

pTagFP635-Cx43 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). TagFP635 amino acids are shown in red, Connexin 43 amino acids are shown in green, linker amino acids are shown in black.



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                                Aat2                               Eci1
                                |                               |
TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTTGTTTTGGCACCACAAAATCAACGGGACTTTCCAAAATGTCGTA
401 | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTTACAGCAT

                                Nhe1  Afel
                                |    |
ACAACCTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * 600
TGTTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

      Xho1    Hind3    EcoR1
      |      |      |
BpuE1  Bgl2    Sac1  BstB1
|      |      |      |
CCGGACTCAGATCTCGAGCTCAAGCTTCGAATTCGGCAGCACTTTTCTTTTCATTGGGGGAAGGCGTGAGGAAAGTACCAAACAGCAGCAGACTTTTAAA
601 | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * 700
GGCCTGAGTCTAGAGCTCGAGTTTCAAGCTTAAAGCCGTCTGAAAAGAAAAGTAAACCCCCCTTCCGCACTCCTTTTCATGGTTTTGTCGTCGTCTGAAAATTT

                                Nae1
                                |
      BssH2  NgoM4
      |      |
      Asc1   |
      |      |
Dra1       Eco57                               SpDon
|          |                                   |
CTTTAAACAGACAGGTCTGAGAGCCTGAACTCTCATTTTTTTCTTTGACTTCAGCCTCCAAGGAGTTCCACCAACTTTGGCGCGCCGGCTTCACTTTTCATT
701 | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * 800
GAAATTTGTCTGTCCAGACTCTCGGACTTGAGAGTAAAAAGGAAACTGAAAGTCGGAGGTTCTCAAGGTGGTTGAAACC GCGCGGCCGAAGTGAAAGTAA

                                Hind3  Bpm1  PflF1                               BsaXaSpAcc
                                |    |    |                               |    |
AAGTGAAAGAGAGGTTGCCAGACATGGGTGACTGGAGTGCCTTGGGGAAGCTTCTGGACAAGGTCCAAGCCTACTCCACCGCTGGAGGGAAGGTGTGGCT
801 | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * | | | | | | | | | * 900
TTCACTTTCTCTCCACGGGCTGTACCCACTGACCTCACGGAAACCCCTTCAAGACCTGTTCAGGTTTCGGATGAGGTGGCGACCTCCCTTCCACACCGA
Cx43 >           M G D W S A L G K L L D K V Q A Y S T A G G K V W L

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      BsaXb      Sap1
      Bpm1      |      Ear1
                    |
                    Pvu2
901  GTCAGTGCTCTTCATATTCAGAATCCTGCTCCTGGGGACAGCTGTTGAGTCAGCTTGGGGTGATGAACAGTCTGCCTTTTCGCTGTAACACTCAACAACCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
    CAGTCACGAGAAGTATAAGTCTTAGGACGAGGACCCCTGTCGACAACCTCAGTCGAACCCCACTACTTGTGACACGGAAAGCGACATTGTGAGTTGTTGGA
Cx43 > S V L F I F R I L L L G T A V E S A W G D E Q S A F R C N T Q Q P

