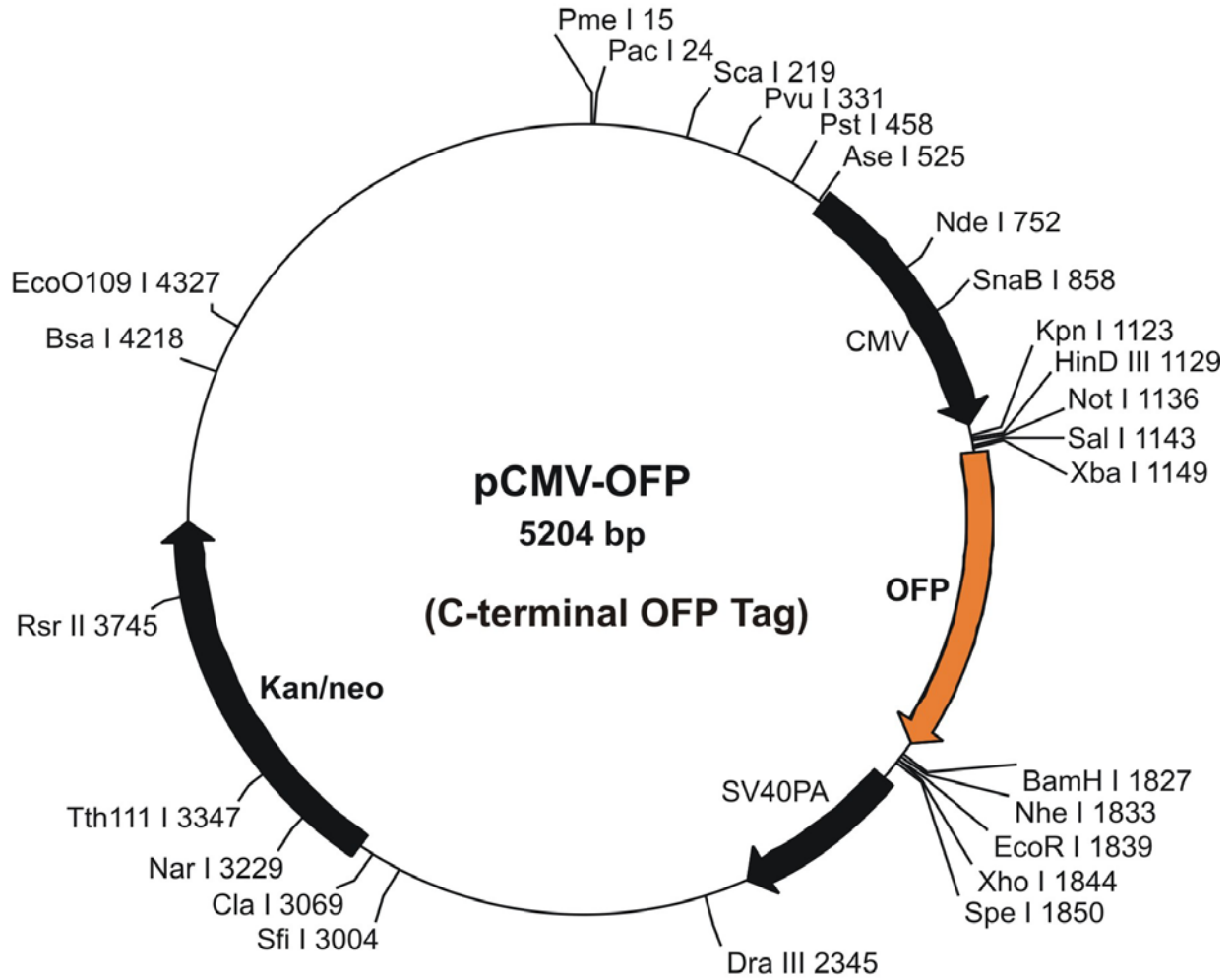
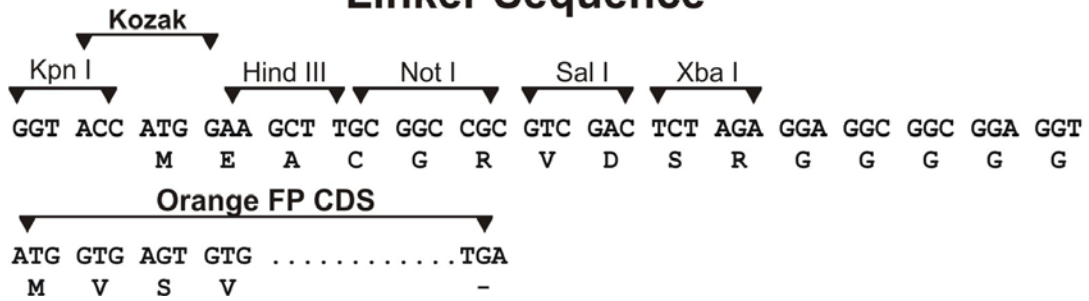


