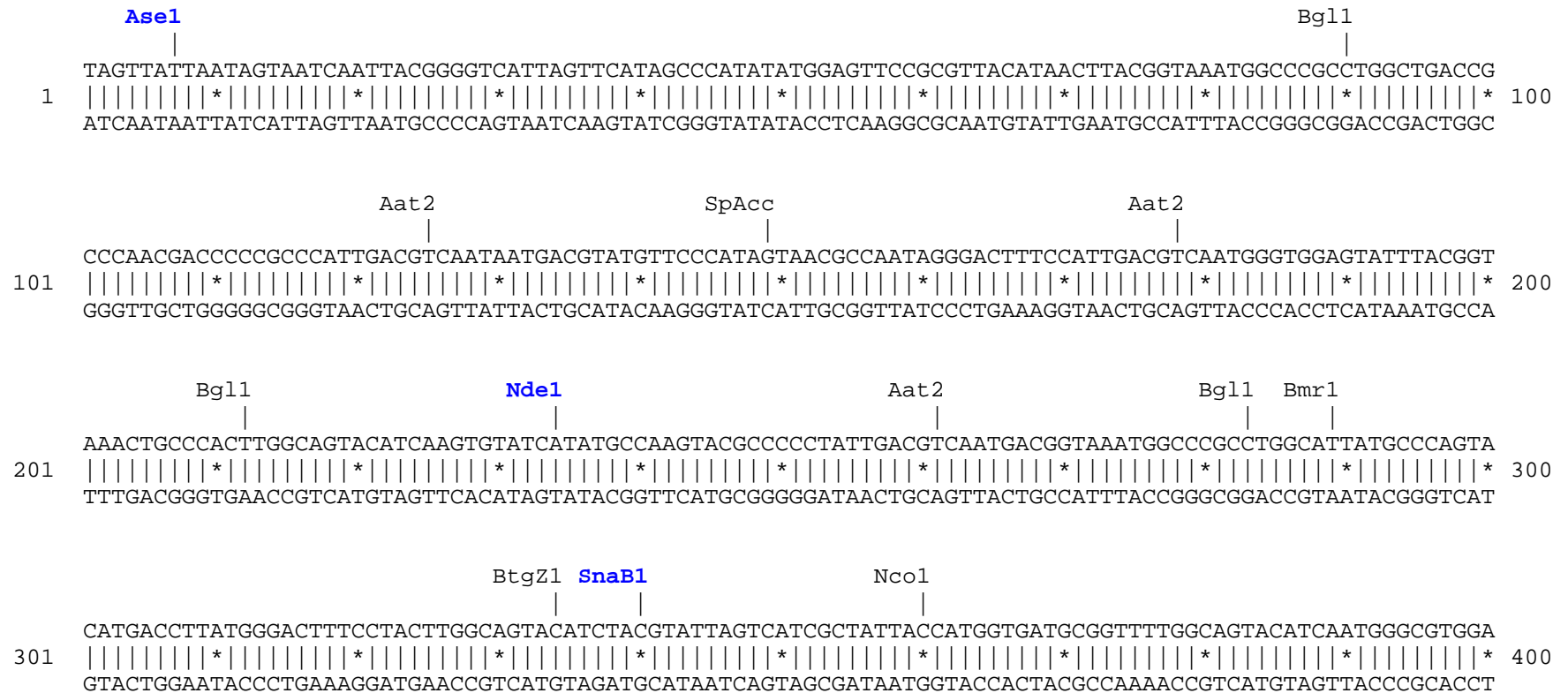


pFusionRed-CD151 vector restriction map

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, CD151 amino acids are shown in green, linker amino acids are shown in black.



401 TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTA
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

Aat2

Ecil

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 600
TGTTGAGGCGGGTAACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Nhe1

Afe1

601 CCGGTCGCCACCATGGTGAGCGAGCTGATTAAGGAGAACATGCCCATGAAGCTGTACATGGAGGGCACCCTGAACAACCACCACTTCAAGTGCACATCCG
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 700
GGCCAGCGGTGGTACCCTCGCTCGACTAATTCTCTTTGTACGGGTACTTCGACATGTACCTCCCGTGGCACTTGTGTTGGTGGTGAAGTTTCACGTGTAGGC

