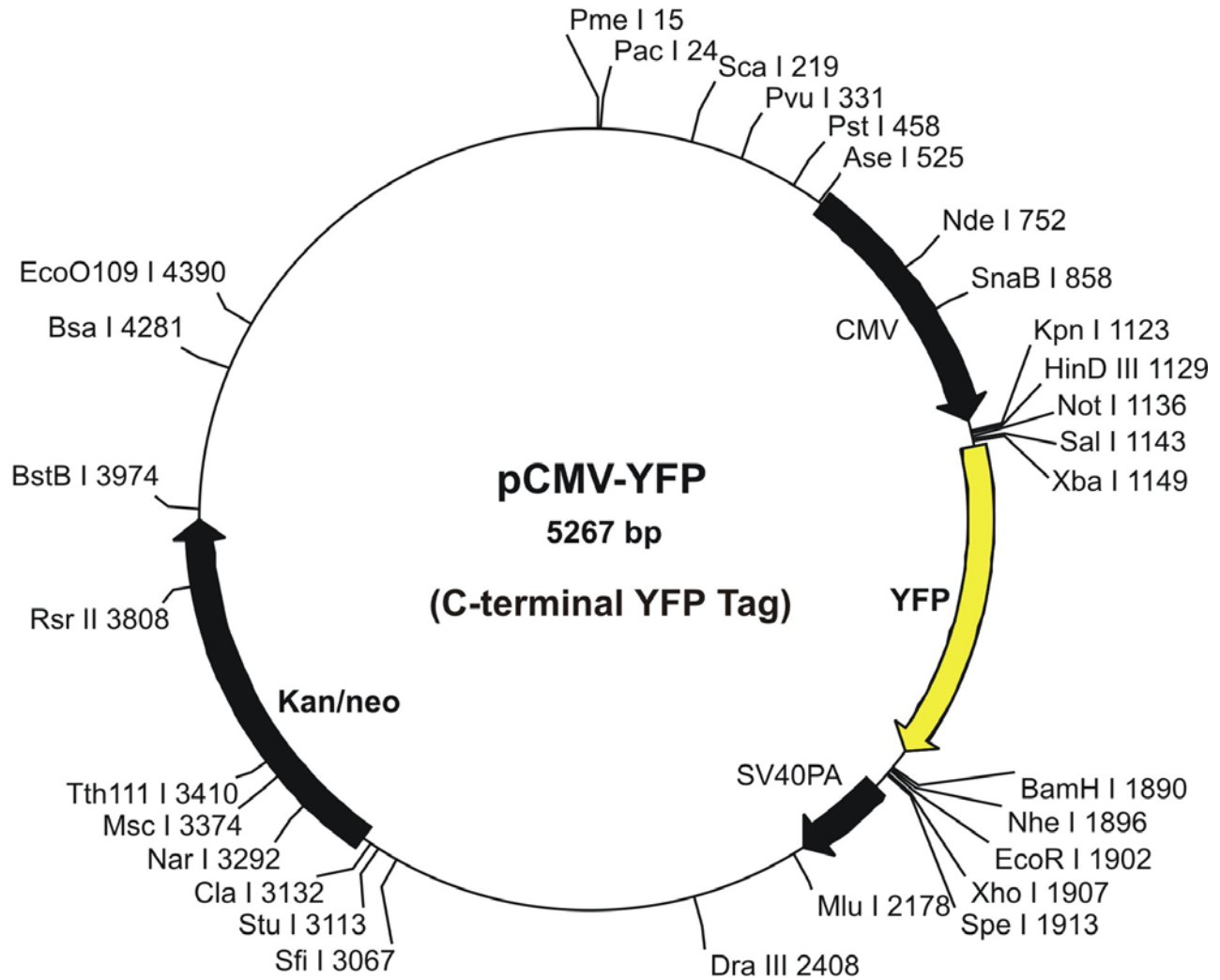
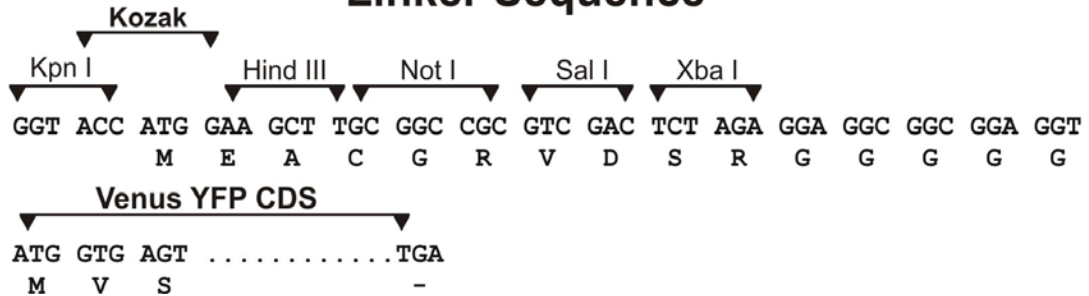