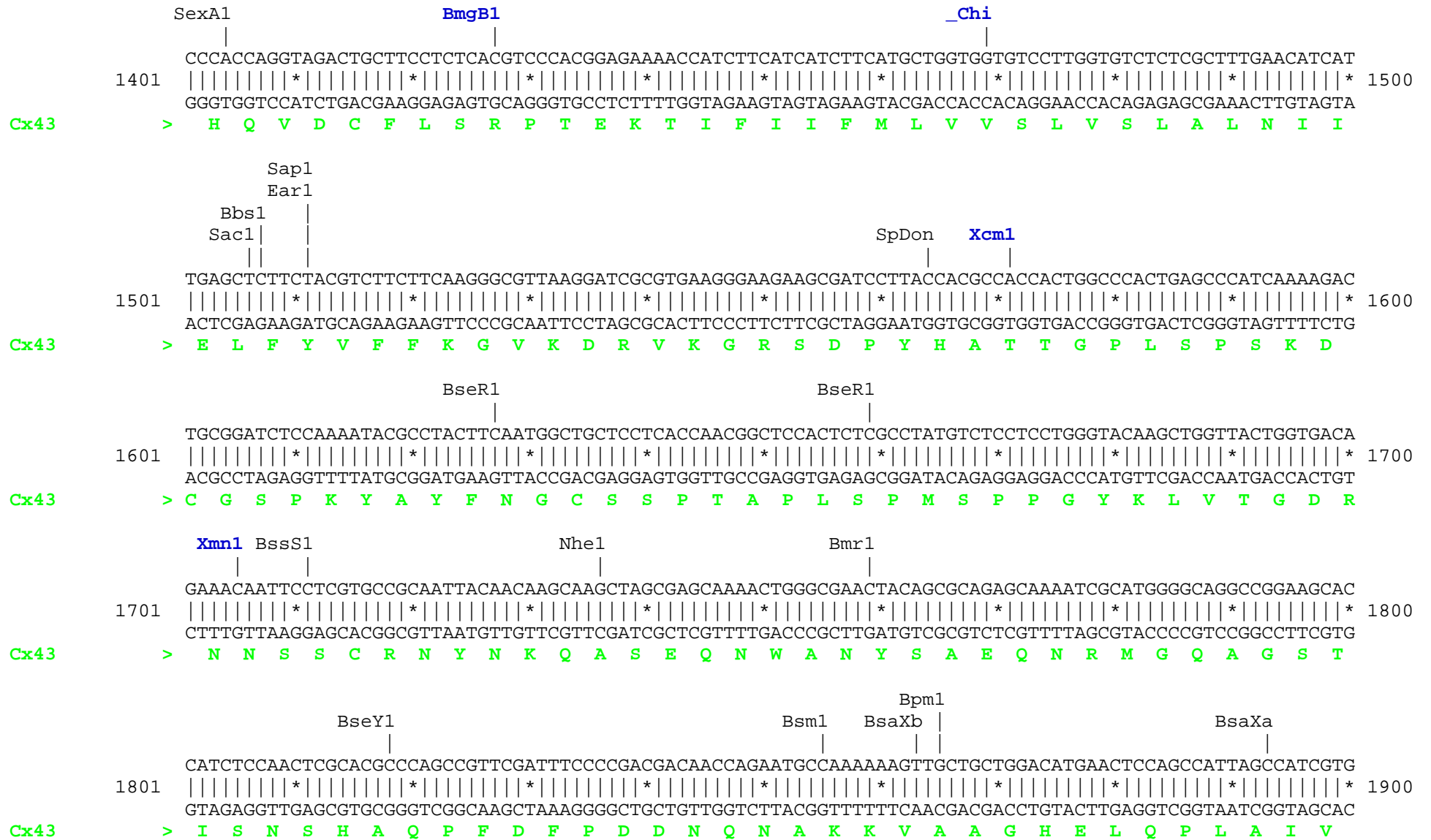
      SpAcc      Eco57
      |          Pml1
      |          ||
1001 GGCTGCGAAAACGTCTGCTATGACAAGTCCTTCCCATCTCTCACGTGCGCTTCTGGGTCCTTCAGATCATATTCGTGTCTGTGCCACACTCCTGTACT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    CCGACGCTTTTGCAGACGATACTGTTTCTCAGGAAGGGGTAGAGAGTGCACGCGAAGACCCAGGAAGTCTAGTATAAGCACAGACACGGGTGTGAGGACATGA
Cx43 > G C E N V C Y D K S F P I S H V R F W V L Q I I F V S V P T L L Y L

      Ear1      Ear1      Sac1      BseR1      PflF1
      |          |          |          |          |
1101 TGGCCCATGTGTTCTATGTGATGAGGAAGGAAGAGAAGCTAAACAAGAAAAGAAGAGGAGCTCAAAGTGGCCCAGACTGACGGGGTCAACGTGGAGATGCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    ACCGGGTACACAAGATACTACTCCTTCTCTTCTCTTCGATTTGTTCTTTCTTCTCCTCGAGTTTACCCGGGTCTGACTGCCCCAGTTGCACCTCTACGT
Cx43 > A H V F Y V M R K E E K L N K K E E E L K V A Q T D G V N V E M H

      BsaB1      Eco57      Sap1      SpDon
      |          |          |          |
1201 CCTGAAGCAGATTGAAATCAAGAAGTTCAAGTACGGGATTGAAGAGCACGGCAAGGTGAAAATGAGGGGCGGCTTGCTGAGAACCTACATCATCAGCATC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    GGACTTCGTCTAACTTTAGTTCTTCAAGTTCATGCCCTAACTTCTCGTGCCGTTCCACTTTTACTCCCCGCCGAACGACTCTTGATGTAGTAGTCGTAG
Cx43 > L K Q I E I K K F K Y G I E E H G K V K M R G G L L R T Y I I S I

