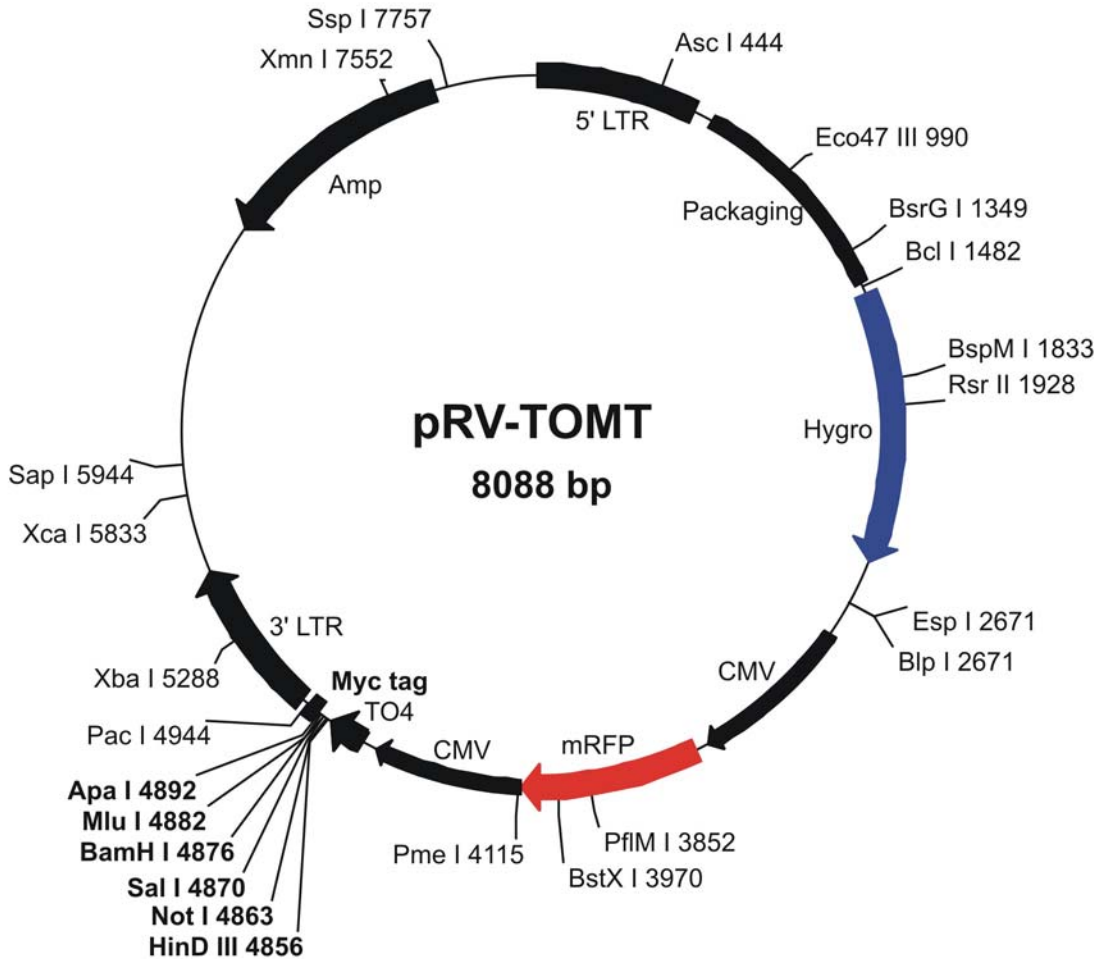


Name of Vector: pRV-TOMT  
 Antibiotic Selection: Amp  
 Created by: Hong Yin  
 (He Lab @ The University of Chicago)  
 Date of Creation: February 2005



### Linker Sequence

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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

gaa caa aaa ctc atc tca gaa gag gat ctg TGA attcttaattaa
E  Q  K  L  I  S  E  E  D  L  TGA attcttaattaa
|-----| |-----|
EcoR I (1/4)  Pac I

Myc Tag
  
```

## prRV-TOMT (Myc tag) Full-length Sequence

TTTGAAAGAC CCCACCCGTA GGTGGCAAGC TAGCTTAAGT AACGCCACTT TGCAAGGCAT GGAAAAATAC  
ATAACTGAGA ATAGAAAAGT TCAGATCAAG GTCAGGAACA AAGAAACAGC TGAATACCAA ACAGGATATC  
TGTGGTAAGC GGTTCCCTGCC CCGGCTCAGG GCCAAGAACA GATGAGACAG CTGAGTGATG GGCCAAACAG  
GATATCTGTG GTAAGCAGTT CCTGCCCCGG CTCGGGGCCA AGAACAGATG GTCCCCAGAT GCGGTCCAGC  
CCTCAGCAGT TTCTAGTGAA TCATCAGATG TTCCAGGGT GCCCAAGGA CCTGAAAATG ACCCTGTACC  
TTATTTGAAC TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC CGCTCTCCGA GCTCAATAAA  
AGAGCCCACA ACCCTCACT CGGCGCGCCA GTCTTCCGAT AGACTGCGTC GCCCGGTAC CCGTATTCCC  
AATAAAGCCT CTTGCTGTTT GCATCCGAAT CGTGGTCTCG CTGTTCCCTG GGAGGGTCTC CTCTGAGTGA  
TTGACTACCC ACGACGGGGG TCTTTCAATTT GGGGGTCTCG CCGGGATTTG GAGACCCCTG CCCAGGGACC  
ACCGACCCAC CACCGGGAGG TAAGCTGGCC AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG  
TTTGATGTTA TGCGCCTGCG TCTGTACTAG TTAGCTAACT AGCTCTGTAT CTGGCGGACC CGTGGTGGAA  
CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG  
CCCGACCTGA GGAAGGGAGT CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTCTGGT AGGAGACGAG  
AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA CCGAAGCCGC GCGTCTGTG  
TGCTGCAGCG CTGCAGCATC GTTCTGTGTT GTCTCTGTCT GACTGTGTTT CTGTATTTGT CTGAAAATTA  
GGGCCAGACT GTTACCACCT CCTTAAGTTT GACCTTAGGT CACTGGAAAG ATGTCGAGCG GATCGCTCAC  
AACCAGTCGG TAGATGTCAA GAAGAGACGT TGGGTTACCT TCTGCTCTGC AGAATGGCCA ACCTTTAACG  
TCGGATGGCC GCGAGACGGC ACCTTTAACG GAGACCTCAT CACCCAGGTT AAGATCAAGG TCTTTTCACC  
TGCCCCGCAT GGACACCCAG ACCAGGTCCC CTACATCGTG ACCTGGGAAG CCTTGGCTTT TGACCCCCCT  
CCCTGGGTCA AGCCCTTTGT ACACCCTAAG CCTCCGCCTC CTCTTCCTCC ATCCGCCCCG TCTCTCCCC  
TTGAACCTCC TCGTTCGACC CCGCCTCGAT CCTCCCTTTA TCCAGCCCTC ACTCCTTCTC TAGGCGCCGG  
AATTCGGATC TGATCAGCTT GCCACAACC GTACCAAAGA TGGATAGATC CGGAAAGCCT GAACTCACCG  
CGACGCTGT CGAGAAGTTT CTGATCGAAA AGTTCGACAG CGTCTCCGAC CTGATGCAGC TCTCGGAGGG  
CGAAGAATCT CGTGCCTTCA GCTTCGATGT AGGAGGGCGT GGATATGTC TGCGGGTAAA TAGCTGCGCC  
