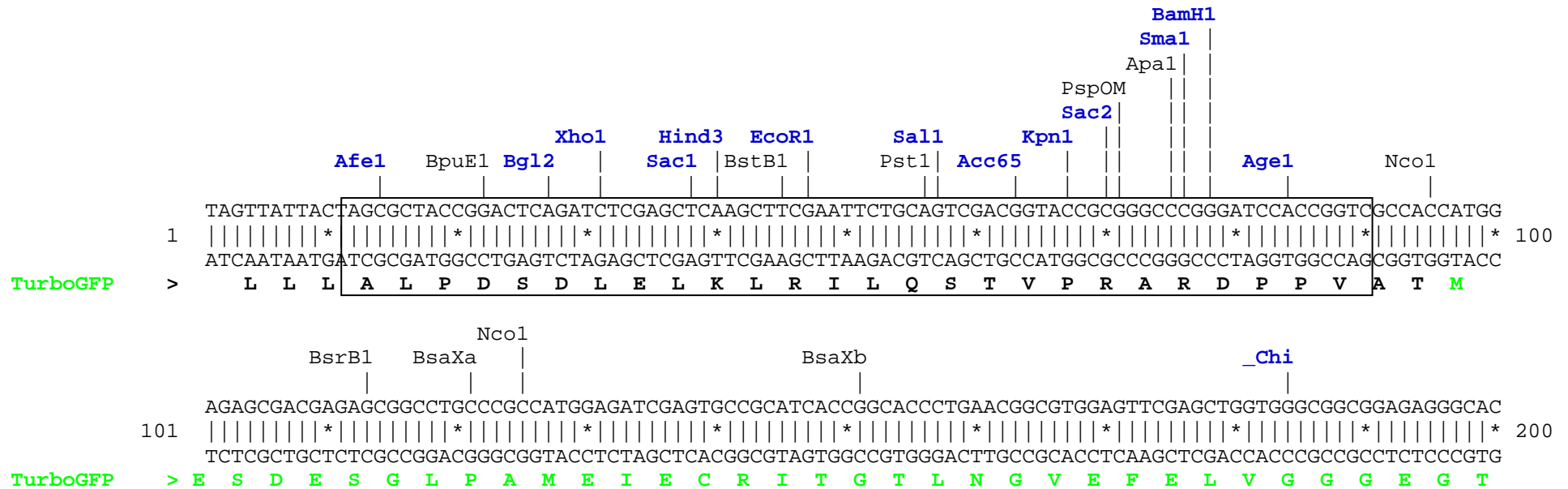


**pTurboGFP-PRL vector restriction map**

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).

