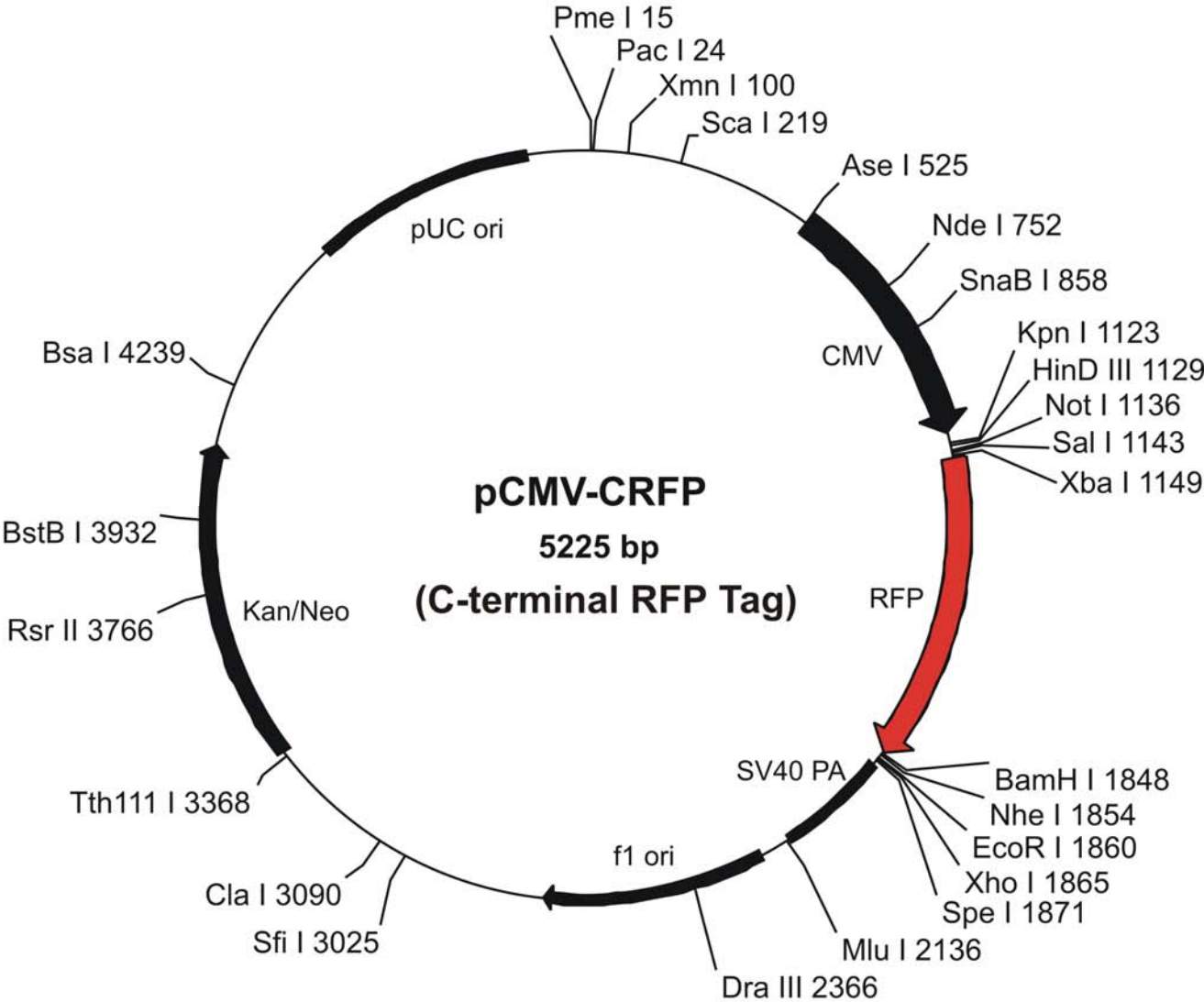


**Name of Vector:** pCMV-CRFP  
**Antibiotic Selection:** Kan  
**Created by:** Wei Jiang and Yien Li  
 (He Lab @ The University of Chicago)  
**Date of Creation:** July 2004



**Linker Sequence**

Kozak  
 Kpn I      Hind III      Not I      Sal I      Xba I  
 GGT ACC ATG GAA GCT TGC GGC CGC GTC GAC TCT AGA GGA GGC GGC GGA GGT  
           M E A C G R V D S R G G G G G