GATGGTTTCT ACAAAGATCG TTATGTTTAT CGGCACTTT CATCGGCCGC GCTCCCGATT CCGGAAGTGC  
TTGACATTGG GGAATTCAGC GAGAGCCTGA CCTATTGCAT CTCCCGCGT GCACAGGGTG TCACGTGCA  
AGACTGCCT GAAACCGAAC TGCCCGCTGT TCTGACCGCG GTGCGGAGG CCATGGATGC CATCGTTCG  
GCCGATCTTA GCCAGCAGC CGGGTTCGGC CCAATCGGAC CGCAAGGAAT CGGTCAATAC ACTACATGGC  
GTGATTTTCAT ATGCGCGATT GCTGATCCCC ATGTGTATCA CTGGCAAAC GTGATGGACG ACACCGTACG  
TGCGTCCGTC GCGCAGGCTC TCGATGAGCT GATGCTTTGG GCCGAGGACT GCCCCGAAGT CCGGCACCTC  
GTGCACGCGG ATTTCCGGCT CAACAATGTC CTGACGGACA ATGGCCGCAT AACAGCGGTC ATTGACTGGA  
GCGAGGCGAT GTTCGGGGAT TCCCAATACG AGGTCGCCAA CATCTTCTTC TGGAGGCCGT GGTGGCCTT  
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CAGAAGCGCG GCCGTCTGGA CCGATGGCTG TGTAGAAGTA CTCGCCGATA GTGGAAACCG ACGCCCAGC  
ACTCGTCCGA GGGCAAAGGA ATAGAGTAGA TGCCGACCGA ACAAGAGCTG ATTTTCGAGAA CGCCTCAGCC  
AGCAACTCGC GCGAGCCTAG CAAGGCAAAT GCGAGAGAAC GGCCTTACGC TTGGTGGCAC AGTTCCTCGT  
CACAGTTCGC TAAGCTCGCT CGGCTGGGTC GCGGGAGGGC CGGTCGCAGT GATTCAGGCC CTTCTGGATT  
GTGTTGGTCC CCAGGGCAGC ATTGTCAATG CCACGCCTC GGGTGATCTG ACTGATCCCC CAGATTGGAG  
ATCGCCGCC GTGCCGTGCC ATTGGGTGC **caga tcc**  
TAATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCGCGCTTACATAACTTACGGTAAATGGCCCCG  
CTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTTCCA  
TTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCT  
ATTGACGTCAATGACGGTAAATGGCCCGCTGGCATTATGCCAGTACATGACCTTATGGGACTTTTCTACTTGGCAGTACA  
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cgtgcagctgcccggcgctacaagaccgacatcaagctggacatcacctcccacaacgaggactacaccatcgtggaacg  
tacgagcgcgcccagggccgcccactccaccggcgcttaaggatct **gtt taa ac**ATTGATTATTGACTAGTTATTA  
ATAGTAATCAATTACGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCGCGCTTACATAACTTACGGTAAATGGCCCCCT

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**cgg atc cA CGC GT GGGCCC** gga ggc ggc gaa caa aaa ctc atc tca gaa gag gat ctg TGA  
attctt aat taa cgATAAAAATA AAAGATTTTA TTTAGTCTCC AGAAAAAGGG GGGAAATGAAA  
GACCCACCT GTAGTTTTGG CAAGCTAGCT TAAGTAACGC CATTTTTGCAA GGCATGGAAA AATACATAAC  
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ATGCGTAAGG AGAAAAATACC GCATCAGGCG CTCTTCCGCT TCCTCGCTCA CTGACTCGCT CCGCTCGGTC  
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ACGCAGGAAA GAACATGTGA GCAAAAGGCC AGCAAAAGGC CAGGAACCGT AAAAAAGGCC CGTTGCTGGC  
GTTTTTCCAT AGGCTCCGCC CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC  