**Name of Vector:** pCMV-YFP (Venus by Miyawaki)  
**Antibiotic Selection:** Kan  
**Created by:** Wei Jiang and Hue Luu  
 (He Lab @ The University of Chicago)  
**Date of Creation:** October 2004



### Linker Sequence



**pCMV-YFP Full-length Sequence and Restriction Sites**  
**(a.k.a., Venus by Miyawaki)**  
**(EYFP with F64L/M153T/V163A/S175G Mutations)**

TAGTTATTATGTTTAAacttaattaagtgcacgagtggggttacatcgaactggatctcaa 60  
cagcggtaagatccttgagagtttctgccccgaagaacgtttccaatgatgagcacttt 120  
taaagttctgctatgtggcgcggtattatcccgtgttgacgcgggcaagagcaactcgg 180  
tcgcccatacactattctcagaatgacttgggtgagtagtaccagtcacagaaaagca 240  
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacctgatgataa 300  
cactgcggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360  
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420  
cataccaaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgctgcgcaa 480  
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540  
CGGGGTCATTAGTTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG 600  
GCCCGCTGGCTGACCGCCCAACGACCCCCGCCATTGACGTCAATAATGACGTATGTTT 660  
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720  
CTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780  
ATGACGGTAAATGGCCCCGCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTTCTTA 840  
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTTGGCAGT 900  
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTG 960  
ACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020  
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080  
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcgggtaccATGGAAGCTTGC GGCCG 1140  
CGTCGACTCTAGAGGAGGCGGCGGAGGTatgggtgagcaagggcgaggagctgttcaccgg 1200  
gggtgggtgcccactcctgggtcgagctggacggcgacgtaaacggccacaagttcagcgtgtc 1260  
cggcagggcgagggcgatgccacctacggcaagctgacctgaagttcatctgcaccac 1320  
cggcaagctgcccgtgccctggcccacctcgtgaccttccggctacggcctgatgtg 1380  
cttcgcccgtaccccgaccacatgaagcagcagcacttcttcaagtcggccatgcccga 1440  
aggctacgtccaggagcgcaccatcttcttcaaggacgacggcaactacaagaccgcgc 1500  
cgaggtgaagttcgagggcgacaccctgggtgaaccgcatcgagctgaagggcatcgactt 1560  
caaggaggacggcaacatcctggggcacaagctggagtacaactacaacagccacaacgt 1620  
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catcgaggacggcagcgtgcagctcggccgaccactaccagcagaacacccccatcggcga 1740  
cggccccgtgctgctgcccgcacaaccactacctgagctaccagtcggccctgagcaaaaga 1800  
ccccaacgagaagcgcgatcacatgggtcctgctggagttcgtgaccgcccggggatcac 1860  
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TTTTACTTGTCTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATG 2040  
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TCACAAATTTACAAATAAAGCATTTTTTTACTGCATTCTAGTTGTGGTTTTGTCCAAAC 2160  
TCATCAATGTATCTTAAACGCGTAAATTTGTAAGCGTTAATATTTTTGTTAAAATTCGCGTTA 2220  
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AAATCAAAGAATAGACCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAAACAAGAGTCCA 2340  
CTATTAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCAGGGCGATGGC 2400  
CCACTACGTGAACCATCACCTAATCAAGTTTTTTTTGGGGTCGAGGTGCCGTAAAGCACTA 2460  
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GTCACGCTGCGCGTAAACCACACCCCGCGCTTAATGCGCGCTACAGGGCGCGTCA 2640  
GGTGGCACTTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACAT 2700  
TCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAA 2760  
AGGAAGAGTCTTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAGTTAGGGTGTGGAA 2820  
AGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGTCAGCAA 2880  
CCAGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCA 2940  
ATTAGTCAGCAACCATAGTCCCGCCCCCTAACTCCGCCCCATCCCCCCCCCTAACTCCGCCCA 3000  
GTTCCGCCCATTTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGG 3060  
CCGCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTTGGAGGCTTAGGCT 3120  
TTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTTCGCATGATTGAACAAGATGGA 3180  
TTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTTCGGCTATGACTGGGCACAA 3240  
CAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGGGCGCCCCGTT 3300  
CTTTTTGTCAAGACCGACCTGTCCGGTCCCTGAATGAACTGCAAGACGAGGCGAGCGCG 3360  
CTATCGTGGCTGGCCACGACGGGCGTTCCCTTGCGCAGCTGTGCTCGACGTTGTCACTGAA 3420  
GCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCCTGTCTATCTCAC 3480

CTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATACGCTT 3540  
 GATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCGAGCACGTACT 3600  
 CGGATGGAAGCCGGTCTTGTGCGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCG 3660  
 CCAGCCGAAGTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGATCTCGTCTGTG 3720  
 ACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTTTTCTGGATTTC 3780  
 ATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTTGGCTACCCGT 3840  
 GATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCTCTCGTGCTTTACGGTATC 3900  
 GCCGCTCCCGATTTCGAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTTCTTCTGAGCG 3960  
 GGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCAACCTGCCATCACGAGATTTTCG 4020  
 ATTCACCCCGCCCTTCTATGAAAGGTTGGGCTTTCGGAATCGTTTTCCGGGACGGCCGGCT 4080  
 GGATGATCCTCCAGCGGGGATCTCATGTGGAGTTCTTTCGCCACCCTAGGCGGGGAGGC 4140  
 TAACTGAAACACGGAAGGAGACAATACCGGAAGGAATCCCGCGCTATGACGGCAATAAAAA 4200  
 GACAGAATAAAACGCACGGTGTGGGTTCGTTTGTTCATAAAACGCGGGTTCGGTCCCAGG 4260  
 GCTGGCACTCTGTGATACCCACCGAGACCCCATTTGGGGCCAATACGCCCGGTTTTCTT 4320  
 CCTTTTCCCCACCCCAAGTTTCGGGTGAAGGCCAGGGCTCGCAGCCAACGTTCG 4380  
 GGGCGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATTGATTTAAAAAC 4440  
 TTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTTGATAATCTCATGACCAAAA 4500  
 TCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAGATCAAAGGAT 4560  
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 TACCAGCGGTGGTTTTGTTTCCCGGATCAAGAGCTACCAACTCTTTTTCCGAAGGTAAGT 4680  
 GCTTCAGCAGAGCGCAGATACCAATACTGTCTTCTAGTGTAGCCGTAGTTAGGCCACC 4740  
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 CTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGGACTCAAGACGATAGTTACCGG 4860  
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 GGGAGCTTCCAGGGGAAACGCCTGGTATCTTTATAGTCTGTTCGGGTTTCGCCACCTCT 5100  
 GACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGCGGAGCCTATGGAAAAACGCCA 5160  
 GCAACGGCCCTTTTTACGGTTTCTGGCCTTTTGTCTGGCCTTTTGTCTCACATGTTCTTTC 5220  
 CTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 5267