**Red Fluorescence Protein Tag**  
 ATG GCC TCC TCC .....TAA GGA TCC  
 monomeric RFP-1 coding region

## pCMV-CRFP Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60  
cagcggtaagatccttgagagttttcgcgccgaagaacgttttccaatgatgagcacttt 120  
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180  
tcgccgcatacactattctcagaatgacttgggtgagtaactcaccagtcacagaaaagca 240  
tcttacggatggcatgacagtaagagaattatgcagtgtgcccataacatgagtgataa 300  
cactgcccgaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360  
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420  
catacacaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480  
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540  
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600  
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660  
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720  
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780  
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTTCTTA 840  
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGT 900  
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960  
ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020  
ACTCCGCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080  
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagcaccATGGAAGCTTGCGGCCG 1140  
CGTCGACTCTAGAGGAGGCGGCGGAGGTatggcctcctccgaggacgtcatcaaggagtt 1200  
catgagcctcaaggtgagcagtgaggggcctccgtgaacggccacgagttcgagatcgaggg 1260  
cgagggcgagggccgcccctacgagggcaccagaccgccaagctgaaggtgaccaaggg 1320  
cggccccctgcccttcgcctgggacatcctgtcccctcagttccagtagcggctccaaggg 1380  
ctacgtgaagcaccgcccgcacatccccgactacttgaagctgtccttccccgagggctt 1440  
caagtgggagcgcgtgatgaacttcgaggacggcggcgtggtgaccgtgaccaggactc 1500  
ctccctgcaggacggcaggttcatctacaaggtgaagctgagcggcaccacttcccctc 1560  
cgacggccccgtaatgcagaagaagaccatgggctgggaggcctccaccgagcggatgta 1620  
ccccgaggacggcgcctgaagggcgagatcaagatgaggctgaagctgaaggacggcgg 1680  
ccactacgacgcccaggtcaagaccacctacatggccaagaagcccgtgcagctgcccgg 1740  
cgcctacaagaccgacatcaagctggacatcacctcccacaacgaggactacaccatcgt 1800  
ggaacagtagcagcgcgcccagggccgcccactccaccggcgcctaaGGATCCGCTAGCGA 1860  
ATTCTCGAGACTAGTGATCTatccgatccaccggannnnnnTAAC'TGATCATAATCAGCC 1920  
ATACCACATTTGTAGAGGTTTTACTTGGTTTTAAAAACCTCCCACACCTCCCCCTGAACC 1980  
TGAAACATAAAAATGAATGCAATTGTTGTTGTTAACTTGTATTATTGCAGCTTATAATGGTT 2040  
ACAAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTA 2100  
GTTGTGGTTTTGTCCAAACTCATCAATGTATCTTAAACGCGTAAATTTGTAAGCGTTAATATT 2160  
TTGTTAAAATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAAACCAATAGGCCGAA 2220  
ATCGGCAAAATCCCTTATAAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCA 2280  
GTTTGAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACC 2340  
GTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCTAATCAAGTTTTTTGGGGTCCG 2400  
AGGTGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCGATTTAGAGCTTGACGG 2460  
GGAAAGCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGG 2520  
GCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCGCCGCGCTAATGCG 2580  
CCGCTACAGGGCGCGTCAGGTGGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGT 2640  
TTATTTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATG 2700  
CTTCAATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGT 2760  
GTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGC 2820  
ATCTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTA 2880  
TGCAAAGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACCTCCGCCCATCC 2940  
CGCCCCTAACCTCCGCCAGTTCGCCCATCTCCGCCCATGGCTGACTAATTTTTTTTTTA 3000  
TTTATGCAGAGGCCGAGGCCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCT 3060  
TTTTTGGAGGCCTAGGCTTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGC 3120  
ATGATTGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTC 3180

GGCTATGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCA 3240  
GCGCAGGGGCGCCCGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTG 3300  
CAAGACGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTG 3360  
CTCGACGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAG 3420  
GATCTCCTGTCACTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATG 3480  
CGGCGGCTGCATACGCTTGATCCGGCTACCTGCCATTTCGACCACCAAGCGAAACATCGC 3540  
ATCGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAA 3600  
GAGCATCAGGGGCTCGCGCCAGCCGAAGTTCGCCAGGCTCAAGGCGAGCATGCCCGAC 3660  
GGCGAGGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAAT 3720  
GGCCGCTTTTCTGATTTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGAC 3780  
ATAGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGCGGGCGAATGGGCTGACCGCTTC 3840  
CTCGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTT 3900  
GACGAGTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACC 3960  
TGCCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCG 4020  
TTTTCCGGGACCGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCG 4080  
CCCACCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCG 4140  
CTATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTGCTTTGTTTCATAAAC 4200  
GCGGGGTTCCGGTCCAGGGCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCC 4260  
AATACGCCCGCGTTTCTTCTTTTCCCCACCCCAAGTTCGGGTGAAGGCCAG 4320  
GGCTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATAC 4380  
TTTAGATTGATTTAAAACCTTCATTTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTG 4440  
ATAATCTCATGACCAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCG 4500  
TAGAAAAGATCAAAGGATCTTCTTGAGATCCTTTTTTTTCTGCGCGTAATCTGCTGCTTGC 4560  
AAACAAAAAAACCACCGCTACCAGCGGTGGTTTGTGGCCGATCAAGAGCTACCAACTC 4620  
TTTTTCCGAAGGTAACCTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGT 4680  
AGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACTCGCTCTGC 4740  
TAATCCTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGCTTACCAGGTTGGACT 4800  
CAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGGGGTTCGTGCACAC 4860  
AGCCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAG 4920  
AAAGCGCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCG 4980  
GAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTG 5040  
TCGGGTTTTCGCCACCTCTGACTTGAGCGTTCGATTTTTGTGATGCTCGTCAGGGGGGCGGA 5100  
GCCTATGGA AAAACGCCAGCAACGCGCCTTTTTACGGTTCTTGCCTTTTGCTGGCCTT 5160  
TTGCTCACATGTTCTTCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCA 5220  
TGCAT 5225

**Unique enzymes in pCMV-CRFP:**

Pme I	CTTT AAAC	15
Pac I	TTA,AT`TAA	24
Xmn I	GAANN NNTTC	100
Sca I	AGT ACT	219
Pvu I	CG,AT`CG	331
EcoN I	CCTNN`N,NNAGG	339
Ase I	AT`TA,AT	525
Vsp I	AT`TA,AT	525
Nde I	CA`TA,TG	752
SnaB I	TAC GTA	858
Acc65 I	G`GTAC,C	1119
Asp718	G`GTAC,C	1119
Kpn I	G,GTAC`C	1123
Hind III	A`AGCT,T	1129
Not I	GC`GGCC,GC	1136
Sal I	G`TCGA,C	1143
Acc I	GT`MK,AC	1144
Xba I	T`CTAG,A	1149
Ahd I	GACNN,N`NNGTC	1349
Bbv II	GAAGAC 7/11	1589
Bbs I	GAAGAC 8/12	1590
Bsg I	GTGCAG 22/20	1749
BssH II	G`CGCG,C	1814
BamH I	G`GATC,C	1848

Nhe I	G`CTAG,C	1854
EcoR I	G`AATT,C	1860
Paer7 I	C`TCGA,G	1865
Xho I	C`TCGA,G	1865
Spe I	A`CTAG,T	1871
Bcl I	T`GATC,A	1907
Mun I	C`AATT,G	2000
Hpa I	GTT AAC	2013
Mlu I	A`CGCG,T	2136
Dra III	CAC,NNN`GTG	2366
Sfi I	GGCCN,NNN`NGGCC	3025
Cla I	AT`CG,AT	3090
Tth111 I	GACN`N,NGTC	3368
Rsr II	CG`GWC,CG	3766
BsiC I	TT`CG,AA	3932
BstB I	TT`CG,AA	3932
Bsa I	GGTCTC 7/11	4239
Eco0109 I	RG`GNC,CY	4348
Number of enzymes = 42		

**The following enzymes do not cut in pCMV-CRFP:**

Afl II	Age I	Apa I	Asc I	Bgl II
Blp I	BsiW I	BsmB I	Bsp120 I	BspM II
BsrG I	Bst1107 I	Eco47 III	Eco72 I	EcoR V
Esp I	Fse I	Nru I	Pml I	PpuM I
PspA I	Sac I	Sac II	Sma I	Spl I

pcMV-CRFP: sites sorted by name:

						3020	3159	3211	3222
						3312	3317	3354	3395
						3482	3485	3488	3724
						3820	3861	3875	3989
						4328	4343	4554	4760
						4763	4828	4971	5126
Aat II	(5)	643	696	779	965				
		1189							
Acc I	(1)	1144				Bsp1286 I	(2)	117	3553
Acc65 I	(1)	1119				BspH I	(2)	2676	4448
Aci I	(73)	64	141	185	306	BspM I	(3)	3137	3518
		352	576	604	616	Bsr I	(12)	54	226
		630	797	888	921			493	814
		1025	1046	1107	1135			2280	2958
		1139	1159	1162	1274	BsrB I	(5)	1613	2510
		1297	1321	1396	1474			3917	
		1543	1613	1678	1826	BsrD I	(2)	466	3483
		1852	2510	2537	2565	BssH II	(1)	1814	
		2568	2582	2625	2672	BssS I	(5)	31	1242
		2735	2920	2932	2941			4995	3842
		2953	2963	2974	3020	BstB I	(1)	3932	3968
		3159	3222	3316	3380	BstE II	(2)	1310	1481
		3481	3484	3724	3764	BstN I	(13)	608	801
		3769	3819	3835	3861			2786	1340
		3917	3986	3989	4055			4216	2858
		4137	4202	4269	4342			5143	5009
		4576	4585	4720	4830	BstU I	(20)	141	578
		4951	4970	5097	5125			1543	1141
		5216						1816	2138
Afl III	(2)	2136	5168					2550	2570
Aha II	(13)	160	640	693	776			3316	3617
		962	1186	1633	1690			4202	4055
		1741	1840	3250	3952	BstX I	(2)	1712	1896
		4031				BstY I	(11)	53	70
Ahd I	(1)	1349						3421	3667
Alu I	(22)	347	410	510	1084			4430	4516
		1131	1304	1421	1538	Bsu36 I	(3)	1844	2730
		1667	1733	1763	2029	Cac8 I	(31)	454	604
		2196	2453	2748	3036			1816	1856
		3356	3814	4611	4868			2526	2799
		4914	5004					2890	3144
Alw I	(18)	60	66	381	1099			3615	3621
		1844	1855	1881	3117			3694	3698
		3428	3495	3674	4039			4222	4269
		4066	4425	4426	4523			4558	5118
		4523	4609			Cfr10 I	(5)	1836	2467
AlwN I	(2)	4351	4759					4033	3569
ApaL I	(2)	28	4854					3090	3750
Apo I	(4)	1860	2064	2168	2179			218	736
Ase I	(1)	525						849	900
Asp718	(1)	1119						1367	1619
Ava I	(3)	1431	1623	1865				199	1357
Ava II	(3)	336	3766	4211		Dde I	(9)	3032	3913
Avr II	(2)	3072	4087					4894	4362
BamH I	(1)	1848						55	72
Ban I	(10)	983	1119	1287	1545	Dpn I	(29)	394	1105
		1632	1740	1839	2403			1650	1850
		3249	3284					1909	3089
Ban II	(4)	1230	2441	3615	4325			3423	3501
Ebe I	(4)	1636	1744	1843	3253			3669	4045
Ebs I	(1)	1590						4432	4510
Ebv I	(8)	468	1742	2038	3323			4604	4518
		3365	3886	4339	4839	DpnII	(29)	53	70
		1589						392	1103
Ebv II	(1)	1589						1648	1144
Ecl I	(1)	1907						1907	1876
Ecn I	(7)	165	516	1739	3255			3421	3087
		3415	4028	4792				3667	3499
Bfa I	(11)	507	1110	1150	1855			4430	4043
		1872	2099	2517	3073			4602	4508
		4088	4422	4675				15	122
Bgl I	(4)	608	730	801	3025	Dra I	(5)	4413	1952
Bpm I	(2)	4033	4090					2366	4394
Bsa I	(1)	4239				Dra III	(1)	1695	2321
Bsaa I	(4)	858	1385	2366	3554	Drd I	(4)	878	1123
BsaB I	(2)	1912	3109			Dsa I	(5)	3682	1588
BsaH I	(13)	160	640	693	776			307	1136
		962	1186	1633	1690	Eae I	(9)	1714	3156
		1741	1840	3250	3952			3748	3330
		4031						1136	3156
BsaJ I	(26)	878	1123	1180	1315	Eag I	(2)	2717	3594
		1339	1375	1432	1492	Ear I	(3)	1325	1658
		1588	1624	1693	1819	Eco57 I	(7)	3395	3827
		2784	2856	2979	3014			339	4627
		3023	3072	3413	3682	EcoN I	(1)	4348	
		4087	4214	4215	4317	EcoO109 I	(1)	1860	
		4318	5008			EcoR I	(1)	606	799
BsaW I	(6)	404	1891	3281	4125	EcoR II	(13)	2784	2839
		4815	4962					4214	4317
BseR I	(4)	1166	1168	1490	3068			5141	5007
Bsg I	(1)	1749						1634	1742
BsiC I	(1)	3932				Ehe I	(4)	185	280
BsiE I	(5)	182	331	1139	3159	Fnu4H I	(44)	1136	1139
		4834						1322	1475
BsiHKA I	(5)	32	117	3363	3553			1679	1731
		4858						2027	2546
Bsm I	(2)	2001	2094					3020	3159
BsmA I	(6)	951	1863	2675	3093			3312	3317
		4112	4240					3482	3485
BsmF I	(12)	693	844	1012	1337			3820	3861
		1356	2766	2838	2902			4328	4343
		3401	3933	4042	4197			4763	4828
BsoF I	(44)	185	280	307	457			261	1332
		1136	1139	1160	1274	Fok I	(9)	2923	3117
		1322	1475	1539	1544			4053	3574
		1679	1731	1734	1826	Fsp I	(3)	477	1218
		2027	2546	2568	2582				3352