CCGACAGGAC TATAAAGATA CCAGGCGTTT CCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC  
TGCCGCTTAC CGGATACCTG TCCGCCTTTT CCCCCTCGGG AAGCGTGGCG CTTTCTCATA GCTCACGCTG  
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CGCTCACCGG CTCCAGATTT ATCAGCAATA AACAGCCAG CCGGAAGGGC CGAGCGAGA AGTGGTCTCTG  
CAACTTTATC CGCCTCCATC CAGTCTATTA AATTGTTGCC GGAAGCTAGA GTAAGTAGTT GCCCAGTTAA  
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GTCTTCAAGA ATTCATACCA GATCACCAGG AACTGTCTC CAAATGTGTC CCCCTCACAC TCCCAAATTC  
GCGGGCTTCT GCCTCTTAGA CCACTCTACC CTATTCCCCA CACTCACCGG AGCCAAAGCC GCGGCCCTTC  
CGTTTTCTTTG CT

Unique enzymes in pRV-TOMT:

Asc I	GG`CGCG,CC	444			3410	4113	4872	4883	
Eco47 III	AGC GCT	990			4933	5606	6622	6708	
BsrG I	T`GTAC,A	1349		AlwN I	(4)	232	5152	5227	6476
Bcl I	T`GATC,A	1482		Apa I	(1)	4892			
BspM I	ACCTGC 10/14	1833		ApaL I	(5)	1800	2102	5876	6374
Rsr II	CG`GWC,CG	1928				7620			
Blp I	GC`TNA,GC	2671		Apo I	(6)	939	1471	1763	4934
Esp I	GC`TNA,GC	2671				7946	8002		
PflM I	CCAN,NNN`NTGG	3852		Asc I	(1)	444			
BstX I	CCAN,NNNN`NTGG	3970		Ase I	(2)	4139	7125		
Pme I	CTTT AAAC	4115		Asp718	(2)	477	5471		
Hind III	A`AGCT,T	4856		Ava I	(8)	242	473	2769	3689
Not I	GC`GGCC,GC	4863				3881	5401	5434	5467
Sal I	G`TCGA,C	4870		Ava II	(15)	261	274	329	627
BamH I	G`GATC,C	4876				757	1286	1928	2469
Mlu I	A`CGCG,T	4882		BamH I	(1)	4876	2737	5256	5324
Bsp120 I	G`GGCC,C	4888		Ban I	(15)	319	477	1209	1464
Apa I	G,GGCC`C	4892				2094	3294	3545	3803
Pac I	TTA,AT`TAA	4944		Ban II	(9)	3890	3998	4097	5314
Xba I	T`CTAG,A	5288				5439	5471	6901	
Bst1107 I	GTA TAC	5833		Bbe I	(5)	414	427	598	3488
Xca I	GTA TAC	5833				4700	4892	5408	5421
Sap I	GCTCTTC 8/11	5944		Bbs I	(3)	5592			
Xmn I	GAANN NNTTC	7552		Bbv I	(13)	1468	3894	4002	4101
Ssp I	AAT ATT	7757				5443			
Number of enzymes = 25					Bbv II	(3)	446	3847	7932
				Bcl I	(1)	1482			
				Bcn I	(22)	163	239	475	476
						604	646	791	2307
						2423	3997	4893	5159

The following enzymes do not cut in pRV-TOMT:

Age I	Avr II	BsiC I	BsiW I	Bsm I					
Bsp1286 I	BstB I	Cla I	Eco72 I	Fse I					
Hpa I	Mun I	Nae I	NgoM I	Nru I					
Nsi I	Paer7 I	Pml I	Sfi I	Sph I					

pRV-TOMT: sites sorted by name:

Aat II	(12)	812	1547	2954	3007					Bgl I	(7)	2919	3041	3112	4222
		3090	3276	3447	4257							4344	4415	7073	
		4310	4393	4579	7875					Bgl II	(4)	4718	4739	4760	4850
Acc I	(2)	4871	5832							Blp I	(1)	2671			
