCCTGTAGTACGCGGAGGCCCTCTTT
vimentin > E L R R Q V D Q L T N D K A R V E V E R D N L A E D I M R L R E K

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Eco57                                     BseR1                                     Ahd1  BsmB1BmgB1
|                                     |                                     |      |      |
TTGCAGGAGGAGATGCTTCAGAGAGAGGAAGCCGAAAAACACCTGCAATCTTTTCAGACAGGATGTTGACAATGCGTCTCTGGCAGCTCTTGACCTTGAAC
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
AACGTCCTCCTCTACGAAGTCTCTCTCCTTCGGCTTTTGTGGGACGTTAGAAAGTCTGTCTTACAACCTGTTACGCAGAGACCGTGCAGAACTGGAACCTTG
vimentin > L Q E E M L Q R E E A E N T L Q S F R Q D V D N A S L A R L D L E R

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          Ear1              Ear1              AlwN1 Pst1
          |                   |                   |   |
GCAAAGTGGAATCTTTGCAAGAAGAGATTGCCCTTTTGAAGAAACTCCACGAAGAGGAAATCCAGGAGCTGCAGGCTCAGATTCCAGGAACAGCATGTCCA
1301 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1400
CGTTTCACCTTAGAAACGTTCTTCTCTAACGGAAAAACTTCTTTGAGGTGCTTCTCCTTTAGGTCCTCGACGTCCGAGTCTAAGTCCTTGTTCGTACAGGT
vimentin  >  K V E S L Q E E I A F L K K L H E E E I Q E L Q A Q I Q E Q H V Q

                                                BspM1
                                                BfuA1
                                                Sbf1 |
                                                Pst1 |
Cla1             PshA1             SpAcc     EcoN1 |
|                   |                 ||     | |
AATCGATGTGGATGTTTCCAAGCCTGACCTCACGGCTGCCCTGCGTGACGTACGTACGCATATATGAAAGTGTGGCTGCCAAGAACCTGCAGGAGGCAGAA
1401 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1500
TTAGCTACACCTACAAAGGTTCCGACTGGAGTGCCGACGGGACGCACTGCATGCAGTCGTTATACTTTACACCCGACGGTTCTTGGACGTCCCTCCGTCTT
vimentin  >  I D V D V S K P D L T A A L R D V R Q Q Y E S V A A K N L Q E A E

                    EcoN1              EcoN1
                    |                   |
GAATGGTACAAATCCAAGTTTGCTGACCTCTCTGAGGCTGCCAACCGGAACAATGACGCCCTGCGCCAGGCAAAGCAGGAGTCCACTGAGTACCGGAGAC
1501 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1600
CTTACCATGTTTAGGTTCAAACGACTGGAGAGACTCCGACGGTTGGCCTTGTTACTGCGGGACGCGGTCCGTTTTTCGTCTCAGGTGACTCATGGCCTCTG
vimentin  >  E W Y K S K F A D L S E A A N R N N D A L R Q A K Q E S T E Y R R Q

    SpDon    Bsg1              Xcm1              Ear1
    |         |                 |                   |
AGGTGCAGTCCCTCACCTGTGAAGTGATGCCCTTAAAGGAACCAATGAGTCCCTGGAACGCCAGATGCGTGAAATGGAAGAGAACTTTGCCGTTGAAGC
1601 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1700
TCCACGTCAGGGAGTGGACACTTCACCTACGGGAATTTCTTTGGTTACTCAGGGACCTTGCGGTCTACGCACTTTACCTTCTCTTGAAACGGCAACTTCG
vimentin  >  V Q S L T C E V D A L K G T N E S L E R Q M R E M E E N F A V E A

          Sbf1              BspM1
          |                   |
          Xcm1             Pst1             Ale1             BfuA1
          |                 |                 |                   |
TGCTAACTACCAAGACTATTGGCCGCTGCAGGATGAGATTCAGAATATGAAGGAGGAAATGGCTCGTACCTTCGTGAATACCAAGACCTGCTCAAT
1701 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1800
ACGATTGATGGTTCTGTGATAACCGGCGGACGTCTACTCTAAGTCTTATACTTCTCCTTTACCGAGCAGTGGAAGCACTTATGGTTCTGGACGAGTTA
vimentin  >  A N Y Q D T I G R L Q D E I Q N M K E E M A R H L R E Y Q D L L N