SpDon

Ale1

Age1

Nco1

BsrG1

ApaL1

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

701 AGGGCGAAGGCAAGCCCTACGAGGGCACCCAGACCATGAGAATCAAGGTCGTGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTT
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 800
TCCCCTTCGTTTCGGGATGCTCCCGTGGGTCTGGTACTCTTAGTTCCAGCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAA

SpAcc

FusionRed > G E G K 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

801 CATGTACGGCAGCAGAACCCTTCATCAAGCACCCCTCCGGGCATCCCCGACTTCTTTAAGCAGTCCCTTCAGGGCTTCACATGGGAGAGAGTCCACCACA
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 900
GTACATGCCGTCGTCTTGGAAGTAGTTTCGTGGGAGGCCCCGTAGGGGCTGAAGAAATTCGTAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGT

Bsu36

SpDon

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

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          Bbs1          Bpm1          BseY1
          |             |             |
TACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCAGCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGGTTAGAGGGGTGAACTTCCCAGCCA
101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
ATGCTTCTGCCCCGCACGACTGGCGATGGGTCTGTGGTCCGAGGTCCTGCCGACGGAGTAGATGTTGCAGTTCCAATCTCCCCACTTGAAGGGTTCGGT
FusionRed > Y E D G G V L T A T Q D T S L Q D G C L I Y N V K V R G V N F P A N

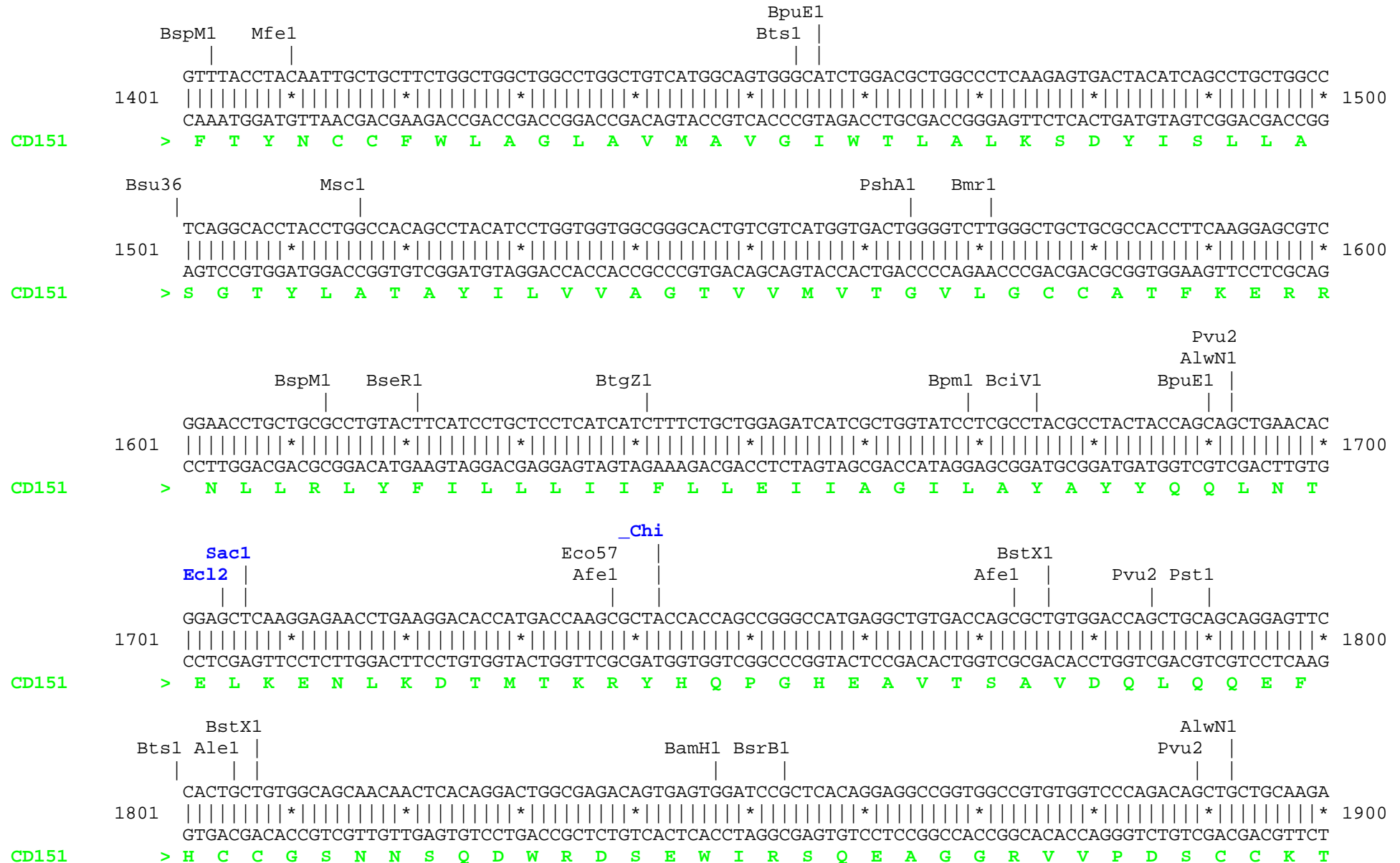
          BsmB1
          |
          BseY1  Stul  Bgl1
          |      |      |
ACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGCCTCCACCGAGACGATGTACCCCGCTGACGGCGGCCTGGAAGGCGCATGTGACATGGCCCT
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
TGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCGGAGGTGGCTCTGCTACATGGGGCGACTGCCGCGGACCTTCCGCGTACACTGTACCGGGA
FusionRed > G P V M Q K K T L G W E A S T E T M Y P A D G G L E G A C D M A L

