

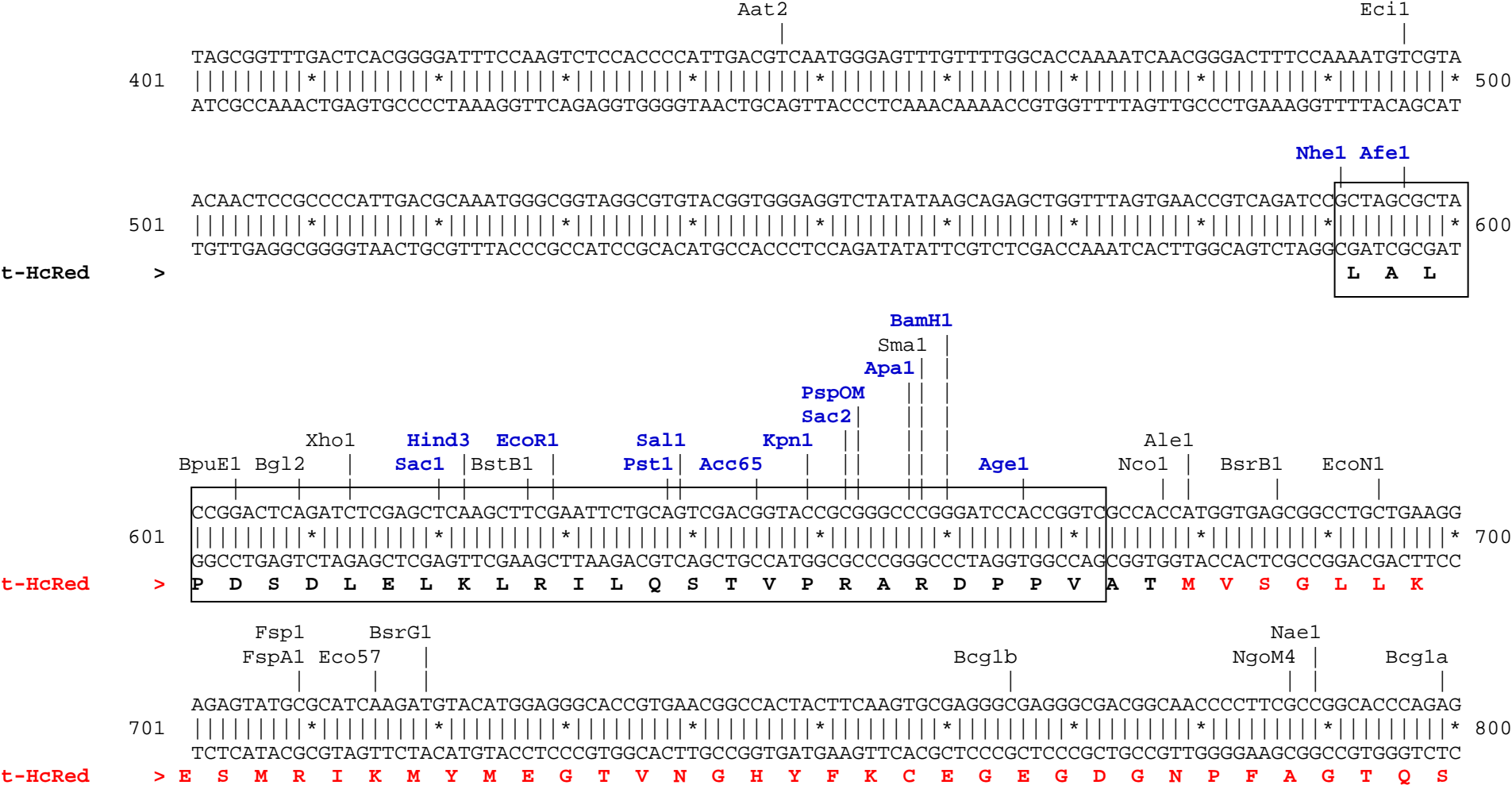
pHcRed-Tandem-N1 vector restriction map

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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                SfiI          BspM1          Bgl2          SmaI          BsrB1          EcoN1
                |            |            |            |            |            |
    Scal        BglI          BfuA1          Bgl2          SmaI          BsrB1          EcoN1
    |           |           |           |           |           |           |
1301  AGTACTTTCGAGCTGTACGAGGCCAGCGTGGCCCCGGTACAGCGACCTGCCCGAGAAGGCCAACAGATCTCCCGGGATGGTGAGCGGCCTGCTGAAGGAGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    TCATGAAGCTCGACATGCTCCGGTTCGCACCCGGGCCATGTCGCTGGACGGGCTCTTCCGGTTGTCTAGAGGGCCCTACCACTCGCCGGACGACTTCCTCTC
t-HcRed  > E Y F E L Y E A S V A R Y S D L P E K A N R S P G M V S G L L K E S

                FspI          BsrG1          NaeI
                |           |           |           |           |           |
    FspA1 Eco57 |           |           |           |           |           |
1401  TATGCGCATCAAGATGTACATGGAGGGCACCGTGAACGGCCACTACTTCAAGTGCAGGGGCGAGGGCGACGGCAACCCCTTCGCCGGCACCCAGAGCATG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
