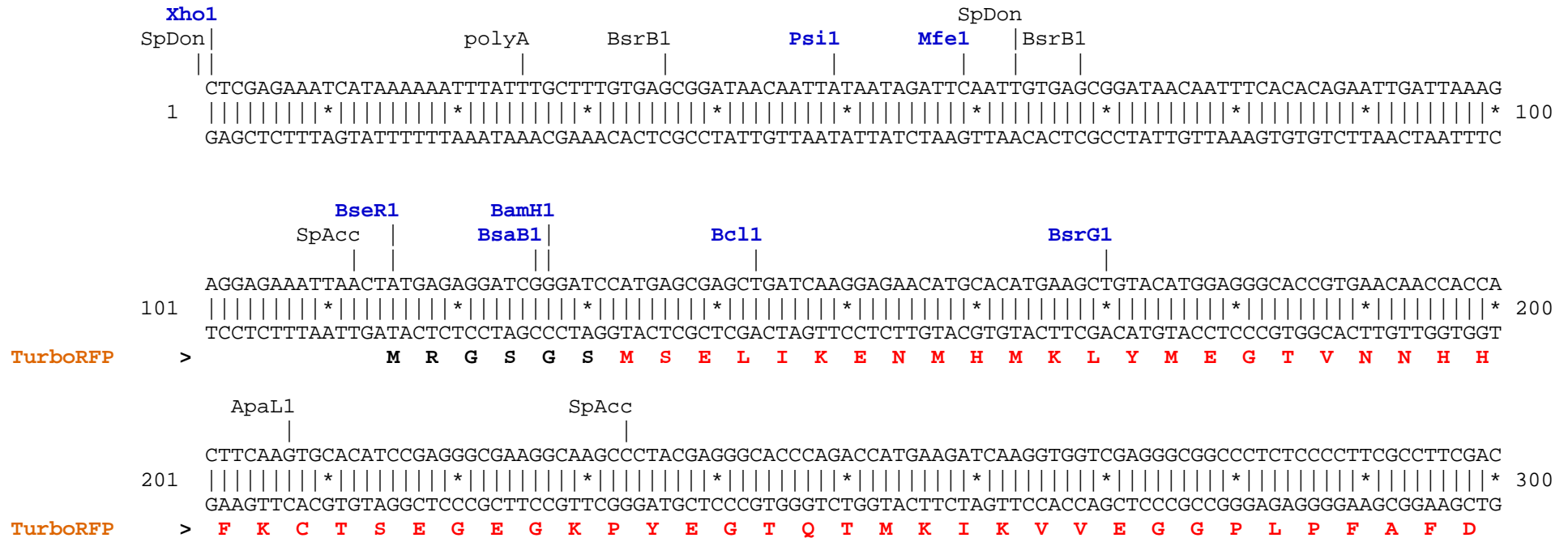


### pTurboRFP-B vector restriction map

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.





```

      SpAcc      Bmr1Hind3      Blp1
      |          |          |
      CCTCCCTAGCAAACCTGGGGCACAGATGAAGCTTAATTAGCTGAGCTTGGACTCCTGTTGATAGATCCAGTAATGACCTCAGAACTCCATCTGGATTTGTT
801  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 900
      GGAGGGATCGTTTGACCCCGTGTCTACTTTCGAATTAATCGACTCGAACCTGAGGACAACCTATCTAGGTCATTACTGGAGTCTTGAGGTAGACCTAAACAA
TurboRFP > L P S K L G H R *

      polyA      Nhe1      Bpu10
      |          |          |
      CAGAACGCTCGGTTGCCGCCGGCGTTTTTTTATTGGTGAGAATCCAAGCTAGCTTGGCGAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAAT
901  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1000
      GTCTTGCGAGCCAACGGCGGCCCGCAAAAAATAACCACTCTTAGGTTTCGATCGAACCGCTCTAAAAGTCTCGATTCTTCGATTTTACCTCTTTTTTTA

      CACTGGATATAACCACCGTTGATATATCCCAATGGCATCGTAAAGAACATTTTGGAGGCATTTTCAGTCAGTTGCTCAATGTACCTATAACCAGACCGTTTCAG
1001  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1100
      GTGACCTATATGGTGGCAACTATATAGGGTTACCGTAGCATTTCTTGTAAAACTCCGTAAAGTCAGTCAACGAGTTACATGGATATTGGTCTGGCAAGTC

      Pvu2      Dra1      SpDon      BspE1
      |          |          |          |          |          |
      CTGGATATTACGGCCTTTTTTAAAGACCGTAAAGAAAAATAAGCACAAAGTTTTATCCGGCCTTTATTACATTCTTGCCCGCCTGATGAATGCTCATCCGG
1101  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
      GACCTATAATGCCGGAATAATTTCTGGCATTCTTTTTTATTTCGTGTTCAAATAGGCCGGAAATAAGTGTAAGAACGGGCGGACTACTTACGAGTAGGCC

      BsrD1      BtgZ1      Acl1
      |          |          |
      AATTTTCGTATGGCAATGAAAAGACGGTGAGCTGGTGATATGGGATAGTGTTCACCCCTTGTTACACCGTTTTCCATGAGCAAACCTGAAAACGTTTTTCATCGCT
1201  |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
      TTAAAGCATACCGTTACTTTCTGCCACTCGACCACTATACCCTATCACAAGTGGGAACAATGTGGCAAAAGGTACTCGTTTGACTTTGCAAAAGTAGCGA

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

polyA          BsmB1    PflM1          SpDon          Dra1    Msc1
|              |        |              |              |        |
ATFGAGAAATATGTTTTTCGTCTCAGCCAATCCCTGGGTGAGTTTCACACAGTTTGGATTAAACGTGGCCAATATGGACAACCTTCTTCGCCCCGTTTTCA
1401 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
TAACTCTTATACAAAAAGCAGAGTCGGTTAGGGACCCACTCAAAGTGGTCAAAACTAAATTTGCACCGTTTATACCTGTTGAAGAAGCGGGGGCAAAGT

SpDon
Nco1          Ssp1
|              |
CCATGGGCAAATATTTATACGCAAGGCGACAAGGTGCTGATGCCGCTGGCGATTTCAGTTTCATCATGCCGTCTGTGATGGCTTCCATGTCGGCAGAATGCT
1501 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
GGTACCCGTTTATAATATGCGTTCCGCTGTTCCACGACTACGGCGACCGCTAAGTCCAAGTAGTACGGCAGACACTACCGAAGGTACAGCCGTCTTACGA

Bsm1          Scal          BtgZ1
|              |              |
TAATGAATTACAACAGTACTGCGATGAGTGGCAGGGCGGGCGTAATTTTTTTTAAAGGCAGTTATTGGTGCCCTTAAACGCCTGGGGTAATGACTCTCTAG
1601 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
ATTACTTAATGTTGTCATGACGCTACTCACCGTCCC GCCCGCATTAATAAATTCGTCATAAACCACGGGAATTTGCGGACCCCATTAAGTACTGAGAGATC

polyA          BpuE1          Bmr1T7Ter          Eci1
|              |              |              |
CTTGAGGCATCAAAATAAACGAAAGGCTCAGTCGAAAGACTGGGCCTTTTCGTTTTATCTGTTGTTTGTGCGGTGAACGCTCTCCTGAGTAGGACAAATCCG
1701 |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1800
