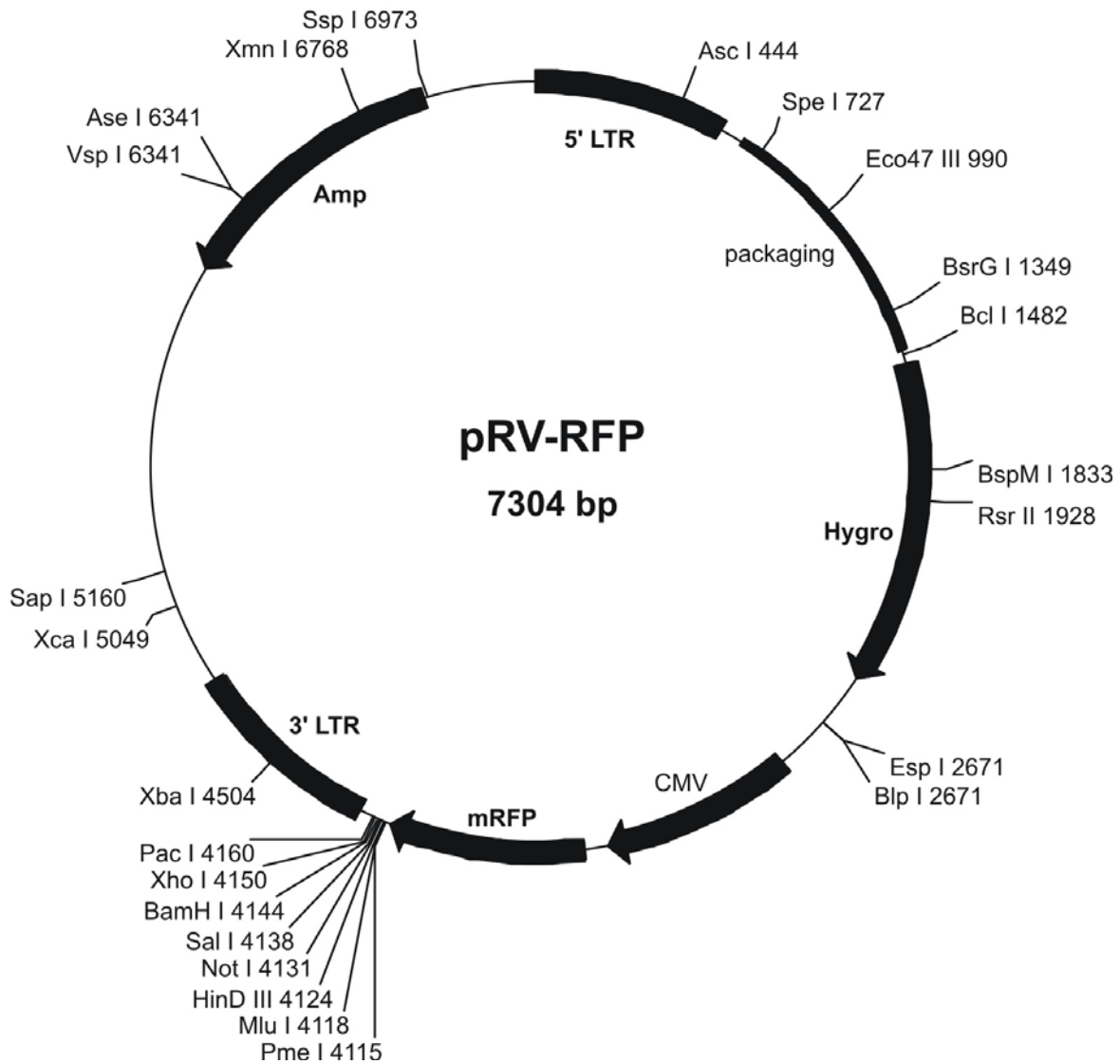


Name of Vector: pRV-RFP
Antibiotic Selection: Amp
Created by: Wei Jiang and Hong Yin
(He Lab @ The University of Chicago)
Date of Creation: February 2005



