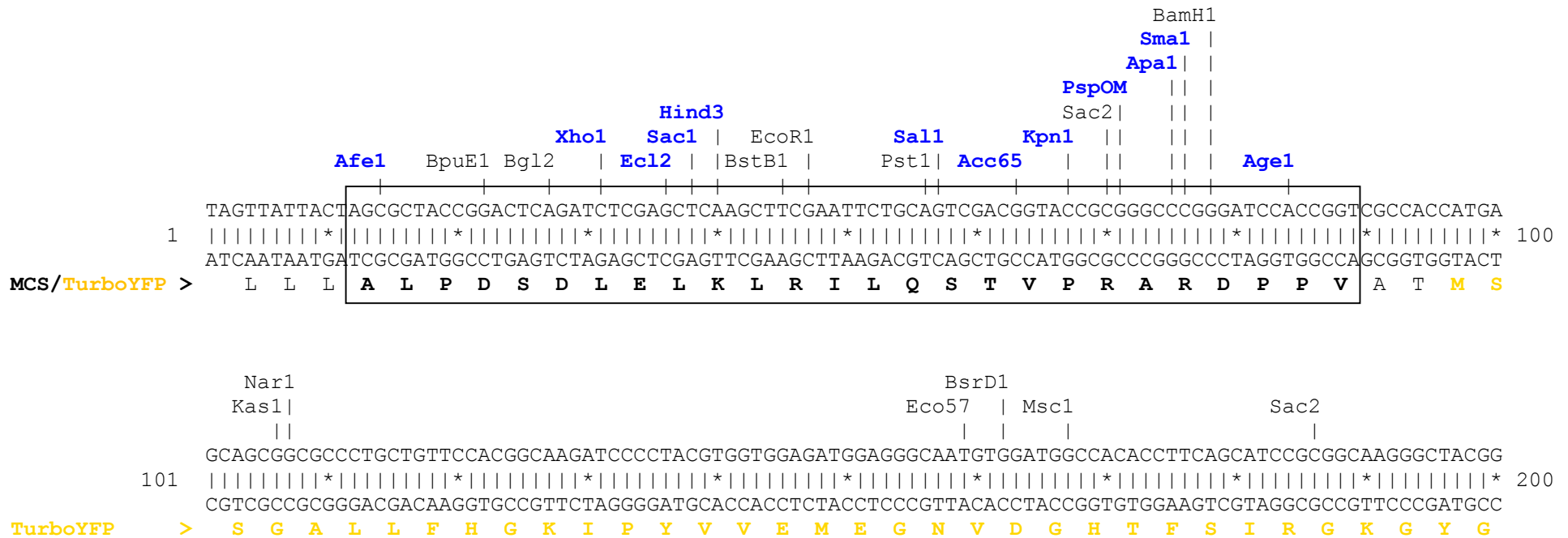


peTurboYFP-PRL-dest1 vector restriction map

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 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.




```

                                Nar1
                                Kas1 |
                                ||
                                Drd1
                                |
3401 CGGCTGCTCTGATGCCGCGTGTTCGGCTGTCAGCGCAGGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGAC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3500
    GCCGACGAGACTACGGCGGCACAAGGCCGACAGTCGCGTCCCCGCGGGCCAAGAAAAACAGTTCTGGCTGGACAGGCCACGGGACTTACTTGACGTTCTG

                                Msc1
                                |
                                Pvu2
                                | |
                                Fsp1 |
                                | |
                                PflF1
                                |
                                Eco57
                                |
3501 GAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCG
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3600
    CTCCGTCGCGCCGATAGCACCGACCGGTGCTGCCCGAAGGAACGCGTCGACACGAGCTGCAACAGTGACTTCGCCCTTCCCTGACCGACGATAACCCGC

                                SpDon
                                |
                                BciV1
                                |
                                BsrD1
                                |
3601 AAGTGCCGGGGCAGGATCTCCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCCGGGCTGCATACGCTTGATCCGGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3700
    TTCACGGCCCCGTCCTAGAGGACAGTAGAGTGGAAACGAGGACGGCTCTTTCATAGGTAGTACCGACTACGTTACGCCGCCGACGTATGCGAACTAGGCCG

                                BtgZ1
                                BspM1 |
                                | |
                                Sap1
                                Ear1
                                |
3701 TACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTA CTGGATGGAAGCCGGTCTTGTGTCGATCAGGATGATCTGGACGAAGAGCAT
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3800
    ATGGACGGGTAAGCTGGTGGTTCGCTTTGTAGCGTAGCTCGCTCGTGCATGAGCCTACCTTCGGCCAGAACAGCTAGTCCTACTAGACCTGCTTCTCGTA

                                BpuE1
                                |
