

pHcRed-Tandem-N3 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 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 shown in frame, amino acids coded by MCS and by a linker between two HcRed1 coding sequences (see vector description) shown in black.



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                                         Aat2                      EciI
                                         |                      |
TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTA
401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACGCAGTTACCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                         NheI AfeI
                                         |     |
ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT
t-HcRed > A S A

                                         Agel
                                         Rsr2
                                         BspE1
                                         BamH1
                                         SmaI
                                         ApaI
                                         Hind3 EcoR1 Sall PspOM
                                         BpuE1 Bgl2 Xho1 Sac1 BstB1 Pst1 Sac2 NcoI BsrB1 EcoNI
                                         AleI
CCGGA CT CAGATCTCGAGCTCAAGCTTCGAATTCTGCAGTCGACCCTACCGCGGGCCCGGGATCCGGACC GGTCGCCACCATGGTGAGCGGCCTGCTGAA
601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
GGCCTGAGTCTAGAGCTCGAGTTTCAAGCTTAAGACGTCAGCTGGGATGGCGCCCGGGCCCTAGGCCTGGCCAGCGGTGGTACCACTCGCCGGACGACTT
t-HcRed > T G L R S R A Q A S N S A V D P T A G P G S G P V A T M V S G L L K

                                         FspI BsrGI NaeI
                                         FspAI Eco57 BcgIb NgoM4
GGAGAGTATGCGCATCAAGATGTACATGGAGGGCACC GTGAACGGCCACTACTTCAAGTGGCAGGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAG
701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
CCTCTCATA CGGTAGTTCTACATGTACCTCCCGTGGCACTTGC CGGTGATGAAGTTACGCTCCC GCTCCC GCTGCC GTTGGGGAAGCGGCCGTGGGTC
t-HcRed > E S M R I K M Y M E G T V N G H Y F K C E G E G D G N P F A G T Q
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      Nar1
      Kas1
Bcg1a  Pml1  Kas1  Bcg1b  ApaL1
|      |      |      |      |
AGCATGAGAAATCCACGTGACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACCTTCGTGCACCACA
801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
TCGTACTCTTAGGTGCACTGGCTCCCCGCGGGGGGACGGGAAGCGGAAGCTGTAGGACCGGGGGACGACGCTCATGCCGTGCTCCTGGAAGCACGTGGTGT
t-HcRed  > S M R I H V T E G A P L P F A F D I L A P C C E Y G S R T F V H H

      Bcg1a
      Bgl1  Bpm1  ApaL1  BsrB1  BseY1
      |      |      |      |      |
CCGCCGAGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTCACCTGGGAGAGAACCACCACCTACGAGGACGGCGGCATCCTGACCGCCCACCA
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
GGCGGCTCTAGGGGCTGAAGAAGTTCGTCTCGAAGGGGCTCCCGAAGTGGACCCTCTCTTGGTGGTGGATGCTCCTGCCGCCGTAGGACTGGCGGGTGGT
t-HcRed  > T A E I P D F F K Q S F P E G F T W E R T T T Y E D G G I L T A H Q

