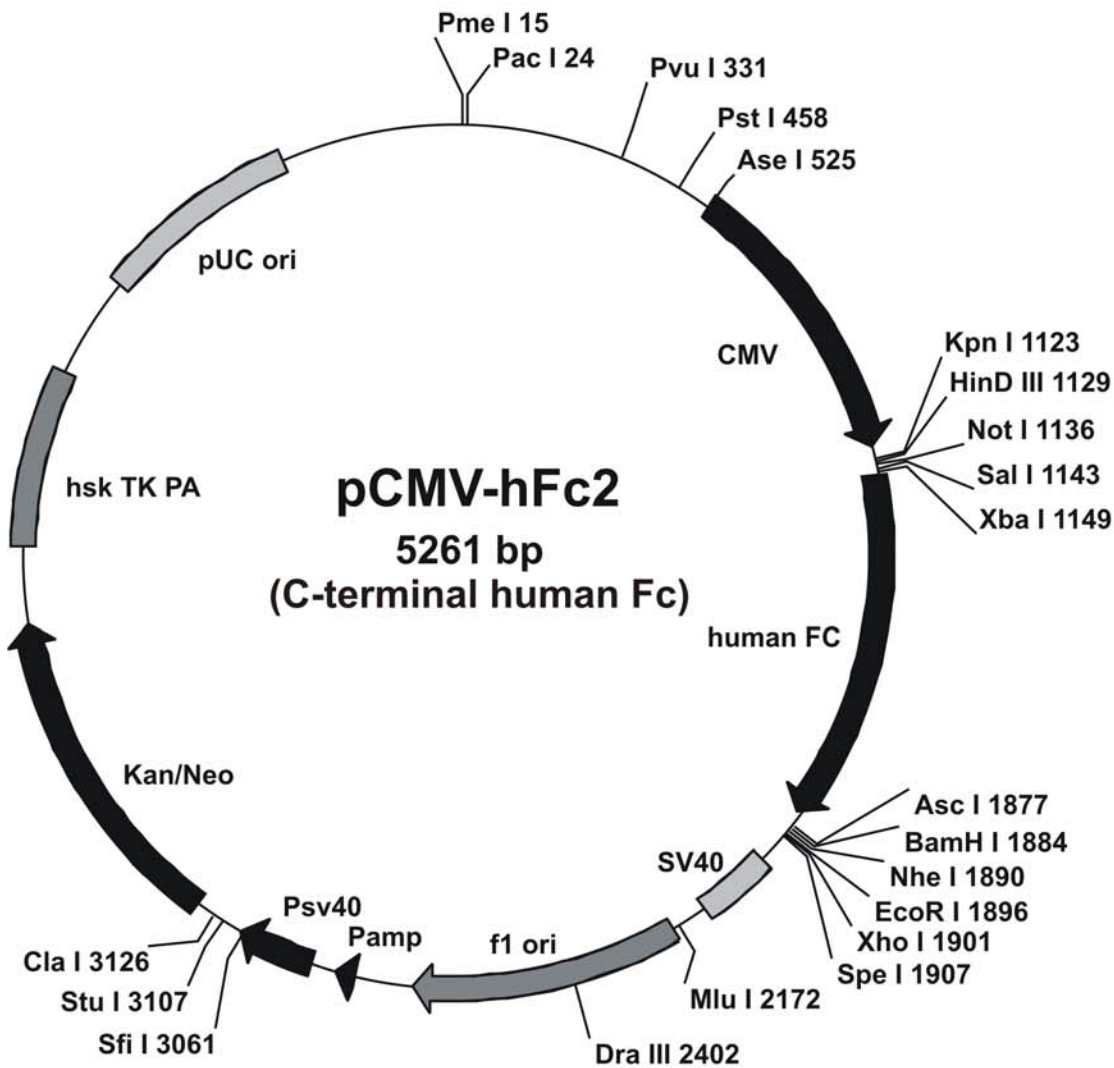
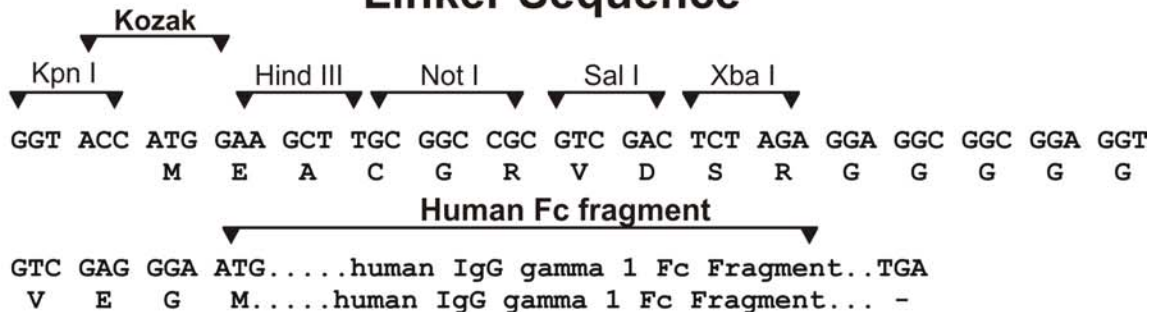


**Name of Vector: pCMV-hFc2**  
**Antibiotic Selection: Kan**  
**Created by: Wei Jiang, and Yien Li**  
**(He Lab @ The University of Chicago)**  
**Date of Creation: June 2004**



### Linker Sequence



## pCMV-hFc2 Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtggggttacatcgaactggatctcaa 60  
cagcggtaagatccttgagagttttcgcgccgaagaacgttttccaatgatgagcacttt 120  
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180  
tcgccgcatacactattctcagaatgacttgggtgagtaactcaccagtcacagaaaagca 240  
tcttacggatggcatgacagtaagagaattatgcagtgctgccataacatgagtgataa 300  
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360  
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420  
catacacaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480  
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540  
CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600  
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCCATTTGACGTCAATAATGACGTATGTTT 660  
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720  
CTGCCACTTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780  
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTCCCTA 840  
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900  
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTG 960  
ACGTCAATGGGAGTTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020  
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080  
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagcatggaagcttgcgccg 1140  
cgtcgaactctagaggaggcggcgagggtgctcagagcccaaatcttgtgacaaaactcacac 1200  
atgccaccgctgccagcacctgaactcctggggggaccgctcagctcttctcttcccccc 1260  
aaaaccgaaggacaccctcatgatctcccggaccctgaggtcacatgcgtgggtgggga 1320  
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taatgccaagacaaagccgcgggaggagcagtagacaacagcacgtaccgtgtggtagcgt 1440  
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GTGGAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTCAATTAGT 2940  
CAGCAACCATAGTCCCGCCCCTAACCTCCGCCCATCCCGCCCCTAACCTCCGCCAGTTCCG 3000  
CCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTATTTATGCAGAGGCCGAGGCCGCT 3060  
CGGCTCTGAGCTATTCCAGAAGTAGTGAGGAGCTTTTTTTGGAGGCCCTAGGCTTTTTGCA 3120  
AAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGATTGAACAAGATGGATTGCAC 3180  
