

pTagRFP-Golgi 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, human beta 1,4-galactosyltransferase amino acids (Golgi targeting sequence, GTS) are shown in bold black.



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                                Aat2                               Ecil
                                |                               |
TACGGGTTTGGACTCACGGGGATTTCCAAGTCTCCACCCCATTGACGTCAATGGGAGTTTGTGGTGGCACCAAATCAACGGGACTTTCCAAAATGTCGTA
401 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 500
ATCGCCAAACTGAGTGCCCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGGTTTTACAGCAT

                                                                    Nhe1
                                                                    |
ACAAC TCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCATGA
501 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 600
TGTTGAGGCGGGGTA ACTGCGTTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGTACT

GTS > M R

        BsrB1
        Bpu10
        BsrB1                BtgZ1   SpAcc                BssS1       Bsg1
        |                     |           |                 |               |
GGCTTCGGGAGCCGCTCCTGAGCGGCAGCGCCGCGATGCCAGGCGCGTCCCTACAGCGGGCCTGCCGCTGCTCGTGGCCGTCTGCGCTCTGCACCTTGG
601 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 700
CCGAAGCCCTCGGCGAGGACTCGCCGTCGCGGGCGCTACGGTCCGCGCAGGGATGTCGCCCGGACGGCGGACGAGCACCGGCAGACGCGAGACGTGGAACC

GTS > L R E P L L S G S A A M P G A S L Q R A C R L L V A V C A L H L G

        SpDon                Bpu10                Pst1
        |                     |                       |
CGTCACCCCTCGTTTACTACCTGGCTGGCCGCGACCTGAGCCGCTGCCCAACTGGTTCGGAGTCTCCACACCCGCTGCAGGGCGGGCTCGAACAGTGCCGCC
701 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 800
GCAGTGGGAGCAAATGATGGACCGACCGGCGCTGGACTCGGCGGACGGGTTGACCAGCCTCAGAGGTGTGGCGACGTCCCGCCGAGCTTGTTCACGGGCGG

GTS > V T L V Y Y L A G R D L S R L P Q L V G V S T P L Q G G S N S A A

                Rsr2
                Sac1       BspE1             BamH1   Age1             Ale1             Sap1
                |         |                   |         |           |               |
GCCATCGGGCAGTCTTCCGGGGAGCTCCGGACCGGAGGGGCCAAGGATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGCTGATTAAGGAGAACA
801 | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | | | | | * | 900
CGGTAGCCCGTCAGGAGGCCCTCGAGGCCCTGGCCTCCCCGTTCTAGTTGCCAGCGGTTGGTACCACAGATTCCCGCTTCTCGACTAATTCCTCTTGT

GTS/TagRFP > A I G Q S S G E L R T G G A K D P P V A T M V S K G E E L I K E N M

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          BsrG1                      ApaL1                      SpAcc
          |                          |                          |
    TGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCCCTACGAGGGCACCCAGACCATGAG
  901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
    ACGTGTACTTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTTACGTGTAGGCTCCCGCTTCCGTTTCGGGATGCTCCCGTGGGTCTGGTACTC
TagRFP > H M K L Y M E G T V N N H H F K C T S E G E G K P Y E G T Q T M R

