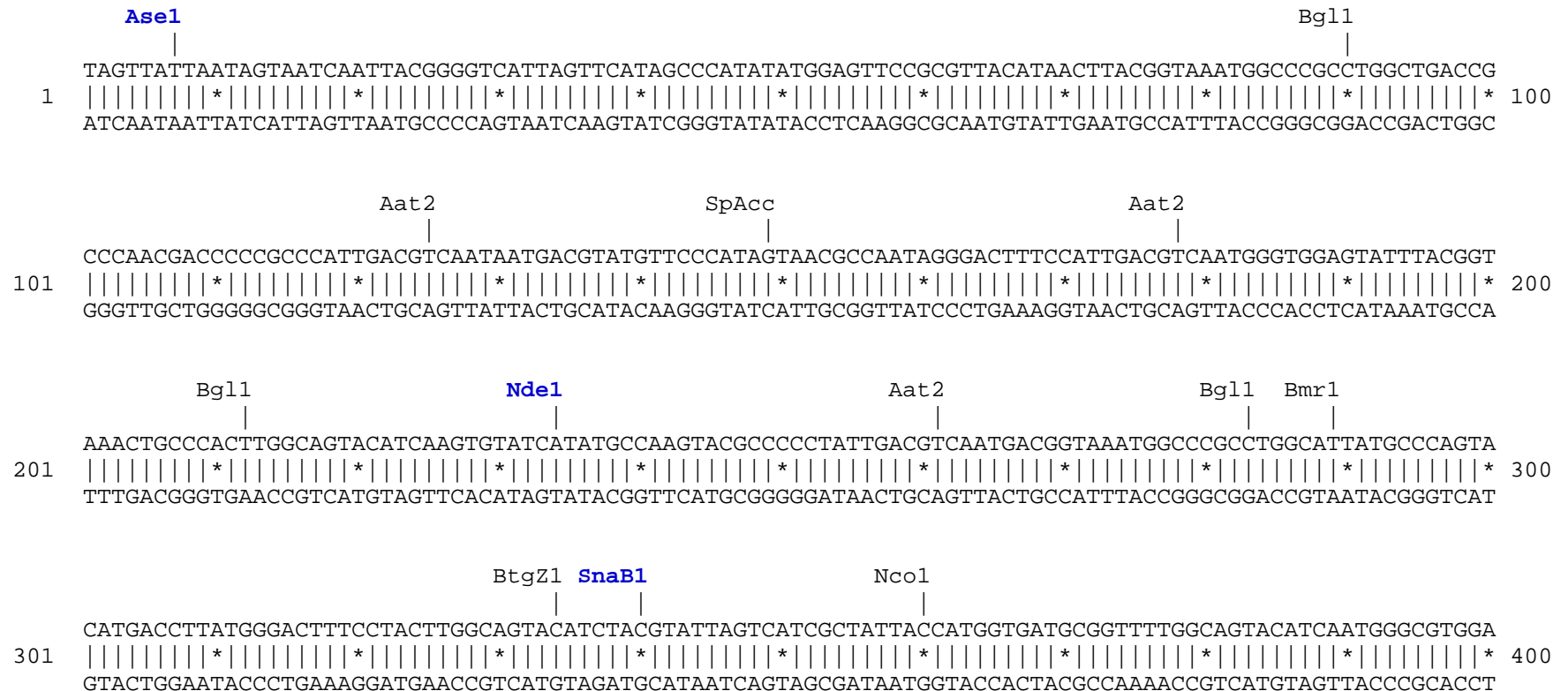


pTagRFP-Cx26 vector restriction map

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, Connexin 26 amino acids are shown in green, linker amino acids are shown in black.



Aat2 | Ecil1
TAGCGGTTTGACTCACGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTTCAGACCAAAAATCAACGGGACTTTCCAAAATGTTCGTA
401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
ATCGCCAAACTGAGTGCCCTAAAGGTTGAGAGGTGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTCAGTTGCCCTGAAAGGTTTTACAGCAT

Nhe1 Afel
ACAACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGCGCTA
501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
TGTGAGGCGGGTAACTGCGTTTACCCGCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

Bcg1b BseR1
Xho1 Hind3 EcoR1 Not1
BpuE1 Bgl2 Sac1 BstB1 Eag1 Bcg1a
CCGACTCAGATCTCGAGCTCAAGCTTTCGAATTCGCGGCCGCACGCTCCTCGGGACACAGTGCCAACCATCCAGAGGACAAGATGGATTGGGGCACACTA
601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
GGCTGAGTCTAGAGCTCGAGTTTCGAAGCTTAAGCGCCGGCGTGCGAGGAGCCCTGTGTCACGGTTGGTAGGTCTCCTGTTCTACCTAACCCCGTGTGAT