pRV-RFP

TTTGAAAGAC CCCACCCGTA GGTGGCAAGC TAGCTTAAGT AACGCCACTT TGCAAGGCAT GGAAAAATAC
ATAACTGAGA ATAGAAAAGT TCAGATCAAG GTCAGGAACA AAGAAACAGC TGAATACCAA ACAGGATATC
TGTGGTAAGC GGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGAGACAG CTGAGTGATG GGCCAAACAG
GATATCTGTG GTAAGCAGTT CCTGCCCCGG CTCGGGGCCA AGAACAGATG GTCCCCAGAT GCGGTCCAGC
CCTCAGCAGT TTCTAGTGAA TCATCAGATG TTTCCAGGGT GCCCAAGGA CCTGAAAATG ACCCTGTACC
TTATTTGAAC TAACCAATCA GTTCGCTTCT CGCTTCTGTT CGCGCGCTTC CGCTCTCCGA GCTCAATAAA
AGAGCCACA ACCCTCACT CGGCGGCCA GTCTTCCGAT AGACTGCGTC GCCCGGTAC CCTTATCC
AATAAAGCCT CTTGCTGTTT GCATCCGAAT CGTGGTCTCG CTGTTCCCTG GGAGGGTCTC CTCTGAGTGA
TTGACTACCC ACGACGGGGG TCTTTCATTT GGGGGCTCGT 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 TGGTTCCTGGT AGGAGACGAG
AACCTAAAAC AGTTCCTGCC TCCGTCTGAA TTTTTGCTTT CGTTTTGGAA CCGAAGCCGC GCGTCTGTGTC
TGCTGCAGCG CTGCAGCAT 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
TGGCCCGCAT GGACACCCAG ACCAGGTCCC CTACATCGTG ACCTGGGAAG CCTTGGCTTT TGACCCCCCT
CCCTGGGTCA AGCCCTTTGT ACACCTAAG CCTCCGCTC CTCTTCCCTC ATCCGCCCCG TCTCTCCCC
TTGAACCTCC TCGTTCGACC CCGCTCGAT CCTCCCTTTA TCCAGCCCTC ACTCCTTCTC TAGGCGCCGG
AATTCGATC TGATCAGCTT GCCACAACC GTACCAAAGA TGGATAGATC CGGAAAGCCT GAACTCACCG
CGACGTCTGT CGAGAAGTTT CTGATCGAAA AGTTCGACAG CGTCTCCGAC CTGATGCAGC TCTCGGAGG
CGAAGAATCT CGTCTTTTCA GCTTCGATGT AGGAGGGCGT GGATATGTCC TGCGGGTAAA TAGCTGCGCC
GATGGTTTCT ACAAAGATCG TTATGTTTAT CGGCACTTTG CATCGGCCG CTCCCGATT GCTCCAGTGC
TTGACATTGG GGAATTCAGC GAGAGCCTGA CCTATTGCAT CTCCCGCCGT GCACAGGGTG TCACGTTGCA
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GCCGATCTTA GCCAGACGAG CGGGTTCGGC CCATTCGGAC CGCAAGGAAT CCGTCAATAC ACTACATGGC
GTGATTTTCAT ATGCGCGATT GCTGATCCCC ATGTGTATCA CTGGCAAAC GTGATGGACG ACACCGTCAG
TGCGTCCGTC GCGCAGGCTC TCGATGAGCT GATGCTTTGG GCCGAGGACT GCCCGAAGT CCGGCACCTC
GTGCACGCGG ATTTCCGGCTC CAACAATGTC CTGACGGACA ATGGCCGCAT AACAGCGGTC ATTGACTGGA
GCGAGGCGAT GTTCGGGGAT TCCCAATACG AGGTCGCCAA CATCTTCTTC TGGAGCCGT GGTGGCTTG
TATGGAGCAG CAGACGCGCT ACTTCGAGCG GAGGCATCCG GAGCTTGCAG GATCGCCCG GCTCCGGGCG
TATATGCTCC GCATTGGTCT TGACCAACTC TATCAGAGCT TGGTTGACGG CAATTTTCGAT GATGCAGCTT
GGGCGCAGGG TCGATGCGAC GCAATCGTCC GATCCGGAGC CGGGACTGTC GGGCGTACAC AAATCGCCCC
CAGAAGCGCG GCCGTCTGGA CCGATGGCTG TGTAGAAGTA CTCGCCGATA GTGGAAACCG ACGCCCCAGC

ACTCGTCCGA GGGCAAAGGA ATAGAGTAGA TGCCGACCGA ACAAGAGCTG
ATTTGAGAA CGCCTCAGCC AGCAACTCGC GCGAGCCTAG CAAGGCAAAT
GCGAGAGAAC GGCCTTACGC TTGGTGGCAC AGTTCTCGTC CACAGTTCGC
TAAGCTCGCT CGGCTGGGTC GCGGGAGGGC CGGTCGCAGT GATTCAGGCC
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GGGTGATCTG ACTGATCCCG CAGATTGGAG ATCGCCGCC GTGCCTGCCG
ATTGGGTGCaga tcc

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CGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATG
ACCTTATGGGACTTTCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATG
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CGGTGGGAGGTCTATATAAGCAGAGCTGGTTTAGTGAACCGTCAGATCCGCTAGaccatgg
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ctccaccggcgccctaaggatct **gttt aaa cgc gta agc ttg cgg ccg cgt cga cgg atc cct cga gtt aat**
taa cgATAAAATA AAAGATTTTA TTAGTCTCC AGAAAAGGG GGAATGAAA