                                Sph1
                                |
                                Nco1
                                |
                                BtgZ1
                                |
3801 CAGGGGCTCGCGCCAGCCGAACTGTTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTTCGTGACCCATGGCGATGCCTGCTTGCCGAATA
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 3900
    GTCCCCGAGCGCGGTCGGCTTGACAAGCGGTCCGAGTTCGGCTCGTACGGGCTGCCGCTCCTAGAGCAGCACTGGGTACCGCTACGGACGAACGGCTTAT

                                BseY1
                                Nae1 |
                                NgoM4 | |
                                | |
                                Rsr2
                                |
                                Eci1
                                |
                                Sap1
                                Ear1
                                |
3901 TCATGGTGGAAAATGGCCGCTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGATATTGC
    |||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||*|||||* 4000
    AGTACCACCTTTTACCGGCGAAAAGACCTAAGTAGCTGACACCGGCCGACCCACACCGCTGGCGATAGTCCTGTATCGCAACCGATGGGCACTATAACG

```


Found:

Acc65	Afe1	Afl2	Age1	Ale1	AlwN1	Apa1	ApaL1	Avr2	BamH1	BciV1	BfrB1	Bgl1	Bgl2
Blp1	Bmr1	Bpm1	BpuE1	Bsa1	BsaB1	BsaXa	BsaXb	BseR1	BseY1	Bsg1	Bsm1	BspE1	BspH1
BspLU	BspM1	BsrB1	BsrD1	BsrG1	BssH2	BssS1	BstAP	BstB1	BstE2	BstX1	Bsu36	BtgZ1	Bts1
Cla1	Dra1	Dra3	Drd1	Eag1	Ear1	Eci1	Ecl2	Eco57	EcoR1	Fsp1	Hind3	Hpa1	Kas1
Kpn1	Mfe1	Msc1	Nae1	Nar1	Nco1	NgoM4	Not1	Nsi1	PflF1	PflM1	Pml1	polyA	Psi1
PspOM	Pst1	Pvu2	Rsr2	Sac1	Sac2	Sall1	SanD1	Sap1	SexA1	Sfi1	SgrA1	Sma1	SpAcc
SpDon	Sph1	Ssp1	Stu1	Xba1	Xho1	Xmn1							

Unique:

Acc65	Afe1	Afl2	Age1	Ale1	Apa1	Bgl1	Blp1	BsaXa	BsaXb	BseR1	BspE1	BspLU	BssH2
BstX1	Cla1	Dra3	Ecl2	Fsp1	Hind3	Hpa1	Kpn1	Not1	PflF1	PflM1	PspOM	Rsr2	Sac1
Sall1	SanD1	SexA1	Sfi1	Sma1	Stu1	Xba1	Xho1	Xmn1					

Not found:

Aar1	Aat2	Ac11	Ahd1	Asc1	Ase1	AsiS1	Baela	Baelb	Bbs1	BbvC1	Bcg1a	Bcg1b	Bcl1
BmgB1	Bpu10	BsiW1	BsmB1	BstZ1	BxatB	BxatL	BxatR	BxatP	_Chi	EcoK	EcoN1	EcoRV	FCatB
FCatL	FCatR	FCatP	ScFRT	Fse1	FspA1	I_Ceu	loxP	Mlu1	Nde1	Nhe1	Nru1	Pac1	Pme1
PshA1	Pvu1	R4atB	R4atL	R4atP	R4atR	Sbf1	Sca1	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	Tfi1	Tse1	Tsp45	Tsp50
TspR1													