Cx26

> M D W G T L

BsaXb _Chi BsaXa Ear1 BspH1 BssS1
CAGAGCATCCTCGGGGTTGTCAACAAGCACTCCACCAGCATTTGGGAAAATCTGGCTCACTGTCTCTTCATCTTCCGCATCATGATCCTCGTGGTGGCCG
701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
GTCTCGTAGGAGCCCCACAGTTGTTTCGTGAGGTGGTTCGTAACCTTTTTCAGACCGAGTGACAGGAGAAGTAGAAGGCGTAGTACTAGGAGCACCACCGGC

Cx26

> Q S I L G G V N K H S T S I G K I W L T V L F I F R I M I L V V A A

Bpm1 SpAcc
CGAAGGAGGTGTGGGAGATGAGCAAGCCGATTTTGTTCGCAACACTCTCCAGCCTGGGTGTAAGAATGTGTGCTACGACCACTACTTCCCCATCTCTCA
801 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
GCTTCTCCACACCCCTCTACTCGTTCGGCTAAAACAAACGTTGAGAGGTCGGACCCGACATTCTTACACACGATGCTGGTGTGTAAGGGGTAGAGAGT

Cx26

> K E V W G D E Q A D F V C N T L Q P G C K N V C Y D H Y F P I S H

Bcl1

Pvu2 | Nae1 |

SpDon | Pst1 | NgoM4 | Pml1 | BspH1 |

901 CATCCGGCTCTGGGCTCTGCAGCTGATCATGGTGTCCACGCCGCCCTCCTGGTAGCTATGCACGTGGCCTACCCGGAGACACGAAAAGAAACGGAAGTTC 1000
 GTAGGCCGAGACCCGAGACGTCGACTAGTACACAGGTGCGGCCGGGAGGACCATCGATACGTGCACCCGGATGGCCTCTGTGCTTTTCTTTGCCTTCAAG
 Cx26 > I R L W A L Q L I M V S T P A L L V A M H V A Y R R H E K K R K F

Ear1 | Sand1 | _Chi |

1001 ATGAAGGGAGAGATAAAGAACGAGTTTAAAGGACATCGAAGAGATCAAAACCAGAAGGTCCGTATCGAAGGGTCCCTGTGGTGGACCTACACCACAGCA 1100
 TACTTCCCTCTCTATTTCTTGCTCAAATTCCTGTAGCTTCTCTAGTTTTGGGTCTTCCAGGCATAGCTTCCAGGGACACCACCTGGATGTGGTGGTTCGT
 Cx26 > M K G E I K N E F K D I E E I K T Q K V R I E G S L W W T Y T T S I

Bbs1 | SpDon | AlwN1 |

BstB1 | SpDonBsrG1 |

1101 TCTTCTTCCGGGTCATCTTCGAAGCTGTCTTCATGTATGTCTTTTACATCATGTACAATGGCTTCTTTCATGCAGCGTCTGGTGAAGTGTAACGCCTGGCC 1200
 AGAAGAAGGCCAGTAGAAGCTTGCACAGAAGTACATACAGAAAATGTAGTACATGTTACCGAAGAAGTACGTGCAGACCACCTTACATTGCGGACCCGG
 Cx26 > F F R V I F E A V F M Y V F Y I M Y N G F F M Q R L V K C N A W P