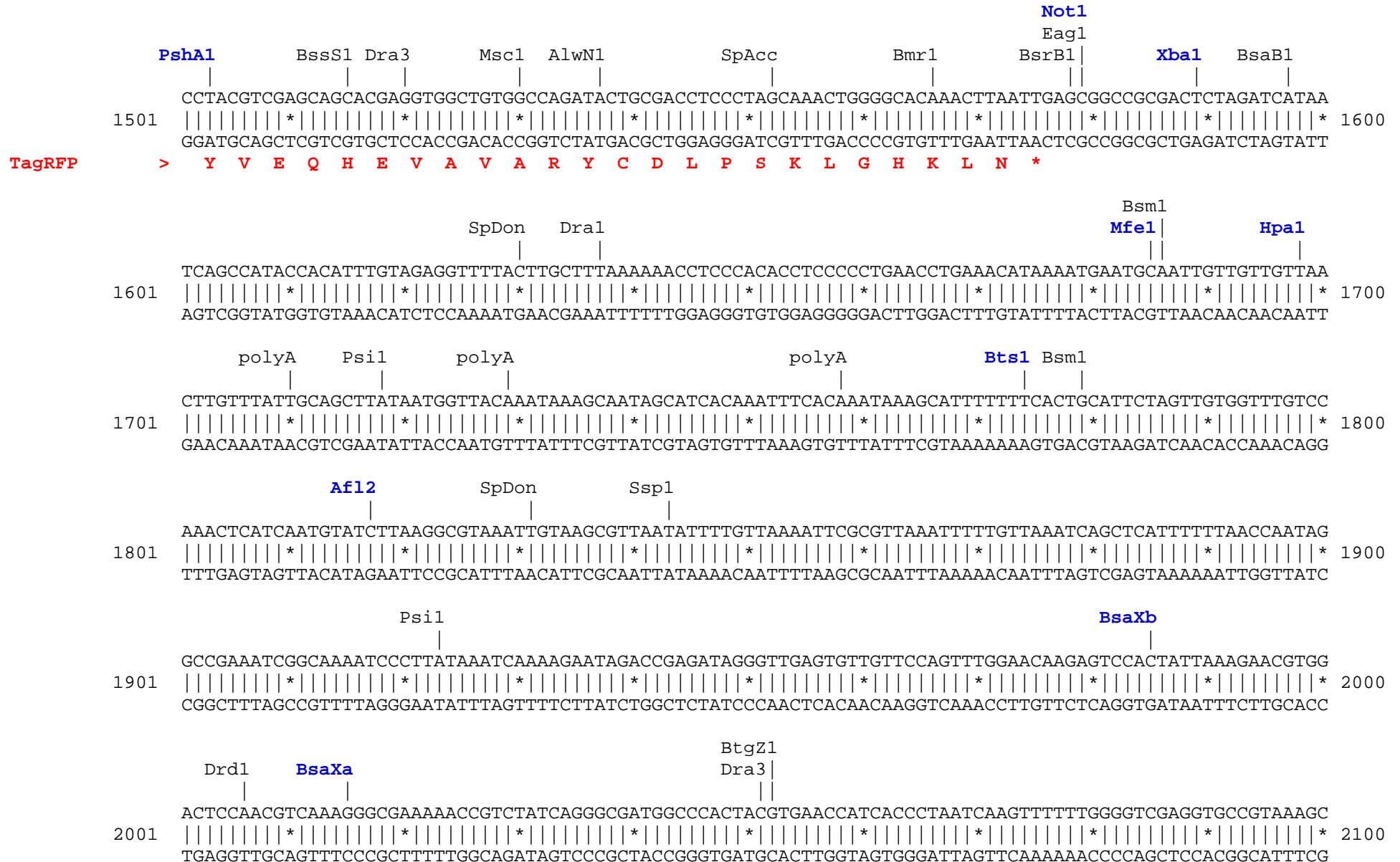
    AATCAAGGTGGTTCGAGGGCGGCCCTCTCCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAGAACCTTCATCAACCACACCCAGGGC
  1001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
    TTAGTTCCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTTCGTTGGAAAGTAGTTGGTGTGGGTCCCG
TagRFP > I K V V E G G P L P F A F D I L A T S F M Y G S R T F I N H T Q G

