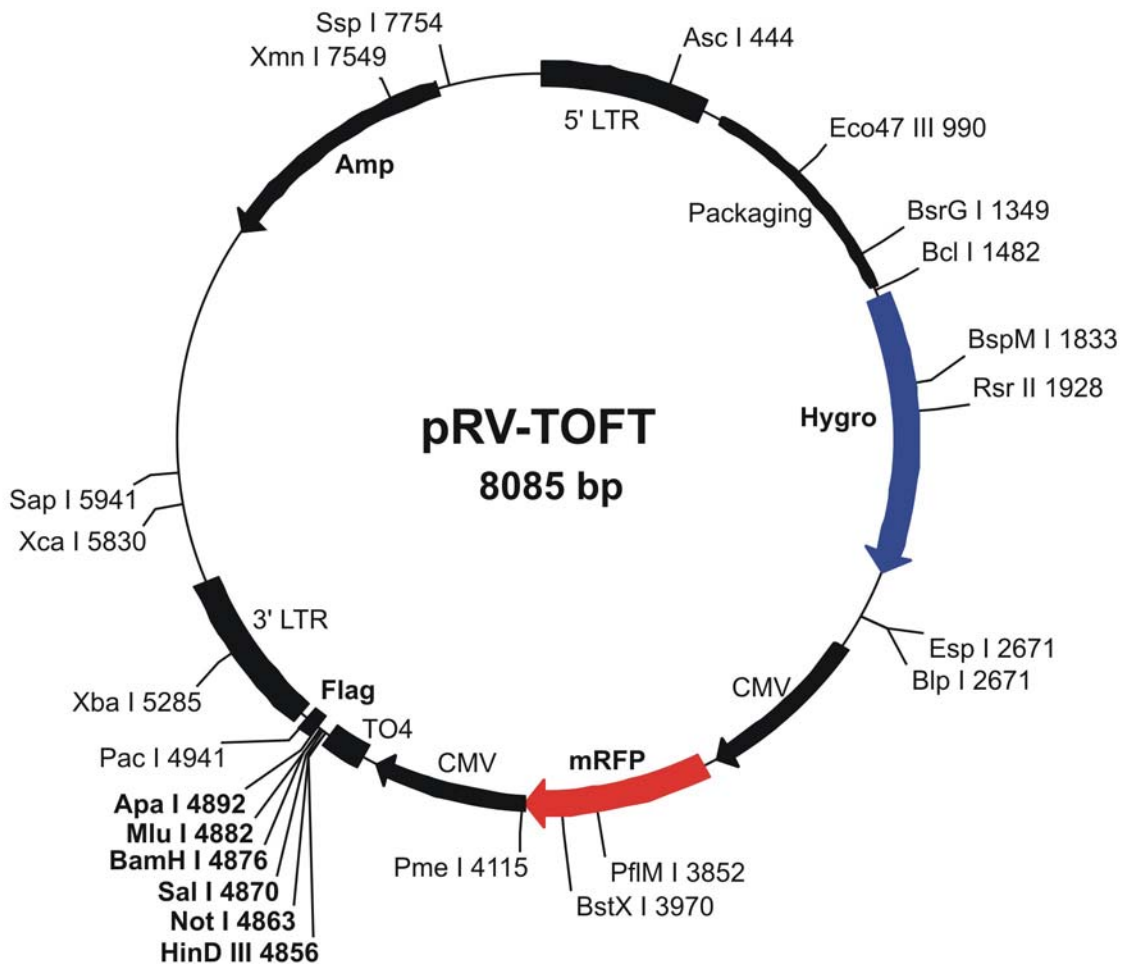


Name of Vector: pRV-TOFT
 Antibiotic Selection: Amp
 Created by: Hong Yin
 (He Lab @ The University of Chicago)
 Date of Creation: February 2005



Linker Sequence

```

Bgl II (1/4)  Hind III  Not I  Sal I  BamH I  Mlu I  Apa I
|-----| |-----| |-----| |-----| |-----| |-----| |-----|
agatc taa gct tgc ggc cgc gtc gac gga tcc acg cgt ggg ccc gga ggc ggc
      -  A  C  G  R  V  D  G  S  T  R  G  P  G  G  G
gat tac aag gat gac gac gat aag ata TGA attcttaattaa
D  Y  K  D  D  D  D  K  I  |-----| |-----|
                        EcoR I (1/4)  Pac I
Flag
  