Name of Vector: pCMV-OFP (mKO1 by Miyawaki)
Antibiotic Selection: Kan
Created by: Wei Jiang and Hue Luu
(He Lab @ The University of Chicago)
Date of Creation: October 2004



Linker Sequence



pCMV-OFP Full-length Sequence and Restriction Sites

(a.k.a., monomeric Kusabira-Orange FP, or mKO1 by Miyawaki)

TAGTTATTATGTTTAAacttaattaagtgcacgagtgagggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120
taaagttctgctattgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgcccatacactattctcagaatgacttgggtgagtagtactcaccagtacagaaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgctgccataaccatgagtgataa 300
cactgcgcccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
cataccaaaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacggttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 600
GCCCCCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCCGCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCTTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTG 960
ACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTTCGTAACA 1020
ACTCCGCCCCATTGACGCAAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcgggtaccATGGAAGCTTGGCGCCG 1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTatgggtgagtgatgattaaaccagagatgaagat 1200
gaggtactacatggacggctccgtcaatgggcatgagttcacaattgaaggtgaaggcac 1260
agccagaccttacgagggacatcaagagatgacactacgcgtcacaatggccaagggcgg 1320
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ccttagaggaaacaccttctaccacaaatccaaatctactgggggtaactttctgcccga 1560
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aagccattacatcagccatcgcctcgtcaggaaaaccgaaggcaacattactgagctggt 1800
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CAAATTTTCAAAAATAAAGCATTTTTTTTTCACTGCATTCTAGTTGTGGTTTTGTCCAAACTCA 2100
TCAATGTATCTTAAACGCGTAAATTTGTAAGCGTTAATATTTTTGTTAAAATTCGCGTTAAAT 2160
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TTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAACCGTCTATCAGGGCGATGGCCCA 2340
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CGGAACCCTAAAGGGAGCCCCGATTTAGAGCTTGACGGGGAAAGCCGGCGAACGTGGCG 2460
AGAAAGGAAGGGAAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGCAAGTGTAGCGGTC 2520
ACGCTGCGCGTAACCACCACACCCGCGCGCTTAATGCGCCGCTACAGGGCGCGTCAGGT 2580
GGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTTATTTTTCTAAATACATTCA 2640
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CCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCCTAGGCTTTTT 3060
GCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTTCGCATGATTGAACAAGATGGATTG 3120
CACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAACAG 3180
ACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTGACGCGAGGGGCGCCCGGTTCTT 3240
TTTGTCAAGACCGACCTGTCCGGTGCCTGAATGAACTGCAAGACGAGGCAGCGCGGCTA 3300
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GGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGCGCCAGGATCTCCTGTCACTGCACCTT 3420
GCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCTGCATACGCTTGAT 3480
CCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTAACG 3540

ATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCA 3600
 GCCGAAGTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCTGTGACC 3660
 CATGGCGATGCCTGCTTGC CGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTCATC 3720
 GACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGTGAT 3780
 ATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTGTGCTTTACGGTATCGCC 3840
 GCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGGACGAGTTCTTCTGAGCGGGA 3900
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 CCACCGCCGCTTCTATGAAAGGTTGGGCTTTCGGAATCGTTTTCCGGGACGCCGGCTGGA 4020
 TGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTTCGCCCACCCTAGGGGGAGGCTAA 4080
 CTGAAACACGGAAGGAGACAATACCGGAAGGAACCCCGCGCTATGACGGCAATAAAAAGAC 4140
 AGAATAAAAACGACCGGTGTTGGGTGTTGGTTTTCATAAACCGCGGGGTTTCGGTCCCAGGCT 4200
 GGCATCTGTGCGATACCCCAACCGAGACCCCAATTGGGGCCAATACGCCCGGTTTCTTCTCT 4260
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 CTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGATCTT 4500
 CTTGAGATCCTTTTTTCTGCGCGTAATCTGCTGCTTTCGAAAACAAAAAACCCACCGCTAC 4560
 CAGCGGTGGTTTTGTTTCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAACCTGGCT 4620
 TCAGCAGAGCGCAGATACCAAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACCACT 4680
 TCAAGAACTCTGTAGCACCCGCTACATACTCGCTCTGCTAATCCTGTTACCAGTGGCTG 4740
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 AGGCGCAGCGGTTCGGGCTGAACGGGGGGTTTCGTGCACACAGCCAGCTTGGAGCGAACGA 4860
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 AGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTTCGGGTTTTCGCCACCTCTGAC 5040
 TTGAGCGTGCATTTTTGTGATGCTCGTCAGGGGGGGCGGAGCCTATGGAAAACGCCAGCA 5100
 ACGCGCCTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTTGTCTACATGTTCTTTCTGT 5160
 CGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 5204

Unique enzymes in pCMV-OFP:

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
Pst I	C,TGCA`G	458
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	1346
Eco72 I	CAC GTG	1355
Pml I	CAC GTG	1355
BamH I	G`GATC,C	1827
Nhe I	G`CTAG,C	1833
EcoR I	G`AATT,C	1839
Ava I	C`YCGR,G	1844
Paer7 I	C`TCGA,G	1844
Xho I	C`TCGA,G	1844
Spe I	A`CTAG,T	1850
Pf1M I	CCAN,NNN`NTGG	1874
BstX I	CCAN,NNNN`NTGG	1875
Bcl I	T`GATC,A	1886
Dra III	CAC,NNN`GTG	2345
Sfi I	GGCCN,NNN`NGGCC	3004
Cla I	AT`CG,AT	3069
Kas I	G`GCGC,C	3228
Nar I	GG`CG,CC	3229
Ehe I	GGC GCC	3230
Bbe I	G,GCGC`C	3232
Tth111 I	GACN`N,NGTC	3347
Rsr II	CG`GWC,CG	3745
Bsa I	GGTCTC 7/11	4218
Eco109 I	RG`GNC,CY	4327

Number of enzymes = 43

pCMV-OFP: sites sorted by name:

Aat II	(4)	643	696	779	965
Acc I	(1)	1144			
Acc65 I	(1)	1119			
Aci I	(68)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1135
		1139	1159	1162	1318
		1477	1675	1713	1831
		2489	2516	2544	2547
		2561	2604	2651	2714
		2899	2911	2920	2932
		2942	2953	2999	3138
		3201	3295	3359	3460
		3463	3703	3743	3748
		3798	3814	3840	3896
		3965	3968	4034	4116
		4181	4248	4321	4555
		4564	4699	4809	4930
		4949	5076	5104	5195
Afl III	(5)	1298	1352	1354	2115
		5147			
Aha II	(8)	160	640	693	776
		962	3229	3931	4010
Ahd I	(1)	1346			
Alu I	(18)	347	410	510	1084
		1131	1796	1815	2008
		2175	2432	2727	3015
		3335	3793	4590	4847
		4893	4983		
Alw I	(18)	60	66	381	1099
		1823	1834	1860	3096
		3407	3474	3653	4018
		4045	4404	4405	4502
		4502	4588		
AlwN I	(2)	4330	4738		
ApaL I	(2)	28	4833		
Apo I	(5)	1533	1839	2043	2147
		2158			
Ase I	(1)	525			
Asp718	(1)	1119			
Ava I	(1)	1844			
Ava II	(5)	336	1474	1563	3745
		4190			
Avr II	(2)	3051	4066		
BamH I	(1)	1827			
Ban I	(5)	983	1119	2382	3228
		3263			
Ban II	(3)	2420	3594	4304	
Bbe I	(1)	3232			
Bbv I	(7)	468	2017	3302	3344
		3865	4318	4818	
Bcl I	(1)	1886			
Bcn I	(6)	165	516	3234	3394

