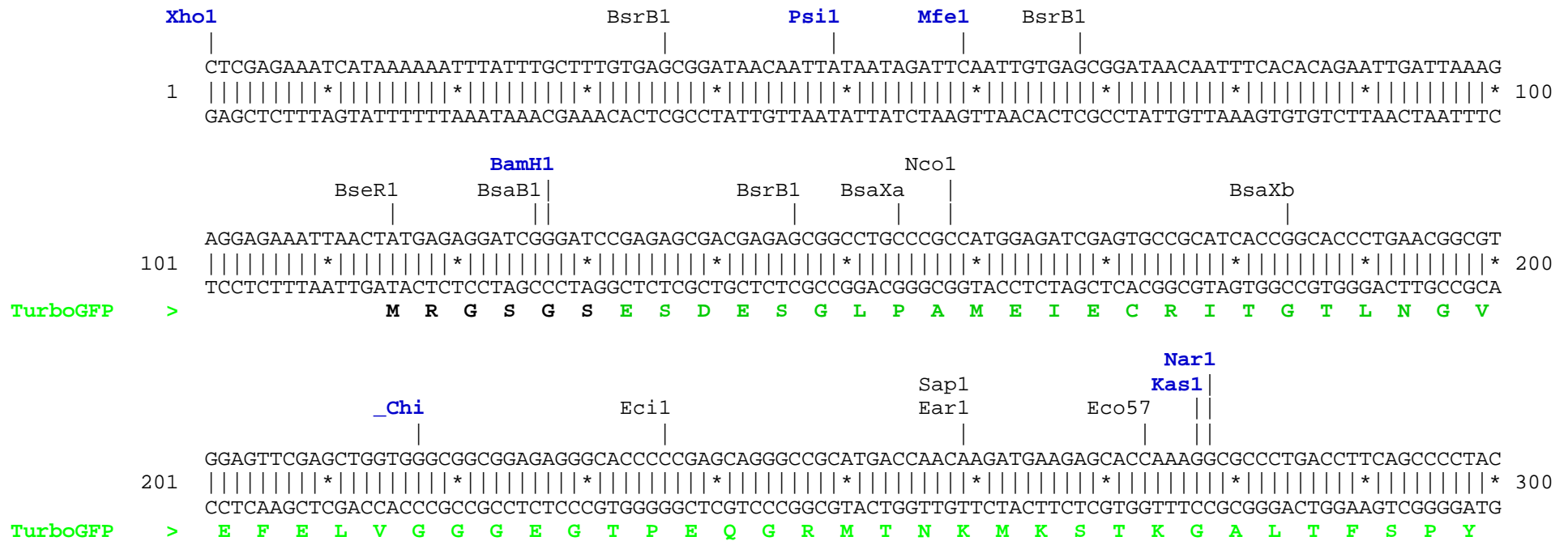


pTurboGFP-B vector restriction map

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). Amino acids coded by vector's backbone sequence are shown in black.