GACCCACCT GTAGTTTTGG CAAGCTAGCT TAAGTAACGC CATTTTGCAA GGCATGAAAA AATACATAAC
TGAGAATAGA GAAGTTCAGA TCAAGGTCAG GAACAGATGG AACAGCTGAA TATGGGCCAA ACAGGATATC
TGTGGTAAGC AGTTCCTGCC CCGGCTCAGG GCCAAGAACA GATGGAACAG CTGAATATGG GCCAAACAGG
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CTCAGCAGTT TCTAGAGAAC CATCAGATGT TTCCAGGGTG CCCAAGGAC CTGAAATGAC CCTGTGCCTT
ATTTGAACTA ACCAATCAGT TCGCTTCTCG CTCTGTTCG CGCGCTTCTG CTCCCCGAGC TCAATAAAAAG
AGCCACAAC CCCTCACTCG GGGCGCCAGT CCTCCGATTG ACTGAGTCGC CCGGGTACCC GTGTATCCAA
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GGCTTAACTA TGCGGCATCA GAGCAGATTG TACTGAGAGT GCACCATATG CCGTGTGAAA TACCGCACAG
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GCGGGCTTCT GCCTCTTAGA CCACTCTACC CTATTCCCCA CACTCACCGG AGCCAAAGCC GCGGCCCTTC
CGTTTCTTTG CT

Unique enzymes in pRV-RFP:

Aac I	GG`CGCG,CC	444				5024	5695	5698	5904
Spe I	A`CTAG,T	727				6598			
Eco47 III	AGC GCT	990			Bbv II (3)	446	3847	7148	
BsrG I	T`GTAC,A	1349			Bcl I (1)	1482			
Bcl I	T`GATC,A	1482			Bcn I (21)	163	239	475	476
BspM I	ACCTGC 10/14	1833				604	646	791	2307
Rsr II	CG`GWC,CG	1928				2423	3997	4375	4450
Blp I	GC`TNA,GC	2671				4685	4686	4814	4856
Bsp I	GC`TNA,GC	2671				4923	4958	5657	6353
SnaB I	TAC GTA	3169				6704			
PflM I	CCAN,NNN`NTGG	3852			Bfa I (13)	31	294	690	728
BstX I	CCAN,NNNN`NTGG	3970				740	1461	2608	3421
Pme I	CTTT AAAC	4115				4238	4505	5771	6024
Mlu I	A`CGCG,T	4118				6359			
Hind III	A`AGCT,T	4124			Bgl I (4)	2919	3041	3112	6289
Not I	GC`GGCC,GC	4131			Blp I (1)	2671			
Sal I	G`TCGA,C	4138			Bpm I (4)	2188	2242	4175	6239
BamH I	G`GATC,C	4144			Bsa I (8)	531	552	606	1216
PaeR7 I	C`TCGA,G	4150				4740	4761	4816	6230
Xho I	C`TCGA,G	4150			BsaA I (3)	3169	3643	5030	
Pac I	TTA,AT`TAA	4160			BsaH I (16)	809	1465	1544	2512
Xba I	T`CTAG,A	4504				2951	3004	3087	3273
Bst1107 I	GTA TAC	5049				3444	3891	3948	3999
Xca I	GTA TAC	5049				4098	4656	6706	7088
Sap I	GCTCTTC 8/11	5160			BsaJ I (47)	160	236	315	325
Ase I	AT`TA,AT	6341				473	537	622	623
Vsp I	AT`TA,AT	6341				761	800	801	813
Xmn I	GAANN NNTTC	6768				814	1234	1303	1312
Ssp I	AAT ATT	6973				1332	1333	1872	2073
Number of enzymes = 29									

The following enzymes do not cut in pRV-RFP:

Age I	Apa I	Avr II	Bgl II	BsaB I
BsiC I	BsiW I	Bsm I	Bsp120 I	Bspl286 I
BstB I	Cla I	Eco72 I	Fse I	Hpa I
Mun I	Nae I	Ngm I	Nru I	Nsi I
Pml I	Sfi I	Sph I	Spl I	Srf I

pRV-RFP: sites sorted by name:

Aat II (8)	812	1547	2954	3007					
	3090	3276	3447	7091					
Acc I (2)	4139	5048							
Acc65 I (2)	477	4687							
Aci I (90)	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	4130	4134	4483					
	4785	4949	4988	4998					
	5040	5065	5103	5116					
	5142	5159	5202	5209					
	5230	5321	5349	5476					
	5495	5616	5726	5861					
	5870	6232	6323	6514					
	6560	6681	6725	6802					
	6911	7010	7057	7224					
	7282	7284							
Afl II (3)	35	1073	4242						
Afl III (2)	4118	5276							
Aha II (16)	809	1465	1544	2512					
	2951	3004	3087	3273					
	3444	3891	3948	3999					
	4098	4656	6706	7088					
Ahd I (5)	1087	3607	4732	4778					
	6169								
Alu I (42)	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	4126	4237	4241					
	4328	4403	4622	4865					
	4918	4937	5218	5444					
	5534	5580	5837	6358					
	6458	6521							
Alw I (21)	1118	1424	1513	1980					
	2298	2407	2780	2827					
	3410	4113	4140	4151					
	4822	5838	5924	5924					
	6021	6022	6486	6801					
	6807								
AlwN I (4)	232	4368	4443	5692					
Apal I (5)	1800	2102	5092	5590					
	6836								
Apo I (5)	939	1471	1763	7162					
	7218								
Asc I (1)	444								
Ase I (1)	6341								
Asp718 (2)	477	4687							
Ava I (9)	242	473	2769	3689					
	3881	4150	4617	4650					
	4683								
Ava II (15)	261	274	329	627					
	757	1286	1928	2469					
	2737	4472	4485	4540					
	4837	6307	6529						
BamH I (1)	4144								
Ban I (15)	319	477	1209	1464					
	2094	3294	3545	3803					
	3890	3998	4097	4530					
	4655	4687	6117						
Ban II (7)	414	427	598	3488					
	4624	4637	4808						
Bbe I (5)	1468	3894	4002	4101					
	4659								
Bbs I (3)	445	3848	7147						
Bbv I (13)	998	1006	1609	1867					
	2260	2387	4000	4927					
					Bbv II (3)	446	3847	7148	
					Bcl I (1)	1482			
					Bcn I (21)	163	239	475	476
						604	646	791	2307
						2423	3997	4375	4450
						4685	4686	4814	4856
						4923	4958	5657	6353
						6704			
					Bfa I (13)	31	294	690	728
						740	1461	2608	3421
						4238	4505	5771	6024
						6359			
					Bgl I (4)	2919	3041	3112	6289
					Blp I (1)	2671			
					Bpm I (4)	2188	2242	4175	6239
					Bsa I (8)	531	552	606	1216
						4740	4761	4816	6230
					BsaA I (3)	3169	3643	5030	
					BsaH I (16)	809	1465	1544	2512
						2951	3004	3087	3273
						3444	3891	3948	3999
						4098	4656	6706	7088
					BsaJ I (47)	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	4372	4447	4526
						4536	4683	4746	4832
						4833	5436	7282	
					BsaW I (8)	1520	1741	2278	2414
						5482	5629	6460	7269
						540	1360	1399	3424
					BseR I (6)	3748	4749		
						2848	4007		
					Bsg I (2)	794	1728	1863	1884
					BsiE I (13)	1893	2463	2558	2705
						4134	5192	5616	6539
						6688			
					BsiHKA I (8)	414	1804	2106	4624
						5096	5594	6755	6840
					BsmA I (20)	180	530	551	607
						801	899	1016	1140
						1199	1217	1395	1587
						3262	4192	4739	4760
						4817	4920	6231	7005
					Bsmb I (7)	800	898	1139	1198
						1396	1588	4919	
					BsmF I (15)	247	640	796	831
						1272	2437	2723	3004
						3155	3323	3595	3614
						4458	4850	7186	
					BsoF I (52)	794	968	984	987
						992	995	1200	1598
						1675	1728	1856	1887
						1890	2146	2249	2297
						2300	2376	2460	2806
						3532	3580	3733	3797
						3802	3937	3989	3992
						4084	4131	4134	4870
						4916	5013	5066	5182
						5200	5203	5321	5476
						5619	5684	5687	5893
						6221	6410	6560	6587
						6682	6911	7282	7285
					BspH I (3)	5996	7004	7109	
					BspM I (1)	1833			
					BspM II (4)	1520	1741	227	

