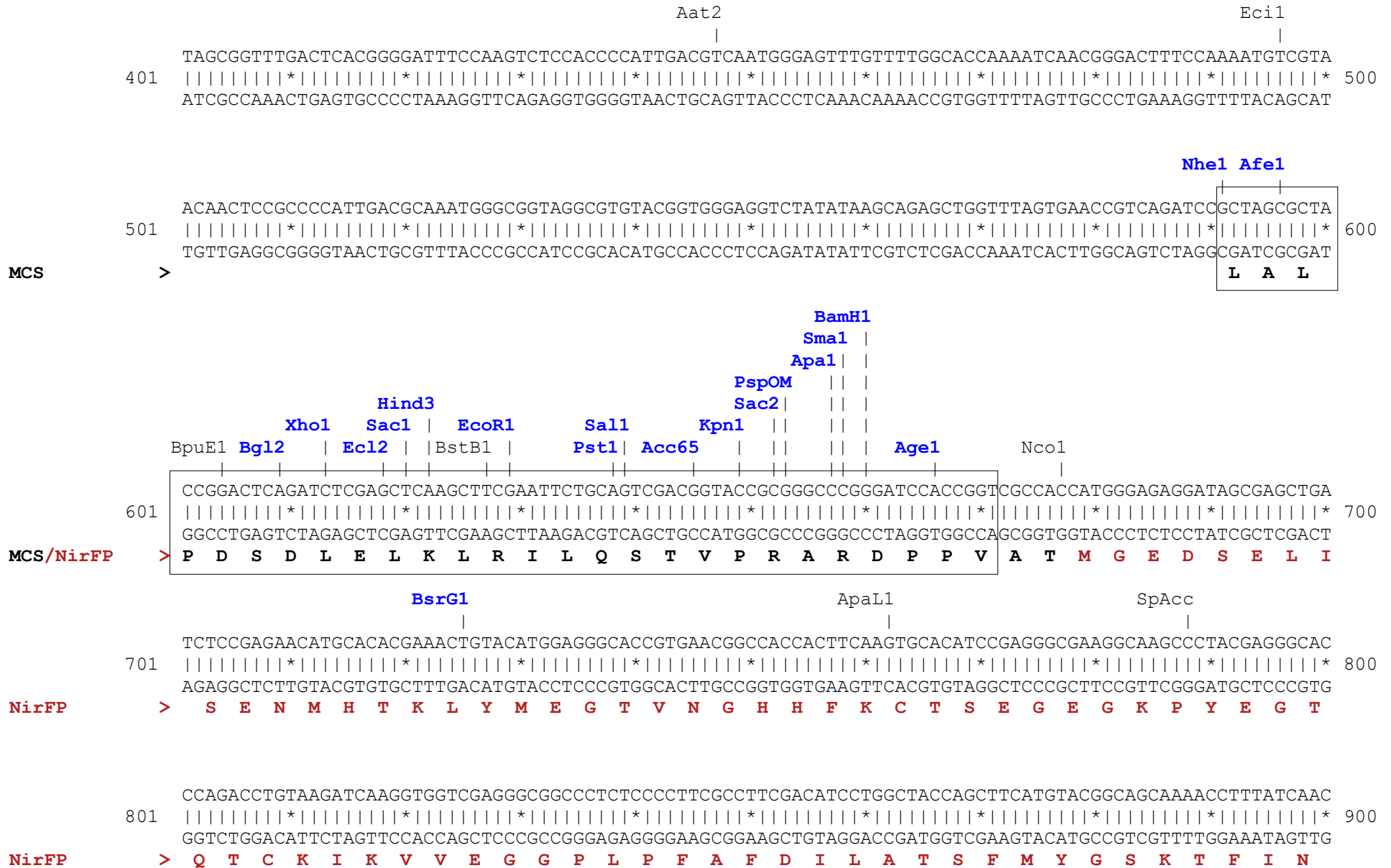


**pNirFP-N vector restriction map**

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). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.





Bs36                                  SpDon                                  Bbs1

|                                  |                                  |

901    CACACCCAGGGCATCCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGGATCACCACATACGAAGACGGGGCGTGCTGACCGCTA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|| 1000  
 GTGTGGGTCCCGTAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCCTAGTGGTGTATGCTTCTGCCCCCGCAGACTGGCGAT

**NirFP**    > H T Q G I P D F F K Q S F P E G F T W E R I T T Y E D G G V L T A T

Bpm1

|

1001    CCCAGGACACCAGCCTCCAGAACGGGTGCCTCATCTACAACGTCAAGATCAACGGGGTGAAGTTCATCAACGGCCCTGTGATGCAGAAGAAAACACT  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|| 1100  
 GGGTCTGTGGTCCGAGGCTTGCAGCAGGAGTAGATGTTGCAGTTCTAGTTGCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTTTGTGA

**NirFP**    > Q D T S L Q N G C L I Y N V K I N G V N F P S N G P V M Q K K T L

BseY1                                  PshA1                                  BssS1                                  Bsg1                                  Eco57  
 |                                  |                                  |                                  |                                  |                                  |                                  |