**Unique enzymes in pCMV-YFP:**

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
BsrG I	T`GTAC,A	1879
BamH I	G`GATC,C	1890
Nhe I	G`CTAG,C	1896
EcoR I	G`AATT,C	1902
Ava I	C`YCGR,G	1907
Paer7 I	C`TCGA,G	1907
Xho I	C`TCGA,G	1907
Spe I	A`CTAG,T	1913
PfI M I	CCAN,NNN`NTGG	1937
BstX I	CCAN,NNNN`NTGG	1938
Bcl I	T`GATC,A	1949
Mun I	C`AATT,G	2042
Hpa I	GTT AAC	2055
Mlu I	A`CGCG,T	2178
Dra III	CAC,NNN`GTG	2408
Sfi I	GGCCN,NNN`NGGCC	3067
Stu I	AGG CCT	3113
Cla I	AT`CG,AT	3132
Kas I	G`GCGC,C	3291
Nar I	GG`CG,CC	3292
Ehe I	GGC GCC	3293
Bbe I	G,GCGC`C	3295
Msc I	TGG CCA	3374
Tth111 I	GACN`N,NGTC	3410
Rsr II	CG`GWC,CG	3808
BsiC I	TT`CG,AA	3974
BstB I	TT`CG,AA	3974
Bsa I	GGTCTC 7/11	4281
EcoO109 I	RG`GNC,CY	4390

Number of enzymes = 48

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

Afl II	Age I	Ahd I	Apa I	Asc I
Bbs I	Bbv II	Bgl II	Blp I	BsiW I
BsmB I	Bsp120 I	BspM II	BssH II	Bst1107 I
BstE II	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	Srf I

**pCMV-YFP: sites sorted by name:**

Aat II	(4)	643	696	779	965
Acc I	(1)	1144			
Acc65 I	(1)	1119			
Aci I	(72)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1135
		1139	1159	1162	1388
		1429	1496	1535	1673
		1786	1846	1849	1894
		2552	2579	2607	2610
		2624	2667	2714	2777
		2962	2974	2983	2995
		3005	3016	3062	3201
		3264	3358	3422	3523
		3526	3766	3806	3811
		3861	3877	3903	3959
		4028	4031	4097	4179
		4244	4311	4384	4618
		4627	4762	4872	4993
		5012	5139	5167	5258
Afl III	(2)	2178	5210		
Aha II	(8)	160	640	693	776
		962	3292	3994	4073
Alu I	(25)	347	410	510	1084
		1131	1190	1223	1295
		1328	1544	1592	1703
		1777	1877	2071	2238
		2495	2790	3078	3398
		3856	4653	4910	4956
		5046			
Alw I	(20)	60	66	381	1099
		1665	1862	1886	1897
		1923	3159	3470	3537
		3716	4081	4108	4467
		4468	4565	4565	4651
AlwN I	(2)	4393	4801		
ApaL I	(2)	28	4896		
Apo I	(4)	1902	2106	2210	2221
Ase I	(1)	525			