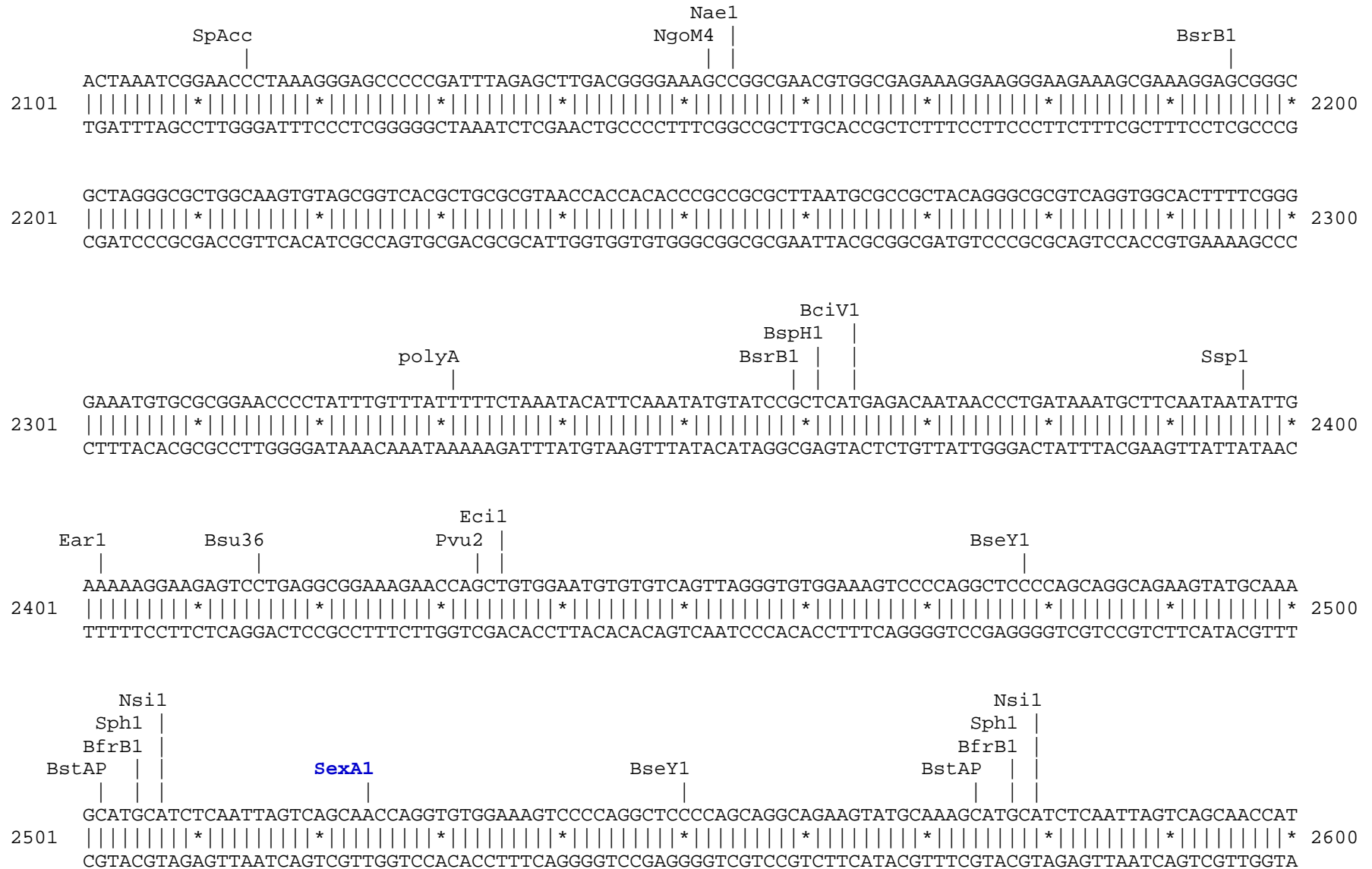
          Bsu36          SpDon                      Bbs1                      Bpm1
          |              |                          |                          |
    ATCCCCGACTTCTTTAAGCAGTCCTTCCCTTGAGGGCTTCACATGGGAGAGAGTCACCACATACGAAGACGGGGCGTGCTGACCGCTACCCAGGACACCA
  1101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    TAGGGGCTGAAGAAATTCGTCAGGAAGGGACTCCCGAAGTGTACCCTCTCTCAGTGGTGTATGCTTCTGCCCGGCACGACTGGCGATGGGTCTGTGGT
TagRFP > 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 V L T A T Q D T S

