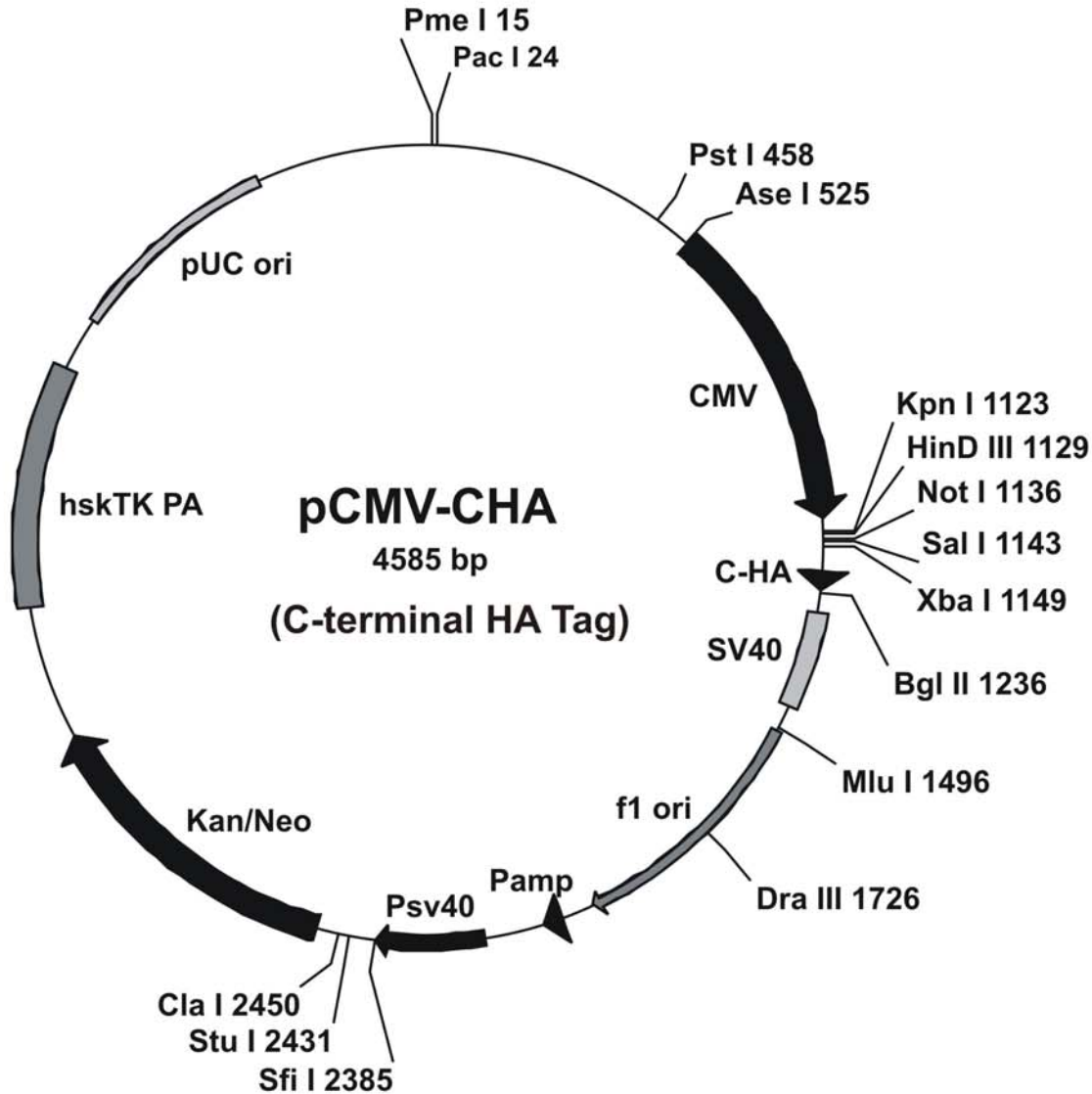
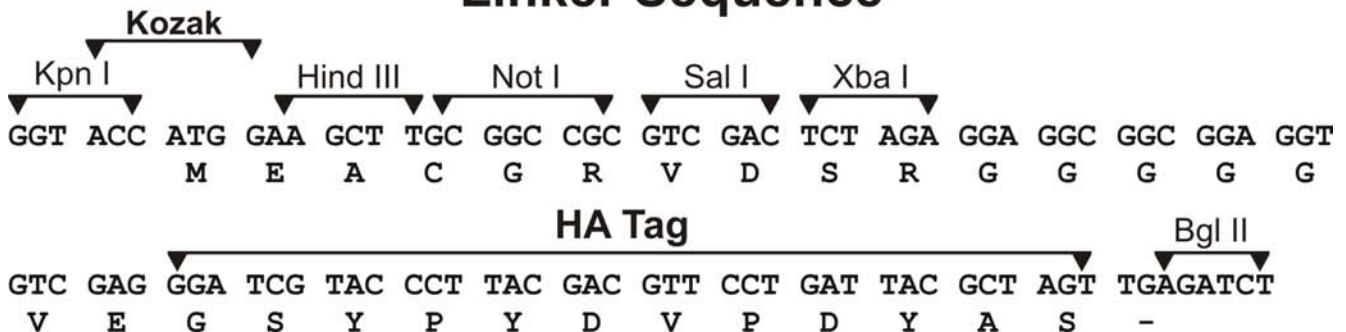