```

prV-TOFT (Flag tag) Full-length Sequence

TTTGAAAGAC CCCACCCGTA GGTGGCAAGC TAGCTTAAAGT AACGCCACTT TGCAAGGCAT GGAAAAATAC
ATAACTGAGA ATAGAAAAGT TCAGATCAAG GTCAGGAACA AAGAAACAGC TGAATACCAA ACAGGATATC
TGTGGTAAGC GGTTCCCTGCC CCGGCTCAGG GCCAAGAACA GATGAGACAG CTGAGTGATG GGCCAAACAG
GATATCTGTG GTAAGCAGTT CCTGCCCCCG CTCCGGGGCCA AGAACAGATG GTCCCCAGAT GCGGTCCAGC
CCTCAGCAGT TTCTAGTGAA TCATCAGATG TTCCAGGGT GCCCAAGGA CCTGAAAATG ACCCTGTACC
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CCCGACCTGA GGAAGGGAGT CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTCTGGT AGGAGACGAG
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ATCGCCGCC GTGCCCTGCC ATTGGGTGC **caga tcc**
TAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATGGCCCCG
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GCGGGCTTCT GCCTCTTAGA CCACTCTACC CTATTCCECA CACTCACCGG AGCCAAAGCC GCGGCCCTTC
CGTTTTCTTG CT

Unique enzymes in pRV-TOFT:

Asc I	GG`CGCG,CC	444			3410	4113	4872	4883	
Eco47 III	AGC GCT	990			5603	6619	6705	6705	
BsrG I	T`GTAC,A	1349		AlwN I	(4)	232	5149	5224	6473
Bcl I	T`GATC,A	1482		Apa I	(1)	4892			
BspM I	ACCTGC 10/14	1833		ApaL I	(5)	1800	2102	5873	6371
Rsr II	CG`GWC,CG	1928		Apo I	(6)	939	1471	1763	4931
Blp I	GC`TNA,GC	2671				7943	7999		
Esp I	GC`TNA,GC	2671		Asc I	(1)	444			
PflM I	CCAN,NNN`NTGG	3852		Ase I	(2)	4139	7122		
BstX I	CCAN,NNNN`NTGG	3970		Asp718	(2)	477	5468		
Pme I	CTTT AAAC	4115		Ava I	(8)	242	473	2769	3689
HinD III	A`AGCT,T	4856				3881	5398	5431	5464
Not I	GC`GGCC,GC	4863		Ava II	(15)	261	274	329	627
Sal I	G`TCGA,C	4870				757	1286	1928	2469
BamH I	G`GATC,C	4876		BamH I	(1)	4876	7088	5253	5321
Mlu I	A`CGCG,T	4882		Ban I	(15)	319	477	1209	1464
Bspl20 I	G`GGCC,C	4888				2094	3294	3545	3803
Apa I	G,GGCC`C	4892				3890	3998	4097	5311
Pac I	TTA,AT`TAA	4941		Ban II	(9)	414	427	598	3488
Xba I	T`CTAG,A	5285				4700	4892	5405	5418
Bst1107 I	GTA TAC	5830		Bbe I	(5)	1468	3894	4002	4101
Xca I	GTA TAC	5830				5589			
Sap I	GCTCTC 8/11	5941		Bbs I	(3)	445	3848	7928	
Xmn I	GAANN NNTTC	7549		Bbv I	(13)	998	1006	1609	1867
Ssp I	AAT ATT	7754				2260	2387	4000	5708
						5805	6476	6479	6685
				Bbv II	(3)	446	3847	7929	
Number of enzymes = 25				Bcl I	(1)	1482			
				Bcn I	(22)	163	239	475	476
						604	646	791	2307
						2423	3997	4893	5156
						5231	5466	5467	5595
						5637	5704	5739	6438
						7134	7485		
				Bfa I	(14)	31	294	690	728
						740	1461	2608	3421
						4132	5019	5286	6552
						6805	7140		
				Bgl I	(7)	2919	3041	3112	4222
						4344	4415	7070	
				Bgl II	(4)	4718	4739	4760	4850
				Blp I	(1)	2671			
				Bpm I	(5)	2188	2242	4834	4956
						7020			
				Bsa I	(8)	531	552	606	1216
						5521	5542	5597	7011
				BsaA I	(4)	3169	3643	4472	5811
				BsaB I	(4)	4717	4738	4759	4780
				BsaH I	(21)	809	1465	1544	2512
						2951	3004	3087	3273
						3444	3891	3948	3999
						4098	4254	4307	4390
						4576	4819	5437	7487
						7869			
				BsaJ I	(48)	160	236	315	325
						473	537	622	623
						761	800	801	813
						814	1234	1303	1312
						1332	1333	1872	2073
						2228	2297	2528	2741
						2742	3189	3426	3438
						3573	3597	3633	3690
						3750	3846	3882	3951
						4077	4492	5153	5228
						5307	5317	5464	5527
						5613	5614	6217	8063
				BsaW I	(8)	1520	1741	2278	2414
						6263	6410	7241	8050
				BseR I	(6)	540	1360	1399	3424
						3748	5530		
				Bsg I	(2)	2848	4007		
				BsiE I	(13)	794	1728	1863	1884
						1893	2463	2558	2705
						4866	5973	6397	7320
						7469			
				BsiHKA I	(9)	414	1804	2106	4700
						5405	5877	6375	7536
						7621			
				BsmA I	(22)	180	530	551	607
						801	899	1016	1140
						1199	1217	1395	1587
						3262	4565	4811	4973
						5520	5541	5598	5701
						7012	7786		
				BsmB I	(8)	800	898	1139	1198
						1396	1588	4810	5700
				BsmF I	(18)	247	640	796	831
						1272	2437	2723	3004
						3155	3323	3595	3614
						4307	4458	4626	5239
						5631	7967		
				BsoF I	(53)	794	968	984	987
						992	995	1200	1598

