

pFusionRed-cadherin 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, VE-Cadherin amino acids are shown in green, linker amino acids are shown in black.



Aat2 Eci1

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              |                                      |
TAGCGGTTTACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTTGTTTTGGCACCAAAAATCAACGGGACTTTCCAAAATGTCGTA
401 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTAGAGGTTGGGTAAGTGCAGTTACCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

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Nhe1

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                                     |
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCCGCC
501 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 600
TGTTGAGGCGGGTAAGTGCCTTACCCGCATCCGACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGCCAGTCTAGGCGATCGGCGG

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BspH1 Nar1 BspM1 Bts1

BseR1 Kas1 Aar1 BstAP

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              |          |          |          |          |          |          |          |          |
ACCATGCAGAGGCTCATGATGCTCCTCGCCACATCGGGCGCCTGCCTGGGCCTGCTGGCAGTGGCAGCAGTGGCAGCAGCAGGTGCTAACCTGCCAAC
601 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 700
TGGTACGTCTCCGAGTACTACGAGGAGCGGTGTAGCCCCGGGACGGACCCGGACGACCGTCAACCGTCGTCACCGTCGTCGTCACGATTGGGACGGGTTG

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Cadherin > M Q R L M M L L A T S G A C L G L L A V A A V A A A G A N P A Q R

Nar1 Ear1 SpDon

Kas1 SgrA1

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              |          |          |          |          |          |          |          |          |
GGGACACCCACAGCCTGCTGCCCCACCCACCGGCGCCAAAAGAGAGATTGGATTTGGAACCAGATGCACATTGATGAAGAGAAAAACACCTCACTTCCCCA
701 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 800
CCCTGTGGGTGTCGGACGACGGGTGGGTGGCCGCGGTTTTCTCTCTAACTAAACCTTGGTCTACGTGTAAGTAACTTCTCTTTTTGTGGAGTGAAGGGGT

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Cadherin > D T H S L L P T H R R Q K R D W I W N Q M H I D E E K N T S L P H

Bsm1 BsaXa BspM1 Bbs1 BsaXb BsmB1

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              |          |          |          |          |          |          |          |          |
TCATGTAGGCAAGATCAAGTCAAGCGTGAGTTCGCAAGAATGCCAAGTACCTGCTCAAAGGAGAATATGTGGGCAAGGTCTTCCGGGTCCGATGCAGAGACA
801 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 900
AGTACATCCGTTCTAGTTCAGTTCGCACTCAGCGTTCTTACGGTTCATGGACGAGTTTTCTCTTATACACCGGTTCCAGAAGGCCAGCTACGTCTCTGT

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Cadherin > H V G K I K S S V S R K N A K Y L L K G E Y V G K V F R V D A E T


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                Drd1                SpAcc                BstX1                SpAcc
                |                    |                    |                    |
1901  TGGACAGAGAAGTCTACCCCTGGTATAACCTGACTGTGGAGGCCAAAGAAGTGGATTCCACTGGAACCCCCACAGGAAAAGAATCCATTGTGCAAGTCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2000
      ACCTGTCTCTTCAGATGGGGACCATATTGGACTGACACCTCCGGTTTCTTGACCTAAGGTGACCTTGGGGGTGTCCTTTTCTTAGGTAACACGTTTCAGGT
Cadherin >  D R E V Y P W Y N L T V E A K E L D S T G T P T G K E S I V Q V H

                                                Nco1  Msc1  Pvu2  Pst1  Bgl2
                                                |    |    |    |    |
2001  CATTGAAGTTTTGGATGAGAATGACAATGCCCCGGAGTTTGCCAAGCCCTACCAGCCCAAAGTGTGTGAGAACGCTGTCCATGGCCAGCTGGTCCTGCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
      GTAACTTCAAAACCTACTCTTACTGTTACGGGGCCTCAAACGGTTCGGGATGGTCGGGTTTCACACACTCTTGCGACAGGTACCGGTCGACCAGGACGTC
Cadherin >  I E V L D E N D N A P E F A K P Y Q P K V C E N A V H G Q L V L Q