Acc65 I	(2)	477	5471							Bpm I	(5)	2188	2242	4834	4959
Aci I	(100)	150	272	401	755							7023			
		794	927	968	1109					Bsa I	(8)	531	552	606	1216
		1200	1266	1365	1384							5524	5545	5600	7014
		1422	1539	1663	1728					BsaA I	(4)	3169	3643	4472	5814
		1795	1845	1865	1889					BsaB I	(4)	4717	4738	4759	4780
		1911	1931	2108	2146					BsaH I	(21)	809	1465	1544	2512
		2156	2269	2297	2299							2951	3004	3087	3273
		2320	2449	2459	2692							3444	3891	3948	3999
		2789	2806	2887	2915							4098	4254	4307	4390
		2927	2941	3108	3199							4576	4819	5440	7490
		3232	3336	3357	3418					BsaJ I	(48)	160	236	315	325
		3532	3555	3579	3654							473	537	622	623
		3732	3801	3871	3936							761	800	801	813
		4084	4190	4218	4230							814	1234	1303	1312
		4244	4411	4502	4535							1332	1333	1872	2073
		4639	4660	4862	4866							2228	2297	2528	2741
		4898	5267	5569	5733							2742	3189	3426	3438
		5772	5782	5824	5849							3573	3597	3633	3690
		5887	5900	5926	5943							3750	3846	3882	3951
		5986	5993	6014	6105							4077	4492	5156	5231
		6133	6260	6279	6400							5310	5320	5467	5530
		6510	6645	6654	7016							5616	5617	6220	8066
		7107	7298	7344	7465					BsaW I	(8)	1520	1741	2278	2414
		7509	7586	7695	7794							6266	6413	7244	8053
		7841	8008	8066	8068					BseR I	(6)	540	1360	1399	3424
												3748	5533		
Afl II	(3)	35	1073	5026						Bsg I	(2)	2848	4007		
Afl III	(2)	4882	6060							BsiE I	(13)	794	1728	1863	1884
Aha II	(21)	809	1465	1544	2512							1893	2463	2558	2705
		2951	3004	3087	3273							4866	5976	6400	7323
		3444	3891	3948	3999							7472			
		4098	4254	4307	4390					BsiHKA I	(9)	414	1804	2106	4700
		4576	4819	5440	7490							5408	5880	6378	7539
		7872										7624			
Ahd I	(5)	1087	3607	5516	5562					BsmA I	(22)	180	530	551	607
		6953										801	899	1016	1140
Alu I	(44)	30	34	120	191							1199	1217	1395	1587
		412	655	735	743							3262	4565	4811	4976
		1488	1600	1632	1674							5523	5544	5601	5704
		2059	2284	2349	2378							7015	7789		
		2568	2675	3395	3562					BsmB I	(8)	800	898	1139	1198
		3679	3796	3925	3991							1396	1588	4810	5703
		4021	4698	4788	4858					BsmF I	(18)	247	640	796	831
		5021	5025	5112	5187							1272	2437	2723	3004
		5406	5649	5702	5721							3155	3323	3595	3614
		6002	6228	6318	6364							4307	4458	4626	5242
		6621	7142	7242	7305							5634	7970		
Alw I	(22)	1118	1424	1513	1980					BsoF I	(53)	794	968	984	987