Asp718	(1)	1119				3154	3465	3543	3624	
Ava I	(1)	1907				3633	3711	4087	4103	
Ava II	(4)	336	1826	3808	4253	4462	4474	4552	4560	
Avr II	(2)	3114	4129			4571	4646			
BamH I	(1)	1890				DpnII (30)	53	70	328	374
Ban I	(6)	983	1119	1205	2445		392	1103	1114	1669
		3291	3326				1817	1855	1890	1918
Ban II	(3)	2483	3657	4367			1927	1949	3129	3133
Bbe I	(1)	3295					3152	3463	3541	3622
Bbv I	(10)	468	1421	1705	1712		3631	3709	4085	4101
		2080	3365	3407	3928		4460	4472	4550	4558
		4381	4881				4569	4644		
Bcl I	(1)	1949				Dra I (5)	15	122	1994	4436
Bcn I	(8)	165	516	1200	1854		4455			
		3297	3457	4070	4834	Dra III (1)	2408			
Bfa I	(11)	507	1110	1150	1897	Drd I (3)	2363	3319	5108	
		1914	2141	2559	3115	Dsa I (4)	878	1123	3021	3724
		4130	4464	4717		Eae I (8)	307	1136	1241	1630
Bgl I	(4)	608	730	801	3067		3198	3372	3763	3790
Bpm I	(4)	1614	1854	4075	4132	Eag I (2)	1136	3198		
Bsa I	(1)	4281				Ear I (3)	2759	3636	3846	
BsaA I	(3)	858	2408	3596		Eco57 I (5)	1322	1565	3437	3869
BsaB I	(2)	1954	3151				4669			
BsaH I	(8)	160	640	693	776	EcoN I (1)	339			
		962	3292	3994	4073	EcoO109 I (1)	4390			
BsaJ I	(21)	878	1123	1198	1338	EcoR I (1)	1902			
		1501	1525	1580	2826	EcoR II (16)	606	799	1213	1338
		2898	3021	3056	3065		1450	1525	1579	2826
		3114	3455	3724	4129		2881	2898	3677	4256
		4256	4257	4359	4360		4359	5049	5062	5183
		5050				Ehe I (1)	3293			
BsaW I	(6)	404	1933	3323	4167	Fnu4H I (42)	185	280	307	457
		4857	5004				1136	1139	1160	1329
BbeR I	(3)	1168	1200	3110			1410	1694	1701	1752
Bbg I	(2)	1298	1719				1755	1849	2069	2588
BsiC I	(1)	3974					2610	2624	3062	3201
BsiE I	(5)	182	331	1139	3201		3253	3264	3354	3359
		4876					3396	3437	3524	3527
BsiHKA I	(5)	32	117	3405	3595		3530	3766	3862	3903
		4900					3917	4031	4370	4385
Bsm I	(2)	2043	2136				4596	4802	4805	4870
BsmA I	(6)	951	1905	2717	3135		5013	5168		
		4154	4282			Fok I (8)	261	1197	1563	2965
BsmF I	(10)	693	844	1012	2808		3159	3616	3641	4095
		2880	2944	3443	3975	Fsp I (2)	477	3394		
		4084	4239			Gdi II (9)	308	1135	1137	1242
BsoF I	(42)	185	280	307	457		1629	3197	3199	3762
		1136	1139	1160	1329		3789			
		1410	1694	1701	1752	Gsu I (4)	1613	1853	4076	4131
		1755	1849	2069	2588	Hae I (5)	3113	3374	4736	5188
		2610	2624	3062	3201		5199			
		3253	3264	3354	3359	Hae II (4)	2559	2567	3295	4970
		3396	3437	3524	3527	Hae III (26)	309	602	795	1138
		3530	3766	3862	3903		1243	1343	1372	1632
		3917	4031	4370	4385		1744	2258	2400	3055
		4596	4802	4805	4870		3061	3070	3113	3200
		5013	5168				3374	3765	3792	4301
Bspl286 I	(2)	117	3595				4358	4391	4736	5170
BspH I	(2)	2718	4490				5188	5199		
BspM I	(3)	3179	3560	4010		Hga I (8)	167	1043	1131	2626
Bsr I	(12)	54	226	493	814		4001	4080	4521	5099
		1782	2322	3000	3235	HgiA I (5)	32	117	3405	3595
		3436	4682	4796	4809		4900			
BsrB I	(4)	2552	2716	3905	3959	HgiE II (2)	1931	4621		
BsrD I	(2)	466	3525			Hha I (25)	141	478	1459	1500
BsrG I	(1)	1879					1816	2558	2566	2592
BssS I	(5)	31	1350	3884	4010		2614	2623	2636	2667
		5037					3286	3294	3358	3395
BstB I	(1)	3974					3661	3921	4097	4183
BstN I	(16)	608	801	1215	1340		4586	4695	4869	4969
		1452	1527	1581	2828		5036			
		2883	2900	3679	4258	HinC II (3)	158	1145	2055	
		4361	5051	5064	5185	Hind II (3)	158	1145	2055	
BstU I	(19)	141	578	1141	1498	Hind III (1)	1129			
		1816	2180	2216	2592	Hinf I (12)	928	1146	2335	2357
		2612	2636	2667	3358		2767	3777	3911	3963
		3659	4097	4181	4244		4021	4058	4840	5236
		4313	4586	5167		HinI I (8)	160	640	693	776
BstX I	(1)	1938					962	3292	3994	4073
BstY I	(12)	53	70	1103	1669	HinP I (25)	139	476	1457	1498
		1890	3463	3709	4101		1814	2556	2564	2590
		4460	4472	4558	4569		2612	2621	2634	2665
Bsu36 I	(2)	2772	4404				3284	3292	3356	3393
Cac8 I	(35)	454	604	797	1133		3659	3919	4095	4181
		1293	1326	1388	1698		4584	4693	4867	4967
		1705	1898	2511	2554		5034			
		2568	2841	2860	2913	Hpa I (1)	2055			
		2932	3186	3372	3591	Hpa II (24)	163	405	515	1198
		3657	3663	3691	3695		1261	1321	1852	1934
		3736	3740	3794	4077		2510	3197	3274	3296
		4264	4311	4367	4389		3324	3455	3545	3612
		4600	5160	5197			3793	4068	4076	4168
Cfr10 I	(5)	1320	2509	3611	3792		4642	4832	4858	5005
		4075				Hph I (11)	215	893	1183	1188
		3132					1516	1540	1669	2410
Cla I	(1)	3132					3471	4362	4478	
Csp6 I	(11)	218	736	761	816	Kas I (1)	3291			
		849	900	1057	1120	Kpn I (1)	1123			
		1598	1880	3597		Mae I (11)	507	1110	1150	1897
Dde I	(9)	199	1773	1791	2772		1914	2141	2559	3115
		3074	3955	4404	4527		4130	4464	4717	
		4936					98	471	640	652
Dpn I	(30)	55	72	330	376	Mae II (19)	693	776	857	962
		394	1105	1116	1671		1234	1447	1618	2352
		1819	1857	1892	1920		2364	2407	2517	3408
		1929	1951	3131	3135					