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 AGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCTCTGTCACTCACCTTGCT 3480  
 CCTGCCGAGAAAAGTATCCATCATGGCTGATGCAATGCGGGCGGCTGCATACGCTTGATCCG 3540  
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 GAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGAGCATCAGGGGCTCGCGCCAGCC 3660  
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 CGGCCTTTTTACGGTTCTTGCCCTTTTGCTGGCCTTTTGCTCACATGTTCTTTCTGCGT 5220  
 TATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT 5261

Unique enzymes in CMVHFC2.TXT:

Pme I	CTTT AAAC	15	Nhe I	G`CTAG,C	1890
Pac I	TTA,AT`TAA	24	EcoR I	G`AATT,C	1896
Sca I	AGT ACT	219	Paer7 I	C`TCGA,G	1901
Pvu I	CG,AT`CG	331	Xho I	C`TCGA,G	1901
Pst I	C,TGCA`G	458	Spe I	A`CTAG,T	1907
Ase I	AT`TA,AT	525	PflM I	CCAN,NNN`NTGG	1931
Vsp I	AT`TA,AT	525	BstX I	CCAN,NNNN`NTGG	1932
Nde I	CA`TA,TG	752	Bcl I	T`GATC,A	1943
SnaB I	TAC GTA	858	Mun I	C`AATT,G	2036
Acc65 I	G`GTAC,C	1119	Hpa I	GTT AAC	2049
Asp718	G`GTAC,C	1119	Mlu I	A`CGCG,T	2172
Kpn I	G,GTAC`C	1123	Dra III	CAC,NNN`GTG	2402
Hind III	A`AGCT,T	1129	Sfi I	GGCCN,NNN`NGGCC	3061
Not I	GC`GGCC,GC	1136	Stu I	AGG CCT	3107
Sal I	G`TCGA,C	1143	Cla I	AT`CG,AT	3126
Acc I	GT`MK,AC	1144	Kas I	G`GCGC,C	3285
Xba I	T`CTAG,A	1149	Nar I	GG`CG,CC	3286
Ahd I	GACNN,N`NNGTC	1242	Ehe I	GGC GCC	3287
Sac II	CC,GC`GG	1401	Bbe I	G,GCGC`C	3289
BsrG I	T`GTAC,A	1570	Msc I	TGG CCA	3368
PspA I	C`CCGG,G	1588	Tth111 I	GACN`N,NGTC	3404
Xma I	C`CCGG,G	1588	Rsr II	CG`GWC,CG	3802
Sma I	CCC GGG	1590	BsiC I	TT`CG,AA	3968
Asc I	GG`CGCG,CC	1877	BstB I	TT`CG,AA	3968
BssH II	G`CGCG,C	1877	EcoO109 I	RG`GNC,CY	4384
BamH I	G`GATC,C	1884			

Number of enzymes = 51

The following enzymes do not cut in CMVHFC2.TXT:

Afl II	Age I	643	696	779	965	Bsp1286 I	(2)	117	3589	3760	3856
BsiW I	BsmB I	(1) 1144				BspH I	(3)	1279	2712	4484	4364
BstE II	Eco47 III	(1) 1119				BspM I	(5)	1632	1762	3173	4799
Fse I	Nru I	(66) 64	141	185	306			4004			
		352	576	604	616	Bsr I	(13)	54	226	493	814
		630	797	888	921			1358	1466	2316	2994
		1025	1046	1107	1135	BsrB I	(4)	2546	2710	3899	3953
		1139	1159	1162	1398	BsrD I	(3)	466	1682	3519	
		1400	1888	2546	2573	BsrG I	(1)	1570			
		2601	2604	2618	2661	BssH II	(1)	1877			
		2708	2771	2956	2968	BssS I	(4)	31	3878	4004	5031
		2977	2989	2999	3010	BstB I	(1)	3968			
		3056	3195	3258	3352	BstN I	(15)	608	801	1230	1458
		3416	3517	3520	3760			1611	1629	2822	2877
		3800	3805	3855	3871			2894	3673	4252	4355