Gdi II	(9)	308	1135	1137	1239			486	525	1951	2012
		1680	3155	3157	3720			2133	2154	2165	2177
		3747						2188	2205	2303	2574
Gsu I	(2)	4034	4089					4393	4407	4412	4464
Hae I	(9)	1173	1380	1602	1716	Msl I	(4)	288	883	1896	3687
		3071	3332	4694	5146	Msp I	(22)	163	405	515	1738
		5157						1837	1892	2468	3155
Hae II	(7)	1636	1744	1843	2517			3232	3254	3282	3413
		2525	3253	4928				3503	3570	3751	4026
Hae III	(31)	309	602	795	1138			4034	4126	4600	4790
		1173	1240	1273	1324			4816	4963		
		1380	1567	1602	1681	MspA1 I	(6)	64	1733	2748	3356
		1716	1825	2216	2358			4585	4830		
		3013	3019	3028	3071	Mun I	(1)	2000			
		3158	3332	3723	3750	Nae I	(3)	2469	3752	4035	
		4259	4316	4349	4694	Nar I	(4)	1633	1741	1840	3250
		5128	5146	5157		Nci I	(7)	164	515	1738	3254
Hga I	(9)	167	1043	1131	1697			3414	4027	4791	
		2584	3959	4038	4479	Nco I	(5)	878	1123	1588	2979
		5057						3682			
HgiA I	(5)	32	117	3363	3553	Nde I	(1)	752			
		4858				Ngom I	(3)	2467	3750	4033	
HgiE II	(2)	1889	4579			Nhe I	(1)	1854			
Hha I	(31)	141	478	1207	1219	Nla III	(24)	257	293	371	381
		1453	1543	1635	1743			822	882	1127	1205
		1816	1818	1842	2516			1223	1592	1715	2680
		2524	2550	2572	2581			2820	2892	2983	3124
		2594	2625	3244	3252			3469	3655	3686	3712
		3316	3353	3619	3879			4068	4452	5172	5223
		4055	4141	4544	4653	Nla IV	(26)	403	985	1121	1229
		4827	4927	4994				1289	1325	1373	1547
HinC II	(3)	158	1145	2013				1568	1634	1742	1841
Hind II	(3)	158	1145	2013				1850	2405	2426	2438
Hind III	(1)	1129						2629	2790	2862	3251
Hinf I	(13)	928	1146	1497	2293			3286	4134	4213	4258
		2315	2725	3735	3869			5101	5140		
		3921	3979	4016	4798	Not I	(1)	1136			
		5194				Nsi I	(3)	2822	2894	5225	
HinI I	(13)	160	640	693	776	Nsp7524 I	(4)	2816	2888	3651	5168
		962	1186	1633	1690	NspB II	(6)	64	1733	2748	3356
		1741	1840	3250	3952			4585	4830		
		4031				NspH I	(4)	2820	2892	3655	5172
HinP I	(31)	139	476	1205	1217	Pac I	(1)	24			
		1451	1541	1633	1741	PaeR7 I	(1)	1865			
		1814	1816	1840	2514	Pal I	(31)	309	602	795	1138
		2522	2548	2570	2579			1173	1240	1273	1324
		2592	2623	3242	3250			1380	1567	1602	1681
		3314	3351	3617	3877			1716	1825	2216	2358
		4053	4139	4542	4651			3013	3019	3028	3071
		4825	4925	4992				3158	3332	3723	3750
Hpa I	(1)	2013						4259	4316	4349	4694
Hpa II	(22)	163	405	515	1738			5128	5146	5157	
		1837	1892	2468	3155	Pf1M I	(2)	1594	1895		
		3232	3254	3282	3413	Ple I	(2)	2301	2733		
		3503	3570	3751	4026	Pme I	(1)	15			
		4034	4126	4600	4790	Psp1406 I	(2)	98	471		
		4816	4963			Pst I	(2)	458	1510		
Hph I	(10)	215	893	1321	1492	Pvu I	(1)	331			
		1543	1764	2368	3429	Pvu II	(3)	1733	2748	3356	
		4320	4436			Rsa I	(12)	219	737	762	817
Kas I	(4)	1632	1740	1839	3249			850	901	1058	1121
Kpn I	(1)	1123						1368	1620	1809	3556
Mae I	(11)	507	1110	1150	1855	Rsr II	(1)	3766			
		1872	2099	2517	3073	Sal I	(1)	1143			
		4088	4422	4675		Sap I	(2)	3594	3804		
Mae II	(18)	98	471	640	652	Sau3A I	(29)	53	70	328	374
		693	776	857	962			392	1103	1114	1252
		1186	1384	2310	2322			1648	1848	1876	1885
		2365	2475	3366	3553			1907	3087	3091	3110
		4334	4467					3421	3499	3580	3589
Mae III	(19)	39	227	380	438			3667	4043	4059	4418
		579	666	1015	1310			4430	4508	4516	4527
		1481	1487	2038	2539			4602			
		2551	3370	3676	4366	Sau96 I	(13)	336	601	794	1271
		4632	4748	4811				1323	1566	1823	2357
Mbo I	(29)	53	70	328	374			3766	4211	4257	4315
		392	1103	1114	1252			4348			
		1648	1848	1876	1885	Sca I	(1)	219			
		1907	3087	3091	3110	ScrF I	(20)	164	515	608	801
		3421	3499	3580	3589			1340	1494	1738	2786
		3667	4043	4059	4418			2841	2858	3254	3414
		4430	4508	4516	4527			3637	4027	4216	4319
		4602						4791	5009	5022	5143
Mbo II	(12)	104	1591	1594	2505	Sec I	(26)	878	1123	1180	1315
		2733	3610	3820	3902			1339	1375	1432	1492
		4069	4269	4439	4512			1588	1624	1693	1819
Mlu I	(1)	2136						2784	2856	2979	3014
Mme I	(4)	1584	2342	4776	4960			3023	3072	3413	3682
Mnl I	(49)	327	1059	1146	1149			4087	4214	4215	4317
		1158	1175	1183	1186			4318	5008		
		1217	1250	1256	1262	SfaN I	(13)	247	440	876	2065
		1277	1365	1427	1460			2828	2900	3209	3464
		1510	1567	1592	1612			3548	3612	3680	3887
		1619	1651	1688	1778			5072			
		1783	1814	1929	1968	Sfc I	(5)	454	1506	2585	4712
		1977	2394	2725	3003			4903			
		3009	3032	3038	3046	Sfi I	(1)	3025			
		3049	3061	3101	3165	SnaB I	(1)	858			
		3301	3658	3850	4056	Spe I	(1)	1871			
		4088	4370	4740	4991	Sph I	(3)	2820	2892	3655	
		5064				Ssp I	(2)	2158	2711		
Msc I	(2)	1716	3332			Stu I	(3)	1380	1602	3071	
Mse I	(20)	14	20	24	121	Sty I	(9)	878	1123	1315	1375