		3368	3625	3877	4066			2951	3004	3087	3273
		4688	5083	6648				3444	3891	3948	3999
Dde I	(26)	76	166	192	283			4098	4656	6706	7088
		554	848	1085	1357	HinP I	(42)	393	395	444	446
		1898	2585	2671	3615			713	970	989	1465
		4102	4283	4378	4453			1677	1730	1974	2042
		4494	4675	4763	5086			2257	2384	2457	2600
		5551	5960	6126	6666			3463	3475	3709	3799
		7092	7238					3891	3999	4072	4074
Dpn I	(39)	96	1113	1245	1430			4098	4603	4605	4656
		1479	1484	1519	1565			4877	4980	5010	5151
		1598	1883	1896	1986			5184	5454	5521	5621
		2293	2413	2777	2786			5795	5904	6297	6390
		2802	2833	3416	3512			6727	7059		
		3908	4108	4146	4303	Hpa II	(35)	162	238	474	602
		4817	5844	5919	5930			644	790	1468	1521
		5938	6016	6028	6133			1742	1859	2092	2279
		6474	6492	6538	6796			2305	2415	2421	2701
		6813	6849	7175				3996	4095	4374	4449
DpnII	(39)	94	1111	1243	1428			4684	4812	4854	4922
		1477	1482	1517	1563			4956	5483	5630	5656
		1696	1881	1894	1984			5846	6250	6284	6351
		2291	2411	2775	2784			6461	6703	7270	
		2800	2831	3414	3510	Hph I	(18)	1224	1250	1529	2784
		3906	4106	4144	4301			3204	3579	3750	3801
		4815	5842	5917	5928			4022	4897	4906	6013
		5936	6014	6026	6131			6240	6654	6862	6895
		6472	6490	6536	6794			7169	7260		
		6811	6847	7173		Kas I	(5)	1464	3890	3998	4097
Dra I	(4)	4115	6035	6054	6746			4655			
Dra III	(2)	1808	2101			Xpn I	(2)	481	4691		
Drd I	(5)	2024	2405	3953	4971	Mae I	(13)	31	294	690	728
		5384						740	1461	2608	3421
		761	1872	2228	2297			4238	4505	5771	6024
Dsa I	(8)	3189	3426	3846	7282			6359			
Eae I	(13)	657	791	1176	1197	Mae II	(18)	809	1148	1189	1544
		1725	1890	2143	2460			1814	2951	2963	3004
		3496	3937	3972	4131			3087	3168	3273	3444
		6557						3642	5029	5979	6395
Eag I	(5)	791	1725	1890	2460			6768	7088		
		4131				Mae III	(23)	39	1061	1089	1154
Ear I	(4)	1137	1378	5160	6964			1298	1810	2890	2977
Eco47 III	(1)	990						3326	3568	3739	3745
Eco57 I	(6)	3583	3916	3940	3946			4246	4930	5025	5632
		5823	6837					5695	5811	6094	6425
EcoN I	(2)	851	1459					6483	6636	6824	
EcoO109 I	(5)	329	1286	2718	4540	Mbo I	(39)	94	1111	1243	1428
		7145						1477	1482	1517	1563
		1471	1763	7162				1696	1881	1894	1984
EcoR I	(3)	314	622	800	813			2291	2411	2775	2784
EcoR II	(19)	1234	1259	1282	1302			2800	2831	3414	3510
		1332	2741	2917	3110			3906	4106	4144	4301
		3596	3750	4525	4832			4815	5842	5917	5928
		5302	5423	5436				5936	6014	6026	6131
EcoR V	(4)	138	214	4350	4425			6472	6490	6536	6794
Ehe I	(5)	1466	3892	4000	4099			6811	6847	7173	
		4657				Mbo II	(15)	446	1153	1366	1624
Esp I	(1)	2671						2207	2210	3849	3852
Fnu4H I	(52)	794	968	984	987			5148	5937	6010	6765
		992	995	1200	1598			6843	6952	7148	
		1675	1728	1856	1887						
		1890	2146	2249	2297	Mlu I	(1)	4118			
		2300	2376	2460	2806			896	1173	1610	2144
		3532	3580	3733	3797			3842	4748	5490	5674
		3802	3937	3989	3992	Mme I	(8)	291	444	508	536
		4084	4131	4134	4870			560	641	843	939
		4916	5013	5066	5182	Mnl I	(75)	1235	1338	1371	1377
		5200	5203	5321	5476			1380	1386	1416	1419
		5619	5684	5687	5893			1434	1441	1457	1600
		6221	6410	6560	6587			1637	1861	2068	2107
		6682	6911	7282	7285			2167	2194	2217	2265
Fok I	(13)	499	1207	1367	1889			2523	2593	2689	3370
		2262	3590	3647	3886			3433	3441	3444	3475
		4708	4964	6135	6316			3508	3514	3520	3535
		6603						3623	3685	3718	3768
		3476	6391					3825	3850	3870	3877
Fsp I	(2)	790	792	1196	1724			3909	3946	4036	4041
Gdi II	(15)	1726	1889	1891	2142			4072	4158	4502	4654
		2459	2461	3497	3938			4673	4718	4745	4769
		4130	4132	6556				4851	4882	4912	5174
Gsu I	(4)	2187	2241	4176	6240			5384	5457	5708	6108
Hae I	(10)	659	1178	1871	3431			6189	6335	6541	7136
		3638	3860	3974	5291			7199	7215	7244	
		5302	5754			Msc I	(3)	659	1178	3974	
Hae II	(8)	992	1468	3894	4002	Mse I	(19)	36	1074	1186	1216
		4101	4659	5154	5524			1240	4114	4156	4160
Hae III	(48)	172	203	248	659			4243	5057	5982	6034
		793	829	841	1054			6039	6053	6106	6341
		1178	1199	1264	1727			6380	6745	7117	
		1871	1892	1920	2072	Msl I	(3)	3194	6421	6580	
		2145	2227	2462	2633			162	238	474	602
		2700	2719	2913	3106	Msp I	(35)	644	790	1468	1521
		3431	3498	3531	3582			1742	1859	2092	2279
		3638	3825	3860	3939			2305	2415	2421	2701
		3974	4083	4133	4339			3996	4095	4374	4449
		4384	4414	4459	5291			4684	4812	4854	4922
		5302	5320	5754	6212			4956	5483	5630	5656
		6292	6559	7146	7287			5846	6250	6284	6351
Hga I	(15)	457	709	962	1571			6461	6703	7270	
		2023	2262	2407	2519	MspAl I	(14)	120	191	1847	2156
		3354	3955	4126	4972			2299	3991	4328	4403
		5386	5964	6966				4785	4988	5618	5863
HgiA I	(8)	414	1804	2106	4624			6804	7284		
		5096	5594	6755	6840	Nar I	(5)	1465	3891	3999	4098
HgiE II	(2)	5094	5855					4656			
Hha I	(42)	395	397	446	448	Nci I	(21)	162	238	474	475
		715	972	991	1467			603	645	790	2306
		1679	1732	1976	2044			2422	3996	4374	4449
		2259	2386	2459	2602			4684	4685	4813	4855
		3465	3477	3711	3801			4922	4957	5656	6352
		3893	4001	4074	4076			6703			
		4100	4605	4607	4658	Nco I	(4)	1872	3189	3426	3846
		4879	4982	5012	5153	Nde I	(3)	1970	3063	5099	
		5186	5456	5523	5623	Nhe I	(2)	30	4237		
		5797	5906	6299	6392	Nla III	(24)	62	1272	1876	1959
		6729	7061					1994	2760	3133	3193
HinC II	(3)	2356	4140	6710				3430	3463	3481	3850
Hind II	(3)	2356	4140	6710				3973	4269	4915	5020
Hind III	(1)	4124						5280	6000	6491	6501
Hinf I	(16)	299	518	858	869			6579	6615	7008	7113
		1616	1738	1938	2189						
		2712	3239	3755	4677	Nla IV	(41)	154	247	263	321
		5176	5251	5647	6164			479	628	759	828
HinI I	(16)	809	1465	1544	2512			960	1211	1288	1466
								2096	2119	2303	2419
								2739	3296	3487	3547

