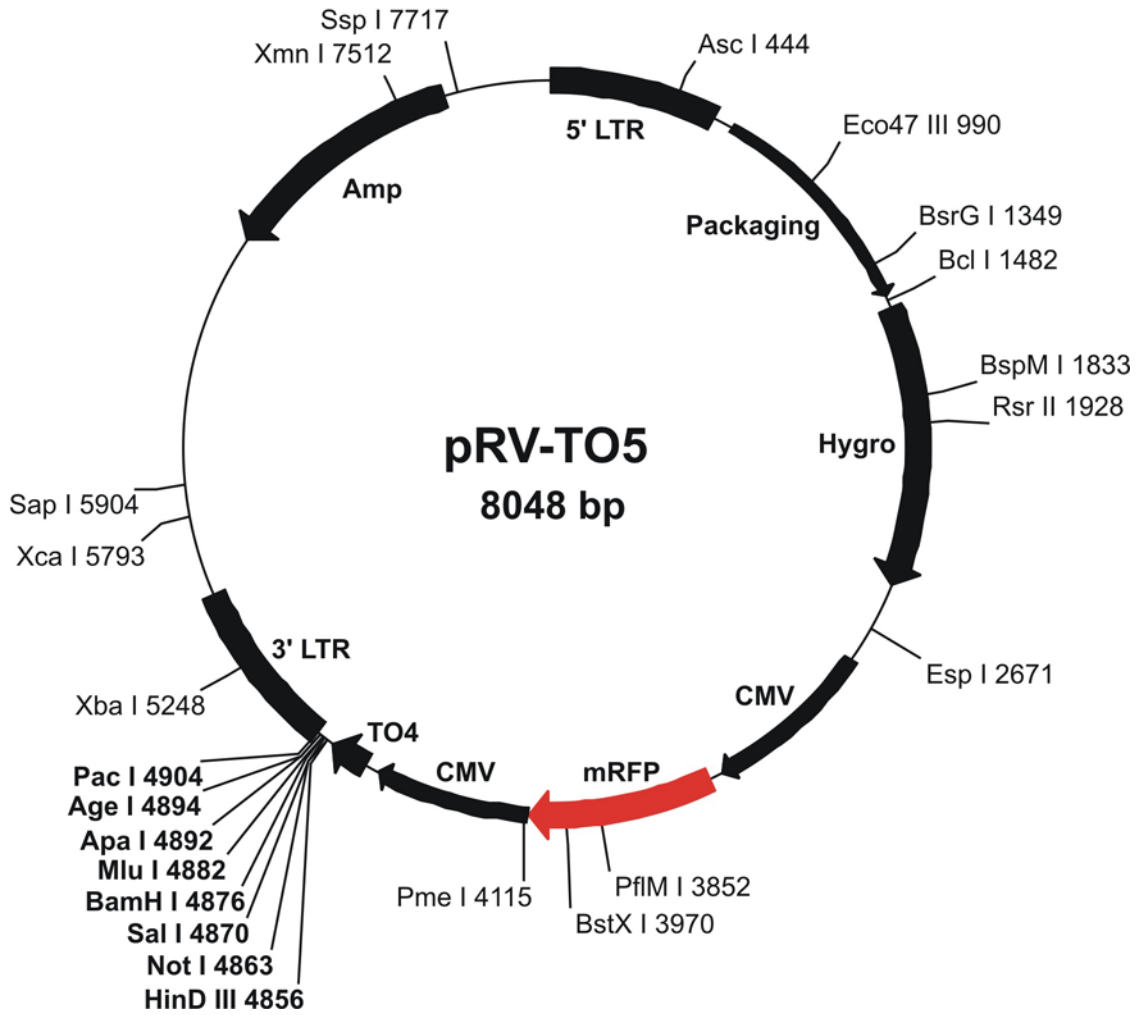


Name of Vector: pRV-TO5  
Antibiotic Selection: Amp  
Created by: Hong Yin  
(He Lab @ The University of Chicago)  
Date of Creation: February 2005