		2298	2407	2780	2827							992	995	1200	1598



		4098	4254	4307	4390			7135	7245	7487	8054
		4576	4819	5440	7490	MspAl I	(14)	120	191	1847	2156
		7872						2299	3991	5112	5187
HinP I	(42)	393	395	444	446			5569	5772	6402	6647
		713	970	989	1465			7588	8068		
		1677	1730	1974	2042	Nar I	(5)	1465	3891	3999	4098
		2257	2384	2457	2600			5440			
		3463	3475	3709	3799	Nci I	(22)	162	238	474	475
		3891	3999	4072	4074			603	645	790	2306
		4098	5387	5389	5440			2422	3996	4892	5158
		5661	5764	5794	5935			5233	5468	5469	5597
		5968	6238	6305	6405			5639	5706	5741	6440
		6579	6688	7081	7174			7136	7487		
		7511	7843			Nco I	(5)	1872	3189	3426	3846
Hpa II	(36)	162	238	474	602			4492			
		644	790	1468	1521	Nde I	(4)	1970	3063	4366	5883
		1742	1859	2092	2279	Nhe I	(2)	30	5021		
		2305	2415	2421	2701	Nla III	(26)	62	1272	1876	1959
		3996	4095	4892	5158			1994	2760	3133	3193
		5233	5468	5596	5638			3430	3463	3481	3850
		5706	5740	6267	6414			3973	4436	4496	5053
		6440	6630	7034	7068			5699	5804	6064	6784
		7135	7245	7487	8054			7275	7285	7363	7399
Hph I	(19)	1224	1250	1529	2784			7792	7897		
		3204	3579	3750	3801	Nla IV	(43)	154	247	263	321
		4022	4507	5681	5690			479	628	759	828
		6797	7024	7438	7646			960	1211	1288	1466
		7679	7953	8044				2096	2119	2303	2419
Kas I	(5)	1464	3890	3998	4097			2739	3296	3487	3547
		5439						3583	3631	3805	3826
Kpn I	(2)	481	5475					3892	4000	4099	4599
Mae I	(14)	31	294	690	728			4878	4890	5258	5316
		740	1461	2608	3421			5441	5473	5622	6092
		4132	5022	5289	6555			6131	6903	6997	7038
		6808	7143					7249	7839	8058	
Mae II	(24)	809	1148	1189	1544	Not I	(1)	4863			
		1814	2951	2963	3004	Nsp7524 I	(2)	5695	6060		
		3087	3168	3273	3444	NspB II	(14)	120	191	1847	2156
		3642	4254	4266	4307			2299	3991	5112	5187
		4390	4471	4576	5813			5569	5772	6402	6647
		6763	7179	7552	7872			7588	8068		
Mae III	(26)	39	1061	1089	1154	NspH I	(2)	5699	6064		
		1298	1810	2890	2977	Pac I	(1)	4944			
		3326	3568	3739	3745	Pal I	(51)	172	203	248	659
		4193	4280	4629	5030			793	829	841	1054
		5714	5809	6416	6479			1178	1199	1264	1727
		6595	6878	7209	7267			1871	1892	1920	2072
		7420	7608					2145	2227	2462	2633
Mbo I	(46)	94	1111	1243	1428			2700	2719	2913	3106
		1477	1482	1517	1563			3431	3498	3531	3582
		1696	1881	1894	1984			3638	3825	3860	3939
		2291	2411	2775	2784			3974	4083	4216	4409
		2800	2831	3414	3510			4865	4890	5123	5168
		3906	4106	4718	4739			5198	5243	6075	6086