Name of Vector: pCMV-CHA
 Antibiotic Selection: Kan
 Created by: Wei Jiang and Qing Luo
 (He Lab @ The University of Chicago)
 Date of Creation: February 2004



Linker Sequence



pCMV-CHA Full-length Sequence and Restriction Sites

TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa 60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt 120
taaagttctgctatgtggcgcggtattatcccgtgttgacgcccgggcaagagcaactcgg 180
tcgccgcatacactattctcagaatgacttgggtgagtactcaccagtcacagaaaagca 240
tcttacggatggcatgacagtaagagaattatgcagtgtgcccataacatgagtataa 300
cactgcgggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgctttttt 360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc 420
catacceaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa 480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA 540
CGGGTCCATTAGTTCATAGCCCATATATGGAGTTCGCGTTACATAACTTACGGTAAATG 600
GCCCGCCTGGCTGACCGCCCAACGACCCCGCCATTGACGTCAATAATGACGTATGTTT 660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA 720
CTGCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA 780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCAGTACATGACCTTATGGGACTTTTCTTA 840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGTATGCGGTTTTGGCAGT 900
ACATCAATGGGCGTGGATAGCGGTTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATG 960
ACGTCAATGGGAGTTTTGTTTTGGCACAAAATCAACGGGACTTTCCAAAATGTCGTAACA 1020
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA 1080
GAGCTGGTTTTAGTGAACCGTCAGATCCgctagagatcggtagaccATGGAAGCTTGCGGCCG 1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTGAGGGATCGTACCCTTACGACGTTCTCTGA 1200
TTACGCTAGTTGagatctatccgatccaccggannnnnnTAACTGATCATAATCAGCCAT 1260
ACCACATTTGTAGAGGTTTTACTTGTCTTAAAAAACCTCCCACACC'TCCCCCTGAACCTG 1320
AAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTAC 1380
AAATAAAGCAATAGCATCACAAATTTACAAATAAAGCATTTTTTTTCACTGCATTCTAGT 1440
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GCTGGCAAGTGTAGCGGTACGCTGCGCGTAACCACCACACCCCGCGCGCTTAATGCGCC 1920
GCTACAGGGCGCGTACGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTT 1980
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CAGTTAGGGTGTGGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATGCAAAGCATGCAT 2160
CTCAATTAGTCAGCAACCAGGTGTGGAAAGTCCCAGGCTCCCAGCAGGCAGAAGTATG 2220
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CCCCTAACTCCGCCAGTTCCGCCATTCTCCGCCCATGGCTGACTAATTTTTTTTTTATT 2340
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CGAGCGAGCACGTACTCGGATGGAAGCCGGTCTTGTGATCAGGATGATCTGGACGAAGA 2940
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AGCGTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCT 3180
CGTGCTTTACGGTATCGCCGCTCCCGATTTCGACGCGCATCGCCTTCTATCGCCTTCTTGA 3240