    ATACGCGTAGTTCTACATGTACCTCCCGTGGCACTTGCCGGTGATGAAGTTCACGCTCCCCTGCCGTTGGGGAAGCGGCCGTGGGTCTCGTAC
t-HcRed  > 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 S M

                NarI
                |           |           |           |           |           |
    PmlI    KasI |           |           |           |           |           |
1501  AGAATCCACGTGACCGAGGGCGCCCCCTGCCCTTCGCCTTCGACATCCTGGCCCCCTGCTGCGAGTACGGCAGCAGGACCTTCGTGCACCACACCCGCCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
    TCTTAGGTGCACTGGCTCCCGCGGGGGGACGGGAAGCGGAAGCTGTAGGACCGGGGGACGACGCTCATGCCGTGCTCCTGGAAGCACGTGGTGTGGCGGC
t-HcRed  > 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 T A

                BspM1          Bgl2          ApaI          BsrB1          BseY1
                |           |           |           |           |           |
    BglI          BpmI          ApaL1          BsrB1          BseY1
    |           |           |           |           |           |           |
1601  AGATCCCCGACTTCTTCAAGCAGAGCTTCCCCGAGGGCTTTCACCTGGGAGAGAACCACCACCTACGAGGACGGCGGCATCCTGACCCGCCACCAGGACAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
    TCTAGGGGCTGAAGAAGTTCGTCTCGAAGGGGCTCCCGAAGTGGACCTCTCTTGGTGGTGGATGCTCCTGCCGCCGTAGGACTGGCGGGTGGTCTCTGTG
t-HcRed  > 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 D T