                                SpDon
                                |
2101  ATCTCCGCAACAGACAAGGACATAACACCACGAAACGTGAAGTTCAAATTCACCTTTGAATACTGAGAACAACCTTTACCCTCACGGATAATCACGATAACA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
      TAGAGGCGTTGTCTGTTCTGTATTGTGGTGCTTTGCACTTCAAGTTTAAAGTAAAACCTTATGACTCTTGTTGAAATGGGAGTGCCTATTAGTGCTATTGT
Cadherin >  I S A T D K D I T P R N V K F K F T L N T E N N F T L T D N H D N T

2201  CGGCCAACATCACAGTCAAGTATGGGCAGTTTGACCGGGAGCATAACCAAGGTCCACTTCTACCCGTGGTCATCTCAGACAATGGGATGCCAAGTTCGCAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
      GCCGGTTGTAGTGTTCAGTTTCATACCCGTCAAACCTGGCCCTCGTATGGTTCCAGGTGAAGGATGGGCACCAGTAGAGTCTGTTACCCTACGGTTCAGCGTG
Cadherin >  A N I T V K Y G Q F D R E H T K V H F L P V V I S D N G M P S R T

                                SpAcc
                                |
                                SpDon
                                |
2301  GGGCACCAGCACGCTGACCGTGGCCGTGTGCAAGTGCAACGAGCAGGGCGAGTTACCTTCTGCGAGGATATGGCCGCCAGGTGGGCGTGAGCATCCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      CCCGTGGTTCGTGCGACTGGCACCAGGCACACGTTTACGTTGCTCGTCCCCTCAAGTGAAGACGCTCCTATACCGGCGGGTCCACCCGCACTCGTAGGTC
Cadherin >  G T S T L T V A V C K C N E Q G E F T F C E D M A A Q V G V S I Q

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PflM1 Bts1          SpDon      Bcl1          BspE1          BssH2
|         |          |          |          |          |
GCAGTGGTAGCCATCTTACTCTGCATCCTCACCATCACAGTGATCACCTGCTCATCTTCTGCGGCGGGCTCCGGAAGCAGGCCCGCGCGCACGGCA
2401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
CGTCACCATCGGTAGAATGAGACGTAGGAGTGGTAGTGTCACTAGTGGGACGAGTAGAAGGACGCCGCCGCGGAGGCCCTTCGTCCGGGCGCGCGTGCCGT
Cadherin > A V V A I L L C I L T I T V I T L L I F L R R R L R K Q A R A H G K

          BstE2
        BssS1  Pvu2  |          BseR1  _Chi
          |         |         |          |         |
AGAGCGTGCCGGAGATCCACGAGCAGCTGGTCACCTACGACGAGGAGGGCGGGCGGCGAGATGGACACCACCAGCTACGATGTGTGGTGTCAACTCGGT
2501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
TCTCGCACGGCCTCTAGGTGCTCGTCGACCAGTGGATGCTGCTCCTCCCGCCGCGCTCTACCTGTGGTGGTTCGATGCTACACAGCCACGAGTTGAGCCA
Cadherin > S V P E I H E Q L V T Y D E E G G G E M D T T S Y D V S V L N S V

          Sac2          BspM1          Bgl1  Bsg1
          |         |         |         |         |         |         |
GCGCCGCGGGCGGGGCCAAGCCCCCGGGCCCGCGCTGGACGCCCGGCTTCCCTCTATGCGCAGGTGCAGAAGCCACCGAGGCACGCGCCTGGGGCACAC
2601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
CGCGGCGCCGCCCGGTTCCGGGGCGCCGGGCGCGACCTGCGGGCCGGAAGGGAGATACGCGTCCACGTCTTCGGTGGCTCCGTGCGCGGACCCCGTGTG
Cadherin > R R G G A K P P R P A L D A R P S L Y A Q V Q K P P R H A P G A H