		3583	3631	3805	3826
		3892	4000	4099	4146
		4474	4532	4657	4689
		4838	5308	5347	6119
		6213	6254	6465	7055
		7274			
Not I	(1)	4131			
Nsp7524 I	(2)	4911	5276		
NspB II	(14)	120	191	1847	2156
		2299	3991	4328	4403
		4785	4988	5618	5863
		6804	7284		
NspH I	(2)	4915	5280		
Pac I	(1)	4160			
PaeR7 I	(1)	4150			
Pal I	(48)	172	203	248	659
		793	829	841	1054
		1178	1199	1264	1727
		1871	1892	1920	2072
		2145	2227	2462	2633
		2700	2719	2913	3106
		3431	3498	3531	3582
		3638	3825	3860	3939
		3974	4083	4133	4339
		4384	4414	4459	5291
		5302	5320	5754	6212
		6292	6559	7146	7287
Pf1M I	(1)	3852			
Ple I	(3)	866	4685	5655	
Pme I	(1)	4115			
PpuM I	(3)	329	1286	4540	
Psp1406 I	(2)	6395	6768		
PspA I	(2)	473	4683		
Pst I	(6)	988	996	1172	1857
		3768	6414		
Pvu I	(2)	1884	6539		
Pvu II	(5)	120	191	3991	4328
		4403			
Rsa I	(19)	348	479	726	1351
		1503	2437	2490	3048
		3073	3128	3161	3212
		3369	3626	3878	4067
		4689	5084	6649	
Rsr II	(1)	1928			
Sac I	(2)	414	4624		
Sac II	(2)	2300	7285		
SaI I	(1)	4138			
Sap I	(1)	5160			
Sau3A I	(39)	94	1111	1243	1428
		1477	1482	1517	1563
		1696	1881	1894	1984
		2291	2411	2775	2784
		2800	2831	3414	3510
		3906	4106	4144	4301
		4815	5842	5917	5928
		5936	6014	6026	6131
		6472	6490	6536	6794
		6811	6847	7173	
Sau96 I	(40)	170	201	246	261
		274	329	627	757
		827	840	1052	1263
		1286	1919	1928	2070
		2469	2698	2718	2737
		2912	3105	3529	3581
		3824	4081	4337	4382
		4412	4457	4472	4485
		4540	4837	6211	6290
		6307	6529	7145	7286
Sca I	(2)	2490	6649		
ScrF I	(40)	162	238	316	474
		475	603	624	645
		790	802	815	1236
		1261	1284	1304	1334
		2306	2422	2743	2919
		3112	3598	3752	3996
		4374	4449	4527	4684
		4685	4813	4834	4855
		4922	4957	5304	5425
		5438	5656	6352	6703
Sec I	(47)	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	4372	4447	4526
		4536	4683	4746	4832
SfaN I	(23)	4833	5436	7282	
		260	520	1005	1585
		1729	1796	1868	2053
		2283	2363	2385	2541
		3187	4471	4729	4943
		5076	5114	5152	5372
Sfc I	(9)	6424	6617	6864	
		984	992	1168	1853
		3764	4222	5541	5732
		6410			
Sma I	(2)	475	4685		
SnaB I	(1)	3169			
Spe I	(1)	727			
Ssp I	(1)	6973			
Stu I	(2)	3638	3860		
Sty I	(11)	325	537	1312	1872
		3189	3426	3573	3633
		3846	4536	4746	
Taq I	(20)	861	1105	1416	1427
		1551	1566	1575	1635
		2052	2265	2367	2392
		2575	3507	3513	3723
		4139	4151	5376	6820
Tfi I	(9)	299	518	869	1616
		1738	1938	2189	2712
		5251			
Tsp45 I	(10)	1089	1298	1810	3568
		3739	3745	4930	5025
		6425	6636		