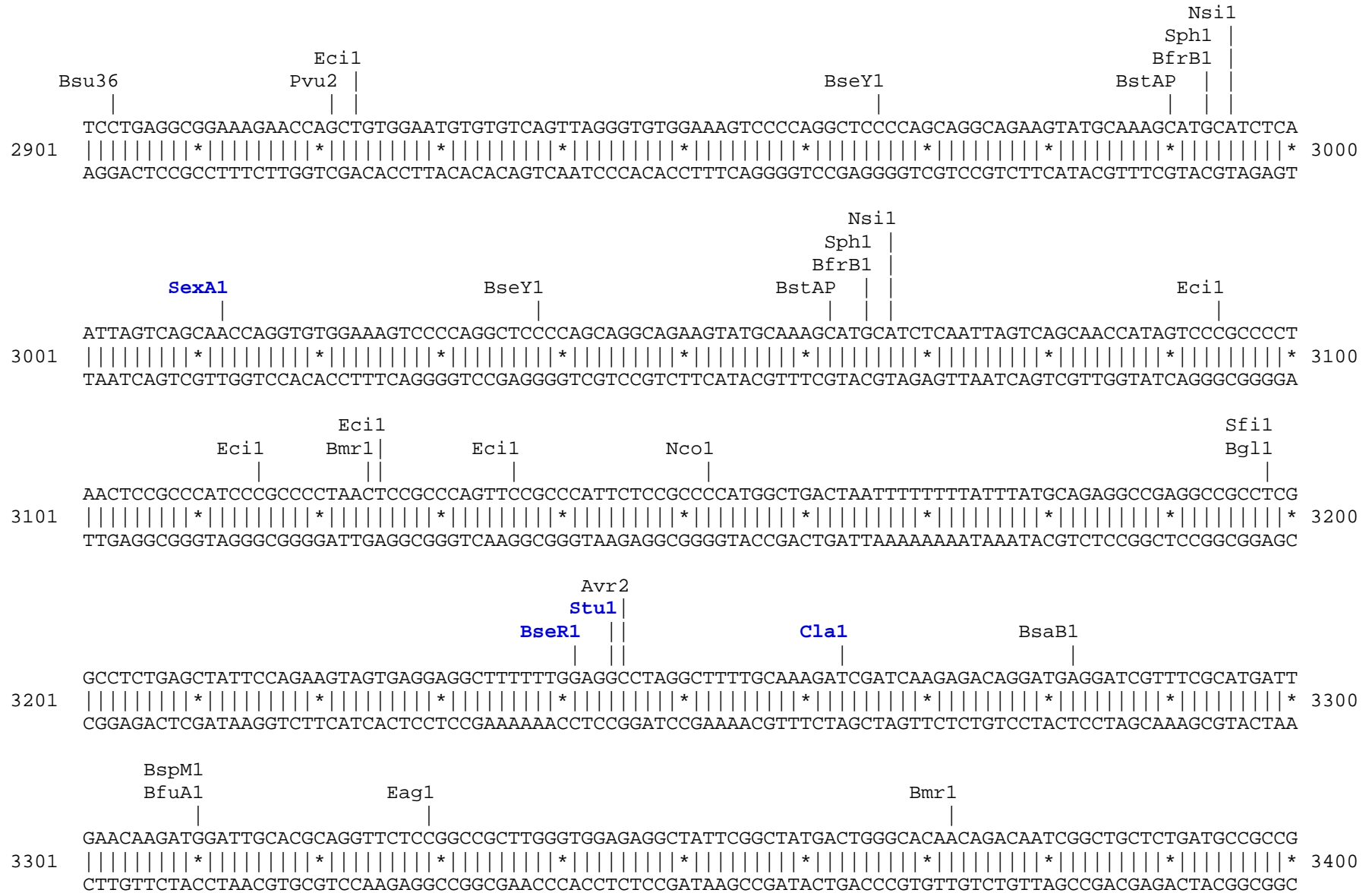
                BglI          BpmI          ApaL1          BsrB1          BseY1
                |           |           |           |           |           |
1701  CAGCCTGGAGGGCAACTGCCTGATCTACAAGGTGAAGGTGCACGGCACCAACTTCCCCGCCGACGGCCCCGTGATGAAGAACAAGAGCGGGCGGCTGGGAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
    GTCGGACCTCCCGTTGACGGACTAGATGTTCCACTTCCACGTGCCGTGGTTGAAGGGGCGGCTGCCGGGGCACTACTTCTTGTCTCGCCGCCGACCCTC
t-HcRed  > 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 W E