## pRV-T05 Full-length Sequence

TTTCAAAGAC 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  
TTATTTGAAC TAACCAATCA GTTCGCTTCT CGTTCCTGTT CGCGCGCTTC CGCTCTCCGA GCTCAATAAA  
AGAGCCCACA ACCCTCACT CGGCGCGCCA GTCTTCCGAT AGACTGCGTC GCCCGGTAC CCGTATTCCC  
AATAAAGCCT CTTGCTGTTT GCATCCGAAT CGTGGTCTCG CTGTTCCCTG GGAGGGTCTC CTCTGAGTGA  
TTGACTACCC ACGACGGGGT TCTTTCAATTT GGGGGTCTCG CCGGGATTTG GAGACCCCTG CCCAGGGACC  
ACCGACCCAC CACCGGGAGG TAAGCTGGCC AGCAACTTAT CTGTGTCTGT CCGATTGTCT AGTGTCTATG  
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CTGACGAGTT CTGAACACCC GGCCGCAACC CTGGGAGACG TCCCAGGGAC TTTGGGGGCC GTTTTTGTGG  
CCCGACCTGA GGAAGGGAGT CGATGTGGAA TCCGACCCCG TCAGGATATG TGGTCTGGT AGGAGACGAG  
AACCTAAAAC AGTTCCCGCC TCCGTCTGAA TTTTTGCTTT CGGTTTGGAA CCGAAGCCGC GCGTCTGTG  
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TGCCCCGCAT GGACACCCAG ACCAGGTCCC CTACATCGTG ACCTGGGAAG CCTTGGCTTT TGACCCCCCT  
CCCTGGGTCA AGCCCTTTGT ACACCCTAAG CCTCCGCCTC CTCTTCCTCC ATCCGCCCCG TCTCTCCCC  
TTGAACCTCC TCGTTCGACC CCGCCTCGAT CCTCCCTTTA TCCAGCCCTC ACTCCTTCTC TAGGCGCCCG  
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CGACGCTGT CGAGAAGTTT CTGATCGAAA AGTTCGACAG CGTCTCCGAC CTGATGCAGC TCTCGGAGGG  
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GGGCGCAGGG TCGATGCGAC GCAATCGTCC GATCCGGAGC CGGGACTGTC GGGCGTACAC AAATCGCCCG  
CAGAAGCGCG GCCGTCTGGA CCGATGGCTG TGTAGAAGTA CTCGCCGATA GTGGAAACCG ACGCCCCAGC  
ACTCGTCCGA GGGCAAAGGA ATAGAGTAGA TGCCGACCGA ACAAGAGCTG ATTTTCGAGAA CGCCTCAGCC  
AGCAACTCGC GCGAGCCTAG CAAGGCAAAT GCGAGAGAAC GGCCTTACGC TTGGTGGCAC AGTTCCTCGT  
CACAGTTCGC TAAGCTCGCT CCGGTGGGTC GCGGGAGGGC CGGTCGCAGT GATTTCAGGC CTTCTGGATT  
GTGTTGGTCC CCAGGGCAGC ATTGTCAATG CCACGCCTC GGGTGATCTG ACTGATCCCC CAGATTGGAG  
ATCGCCGCC GTGCCTGCC ATTGGGTGC **caga tcc**  
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**cgg atc cA CGC GTG GGC CCA CCG GTtt aat taa cgATAAAAATA AAAGATTTTA TTTAGTCTCC**  
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GTCTTCAAGA ATTCATACCA GATCACCGAA AACTGTCTC CAAATGTGTC CCCCACAC TCCCAAATTC  
GCGGGCTTCT GCCTCTTAGA CCACTCTACC CTATTCCCCA CACTCACCGG AGCCAAAGCC GCGGCCCTTC  
CGTTTTCTTTG CT

**Unique enzymes in prV-T05:**

Asc I	GG`CGCG,CC	444
Eco47 III	AGC GCT	990
BsrG I	T`GTAC,A	1349
Bcl I	T`GATC,A	1482
BspM I	ACCTGC 10/14	1833
Rsr II	CG`GWC,CG	1928
Blp I	GC`TNA,GC	2671
Esp I	GC`TNA,GC	2671
PflM I	CCAN,NNN`NTGG	3852
BstX I	CCAN,NNNN`NTGG	3970
Pme I	CTTT AAAC	4115
HinD III	A`AGCT,T	4856
Not I	GC`GGCC,GC	4863
Sal I	G`TCGA,C	4870
BamH I	G`GATC,C	4876
Mlu I	A`CGCG,T	4882
Bsp120 I	G`GGCC,C	4888
Apa I	G,GGCC`C	4892
Age I	A`CCGG,T	4894
Pac I	TTA,AT`TAA	4904
Xba I	T`CTAG,A	5248
Bst1107 I	GTA TAC	5793
Xca I	GTA TAC	5793
Sap I	GCTCTTC 8/11	5904
Xmn I	GAANN NNTTC	7512
Ssp I	AAT ATT	7717