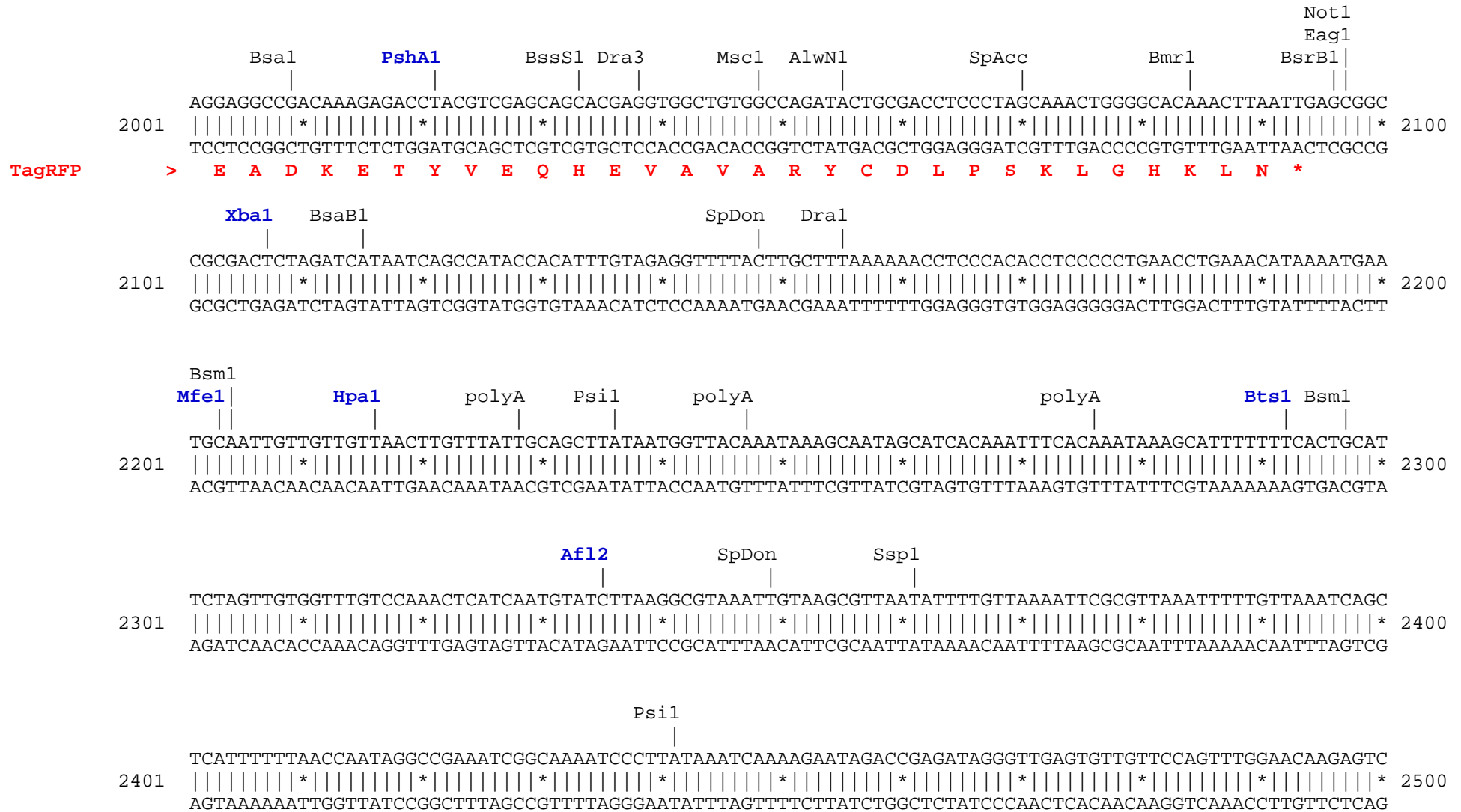
BstX1 | Bbs1 | BspH1 |

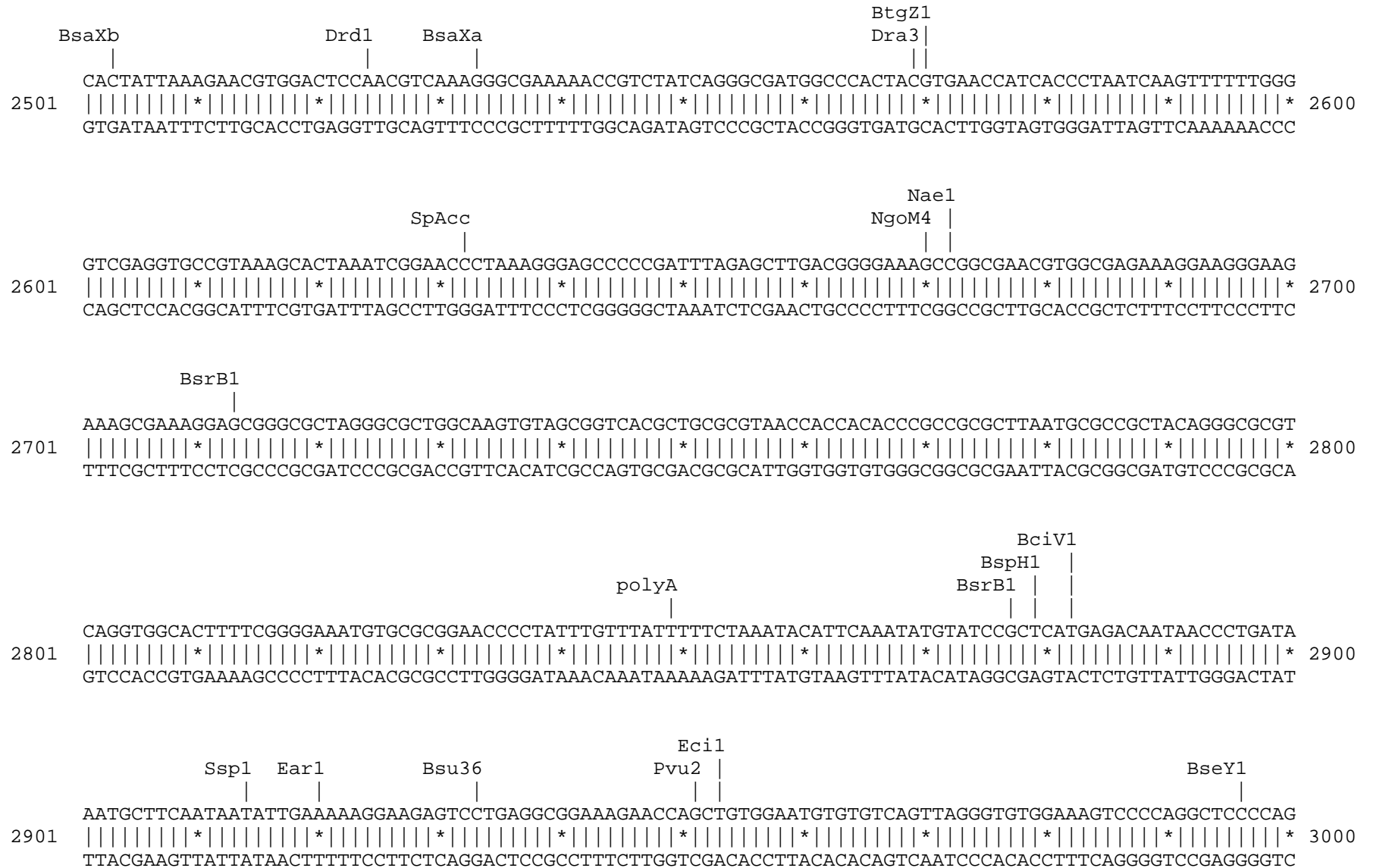
1201 TTGTCCAATACAGTGGACTGCTTTCATTTCCAGGCCACAGAAAAGACTGTCTTCCAGGTGTTTCATGATCTCTGTGTCTGGAATTTGCATCCTGCTAAAC 1300
 AACAGGGTTATGTCACCTGACGAAGTAAAGGTCCGGGTGTCTTTTCTGACAGAAGTCCACAAGTACTAGAGACACAGACCTTAAACGTAGGACGATTTG
 Cx26 > C P N T V D C F I S R P T E K T V F T V F M I S V S G I C I L L N