CGAGTTCTTCTGAGCGGGACTCTGGGGTTTCGAAATGACCGACCAAGCGACGCCAACCTG 3300
 CCATCACGAGATTTTCGATTCCACCGCCGCTTCTATGAAAGGTTGGGCTTCGGAATCGTT 3360
 TTCCGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCC 3420
 CACCCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCT 3480
 ATGACGGCAATAAAAAGACAGAATAAAACGCACGGTGTGGGTCGTTTGTTCATAAACGC 3540
 GGGGTTTCGGTCCAGGGCTGGCACTCTGTTCGATACCCACCGAGACCCATTGGGGCCAA 3600
 TACGCCCGCGTTTCTTCTTTTCCCCACCCACCCCAAGTTCGGGTGAAGGCCAGGG 3660
 CTCGCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTT 3720
 TAGATTGATTTAAAACCTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTTGAT 3780
 AATCTCATGACCAAATCCCTTAACGTGAGTTTTTCGTTCCACTGAGCGTCAGACCCCGTA 3840
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 CCGTAGTTAGGCCACCCTTCAAGAACTCTGTAGCACCAGCCTACATACCTCGCTCTGCTA 4080
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 GGGTTTCGCCACCTCTGACTTGGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGC 4440
 CTATGGA AAAACGCCAGCAACGCGCCTTTTTTACGGTTCCTGGCCTTTTGTGCTGGCCTTTT 4500
 GCTCACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATG 4560
 CAT 4563

Unique enzymes in CMVCHA

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
Bgl II	A`GATC,T	1214
PflM I	CCAN,NNN`NTGG	1233
BstX I	CCAN,NNNN`NTGG	1234
Bcl I	T`GATC,A	1245
Mun I	C`AATT,G	1338
Hpa I	GTT AAC	1351
Mlu I	A`CGCG,T	1474
Dra III	CAC,NNN`GTG	1704
Sfi I	GGCCN,NNN`NGGCC	2363
Stu I	AGG CCT	2409
Cla I	AT`CG,AT	2428
Kas I	G`GCGC,C	2587
Nar I	GG`CG,CC	2588
Ehe I	GGC GCC	2589
Ebe I	G,GCGC`C	2591
Msc I	TGG CCA	2670
Tth111 I	GACN`N,NGTC	2706
Rsr II	CG`GWC,CG	3104
BsiC I	TT`CG,AA	3270
BstB I	TT`CG,AA	3270
Bsa I	GGTCTC 7/11	3577
EcoO109 I	RG`GNC,CY	3686