The following enzymes do not cut in pCMV-OFP:

Afl II	Age I	Apa I	Asc I	Bbs I
Bbv II	Bgl II	Blp I	Bsg I	BsiW I
BsmB I	Bsp120 I	BspM II	BsrG I	BssH III
Bst1107 I	BstE II	Eco47 III	EcoR V	Esp I
Fse I	Nru I	PpuM I	PspA I	Sac I
Sac II	Sma I	Spl I	Srf I	Xca I

Bfa I	(11)	4007	4771			EcoN I	(1)	339					
		507	1110	1150	1834	EcoO109 I	(1)	4327					
		1851	2078	2496	3052	EcoR I	(1)	1839					
		4067	4401	4654		EcoR II	(12)	606	799	1736	2763		
Bgl I	(4)	608	730	801	3004			2818	2835	3614	4193		
Bpm I	(2)	4012	4069					4296	4986	4999	5120		
Bsa I	(1)	4218				Ehe I	(1)	3230					
BsaA I	(4)	858	1355	2345	3533	Fnu4H I	(37)	185	280	307	457		
BsaB I	(2)	1891	3088					1136	1139	1160	1676		
BsaH I	(8)	160	640	693	776			1714	2006	2525	2547		
		962	3229	3931	4010			2561	2999	3138	3190		
BsaJ I	(17)	878	1123	1312	2763			3201	3291	3296	3333		
		2835	2958	2993	3002			3374	3461	3464	3467		
		3051	3392	3661	4066			3703	3799	3840	3854		
		4193	4194	4296	4297			3968	4307	4322	4533		
		4987						4739	4742	4807	4950		
BsaW I	(6)	404	1870	3260	4104			5105					
		4794	4941			Fok I	(6)	261	2902	3096	3553		
BseR I	(2)	1168	3047					3578	4032				
BsiC I	(2)	1462	3911			Fsp I	(3)	477	1492	3331			
BsiE I	(5)	182	331	1139	3138	Gdi II	(8)	308	1135	1137	1368		
		4813						3134	3136	3699	3726		
BsiHKA I	(5)	32	117	3342	3532	Gsu I	(2)	4013	4068				
		4837				Hae I	(7)	1311	1435	3050	3311		
Bsm I	(2)	1980	2073					4673	5125	5136			
BsmA I	(6)	951	1842	2654	3072	Hae II	(4)	2496	2504	3232	4907		
		4091	4219			Hae III	(25)	309	602	795	1138		
BsmF I	(11)	693	844	1012	1291			1311	1322	1369	1435		
		2745	2817	2881	3380			2195	2337	2992	2998		
		3912	4021	4176				3007	3050	3137	3311		
BsoF I	(37)	185	280	307	457			3702	3729	4238	4295		
		1136	1139	1160	1676			4328	4673	5107	5125		
		1714	2006	2525	2547			5136					
		2561	2999	3138	3190	Hga I	(9)	167	1043	1131	1290		
		3201	3291	3296	3333			2563	3938	4017	4458		
		3374	3461	3464	3467			5036					
		3703	3799	3840	3854			32	117	3342	3532		
		3968	4307	4322	4533			4837					
		4739	4742	4807	4950	HgiE II	(2)	1868	4558				
		5105				Hha I	(23)	141	478	1493	2495		
Bspl286 I	(2)	117	3532					2503	2529	2551	2560		
BspH I	(2)	2655	4427					2573	2604	3223	3231		
BspM I	(3)	3116	3497	3947				3295	3332	3598	3858		
Bsr I	(12)	54	226	493	814			4034	4120	4523	4632		
		1543	2259	2937	3172			4806	4906	4973			
		3373	4619	4733	4746	HinC II	(4)	158	1145	1547	1992		
BsrB I	(4)	2489	2653	3842	3896	Hind II	(4)	158	1145	1547	1992		
BsrD I	(2)	466	3462			HinD III	(1)	1129					
BssS I	(4)	31	3821	3947	4974	Hinf I	(13)	928	1146	1724	2272		