1101    CGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACAGCGGTCTGAGAGGCCATAATCAGATGGCCCTGAAGCTCGTGGGCGGGGGCTACCTGCAC  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|| 1200  
 GCCGACCTCCGGTTGTGGCTCTACGACATGGGGCGACTGTCCGACTCTCCGGTATTAGTCTACCGGGACTTCCAGCACCAGCCCGCCCGATGGACGTG

**NirFP**    > G W E A N T E M L Y P A D S G L R G H N Q M A L K L V G G G Y L H

BspM1                                  BpuE1                                  SpAcc

|                                  |                                  |

1201    TGCTCCCTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCCGGCTTCTACTTCGTGGACCGTAAACTGGAAAGAATCAAGGAGG  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|| 1300  
 ACGAGGAGTTCTGGTGTATGTCTAGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAAGATGAAGCACCTGGCATTGACCTTTCTTAGTTCTCTCC

**NirFP**    > C S L K T T Y R S K K P A K N L K M P G F Y F V D R K L E R I K E A

Not1  
 Eag1  
 BsrB1  
 Blp1  
 Pvu2  
 Bmr1

|                                  |                                  |                                  |                                  |                                  |                                  |                                  |

Bsa1                                  PshA1                                  BssS1                                  Msc1                                  AlwN1                                  BspM1                                  Xba1

1301    CCGACAAAGAGACCTACGTCGAGCAGCAGATGGCTGTGGCCAGGTACTGCGACCTGCCTAGCAAAGTGGGGCACAGCTGAGCGGCCGCGACTCTAGA  
 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|| 1400  
 GGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCTACCGACACCGGTCCATGACGCTGGACGGATCGTTTACCCCGTGTGCGACTCGCCGGCGCTGAGATCT

**NirFP**    > D K E T Y V E Q H E M A V A R Y C D L P S K L G H S \*



```
BsrB1
|
GCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTT
2001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
CGCCGCGATCCCGGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAA

                                polyA
                                |
                                BciV1
                                BspH1 |
                                BsrB1 | |
                                | | |
TTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATA
2101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
AAGCCCCTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTAT

                                Ecil
                                |
                                |
Ssp1  Ear1      Bsu36      Pvu2 |      BseY1
|    |          |          | |          |
ATATTGAAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTA
2201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
TATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTCGACACCTTACACACAGTCAATCCACACCTTTTCAGGGGTCCGAGGGGTCCGTCCGTCTTCAT

                                NsiI
                                Sph1 |
                                BfrB1 |
                                BstAP | |
                                | | |
                                SexA1
                                |
                                BseY1
                                |
                                BstAP | |
                                | | |
TGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGC
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
ACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCCGAGGGGTCCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCG

                                Ecil
                                |
                                Ecil      Bmr1 |      Ecil      Nco1      polyA
                                |      | |      |      |      |
AACCATAGTCCC GCCCTAACTCCGCCCATCCC GCCCTAACTCCGCCCATTC CGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCA
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
TTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAATAAATAACGT
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                                polyA          polyA
                                |              |
3601  ACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGGTCGTTTGTTCATAAACCGGGGTT
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3700
      TGCCTTCCTCTGTTATGGCCTTCCTTGGGCGGATACTGCCGTTATTTTTCTGTCTTATTTTTCGCGTGCCACAACCCAGCAAACAAGTATTTGCGCCCAA

                                BsaI
                                |
3701  CGGTCCCAGGGCTGGCACTCTGTCGATACCCACCGAGACCCCATTTGGGGCCAATACGCCC GCGTTTCTTCCTTTTCCCCACCCCAAGTTCGG
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3800
      GCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCC

                                BstAP          AlwN1          Bsu36          DraI
                                |              |              |              |
3801  GTGAAGGCCCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTTA
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3900
      CACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAAT

                                DraI          BspH1
                                |              |
3901  ATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAAATCCCTTAACTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAG
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4000
      TAAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTC

                                BpuE1
                                |
4001  ATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAAACAAAAAACCCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAG
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4100
      TAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAAACAAACGGCCTAGTTC

                                Eco57          SpAcc
                                |              |
4101  AGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAA
      |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 4200
      TCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTT
  
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                                     AlwN1                               BpuE1
                                     |                               |
4201 CTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
GAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAATGGCCCAACCTGAGTTCTGCT

                                     ApaL1           BseY1
                                     |               |
4301 TAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
ATCAATGGCCTATTCCGCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTCTGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTCTG

                                     BciV1
                                     |
SpAcc                               Eci1 |                               BssS1
|                                     |
4401 GTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
CACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGG

                                     SpAcc           Drd1           BpuE1           SpAcc
                                     |               |               |               |
4501 AGGGGAAACGCCTGGTATCTTTATAGTCTGTCTGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
TCCCCCTTTCGCGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATAACC

                                     SpDon
                                     |
Eci1                               BspLU|
|                                   ||
4601 AAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
TTTTTTCGGGTCGTTGCGCCGAAAAATGCCAAGGACCGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGG

                                     NsiI
                                     |
BfrB1 |
|
4701 GTATTACCGCCATGCAT
   |||||*||||| 4717
CATAATGGCGGTACGTA
```