Number of enzymes = 41

CMVCHA: sites sorted by name

Aat II	(4)	643	696	779	965
Acc I	(1)	1144			
Acc65 I	(1)	1119			
Aci I	(63)	64	141	185	306
		352	576	604	616
		630	797	888	921
		1025	1046	1107	1135
		1139	1159	1162	1848
		1875	1903	1906	1920
		1963	2010	2073	2258
		2270	2279	2291	2301
		2312	2358	2497	2560
		2654	2718	2819	2822
		3062	3102	3107	3157
		3173	3199	3255	3324
		3327	3393	3475	3540
		3607	3680	3914	3923
		4058	4168	4289	4308
		4435	4463	4554	
Afl III	(2)	1474	4506		
Aha II	(8)	160	640	693	776
		962	2588	3290	3369
Alu I	(16)	347	410	510	1084
		1131	1367	1534	1791
		2086	2374	2694	3152
		3949	4206	4252	4342
Alw I	(17)	60	66	381	1099
		1183	1219	2455	2766
		2833	3012	3377	3404
		3763	3764	3861	3861
		3947			
AlwN I	(2)	3689	4097		
ApaL I	(2)	28	4192		
Apo I	(3)	1402	1506	1517	
Ase I	(1)	525			
Asp718	(1)	1119			
Ava II	(3)	336	3104	3549	
Avr II	(2)	2410	3425		
Ban I	(5)	983	1119	1741	2587
		2622			
Ban II	(3)	1779	2953	3663	
Bbe I	(1)	2591			
Bbv I	(7)	468	1376	2661	2703
		3224	3677	4177	
Bcl I	(1)	1245			
Bcn I	(6)	165	516	2593	2753
		3366	4130		
Bfa I	(10)	507	1110	1150	1207
		1437	1855	2411	3426
		3760	4013		
Bgl I	(4)	608	730	801	2363
Bgl II	(1)	1214			
Bpm I	(2)	3371	3428		
Bsa I	(1)	3577			
BsaA I	(3)	858	1704	2892	
BsaB I	(2)	1250	2447		

The following enzymes do not cut in CMVCHA

Afl II	Age I	Ahd I	Apa I	Asc I
Ava I	BamH I	Bbs I	Bbv II	Blp I
Bsg I	BsiW I	BsmB I	Bsp120 I	BspM II
BsrG I	BssH II	Bst1107 I	BstE II	Eco47 III
Eco72 I	EcoR I	EcoR V	Esp I	Fse I
Nhe I	Nru I	PaeR7 I	Pml I	PpuM I
PspA I	Sac I	Sac II	Sma I	Spe I
Spl I	Srf I	Xca I	Xcm I	Xho I