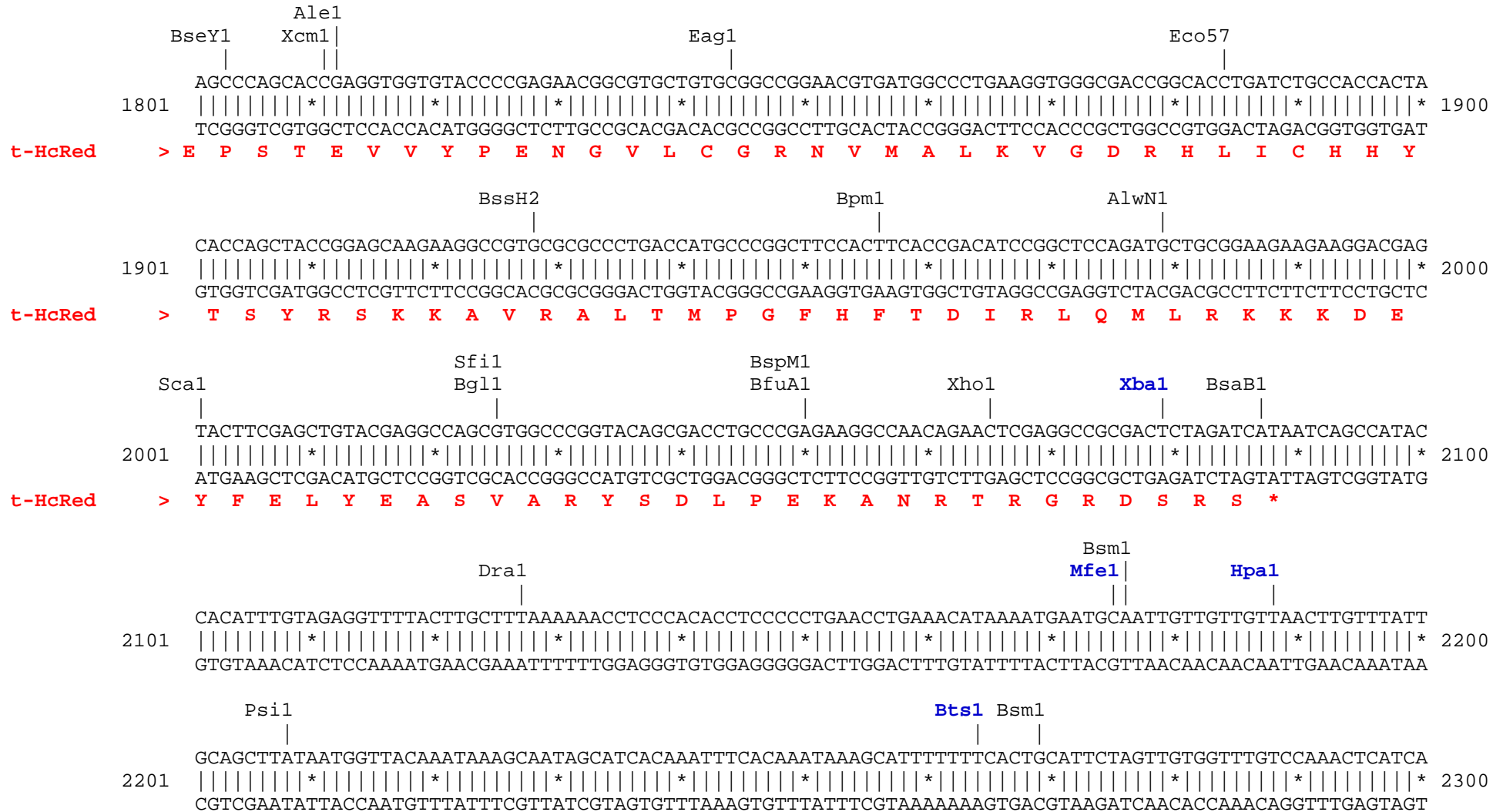
      Bgl1  Bpm1  ApaL1  BsrB1  BseY1
      |      |      |      |      |
GGACACCAGCCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAACAAGAGCGGCGGC
1001 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
CCTGTGGTTCGGACCTCCCCGTTGACGGACTAGATGTTCCACTTCCACGTGCCGTGGTTGAAGGGGGCGGCTGCCGGGGCACTACTTCTTGTCTCGCCGCCG
t-HcRed  > D T S L E G N C L I Y K V K V H G T N F P A D G P V M K N K S G G