          BpuE1
          |
BssS1  Eco57  Bsa1  BpuE1
|      |      |      |
GAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACCTTGAGACCACATACAGATCCAAGAAACCCGCTACGAACCTCAAGATGCCCGGCGTCTACAACGTG
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
CTTCGAGCACCCGCCCCGGTGGACTAGACGTTGGAACCTCTGGTGTATGTCTAGGTTCTTTGGGCGATGCTTGGAGTTCTACGGGCCGAGATGTTGCAC
FusionRed > K L V G G G H L I C N L E T T Y R S K K P A T N L K M P G V Y N V

          SpAcc
          PflM1
          |
          Bsa1  PshA1  BssS1  Dra3  Msc1
          |      |      |      |      |
GACCACAGACTGGAAAGAATCAAGGAGGCCGACGATGAGACCTACGTCGAGCAGCAGAGGTGGCTGTGGCCAGATACTCTACTGGTGGCGCTGGTGTATG
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
CTGGTGTCTGACCTTTCTTAGTTCTCCTCCGGCTGCTACTCTGGATGCAGCTCGTCTGCTCCACCGACACCGGTCTATGAGATGACCACCGCGACCACTAC
FusionRed > D H R L E R I K E 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

          BpuE1
          |
          SpDon  BspE1  Bgl2  BseR1  BspLU  Bbs1  BstAP
          |      |      |      |      |      |      |
GAGGTAAAGGTGGAGGAGGTTCCGGACTCAGATCTGGCGGTATGGGTGAGTTCAACGAGAAGAACAACATGTGGCACCGTTTGCCTCAAGTACCTGCT
1301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
CTCCATTTCCACCTCCTCCAAGGCCTGAGTCTAGACCGCCATAACCACTCAAGTTGCTCTTCTTCTGTTGTACACCGTGGCAAACGGAGTTCATGGACGA
FusionRed > G K G G G G S G L R S G G M G E F N E K K T T C G T V C L K Y L L

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polyA      Bts1 Bsm1      Mlu1      SpDon
|          |   |      |          |          |
GCAATAGCATCACAAATTTTCACAAATAAAGCATTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAA
2301 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
CGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAGTAGTTACATAGAATTGCGCATTTAACATT

      Ssp1                                Psi1
      |                                |
GCGTTAATATTTTTGTTAAAAATTCGCGTTAAATTTTTTGTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAGA
2401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
CGCAATTATAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTTCT

                                BsaXb      Drd1      BsaXa
                                |          |          |
ATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAG
2501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
TATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTCTCAGGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCGCTTTTTGGCAGATAGTC

      BtgZ1      Dra3                                SpAcc
      ||        ||                                |
GGCGATGGCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTA
2601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
CCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAAT

      Nae1      NgoM4                                BsrB1
      |        |                                |
GAGCTTGACGGGGAAAAGCCGGCGAACGTGGCGAGAAAGGAAGGAAGAAAGCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACAGCTGCG
2701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
CTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTTCGCTTTCCTCGCCCGCGATCCCGCGACCGTTACATCGCCAGTGCGACGC