BsaH I	(8)	160	640	693	776					3199	3213	3327	3666
		962	2588	3290	3369					3681	3892	4098	4101
BsaJ I	(16)	878	1123	2122	2194					4166	4309	4464	
		2317	2352	2361	2410		Fok I	(6)	261	2261	2455	2912	
		2751	3020	3425	3552					2937	3391		
BsaW I	(6)	3553	3655	3656	4346		Fsp I	(2)	477	2690			
		404	1229	2619	3463		Gdi II	(7)	308	1135	1137	2493	
		4153	4300							2495	3058	3085	
BseR I	(2)	1168	2406				Gsu I	(2)	3372	3427			
BsiC I	(1)	3270					Hae I	(5)	2409	2670	4032	4484	
BsiE I	(5)	182	331	1139	2497					4495			
		4172					Hae II	(4)	1855	1863	2591	4266	
BsiHKA I	(5)	32	117	2701	2891		Hae III	(21)	309	602	795	1138	
		4196								1554	1696	2351	2357
Bsm I	(2)	1339	1432							2366	2409	2496	2670
BsmA I	(5)	951	2013	2431	3450					3061	3088	3597	3654
		3578								3687	4032	4466	4484
BsmF I	(10)	693	844	1012	2104					4495			
		2176	2240	2739	3271		Hga I	(8)	167	1043	1131	1922	
		3380	3535							3297	3376	3817	4395
BsoF I	(35)	185	280	307	457		HgiA I	(5)	32	117	2701	2891	
		1136	1139	1160	1365					4196			
		1884	1906	1920	2358		HgiE II	(2)	1227	3917			
		2497	2549	2560	2650		Hha I	(22)	141	478	1854	1862	
		2655	2692	2733	2820					1888	1910	1919	1932
		2823	2826	3062	3158					1963	2582	2590	2654
		3199	3213	3327	3666					2691	2957	3217	3393
		3681	3892	4098	4101					3479	3882	3991	4165
		4166	4309	4464						4265	4332		
Bsp1286 I	(2)	117	2891				HinC II	(3)	158	1145	1351		
BspH I	(2)	2014	3786				Hind II	(3)	158	1145	1351		
BspM I	(3)	2475	2856	3306			Hind III	(1)	1129				
Bsr I	(11)	54	226	493	814		Hinf I	(12)	928	1146	1631	1653	
		1618	2296	2531	2732					2063	3073	3207	3259
		3978	4092	4105						3317	3354	4136	4532
BsrB I	(4)	1848	2012	3201	3255		HinI I	(8)	160	640	693	776	
BsrD I	(2)	466	2821							962	2588	3290	3369
Bsss I	(4)	31	3180	3306	4333		HinP I	(22)	139	476	1852	1860	
BstB I	(1)	3270								1886	1908	1917	1930
BstN I	(11)	608	801	2124	2179					1961	2580	2588	2652
		2196	2975	3554	3657					2689	2955	3215	3391
		4347	4360	4481						3477	3880	3989	4163
BstU I	(17)	141	578	1141	1476					4263	4330		
		1512	1888	1908	1932		Hpa I	(1)	1351				
		1963	2654	2955	3393		Hpa II	(20)	163	405	515	1230	
		3477	3540	3609	3882					1806	2493	2570	2592
		4463								2620	2751	2841	2908
BstX I	(1)	1234								3089	3364	3372	3464
BstY I	(11)	53	70	1103	1214					3938	4128	4154	4301
		2759	3005	3397	3756		Hph I	(6)	215	893	1706	2767	
		3768	3854	3865						3658	3774		
