

pTagRFP-FAK 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). TagRFP amino acids are shown in red, Fokal adhesion kinase (FAK) amino acids are shown in green, linker amino acids are shown in black.



BseY1 Bgl1

1001 TCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAGCGA 1100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
 AGGGTAGGTTGCCGGGACACTACGTCTTCTTTGTGAGCCGACCCTCCGGTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTCGCT
TagRFP > P S N G P V M Q K K T L G W E A N T E M L Y P A D G G L E G R S D

BssS1 Eco57 BpuE1

1101 CATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTC 1200
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
 GTACCGGGACTTCGAGCACCCGCCCGGTGGACTAGACGTTGAAGTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGCGAG
TagRFP > M A L K L V G G G H L I C N F K T T Y R S K K P A K N L K M P G V

SpAcc
 PflM1 Bsa1 PshA1 BssS1 Dra3 Msc1 AlwN1

1201 TACTATGTGGACCACAGACTGGAAAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTA 1300
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
 ATGATACACTGGTGTCTGACCTTTCTTAGTTCCTCCGGCTGTTTCTCTGGATGCAGCTCGTCGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGAT
TagRFP > Y Y V D H R L E R I K E A D K E T Y V E Q H E V A V A R Y C D L P S

SpAcc Bmr1 BspE1 Bgl2 SpDon

1301 GCAAACCTGGGGCACAACCTTAATTCCGGACTCAGATCTATGGCAGCAGCTTACCTTTGATCCAAACTTGAATCATAACCAAGTTCAAGTGCAAAGACGCA 1400
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
 CGTTTGACCCCGTGTGTTGAATTAAGGCCTGAGTCTAGATACCGTCGTCGAATGGAACCTAGGTTTGAACCTAGTATGTGGTTCAAGTTTACGTTTTCTGCGT
TagRFP/FAK > K L G H K L N S G L R S M A A A Y L D P N L N H T P S S S A K T H

Bmr1 Sma1 Nco1 SpDon BstX1 BmgB1

1401 CCTCGGTACTGGGATGGAGCGTTCCCCGGGGGCCATGGAGCGAGTCCTAAAGGTTTTTCACTACTTTGAAAACAGCAGCGAGCCAACGACGTGGGCCAGC 1500
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
 GGAGCCATGACCTACCTCGCAAGGGGCCCGGTACCTCGCTCAGGATTTCCAAAAGTGATGAAACTTTTGTGCTCGCTCGGTTGCTGCACCCGGTTCG
FAK > L G T G M E R S P G A M E R V L K V F H Y F E N S S E P T T W A S


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                polyA                SpDon                SpDon                MscI
                |                |                |                |
ACGCAATCTTTTATTATCAGGCCACAGAAAGAAGGTGAAAGAGCTTTACCATCAATACCAAAGCTGGCCAACAATGAGAAGCAAGGAGTAAGGTGCGACA
2401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
TGC GTTAGAAAATAATAGTCCGGTGTCTTTCTTCCACTTTCTCGAAATGGTAGTTATGGTTTTCGACCGGTTGTTACTCTTCGTTCCCTCATTCCAGCGTGT
FAK    > T Q S F I I R P Q K E G E R A L P S I P K L A N N E K Q G V R S H T

                AlwN1                T7Ter
                |                |
CAGTCTCTGTATCAGAAAACAGATGACTATGCAGAGATAATAGATGAAGAAGATACTTATACAATGCCATCAACCAGAGATTATGAAATTCAAAGGGAGAG
2501  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
GTCAGAGACATAGTCTTTGTCTACTGATACGTCTCTATTATCTACTTCTTCTATGAATATGTTACGGTAGTTGGTCTCTAATACTTTAAGTTTCCCTCTC
FAK    > V S V S E T D D Y A E I I D E E D T Y T M P S T R D Y E I Q R E R