          Sma1
        BspOM  Apal  |          SpDon          Eci1  Bsg1          BsaXb  SpAcc
          |         |         |         |         |         |         |         |
GGAGGGCCCGGGGAGATGGCAGCCATGATCGAGGTGAAGAAGGACGAGGCGGACCACGACGGCGACGGCCCCCCTACGACACGCTGCACATCTACGGCT
2701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
CCTCCCGGGCCCCCTCTACCGTCCGTTACTAGCTCCACTTCTTCCCTGCTCCGCTGGTGTGCGGCTGCCGGGGGGGATGCTGTGCGACGTGTAGATGCCGA
Cadherin > G G P G E M A A M I E V K K D E A D H D G D G P P Y D T L H I Y G Y

          BsaXa  Bpu10  BbvC1          BmgB1          SanD1  Bmr1
          |         |         |         |         |         |         |
ACGAGGGCTCCGAGTCCATAGCCGAGTCCCTCAGCTCCCTGGGCACCGACTCATCCGACTCTGACGTGGATTACGACTTCCCTTAACGACTGGGGACCCAG
2801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
TGCTCCCGAGGCTCAGGTATCGGCTCAGGGAGTCGAGGGACCCGTGGCTGAGTAGGCTGAGACTGCACCTAATGCTGAAGGAATTGCTGACCCCTGGGTC
Cadherin > E G S E S I A E S L S S L G T D S S D S D V D Y D F L N D W G P R

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BseY1 BsmB1 Stul Bgl1 BssS1 Eco57
TCGGCTGGGAGGCTCCACCGAGACGATGTACCCCGCTGACGGCGGCTGGAAGGCGCATGTGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGAT
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
AGCCGACCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCCGGACCTTCCGCGTACACTGTACCGGGACTTCGAGCACCCGCCCGGTGGACTA
FusionRed > **G W E A S T E T M Y P A D G G L E G A C D M A L K L V G G G H L I**

Bsa1 BpuE1 SpAcc PflM1
CTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCCGGCTCTACAACGTGGACCACAGACTGGAAAGAATCAAGGAG
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
GACGTTGGAACCTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGAGATGTTGCACCTGGTGTCTGACCTTTCTTAGTTCTC
FusionRed > **C N L E T T Y R S K K P A T N L K M P G V Y N V D H R L E R I K E**

Bsa1 PshA1 BssS1 Dra3 Msc1 SpDon BsrB1 Not1 Eagl Xba1
GCCGACGATGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGATGGAGGTAAATGAGCGGCCGCGACTCTAG
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CGGCTGCTACTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGAGATGACCACCGCACCCTACCTCCATTTACTCGCCGGCGCTGAGATC
FusionRed > **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 G K ***

BsaB1 SpDon Dra1 Bsm1 MfeI
ATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGTCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTG
3701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
TAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGGACTTTGTATTTTACTTACGTTAACAAC

HpaI polyA PstI polyA polyA Bts1 Bsm1
TTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGG
3801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
AACAAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACC


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                                     Af12      SpDon      Ssp1
                                     |          |          |
3901 TTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAAATTTCGCGTTAAATTTTGTAAATCAGCTCATTTTTTTAA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
AAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATT

                                     Psil      BsaXb
                                     |          |
4001 CCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGTCCACTATTAAG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
GGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTTC

                                     BtgZ1
                                     Dra3 |
                                     ||
   Drd1      BsaXa
   |          |
4101 AACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
TTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACCTTGGTAGTGGGATTAGTTCAAAAAACCCCAGCTCCACGG

                                     Nae1
                                     NgoM4 |
                                     ||
   SpAcc
   |
4201 GTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CATTTGCGTATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCCCTTTCGGCCGCTTGACCCGCTCTTTCCTTCCCTTCTTTTCGCTTTCC

BsrB1
|
4301 AGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
TCGCCC CGGATCCC CGGACCGTT CACATCGCCAGT GCGACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCATGTCGCGCAGTCCACCGTGA

                                     BciV1
                                     BspH1 |
                                     BsrB1 |
                                     ||
   polyA
   |
4401 TTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAAT
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
AAAGCCCCTTTACACGCGCTTGGGGATAAAACAAATAAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTA

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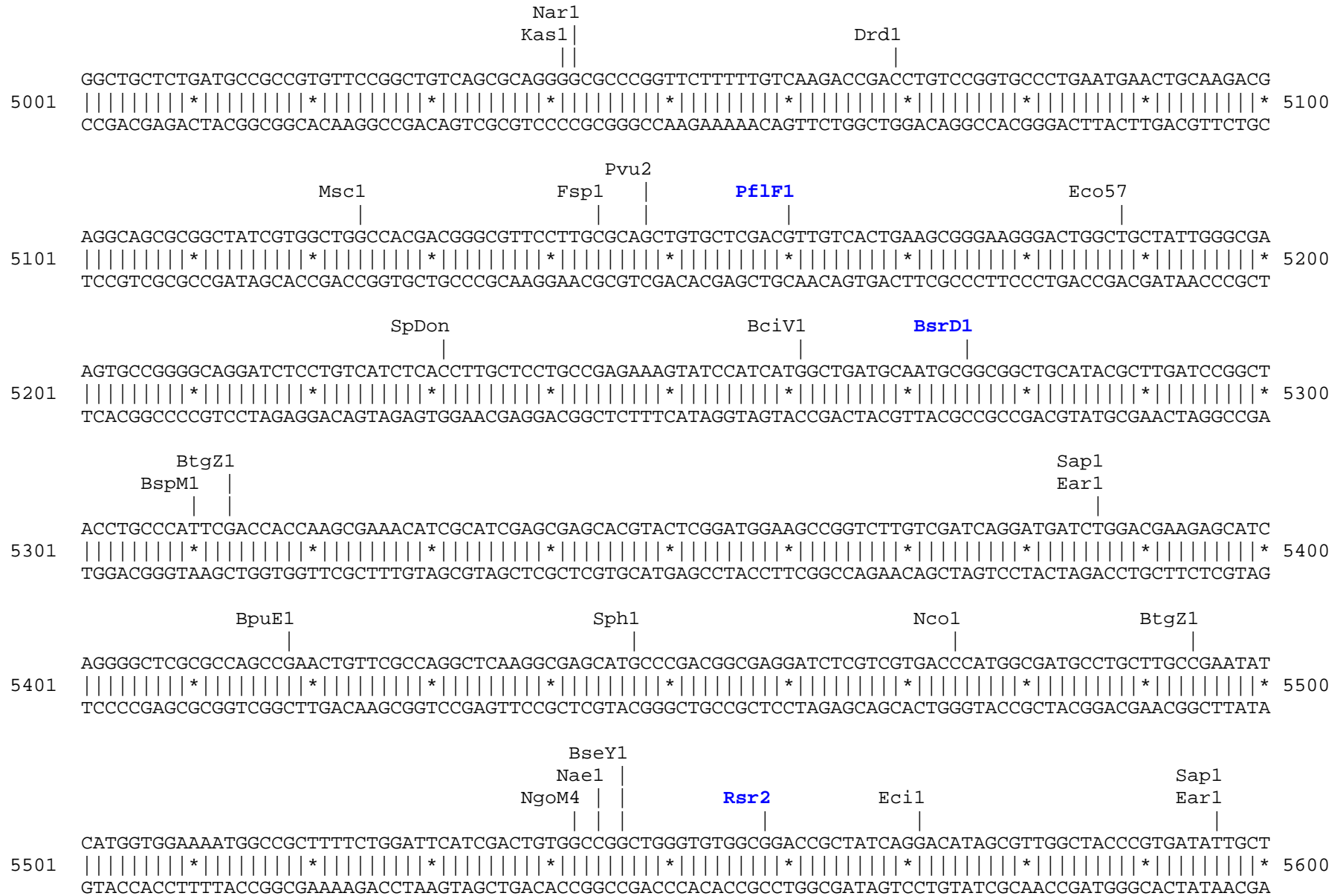
SspI EarI Bsu36 EciI Pvu2 BseY1
AATATTGAAAAAGGAAGAGTCTTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGT
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
TTATAACTTTTTCCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCA

NsiI SphI BfrB1 BstAP SexA1 BseY1 BstAP SphI BfrB1 NsiI
ATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAG
4601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
TACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTC

EciI EciI BmrI EciI NcoI polyA
CAACCATAGTCCCGCCCTAACTCCGCCATCCCGCCCTAACTCCGCCAGTTCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGC
4701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
GTTGGTATCAGGGCGGGATTGAGGCGGGTAGGGCGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGTACCGACTGATTAATAAATAAATAACG

BglI sfiI SpDon BseR1 Avr2 StuI ClaI
AGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTGC AAAGATCGATCAAGAGACAGGATG
4801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
TCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCTCCGAAAAAACCCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTTAC

BsaB1 BspM1 Eag1 Bmr1
AGGATCGTTTCGCATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAACAGACAATC
4901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
TCTTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCCAAGAGGCCGGCGAACCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAG




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                                BstAP
                                AlwN1      Bsu36                                Dra1
                                |           |                                |
6101 GGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6200
    CCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAA

    Dra1                                BspH1
    |                                   |
6201 AATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6300
    TTAAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTT

                                BpuE1
                                |
6301 GATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6400
    CTAGTTTCTAGAAAGACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTT

                                Eco57                                SpAcc
                                |                                   |
6401 GAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6500
    CTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCT

                                AlwN1                                BpuE1
                                |                                   |
6501 ACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6600
    TGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTGAGCACAGAATGGCCCAACCTGAGTTCTGC

                                ApaL1      BseY1
                                |           |
6601 ATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6700
    TATCAATGGCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGGACTCTATGGATGTC

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SpAcc
|
CGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTC
6701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6800
GCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAG

BciV1
|
EciI
|
BssS1
|

SpAcc
|
CAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATG
6801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6900
GTCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCCTCGGATAC

SpAcc
|
Drd1
|
BpuE1
|
SpAcc
|

EciI
|
GAAAAACGCCAGCAACCGGCCTTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAAC
6901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 7000
CTTTTTGCGGTTCGTTGCGCCGAAAAATGCCAAGGACCGAAAAACGACCGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTG

SpDon
|
BspLU
|

NsiI
|
BfrB1
|
CGTATTACCGCCATGCAT
7001 |||||*||||| 7018
GCATAATGGCGGTACGTA

Found:

Aar1	Aat2	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BbvC1	BciV1
Bcl1	BfrB1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb
BseR1	BseY1	Bsg1	Bsm1	BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1
BstAP	BstB1	BstE2	BstX1	Bsu36	BtgZ1	Bts1	_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1
Eci1	Eco57	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1
Not1	Nsil	PflF1	PflM1	polyA	PshA1	Psil	PspOM	Pst1	Pvu2	Rsr2	Sac2	SanD1	Sap1
SexA1	Sfil	SgrA1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1	Xcm1		

Unique:

Afl2	Age1	Apa1	Ase1	BamH1	BbvC1	Bcl1	Bgl2	Blp1	Bpu10	BspE1	BspLU	BsrD1	BsrG1
BssH2	BstB1	BstE2	_Chi	Hind3	Hpa1	Mfe1	Nde1	Nhe1	Not1	PflF1	PspOM	Pst1	Rsr2
SanD1	SexA1	Sfil	SgrA1	SnaB1	Xba1								

Not found:

Acc65	Acc1	Afe1	Ahd1	Asc1	AsiS1	Baela	Baelb	BcglA	Bcglb	BsiW1	BstZ1	BxatB	BxatL
BxatR	BxatP	Ecl2	EcoK	EcoN1	EcoR1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1
I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	Pml1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac1
Sall	Sbf1	Sca1	Sgf1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce	Xho1	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	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													