		4760	4781	4806	4850			6104	6538	6996	7076
		4876	4926	5085	5599			7343	7930	8071	
		6626	6701	6712	6720	PflM I	(1)	3852			
		6798	6810	6915	7256	Ple I	(3)	866	5469	6439	
		7274	7320	7578	7595	Pme I	(1)	4115			
		7631	7957			PpuM I	(3)	329	1286	5324	
Mbo II	(17)	446	1153	1366	1624	Psp1406 I	(2)	7179	7552		
		2207	2210	3849	3852	PspA I	(2)	473	5467		
		4859	4932	5932	6721	Pst I	(6)	988	996	1172	1857
		6794	7549	7627	7736			3768	7198		
		7932				Pvu I	(2)	1884	7323		
Mlu I	(1)	4882				Pvu II	(5)	120	191	3991	5112
Mme I	(8)	896	1173	1610	2144			5187			
		3842	5532	6274	6458	Rsa I	(25)	348	479	726	1351
Mnl I	(78)	291	444	508	536			1503	2437	2490	3048
		560	641	843	939			3073	3128	3161	3212
		1235	1338	1371	1377			3369	3626	3878	4067
		1380	1386	1416	1419			4351	4376	4431	4464
		1434	1441	1457	1600			4515	4672	5473	5868
		1637	1861	2068	2107			7433			
		2167	2194	2217	2265	Rsr II	(1)	1928			
		2523	2593	2689	3370	Sac I	(3)	414	4700	5408	
		3433	3441	3444	3475	Sac II	(2)	2300	8069		
		3508	3514	3520	3535	Sal I	(1)	4870			
		3623	3685	3718	3768	Sap I	(1)	5944			
		3825	3850	3870	3877	Sau3A I	(46)	94	1111	1243	1428
		3909	3946	4036	4041			1477	1482	1517	1563
		4072	4673	4849	4888			1696	1881	1894	1984
		4917	5286	5438	5457			2291	2411	2775	2784
		5502	5529	5553	5635			2800	2831	3414	3510
		5666	5696	5958	6168			3906	4106	4718	4739
		6241	6492	6892	6973			4760	4781	4806	4850
		7119	7325	7920	7983			4876	4926	5085	5599
		7999	8028					6626	6701	6712	6720
Msc I	(3)	659	1178	3974				6798	6810	6915	7256
Mse I	(20)	36	1074	1186	1216			7274	7320	7578	7595
		1240	4114	4139	4940			7631	7957		
		4944	5027	5841	6766	Sau96 I	(44)	170	201	246	261
		6818	6823	6837	6890			274	329	627	757
		7125	7164	7529	7901			827	840	1052	1263
Msl I	(4)	3194	4497	7205	7364			1286	1919	1928	2070
Msp I	(36)	162	238	474	602			2469	2698	2718	2737
		644	790	1468	1521			2912	3105	3529	3581
		1742	1859	2092	2279			3824	4081	4215	4408
		2305	2415	2421	2701			4888	4889	5121	5166
		3996	4095	4892	5158			5196	5241	5256	5269
		5233	5468	5596	5638			5324	5621	6995	7074
		5706	5740	6267	6414			7091	7313	7929	8070
		6440	6630	7034	7068	Sca I	(2)	2490	7433		

ScrF I	(44)	162	238	316	474	Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	7
		475	603	624	645	Bgl II	A`GATC,T	4	Blp I	GC`TNA,GC	1
		790	802	815	1236	Bpm I	CTGGAG 22/20	5	Bsa I	GGTCTC 7/11	8
		1261	1284	1304	1334	BsaA I	YAC GTR	4	BsaB I	GATNN NNATC	4