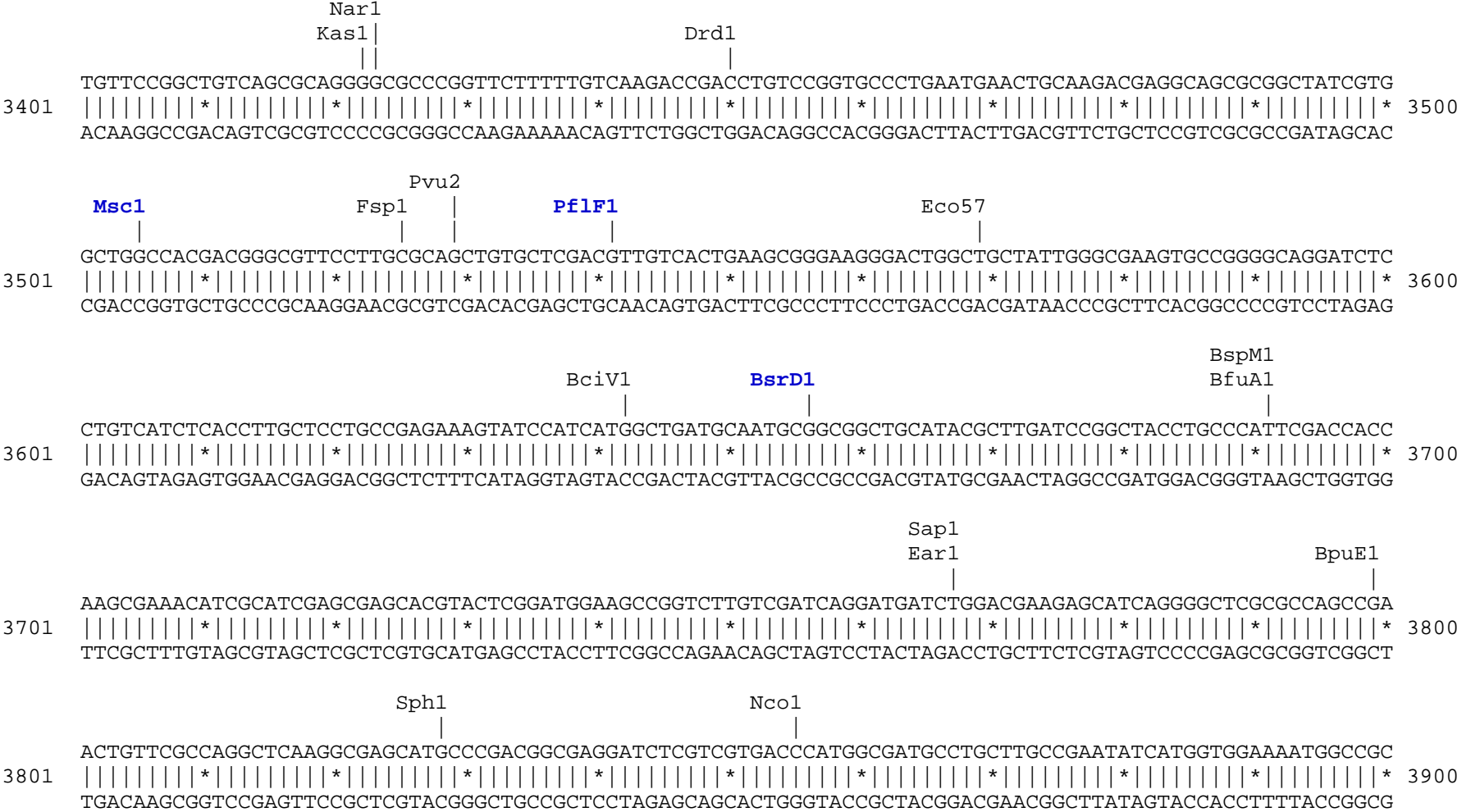
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