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SpDon | Bbs1 | Bpm1 |

2301 GCAGTCCTTCCCGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGC 2400
||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2400
CGTCAGGAAGGGCTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCCCGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCTGCCGACG

mKate2 > Q S F P E G F T W E R V T T Y E D G G V L T A T Q D T S L Q D G C

BseY1 Bsa1 | Stul |

2401 CTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACCCTGT 2500
||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2500
GAGTAGATGTTGCAGTTCAGTCTCCCCTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGGGACA

mKate2 > L I Y N V K I R G V N F P S N G P V M Q K K T L G W E A S T E T L Y

Bgl1 Bgl1 BssS1 Eco57 | Bbs1 |

2501 ACCCCGCTGACGGCGGCCTGGAAGGCAGAGCCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAA 2600
||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2600
TGGGGCGACTGCCGCCGACCTTCCGTCTCGGCTGTACCGGGACTTCGAGCACCCGCCCGGTGGACTAGACGTTGAACTTCTGGTGTATGTCTAGGTT

mKate2 > P A D G G L E G R A D M A L K L V G G G H L I C N L K T T Y R S K

BpuE1 | Bbs1 | SpAcc | Bsa1 | PshA1 | BssS1 |

2601 GAAACCCGCTAAGAACCCTCAAGATGCCCCGGCGTCTACTATGTGGACAGAAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAC 2700
||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2700
CTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGTCTTCTGACCTTTCTTAGTTCTCCGGCTGTTTCTCTGGATGCAGCTCGTCTGTG

mKate2 > K P A K N L K M P G V Y Y V D R R L E R I K E A D K E T Y V E Q H

Not1 | Eag1 |

Dra3 Msc1 AlwN1 | SpAcc | Bmr1 BsrB1 | Xba1 | BsaB1 |

2701 GAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAAACCTGGGGCACAGATGAGCGGCCGCGACTCTAGATCATAATCAGCCATAACCACATTTGTAGAG 2800
||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 2800
CTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTTGACCCCGTGTCTACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTC

mKate2 > E V A V A R Y C D L P S K L G H R *


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                    NaeI
                    NgoM4 |
                    | |
3301  GCGGCGCGCTAGGGCGCTGGCAAGTGTAGC
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3400
CGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGACCCGCTCTTTCCTTCCCTTCTTTTCGCTTTCTCCTCGCCCAGATCCCAGCACCATTACATCG

GGTCACGCTGCGCGTAACCACACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAAATGTGCGCGGAACCCCTATT
3401  | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3500
CCAGTGCGACGCGCATTTGGTGGTGTGGGCGGCGGAATTACGCGCGCATGTCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGCCTTGGGGATAA

                    BciV1
                    BspH1 |
                    | |
                    polyA
                    |
                    | | | | | | | | | | | | | |
                    | | | | | | | |
                    | | | | | | | | | | | | | |
3501  TGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCGTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCTTGAGGCGG
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3600
ACAAATAAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCC

                    NsiI
                    SphI |
                    BfrB1 |
                    BstAP | |
                    | | |
                    EciI
                    Pvu2 |
                    | |
                    | | | | | | | | | | | | | |
                    | | | | | | | |
                    | | | | | | | | | | | | | |
3601  AAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCA
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3700
TTTCTTTGGTTCGACACCTTACACACAGTCAATCCACACCTTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGT

                    NsiI
                    SphI |
                    BfrB1 |
                    BstAP | |
                    | | |
                    SexA1
                    |
                    | | | | | | | | | | | | | |
                    | | | | | | | |
                    | | | | | | | | | | | | | |
3701  ACCAGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCCGCCCTAACTCCGCCCA
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 3800
TGGTCCACACCTTTTCAGGGGTCCGAGGGGTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGT

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                BssS1
                BspM1
                BfuA1
                SpAcc
                NaeI
                NgoM4 |
                Bpm1 |
                |
4801 GACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
    CTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCG
  
```

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                Bpm1
                SpAcc |
                Avr2 |
                |
4901 TGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
    ACCTACTAGGAGGTCGCGCCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTCCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGG
  