Bsu36 I	(2)	2068	3700				Kas I	(1)	2587				
Cac8 I	(29)	454	604	797	1133		Kpn I	(1)	1123				
		1807	1850	1864	2137		Mae I	(10)	507	1110	1150	1207	
		2156	2209	2228	2482					1437	1855	2411	3426
		2668	2887	2953	2959					3760	4013		
		2987	2991	3032	3036		Mae II	(17)	98	471	640	652	
		3090	3373	3560	3607					693	776	857	962
		3663	3685	3896	4456					1192	1648	1660	1703
		4493								1813	2704	2891	3672
Cer10 I	(4)	1805	2907	3088	3371					3805			
Clf I	(1)	2428					Mae III	(16)	39	227	380	438	
Csp6 I	(10)	218	736	761	816					579	666	1015	1376
		849	900	1057	1120					1877	1889	2708	3014
		1181	2893							3704	3970	4086	4149
Dde I	(7)	199	2068	2370	3251		Mbo I	(27)	53	70	328	374	
		3700	3823	4232						392	1103	1114	1176
Dpn I	(27)	55	72	330	376					1214	1223	1245	2425
		394	1105	1116	1178					2429	2448	2759	2837
		1216	1225	1247	2427					2918	2927	3005	3381
		2431	2450	2761	2839					3397	3756	3768	3846
		2920	2929	3007	3383					3854	3865	3940	
		3399	3758	3770	3848		Mbo II	(10)	104	1843	2071	2948	
		3856	3867	3942						3158	3240	3407	3607
DpnII	(27)	53	70	328	374					3777	3850		
		392	1103	1114	1176		Mlu I	(1)	1474				
		1214	1223	1245	2425		Mme I	(3)	1680	4114	4298		
		2429	2448	2759	2837		Mnl I	(29)	327	1059	1146	1149	
		2918	2927	3005	3381					1158	1166	1267	1306
		3397	3756	3768	3846					1315	1732	2063	2341
		3854	3865	3940						2347	2370	2376	2384
Dra I	(5)	15	122	1290	3732					2387	2399	2439	2503
		3751								2639	2996	3188	3394
Dra III	(1)	1704								3426	3708	4078	4329
Drd I	(3)	1659	2615	4404						4402			
Dsa I	(4)	878	1123	2317	3020		Msc I	(1)	2670				
Eae I	(6)	307	1136	2494	2668		Mse I	(20)	14	20	24	121	
		3059	3086							486	525	1289	1350
Eag I	(2)	1136	2494							1471	1492	1503	1515
Ear I	(3)	2055	2932	3142						1526	1543	1641	1912
Eco57 I	(3)	2733	3165	3965						3731	3745	3750	3802
EcoN I	(1)	339					Msl I	(4)	288	883	1234	3025	
EcoO109 I	(1)	3686					Msp I	(20)	163	405	515	1230	
EcoR II	(11)	606	799	2122	2177					1806	2493	2570	2592
		2194	2973	3552	3655					2620	2751	2841	2908
		4345	4358	4479						3089	3364	3372	3464
Ehe I	(1)	2589								3938	4128	4154	4301
Fnu4H I	(35)	185	280	307	457		MspAl I	(5)	64	2086	2694	3923	
		1136	1139	1160	1365					4168			
		1884	1906	1920	2358		Mun I	(1)	1338				
		2497	2549	2560	2650		Nae I	(3)	1807	3090	3373		
		2655	2692	2733	2820		Nar I	(1)	2588				
		2823	2826	3062	3158		Nci I	(6)	164	515	2592	2752	

