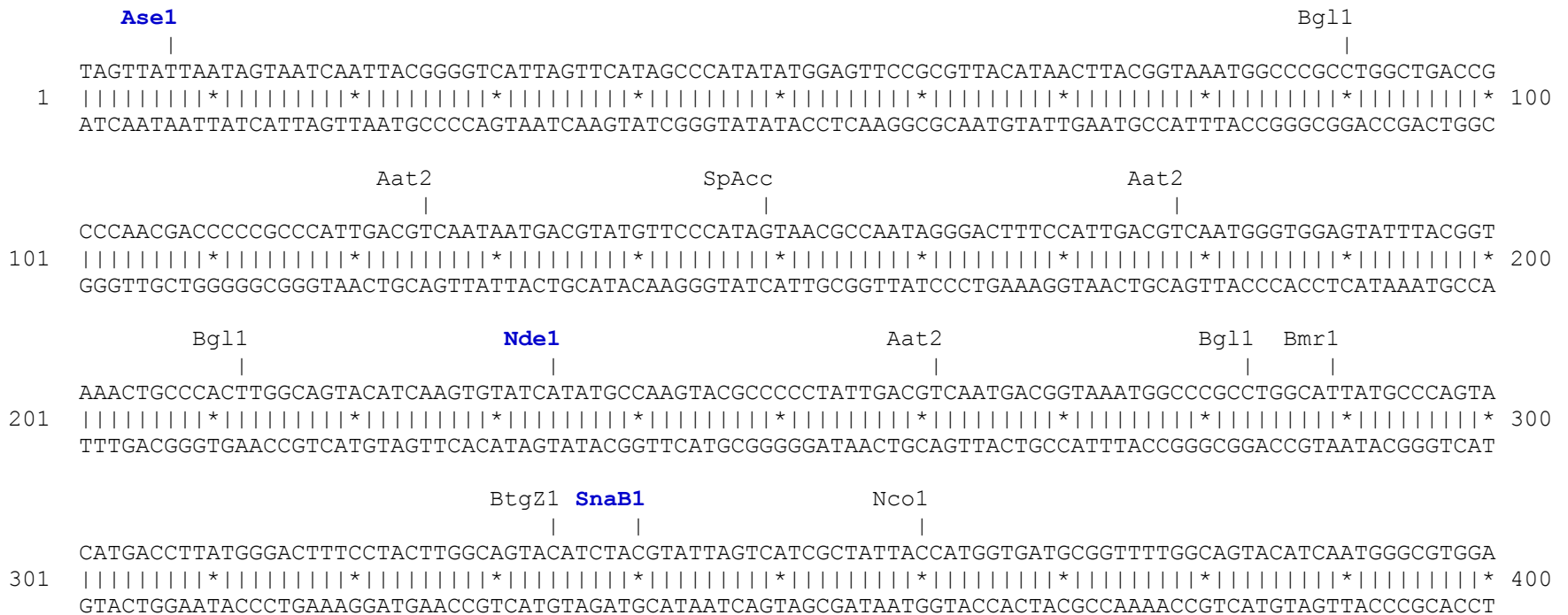


pTagFP635-N vector restriction map

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). MCS sequence is shown in frame, amino acids encoded by MCS are shown in black.



Aat2 | Eci1

401 TAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTTGACGTCAATGGGAGTTTGTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
 ATCGCCAAACTGAGTGCCCTAAAGGTTTCAGAGGTGGGGTAACTGCAGTTACCCTCAAACAAAACCGTGGTTTTAGTTGCCCTGAAAGTTTTACAGCAT

Nhe1 Afel

501 ACAACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCTGGTTTTAGTGAACCGTCAGATCCGCTAGCGCTA
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
 TGTTGAGGCGGGTAACTGCGTTTACCCGCCATCCGCACATGCCACCCTCCAGATATATTCGTCTCGACCAAATCACTTGGCAGTCTAGGCGATCGCGAT