GAACTCCGTAGTTTATTTTGCTTTCCGAGTCAGCTTTCTGACCCGAAAGCAAATAGACAACAAACAGCCACTTGCAGAGAGGACTCATCCTGTTTAGGC

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      BpuE1          Drd1          SpAcc          BssS1
      |             |             |             |
2301 GACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAAACCCGACAGGACTATAAAGATAACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
      CTGCTCGTAGTGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTTGGGCTGTCCTGATATTTCTATGGTCCGCAAAGGGGGACCTTCGAGGGAGCACGCGA

      BciV1  Eci1
      |      |
2401 CTCTGTTCGGACCCCTGCCGCTTACCGGATACCTGTCCGCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
      GAGGACAAGGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGGAAGCCCTTCGCACCGCGAAAGAGTTACGAGTGCGACATCCATAGAGTCAAG

      BseY1      ApaL1
      |          |
2501 GGTGTAGGTCGTTTCGCTCCAAGCTGGGCTGTGTGCACGAACCCCCCGTTTCAGCCCGACCGCTGCGCCTTATCCGGTA ACTATCGTCTTGAGTCCAACCCG
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
      CCACATCCAGCAAGCGAGGTTTCGACCCGACACACGTGCTTGGGGGGCAAGTCGGGCTGGCGACGCGGAATAGGCCATTGATAGCAGAACTCAGGTTGGGC

      BpuE1          AlwN1
      |             |
2601 GTAAGACACGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCTA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
      CATTCTGTGCTGAATAGCGGTGACCGTCGTCGGTGACCATTGTCCTAATCGTCTCGCTCCATACATCCGCCACGATGTCTCAAGAACTTCACCACCGGAT

      SpAcc          Eco57
      |             |
2701 ACTACGGCTACACTAGAAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAACAAAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
      TGATGCCGATGTGATCTTCCTGTCATAAACCATAGACGCGAGACGACTTCGGTCAATGGAAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTTTG
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          SpDon SpDon
          |     |
3801 TCTTTTACTTTTACCAGCGTTTCTGGGTGAGCAAAAAACAGGAAGGCAAAATGCCGCAAAAAAGGGAATAAGGGCGACACGGAAATGTTGAATACTCATAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
      AGAAAAATGAAAGTGGTCGCAAAGACCCACTCGTTTTTGTCTTCCGTTTTACGGCGTTTTTCCCTTATTCCCGCTGTGCCTTTACAACCTTATGAGTATG

                                     BsrB1
                                     |
          BciV1
          |
          BspH1 |
Earl      Ssp1
|         |
3901 TCTTCCTTTTTCAATATTATTGAAGCATTATCAGGGTTATTGTCTCATGAGCGGATACATATTTGAATGTATTTAGAAAAATAAACAAATAGGGGTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
      AGAAGGAAAAAGTTATAATAACTTCGTAAATAGTCCCAATAACAGAGTACTCGCCTATGTATAAACTTACATAAATCTTTTTATTTGTTTATCCCCAAGG

                                     Aat2
                                     |
                                     BspH1
                                     |
                                     SpAcc
                                     |
                                     BssS1
                                     |
                                     Bbs1
                                     |
4001 GCGCACATTTCCCCGAAAAGTGCCACCTGACGTCTAAGAAACCATTATTATCATGACATTAACCTATAAAAAATAGGCGTATCACGAGGCCCTTTTCGTCTT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
      CGCGTGTAAGGGGCTTTTCACGGTGGACTGCAGATTCTTTGGTAATAATAGTACTGTAATTGGATATTTTATCCGCATAGTGCTCCGGGAAAGCAGAA

4101 CAC
      ||| 4103
      GTG
  