                Bmr1                ApaL1                SpDon BspE1                Bsg1
                |                |                |                |                |
AATTGAACTGGGGCGCTGCATTGGTGAAGGACAGTTTGGAGATGTGCACCAAGGAATTTACATGAGTCCGGAAAATCCAGCTATGGCTGTAGCAATCAAAA
2601  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
TTAACTTGAACCCCGCGACGTAACCACTTCTGTCAAACCTCTACACGTGGTTCTTAAATGTACTCAGGCCTTTTAGGTCGATACCGACATCGTTAGTTT
FAK    > I E L G R C I G E G Q F G D V H Q G I Y M S P E N P A M A V A I K

                SpDon                SpDon                SpDon                SpDon                SpDon
                |                |                |                |                |
                BspLU                SpAcc                Bcl1                Dra3
                |                |                |                |                |
ACATGTAAAAACTGCACCTCAGACAGCGTTAGAGAAAAGTTCCTACAAGAAGCCTTAACAATGCGTCAGTTTGTATCATCCTCACATTGTGAAGCTCATTG
2701  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
TGTACATTTTTGACGTGGAGTCTGTGCGCAATCTCTTTTCAAGGATGTTCTTCGGAATTGTTACGCAGTCAAAGTCTAGTAGGAGTGTAACACTTCGAGTAAC
FAK    > T C K N C T S D S V R E K F L Q E A L T M R Q F D H P H I V K L I G

                Bmr1                BsrG1                SpDon                BsaXb
                |                |                |                |
GAGTTATTACAGAAAACCCAGTGTGGATAATCATGGAGCTCTGTACACTTGGAGAGTTGAGATCGTTTCTGCAAGTAAGAAAATTCAGCTTGGACCTGGC
2801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
CTCAATAATGTCTTTTGGGTCACACCTATTAGTACCTCGAGACATGTGAACCTCTCAACTCTAGCAAAGACGTTTCAATTCTTTAAGTCGAACCTGGACCG
FAK    > V I T E N P V W I I M E L C T L G E L R S F L Q V R K F S L D L A

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                BsaXa      SpDon      Bsp1      BsrG1
                |         |         |         |
2901  CTCCCTCATCCTCTACGCTTACCAGCTTAGCACAGCACTTGCTTACCTAGAGAGCAAAAAGATTTGTACATAGAGATATTGCTGCTAGGAACGTGCTGGTA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
      GAGGGAGTAGGAGATGCGAATGGTTCGAATCGTGTCTGTCGTGAACGAATGGATCTCTCGTTTTCTAAACATGTATCTCTATAACGACGATCCTTGCACGACCAT
FAK   >  S L I L Y A Y Q L S T A L A Y L E S K R F V H R D I A A R N V L V
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                               ScaI
                               |         |         |         |
3001  TCTGCCACTGACTGTGTGAAATTGGGTGACTTTGGCTTATCCCGATACATGGAAGACAGTACTTACTATAAAGCTTCCAAAGGAAAGTTACCTATCAAAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
      AGACGGTGACTGACACACTTTAACCCACTGAAACCGAATAGGGCTATGTACCTTCTGTCTCATGAATGATATTTTGAAGGTTTCCTTTCAATGGATAGTTTA
FAK   >  S A T D C V K L G D F G L S R Y M E D S T Y Y K A S K G K L P I K W
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                Bpu10      BbvC1      SpDon      BtgZ1      NsiI      BfrB1
                |         |         |         |         |         |
3101  GGATGGCTCCAGAGTCAATCAACTTCCGACGGTTTACCTCAGCAAGCGATGTGTGGATGTTTGGTGTGTGTATGTGGGAGATCCTGATGCATGGGGTAAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      CCTACCGAGGTCTCAGTTAGTTGAAGGCTGCCAAATGGAGTCGTTTCGTACACACCTACAAACCACACACATACACCCTCTAGGACTACGTACCCCATTT
FAK   >  M A P E S I N F R R F T S A S D V W M F G V C M W E I L M H G V K
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                SpAcc      BsrB1      SpAcc
                |         |         |
3201  GCCCTTCCAGGGAGTGAAAAATAATGATGTTATTGGTCCGATTGAGAACGGTGAGCGGCTCCCCATGCCTCCGAACTGCCCTCCCACCCTCTACAGCCTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
      CGGGAAGGTCCCTCACTTTTTTATTACTACAATAACCAGCCTAACTCTTGCCACTCGCCGAGGGGTACGGAGGCTTGACGGGAGGGTGGGAGATGTGGAA
FAK   >  P F Q G V K N N D V I G R I E N G E R L P M P P N C P P T L Y S L
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                                     PflM1
                                     BseY1
                                     |
ATGACCAAGTGCTGGGCATACGACCCTAGTAGACGACCCAGGTTTACTGAACTTAAAGCACAACCTCAGTACAATACTGGAGGAGGAGAAGCTGCAGCAAG
3301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
TACTGGTTCACGACCCGTATGCTGGGATCATCTGCTGGGTCCAAATGACTTGAATTTTCGTGTTGAGTCATGTTATGACCTCCTCCTCTTCGACGTCGTTTC
FAK > M T K C W A Y D P S R R P R F T E L K A Q L S T I L E E E K L Q Q E