Mae III	(18)	3595	4376	4509	
		39	227	380	438
		579	666	1015	1352
		1841	2080	2581	2593
		3412	3718	4408	4674
		4790	4853		
Mbo I	(30)	53	70	328	374
		392	1103	1114	1669
		1817	1855	1890	1918
		1927	1949	3129	3133
		3152	3463	3541	3622
		3631	3709	4085	4101
		4460	4472	4550	4558
		4569	4644		
Mbo II	(14)	104	1413	1458	1461
		1654	2547	2775	3652
		3862	3944	4111	4311
		4481	4554		
Mlu I	(1)	2178			
Mme I	(3)	2384	4818	5002	
Mnl I	(36)	327	1059	1146	1149
		1158	1178	1259	1265
		1358	1496	1508	1559
		1679	1971	2010	2019
		2436	2767	3045	3051
		3074	3080	3088	3091
		3103	3143	3207	3343
		3700	3892	4098	4130
		4412	4782	5033	5106
Msc I	(1)	3374			
Mse I	(20)	14	20	24	121
		486	525	1993	2054
		2175	2196	2207	2219
		2230	2247	2345	2616
		4435	4449	4454	4506
Msl I	(5)	288	883	1656	1938
		3729			
Msp I	(24)	163	405	515	1198
		1261	1321	1852	1934
		2510	3197	3274	3296
		3324	3455	3545	3612
		3793	4068	4076	4168
		4642	4832	4858	5005
MspA1 I	(5)	64	2790	3398	4627
		4872			
Mun I	(1)	2042			
Nae I	(3)	2511	3794	4077	
Nar I	(1)	3292			
Nci I	(8)	164	515	1199	1853
		3296	3456	4069	4833
Nco I	(4)	878	1123	3021	3724
Nde I	(1)	752			
NgoM I	(3)	2509	3792	4075	
Nhe I	(1)	1896			
Nla III	(25)	257	293	371	381
		822	882	1127	1406
		1436	1631	1826	1871
		2722	2862	2934	3025
		3166	3511	3697	3728
		3754	4110	4494	5214
		5265			
Nla IV	(19)	403	985	1121	1207
		1745	1892	2447	2468
		2480	2671	2832	2904
		3293	3328	4176	4255
		4300	5143	5182	
Not I	(1)	1136			
Nsi I	(3)	2864	2936	5267	
Nsp7524 I	(4)	2858	2930	3693	5210
NspB II	(5)	64	2790	3398	4627
		4872			
NspH I	(4)	2862	2934	3697	5214
Pac I	(1)	24			
Paer7 I	(1)	1907			
Pal I	(26)	309	602	795	1138
		1243	1343	1372	1632
		1744	2258	2400	3055
		3061	3070	3113	3200
		3374	3765	3792	4301
		4358	4391	4736	5170
		5188	5199		
Pf1M I	(1)	1937			
Ple I	(2)	2343	2775		
Pme I	(1)	15			
Psp1406 I	(2)	98	471		
Pst I	(1)	458			
Pvu I	(1)	331			
Pvu II	(2)	2790	3398		
Rsa I	(11)	219	737	762	817
		850	901	1058	1121
		1599	1881	3598	
Rsr II	(1)	3808			
Sal I	(1)	1143			
Sap I	(2)	3636	3846		
Sau3A I	(30)	53	70	328	374
		392	1103	1114	1669
		1817	1855	1890	1918
		1927	1949	3129	3133
		3152	3463	3541	3622
		3631	3709	4085	4101
		4460	4472	4550	4558
		4569	4644		
Sau96 I	(12)	336	601	794	1342
		1743	1826	2399	3808
		4253	4299	4357	4390