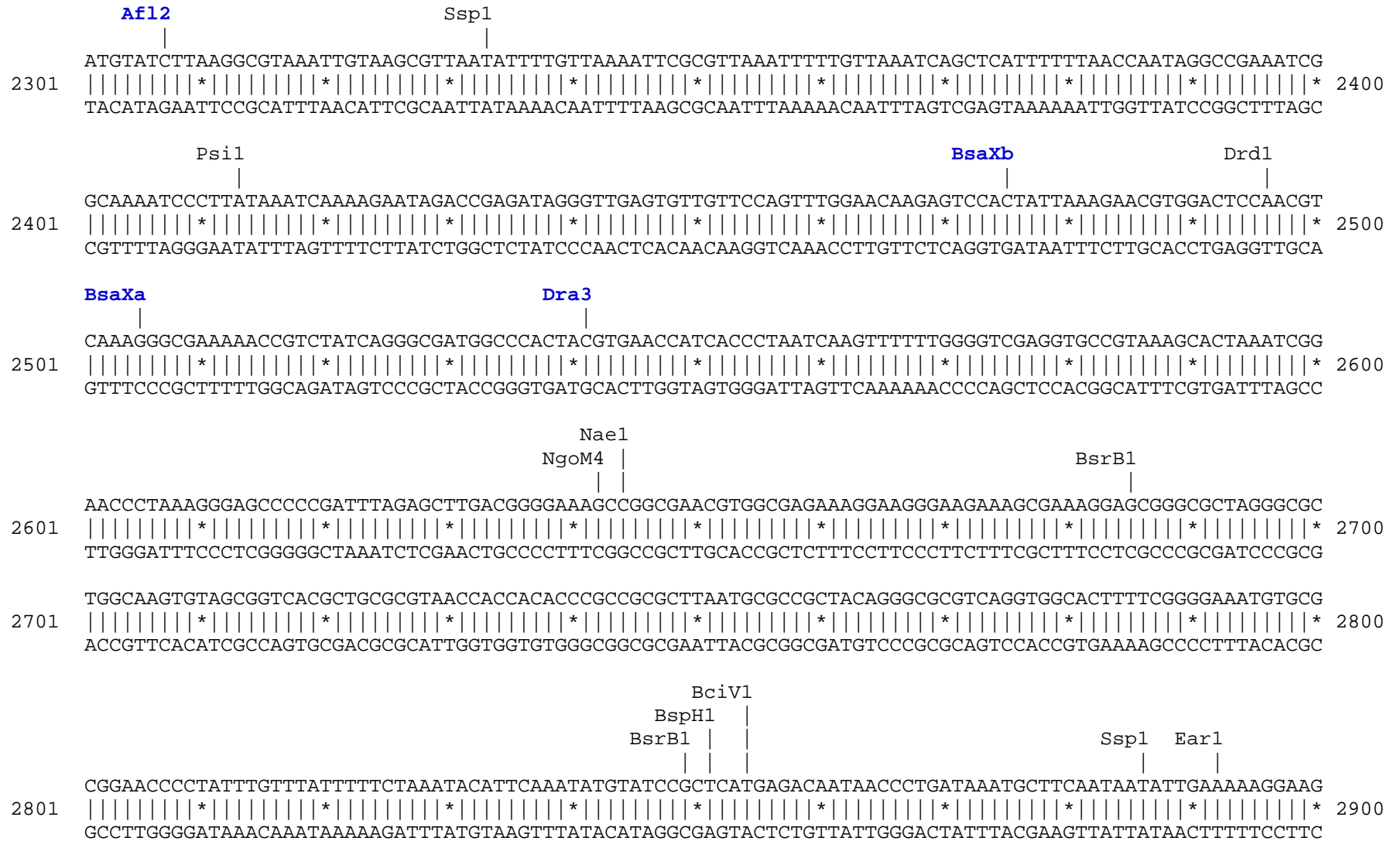
      Ale1
      BseY1  Xcm1  Eag1  Eco57
      |      |      |      |      |
TGGGAGCCCAGCACCGAGGTGGTGTACCCCCGAGAACGGCGTGCTGTGCGGCCGGAACGTGATGGCCCTGAAGGTGGGCGACCGGCACCTGATCTGCCACC
1101 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
ACCCTCGGGTCGTGGCTCCACCACATGGGGCTCTTGCCGCACGACACGCCGGCCTTGCCTACTCCGGGACTTCCACCCGCTGGCCGTGGACTAGACGGTGG
t-HcRed  > W E P S T E V V Y P E N G V L C G R N V M A L K V G D R H L I C H