                                     BseR1
                                     Bpm1
                                     Pst1
                                     |
                                     |
                                     |
                                     SpAcc
                                     |
AGGAACGAATGAGAATGGAATCCAGGCGACAAGTCACAGTATCCTGGGACTCAGGAGGATCAGATGAAGCTCCTCCCAAGCCCAGCAGGCCTGGTTACCC
3401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
TCCTTGCTTACTCTTACCTTAGGTCCGCTGTTTCAGTGTTCATAGGACCTGAGTCCTCCTAGTCTACTTCGAGGAGGGTTTCGGGTCGTCCGGACCAATGGG
FAK > E R M R M E S R R Q V T V S W D S G G S D E A P P K P S R P G Y P

                                     Bpu10
                                     BbvC1 Nde1
                                     |
                                     |
                                     |
                                     SexA1 BstX1
                                     |
                                     |
                                     |
                                     BciV1
                                     |
CAGCCCAAGGTCCAGTGAAGGGTTTTATCCGAGTCCTCAGCATATGGTACAGCCAAATCACTACCAGGTATCTGGCTACTCTGGTTCTCATGGGATACCA
3501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
GTCGGGTTCCAGGTCACTTCCCAAAATAGGCTCAGGAGTCGTATAACCATGTTCGGTTTTAGTGATGGTCCATAGACCGATGAGACCAAGAGTACCCTATGGT
FAK > S P R S S E G F Y P S P Q H M V Q P N H Y Q V S G Y S G S H G I P

Nco1
|
GCCATGGCAGGCAGCATTTATCCTGGGCAAGCTTCTCTCTTGGATCAAACAGATTCTGGAACCATCGACCTCAGGAAGTATCAGCATGGCAGCCAAACA
3601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
CGGTACCGTCCGTCGTAAATAGGACCCGTTTCAAGAGAGAACCTAGTTTGTCTAAGGACCTTGGTAGCTGGAGTCCTTCATAGTCGTACCGTCCGTTTGT
FAK > A M A G S I Y P G Q A S L L D Q T D S W N H R P Q E V S A W Q P N M

                                     BseR1
                                     Bpm1
                                     Pst1
                                     |
                                     |
                                     |
                                     SpAcc
                                     |
                                     |
                                     |
                                     BseY1 Bgl1
                                     |
                                     |
                                     |
                                     BstE2
                                     |
                                     |
                                     |
                                     BseY1
                                     |

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BspM1 BstAP Xcm1
 BfuA1 AlwN1 BsaXa BseR1 BsaXb

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3701  TGGAGGATTCGGGCACTTTGGATGTACGAGGAATGGGGCAGGTTCTGCCACACATCTCATGGAGGAGAGGTTAATAAGACAACAGCAAGAGATGGAAGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      ACCTCCTAAGCCCGTGAAACCTACATGCTCCTTACCCCGTCCAAGACGGGTGTGTAGAGTACCTCCTCTCCAATTATTCTGTTGTGCGTTCTCTACCTTCT
FAK   >  E D S G T L D V R G M G Q V L P T H L M E E R L I R Q Q Q E M E E
    