BstB I	(2)	1462	3911					2294	2704	3714	3848		
BstN I	(12)	608	801	1738	2765			3900	3958	3995	4777		
		2820	2837	3616	4195			5173					
		4298	4988	5001	5122	HinI I	(8)	160	640	693	776		
BstU I	(19)	141	578	1141	1300			962	3229	3931	4010		
		1335	2117	2153	2529	HinP I	(23)	139	476	1491	2493		
		2549	2573	2604	3295			2501	2527	2549	2558		
		3596	4034	4118	4181			2571	2602	3221	3229		
		4250	4523	5104				3293	3330	3596	3856		
BstX I	(1)	1875						4032	4118	4521	4630		
BstY I	(11)	53	70	1103	1827			4804	4904	4971			
		3400	3646	4038	4397	Hpa I	(2)	1547	1992				
		4409	4495	4506		Hpa II	(20)	163	405	515	1871		
Bsu36 I	(3)	1823	2709	4341				2447	3134	3211	3233		
Cac8 I	(32)	454	604	797	1133			3261	3392	3482	3549		
		1320	1622	1835	2448			3730	4005	4013	4105		
		2491	2505	2778	2797			4579	4769	4795	4942		
		2850	2869	3123	3309								
		3528	3594	3600	3628	Hph I	(9)	215	893	1183	1262		
		3632	3673	3677	3731			1652	2347	3408	4299		
		4014	4201	4248	4304			4415					
		4326	4537	5097	5134	Kas I	(1)	3228					
Cfr10 I	(4)	2446	3548	3729	4012	Kpn I	(1)	1123					
Cla I	(1)	3069				Mae I	(11)	507	1110	1150	1834		
Csp6 I	(11)	218	736	761	816			1851	2078	2496	3052		
		849	900	1057	1120			4067	4401	4654			
		1205	1655	3534		Mae II	(17)	98	471	640	652		
Dde I	(11)	199	1343	1503	1792			693	776	857	962		
		1823	2709	3011	3892			1354	2289	2301	2344		
		4341	4464	4873				2454	3345	3532	4313		
Dpn I	(27)	55	72	330	376			4446					
		394	1105	1116	1829	Mae III	(20)	39	227	380	438		
		1857	1866	1888	3068			579	666	1015	1301		
		3072	3091	3402	3480			1348	1362	1646	2017		
		3561	3570	3648	4024			2518	2530	3349	3655		
		4040	4399	4411	4489			4345	4611	4727	4790		
		4497	4508	4583				53	70	328	374		
DpnII	(27)	53	70	328	374			392	1103	1114	1827		
		392	1103	1114	1827			1855	1864	1886	3066		
		1855	1864	1886	3066			3070	3089	3400	3478		
		3070	3089	3400	3478			3559	3568	3646	4022		
		3559	3568	3646	4022			4038	4397	4409	4487		
		4038	4397	4409	4487			4495	4506	4581			
Dra I	(5)	15	122	1931	4373			104	1207	1406	1475		
		4392						1814	2484	2712	3589		
Dra III	(1)	2345						3799	3881	4048	4248		
Drd I	(4)	1221	2300	3256	5045	Mlu I	(2)	1298	2115				
Dsa I	(4)	878	1123	2958	3661	Mme I	(4)	1436	2321	4755	4939		
Eae I	(8)	307	1136	1309	1367	Mnl I	(33)	327	1059	1146	1149		
		3135	3309	3700	3727			1158	1195	1268	1500		
Eag I	(2)	1136	3135					1665	1772	1908	1947		
Ear I	(4)	1390	2696	3573	3783			1956	2373	2704	2982		
Eco57 I	(6)	1449	1466	1655	3374			2988	3011	3017	3025		
		3806	4606					3028	3040	3080	3144		
Eco72 I	(1)	1355						3280	3637	3829	4035		
								4067	4349	4719	4970		