      Ear1      BspM1      BfuA1      Aar1
      Bbs1      |          |          |
      |          |          |          |
      SpAcc      BpuE1
      |          |
1301 CTCTTCAAGTCTGTCTTCGAGGTGGCCTTCCCTGCTCATCCAGTGGTACATCTATGGGTTTCTGAGCGCGGTCTACACCTGCAAGAGAGATCCCTGCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    GAGAAGTTCAGACAGAAGCTCCACCGGAAGGACGAGTAGGTCACCATGTAGATACCCAAGTCGAACTCGCGCCAGATGTGGACGTTCTCTCTAGGGACGG
Cx43 > L F K S V F E V A F L L I Q W Y I Y G F S L S A V Y T C K R D P C P

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StuI
BamHI
AgeI
BpmI
NcoI
AclI

 GACCAACGACCTTCCAGCAGAGCCAGCAGCCGCGCCAGCAGCAGGCCTCGGCCTGATGACCTGGAGATTGCGGATCCACCGGTCCGCCACCATGGTGTCTA
 1901
2000

 CTGGTTGCTGGAAGGTCGTCTCGGTCTCGGCAGCGGTCTCGTCCGGAGCCGGACTACTGGACCTCTAACGCCTAGGTGGCCAGCGGTGGTACCACAGAT

Cx43/TagFp635 > D Q R P S S R A S S R A S S R P R P D D L E I A D P P V A T M V S K

SapI
EarI
BsrGI
ApaLI

 AGGGCGAAGAGCTGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACACCACCTTCAAGTGCACATCCGAGGGCGAAGGCAA
 2001
2100

 TCCCGCTTCTCGACTAATTCCCTCTTGTACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTGTTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTT

TagFp635 > G E E L I K E N M H M K L Y M E G T V N N H H F K C T S E G E G K

SpAcc

 GCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGC
 2101
2200

 CGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCG

TagFp635 > P Y E G T Q T M R I K V V E G G P L P F A F D I L A T S F M Y G S

Bsu36
SpDon
BbsI

 AAAACCTTCATCAACCACACCCAGGGCATCCCGACTTCTTTAAGCAGTCCTTCCCTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGG
 2201
2300

 TTTTGGAAAGTAGTTGGTGTGGGTCCCGTAGGGCTGAAGAAAATTCGTTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCC

TagFp635 > K T F I N H T Q G I P D F F K Q S F P E G F T W E R V T T Y E D G G

BpmI
SpDon

 GCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGAT
 2301
2400

 CGCACGACTGGCGATGGGTCTGTGGTTCGGAGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCACTTGAAGGGTAGGTTGCCGGGACACTA

TagFp635 > V L T A T Q D T S L Q D G C L I Y N V K I R G V N F P S N G P V M

BseY1 StuI Bgl1 BssS1
GCAGAAGAAAACACTCGGCTGGGAGGCCCTCCACCGAGATGCTGTACCCCGCTGACGGCGGCCCTGGAAGGCAGAAGCGACATGGCCCTGAAGCTCGTGGGC
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
CGTCTTCTTTTGTGAGCCGACCCCTCCGGAGGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGTCTTTCGCTGTACCGGGACTTCGAGCACCCG
TagFp635 > Q K K T L G W E A S T E M L Y P A D G G L E G R S D M A L K L V G

Eco57 Bbs1 BpuE1 Bbs1 SpAcc
GGGGGCCACCTGATCTGCAACTTGAAGACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCGTCTACTATGTGGACAGAAGACTGG
2501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
CCCCCGGTGGACTAGACGTTGAACCTTCTGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGTCTTCTGACC
TagFp635 > G G H L I C N L K T T Y R S K K P A K N L K M P G V Y Y V D R R L E

Bsa1 PshA1 BssS1 Dra3 Msc1 AlwN1 SpAcc
AAAGAATCAAGGAGGCCGACAAAGAGACCTACGTCGAGCAGCACGAGGTGGCTGTGGCCAGATACTGCGACCTCCCTAGCAATCTGGGGCACAAACTTAA
2601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
TTTCTTAGTTCTCCGGCTGTTTCTCTGGATGCAGCTCGTCTGTGCTCCACCGACACCGGTCTATGACGCTGGAGGGATCGTTAGACCCCGTGTTTGAATT
TagFp635 > 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 N L G H K L N