Nco I	(4)	3365	4129			Bbe I	G,CGCG`C	1	Bbs I	GAAGAC 8/12	-
Nde I	(1)	878	1123	2317	3020	Bbv I	GCAGC 13/17	7	Bbv II	GAAGAC 7/11	-
NgoM I	(3)	1805	3088	3371		Bcl I	T`GATC,A	1	Bcn I	CC,S`GG	6
Nla III	(20)	257	293	371	381	Bfa I	C`TA,G	10	Bgl I	CCCN,NNN`NGGC	4
		822	882	1127	2018	Bgl II	A`GATC,T	1	Blp I	GC`TNA,GC	-
		2158	2230	2321	2462	Bpm I	CTGGAG 22/20	2	Bsa I	GGTCTC 7/11	1
		2807	2993	3024	3050	BsaA I	YAC GTR	3	BsaB I	GATNN NNATC	2
		3406	3790	4510	4561	BsaH I	GR`CG,YC	8	BsaJ I	C`CNNNG,G	16
Nla IV	(16)	403	985	1121	1743	BsaW I	W`CCGG,W	6	Bse I	GAGGAG 16/14	2
		1764	1776	1967	2128	Bsg I	GTGCAG 22/20	-	BsiC I	TT`CG,AA	1
		2200	2589	2624	3472	BsiE I	CG,RY`CG	5	BsiHKA I	G,WGCW`C	5
		3551	3596	4439	4478	BsiW I	C`GTAC,G	-	Bsm I	GAATG,C 7	2
Not I	(1)	1136				Bsma I	GTCTC`/9	5	BsmB I	CGTCTC 7/11	-
Nsi I	(3)	2160	2232	4563		BsmF I	GGGAC 15/19	10	BsoF I	GC`N,GC	35
Nsp7524 I	(4)	2154	2226	2989	4506	Bsp120 I	G`GGCC,C	-	Bsp1286 I	G,DGCH`C	2
NspB II	(5)	64	2086	2694	3923	BspH I	T`CATG,A	2	BspM I	ACCTGC 10/14	3
		4168				BspM II	T`CCGG,A	-	Bsr I	ACT,GG`	11
NspH I	(4)	2158	2230	2993	4510	BsrB I	GAG CGG	4	BsrD I	GCAATG, 8	2
Pac I	(1)	24				BsrG I	T`GTAC,A	-	Bssh II	G`CCGG,C	-
Pal I	(21)	309	602	795	1138	Bsss I	C`CGT,G	4	Bst1107 I	GTA TAC	-
		1554	1696	2351	2357	BstB I	TT`CG,AA	1	BstE II	G`GTNAC,C	-
		2366	2409	2496	2670	BstN I	CC`W,GG	11	BstU I	CG CG	17
		3061	3088	3597	3654	BstX I	CCAN,NNNN`NTGG	1	BstY I	R`GATC,Y	11
		3687	4032	4466	4484	Bsu36 I	CC`TNA,GG	2	Cac8 I	GCN NGC	29
Pf1M I	(1)	1233				Cfr10 I	R`CCGG,Y	4	ClA I	AT`CG,AT	1
Ple I	(2)	1639	2071			Csp6 I	G`TA,C	10	Dde I	C`TNA,G	7
Pme I	(1)	15				Dpn I	GA TC	27	DpnII	`GATC,	27
Psp1406 I	(2)	98	471			Dra I	TTT AAA	5	Dra III	CAC,NNN`GTG	1
Pst I	(1)	458				Drd I	GACNN,NN`NNGTC	3	Dsa I	C`CRYG,G	4
Pvu I	(1)	331				Eae I	Y`GGCC,R	6	Eag I	C`GGCC,G	2
Pvu II	(2)	2086	2694			Ear I	CTCTTC 7/10	3	Eco47 III	AGC GCT	-
Rsa I	(10)	219	737	762	817	Eco57 I	CTGAAG 21/19	3	Eco72 I	CAC GTG	-
		850	901	1058	1121	EcoN I	CCTNN`N,NNAGG	1	Eco109 I	RG`GNC,CY	1
		1182	2894			EcoR I	G`AATT,C	-	EcoR II	`CCWGG,	11
Rsr II	(1)	3104				EcoR V	GAT ATC	-	Ehe I	GGC GCC	1
Sal I	(1)	1143				Esp I	GC`TNA,GC	-	Fnu4H I	GC`N,GC	35
Sap I	(2)	2932	3142			Fok I	GGATG 14/18	6	Fse I	GG,CCGG`CC	-
Sau3A I	(27)	53	70	328	374	Fsp I	TGC GCA	2	Gdi II	`YGGC,CG	7
		392	1103	1114	1176	Gsu I	CTGGAG 21/19	2	Hae I	WGG CCW	5
		1214	1223	1245	2425	Hae II	R,CGCG`Y	4	Hae III	GG CC	21
		2429	2448	2759	2837	Hga I	GACGC 9/14	8	HgiA I	G,WGCW`C	5
		2918	2927	3005	3381	HgiE II	ACCNNNNNNGGT -1/132	-	Hha I	G,CG`C	22
		3397	3756	3768	3846	Hinc II	GTY RAC	3	Hind II	GTY RAC	3
Sau96 I	(9)	336	601	794	1695	Hind III	A`AGCT,T	1	Hinf I	G`ANT,C	12
		3104	3549	3595	3653	HinI I	GR`CG,YC	8	HinP I	G`CG,C	22
