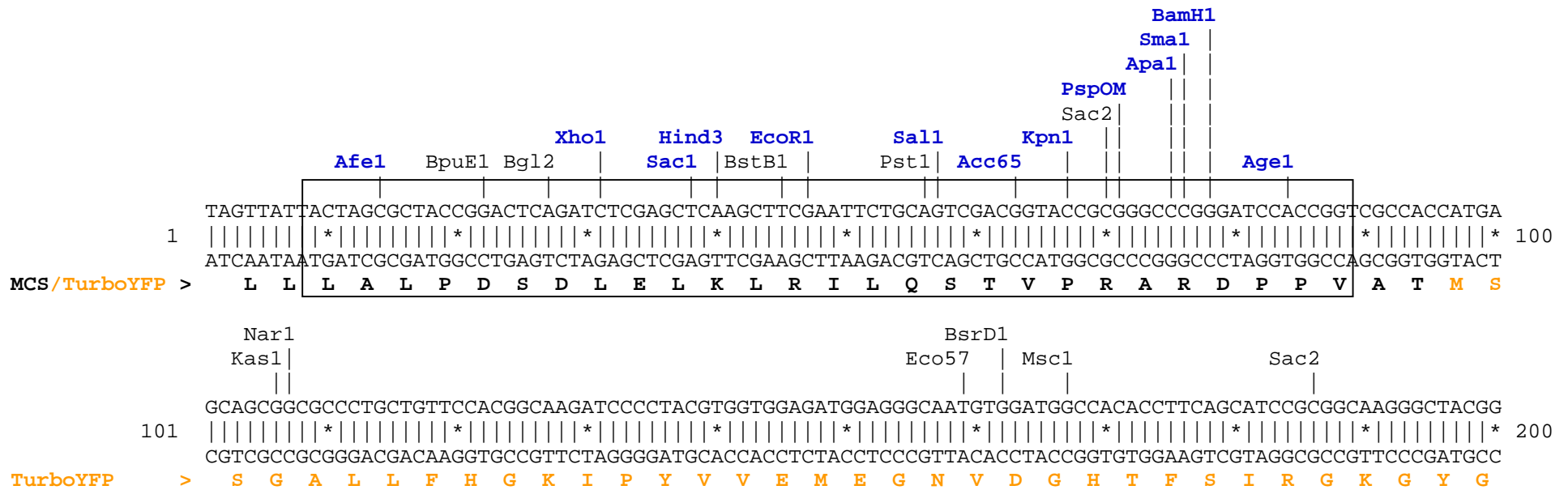


**pTurboYFP-PRL-dest1 vector** restriction map

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 shown in frame, amino acids coded by MCS and MODC amino acids are shown in bold black.



Restriction enzyme sites: BtgZ1, Bsg1, Bmr1, SgrA1, BtgZ1, BstE2, Ale1, Bpm1, Nar1, Kas1, Bmr1

CGATGCCAGCGTGGGCAAGGTGGATGCCCAGTTCATCTGCACCACCGGCGATGTGCCCGTGCCCTGGAGCACCCCTGGTGACCACCCTGACCTACGGCGCC  
201 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 300  
GCTACGGTCGCACCCGTTCCACCTACGGGTCAAGTAGACGTGGTGGCCGCTACACGGGCACGGGACCTCGTGGGACCCTGGTGGGACTGGATGCCGCGG  
TurboYFP > D A S V G K V D A Q F I C T T G D V P V P W S T L V T T L T Y G A

Restriction enzyme sites: SpAcc, Xmn1, Eco57, Sph1, Bsg1

CAGTGCTTCGCCAAGTACGGCCCCGAGCTGAAGGATTTCTACAAGAGCTGCATGCCCGATGGCTACGTGCAGGAGCGCACCATCACCTTCGAGGGCGATG  
301 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 400  
GTCACGAAGCGGTTTCATGCCGGGGCTCGACTTCTAAAGATGTTCTCGACGTACGGGCTACCGATGCACGTCCTCGCGTGGTAGTGGAAGCTCCCGCTAC  
TurboYFP > Q C F A K Y G P E L K D F Y K S C M P D G Y V Q E R T I T F E G D G

Restriction enzyme sites: BtgZ1, BstE2, BsrG1, Msc1, PflM1, BseY1, Pml1

GCAATTTCAAGACCCGCGCCGAGGTGACCTTCGAGAATGGCAGCGTGTACAATCGCGTGAAGCTGAATGGCCAGGGCTTCAAGAAGGATGGCCACGTGCT  
401 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 500  
CGTTAAAGTTCTGGGCGGGCTCCACTGGAAGCTTTACCGTCGCACATGTTAGCGCACTTCGACTTACCGGTCCCGAAGTTCTTCTACCGGTGCACGA  
TurboYFP > N F K T R A E V T F E N G S V Y N R V K L N G Q G F K K D G H V L