Not1
Eag1
BsrB1 Xba1 BsaB1 SpDon Dra1
TTGAGCGGCCCGGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACA
2701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
AACTCGCCGGCGCTGAGATCTAGTATTAGTCGGTATGGTGTAAACATCTCCAAAATGAACGAAATTTTTTGGAGGGTGTGGAGGGGGACTTGACTTTGT
TagFp635 > *

Bsm1
MfeI HpaI polyA PsiI polyA polyA
TAAAAATGAATGCAATTGTTGTTTAACTTGTATTATGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTT
2801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
ATTTTACTTACGTTAACAACAACAATTGAACAAATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTAAAGTGTATTTCGTAAAAAA

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Bts1 Bsm1              Af12              SpDon              Ssp1
|      |              |              |              |
TCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTTGTAAGCGTTAATATTTTGTAAATTCGCGTTAAATTTTTGT
2901 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3000
AGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAAACAATTTTAAGCGCAATTTAAAAACA

              Psil
              |
TAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGG
3001 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3100
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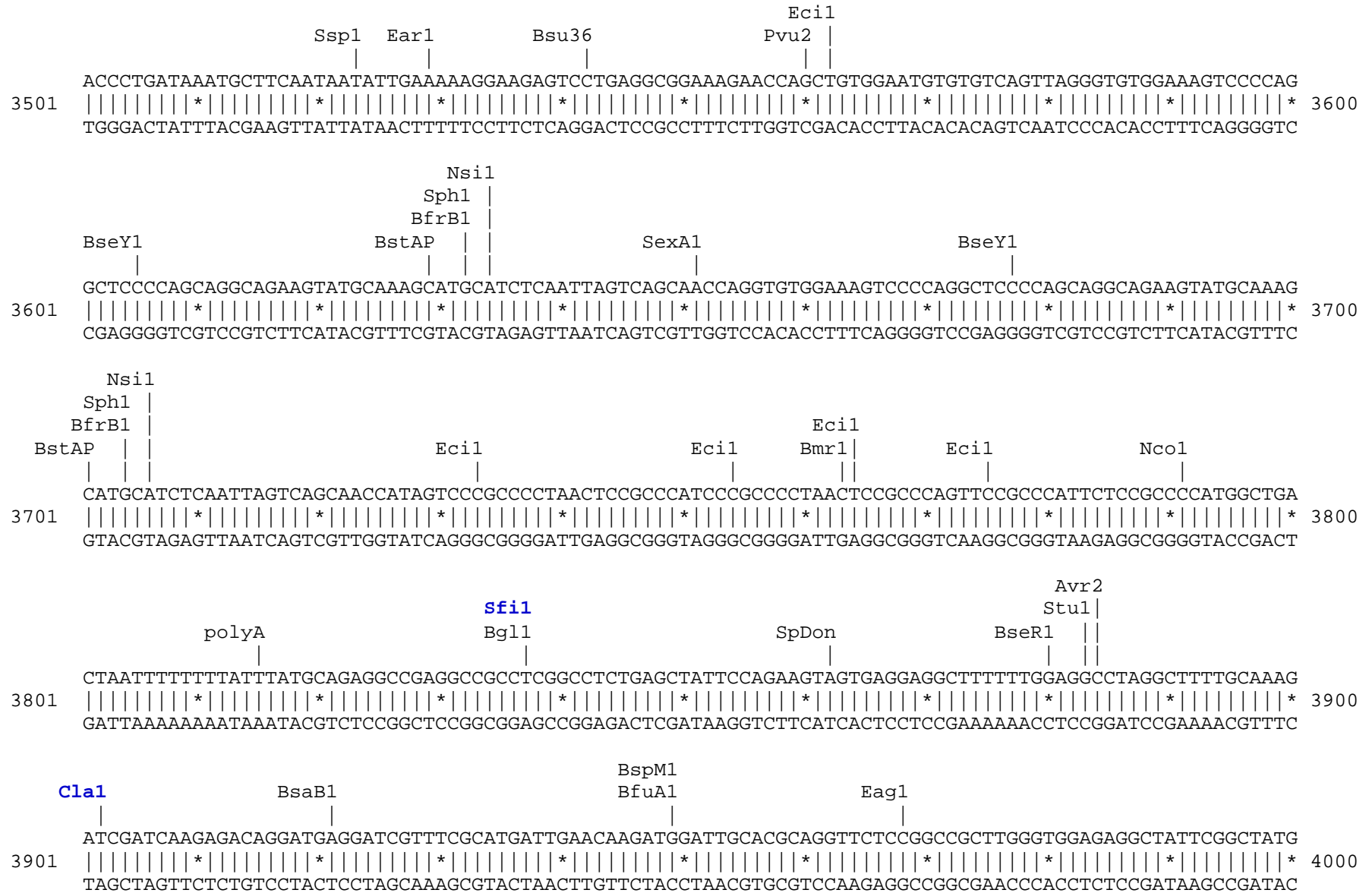
              BsaXb              Drd1              BsaXa              BtgZ1
              |              |              |              |
ACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAG
3101 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3200
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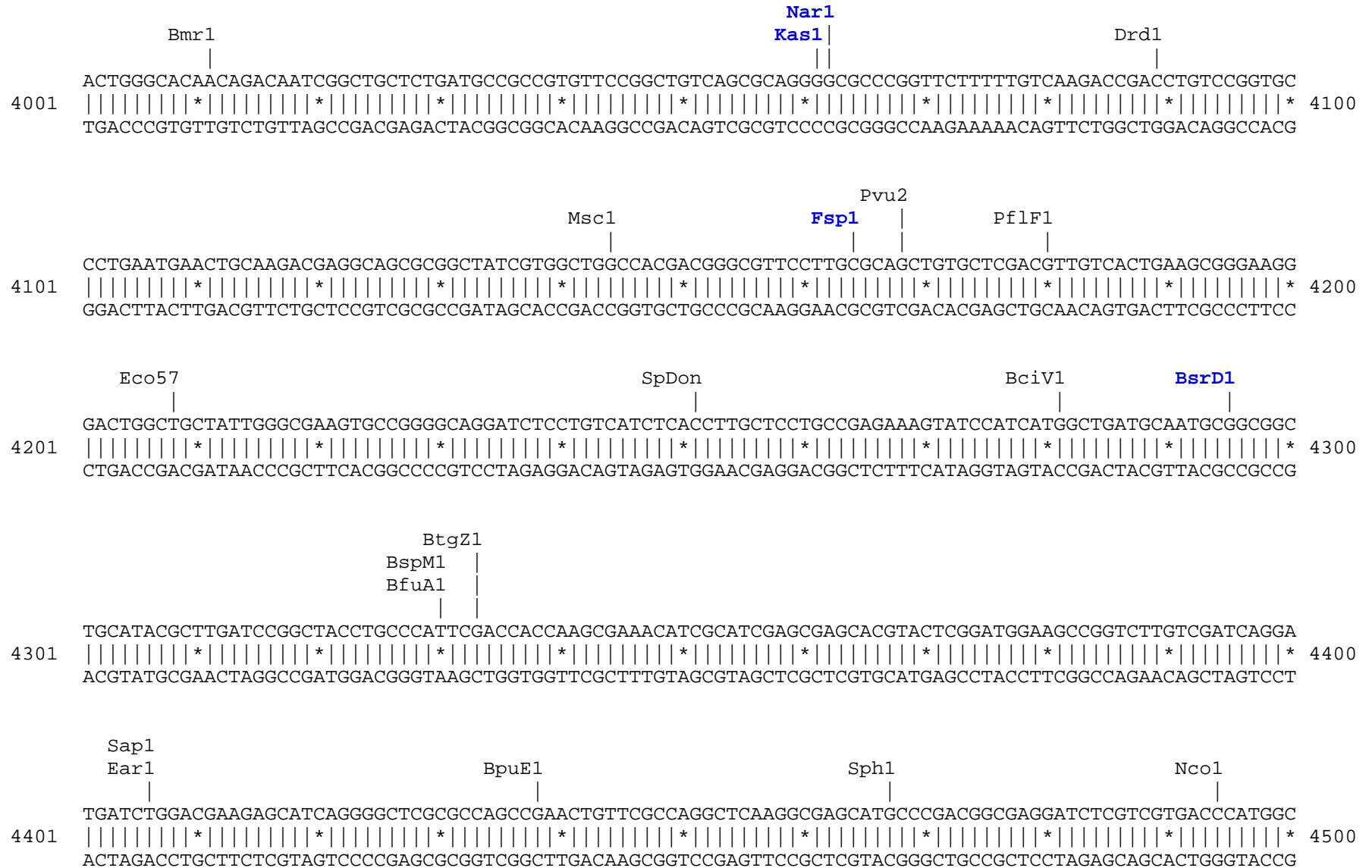
              SpAcc              Nae1
              |              |
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3201 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3300
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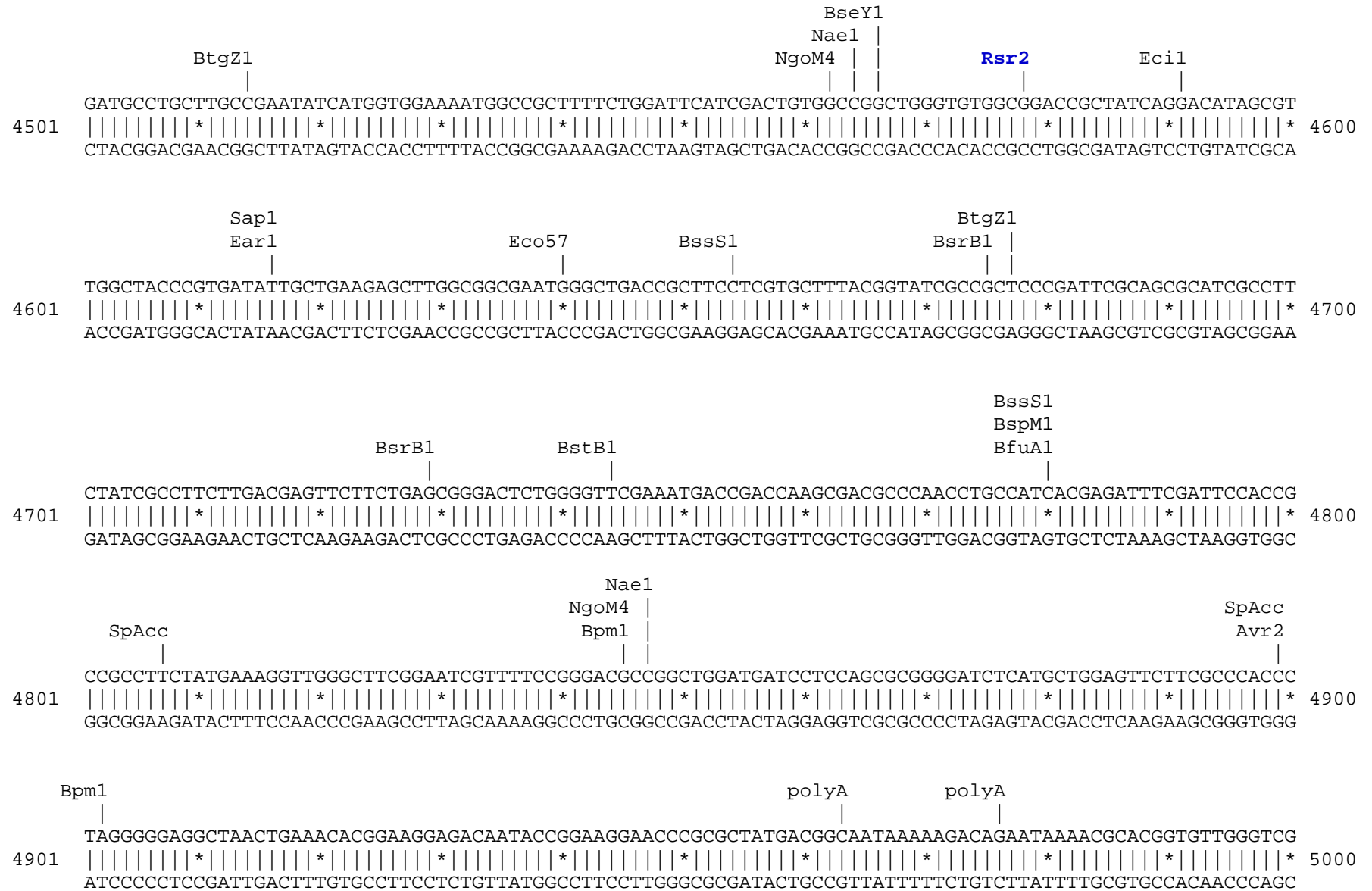
              BsrB1
              |
GAAGGGAAGAAAAGCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTAC
3301 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3400
CTTCCCTTCTTTTCGCTTTCCTCGCCCCGCGATCCC CGGACCGTTTACATCGCCAGTGCACGCGCATTGGTGGTGTGGGGCGGCGGAATTACGCGGCGATG