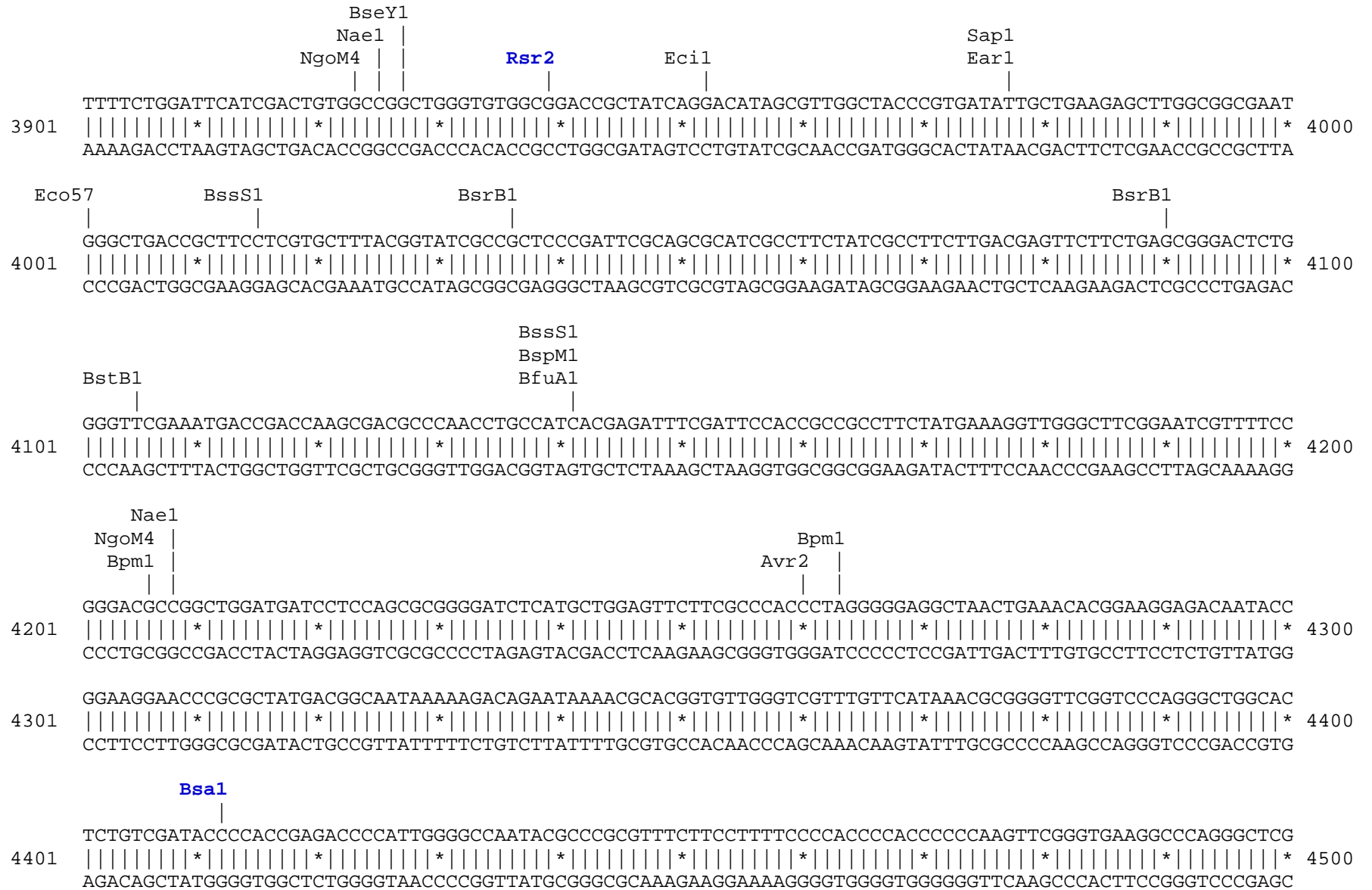