MCS sequence shown in frame, amino acids coded by MCS shown in bold black.







```

                                Psil
                                |
1101 CTCATTTTTTTAACCAATAGGCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGAACAAGAGT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1200
    GAGTAAAAAATTGGTTATCCGGCTTTAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAAACAAGGTCAAACCTTGTTCTCA

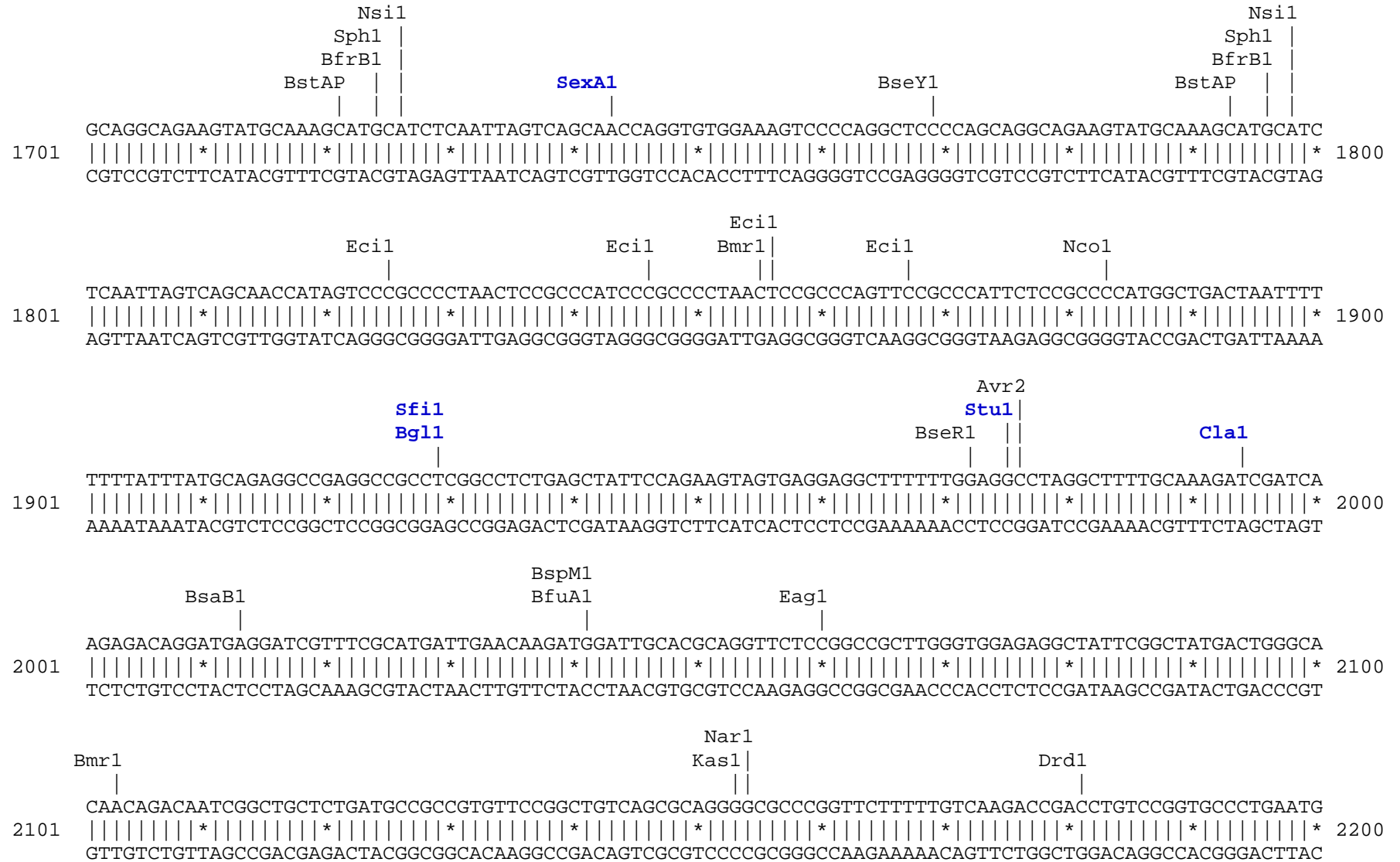
BsaXb          Drd1      BsaXa          Dra3
|              |         |              |
1201 CCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1300
    GGTGATAATTTCTTGCACCTGAGGTTGCAGTTTCCCCTTTTTGGCAGATAGTCCCCTACCGGGTGATGCACCTGGTAGTGGGATTAGTTCAAAAAACC

                                NaeI
                                |
                                NgoM4
                                |
1301 GGTTCGAGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1400
    CCAGCTCCACGGCATTTCGTGATTTAGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCCTTCCCTT

BsrB1
|
1401 GAAAGCGAAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACAGCTGCGCGTAACCACCACACCCGCCGCTTAATGCGCCGCTACAGGGCGCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1500
    CTTTCGCTTTCCTCGCCCGATCCCAGCACCCTTACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGGAATTACGCGGCGATGTCCCAGCGC

                                BciV1
                                |
                                BspH1
                                |
                                BsrB1
                                |
1501 TCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1600
    AGTCCACCGTGAAAAGCCCTTTACACGCGCCTTGGGGATAAAACAAATAAAAAGATTTATGTAAGTTTATACATAGGCGAGTACTCTGTTATTGGGACTA

                                EciI
                                |
                                Ssp1  Ear1      Bsu36          Pvu2  BseY1
                                |    |         |              |         |
1601 AAATGCTTCAATAATATTGAAAAAGGAAGAGTCCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 1700
    TTTACGAAGTTATTATAACTTTTTCTTCTCAGGACTCCGCTTTCTTGGTGCACACCTTACACACAGTCAATCCCACACCTTTCAGGGGTCCGAGGGGT
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                                                                 BssS1
                                                                 BspM1
                                                                 BfuA1
          BsrB1          BstB1
          |              |
2801  TTCTTGACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCGATTCCACCGCCGCCTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2900
      AAGAACTGCTCAAGAAGACTCGCCCTGAGACCCCAAGCTTTACTGGCTGGTTCGCTGCGGGTTGGACGGTAGTGCTCTAAAGCTAAGGTGGCGGGCGGAAG

                                                                 NaeI
                                                                 NgoM4
                                                                 Bpm1
                                                                 Bpm1
                                                                 Avr2
                                                                 |
2901  TATGAAAGGTTGGGCTTCGGAATCGTTTTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCACCCCTAGGGGGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3000
      ATACTTTCCAACCCGAAGCCTTAGCAAAAGGCCCTGCGGCCGACCTACTAGGAGGTCGCGCCCCTAGAGTACGACCTCAAGAAGCGGGTGGGATCCCCCT

3001  GGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACGGCAATAAAAAAGACAGAATAAAACGCACGGTGTGGGTTCGTTTGTTC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3100
      CCGATTGACTTTGTGCCTTCCTCTGTTATGGCCTTCCTTGGGCGCGATACTGCCGTTATTTTTCTGTCTTATTTTTCGTGCCACAACCCAGCAAACAAGT

                                                                 BsaI
                                                                 |
3101  TAAACGCGGGGTTTCGGTCCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTCTTCCTTTTCCCCACCCAC
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3200
      ATTTGCGCCCAAGCCAGGGTCCCAGCCGTGAGACAGCTATGGGGTGGCTCTGGGGTAACCCCGTTATGCGGGCGCAAAGAAGGAAAAGGGGTGGGGTG

                                                                 BstAP
                                                                 AlwN1
                                                                 Bsu36
                                                                 DraI
3201  CCCCCAAGTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3300
      GGGGGTTCAAGCCCACTTCCGGGTCCCAGCGTTCGGTTGCAGCCCCGCGTCCGGGACGGTATCGGAGTCCAATGAGTATATATGAAATCTAACTAAATT

          DraI          BspH1
          |              |
3301  AACTTCATTTTAAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTCATGACCAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGA
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3400
      TTGAAGTAAAAATTAATTTTCTAGATCCACTTCTAGGAAAACTATTAGAGTACTGGTTTTAGGGAATTGCACTCAAAGCAAGGTGACTCGCAGTCT

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                Ecil                               BspLU
                |                                   |
4001  GCGGAGCCTATGGAAAAACGCCAGCAACGGCCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGAT
      |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
      CGCCTCGGATACCTTTTTGCGGTCGTTGCGCCGAAAAATGCCAAGGACCGAAAAACGACCGAAAAACGAGTGTACAAGAAAGGACGCAATAGGGGGACTA

                Nsil
                BfrB1 |
                | |
4101  TCTGTGGATAACCGTATTACCGCCATGCAT
      |||||*|||||*|||||* 4130
      AGACACCTATTGGCATAATGGCGGTACGTA
  