		2306	2422	2743	2919	BsaH I	GR`CG,YC	21	BsaJ I	C`CNNG,G	48
		3112	3598	3752	3996	BsaW I	W`CCGG,W	8	BseR I	GAGGAG 16/14	6
		4222	4415	4813	4892	Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
		5158	5233	5311	5468	BsiE I	CG,RY`CG	13	BsiHKA I	G,WGCW`C	9
		5469	5597	5618	5639	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
		5706	5741	6088	6209	BsmA I	GTCTC`/9	22	BsmB I	CGTCTC 7/11	8
		6222	6440	7136	7487	BsmF I	GGGAC 15/19	18	BsoF I	GC`N,GC	53
Sec I	(48)	160	236	315	325	Bsp120 I	G`GGCC,C	1	Bsp1286 I	G,DGCH`C	-
		473	537	622	623	BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	1
		761	800	801	813	BspM II	T`CCGG,A	4	Bsr I	ACT,GG`	19
		814	1234	1303	1312	BsrB I	GAG CGG	7	BsrD I	GCAATG, 8	2
		1332	1333	1872	2073	BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	4
		2228	2297	2528	2741	BssS I	C`TCGT,G	6	Bst1107 I	GTA TAC	1
		2742	3189	3426	3438	BstB I	TT`CG,AA	-	BstE II	G`GTNAC,C	3
		3573	3597	3633	3690	BstN I	CC`W,GG	22	BstU I	CG CG	37
		3750	3846	3882	3951	BstX I	CCAN,NNNN`NTGG	1	Bsty I	R`GATC,Y	16
		4077	4492	5156	5231	Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	35
		5310	5320	5467	5530	Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	-
SfaN I	(24)	5616	5617	6220	8066	Csp6 I	G`TA,C	25	Dde I	C`TNA,G	28
		260	520	1005	1585	Dpn I	GA TC	46	DpnII	`GATC,	46
		1729	1796	1868	2053	Dra I	TTT AAA	4	Dra III	CAC,NNN`GTG	2
		2283	2363	2385	2541	Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	9
		3187	4490	5255	5513	Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	5
		5727	5860	5898	5936	Ear I	CTCTTC 7/10	5	Eco47 III	AGC GCT	1
		6156	7208	7401	7648	Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	-
Sfc I	(9)	984	992	1168	1853	EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	5
		3764	5006	6325	6516	EcoR I	G`AATT,C	4	EcoR II	`CCWGG,	22
		7194				EcoR V	GAT ATC	4	Ehe I	GGC GCC	5
Sma I	(2)	475	5469			Esp I	GC`TNA,GC	1	Fnu4H I	GC`N,GC	53
SnaB I	(2)	3169	4472			Fok I	GGATG 14/18	14	Fse I	GG,CCGG`CC	-
Spe I	(2)	727	4131			Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	15
Ssp I	(1)	7757				Gsu I	CTGGAG 21/19	5	Hae I	WGG CCW	10
Stu I	(2)	3638	3860			Hae II	R,CGCG`Y	8	Hae III	GG CC	51
Sty I	(12)	325	537	1312	1872	Hga I	GACGC 9/14	17	Hgia I	G,WGCW`C	9
		3189	3426	3573	3633	HgiE II	ACCNNNNNNGGT -1/132	3	Hha I	G,CG`C	42
Taq I	(20)	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	GTT AAC	-	Hpa II	C`CG,G	36