Restriction enzyme sites: Bpm1, Bts1, SpDon, BsrG1, Sap1, Ear1, BssS1, Eco57

GGGCAAGAATCTGGAGTTCAATTTACCCCCACTGCCTGTACATCTGGGGCGATCAGGCCAATCACGGCCTGAAGAGCGCCTTCAAAATCTGCCACGAG  
501 |||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\*|||||\* 600  
CCCGTTCTTAGACCTCAAGTTAAAGTGGGGGTGACGGACATGTAGACCCCGCTAGTCCGGTTAGTGCCGGACTTCTCGCGGAAGTTTTAGACGGGTGCTC  
TurboYFP > G K N L E F N F T P H C L Y I W G D Q A N H G L K S A F K I C H E



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polyA      Psil      polyA      polyA      Bts1 Bsm1
|          |          |          |          |
1101 TATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTTCACAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTC 1200
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
ATAACGTCGAATATTACCAATGTTTATTTTCGTTATCGTAGTGTTTAAAGTGTTTATTTTCGTAAAAAAAGTGACGTAAGATCAACACCAAACAGGTTTGAG

      Afl2      SpDon      Ssp1
      |          |          |
1201 ATCAATGTATCTTAAGGCGTAAATTTGTAAGCGTTAATATTTTTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTTAACCAATAGGCCGAA 1300
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
TAGTTACATAGAATTCCGCATTTAACATTTCGCAATTATAAAAACAATTTTAAAGCGCAATTTAAAAACAATTTAGTCGAGTAAAAAATTGGTTATCCGGCTT

      Psil      BsaXb
      |          |
1301 ATCGGCAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCA 1400
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
TAGCCGTTTTAGGGAATATTTAGTTTTCTTATCTGGCTCTATCCCAACTCACAACAAGGTCAAACCTTGTTCTCAGGTGATAATTTCTTGCACCTGAGGT

      Drd1      BsaXa      BtgZ1      Dra3
      |          |          |          |
1401 ACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCGAGGTGCCGTAAAGCACTAAA 1500
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
TGCAGTTTCCCGCTTTTTTGGCAGATAGTCCCGCTACCGGGTGATGCACTTGGTAGTGGGATTAGTTCAAAAAACCCAGCTCCACGGCATTTCGTGATTT

      SpAcc      NaeI      NgoM4      BsrB1
      |          |          |          |
1501 TCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAAGAAAGCGAAAGGAGCGGGCGCTAGG 1600
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
AGCCTTGGGATTTCCCTCGGGGGCTAAATCTCGAACTGCCCTTTTCGGCCGCTTGCACCGCTCTTTCTTCCCTTCTTTTCGCTTTTCTCGCCCGGATCC

1601 GCGCTGGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATG 1700
| | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | * | | | | | | | *
CGCGACCGTTCACATCGCCAGTGCACGCGCATTGGTGGTGTGGGCGGCGCAATTACGCGGCGATGTCCCGCGCAGTCCACCGTGAAGGACCCCTTTAC
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                BspM1
                BfuA1
                Eag1
                Bmr1
2201  ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2300
    TACTAACTTGTTCACCTAACGTGCGTCCAAGAGGCCGGCGAACCCACCTCTCCGATAAGCCGATACTGACCCGTGTTGTCTGTTAGCCGACGAGACTAC

                Nar1
                Kas1
                Drd1
2301  CCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGAGGCAGCGCGGCT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2400
    GGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTGCTCCGTGCGGCCGA

                Pvu2
                Msc1
                Fsp1
                PflF1
                Eco57
2401  ATCGTGGCTGGCCACGACGGGCGTTCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2500
    TAGCACCGACCGGTGCTGCCCCGAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCTGACCGACGATAACCCGCTTCACGGCCCCGTC

                SpDon
                BciV1
                BsrD1
                BspM1
                BfuA1
2501  GATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGATCCGGCTACCTGCCCATTTCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2600
    CTAGAGGACAGTAGAGTGGAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCGATGGACGGGTAAGC

                BtgZ1
                Sap1
                Ear1
2601  ACCACCAAGCGAAAACATCGCATCGAGCGAGCACGTA CTGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2700
    TGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCTACTAGACCTGCTTCTCGTAGTCCCCGAGCGCGG

                BpuE1
                Sph1
                Nco1
                BtgZ1
2701  AGCCGAAC TGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 2800
    TCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTATAGTACCACCTTTTA
    