		3897	3953	4022	4025	BstU I	(19)	5045	5058	5179	
		4091	4173	4238	4305			141	578	1141	1400
		4378	4612	4621	4756			1879	2174	2210	2586
		4866	4987	5006	5133			2606	2630	2661	3352
		5161	5252					3653	4091	4175	4238
Afl III	(2)	2172	5204			BstX I	(1)	1932			
Aha II	(8)	160	640	693	776	BstY I	(11)	53	70	1103	1884
		962	3286	3988	4067			3457	3703	4095	4454
Ahd I	(1)	1242						4466	4552	4563	
Alu I	(18)	347	410	510	1084	Bsu36 I	(4)	1297	1339	2766	4398
		1131	1598	1754	2065	Cac8 I	(32)	454	604	797	1133
		2232	2489	2784	3072			1752	1879	1892	2505
		3392	3850	4647	4904			2548	2562	2835	2854
		4950	5040					2907	2926	3180	3366
Alw I	(18)	60	66	381	1099			3585	3651	3657	3685
		1880	1891	1917	3153			3689	3730	3734	3788
		3464	3531	3710	4075			4071	4258	4305	4361
		4102	4461	4462	4559			4383	4594	5154	5191
		4559	4645			Cfr10 I	(4)	2503	3605	3786	4069
AlwN I	(3)	1221	4387	4795		Cla I	(1)	3126			
ApaL I	(2)	28	4890			Csp6 I	(14)	218	736	761	816
Apo I	(4)	1896	2100	2204	2215			849	900	1057	1120
Asc I	(1)	1877						1358	1412	1424	1481
Ase I	(1)	525						1571	3591		
Asp718	(1)	1119				Dde I	(9)	199	1297	1339	2766
Ava I	(3)	1555	1588	1901				3068	3949	4398	4521
Ava II	(5)	336	1236	1291	3802			4930			
		4247				Dpn I	(29)	55	72	330	376
Avr II	(2)	3108	4123					394	1105	1116	1284
BamH I	(1)	1884						1873	1886	1914	1923
Ban I	(5)	983	1119	2439	3285			1945	3125	3129	3148
		3320						3459	3537	3618	3627
Ban II	(4)	1177	2477	3651	4361			3705	4081	4097	4456
Bbe I	(1)	3289						4468	4546	4554	4565
Bbs I	(3)	1238	1339	1784				4640			
Bbv I	(10)	468	1562	1694	1790	DpnII	(29)	53	70	328	374
		2074	3359	3401	3922			392	1103	1114	1282
		4375	4875					1871	1884	1912	1921
Bbv II	(3)	1239	1338	1785				1943	3123	3127	3146
Bcl I	(1)	1943						3457	3535	3616	3625
Bcn I	(10)	165	516	1290	1590			3703	4079	4095	4454
		1591	1862	3291	3451			4466	4544	4552	4563
		4064	4828			Dra I	(5)	15	122	1988	4430
Bfa I	(11)	507	1110	1150	1891			4449			
		1908	2135	2553	3109	Dra III	(1)	2402			
		4124	4458	4711		Drd I	(4)	1341	2357	3313	5102
Bgl I	(4)	608	730	801	3061	Dsa I	(7)	878	1123	1398	1660
Bpm I	(2)	4069	4126					1759	3015	3718	
Bsa I	(2)	1499	4275			Eae I	(6)	307	1136	3192	3366
BsaA I	(5)	858	1361	1423	2402			3757	3784		
		3590				Eag I	(2)	1136	3192		
BsaB I	(2)	1948	3145			Ear I	(5)	1257	1836	2753	3630
BsaH I	(8)	160	640	693	776			3840			
		962	3286	3988	4067	Eco57 I	(3)	3431	3863	4663	