The following enzymes do not cut in pRV-TOFT:

Age I	Avr II	BsiC I	BsiW I	Bsm I						
Bsp1286 I	BstB I	Cla I	Eco72 I	Fse I	Bfa I	(14)	294	690	728	
Hpa I	Mun I	Nae I	NgoM I	Nru I			740	1461	2608	3421
Nsi I	Paer7 I	Pml I	Sfi I	Sph I			4132	5019	5286	6552
							6805	7140		
pRV-TOFT: sites sorted by name:					Bgl I	(7)	2919	3041	3112	4222
							4344	4415	7070	
Aat II	(12)	812	1547	2954	3007		4718	4739	4760	4850
		3090	3276	3447	4257		2671			
		4310	4393	4579	7872		2188	2242	4834	4956
Acc I	(2)	4871	5829				7020			
Acc65 I	(2)	477	5468				531	552	606	1216
Aci I	(100)	150	272	401	755		5521	5542	5597	7011
		794	927	968	1109		3169	3643	4472	5811
		1200	1266	1365	1384		4717	4738	4759	4780
		1422	1539	1663	1728		809	1465	1544	2512
		1795	1845	1865	1889		2951	3004	3087	3273
		1911	1931	2108	2146		3444	3891	3948	3999
		2156	2269	2297	2299		4098	4254	4307	4390
		2320	2449	2459	2692		4576	4819	5437	7487
		2789	2806	2887	2915		7869			
		2927	2941	3108	3199		160	236	315	325
		3232	3336	3357	3418		473	537	622	623
		3532	3555	3579	3654		761	800	801	813
		3732	3801	3871	3936		814	1234	1303	1312
		4084	4190	4218	4230		1332	1333	1872	2073
		4244	4411	4502	4535		2228	2297	2528	2741
		4639	4660	4862	4866		2742	3189	3426	3438
		4898	5264	5566	5730		3573	3597	3633	3690
		5769	5779	5821	5846		3750	3846	3882	3951
		5884	5897	5923	5940		4077	4492	5153	5228
		5983	5990	6011	6102		5307	5317	5464	5527
		6130	6257	6276	6397		5613	5614	6217	8063
		6507	6642	6651	7013		1520	1741	2278	2414
		7104	7295	7341	7462		6263	6410	7241	8050
		7506	7583	7692	7791		540	1360	1399	3424
		7838	8005	8063	8065		3748	5530		
Afl II	(3)	35	1073	5023			2848	4007		
Afl III	(2)	4882	6057				794	1728	1863	1884
Aha II	(21)	809	1465	1544	2512		1893	2463	2558	2705
		2951	3004	3087	3273		4866	5973	6397	7320
		3444	3891	3948	3999		7469			
		4098	4254	4307	4390					
		4576	4819	5437	7487					
		7869								
Ahd I	(5)	1087	3607	5513	5559					
		6950								
Alu I	(44)	30	34	120	191					
		412	655	735	743					
		1488	1600	1632	1674					
		2059	2284	2349	2378					