Msc I	(2)	5043			
Mse I	(23)	1311	3311		
		14	20	24	121
		486	525	1183	1546
		1729	1930	1991	2112
		2133	2144	2156	2167
		2184	2282	2553	4372
		4386	4391	4443	
Msl I	(4)	288	883	1875	3666
Msp I	(20)	163	405	515	1871
		2447	3134	3211	3233
		3261	3392	3482	3549
		3730	4005	4013	4105
		4579	4769	4795	4942
MspA1 I	(5)	64	2727	3335	4564
		4809			
Mun I	(2)	1243	1979		
Nae I	(3)	2448	3731	4014	
Nar I	(1)	3229			
Nci I	(6)	164	515	3233	3393
		4006	4770		
Nco I	(4)	878	1123	2958	3661
Nde I	(1)	752			
NgoM I	(3)	2446	3729	4012	
Nhe I	(1)	1833			
Nla III	(24)	257	293	371	381
		822	882	1127	1214
		1236	1444	1574	2659
		2799	2871	2962	3103
		3448	3634	3665	3691
		4047	4431	5151	5202
Nla IV	(20)	403	985	1121	1220
		1475	1597	1829	2384
		2405	2417	2608	2769
		2841	3230	3265	4113
		4192	4237	5080	5119
Not I	(1)	1136			
Nsi I	(3)	2801	2873	5204	
Nsp7524 I	(4)	2795	2867	3630	5147
NspB II	(5)	64	2727	3335	4564
		4809			
NspH I	(4)	2799	2871	3634	5151
Pac I	(1)	24			
Paer7 I	(1)	1844			
Pal I	(25)	309	602	795	1138
		1311	1322	1369	1435
		2195	2337	2992	2998
		3007	3050	3137	3311
		3702	3729	4238	4295
		4328	4673	5107	5125
		5136			
PflM I	(1)	1874			
Ple I	(2)	2280	2712		
Pme I	(1)	15			
Pml I	(1)	1355			
Psp1406 I	(2)	98	471		
Pst I	(1)	458			
Pvu I	(1)	331			
Pvu II	(2)	2727	3335		
Rsa I	(11)	219	737	762	817
		850	901	1058	1121
		1206	1656	3535	
Rsr II	(1)	3745			
Sal I	(1)	1143			
Sap I	(2)	3573	3783		
Sau3A I	(27)	53	70	328	374
		392	1103	1114	1827
		1855	1864	1886	3066
		3070	3089	3400	3478
		3559	3568	3646	4022
		4038	4397	4409	4487
		4495	4506	4581	
Sau96 I	(12)	336	601	794	1320
		1474	1563	2336	3745
		4190	4236	4294	4327
Sca I	(1)	219			
ScrF I	(18)	164	515	608	801
		1738	2765	2820	2837
		3233	3393	3616	4006
		4195	4298	4770	4988
		5001	5122		
Sec I	(17)	878	1123	1312	2763
		2835	2958	2993	3002
		3051	3392	3661	4066
		4193	4194	4296	4297
		4987			
SfaN I	(14)	247	440	876	1797
		2044	2807	2879	3188
		3443	3527	3591	3659
		3866	5051		
Sfc I	(4)	454	2564	4691	4882
Sfi I	(1)	3004			
SnaB I	(1)	858			
Spe I	(1)	1850			
Sph I	(3)	2799	2871	3634	
Ssp I	(2)	2137	2690		
Stu I	(2)	1435	3050		
Sty I	(7)	878	1123	1312	2958
		3051	3661	4066	
Taq I	(15)	46	1144	1462	1845
		2378	3069	3342	3498
		3522	3558	3720	3911
		3956	4211	5049	
Tfi I	(6)	1724	3714	3848	3958
		3995	5173		