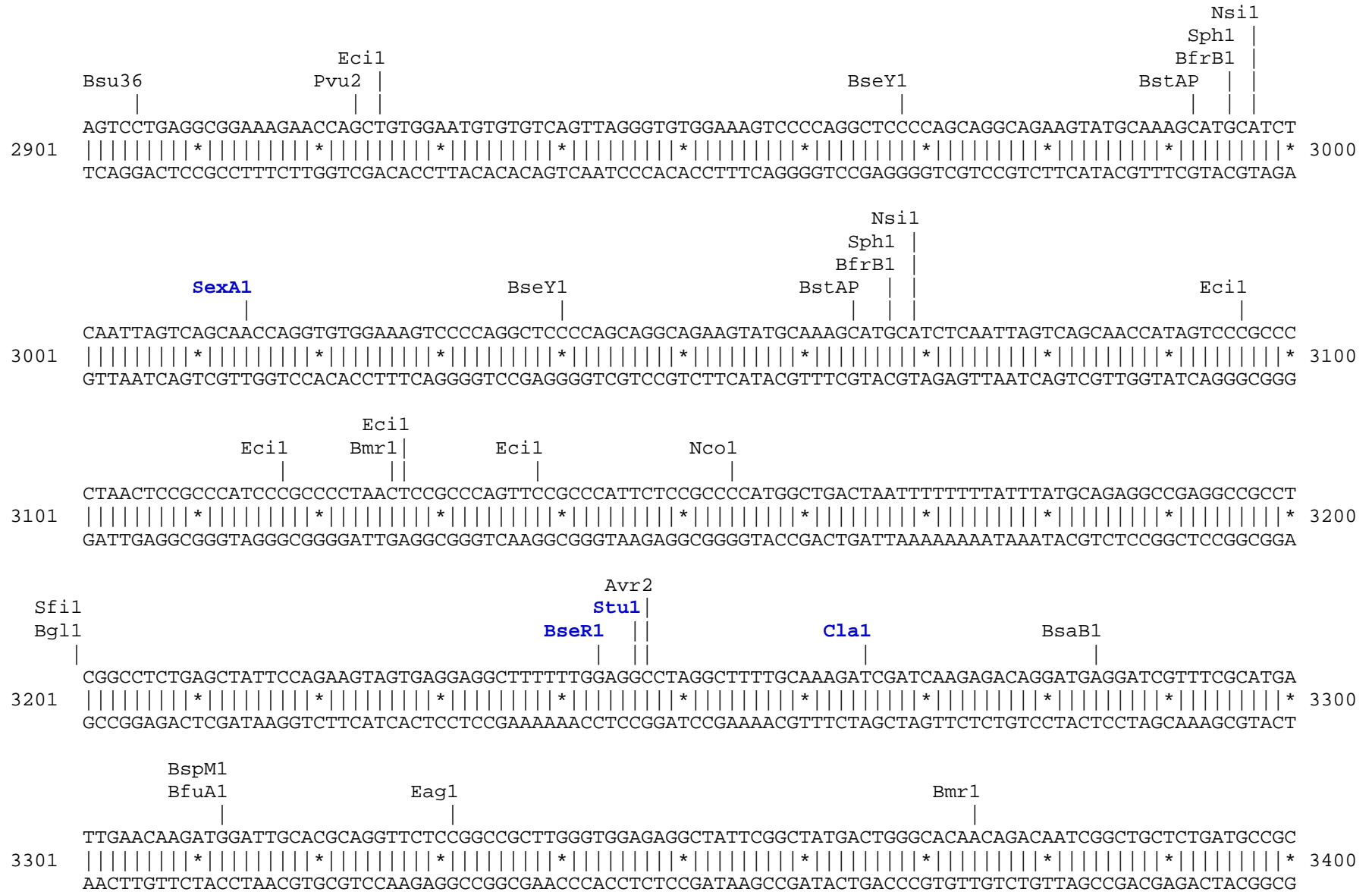
      BssH2  Bpm1  AlwN1
      |      |      |
ACTACACCAGCTACCGGAGCAAGAAGGCCGTGCGCGCCCTGACCATGCCCGGCTTCCACTTACCGACATCCGGCTCCAGATGCTGCGGAAGAAGAAGGA
1201 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
TGATGTGGTTCGATGGCCTCGTTCCTCCGGCACGCGCGGGACTGGTACGGGCCGAAGGTGAAGTGGCTGTAGGCCGAGGTCTACGACGCCTTCTTCTTCT
t-HcRed  > H Y T S Y R S K K A V R A L T M P G F H F T D I R L Q M L R K K K D