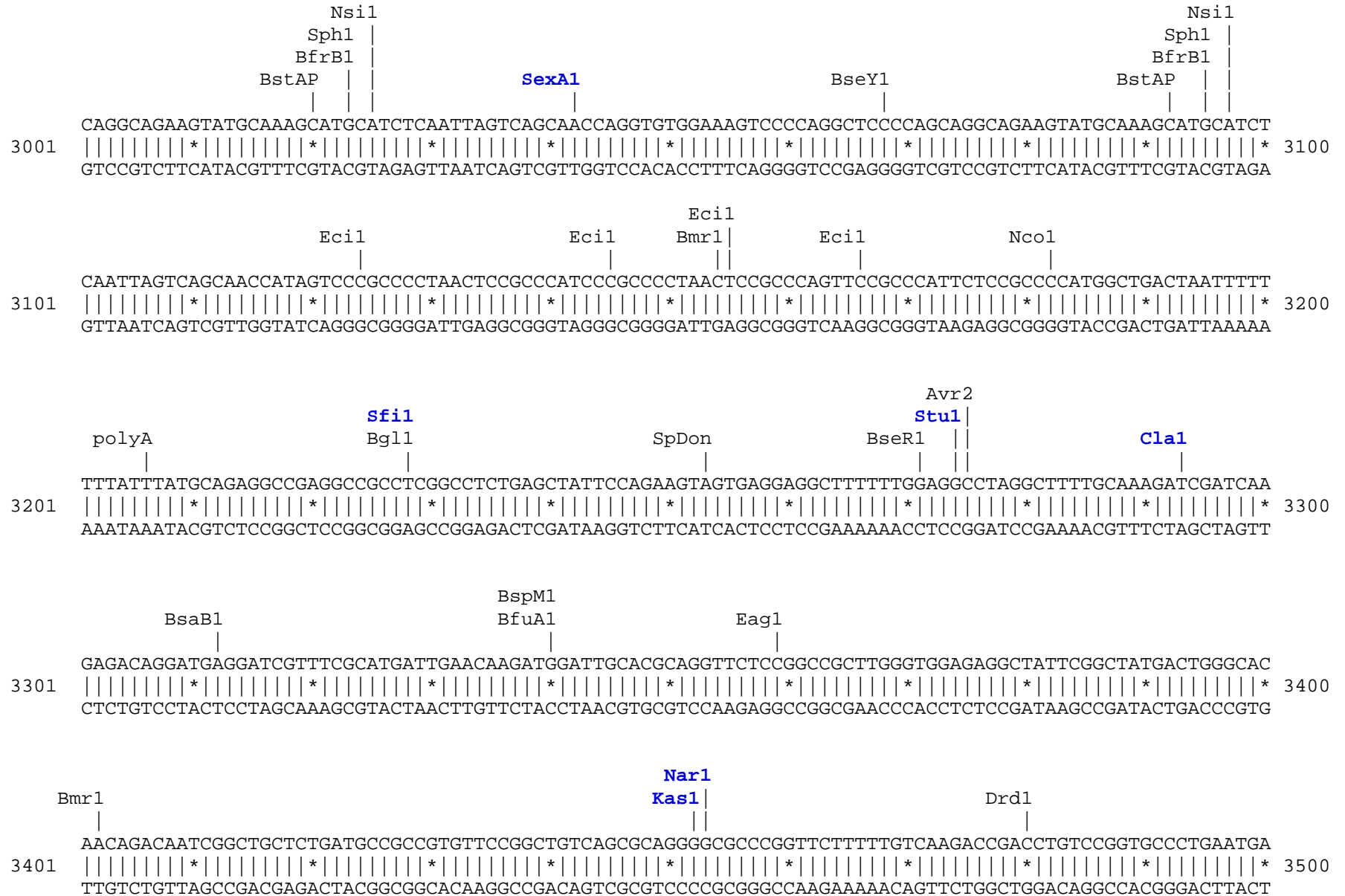
T7Ter | Bpu10 | BamH1 | Age1 | Ale1 | Sap1 |

Nco1 | Ear1 |

1301 ATCACAGAGCTGTGCTATCTGTTTTCATTAGGTTATGCTCAGGGAAGTCCAAAAGACCAGTCGCGGATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAG 1400
 TAGTGTCTCGACACGATAGACAAGTAATCCATAACGAGTCCCTTCAGGTTTTCTGGTCAGCGCCTAGGTGGCCAGCGGTGGTACCACAGATTCCCGCTTC
 Cx26/TagRFP > I T E L C Y L F I R Y C S G K S K R P V A D P P V A T M V S K G E E








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          SapI      Eco57      BssS1      BtgZ1      BsrB1
          EarI
          |          |          |          |          |
4001  GTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGCAGCGCATCGCCTTCTATCGCCT
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4100
      CACTATAACGACTTCTCGAACC GCCGCTTACCCGACTGGCGAAGGAGCACGAAATGCCATAGCGGCGAGGGCTAAGCGTCGCGTAGCGGAAGATAGCGGA

                                     BssS1      BspM1      BfuA1      SpAcc
                                     |          |          |          |
4101  TCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCTTCT
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4200
      AGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGCGGAAGA

                                     NaeI      NgoM4      Bpm1      SpAcc      Bpm1      Avr2
                                     |          |          |          |          |          |          |
4201  ATGAAAAGTTGGGCTTCGGAATCGTTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCTAGGGGGAG
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4300
      TACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTTCGCGCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCTC

                                     polyA      polyA
                                     |          |
4301  GCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTCGTTTGTTCAT
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4400
      CGATTGACTTTGTGCCTTCTCTGTTATGGCCTTCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTTCGCGTGCCACAACCCAGCAAACAAGTA