```

Found:

<a href="#">Aar1</a>	<a href="#">Acc65</a>	<a href="#">Afe1</a>	<a href="#">Afl2</a>	<a href="#">Age1</a>	AlwN1	Apa1	<a href="#">ApaL1</a>	Avr2	<a href="#">BamH1</a>	BciV1	BfrB1	BfuA1	<a href="#">Bgl1</a>
<a href="#">Bgl2</a>	<a href="#">Blp1</a>	Bmr1	Bpm1	BpuE1	<a href="#">Bsa1</a>	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspH1
<a href="#">BspLU</a>	BspM1	BsrB1	<a href="#">BsrD1</a>	BssS1	BstAP	BstB1	Bsu36	<a href="#">Bts1</a>	<a href="#">_Chi</a>	<a href="#">Cla1</a>	Dra1	<a href="#">Dra3</a>	Drd1
Eag1	Ear1	Ecil	Eco57	<a href="#">EcoR1</a>	<a href="#">Fse1</a>	<a href="#">Fsp1</a>	<a href="#">Hind3</a>	<a href="#">Hpa1</a>	Kas1	<a href="#">Kpn1</a>	<a href="#">Mfe1</a>	<a href="#">Msc1</a>	Nae1
Nar1	Nco1	NgoM4	<a href="#">Not1</a>	Nsil	<a href="#">PflF1</a>	<a href="#">PflM1</a>	Pml1	Psi1	PspOM	Pst1	Pvu2	<a href="#">Rsr2</a>	<a href="#">Sac1</a>
<a href="#">Sac2</a>	<a href="#">Sal1</a>	Sap1	<a href="#">SexA1</a>	<a href="#">Sfi1</a>	<a href="#">Sma1</a>	Sph1	Ssp1	<a href="#">Stu1</a>	<a href="#">Xba1</a>	<a href="#">Xho1</a>	<a href="#">Xmn1</a>		

Unique:

Aar1	Acc65	Afe1	Afl2	Age1	ApaL1	BamH1	Bgl1	Bgl2	Blp1	Bsa1	BspLU	BsrD1	Bts1
_Chi	Clal	Dra3	EcoR1	Fse1	Fsp1	Hind3	Hpa1	Kpn1	Mfe1	Msc1	Not1	PflF1	PflM1
Rsr2	Sac1	Sac2	Sall	SexA1	Sfi1	Sma1	Stu1	Xba1	Xho1	Xmn1			

Not found:

Aat2	Acl1	Ahd1	Ale1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1
BmgB1	Bpu10	BsiW1	BsmB1	BspE1	BsrG1	BssH2	BstE2	BstX1	BstZ1	EcoK	EcoN1	EcoRV	ScFRT
FspA1	I_Ceu	loxP	Mlu1	Nde1	Nhe1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Scal
Sgf1	SgrA1	SnaB1	Spe1	Srf1	Swal	PISce	Xcm1						

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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													