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BpuE1 Bpm1 Bpm1 PshA1 Bsa1

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3801  AGATCAACGCTGGCTTGAGAAAAGAGGAACGATTCTGGTAATGAAACCTGATGTGCGGCTCTCCAGAGGCAGCATTGAACGGGAGGACGGAGGTCTCCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      TCTAGTTGCGACCGAACTCTTTCTCCTTGCTAAGGACCATTACTTTGGACTACACGCCGAGAGGTCTCCGTCGTAACCTTGCCCTCCTGCCTCCAGAGGTC
FAK   >  D Q R W L E K E E R F L V M K P D V R L S R G S I E R E D G G L Q
    
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BstE2
 Pvu2
 Xcm1
 Apa1
 BseY1
 PspOM
 BsrB1

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3901  GGCCAGCTGGTAACCAGCACATATATCAGCCTGTGGGTAAACCAGATCATGCCGCTCCACCAAAGAAGCCCCCTCGCCCTGGAGCCCCCACTTGGGCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCGGGTCGACCATTTGGTCGTGTATATAGTCGGACACCCATTTGGTCTAGTACGGCGAGGTGGTTTCTTCGGGGGAGCGGGACCTCGGGGGGTGAACCCGT
FAK   >  G P A G N Q H I Y Q P V G K P D H A A P P K K P P R P G A P H L G S
    
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Bpm1 Nru1 BseR1 BsrB1

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4001  GCCTCGCGAGCCTGAACAGCCCCGTGGACAGCTACAACGAAGGCGTGAAGATCAAGCCACAGGAAATCAGCCCTCCTCCTACGGCCAACCTGGACCGCTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CCGGAGCGCTCGGACTTGTGCGGGCACCTGTCGATGTTGCTTCCGCACTTCTAGTTCGGTGTCTTTAGTCGGGAGGAGGATGCCGGTTGGACCTGGCGAG
FAK   >  L A S L N S P V D S Y N E G V K I K P Q E I S P P P T A N L D R S
    
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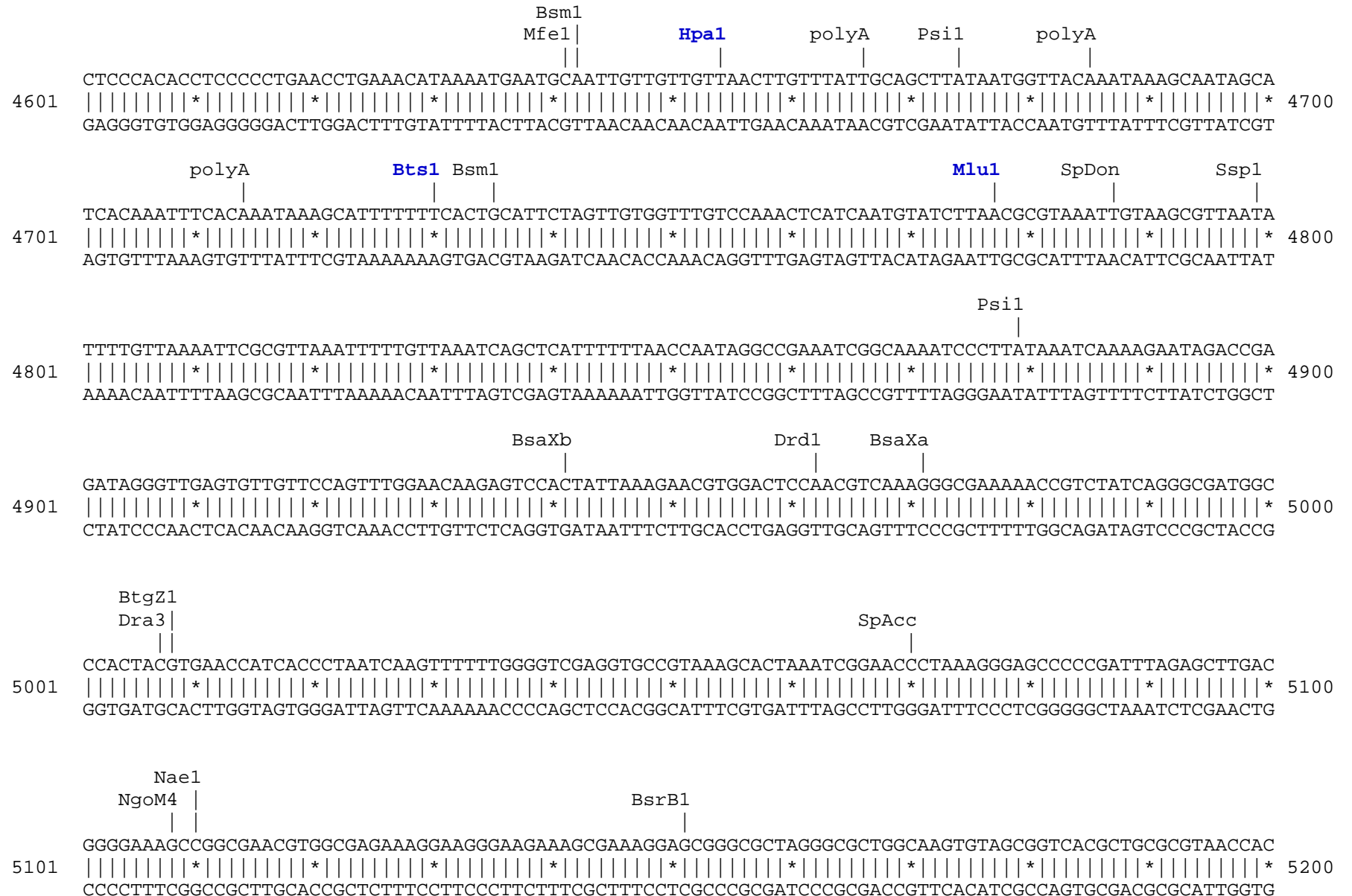
SpAcc PflF1 SpDon Ecil BseR1 Nco1
CAATGACAAAGTCTATGAGAATGTAACCGGGCTGGTGAAAGCTGTCATAGAGATGTCCAGTAAAATACAGCCAGCTCCGCCAGAGGAGTACGTGCCCATG
4101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
GTTACTGTTTCAGATACTCTTACATTGGCCCCGACCACTTTTCGACAGTATCTCTACAGGTCATTTTATGTTCGGTCGAGGCGGTCTCCTCATGCACGGGTAC
FAK > N D K V Y E N V T G L V K A V I E M S S K I Q P A P P E E Y V P M