Tsp45 I	(7)	227	438	1301	1348
			2518	3349	3655
Tth111 I	(1)	3347			
Tth111 II	(6)	1430	1434	3665	4525
		4555	4564		
Vsp I	(1)	525			
Xba I	(1)	1149			
Xho I	(1)	1844			
Xho II	(11)	53	70	1103	1827
		3400	3646	4038	4397
		4409	4495	4506	
Xma III	(2)	1136	3135		
Xmn I	(1)	100			

Site usage in pCMV-OFP:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	68
Afl II	C`TTAA,G	-	Afl III	A`CRYG,T	5
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	1	Alu I	AG CT	18
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	5	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	1	Ava II	G`GWC,C	5
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	5	Ban II	G,RCY`C	3
Bbe I	G,CGCC`C	1	Bbs I	GAAGAC 8/12	-
Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	6
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	8	BsaJ I	C`CNNG,G	17
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	2
Bsg I	GTGCAG 22/20	-	BsiC I	TT`CG,AA	2
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	11	BsoF I	GC`N,GC	37
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	2	BspM I	ACCTCG 10/14	3
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	12
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	-	Bssh II	G`CGCG,C	-
BssS I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	2	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	12	BstU I	CG CG	19
BstX I	CCAN,NNNN`NTGG	1	Bsty I	R`GATC,Y	11
Bsu36 I	CC`TNA,GG	3	Cac8 I	GCM NGC	32
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	1
Csp6 I	G`TA,C	11	Dde I	C`TNA,G	11
Dpn I	GA TC	27	DpnII	`GATC,	27
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	4	Dsa I	C`CRYG,G	4
Eae I	Y`GGCC,R	8	Eag I	C`GGCC,G	2
Ear I	CTCTTC 7/10	4	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	6	Eco72 I	CAC GTG	1
EcoN I	CCTNN`N,NNAGG	1	Eco109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	12
EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	37
Fok I	GGATG 14/18	6	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	3	Gdi II	`YGGC,CG	8
Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	7
Hae II	R,CGCC`Y	4	Hae III	GG CC	25
Hga I	GACGC 9/14	9	HgiA I	G,WGCW`C	5
HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	23
Hinc II	GTY RAC	4	Hind II	GTY RAC	4
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	13
HinI I	GR`CG,YC	8	HinP I	G`CG,C	23
Hpa I	GT AAC	2	Hpa II	C`CG,C	20
Hph I	GGTGA 12/11	9	Kas I	G`GCGC,C	1
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	11
Mae II	A`CG,T	17	Mae III	`GTNAC,	20
Mbo I	`GATC,	27	Mbo II	GAAGA 12/11	14
Mlu I	A`CCGG,T	2	Mme I	TCCRAC 25/23	4
Mnl I	CCTC 10/10	33	Msc I	TGG CCA	2
Mse I	T`TA,A	23	Msl I	CAYNN NNRTG	4
Msp I	C`CG,G	20	MspA1 I	CMG CKG	5
Mun I	C`AATT,G	2	Nae I	GCC GGC	3
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	6
Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	1
Nla III	,CATG`	24	Nla IV	GNN NCC	20
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	5	NspH I	R,CATG`Y	4
Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	1
Pal I	GG CC	25	PflM I	CCAN,NNN`NTGG	1
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Pml I	CAC GTG	1	PpuM I	RG`GWC,CY	-
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Pvu II	CAG CTG	2	Rsa I	GT AC	11
Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
Sap I	GCTCTC 8/11	2	Sau3A I	`GATC,	27
Sau96 I	G`GNC,C	12	Sca I	AGT ACT	1
ScrF I	CC`N,GG	18	Sec I	C`CNNG,G	17
SfaN I	GCATC 9/13	14	Sfc I	C`TRYA,G	4
Sfi I	GCCCN,NNN`NGGCC	1	Sma I	CCC GGG	-

SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1	Tth111 II	CAARCA 16/14	6	Vsp I	AT`TA,AT	1
Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2	Xcm I	CCANNNN,N`NNNNTGG-		Xho I	C`TCGA,G	1
Stu I	AGG CCT	2	Sty I	C`CWWG,G	7	Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	-
Taq I	T`CG,A	15	Tfi I	G`AWT,C	6	Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1
Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	1						