Number of enzymes = 26

Alw I	(21)	1118	1424	1513	1980
		2298	2407	2780	2827
		3410	4113	4872	4883
		5566	6582	6668	6668
		6765	6766	7230	7545
		7551			
AlwN I	(4)	232	5112	5187	6436
Apa I	(1)	4892			
ApaL I	(5)	1800	2102	5836	6334
		7580			
Apo I	(5)	939	1471	1763	7906
		7962			
Asc I	(1)	444			
Ase I	(2)	4139	7085		
Asp718	(2)	477	5431		
Ava I	(8)	242	473	2769	3689
		3881	5361	5394	5427
Ava II	(15)	261	274	329	627
		757	1286	1928	2469
		2737	5216	5229	5284
		5581	7051	7273	
BamH I	(1)	4876			
Ban I	(15)	319	477	1209	1464
		2094	3294	3545	3803
		3890	3998	4097	5274
		5399	5431	6861	
Ban II	(9)	414	427	598	3488
		4700	4892	5368	5381
		5552			
Bbe I	(5)	1468	3894	4002	4101
		5403			
Bbs I	(3)	445	3848	7891	
Bbv I	(13)	998	1006	1609	1867
		2260	2387	4000	5671
		5768	6439	6442	6648
		7342			
Bbv II	(3)	446	3847	7892	
Bcl I	(1)	1482			
Bcn I	(21)	163	239	475	476
		604	646	791	2307
		2423	3997	5119	5194
		5429	5430	5558	5600
		5667	5702	6401	7097
		7448			

**The following enzymes do not cut in prV-T05:**

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	Spl I

prV-T05: sites sorted by name:

Aat II	(12)	812	1547	2954	3007
		3090	3276	3447	4257
		4310	4393	4579	7835
Acc I	(2)	4871	5792		
Acc65 I	(2)	477	5431		
Aci I	(99)	150	272	401	755
		794	927	968	1109
		1200	1266	1365	1384
		1422	1539	1663	1728
		1795	1845	1865	1889
		1911	1931	2108	2146
		2156	2269	2297	2299
		2320	2449	2459	2692
		2789	2806	2887	2915
		2927	2941	3108	3199
		3232	3336	3357	3418
		3532	3555	3579	3654
		3732	3801	3871	3936
		4084	4190	4218	4230
		4244	4411	4502	4535
		4639	4660	4862	4866
		5227	5529	5693	5732
		5742	5784	5809	5847
		5860	5886	5903	5946
		5953	5974	6065	6093
		6220	6239	6360	6470
		6605	6614	6976	7067
		7258	7304	7425	7469
		7546	7655	7754	7801
		7968	8026	8028	
Afl II	(3)	35	1073	4986	
Afl III	(2)	4882	6020		
Age I	(1)	4894			
Aha II	(21)	809	1465	1544	2512
		2951	3004	3087	3273
		3444	3891	3948	3999
		4098	4254	4307	4390
		4576	4819	5400	7450
		7832			
Ahd I	(5)	1087	3607	5476	5522
		6913			
Alu I	(44)	30	34	120	191
		412	655	735	743
		1488	1600	1632	1674
		2059	2284	2349	2378
		2568	2675	3395	3562
		3679	3796	3925	3991
		4021	4698	4788	4858
		4981	4985	5072	5147
		5366	5609	5662	5681
		5962	6188	6278	6324
		6581	7102	7202	7265
Bfa I	(14)	31	294	690	728
		740	1461	2608	3421
		4132	4982	5249	6515
		6768	7103		
Bgl I	(7)	2919	3041	3112	4222
		4344	4415	7033	
Bgl II	(4)	4718	4739	4760	4850
Blp I	(1)	2671			
Bpm I	(5)	2188	2242	4834	4919
		6983			
Bsa I	(8)	531	552	606	1216
		5484	5505	5560	6974
BsaA I	(4)	3169	3643	4472	5774
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	5400	7450
		7832			
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	5116	5191
		5270	5280	5427	5490
		5576	5577	6180	8026
BsaW I	(9)	1520	1741	2278	2414
		4894	6226	6373	7204
		8013			
BseR I	(6)	540	1360	1399	3424
		3748	5493		
Bsg I	(2)	2848	4007		
BsiE I	(13)	794	1728	1863	1884
		1893	2463	2558	2705
		4866	5936	6360	7283
		7432			
BsiHKA I	(9)	414	1804	2106	4700
		5368	5840	6338	7499
		7584			
BsmA I	(22)	180	530	551	607
		801	899	1016	1140
		1199	1217	1395	1587
		3262	4565	4811	4936
		5483	5504	5561	5664
		6975	7749		
BsmB I	(8)	800	898	1139	1198
		1396	1588	4810	5663
BsmF I	(18)	247	640	796	831
		1272	2437	2723	3004
		3155	3323	3595	3614
		4307	4458	4626	5202