SpDon Nhe1
GTAAAGGAGGTTGGCTTGGCGCTGAGAACCTTGCTAGCAACAGTGGATGAGTCGCTGCCAGTGCTTCTGCAAGCACCCACAGAGAGATTGAGATGGCCC
4201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
CATTTCTCCAACCGAACCGGACTCTTGAACGATCGTTGTCACCTACTCAGCGACGGTCACGAAGGACGTTTCGTGGGTGTCTCTCTAACTCTACCGGG
FAK > V K E V G L A L R T L L A T V D E S L P V L P A S T H R E I E M A Q

AlwN1 Bln1 Sac1 BseY1 BspH1 Pst1 EcoN1
AGAAACTGCTGAACTCTGACCTGGCTGAGCTCATTAACAAGATGAAGCTGGCCCAGCAGTACGTCATGACCAGCCTGCAGCAGGAGTACAAGAAGCAAAT
4301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4400
TCTTTGACGACTTGAGACTGGACCGACTCGAGTAATTGTTCTACTTTCGACCGGGTCGTCATGCAGTACTGGTTCGGACGTCGTCCTCATGTTCTTCGTTTA
FAK > K L L N S D L A E L I N K M K L A Q Q Y V M T S L Q Q E Y K K Q M

Xcm1 Cla1 Bcl1
GCTGACGGCTGCTCACGCTCTGGCTGTGGATGCCAAGAAGCTGCTGGATGTCATCGATCAAGCCAGACTGAAAATGATCAGCCAGTCCAGGCCCACTAAG
4401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4500
CGACTGCCGACGAGTGCAGACCGACACCTACGGTCTTGAACGACCTACAGTAGCTAGTTCCGGTCTGACTTTTACTAGTCGGTCAGGTCCGGGTGATTC
FAK > L T A A H A L A V D A K N L L D V I D Q A R L K M I S Q S R P T K