		878	1123	1229	1267	EcoN I	(2)	339	1455		
		1398	1588	1660	1759	EcoO109 I	(1)	4384			
		2820	2892	3015	3050	EcoR I	(1)	1896			
		3059	3108	3449	3718	EcoR II	(15)	606	799	1228	1456
		4123	4250	4251	4353			1609	1627	2820	2875
		4354	5044					2892	3671	4250	4353
BsaW I	(6)	404	1927	3317	4161			5043	5056	5177	
		4851	4998			Ehe I	(1)	3287			
BseR I	(3)	1168	1419	3104		Fnu4H I	(39)	185	280	307	457
Bsg I	(2)	1437	1806					1136	1139	1160	1398
BsiC I	(1)	3968						1551	1683	1779	2063
BsiE I	(5)	182	331	1139	3195			2582	2604	2618	3056
		4870						3195	3247	3258	3348
BsiHKA I	(5)	32	117	3399	3589			3353	3390	3431	3518
		4894						3521	3524	3760	3856
Bsm I	(2)	2037	2130					3897	3911	4025	4364
BsmA I	(8)	951	1498	1860	1899			4379	4590	4796	4799
		2711	3129	4148	4276			4864	5007	5162	
BsmF I	(11)	693	844	1012	1249	Fok I	(8)	261	1571	1605	2959
		2802	2874	2938	3437			3153	3610	3635	4089
		3969	4078	4233		Fsp I	(2)	477	3388		
BsoF I	(39)	185	280	307	457	Gdi II	(7)	308	1135	1137	3191
		1136	1139	1160	1398			3193	3756	3783	
		1551	1683	1779	2063	Gsu I	(2)	4070	4125		
		2582	2604	2618	3056	Hae I	(5)	3107	3368	4730	5182
		3195	3247	3258	3348			5193			
		3353	3390	3431	3518						

Hae II	(4)	2553	2561	3289	4964	Nar I	(1)	3286					
Hae III	(21)	309	602	795	1138	Nci I	(10)	164	515	1289	1589		
		2252	2394	3049	3055			1590	1861	3290	3450		
		3064	3107	3194	3368			4063	4827				
		3759	3786	4295	4352	Nco I	(4)	878	1123	3015	3718		
		4385	4730	5164	5182	Nde I	(1)	752					
		5193				NgoM I	(3)	2503	3786	4069			
Hga I	(9)	167	1043	1131	1428	Nhe I	(1)	1890					
		2620	3995	4074	4515	Nla III	(25)	257	293	371	381		
		5093						822	882	1127	1204		
HgiA I	(5)	32	117	3399	3589			1283	1309	1801	1815		
		4894						2716	2856	2928	3019		
HgiE II	(2)	1925	4615					3160	3505	3691	3722		
Hha I	(24)	141	478	1879	1881			3748	4104	4488	5208		
		2552	2560	2586	2608			5259					
		2617	2630	2661	3280	Nla IV	(20)	403	985	1121	1237		
		3288	3352	3389	3655			1293	1733	1886	2441		
		3915	4091	4177	4580			2462	2474	2665	2826		
		4689	4863	4963	5030			2898	3287	3322	4170		
HinC II	(3)	158	1145	2049				4249	4294	5137	5176		
Hind II	(3)	158	1145	2049		Not I	(1)	1136					
HinD III	(1)	1129				Nsi I	(4)	1813	2858	2930	5261		
Hinf I	(13)	928	1146	1722	2329	Nsp7524 I	(6)	1200	1305	2852	2924		
		2351	2761	3771	3905			3687	5204				
		3957	4015	4052	4834	NspB II	(6)	64	1400	2784	3392		
		5230						4621	4866				