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                                     ApaL1   BseY1                                     SpAcc
                                     |         |                                     |
3901 AAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAG
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
   TTCCGCGTCGCCAGCCCGACTTGCCCCCAAGCACGTGTGTGGGTGCGAACCTCGCTTGCTGGATGTGGCTTGACTCTATGGATGTGCGACTCGATACTC

                                     BciV1
                                     |         |
4001 AAAGCGCCACGCTTCCCGAAGGGAGAAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGAGAGCGCACGAGGGGAGCTTCCAGGGGGAAACGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4100
   TTTCGCGGTGCGAAGGGCTTCCCTCTTTCCGCCTGTCCATAGGCCATTGCGCGTCCCAGCCTTGTCTCTCGCGTGCTCCCTCGAAGGTCCCCCTTTGCG

                                     SpAcc   Drd1   BpuE1   SpAcc   Eci1
                                     |         |         |         |         |
4101 CTGGTATCTTTATAGTCCTGTTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGGAAAAACGCCAGC
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4200
   GACCATAGAAATATCAGGACAGCCCAAAGCGGTGGAGACTGAACTCGCAGCTAAAAAACTACGAGCAGTCCCCCGCCTCGGATACCTTTTTTGCGGTCG

                                     SpDon
                                     BspLU
                                     ||
4201 AACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCA
   |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4300
   TTGCGCCGAAAAATGCCAAGGACCGGAAAACGACCGGAAAACGAGTGTACAAGAAAGGACGCAATAGGGGACTAAGACACCTATTGGCATAATGGCGGT

Nsil
BfrB1 |
      | |
      TGCAT
4301 ||||| 4305
      ACGTA
```

Found:

<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	AlwN1	<b>Apa1</b>	ApaL1	Avr2	<b>BamH1</b>	BciV1	BfrB1	BfuA1	<b>Bgl1</b>
Bgl2	<b>Blp1</b>	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	BseY1	Bsg1	Bsm1	<b>BspE1</b>
BspH1	<b>BspLU</b>	BspM1	BsrB1	BsrD1	BsrG1	<b>BSSH2</b>	BssS1	BstAP	BstB1	BstE2	Bsu36	BtgZ1	Bts1
<b>Clal</b>	Dra1	<b>Dra3</b>	Drd1	Eag1	Ear1	Eci1	Eco57	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	Kas1	<b>Kpn1</b>
<b>Mfe1</b>	Msc1	Nae1	Nar1	Nco1	NgoM4	Nsi1	<b>PflF1</b>	<b>PflM1</b>	Pml1	polyA	Psi1	<b>PspOM</b>	Pst1
Pvu2	<b>Rsr2</b>	<b>Sac1</b>	Sac2	<b>Sall</b>	Sap1	<b>SexA1</b>	<b>Sfi1</b>	SgrA1	<b>Sma1</b>	SpAcc	SpDon	Sph1	Ssp1
<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>										

Unique:

<b>Acc65</b>	<b>Afe1</b>	<b>Afl2</b>	<b>Age1</b>	<b>Ale1</b>	<b>Apa1</b>	<b>BamH1</b>	<b>Bgl1</b>	<b>Blp1</b>	<b>BsaXa</b>	<b>BsaXb</b>	<b>BseR1</b>	<b>BspE1</b>	<b>BspLU</b>
<b>BSSH2</b>	<b>Clal</b>	<b>Dra3</b>	<b>EcoR1</b>	<b>Fsp1</b>	<b>Hind3</b>	<b>Hpa1</b>	<b>Kpn1</b>	<b>Mfe1</b>	<b>PflF1</b>	<b>PflM1</b>	<b>PspOM</b>	<b>Rsr2</b>	<b>Sac1</b>
<b>Sall</b>	<b>SexA1</b>	<b>Sfi1</b>	<b>Sma1</b>	<b>Stu1</b>	<b>Xba1</b>	<b>Xho1</b>	<b>Xmn1</b>						

Not found:

Aar1	Aat2	Acl1	Ahd1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcgl1a	Bcgl1b	Bcl1
BmgB1	Bpu10	BsiW1	BsmB1	BstX1	BstZ1	_Chi	EcoK	EcoN1	EcoRV	ScFRT	Fse1	FspA1	I_Ceu
loxP	Mlu1	Nde1	Nhe1	Not1	Nru1	Pac1	Pme1	PshA1	Pvu1	SanD1	Sbf1	Scal	Sgf1
SnaB1	Spe1	Srf1	Swa1	T3RNA	T7RNA	T7Ter	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	Tfil	Tse1	Tsp45	Tsp50
TspR1													