EcoR1 Pst1 BamH1 Xba1 Bcl1 BsaB1 SpDon Dra1
CTGCCGTAGCCGAATTCTGCAGATGGGATCCACCGGATCTAGATAACTGATCATAATCAGCCATAACCATTTGTAGAGGTTTTACTTTAAAAAAC
4501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
GACGGCATCGGCTTAAGACGTCTACCCTAGGTGGCCTAGATCTATTGACTAGTATTAGTCGGTATGGTGTAACATCTCCAAAATGAACGAAATTTTTTTG
FAK > L P *



polyA
|

5201 CACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACAT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
 GTGTGGGCGGCGCAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCCTTTACACGCGCCTTGGGGATAAACAAATAAAAAGATTTATGTA

BciV1
 BspH1 |
 BsrB1 | | SspI | EarI | Bsu36 | Ecil
 Pvu2 |

5301 TCAAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGT
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
 AGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCCTTTCTTGGTTCGACACCTTACA

NsiI
 SphI |
 BfrB1 |
 BseY1 | BstAP | SexA1

5401 GTGTCAGTTAGGGTGTGGAAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAAGTCCCCA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
 CACAGTCAATCCACACCTTTTCAGGGGTCCGAGGGGTTCGTCCGTCTTCATACGTTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGT

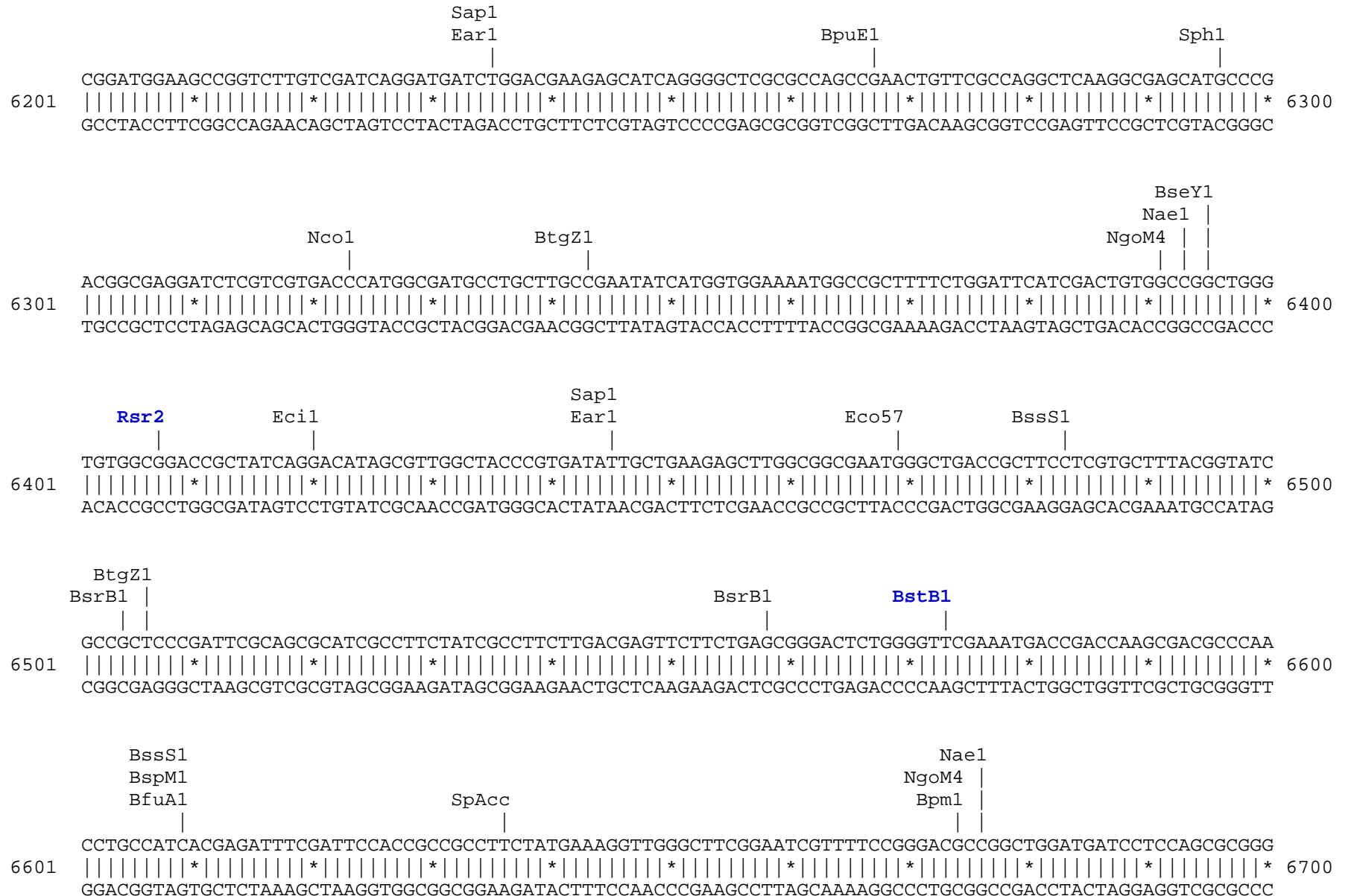
NsiI
 SphI |
 BfrB1 |
 BseY1 | BstAP | Ecil | Ecil | Ecil
 BmrI |