		1588	2979	3072	3682	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
		4087				Pst I	C,TGCA`G	2	Pvu I	CG,AT`CG	1
Taq I	(17)	46	1144	1249	1255	Pvu II	CAG CTG	3	Rsa I	GT AC	12
		1465	1866	2399	3090	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
		3363	3519	3543	3579	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
		3741	3932	3977	4232	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	29
		5070				Sau96 I	G`GNC,C	13	Sca I	AGT ACT	1
Tfi I	(5)	3735	3869	3979	4016	ScrF I	CC`N,GG	20	Sec I	C`CNNG,G	26
		5194				SfaI I	GCATC 9/13	13	Sfc I	C`TRYA,G	5
Tsp45 I	(8)	227	438	1310	1481	Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
		1487	2539	3370	3676	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Tth111 I	(1)	3368				Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Tth111 II	(4)	3686	4546	4576	4585	Srf I	GCCC GGGC	-	Ssp I	AAAT ATT	2
Vsp I	(1)	525				Stu I	AGG CCT	3	Sty I	C`CWVG,G	9
Xba I	(1)	1149				Taq I	T`CG,A	17	Tfi I	G`AWT,C	5
Xho I	(1)	1865				Tsp45 I	`GTSAC,	8	Tth111 I	GACN`N,NGTC	1
Xho II	(11)	53	70	1103	1848	Tth111 II	CAARCA 16/14	4	Vsp I	AT`TA,AT	1
		3421	3667	4059	4418	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
		4430	4516	4527		Xcm I	CCANNNN,N`NNNNTGG-		Xho I	C`TCGA,G	1
Xma III	(2)	1136	3156			Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	-
Xmn I	(1)	100				Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1