		4784	4871	6160	7604	Hph I	GGTGA 12/11	19	Kas I	G`GGCG,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
		6035				Mbo I	`GATC,	46	Mbo II	GAAGA 12/11	17
Tsp45 I	(10)	1089	1298	1810	3568	Mlu I	A`CGCG,T	1	Mme I	TCCRCR 25/23	8
		3739	3745	5714	5809	Mnl I	CCTC 10/10	78	Msc I	TGG CCA	3
		7209	7420			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	5460	5807		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	5140	5215	6649	Nco I	C`CATG,G	5	Nde I	CA`TA,TT	4
		6658	6688			NgoM I	G`CCGG,C	-	Nhe I	G`CTAG,C	2
Vsp I	(2)	4139	7125			Nla III	,CATG`	26	Nla IV	GGN NCC	43
Xba I	(1)	5288				Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Xca I	(1)	5833				Nsi I	A,TGCA`T	-	Nsp7524 I	R`CATG,Y	2
Xho II	(16)	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	4926	6701	6712	Pal I	GG CC	51	PflM I	CCAN,NNN`NTGG	1
		6798	6810	7578	7595	Ple I	GAGTC 9/10	3	Pme I	CTTT AAAC	1
Xma I	(2)	473	5467			Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	3
Xma III	(5)	791	1725	1890	2460	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	2
		4863				Pst I	C,TGCA`G	6	Pvu I	CG,AT`CG	2
Xmn I	(1)	7552				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,	46
						Sau96 I	G`GNC,C	44	Sca I	AGT ACT	2
Site usage in pRV-TOMT:						ScrF I	CC`N,GG	44	Sec I	C`CNNG,G	48
Aat II	G,ACGT`C	12	Acc I	GT`MK,AC	2	SfaN I	GCATC 9/13	24	Sfc I	C`TRYA,G	9
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	100	Sfi I	GGCCN,NNN`NGGCC	-	Sma I	CCC GGG	2
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2	SnaB I	TAC GTA	2	Spe I	A`CTAG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	21	Sph I	G,CATG`C	-	Spl I	C`GTAC,G	-
Ahd I	GACNN,N`NNGTC	5	Alu I	AG CT	44	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	1
Alw I	GGATC 8/9	22	AlwN I	CAG,NNN`CTG	4	Stu I	AGG CCT	2	Sty I	C`CWG,G	12
Apa I	G,GGCC`C	1	Apal I	G`TGCA,C	5	Taq I	T`CG,A	20	Tfi I	G`AWT,C	9
Apo I	R`AATT,Y	6	Asc I	GG`CGCG,CC	1	Tsp45 I	`GTSAC,	10	Tth111 I	GACN`N,NGTC	7
Ase I	AT`TA,AT	2	Asp718	G`GTAC,C	2	Tth111 II	CAARCA 16/14	10	Vsp I	AT`TA,AT	2
Ava I	C`YCGR,G	8	Ava II	G`GWC,C	15	Xba I	T`CTAG,A	1	Xca I	GTA TAC	1
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	-
Ban I	G`GYRC,C	15	Ban II	G,RGCY`C	9	Xho II	R`GATC,Y	16	Xma I	C`CCGG,G	2
Bbe I	G,GGCC`C	5	Bbs I	GAAGAC 8/12	3	Xma III	C`GGCC,G	5	Xmn I	GAANN NNITC	1
Bbv I	GCAGC 13/17	13	Bbv II	GAAGAC 7/11	3	Xma III	C`GGCC,G	5	Xmn I	GAANN NNITC	1
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	22						