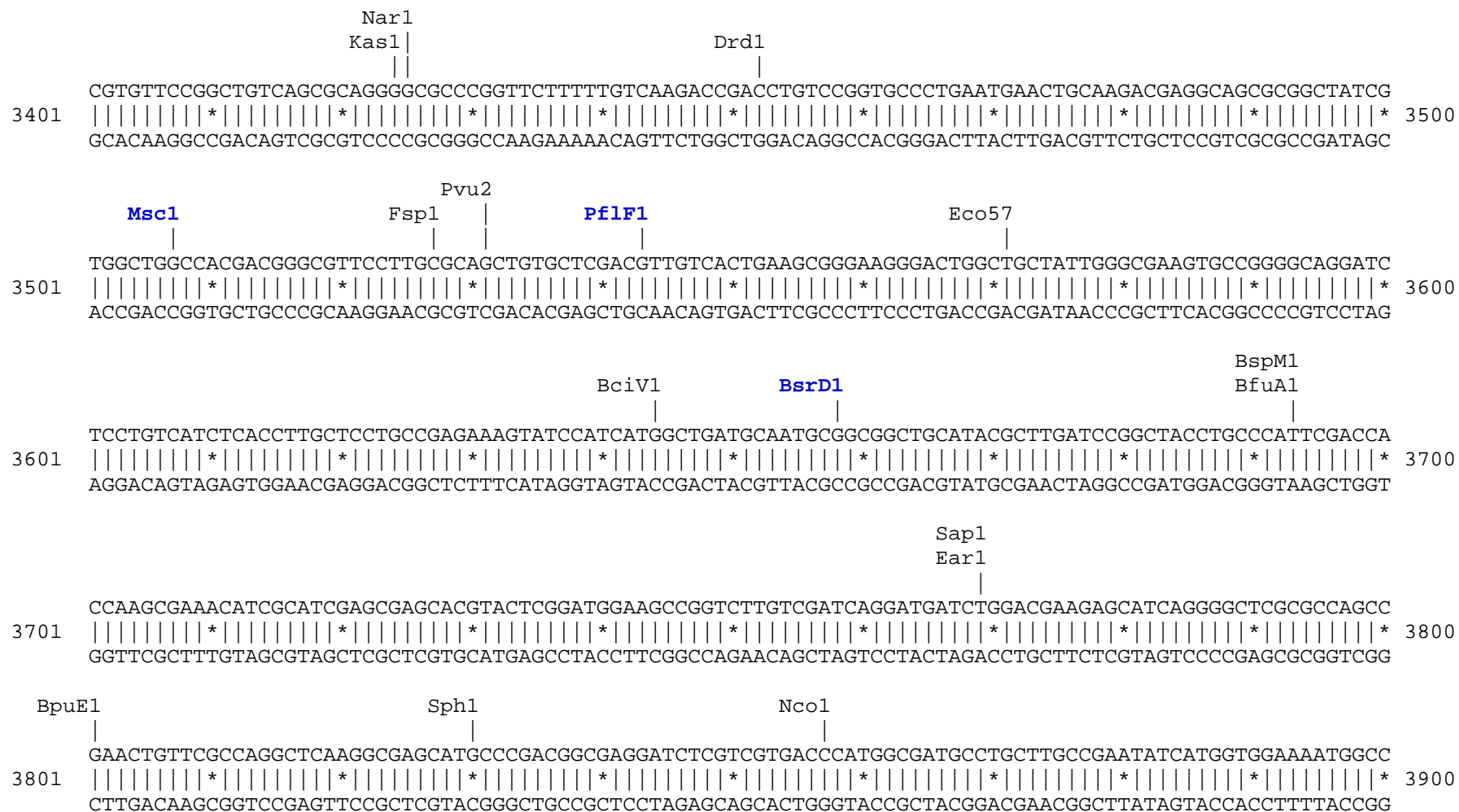
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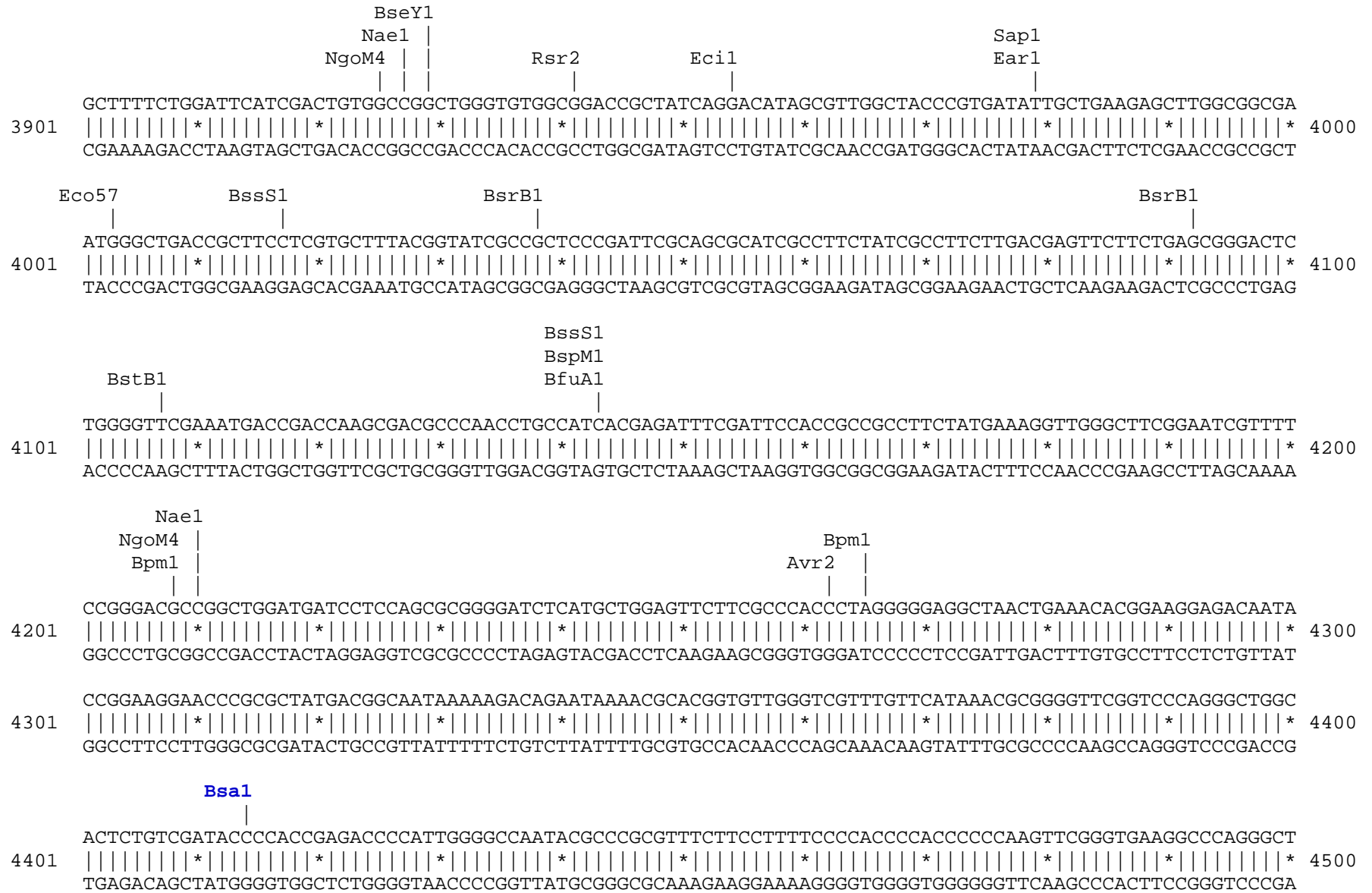
		Scal		SfiI		BspM1		Bgl2		SmaI		BsrB1		EcoN1	
1301															
															1400
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														
t-HcRed	>														