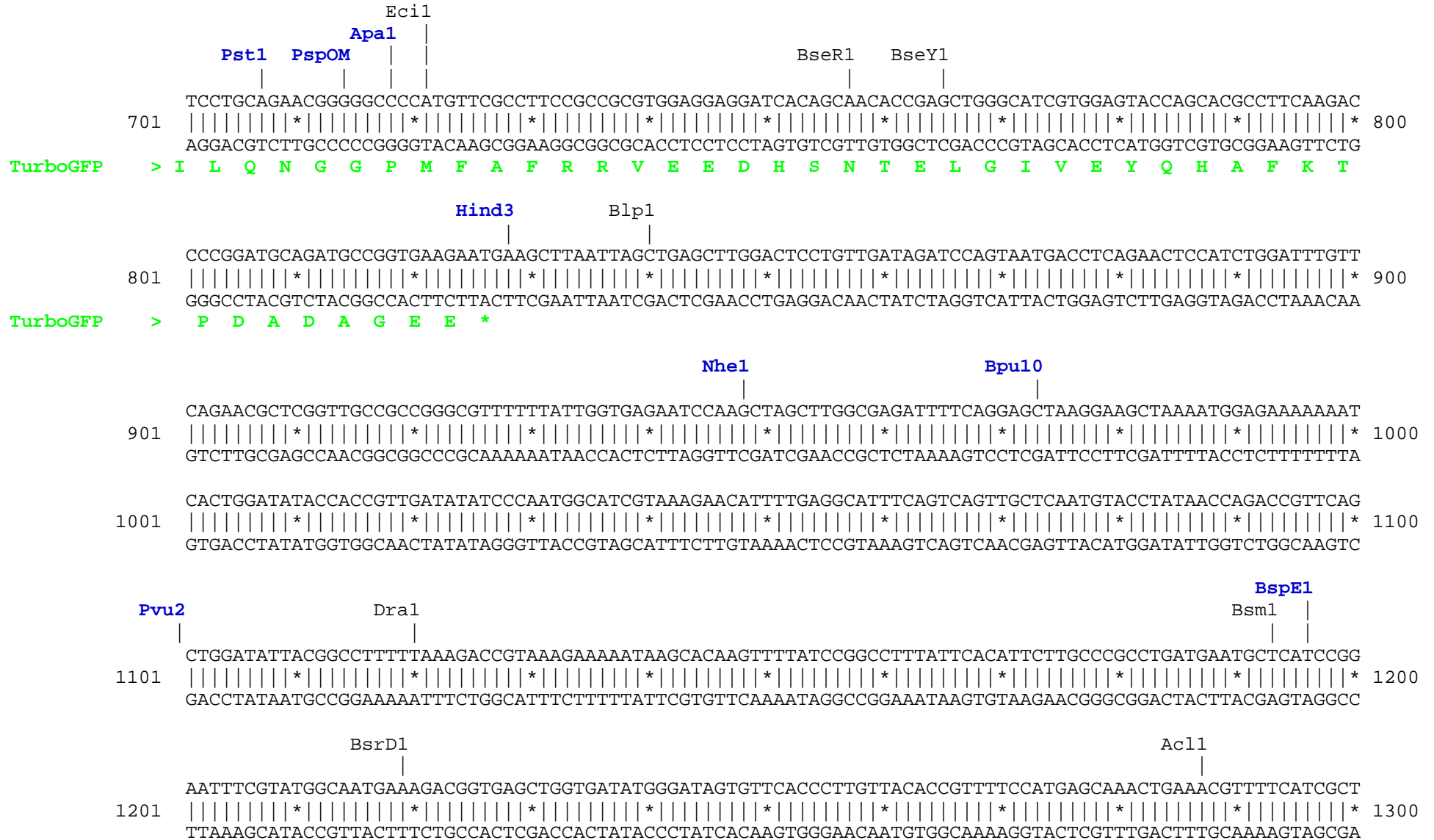
Restriction enzyme sites: PflM1, Pml1, BspM1, BfuA1, Bsp1, BseY1, Bsg1, Xmn1, Fse1, Nae1, Eag1, NgoM4, BsaB1, Nco1, BsaXb, BsaXa, BseY1.

301
CTGCTGAGCCACGTGATGGGCTACGGCTTCTACCACTTCGGCACCTACCCAGCGGCTACGAGAACCCCTTCCTGCACGCCATCAACAACGGCGGCTACA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 400
GACGACTCGGTGCACTACCCGATGCCGAAGATGGTGAAGCCGTGGATGGGGTCGCCGATGCTCTTGGGGAAGGACGTGCGGTAGTTGTTGCCGCCGATGT
TurboGFP > L L S H V M G Y G F Y H F G T Y P S G Y E N P F L H A I N N G G Y

401
CCAACACCCGCATCGAGAAGTACGAGGACGGCGGGCTGCTGCACGTGAGCTTCAGCTACCGCTACGAGGCCGGCCGCGTGATCGGGCACTTCAAGGTGAT
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 500
GGTTGTGGGCGTAGCTCTTCATGCTCCTGCCGCCGACGACGTGCACTCGAAGTCGATGGCGATGCTCCGGCCGGCGCACTAGCCGCTGAAGTTCCACTA
TurboGFP > T N T R I E K Y E D G G V L H V S F S Y R Y E A G R V I G D F K V M

501
GGGCACCGGCTTCCCCGAGGACAGCGTGATCTTCACCGACAAGATCATCCGCAGCAACGCCACCGTGGAGCACCTGCACCCCATGGGCGATAACGATCTG
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 600
CCCGTGGCCGAAGGGGCTCCTGTGCGCACTAGAAGTGGCTGTTCTAGTAGGCGTCTGTTGCGGTGGCACCTCGTGGACGTGGGGTACCCGCTATTGCTAGAC
TurboGFP > G T G F P E D S V I F T D K I I R S N A T V E H L H P M G D N D L