L A L

MCS >

BamH1
Sma1
Apa1
PspOM
Sac2

Xho1 Hind3 EcoR1 Sal1 Kpn1 Ale1 Sap1
BpuE1 Bgl2 Sac1 BstB1 Pst1 Acc65 Age1 Nco1 Ear1

601 CCGGACTCAGATCTCGAGCTCAAGCTTCAAGCTTGAATTCGAGTCGACGGTACCGCGGGCCCGGGATCCACCGGTCGCCACCATGGTGTCTAAGGGCGAAGAGC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
 GGCCCTGAGTCTAGAGCTCGAGTTCGAAGCTTAAGACGTCAGCTGCCATGGCGCCCGGGCCCTAGGTGGCCAGCGGTGGTACCACAGATTCCCCTTCTCG

MCS/TagFP635 > P D S D L E L K L R I L Q S T V P R A R D P P V A T M V S K G E E L

BsrG1 ApaL1 SpAcc

701 TGATTAAGGAGAACATGCACATGAAGCTGTACATGGAGGGCACCGTGAACAACCACCACTTCAAGTGCACATCCGAGGGCGAAGGCAAGCCCTACGAGGG
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 800
 ACTAATTCCTCTTGTACGTGTAATTCGACATGTACCTCCCGTGGCACTTGTGGTGGTGAAGTTCACGTGTAGGCTCCCGCTTCCGTTCCGGGATGCTCCC

TagFP635 > I K E N M 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

801 CACCCAGACCATGAGAATCAAGGTGGTTCGAGGGCGGCCCTCTCCCTTCGCCTTCGACATCCTGGCTACCAGCTTCATGTACGGCAGCAAAACCTTCATC
 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
 GTGGGTCTGGTACTCTTAGTTCACCAGCTCCCGCCGGGAGAGGGGAAGCGGAAGCTGTAGGACCGATGGTTCGAAGTACATGCCGTCGTTTTGGAAGTAG

TagFP635 > 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 M Y G S K T F I


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      BsrB1
      |
2001 GCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2100
      CGCTTTCCTCGCCC GCGATCCC GCGACCGTTCACATCGCCAGTGCGACGCGCATTGGTGGTGTGGGCGGCGCGAATTACGCGGCGATGTCCC GCGCAGTC

                                     polyA
                                     |
                                     BciV1
                                     BspH1 |
                                     BsrB1 | |
                                     | | |
2101 GTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2200
      CACCGTGAAAAGCCCTTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTATTTA

      Ssp1  Ear1      Bsu36      Eci1      Pvu2 |      BseY1
      |    |          |          |          |          |
2201 GCTTCAATAATATTGAAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
      CGAAGTTATTATAACTTTTTCTCTCAGGACTCCGCTTTCTTGGTCGACACCTTACACACAGTCAATCCCACACCTTTTCAGGGGTCCGAGGGGTTCGTC

      Nsi1
      Sph1 |
      BfrB1 |
      BstAP | |
      | | |
2301 GCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      CGTCTTCATACGTTTCGTACGTAGAGTTAATCAGTCGTTGGTCCACACCTTTTCAGGGGTCCGAGGGGTTCGTCCTTCATACGTTTCGTACGTAGAGTT

      Eci1      Eci1      Eci1      Bmr1 |      Eci1      Nco1
      |          |          |          |          |          |
2401 TTAGTCAGCAACCATAGTCCCGCCCTAACTCCGCCCATCCCGCCCTAACTCCGCCCATTTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
      AATCAGTCGTTGGTATCAGGGCGGGGATTGAGGCGGGTAGGGCGGGATTGAGGCGGGTCAAGGCGGGTAAGAGGCGGGGTACCGACTGATTAATAAAAAA

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                Eco57                      SpAcc
                |                          |
4101  CGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGTGGCTTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCA
      |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 4200
      GCCTAGTTCTCGATGGTTGAGAAAAAGGCTTCCATTGACCGAAGTCGTCTCGCGTCTATGGTTTATGACAGGAAGATCACATCGGCATCAATCCGGTGGT