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      Af12                               Ssp1
      |                                 |
2301 GTATCTTAAGGCGTAAATTGTAAGCGTTAATATTTTGTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTTAACCAATAGGCCGAAATCGGC
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      CATAGAATTCCGCATTTAACATTTCGCAATTATAAAAACAATTTTAAGCGCAATTTAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTTTAGCCG
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
2401 AAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCA
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      TTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGACCTGAGGTTGCAGT
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
2501 AAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAATCGGAA
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      TTCCCGCTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTTAGCCTT
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
2601 CCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAAGGAAGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTG
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      GGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTTCTTTTCGCTTTCCTCGCCCGGATCCCGCGAC
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
2701 GCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATGTGCGCG
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      CGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGCAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAAAGCCCCTTTACACGCGC
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
2801 GAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAG
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      CTTGGGGATAAACAAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTACGAAGTTATTATAACTTTTTCTTCTC
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
2900
    
```







```
          BstAP
          AlwN1       Bsu36                                DraI       DraI
          |          |          |          |          |          |
4501  CAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAAGGATCTAGGT 4600
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      GTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTTTGAAGTAAAAATTAATTTTTCTAGATCCA

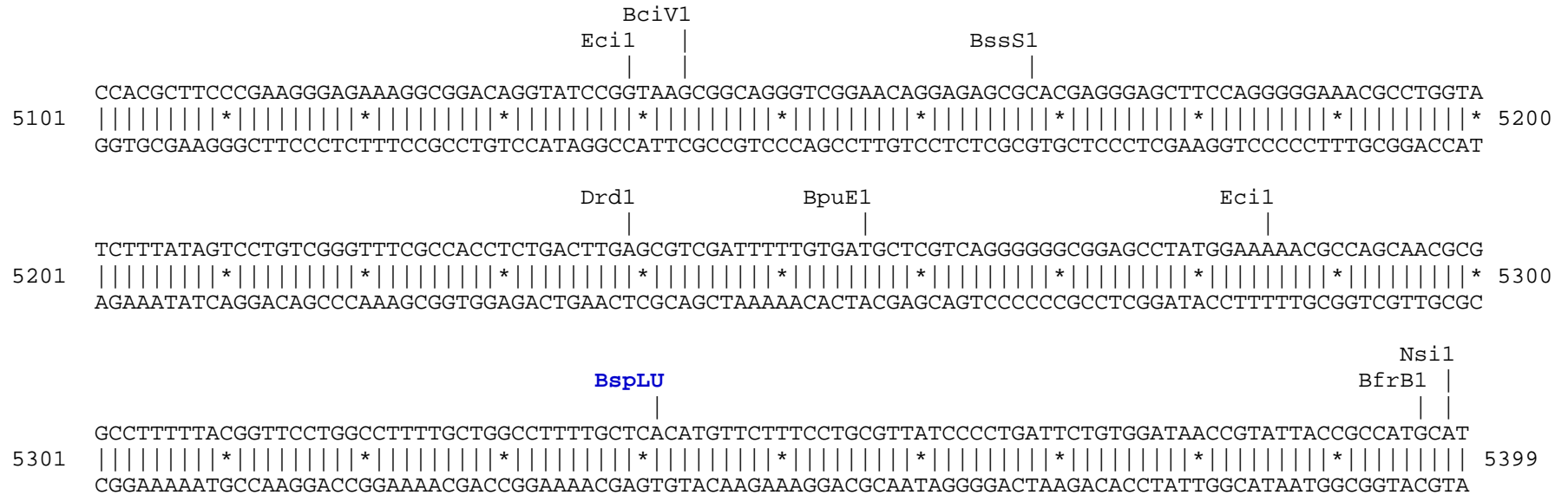
          BspH1
          |
4601  GAAGATCCTTTTTGATAATCTCATGACCAAAAATCCCTTAAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTTCTTGA 4700
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      CTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTTTCTAGAAGAACT

          BpuE1                                Eco57
          |          |
4701  GATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTTC 4800
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      CTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCGCCACCAAACAAACGGCCTAGTTCTCGATGGTTGAGAAAAAG

          CGAAGGTAAGTGGCTTCAGCAGAGCGCAGATAACAAATACTGTCTTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGTAGCACCGCCTAC 4900
4801  | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      GCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACATCGTGGCGGATG

          AlwN1                                BpuE1
          |          |
4901  ATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGGATAAGGCG 5000
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      TATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTGAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAATGGCCTATTCCGC

          ApaL1       BseY1
          |          |
5001  CAGCGGTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCG 5100
      | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | *
      GTCGCCAGCCCGACTTGCCECAAGCACGTGTGTGGGTCGAACCTCGCTTGTGATGTGGCTTGACTCTATGGATGTGCACTCGATACTCTTTTCGC
```



Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	Apal1	Ase1	Avr2	BamH1	Bcg1a	Bcg1b
BciV1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1
Bsm1	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
Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Nsi1	PflF1	Pml1	Psi1	PspOM
Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall1	Sap1	Sca1	SexA1	Sfi1	Sma1	SnaB1	Sph1	Ssp1
Stu1	Xba1	Xcm1	Xho1										

Unique:

Acc65	Afe1	Afl2	Age1	Apa1	Ase1	BamH1	Bsa1	BsaXa	BsaXb	BseR1	BspLU	BsrD1	Bts1
Cla1	Dra3	EcoR1	Hind3	Hpa1	Kpn1	Mfe1	Msc1	Nde1	Nhe1	PflF1	PspOM	Pst1	Rsr2
Sac1	Sac2	Sal1	SexA1	SnaB1	Stu1	Xba1							

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcl1	Blp1	BmgB1	Bpu10	Bsg1
BsiW1	BsmB1	BspE1	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoRV	ScFRT	Fse1	I_Ceu	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	Ap01	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfa1	Bme15
BsaA1	BsaH1	BsaJ1	BsaW1	BseM2	BsiE1	BsiH1	Bs11	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													