		3444	3891	3948	3999	MspAl I	(14)	120	191	1847	2156
		4098	4254	4307	4390			2299	3991	5072	5147
		4576	4819	5400	7450			5529	5732	6362	6607
		7832						7548	8028		
HinP I	(42)	393	395	444	446	Nar I	(5)	1465	3891	3999	4098
		713	970	989	1465			5400			
		1677	1730	1974	2042	Nci I	(21)	162	238	474	475
		2257	2384	2457	2600			603	645	790	2306
		3463	3475	3709	3799			2422	3996	5118	5193
		3891	3999	4072	4074			5428	5429	5557	5599
		4098	5347	5349	5400			5666	5701	6400	7096
		5621	5724	5754	5895			7447			
		5928	6198	6265	6365	Nco I	(5)	1872	3189	3426	3846
		6539	6648	7041	7134			4492			
Hpa II	(36)	7471	7803			Nde I	(4)	1970	3063	4366	5843
		162	238	474	602	Nhe I	(2)	30	4981		
		644	790	1468	1521	Nla III	(26)	62	1272	1876	1959
		1742	1859	2092	2279			1994	2760	3133	3193
		2305	2415	2421	2701			3430	3463	3481	3850
		3996	4095	4895	5118			3973	4436	4496	5013
		5193	5428	5556	5598			5659	5764	6024	6744
		5666	5700	6227	6374			7235	7245	7323	7359
		6400	6590	6994	7028			7752	7857		
Hph I	(19)	7095	7205	7447	8014	Nla IV	(43)	154	247	263	321
		1224	1250	1529	2784			479	628	759	828
		3204	3579	3750	3801			960	1211	1288	1466
		4022	4507	5641	5650			2096	2119	2303	2419
		6757	6984	7398	7606			2739	3296	3487	3547
		7639	7913	8004				3583	3631	3805	3826
Kas I	(5)	1464	3890	3998	4097			3892	4000	4099	4599
		5399						4878	4890	5218	5276
Kpn I	(2)	481	5435					5401	5433	5582	6052
Mae I	(14)	31	294	690	728			6091	6863	6957	6998
		740	1461	2608	3421			7209	7799	8018	
		4132	4982	5249	6515	Not I	(1)	4863			
		6768	7103			Nsp7524 I	(2)	5655	6020		
Mae II	(24)	809	1148	1189	1544	NspB II	(14)	120	191	1847	2156
		1814	2951	2963	3004			2299	3991	5072	5147
		3087	3168	3273	3444			5529	5732	6362	6607
		3642	4254	4266	4307			7548	8028		
		4390	4471	4576	5773			5659	6024		
		6723	7139	7512	7832	NspH I	(2)	5659	6024		
Mae III	(26)	39	1061	1089	1154	Pac I	(1)	4904			
		1298	1810	2890	2977	Pal I	(51)	172	203	248	659
		3326	3568	3739	3745			793	829	841	1054
		4193	4280	4629	4990			1178	1199	1264	1727
		5674	5769	6376	6439			1871	1892	1920	2072
		6555	6838	7169	7227			2145	2227	2462	2633
		7380	7568					2700	2719	2913	3106
Mbo I	(45)	94	1111	1243	1428			3431	3498	3531	3582
		1477	1482	1517	1563			3638	3825	3860	3939