```

Found:

|              |              |             |              |              |              |              |              |              |              |              |              |              |             |
|--------------|--------------|-------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|--------------|-------------|
| <b>Aat2</b>  | AcI1         | <b>Ahd1</b> | <b>AlwN1</b> | ApaL1        | <b>Ase1</b>  | <b>BamH1</b> | Bbs1         | <b>Bcg1a</b> | <b>Bcg1b</b> | BciV1        | <b>Bcl1</b>  | <b>BfuA1</b> | Bgl1        |
| <b>Blp1</b>  | Bmr1         | Bpm1        | <b>Bpu10</b> | BpuE1        | Bsa1         | <b>BsaB1</b> | <b>BseR1</b> | BseY1        | <b>Bsg1</b>  | Bsm1         | BsmB1        | <b>BspE1</b> | BspH1       |
| <b>BspLU</b> | <b>BspM1</b> | BsrB1       | BsrD1        | <b>BsrG1</b> | BssS1        | <b>BstAP</b> | <b>BstZ1</b> | <b>Bsu36</b> | BtgZ1        | Bts1         | Dra1         | <b>Dra3</b>  | Drd1        |
| Ear1         | Eci1         | Eco57       | <b>EcoK</b>  | <b>Fsp1</b>  | <b>Hind3</b> | <b>Mfe1</b>  | Msc1         | <b>Nco1</b>  | <b>Nde1</b>  | <b>Nhe1</b>  | <b>PflF1</b> | PflM1        | polyA       |
| <b>PshA1</b> | <b>Psi1</b>  | <b>Pvu1</b> | <b>Pvu2</b>  | <b>Sap1</b>  | Sca1         | <b>Sfi1</b>  | SpAcc        | SpDon        | Ssp1         | <b>T7Ter</b> | <b>Xba1</b>  | <b>Xho1</b>  | <b>Xmn1</b> |

Unique:

|       |       |       |       |       |       |       |      |       |      |       |       |       |      |
|-------|-------|-------|-------|-------|-------|-------|------|-------|------|-------|-------|-------|------|
| Aat2  | Ahd1  | AlwN1 | Ase1  | BamH1 | Bcg1a | Bcg1b | Bcl1 | BfuA1 | Blp1 | Bpu10 | BsaB1 | BseR1 | Bsg1 |
| BspE1 | BspLU | BspM1 | BsrG1 | BstAP | BstZ1 | Bsu36 | Dra3 | EcoK  | Fsp1 | Hind3 | Mfe1  | Nco1  | Nde1 |
| Nhe1  | PflF1 | PshA1 | Psi1  | Pvu1  | Pvu2  | Sap1  | Sfi1 | T7Ter | Xba1 | Xho1  | Xmn1  |       |      |

Not found:

|       |       |       |       |       |       |       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Aar1  | Acc65 | Afe1  | Afl2  | Age1  | Ale1  | Apa1  | Asc1  | AsiS1 | Avr2  | Baela | Baelb | BbvC1 | BfrB1 |
| Bgl2  | BmgB1 | BsaXa | BsaXb | BsiW1 | BssH2 | BstB1 | BstE2 | BstX1 | _Chi  | Clal  | Eag1  | EcoN1 | EcoR1 |
| EcoRV | ScFRT | Fse1  | FspA1 | Hpa1  | I_Ceu | Kas1  | Kpn1  | loxP  | Mlu1  | Nae1  | Nar1  | NgoM4 | Not1  |
| Nru1  | Nsi1  | Pac1  | Pme1  | Pml1  | PspOM | Pst1  | Rsr2  | Sac1  | Sac2  | Sall  | SanD1 | Sbf1  | SexA1 |
| Sgf1  | SgrA1 | Sma1  | SnaB1 | Spe1  | Sph1  | Srf1  | Stu1  | Swal  | T3RNA | T7RNA | PISce | Xcm1  |       |

Excluded by site complexity:

|       |       |       |       |       |       |       |       |       |       |       |       |       |       |
|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|
| Acc1  | Ac11  | 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 |       |       |       |       |       |       |       |       |       |       |       |       |       |