BstAP
AlwN1
Bsu36
Dra1
Dra1

4501 CGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTTTAATTTAAAAGGATCTAG 4600
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
 GCGTCGGTTGCAGCCCCGCCGTCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTCTAGATC

BspH1

4601 GTGAAGATCCTTTTTGATAATCTCATGACCAAAAATCCCTTAACGTGAGTTTTCGTTCCTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTT 4700
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
 CACTTCTAGGAAAACATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTCTAGAAGAA

BpuE1

4701 GAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAACCAACCCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTACCAACTCTTTT 4800
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
 CTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAACGGCCTAGTTCTCGATGGTTGAGAAAA

Eco57

4801 TCCGAAGGTAACCTGGCTTTCAGCAGAGCGCAGATACCAAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCT 4900
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
 AGGCTTCCATTGACCGAAGTCGTCTCGCTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGA

AlwN1
BpuE1

4901 ACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGG 5000
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
 TGTATGGAGCGAGACGATTAGGACAATGGTCAACGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCC

ApaL1
BseY1

5001 CGCAGCGGTCGGGCTGAACGGGGGTTCGTGCACACAGCCAGCTTGAGCGAACGACCTACACCGAAGTACCTACAGCGTGAGCTATGAGAAAG 5100
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
 GCGTCGCCAGCCGACTTGCCCCCAAGCACGTGTGTGGGTCGAACCTCGCTTGCTGGATGTGGCTTACTCTATGGATGTGCACTCGATACTCTTTTC

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                                BciV1
                                |
                                EciI
                                |
                                BssS1
                                |
5101 CGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5200
    GCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTGCGCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCGGACC

                                Drd1
                                |
                                BpuE1
                                |
                                EciI
                                |
5201 TATCTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGCAACG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5300
    ATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTGTTGC

                                BspLU
                                |
                                BfrB1
                                |
5301 CGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5400
    GCCGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGTACGT

NsiI
|
T
5401 | 5401
A
```

Found:

Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	Apal	ApaL1	Ase1	Avr2	BamH1	Bcgl1a	Bcgl1b	BciV1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BspE1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	Bsu36	Bts1	Cla1
Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoN1	EcoR1	FspA1	Fsp1	Hind3	Hpa1	Kas1
Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	Pml1	Psi1	PspOM	Pst1
Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	Sca1	SexA1	Sfi1	Sma1	SnaB1	Sph1	Ssp1	Stu1
Xba1	Xcm1	Xho1											

Unique:

Afe1	Afl2	Age1	Apal	Ase1	BamH1	Bsa1	BsaXa	BsaXb	BseR1	BspE1	BspLU	BsrD1	Bts1
Cla1	Dra3	EcoR1	Hind3	Hpa1	Mfe1	Msc1	Nde1	Nhe1	PflF1	PspOM	Pst1	Sac1	Sac2
Sall	SexA1	SnaB1	Stu1	Xba1	Not found:								

Aar1	Acc65	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcl1	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoRV	ScFRT	Fse1	I_Ceu	Kpn1	loxP
Mlu1	Not1	Nru1	Pac1	PflM1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Sgf1	SgrA1	Spe1	Srf1
Swal	PISce	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													