                                polyA
                                |
CGTAACCACCACACCCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTC
2801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
GCATTGGTGGTGTGGGGCGGCGGAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCCTTTACACGCGCCTTGGGGATAAAACAATAAAAAAG
```

BciV1
BspH1
BsrB1
Ssp1 Ear1 Bsu36 Pvu2
2901 TAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCT 3000
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
ATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCTTTCTTGGTCTGA

Eci1 BseY1 BstAP Nsil Sph1 BfrB1 SexA1
3001 GTGGAATGTGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGA 3100
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
CACCTTACACACAGTCAATCCCACACCTTTTCAGGGGTCCGAGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCT

BseY1 BstAP Nsil Sph1 BfrB1 Eci1 Eci1
3101 AAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTAA 3200
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
TTCAGGGGTCCGAGGGTTCGTCCGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGGATT

Eci1 Bmr1 Eci1 Nco1 polyA Bgl1 Sfi1
3201 CTCCGCCCAGTTCCGCCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCCTCGGCCTCTGAGCTATTCCAGAAGTA 3300
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
GAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAATAAATAACGTCTCCGGCTCCGGCGGAGCCGGAGACTCGATAAGGTCTTCAT

SpDon Avr2 StuI BseR1 ClaI BsaB1 BspM1
3301 GTGAGGAGGCTTTTTTGGAGGCCTAGGCTTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGATTGCACGCAGG 3400
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
CACTCCTCCGAAAAAACCCTCCGGATCCGAAAACGTTTCTAGCTAGTTCTCTGTCTACTCCTAGCAAAGCGTACTAACTTGTTCTACCTAACGTGCGTCC


```

4501 CCATTGGGGCCAATACGCCC GCGTTTCTTCCTTTTCCCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGC 4600
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGGGGGTTCAAGCCACTTCCGGGTCCCGAGCGTCGGTTGCAGCCCCGCGTCCG

      BstAP
      AlwN1      Bsu36                      DraI                      DraI                      BspH1
      |          |                          |                          |                          |
4601 CCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCA 4700
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAAACTATTAGAGT

                                                                BpuE1
                                                                |
4701 TGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTCTGCGCGTAAT 4800
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      ACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAAGAACTCTAGGAAAAAAGACGCGCATT

                                                                Eco57
                                                                |
4801 CTGCTGCTTGCAAACAAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTCAGCAGA 4900
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      GACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAACGGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCT

                        SpAcc
                        |
4901 GCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCTGCTAATCCTGT 5000
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      CGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACA

      AlwN1                      BpuE1
      |                          |
5001 TACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTGCGGGCTGAACGGGGG 5100
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*
      ATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCAGCTTGCCCCC
  
```


Found:

Aat2	Acc65	Afe1	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	Bcl1
BfrB1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1
BsmB1	BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	Bsu36	BtgZ1
Bts1	_Chi	Clal	Dra1	Dra3	Drd1	Eag1	Ear1	Ecil	Ecl2	Eco57	EcoR1	Fsp1	Hpa1
Kas1	Kpn1	Mfe1	Mlu1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	PflM1
Pml1	polyA	PshA1	Psil	PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1
Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stul	Xba1						

Unique:

Acc65	Age1	Apa1	Ase1	Bcl1	Bgl2	Bsg1	BsmB1	BspE1	BstB1	_Chi	Clal	Eag1	Ecl2
EcoR1	Fsp1	Hpa1	Kas1	Kpn1	Mlu1	Nar1	Nde1	Nhe1	PflF1	PflM1	Pml1	PspOM	Rsr2
Sac1	Sac2	Sall	SexA1	Sfi1	Sma1	SnaB1	Xba1						

Not found:

Aar1	Acl1	Afl2	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcgl1a	Bcgl1b	Blp1	BmgB1	Bpu10
BsiW1	BssH2	BstE2	BstZ1	BxatB	BxatL	BxatR	BxatP	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR
FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	loxP	Not1	Nru1	Pac1	Pme1	Pvu1	R4atB	R4atL
R4atP	R4atR	SanD1	Sbf1	Sca1	Sgf1	SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	PISce
Xcm1	Xho1	Xmn1											

Excluded by site complexity:

Acc1	Acil	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfal	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													