Site usage in pCMV-CRFP:

Aat II	G,ACGT`C	5	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	73
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	13
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	22
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	4	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	3	Ava II	C`GWC,C	3
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	10	Ban II	G,RGCGY`C	4
Bbe I	G,GCGC`C	4	Bbs I	GAAGAC 8/12	1
Bbv I	GCAGC 13/17	8	Bbv II	GAAGAC 7/11	1
Bcl I	T`GATC,A	1	Bcn I	CC,s`GG	7
Bfa I	C`TA,G	11	Bgl I	GCCN,NNN`NGGC	4
Bgl II	A`GATC,T	-	Blp I	GC`TNA,GC	-
Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
BsaA I	YAC GTR	4	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	13	BsaJ I	C`CNNG,G	26
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	4
Bsg I	GTGCAG 22/20	1	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
BsmA I	GTCTC`/9	6	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	12	BsmF I	GC`N,GC	44
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	12
BsrB I	GAG CGG	5	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	-	BssH II	G`CGCG,C	1
Bsss I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	2
BstN I	CC`W,GG	13	BstU I	CG CG	20
BstX I	CCAN,NNNN`NTGG	2	BstY I	R`GATC,Y	11
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCN NGC	31
Cfr10 I	R`CCGG,Y	5	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	12	Dde I	C`TNA,G	9
Dpn I	GA TC	29	DpnII	`GATC,	29
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	5
Eae I	Y`GGCC,R	9	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	7	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	1	Eco109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	13
EcoR V	GAT ATC	-	Ehe I	GGC GCC	4
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	44
Fok I	GGATG 14/18	9	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	9
Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	9
Hae II	R,GCGC`Y	7	Hae III	GG CC	31
Hga I	GACGC 9/14	9	HgiA I	G,WGCW`C	5
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	31
Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	13
HinI I	GR`CG,YC	13	HinP I	G`CG,C	31
Hpa I	GTT AAC	1	Hpa II	C`CG,G	22
Hph I	GGTGA 12/11	10	Kas I	G`GCGC,C	4
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	11
Mae II	A`CG,T	18	Mae III	`GTNAC,	19
Mbo I	`GATC,	29	Mbo II	GAAGA 12/11	12
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	4
Mnl I	CCTC 10/10	49	Msc I	TGG CCA	2
Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	4
Msp I	C`CG,G	22	MspA1 I	CMG CKG	6
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	4	Nci I	CC`s,GG	7
Nco I	C`CATG,G	5	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	1
Nla III	,CATG`	24	Nla IV	GGN NCC	26
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4
NspB II	CMG CKG	6	NspH I	R,CATG`Y	4
Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1
Pal I	GG CC	31	Pfl1 I	CCAN,NNN`NTGG	2
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-