HinI I	(8)	160	640	693	776	NspH I	(6)	1204	1309	2856	2928		
		962	3286	3988	4067			3691	5208				
HinP I	(24)	139	476	1877	1879	Pac I	(1)	24					
		2550	2558	2584	2606	PaeR7 I	(1)	1901					
		2615	2628	2659	3278	Pal I	(21)	309	602	795	1138		
		3286	3350	3387	3653			2252	2394	3049	3055		
		3913	4089	4175	4578			3064	3107	3194	3368		
		4687	4861	4961	5028			3759	3786	4295	4352		
Hpa I	(1)	2049						4385	4730	5164	5182		
Hpa II	(25)	163	405	515	1289			5193					
		1589	1686	1860	1882	Pf1M I	(1)	1931					
		1928	2504	3191	3268	Ple I	(2)	2337	2769				
		3290	3318	3449	3539	Pme I	(1)	15					
		3606	3787	4062	4070	Psp1406 I	(2)	98	471				
		4162	4636	4826	4852	PspA I	(1)	1588					
		4999				Pst I	(1)	458					
Hph I	(8)	215	893	1437	1749	Pvu I	(1)	331					
		2404	3465	4356	4472	Pvu II	(2)	2784	3392				
						Rsa I	(14)	219	737	762	817		
Kas I	(1)	3285						850	901	1058	1121		
Kpn I	(1)	1123						1359	1413	1425	1482		
Mae I	(11)	507	1110	1150	1891			1572	3592				
		1908	2135	2553	3109	Rsr II	(1)	3802					
		4124	4458	4711		Sac II	(1)	1401					
Mae II	(20)	98	471	640	652	Sal I	(1)	1143					
		693	776	857	962	Sap I	(3)	1836	3630	3840			
		1321	1360	1422	1789	Sau3A I	(29)	53	70	328	374		
		2346	2358	2401	2511			392	1103	1114	1282		
		3402	3589	4370	4503			1871	1884	1912	1921		
Mae III	(18)	39	227	380	438			1943	3123	3127	3146		
		579	666	1015	1185			3457	3535	3616	3625		
		1301	2074	2575	2587			3703	4079	4095	4454		
		3406	3712	4402	4668			4466	4544	4552	4563		
		4784	4847					4638					
Mbo I	(29)	53	70	328	374	Sau96 I	(11)	336	601	794	1236		
		392	1103	1114	1282			1291	2393	3802	4247		
		1871	1884	1912	1921			4293	4351	4384			
		1943	3123	3127	3146	Sca I	(1)	219					
		3457	3535	3616	3625	ScrF I	(25)	164	515	608	801		
		3703	4079	4095	4454			1230	1289	1458	1589		
		4466	4544	4552	4563			1590	1611	1629	1861		
Mbo II	(16)	104	1239	1245	1343			2822	2877	2894	3290		
		1731	1785	1852	2541			3450	3673	4063	4252		
		2769	3646	3856	3938			4355	4827	5045	5058		
		4105	4305	4475	4548			5179					
Mlu I	(1)	2172				Sec I	(22)	878	1123	1229	1267		
Mme I	(5)	1521	1749	2378	4812			1398	1588	1660	1759		
		4996						2820	2892	3015	3050		
Mnl I	(40)	327	1059	1146	1149			3059	3108	3449	3718		
		1158	1259	1286	1292			4123	4250	4251	4353		
		1334	1367	1397	1451			4354	5044				
		1517	1719	1751	1808	SfaN I	(14)	247	440	876	1799		
		1856	1965	2004	2013			2101	2864	2936	3245		