		1696	1881	1894	1984			3974	4083	4216	4409
		2291	2411	2775	2784			4865	4890	5083	5128
		2800	2831	3414	3510			5158	5203	6035	6046
		3906	4106	4718	4739			6064	6498	6956	7036
		4760	4781	4806	4850			7303	7890	8031	
		4876	5045	5559	6586	PflM I	(1)	3852			
		6661	6672	6680	6758	Ple I	(3)	866	5429	6399	
		6770	6875	7216	7234	Pme I	(1)	4115			
		7280	7538	7555	7591	PpuM I	(3)	329	1286	5284	
		7917				Psp1406 I	(2)	7139	7512		
Mbo II	(16)	446	1153	1366	1624	PspA I	(2)	473	5427		
		2207	2210	3849	3852	Pst I	(6)	988	996	1172	1857
		4859	5892	6681	6754			3768	7158		
		7509	7587	7696	7892	Pvu I	(2)	1884	7283		
						Pvu II	(5)	120	191	3991	5072
Mlu I	(1)	4882						5147			
Mme I	(8)	896	1173	1610	2144	Rsa I	(25)	348	479	726	1351
		3842	5492	6234	6418			1503	2437	2490	3048
Mnl I	(76)	291	444	508	536			3073	3128	3161	3212
		560	641	843	939			3369	3626	3878	4067
		1235	1338	1371	1377			4351	4376	4431	4464
		1380	1386	1416	1419			4515	4672	5433	5828
		1434	1441	1457	1600			7393			
		1637	1861	2068	2107	Rsr II	(1)	1928			
		2167	2194	2217	2265	Sac I	(3)	414	4700	5368	
		2523	2593	2689	3370	Sac II	(2)	2300	8029		
		3433	3441	3444	3475	Sal I	(1)	4870			
		3508	3514	3520	3535	Sap I	(1)	5904			
		3623	3685	3718	3768	Sau3A I	(45)	94	1111	1243	1428
		3825	3850	3870	3877			1477	1482	1517	1563
		3909	3946	4036	4041			1696	1881	1894	1984
		4072	4673	4849	5246			2291	2411	2775	2784
		5398	5417	5462	5489			2800	2831	3414	3510
		5513	5595	5626	5656			3906	4106	4718	4739
		5918	6128	6201	6452			4760	4781	4806	4850
		6852	6933	7079	7285			4876	5045	5559	6586
		7880	7943	7959	7988			6661	6672	6680	6758
Msc I	(3)	659	1178	3974				6770	6875	7216	7234
Mse I	(20)	36	1074	1186	1216			7280	7538	7555	7591
		1240	4114	4139	4900			7917			
		4904	4987	5801	6726	Sau96 I	(44)	170	201	246	261
		6778	6783	6797	6850			274	329	627	757
		7085	7124	7489	7861			827	840	1052	1263
Msl I	(4)	3194	4497	7165	7324			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	5081	5126
		3996	4095	4895	5118			5156	5201	5216	5229
		5193	5428	5556	5598			5284	5581	6955	7034
		5666	5700	6227	6374			7051	7273	7889	8030
		6400	6590	6994	7028	Sca I	(2)	2490	7393		
		7095	7205	7447	8014	ScrF I	(43)	162	238	316	474