Tth111 I	(7)	466	878	1284	1580
		2024	4676	5023	
Tth111 II	(10)	144	220	498	691
		1740	4356	4431	5865
		5874	5904		
Vsp I	(1)	6341			
Xba I	(1)	4504			
Xca I	(1)	5049			
Xho I	(1)	4150			
Xho II	(11)	1517	2831	3414	4106
		4144	5917	5928	6014
		6026	6794	6811	
Xma I	(2)	473	4683		
Xma III	(5)	791	1725	1890	2460
		4131			
Xmn I	(1)	6768			

site usage in pRV-RFP:

Aat II	G,ACGT`C	8	Acc I	GT`MK,AC	2
Acc65 I	G`GTAC,C	2	Aci I	C`CG,C	90
Afl II	C`TAA,G	3	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	16
Ahd I	GACNN,N`NNGTC	5	Alu I	AG CT	42
Alw I	GGATC 8/9	21	AlwN I	CAG,NNN`CTG	4
Apa I	G,GGCC`C	-	Apal I	G`TGCA,C	5
Apo I	R`AATT,Y	5	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	2
Avr I	C`YGR,G	9	Avr II	G`GWC,C	15
Ban I	G`GYRC,C	-	BamH I	G`GTAC,C	1
Bbe I	G,CGCG`C	5	Ban II	G,`RGCY`C	7
Bbv I	GACG 13/17	13	Bbs I	GAAGAC 8/12	3
Bcl I	T`GATC,A	1	Bbv II	GAAGAC 7/11	3
Bfa I	C`TA,G	13	Bcn I	CC,S`GG	21
Bgl II	A`GATC,T	-	Bgl I	GCCN,NNN`NGGC	4
Bpm I	CTGGAG 22/20	4	Blp I	GC`TNA,GC	1
BsaA I	YAC GTR	3	Bsa I	GGTCTC 7/11	8
BsaH I	GR`CG,YC	16	BsaB I	GATNN NNATC	-
BsaW I	W`CCGG,W	8	BsaJ I	C`CNNG,G	47
Bsg I	GTGCAG 22/20	2	BseR I	GAGGAG 16/14	6
BsiE I	CG,RY`CG	13	BsiC I	TT`CG,AA	-
BsiW I	C`GTAC,G	-	BsiHKA I	G,`GWCW`C	8
BsmA I	GTCTC`/9	20	Bsm I	GAATG,C 7	-
BsmF I	GGGAC 15/19	15	BsmB I	CGTCTC 7/11	7
Bsp120 I	G`GGCC,C	-	BsoF I	GC`N,GC	52
BspH I	T`CATG,A	3	Bsp1286 I	G,`DGCH`C	-
BspM II	T`CCGG,A	4	BspM I	ACCTGC 10/14	1
BsrB I	GAG CGG	7	Bsr I	ACT,GG`	18
BsrG I	T`GTAC,A	1	BsrD I	GCAATG, 8	2
BssS I	C`TCGT,G	6	BssH II	G`CGCG,C	4
BstB I	TT`CG,AA	-	Bst1107 I	GTA TAC	1
BstN I	CC`W,GG	19	BstE II	G`GTNAC,C	3
BstX I	CCAN,NNN`NTGG	1	BstU I	CG CG	36
Bsu36 I	CC`TNA,GG	3	BstY I	R`GATC,Y	11
Cfr10 I	R`CCGG,Y	4	Cac8 I	GCN NGC	33
Csp6 I	G`TA,C	19	Cla I	AT`CG,AT	-
Dpn I	GA TC	39	Dde I	C`TNA,G	26
Dra I	TTT AAA	4	DpnII	`GATC,	39
Drd I	GACNN,NN`NNGTC	5	Dra III	CAC,NNN`GTG	2
Eae I	Y`GGCC,R	13	Dsa I	C`CRYG,G	8
Ear I	CTCTTC 7/10	4	Eag I	C`GGCC,G	5
Eco57 I	CTGAAG 21/19	6	Eco47 III	AGC GCT	1
EcoN I	CCTNN`N,NNAGG	2	Eco72 I	CAC GTG	-