                                     BsaI
                                     |
4401  AAACGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTTCGATAACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTCTTCTTTTCCCCACCCACC
      |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 4500
      TTTGCGCCCCAAGCCAGGGTCCCGACCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTGG
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                                     BstAP
                                     AlwN1
                                     Bsu36
                                     DraI
4501  CCCC AAGTTCGGGTGAAGGCC CAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4600
      GGGGTTC AAGCCCACTTCCGGGTCCCAGCGTCGGTTGCAGCCCCGCCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATTT

      DraI
      BspH1
4601  ACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4700
      TGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCTG

                                     BpuE1
4701  CCCGTAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCTAATCTGCTGCTTGCAAACAAAAAACACCGCTACCAGCGGTGGTTTGTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4800
      GGCATCTTTTCTAGTTTCTTAGAAGAACTCTAGGAAAAAAGACGCGCATTAGACGACGAACGTTTGTTTTTTTGGTGGCGATGGTCCGCCACCAAACAA

                                     Eco57
                                     SpAcc
4801  TGCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAGTTAGGCCA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4900
      ACGCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGT

                                     AlwN1
                                     BpuE1
4901  CCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5000
      GGTGAAGTTCCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCACCGCTATTGAGCAGAGAATGGCCCAAC

                                     ApaL1
                                     BseY1
5001  GACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAAGTGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 5100
      CTGAGTTCCTGCTATCAATGGCCTATTCCGCGTCGCCAGCCCCGACTTGCACCAAGCACGTGTGTCGGGTCGAACCTCGCTTGTGATGTGGCTTGACT
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                                     BciV1
                                     Eci1
                                     |
                                     |
          SpAcc                       |                       BssS1
          |                             |                       |
GATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTTCGGAACAGGAGAGCGCAC
5101 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5200
CTATGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCGCTGTCCATAGGCCATTTCGCCGTCCCAGCCTTGTCTCTCGCGTG

                                     SpAcc                       Drd1                       BpuE1
                                     |                             |                             |
GAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCTGTGCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGGGG
5201 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5300
CTCCCTCGAAGGTCCCCCTTTGCGGACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCC

                                     SpDon
                                     BspLU
                                     ||
          SpAcc                       Eci1                       |
          |                             |                       |
CGGAGCCTATGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTTCTGCGTTATCCCCTGATT
5301 |||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||*||||||* 5400
GCCTCGGATACCTTTTTGCGGTTCGTTGCGCCGGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAA

                                     Nsi1
                                     BfrB1
                                     |
                                     |
          CTGTGGATAACCGTATTACCGCCATGCAT
5401 |||||||*||||||*||||||*||||||*||||||* 5429
          GACACCTATTGGCATAATGGCGGTACGTA
```

Found:

Aat2	Afe1	Afl2	Age1	Ale1	AlwN1	ApaL1	Ase1	Avr2	BamH1	Bbs1	Bcg1a	Bcg1b	BciV1
Bcl1	BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	Bpu10	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1
BseY1	Bsm1	BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	BstX1	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	PflM1	Pml1
polyA	PshA1	Psi1	Pst1	Pvu2	Rsr2	Sac1	SanD1	Sap1	SexA1	Sfi1	SnaB1	SpAcc	SpDon
Sph1	Ssp1	Stu1	T7Ter	Xba1	Xho1								

Unique:

Afe1	Afl2	Age1	Ale1	Ase1	BamH1	Bcg1a	Bcg1b	Bcl1	Bgl2	Bpu10	BspLU	BsrD1	BstX1
Bts1	Clal	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Mfe1	Nar1	Nde1	Nhe1	PflF1	PflM1	Pml1
PshA1	Pst1	Rsr2	Sac1	SanD1	SexA1	Sfi1	SnaB1	Stu1	T7Ter	Xba1	Xho1		

Not found:

Aar1	Acc65	Acc1	Ahd1	Apal	Asc1	AsiS1	Baela	Baelb	BbvC1	Blp1	BmgB1	Bsg1	BsiW1
BsmB1	BspE1	BssH2	BstE2	BstZ1	EcoK	EcoN1	EcoRV	FCatB	FCatL	FCatR	FCatP	ScFRT	Fse1
FspA1	I_Ceu	Kpn1	loxP	Mlu1	Nru1	Pac1	Pme1	PspOM	Pvu1	R4atB	R4atL	R4atP	R4atR
Sac2	Sall	Sbf1	Scal	Sgf1	SgrA1	Sma1	Spe1	Srf1	Swal	T3RNA	T7RNA	PISce	Xcm1
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	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													