		3686				Hpa I	GTT AAC	1	Hpa II	C`CG,G	20
Sca I	(1)	219				Hph I	GGTGA 12/11	6	Kas I	G`CGCG,C	1
ScrF I	(17)	164	515	608	801	Kpn I	G,GTAC`C	1	Mae I	C`TA,G	10
		2124	2179	2196	2592	Mae II	A`CG,T	17	Mae III	`GTNAC,	16
		2752	2975	3365	3554	Mlu I	`GATC,	27	Mbo II	GAAGA 12/11	10
		3657	4129	4347	4360	Mnl I	A`CGCG,T	1	Mme I	TCCRAC 25/23	3
		4481				Mse I	CCTC 10/10	29	Msc I	TGG CCA	1
Sec I	(16)	878	1123	2122	2194	Msp I	T`TA,A	20	Msl I	CAYNN NNRTG	4
		2317	2352	2361	2410	Mun I	C`CG,G	20	MspA1 I	CMG CKG	5
		2751	3020	3425	3552	Nar I	C`AATT,G	1	Nae I	GCC GGC	3
		3553	3655	3656	4346	Nco I	GG`CG,CC	1	Nci I	CC`S,GG	6
SfaN I	(13)	247	440	876	1403	Nco I	C`CATG,G	4	Nde I	CA`TA,TG	1
		2166	2238	2547	2802	NgoM I	G`CCGG,C	3	Nhe I	G`CTAG,C	-
		2886	2950	3018	3225	Nla III	`CATG`	20	Nla IV	GGN NCC	16
Sfc I	(4)	454	1923	4050	4241	Not I	GC`GGCC,GC	1	Nru I	TCG CGA	-
Sfi I	(1)	2363				Nsi I	A,TGCA`T	3	Nsp7524 I	R`CATG,Y	4
SnaB I	(1)	858				NspB II	CMG CKG	5	NspH I	R,CATG`Y	4
Sph I	(3)	2158	2230	2993		Pac I	TTA,AT`TAA	1	Paer7 I	C`TCGA,G	-
Ssp I	(2)	1496	2049			Pal I	GG CC	21	Pf1M I	CCAN,NNN`NTGG	1
Stu I	(1)	2409				Ple I	GAGTC 9/10	2	Pme I	CTTT AAAC	1
Sty I	(6)	878	1123	2317	2410	Pml I	CAC GTG	-	PpuM I	RG`GWC,CY	-
		3020	3425			Psp1406 I	AA`CG,TT	2	PspA I	C`CCGG,G	-
Taq I	(14)	46	1144	1171	1737	Pst I	C,TGCA`G	1	Pvu I	CG,AT`CG	1
		2428	2701	2857	2881	Pvu II	CAG CTG	2	Rsa I	GT AC	10
		2917	3079	3270	3315	Rsr II	CG`GWC,CG	1	Sac I	G,AGCT`C	1
Tfi I	(5)	3073	3207	3317	3354	Sac II	CC,GC`GG	-	Sal I	G`TCGA,C	1
		4532				Sap I	GCTCTTC 8/11	2	Sau3A I	`GATC,	27
Tsp45 I	(5)	227	438	1877	2708	Sau96 I	G`GNC,C	9	Sca I	AGT ACT	1
		3014				ScrF I	CC`N,GG	17	Sec I	C`CNNG,G	16
Tth111 I	(1)	2706				SfaN I	GCATC 9/13	13	Sfc I	C`TRYA,G	4
Tth111 II	(4)	3024	3884	3914	3923	Sfi I	GGCCN,NNN`NGGCC	1	Sma I	CCC GGG	-
Vsp I	(1)	525				SnaB I	TAC GTA	1	Spe I	A`CTAG,T	-
Xba I	(1)	1149				Sph I	G,CATG`C	3	Spl I	C`GTAC,G	-
Xho II	(11)	53	70	1103	1214	Srf I	GCCC GGGC	-	Ssp I	AAT ATT	2
		2759	3005	3397	3756	Stu I	AGG CCT	1	Sty I	C`CWGG,G	6
		3768	3854	3865		Taq I	T`CG,A	14	Tfi I	G`AWT,C	5
Xma III	(2)	1136	2494			Tsp45 I	`GTSAC,	5	Tth111 I	GACN`N,NGTC	1
Xmn I	(1)	100				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	-
						Xho II	R`GATC,Y	11	Xma I	C`CCGG,G	-
						Xma III	C`GGCC,G	2	Xmn I	GAANN NNTTC	1

Site usage in CMVCHA.TXT:

Aat II	G,ACGT`C	4	Acc I	GT`MK,AC	1
Acc65 I	G`GTAC,C	1	Aci I	C`CG,C	63
Afl 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	16
Alw I	GGATC 8/9	17	AlwN I	CAG,NNN`CTG	2
Apa I	G,GGCC`C	-	ApaL I	G`TGCA,C	2
Apo I	R`AATT,Y	3	Asc I	GG`CGCG,CC	-
Ase I	AT`TA,AT	1	Asp718	G`GTAC,C	1
Ava I	C`YCGR,G	-	Ava II	G`GWC,C	3
Avr II	C`CTAG,G	2	BamH I	G`GATC,C	-
Ban I	G`GYRC,C	5	Ban II	G,RGCY`C	3