              polyA              BciV1
              |              BspH1
              |              |
AGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATA
3401 |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 3500
TCCCGCGCAGTCCACCGTGAAAAGCCCTTTACACGCGCCTTGGGGATAAACAATAAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTAT

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                                     Bsa1
                                     |
5001 TTTGTTCATAAACGCGGGTTCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTCTTCCTTTTCCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
    AAACAAGTATTTGCGCCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGG

                                     SpDon
                                     |
                                     BstAP
                                     |
                                     AlwN1
                                     |
                                     Bsu36
                                     |
5101 CACCCACCCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    GTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTA

    Dra1
    |
    Dra1
    |
    BspH1
    |
5201 TGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTTTCGTTCCACTGA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    ACTAAATTTGAAGTAAAAATTAAATTTTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACT

                                     BpuE1
                                     |
5301 GCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGGTAATCTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    CGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTTCGCC

                                     Eco57
                                     |
                                     SpAcc
                                     |
5401 TGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5500
    ACCAAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCAT

                                     AlwN1
                                     |
                                     BpuE1
                                     |
5501 GTTAGCCCACTTCAAGAATCTGTAGCACCGCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5600
    CAATCCGGTGGTGAAGTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTTCAGCACAGAA
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                                     ApaL1      BseY1
                                     |           |
ACC GGG TTG GACT CAAG ACG ATAG TTAC CGG ATAAG GCG CAG CGG TCG GGCTG AAC CGG GGG GTT CGT GCA CAC AG CCC AG CT TGG AG CGA ACG ACCT ACA
5601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5700
TGG CCA ACG CTG AGT TCT GCT ATCA ATGG CCTATT CCG CGT CGC CAG CCC GACTT G CCCC CAAG CAC GTGT GTCG GGT CGA ACCT CGCT TGCT GGAT GT

                                     SpAcc
                                     |
CCG AAC TGAG ATAC CTAC AGCG TGAG CTAT GAG AAA GCG CCAC GCTT CCG AAG GGAG AAA GCG GAC AGG TAT CCG GTA AG CGG CAG GGTC GGA ACAG G
5701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5800
GGCTTGACTCTATGGATGTGCACTCGATACTCTTTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTCGCCGTCCCAGCCTTGTTCC

    BssS1                               SpAcc                               Drd1                               BpuE1
    |                                   |                                   |                                   |
AGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCG
5801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5900
TCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGC

                                     SpDon
                                     |
    SpAcc   Eci1                               BspLU
    |       |                                   |
TCAGGGGGCGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTAT
5901 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6000
AGTCCCCCGCCTCGGATACCTTTTTGCGGTTCGTTGCGCCGGAATAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATA

                                     Nsil
                                     |
    BfrB1
    |
CCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT
6001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 6038
GGGGACTAAGACACCTATTGGCATAATGGCGGTACGTA

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Found:

Aar1	Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Asc1	Ase1	Avr2	BamH1	Bbs1	BciV1
BfrB1	BfuA1	Bgl1	Bgl2	BmgB1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1
_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	Ngom4	Nhe1	Not1	Nsi1	PflF1	Pml1	polyA	PshA1
Psil	Pvu2	Rsr2	Sac1	Sap1	SexA1	Sfil	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1
Xcm1	Xho1	Xmn1											

Unique:

Aar1	Afe1	Afl2	Age1	Ale1	Asc1	Ase1	BamH1	Bgl2	BmgB1	BspLU	BsrD1	BsrG1	BssH2
Bts1	_Chi	Clal	EcoR1	Fsp1	Hpa1	Kas1	Mfe1	Nar1	Nde1	Not1	Pml1	PshA1	Rsr2
Sfil	SnaB1	Xba1	Xcm1	Xho1	Xmn1								

Not found:

Acc65	Acl1	Ahd1	Apa1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1	Bpu10	Bsg1
BsiW1	BsmB1	BspE1	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu	Kpn1
loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	PspOM	Pst1	Pvu1	Sac2	Sall	Sand1	Sbf1	Scal
Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	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	Faul	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													