Sca I	(1)	219			
ScrF I	(24)	164	515	608	801
		1199	1215	1340	1452
		1527	1581	1853	2828
		2883	2900	3296	3456
		3679	4069	4258	4361
		4833	5051	5064	5185
Sec I	(21)	878	1123	1198	1338
		1501	1525	1580	2826
		2898	3021	3056	3065
		3114	3455	3724	4129
		4256	4257	4359	4360
		5050			
SfaN I	(17)	247	440	876	1269
		1545	1560	1659	2107
		2870	2942	3251	3506
		3590	3654	3722	3929
		5114			
Sfc I	(4)	454	2627	4754	4945
Sfi I	(1)	3067			
SnaB I	(1)	858			
Spe I	(1)	1913			
Sph I	(3)	2862	2934	3697	
Ssp I	(2)	2200	2753		
Stu I	(1)	3113			
Sty I	(6)	878	1123	3021	3114
		3724	4129		
Taq I	(19)	46	1144	1219	1513
		1540	1555	1684	1908
		2441	3132	3405	3561
		3585	3621	3783	3974
		4019	4274	5112	
Tfi I	(5)	3777	3911	4021	4058
		5236			
Tsp45 I	(7)	227	438	1352	1841
		2581	3412	3718	
Tth111 I	(1)	3410			
Tth111 II	(5)	1652	3728	4588	4618
		4627			
Vsp I	(1)	525			
Xba I	(1)	1149			
Xho I	(1)	1907			
Xho II	(12)	53	70	1103	1669
		1890	3463	3709	4101
		4460	4472	4558	4569
Xma III	(2)	1136	3198		
Xmn I	(1)	100			