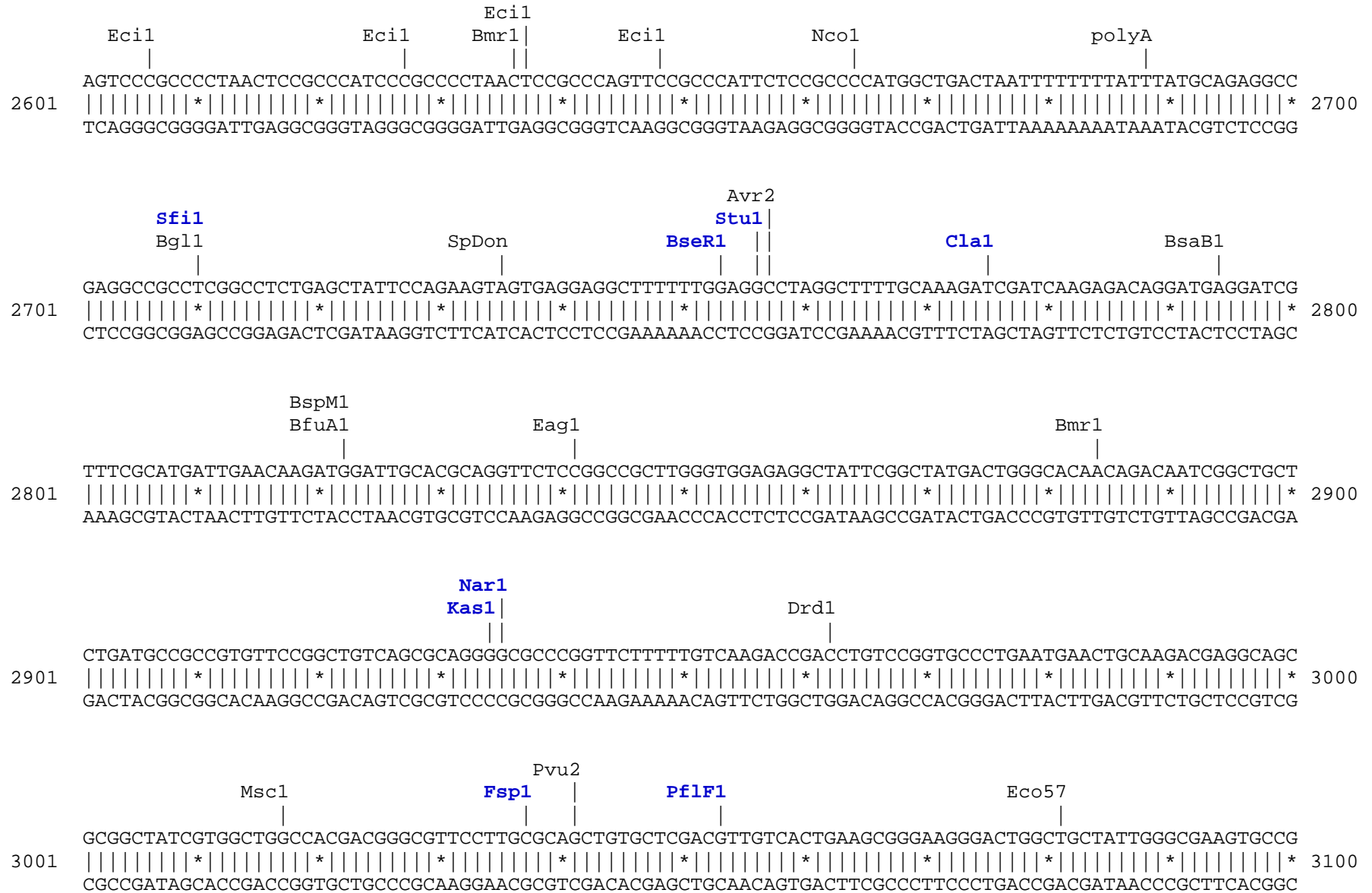
          BseY1
          |
    GCCTCCAGGACGGCTGCCTCATCTACAACGTCAAGATCAGAGGGGTGAACTTCCCATCCAACGGCCCTGTGATGCAGAAGAAAACACTCGGCTGGGAGGC
  1201  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    CGGAGGTCTGCCGACGGAGTAGATGTTGCAGTTCTAGTCTCCCCACTTGAAGGGTAGGTTGCCGGGACACTACGTCTTCTTTTGTGAGCCGACCCTCCG
TagRFP > L Q D G C L I Y N V K I R G V N F P S N G P V M Q K K T L G W E A

          Bgl1                      BssS1                      Eco57
          |                          |                          |
    CAACACCGAGATGCTGTACCCCGCTGACGGCGGCCTGGAAGGCAGAAAGCGACATGGCCCTGAAGCTCGTGGGCGGGGGCCACCTGATCTGCAACTTCAAG
  1301  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    GTTGTGGCTCTACGACATGGGGCGACTGCCGCCGGACCTTCCGCTTTCGCTGTACCGGGACTTCGAGCACCCGCCCCGGTGGACTAGACGTTGAAGTTC
TagRFP > N T E M L Y P A D G G L E G R S D M A L K L V G G G H L I C N F K

          BpuE1                      SpAcc          PflM1                      Bsa1
          |                          |              |                          |
    ACCACATACAGATCCAAGAAACCCGCTAAGAACCTCAAGATGCCCGGCTCTACTATGTGGACCACAGACTGGAAAGAATCAAGGAGGCCGACAAAGAGA
  1401  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
    TGGTGTATGTCTAGGTTCTTTGGGCGATTCTTGGAGTTCTACGGGCCGAGATGATACACCTGGTGTCTGACCTTTCTTAGTTTCTCCGGCTGTTTCTCT
TagRFP > T T Y R S K K P A K N L K M P G V Y Y V D H R L E R I K E A D K E T
  
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SpDon | BciV1 | **BsrD1**
 GGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGTGCATACGCTTGATCCGGCTACCTGCC
 3101 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3200
 CCCGTCCTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGG

BtgZ1 | BspM1 | BfuA1 | Sap1 | Ear1
 CATTCGACCACCAAGCGAAAACATCGCATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGGCT
 3201 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3300
 GTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCACTAGACCTGCTTCTCGTAGTCCCCGA

BpuE1 | Sph1 | Nco1 | BtgZ1
 CGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTG
 3301 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3400
 GCGCGGTCGGCTTGACAAGCGGTCCGAGTTCGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCAC

BseY1 | Nae1 | NgoM4 | Rsr2 | Eci1 | Sap1 | Ear1
 GAAAATGGCCGCTTTTCTGGATTTCATCGACTGTGGCCGGCTGGGTGTGGCCGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGCTGAAGAGC
 3401 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3500
 CTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCCTGGCGATAGTCCTGTATCGCAACCGATGGGCACCTATAACGACTTCTCG

Eco57 | BssS1 | BtgZ1 | BsrB1
 TTGGCGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTACGAGGTTCTTCTG
 3501 |||||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||*|||* 3600
 AACCGCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGAAGAACTGCTCAAGAAGAC

BspH1
|
4101 AAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAA 4200
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4200
TTCCTAGATCCACTTCTAGGAAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAAGCAAGGTGACTCGCAGTCTGGGGCATCTTTTCTAGTTT

BpuE1
|
4201 GGATCTTCTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAAAACCACCGCTACCAGCGGTGGTTTGTGTTGCCGGATCAAGAGCTAC 4300
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4300
CCTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTGGTGGCGATGGTGCACCACAAACAAACGGCCTAGTTCTCGATG

Eco57
|
4301 CAACTCTTTTCCGAAGGTAAGTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAAGTCTGT 4400
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4400
GTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGTGAAGTTCTTGAGACA

AlwN1
|
4401 AGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGATAGTTA 4500
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4500
TCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTCAGCACAGAATGGCCCAACCTGAGTTCTGCTATCAAT

ApaI1
|
4501 BseY1
|
4501 CCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGC 4600
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4600
GGCCTATTCCCGCTGCCAGCCCAGCTTGGCCCCAAGCACGTGTGTGGGTTCGAACCTCGCTTGTGATGTGGCTTACTCTATGGATGTGCGACTCG

BciV1
|
4601 Ecil
|
4601 BssS1
|
4601 TATGAGAAAGCGCCACGCTTCCCGAAGGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGG 4700
|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 4700
ATACTCTTTCCGGTGCAGAGGGCTTCCCTCTTCCGCCTGTCCATAGGCCATTCCCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCC

```

                SpAcc                Drd1                BpuE1                SpAcc                Eci1
                |                    |                    |                    |                    |
4701 AAACGCCTGGTATCTTTATAGTCCTGTCTGGGTTTTCGCCACCTCTGACTTGAGCGTCGATTTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAAC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
   TTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTG

                SpDon
                BspLU|
                ||
4801 GCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGTGGCCTTTTGTCTCACATGTTCTTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
   CGGTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAAT

                Nsil
                BfrB1 |
                | |
4901 CCGCCATGCAT
   |||||*| 4911
   GGCGGTACGTA
```

Found:

Aat2	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1	BfrB1	BfuA1	Bgl1
Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspE1	BspH1
BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal	Dra1	Dra3
Drd1	Eag1	Ear1	Ecil	Eco57	Fsp1	Hpa1	Kas1	Mfe1	Msc1	Nae1	Nar1	Nco1	Nde1
NgoM4	Nhe1	Not1	Nsil	PflF1	PflM1	polyA	PshA1	Psi1	Pst1	Pvu2	Rsr2	Sac1	Sap1
SexA1	Sfil	SnaB1	SpAcc	SpDon	Sph1	Ssp1	Stu1	Xba1					

Unique:

Afl2	Age1	Ale1	Ase1	BamH1	Bbs1	BsaXa	BsaXb	BseR1	Bsg1	BspE1	BspLU	BsrD1	BsrG1
BstB1	Bts1	Clal	Fsp1	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1	Not1	PflF1	PflM1	PshA1
Pst1	Sac1	SexA1	Sfil	SnaB1	Stu1	Xba1							

Not found:

Aar1	Acc65	Ac11	Afe1	Ahd1	Apa1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b	Bcl1
Bgl2	Blp1	BmgB1	BsiW1	BsmB1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoR1	EcoRV
FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	Hind3	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1
Pme1	Pml1	PspOM	Pvu1	R4atB	R4atL	R4atP	R4atR	Sac2	Sall	SanD1	Sbf1	Scal	Sgf1
SgrA1	Sma1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	PISce	Xcm1	Xho1	Xmn1		

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	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													