5501 GGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCCCCCCTAACTCCGCCCATCCCGCCCCTAACTCCGCCCA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
 CCGAGGGGTTCGTCCGTCTTCATACGTTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATTGAGGCGGGT

SfiI

Ecil | NcoI | polyA | BglI | SpDon

5601 GTTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTATTTATGCGAGGCGGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGG
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
 CAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAAAAATAAATACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCATCACTCCTCC




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                                SpAcc
                                |
7301 CCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGG
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 7400
      GGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACC

AlwNI1                                BpuE1                                ApaI1
|                                     |                                     |
7401 CTGCTGCCAGTGGCGATAAGTCGTGCTTACCAGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCTGGGCTGAACGGGGGGTTTCGTGCAC
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 7500
      GACGACGGTCACCGCTATTACAGCACAGAATGGCCAACTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTG

BseY1                                SpAcc
|                                     |
7501 ACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGG
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 7600
      TGTCGGGTGCGAACCTCGCTTGCTGGATGTGGCTTACTGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCC

                                BciV1
                                |
                                Ecil
                                |
                                BssS1
                                |
                                SpAcc
                                |
7601 TATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCT
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 7700
      ATAGGCCATTGCGCGTCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGA

Drd1                                BpuE1                                SpAcc                                Ecil
|                                     |                                     |                                     |                                     |
7701 GACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTTGGCCTTTTGCTGGCC
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 7800
      CTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTGCTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGG

                                SpDon
                                |
                                BspLU
                                |
                                NsiI
                                |
                                BfrB1
                                |
7801 TTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 7867
      AAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA
  
```


Found:

Aar1	Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	BamH1	Bbs1	BbvC1
Bcg1a	Bcg1b	BciV1	Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Blp1	BmgB1	Bmr1	Bpm1	Bpu10	BpuE1
Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1
BsrG1	BssS1	BstAP	BstB1	BstE2	BstX1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3	Drd1	Eag1
Ear1	Eci1	Eco57	EcoK	EcoN1	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Mlu1	Msc1
Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nrul	Nsi1	PflF1	PflM1	polyA	PshA1	Psi1	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sap1	Scal	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1
Stu1	T7Ter	Xba1	Xcm1										

Unique:

Aar1	Acc65	Afe1	Age1	Ale1	Apal	BamH1	Bcg1a	Bcg1b	Bgl2	BmgB1	BstB1	Bts1	Eag1
EcoK	EcoN1	Fsp1	Hpa1	Kas1	Kpn1	Mlu1	Nar1	Nrul	PspOM	Rsr2	Scal	Sfi1	Sma1
SnaB1	Xba1												

Not found:

Ac11	Afl2	Ahd1	Asc1	AsiS1	Baela	Baelb	BsiW1	BsmB1	BssH2	BstZ1	_Chi	EcoRV	FCatB
FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Not1	Pac1	Pme1	Pml1	Pvu1	R4atB
R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA
PIsce	Xho1	Xmn1											

Excluded by site complexity:

Acc1	Ac11	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													