		475	603	624	645	Bfa I	C`TA,G	14	Bgl I	GCCN,NNN`NGGC	7
		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	5118	BsaW I	W`CCGG,W	9	BseR I	GAGGAG 16/14	6
		5193	5271	5428	5429	Bsg I	GTGCAG 22/20	2	BsiC I	TT`CG,AA	-
		5557	5578	5599	5666	BsiE I	CG,R`Y`CG	13	BsiHKA I	G,WGCW`C	9
		5701	6048	6169	6182	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	-
		6400	7096	7447		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	52
		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	5116	5191	BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	15
		5270	5280	5427	5490	Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	35
SfaN I	(24)	5576	5577	6180	8026	Cfr10 I	R`CCGG,Y	5	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	5215	5473	Drd I	GACNN,NN`NNGTC	5	Dsa I	C`CRYG,G	9
		5687	5820	5858	5896	Eae I	Y`GGCC,R	13	Eag I	C`GGCC,G	5
Sfc I	(9)	6116	7168	7361	7608	Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	1
		984	992	1168	1853	Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	-
		3764	4966	6285	6476	EcoN I	CCTNN`N,NNAGG	2	Eco109 I	RG`GNC,CY	5
		7154				EcoR I	G`AATT,C	3	EcoR II	`CCWGG,	22
Sma I	(2)	475	5429			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	52
Spe I	(2)	727	4131			Fok I	GGATG 14/18	14	Fse I	GG,CCGG`CC	-
Ssp I	(1)	7717				Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	15
Stu I	(2)	3638	3860			Gsu I	CTGGAG 21/19	5	Hae I	WGG CCW	10
Sty I	(12)	325	537	1312	1872	Hae II	R,CGCG`Y	8	Hae III	GG CC	51
		3189	3426	3573	3633	Hga I	GACGC 9/14	17	Hgia I	G,WGCW`C	9
		3846	4492	5280	5490	HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	42
Taq I	(20)	861	1105	1416	1427	Hinc II	GTY CAC	3	Hind II	GTY CAC	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	6120	7564	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
		5995				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	TCCRCR 25/23	8
		3739	3745	5674	5769	Mnl I	CCTC 10/10	76	Msc I	TGG CCA	3
		7169	7380			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	5420	5767		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	21
		1740	5100	5175	6609	Nco I	C`CATG,G	5	Nde I	CA`TA,TG	4
		6618	6648			NgoM I	G`CCGG,C	-	Nhe I	G`CTAG,C	2
Vsp I	(2)	4139	7085			Nla III	,CATG`	26	Nla IV	GGN NCC	43
Xba I	(1)	5248				Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Xca I	(1)	5793				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	6661	6672	6758	Pal I	GG CC	51	Pf1M I	CCAN,NNN`NTGG	1
		6770	7538	7555		Ple I	GAGTC 9/10	3	Pme I	CTTT AAC	1
Xma I	(2)	473	5427			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)	7512				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	43	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	-	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`CWVG,G	12
						Taq I	T`CG,A	20	Tfi I	G`AWT,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-TO5:											
Aat II	G,ACGT`C	12	Acc I	GT`MK,AC	2	Acc I	GT`MK,AC	2	Sau96 I	G`GNC,C	44
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	99	Aci I	C`CG,C	99	ScrF I	CC`N,GG	43
Afl II	C`TTAA,G	3	Afl III	A`CRYG,T	2	Afl III	A`CRYG,T	2	SfaN I	GCATC 9/13	24
Age I	A`CCGG,T	1	Aha II	GR`CG,YC	21	Aha II	GR`CG,YC	21	Sfi I	GGCCN,NNN`NGGCC	-
Ahd I	GACNN,N`NNGTC	5	Alu I	AG CT	44	Alu I	AG CT	44	SnaB I	TAC GTA	-
Alw I	GGATC 8/9	21	AlwN I	CAG,NNN`CTG	4	AlwN I	CAG,NNN`CTG	4	Sph I	G,CATG`C	-
Apa I	G,GGCC`C	1	ApaL I	G`TGCA,C	5	ApaL I	G`TGCA,C	5	Srf I	GCCC GGGC	-
Apo I	R`AATT,Y	5	Asc I	GG`CGCG,CC	1	Asc I	GG`CGCG,CC	1	Stu I	AGG CCT	2
Ase I	AT`TA,AT	2	Asp718	G`GTAC,C	2	Asp718	G`GTAC,C	2	Taq I	T`CG,A	20
Ava I	C`YCGR,G	8	Ava II	G`GWC,C	15	Ava II	G`GWC,C	15	Tsp45 I	`GTSAC,	10
Avr II	C`CTAG,G	-	BamH I	G`GATC,C	1	BamH I	G`GATC,C	1	Tth111 II	CAARCA 16/14	10
Ban I	G`GYRC,C	15	Ban II	G,RGCY`C	9	Ban II	G,RGCY`C	9	Xba I	T`CTAG,A	1
Bbe I	G,CGGC`C	5	Bbs I	GAAGAC 8/12	3	Bbs I	GAAGAC 8/12	3	Xcm I	CCANNNN,N`NNNNTGG-	-
Bbv I	GCAGC 13/17	13	Bbv II	GAAGAC 7/11	3	Bbv II	GAAGAC 7/11	3	Xho II	R`GATC,Y	15
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	21	Bcn I	CC,S`GG	21	Xma III	C`GGCC,G	5