### Site usage in pCMV-YFP:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	72
Afl I II	C`TTAA,G	-	Afl III	A`CRYG,T	2
Age I	A`CCGG,T	-	Aha II	GR`CG,YC	8
Ahd I	GACNN,N`NNGTC	-	Alu I	AG CT	25
Alw I	GGATC 8/9	20	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	1	Ava II	G`GWC,C	4
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	1
Ban I	G`GYRC,C	6	Ban II	G,RCYC`C	3
Bbe I	G,CGCC`C	1	Bbs I	GAAGAC 8/12	-
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	-
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	8
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	4	Bsa I	GGTCTC 7/11	1
BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	21
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	3
Bsg I	GTGCG 22/20	2	BsiC I	TT`CG,AA	1
BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
BslW 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	10	BsoF I	GC`N,GC	42
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 CCG	4	BsrD I	GCAATG, 8	2
BsrG I	T`GTAC,A	1	Bssh II	G`CGCG,C	-
BssS I	C`TCGT,G	5	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	16	BstU I	CG CG	19
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	12
Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	35
Cfr10 I	R`CCGG,Y	5	Clal I	AT`CG,AT	1
Csp6 I	G`TA,C	11	Dde I	C`TNA,G	9
Dpn I	GA TC	30	DpnII	`GATC,	30
Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Eae I	Y`GGCC,R	8	Eag I	C`GGCC,C	2
Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	5	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,NNAGG	1	Eco0109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	16
EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	42
Fok I	GGATG 14/18	8	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	9
Gsu I	CTGGAG 21/19	4	Hae I	WGG CCW	5
Hae II	R,CGCC`Y	4	Hae III	GG CC	26
Hga I	GACGC 9/14	8	HgiA I	G,WGCW`C	5
HgiE II	ACCCNNNNNGGT -1/132	-1/132	Hha I	G,CG`C	25

Hinc II	GTY RAC	3	Hind II	GTY RAC	3	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12	Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
HinI I	GR`CG,YC	8	HinP I	G`CG,C	25	Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Hpa I	GTT AAC	1	Hpa II	C`CG,G	24	Pvu II	CAG CTG	2	Rsa I	GT AC	11
Hph I	GGTGA 12/11	11	Kas I	G`GCGC,C	1	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	11	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
Mae II	A`CG,T	19	Mae III	`GTNAC,	18	Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	30
Mbo I	`GATC,	30	Mbo II	GAAGA 12/11	14	Sau96 I	G`GNC,C	12	Sca I	AGT ACT	1
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3	ScrF I	CC`N,GG	24	Sec I	C`CNNG,G	21
Mnl I	CCTC 10/10	36	Msc I	TGG CCA	1	SfaN I	GCATC 9/13	17	Sfc I	C`TRYA,G	4
Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	5	Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
Msp I	C`CG,G	24	MspAl I	CMG CKG	5	SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Mun I	C`AATT,G	1	Nae I	GCC GGC	3	Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	8	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1	Stu I	AGG CCT	1	Sty I	C`CWWG,G	6
NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	1	Taq I	T`CG,A	19	Tfi I	G`AWT,C	5
Nla III	,CATG`	25	Nla IV	GGN NCC	19	Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	1
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-	Tth111 II	CAARCA 16/14	5	Vsp I	AT`TA,AT	1
Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4	Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
NspB II	CMG CKG	5	NspH I	R,CATG`Y	4	Xcm I	CCANNNN,N`NNNNTGG-	-	Xho I	C`TCGA,G	1
Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,C	1	Xho II	R`GATC,Y	12	Xma I	C`CCGG,G	-
Pal I	GG CC	26	PflM I	CCAN,NNN`NTGG	1	Xma III	C`GGCC,G	2	Xmn I	GAANN NNITC	1
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1						