                AlwN1                      BpuE1
                |                          |
4201  CTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCTGCTAATCCTGTTACCACTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGAC
      |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 4300
      GAAGTTCTTGAGACATCGTGGCGGATGTATGGAGCGAGACGATTAGGACAATGGTCACCGACGACGGTCAACCGTATTTCAGCACAGAATGGCCCAACCTG

                ApaL1    BseY1
                |        |
4301  TCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGAT
      |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 4400
      AGTTCTGCTATCAATGGCCTATTCCCGCTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTTCGGGTCGAACCTCGCTTGCTGGATGTGGCTTGACTCTA

                BciV1
                |
                SpAcc          Eci1    |          BssS1
                |             |        |          |
4401  ACCTACAGCGTGAGCTATGAGAAAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAG
      |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 4500
      TGGATGTCGCACTCGATACTCTTTCGCGGTGCGAAGGGCTTCCCTCTTTCGCTGTCCATAGGCCATTCCGCCGTCCAGCCTTGCTCTCTCGCGTGCTC

                SpAcc          Drd1          BpuE1
                |             |             |
4501  GGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGGGGCGG
      |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 4600
      CCTCGAAGGTCCCCCTTTCGCGGACCATAGAAAATATCAGGACAGCCCAAGCGGTGGAGACTGAACTCGCAGCTAAAAACACTACGAGCAGTCCCCCGCC

                SpAcc    Eci1                      SpDon
                |       |                       BspLU
                |       |                       |
4601  AGCCTATGGAAAAACGCCAGCAACCGGCCTTTTTACGGTTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTCTCGGTTATCCCCCTGATTCTG
      |||||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||*||* 4700
      TCGGATACCTTTTTCGCGTCTGCGCCGAAAAATGCCAAGGACCGGAAAAACGACCGGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGAC
  
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                NsiI
                BfrB1 |
                | |
TGGATAACCGTATTACCGCCATGCAT
4701 | | | | | | | | * | | | | | | | * | | | | | | | 4726
ACCTATTGGCATAAATGGCGGTACGTA

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Found:

Aat2	Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Ase1	Avr2	BamH1	Bbs1	BciV1
BfrB1	BfuA1	Bgl1	Bgl2	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsm1
BspH1	BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssS1	BstAP	BstB1	Bsu36	BtgZ1	Bts1	Clal	Dra1
Dra3	Drd1	Eag1	Ear1	Eci1	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Msc1
Nae1	Nar1	Nco1	Nde1	NgoM4	Nhe1	Not1	Nsi1	PflF1	polyA	PshA1	Psi1	PspOM	Pst1
Pvu2	Rsr2	Sac1	Sac2	Sall	Sap1	SexA1	Sfi1	Sma1	SnaB1	SpAcc	SpDon	Sph1	Ssp1
Stu1	Xba1	Xho1											

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	Ase1	BamH1	Bgl2	BsaXa	BsaXb	BseR1	BspLU	BsrD1
BsrG1	Bts1	Clal	EcoR1	Fsp1	Hind3	Hpa1	Kas1	Kpn1	Mfe1	Nar1	Nde1	Nhe1	Not1
PflF1	PshA1	PspOM	Pst1	Rsr2	Sac1	Sac2	Sall	SexA1	Sfi1	Sma1	SnaB1	Xba1	Xho1

Not found:

Aar1	Acl1	Ahd1	Asc1	AsiS1	Baela	Baelb	BbvC1	Bcg1a	Bcg1b	Bcl1	Blp1	BmgB1	Bpu10
Bsg1	BsiW1	BsmB1	BspE1	BssH2	BstE2	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1
FspA1	I_Ceu	loxP	Mlu1	Nru1	Pac1	PflM1	Pme1	Pml1	Pvu1	SanD1	Sbf1	Sca1	Sgf1
SgrA1	Spe1	Srf1	Swal	T3RNA	T7RNA	T7Ter	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	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													