		2430	2761	3039	3045			3500	3584	3648	3716		
		3068	3074	3082	3085			3923	5108				
		3097	3137	3201	3337			Sfc I	(5)	454	1745	2621	4748
		3694	3886	4092	4124			4939					
		4406	4776	5027	5100	Sfi I	(1)	3061					
Msc I	(1)	3368				Sma I	(1)	1590					
Mse I	(20)	14	20	24	121	SnaB I	(1)	858					
		486	525	1987	2048	Spe I	(1)	1907					
		2169	2190	2201	2213	Sph I	(3)	2856	2928	3691			
		2224	2241	2339	2610	Ssp I	(2)	2194	2747				
		4429	4443	4448	4500	Stu I	(1)	3107					
Msl I	(5)	288	883	1659	1932	Sty I	(7)	878	1123	1267	3015		
		3723						3108	3718	4123			
Msp I	(25)	163	405	515	1289	Taq I	(16)	46	1144	1171	1522		
		1589	1686	1860	1882			1902	2435	3126	3399		
		1928	2504	3191	3268			3555	3579	3615	3777		
		3290	3318	3449	3539			3968	4013	4268	5106		
		3606	3787	4062	4070	Tfi I	(5)	3771	3905	4015	4052		
		4162	4636	4826	4852			5230					
		4999				Tsp45 I	(7)	227	438	1185	1301		
MspAl I	(6)	64	1400	2784	3392			2575	3406	3712			
		4621	4866			Tth111 I	(1)	3404					
Mun I	(1)	2036				Tth111 II	(4)	3722	4582	4612	4621		
Nae I	(3)	2505	3788	4071		Vsp I	(1)	525					

Xba I	(1)	1149			
Xho I	(1)	1901			
Xho II	(11)	53	70	1103	1884
		3457	3703	4095	4454
		4466	4552	4563	
Xma I	(1)	1588			
Xma III	(2)	1136	3192		
Xmn I	(2)	100	1791		

Tag I	T`CG,A	16	Tfi I	G`AWT,C	5
Tsp45 I	`GTSAC,	7	Tth111 I	GACN`N,NGTC	1
Tth111 II	CAARCA 16/14	4	Vsp I	AT`TA,AT	1
Xba I	T`CTAG,A	1	Xca I	GTA TAC	-
Xcm I	CCANNNN,N`NNNNTGG-		Xho I	C`TCGA,G	1
Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	1
Xma III	C`GGCC,G	2	Xmn I	GAANN NNITC	2

Site usage in CMVHFC2.TXT:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	66
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	1	Alu I	AG CT	18
Alw I	GGATC 8/9	18	AlwN I	CAG,NNN`CTG	3
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	4	Asc I	GG`CGCG,CC	1
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	3	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	4
Bbe I	G,CGCG`C	1	Bbs I	GAAGAC 8/12	3
Bbv I	GCAGC 13/17	10	Bbv II	GAAGAC 7/11	3
Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	10
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	2
BsaA I	YAC GTR	5	BsaB I	GATNN NNATC	2
BsaH I	GR`CG,YC	8	BsaJ I	C`CNNG,G	22
BsaW I	W`CCGG,W	6	BseR I	GAGGAG 16/14	3
Bsg I	GTGCAG 22/20	2	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	8	BsmB I	CGTCTC 7/11	-
BsmF I	GGGAC 15/19	11	BsoF I	GC`N,GC	39
Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
BspH I	T`CATG,A	3	BspM I	ACCTGC 10/14	5
BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	13
BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	3
BsrG I	T`GTAC,A	1	BssH II	G`CGCG,C	1
Bsss I	C`TCGT,G	4	Bst1107 I	GTA TAC	-
BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
BstN I	CC`W,GG	15	BstU I	CG CG	19
BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	11
Bsu36 I	CC`TNA,GG	4	Cac8 I	GCN NGC	32
Cfr10 I	R`CCGG,Y	4	Cla I	AT`CG,AT	1
Cep6 I	G`TA,C	14	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	7
Eae I	Y`GGCC,R	6	Eag I	C`GGCC,C	2
Ear I	CTCTTC 7/10	5	Eco47 III	AGC GCT	-
Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
EcoN I	CCTNN`N,MNAGG	2	Eco0109 I	RG`GNC,CY	1
EcoR I	G`AATT,C	1	EcoR II	`CCWGG,	15
EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	39
Fok I	GGATG 14/18	8	Fse I	GG,CCGG`CC	-
Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	7
Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	5
Hae II	R,CGCG`Y	4	Hae III	GG CC	21
Hga I	GACGC 9/14	9	HgiA I	G,WGCW`C	5
HgiE II	ACCNNNNNNGGT -1/132		Hha I	G,CG`C	24
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	8	HinP I	G`CG,C	24
Hpa I	GTT AAC	1	Hpa II	C`CG,G	25
Hph I	GGTGA 12/11	8	Kas I	G`GCGC,C	1
Kpn I	G,GTAC`C	1	Mae I	C`TA,G	11
Mae II	A`CG,T	20	Mae III	`GTNAC,	18
Mbo I	`GATC,	29	Mbo II	GAAGA 12/11	16
Mlu I	A`CGCG,T	1	Mme I	TCCRAC 25/23	5
Mnl I	CCTC 10/10	40	Msc I	TGG CCA	1
Mse I	T`TA,A	20	Msl I	CAYNN NNRTG	5
Msp I	C`CG,G	25	MspA1 I	CMG CKG	6
Mun I	C`AATT,G	1	Nae I	GCC GGC	3
Nar I	GG`CG,CC	1	Nci I	CC`S,GG	10
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`	25	Nla IV	GGN NCC	20
Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Nsi I	A,TGCA`T	4	Nsp7524 I	R`CATG,Y	6
NspB II	CMG CKG	6	NspH I	R,CATG`Y	6
Pac I	TTA,AT`TAA	1	PaeR7 I	C`TCGA,G	1
Pal I	GG CC	21	PflM I	CCAN,NNN`NTGG	1
Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	1
Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
Pvu II	CAG CTG	2	Rsa I	GT AC	14
Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	-
Sac II	CC,GC`GG	1	Sal I	G`TCGA,C	1
Sap I	GCCTCTC 8/11	3	Sau3A I	`GATC,	29
Sau96 I	G`GNC,C	11	Sca I	AGT ACT	1
ScrF I	CC`N,GG	25	Sec I	C`CNNG,G	22
SfaN I	GCATC 9/13	14	Sfc I	C`TRYA,G	5
Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	1
SnaB I	TAC GTA	1	Spe I	A`CTAG,T	1
Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
Stu I	AGG CCT	1	Sty I	C`CWVG,G	7