	790	802	815	1236	Bgl II	A`GATC,T	4	Blp I	GC`TNA,GC	1	
	1261	1284	1304	1334	Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	8	
	2306	2422	2743	2919	BsaA I	YAC GTR	4	BsaB I	GATNN NNATC	4	
	3112	3598	3752	3996	BsaH I	GR`CG,YC	21	BsaJ I	C`CNNG,G	48	
	4222	4415	4813	4892	BsaW I	W`CCGG,W	8	BseR I	GAGGAG 16/14	6	
	5155	5230	5308	5465	Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-	
	5466	5594	5615	5636	BsiE I	CG,RY`CG	13	BsiHKA I	G,WGCW`C	9	
	5703	5738	6085	6206	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-	
	6219	6437	7133	7484	BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	8	
Sec I	(48)	160	236	315	325	BsmF I	GGGAC 15/19	18	BsoF I	GC`N,GC	53
		473	537	622	623	Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
		761	800	801	813	BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	1
		814	1234	1303	1312	BspM II	T`CCGG,A	4	Bsr I	ACT,GG`	19
		1332	1333	1872	2073	BsrB I	GAG CGG	7	BsrD I	GCAATG, 8	2
		2228	2297	2528	2741	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4
		2742	3189	3426	3438	BssS I	C`TCGT,G	6	Bst1107 I	GTA TAC	1
		3573	3597	3633	3690	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	3
		3750	3846	3882	3951	BstN I	CC`W,GG	22	BstU I	CG CG	37
		4077	4492	5153	5228	BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	15
		5307	5317	5464	5527	Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	35
SfaN I	(24)	5613	5614	6217	8063	Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-
		260	520	1005	1585	Csp6 I	G`TA,C	25	Dde I	C`TNA,G	27
		1729	1796	1868	2053	Dpn I	GA TC	45	DpnII	`GATC,	45
		2283	2363	2385	2541	Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	2
		3187	4490	5252	5510	Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	9
		5724	5857	5895	5933	Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	5
		6153	7205	7398	7645	Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	1
Sfc I	(9)	984	992	1168	1853	Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	5
		3764	5003	6322	6513	EcoN I	CCTNN`N,NNAGG	2	EcoO109 I	RG`GNC,CY	5
		7191				EcoR I	G`AATT,C	4	EcoR II	`CCWGG,	22
Sma I	(2)	475	5466			EcoR V	GAT ATC	4	Ehe I	GGC GCC	5
SnaB I	(2)	3169	4472			Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	53
Spe I	(2)	727	4131			Fok I	GGATG 14/18	15	Fse I	GG,CCGG`CC	-
Ssp I	(1)	7754				Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	15
Stu I	(2)	3638	3860			Gau I	CTGGAG 21/19	5	Hae I	WGG CCW	10
Sty I	(12)	325	537	1312	1872	Hae II	R,GCCG`Y	8	Hae III	GG CC	51
		3189	3426	3573	3633	Hga I	GAGCG 9/14	17	HgiA I	G,WGCW`C	9
Taq I	(20)	3846	4492	5317	5527	HgiE II	ACNNNNNNNGGT -1/132		Hha I	G,CG`C	42
		861	1105	1416	1427	HinC II	GTY RAC	3	Hind II	GTY RAC	3
		1551	1566	1575	1635	HinD III	A`AGCT,T	1	Hinf I	G`ANT,C	17
		2052	2265	2367	2392	HinI I	GR`CG,YC	21	HinP I	G`CG,C	42
		2575	3507	3513	3723	Hpa I	GT AAC	-	Hpa II	C`CG,G	36
		4784	4871	6157	7601	Hph I	GGTGA 12/11	19	Kas I	G`GGCC,C	5
Tfi I	(9)	299	518	869	1616	Kpn I	G,GTAC`C	2	Mae I	C`TA,G	14
		1738	1938	2189	2712	Mae II	A`CG,T	24	Mae III	`GTNAC,	26