EcoR I	G`AATT,C	3	EcoO109 I	RG`GNC,CY	5
EcoRV	GAT ATC	4	EcoR II	`CGWG,G	19
Esp I	GC`TNA,GC	1	Ehe I	GCC GCC	5
Fok I	GGATG 14/18	13	Fnu4H I	GC`N,GC	52
Fsp I	TGC GCA	2	Fse I	GG,CCGG`CC	-
Gsu I	CTGGAG 21/19	4	Gdi II	`YGGC,CG	15
Hae II	R,CGCG`Y	8	Hae I	WGG CCW	10
Hga I	GACGC 9/14	15	Hae III	GG CC	48
HgiE II	ACCNNNNNGGT -1/132	-	HgiA I	G,`GWCW`C	8
Hinc II	GTY RAC	3	Hha I	G,CG`C	42
Hind III	A`AGCT,T	1	Hind II	GTY RAC	3
HinI I	GR`CG,YC	16	Hinf I	G`ANT,C	16
Hpa I	GTT AAC	-	HinP I	G`CG,C	42
Hph I	GGTGA 12/11	18	Hpa II	C`CG,G	35
Kpn I	G,GTAC`C	2	Kas I	G`CGCG,C	5
Mae II	A`CG,T	18	Mae I	C`TA,G	13
Mbo I	`GATC,	39	Mae III	`GTNAC,	23
Mlu I	A`CGCG,T	1	Mbo II	GAAGA 12/11	15
Mnl I	CCTC 10/10	75	Mme I	TCCRC 25/23	8
Mse I	T`TA,A	19	Msc I	TGG CCA	3
Msp I	C`CG,G	35	Msl I	CAYNN NRRTG	3
Mun I	C`AATT,G	-	MspAl I	CMG CGK	14
Nar I	GG`CG,CC	5	Nae I	GCC GGC	-
Nco I	C`CATG,G	4	Nci I	CC`S,GG	21
NgoM I	G`CCGG,C	-	Nde I	CA`TA,TG	3
Nla III	,CATG`	24	Nhe I	G`CTAG,C	2
Not I	GC`GGCC,GC	1	Nla IV	GGN NCC	41
Nsi I	A,TGCA`T	-	Nru I	TCG CGA	-
NspB II	CMG CKG	14	Nsp7524 I	R`CATG,Y	2
Pac I	TTA,AT`TAA	1	NspH I	R,CATG`Y	2
Pal I	GG CC	48	PaeR7 I	C`TCGA,G	1
Ple I	GAGTC 9/10	3	Pf1M I	CCAN,NNN`NTGG	1
Pml I	CAC GTG	-	Pme I	CTTT AAAC	1
Psp1406 I	AA`CG,TT	2	PpuM I	RG`GWC,CY	3
Pst I	C,TGCA`G	6	PspA I	C`CCGG,G	2
Pvu II	CAG CTG	5	Pvu I	CG,AT`CG	2
Rsr II	CG`GWC,CG	1	Rsa I	GT AC	19
Sac II	CC,GC`GG	2	Sac I	G,AGCT`C	2
Sap I	GCTCTCT 8/11	1	SaI I	G`TCGA,C	1
Sau96 I	G`GNC,C	40	Sau3A I	`GATC,	39
ScrF I	CC`N,GG	40	Sca I	AGT ACT	2
SfaN I	GCATC 9/13	23	Sec I	C`CNNG,G	47
Sfi I	GGCCN,NNN`NGGCC	-	Sfc I	C`TRYA,G	9
SnaB I	TAC GTA	1	Sma I	CCC GGG	2
Sph I	G,CATG`C	-	Spe I	A`CTAG,T	1
Srf I	GCCC GGGC	-	Spl I	C`GTAC,G	-
Stu I	AGG CCT	2	Ssp I	AAT ATT	1
Taq I	T`CG,A	20	Sty I	C`CWG,G	11
Tsp45 I	`GTSAC,	10	Tfi I	G`AWT,C	9
Tth111 II	CAARCA 16/14	10	Tth111 I	GACN`N,NGTC	7
Xba I	T`CTAG,A	1	Vsp I	AT`TA,AT	1
Xcm I	CCANNNN,N`NNNNTGG-	-	Xca I	GTA TAC	1
Xho II	R`GATC,Y	11	Xho I	C`TCGA,G	1
Xma III	C`GGCC,G	5	Xma I	C`CCGG,G	2
			Xmn I	GAANN NNITTC	1