601
GATGGCAGCTTCACCCGACCTTCAGCCTGCGCGACGGCGGCTACTACAGCTCCGTGGTGGACAGCCACATGCACTTCAAGAGCGCCATCCACCCAGCA
|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 700
CTACCGTCGAAGTGGGCGTGAAGTCGGACGCGCTGCCGCCGATGATGTGCGAGGCACCACCTGTGCGGTGTACGTGAAGTTCTCGCGGTAGGTGGGGTCGT
TurboGFP > D G S F T R T F S L R D G G Y Y S S V V D S H M H F K S A I H P S



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          Bpm1
          |
1301  CTGGAGTGAATACCACGACGATTTCCGGCAGTTTCTACACATATATTTCGCAAGATGTGGCGTGTTACGGTGAAAACCTGGCCTATTTCCCTAAAGGGTTT
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1400
      GACCTCACTTATGGTGCTGCTAAAGGCCGTCAAAGATGTGTATATAAGCGTTCTACACCGCACAAATGCCACTTTTGGACCGGATAAAGGGATTTCCCAA

          BsmB1   PflM1
          |       |
1401  ATTGAGAAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACCAGTTTGTGATTTAAACGTGGCCAATATGGACAACCTTCTTCGCCCCGTTTTCA
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1500
      TAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAAACTAAATTTGCACCGGTTATACCTGTTGAAGAAGCGGGGGCAAAAGT

Nco1     Ssp1
|         |
1501  CCATGGGCAAATATTATACGCAAGGGCACAAGGTGCTGATGCCGCTGGCGATTTCAGGTTTCATCATGCCGCTGTGTGATGGCTTCCATGTCGGCAGAATGCT
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1600
      GGTACCCGTTTATAATATGCGTTCCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGACACTACCGAAGGTACAGCCGTTTACGA

Bsm1     Scal
|         |
1601  TAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGCGTAATTTTTTTAAGGCAGTTATTGGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAG
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1700
      ATTACTTAATGTTGTCATGACGCTACTCACCGTCCC GCCCCGATTAAAAAATTCCGTCAATAACCACGGGAATTTGCGGACCCCATTACTGAGAGATC

          BpuE1           Bmr1           Eci1
          |               |               |
1701  CTTGAGGCATCAAATAAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCG
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1800
      GAACTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAACAGCCACTTGCGAGAGGACTCATCCTGTTTATAGGC

Xba1
BsrB1 |
|     |
1801  CCGCTCTAGAGCTGCCTCGCGGTTTTCGGTGATGACGGTGAAAACCTCTGACACATGCAGCTCCCGGAGACGGTCACAGCTTGTCTGTAAGCGGATGCCG
      |||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||*|||||||* 1900
      GCGGAGATCTCGACGGAGCGCGCAAAGCCACTACTGCCACTTTTGGAGACTGTGTACGTCGAGGGCCTCTGCCAGTGTGCGAACAGACATTGCGCTACGGC

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Unique:

Aar1	Aat2	Ahd1	AlwN1	Apa1	Ase1	BamH1	Bbs1	Bcg1a	Bcg1b	Bgl1	Bpu10	Bsa1	BspE1
BspLU	BstAP	BstZ1	_Chi	Eag1	EcoK	Fse1	Fsp1	Hind3	Kas1	Mfe1	Msc1	Nae1	Nar1
Nde1	NgoM4	Nhe1	PflF1	Psi1	PspOM	Pst1	Pvu1	Pvu2	Xba1	Xho1			

Not found:

Acc65	Afe1	Afl2	Age1	Ale1	Asc1	AsiS1	Avr2	Baela	Baelb	BbvC1	Bcl1	BfrB1	Bgl2
BmgB1	BsiW1	BsrG1	BssH2	BstB1	BstE2	BstX1	Bsu36	Clal	Dra3	EcoN1	EcoR1	EcoRV	ScFRT
FspA1	Hpa1	I_Ceu	Kpn1	loxP	Mlu1	Not1	Nru1	Nsi1	Pac1	Pme1	PshA1	Rsr2	Sac1
Sac2	Sall	SanD1	Sbf1	SexA1	Sfi1	Sgf1	SgrA1	Sma1	SnaB1	Spe1	Sph1	Srf1	Stu1
Swal	PISce	Xcm1											

Excluded by site complexity:

Acc1	Ac11	Afl3	Alu1	Alw1	Apo1	Ava1	Ava2	Ban1	Ban2	Bbv1	BceA1	Bfal	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													