```

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                polyA
                polyA
                |
5001 GCGCTATGACGGCAATAAAAAAGACAGAATAAAAACGCACGGTGTGGGTCGTTTGTTCATAAACCGGGGTTCGGTCCCAGGGCTGGCACTCTGTCGATAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
    CGCGATACTGCCGTTATTTTTCTGTCTTATTTTGCCTGCCACAACCCAGCAAACAAGTATTTGCGCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATG
  
```

```

Bsa1
|
5101 CCCACCGAGACCCCATTTGGGGCCAATAACGCCCGGTTTCTTCCTTTTCCCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    GGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGTGGGGTGGGGGTTCAGCCCACTTCCGGGTCCCGAGCGTCGGTTGCAG
  
```

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                BstAP
                AlwN1
                Bsu36
                Dra1
                Dra1
2521 GGGGCGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAACTTCATTTTTAATTTAAAGGATCTAGGTGAAGATCCTTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    CCCCOCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAA
  
```

BspH1
|
TTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTT
5301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
AACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAA

BpuE1
|
TCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCGGTGGTTTGTGGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTA
5401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
AGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAGGCTTCCATTGA

Eco57
|

SpAcc
|
GGCTTCAGCAGAGCGCAGATAACAAATACTGTCCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCAGCTACATACCTCGCTC
5501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
CCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAG

AlwN1
|

BpuE1
|

TGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGG
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
ACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCTGCCAGCCC

ApaL1
|

BseY1
|

SpAcc
|

CTGAACGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCC
5701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
GACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTACTCTATGGATGTCGACTCGATACTCTTTCGCGGTGCGAAGGG

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                BciV1
            Eci1  |               BssS1              SpAcc
                |               |                 |
5801  GAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTC
      | | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 5900
      CTCCCTCTTTCCGCCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAG
  
```

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                Drd1           BpuE1           SpAcc           Eci1
                |             |             |             |
5901  CTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTTACG
      | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * 6000
      GACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTTCGTTGCGCCGAAAAATGC
  
```

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                SpDon           Nsi1
                BspLU |         BfrB1 |
                    ||           |  |
6001  GTTCCTGGCCTTTTGTGGCCTTTTGTGCATGTTCTTTCTGCGTTATCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
      | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | 6088
      CAAGGACCGAAAAACGACCGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
  
```

Found:

Aar1	Aat2	Afe1	Afl2	Age1	Ahd1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	Bcg1a
Bcg1b	BciV1	BfrB1	BfuA1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb
BseR1	BseY1	Bsg1	BsiW1	Bsm1	BsmB1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1
BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57
EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1
Not1	Nsi1	PflF1	polyA	PshA1	Psi1	Pst1	Pvu2	Rsr2	Sac1	Sap1	Sbf1	SexA1	Sfi1
Sma1	SnaB1	SpAcc	SpDon	Sph1	Srf1	Ssp1	Stu1	Xba1	Xcm1	Xho1			

Unique:

Aar1	Afe1	Afl2	Age1	Ahd1	Ase1	BamH1	Bcg1a	Bcg1b	Bgl2	BmgB1	Bsg1	BsiW1	BsmB1
BspLU	BsrD1	BsrG1	BssH2	Bts1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1
Not1	Rsr2	Sfi1	SnaB1	Srf1	Xba1								

Not found:

Acc65	Acl1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcl1	Blp1	Bpu10	BspE1	BstE2	BstX1
BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL
R4atP	R4atR	Sac2	Sall	SanD1	Sca1	Sgf1	SgrA1	Spe1	Swa1	T3RNA	T7RNA	T7Ter	PISce
Xmn1													

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	Bs11	BsmA1	BsmF1	Bsp12	BspCa	BspCb	Bsr1
BsrF1	BssK1	BstF5	BstN1	BstU1	BstY1	Btg1	Cac8	CviJ1	Dde1	Eae1	EcoO1	Fau1	Fnu4H
Fok1	Hae2	Hae3	Hga1	Hha1	Hinc2	Hinf1	HinP1	Hpa2	Hph1	Hpy99	Hpy1	Hpy3	HpyC3
HpyC4	HpyC5	Mae3	Mbo2	Mnl1	Mse1	Msl1	MspA1	Mwo1	Nci1	Nla3	Nla4	Nsp1	Ple1
PpuM1	Rsa1	Sau3A	Sau96	SfaN1	Sfc1	Sml1	Sty1	Taq1	Tat1	Tfi1	Tse1	Tsp45	Tsp50
TspR1													