		6032				Mbo I	`GATC,	45	Mbo II	GAAGA 12/11	16
Tsp45 I	(10)	1089	1298	1810	3568	Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	8
		3739	3745	5711	5806	Mnl I	CCTC 10/10	77	Msc I	TGG CCA	3
		7206	7417			Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	4
Tth111 I	(7)	466	878	1284	1580	Msp I	C`CG,G	36	MspA1 I	CMG CKG	14
		2024	5457	5804		Mun I	C`AATT,G	-	Nae I	GCC GGC	-
Tth111 II	(10)	144	220	498	691	Nar I	GG`CG,CC	5	Nci I	CC`S,GG	22
		1740	5137	5212	6646	Nco I	C`CATG,G	5	Nde I	CA`TA,TG	4
		6655	6685			NgoM I	G`CCGG,C	-	Nhe I	G`CTAG,C	2
Vsp I	(2)	4139	7122			Nla III	,CATG`	26	Nla IV	GGN NCC	43
Xba I	(1)	5285				Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Xca I	(1)	5830				Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	2
Xho II	(15)	1517	2831	3414	4106	NspB II	CMG CKG	14	NspH I	R,CATG`Y	2
		4718	4739	4760	4850	Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
		4876	6698	6709	6795	Pal I	GG CC	51	PflM I	CCAN,NNN`NTGG	1
		6807	7575	7592		Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Xma I	(2)	473	5464			Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
Xma III	(5)	791	1725	1890	2460	Pepl406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
		4863				Pet I	C,TGCA`G	6	Pvu I	CG,AT`CG	2
Xmn I	(1)	7549				Pvu II	CAG CTG	5	Rsa I	GT AC	25
						Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	3
						Sac II	CC,GC`GG	2	Sal I	G`TCGA,C	1
						Sap I	GCTCTTC 8/11	1	Sau3A I	`GATC,	45
						Sau96 I	G`GNC,C	44	Sca I	AGT ACT	2
						ScrF I	CC`N,GG	44	Sec I	C`CNNG,G	48
						SfaN I	GCATC 9/13	24	Sfc I	C`TRYA,G	9
						Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
						SnaB I	TAC GTA	2	Spe I	A`CTAG,T	2
						Sph I	G,CATG`C	-	Spl I	C`GTAC,G	-
						Srf I	GCCC GGGC	-	Ssp I	AAT ATT	1
						Stu I	AGG CCT	2	Sty I	C`CWG,G	12
						Taq I	T`CG,A	20	Tfi I	G`ANT,C	9
						Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTC	7
						Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	2
						Xba I	T`CTAG,A	1	Xca I	GTA TAC	1
						Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
						Xho II	R`GATC,Y	15	Xma I	C`CCGG,G	2
						Xma III	C`GGCC,G	5	Xmn I	GAANN NNTTC	1
Site usage in pRV-TOFT:											
Aat II	G,ACGT`C	12	Acc I	GT`MK,AC	2						
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	100						
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2						
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	21						
Ahd I	GACNN,N`NNGTC	5	Alu I	AG CT	44						
Alw I	GGATC 8/9	21	AlwN I	CAG,NNN`CTG	4						
Apa I	G,GGCC`C	1	Apal I	G`TGCA,C	5						
Apo I	R`AATT,Y	6	Asc I	GG`CGCG,CC	1						
Ase I	AT`TA,AT	2	Asp718	G`GTAC,C	2						
Ava I	C`YCGR,G	8	Ava II	G`GWC,C	15						
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1						
Ban I	G`GYRC,C	15	Ban II	G,RGCY`C	9						
Bbe I	G,GCGC`C	5	Bbs I	GAAGAC 8/12	3						
Bbv I	GCAGC 13/17	13	Bbv II	GAAGAC 7/11	3						
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	22						
Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	7						