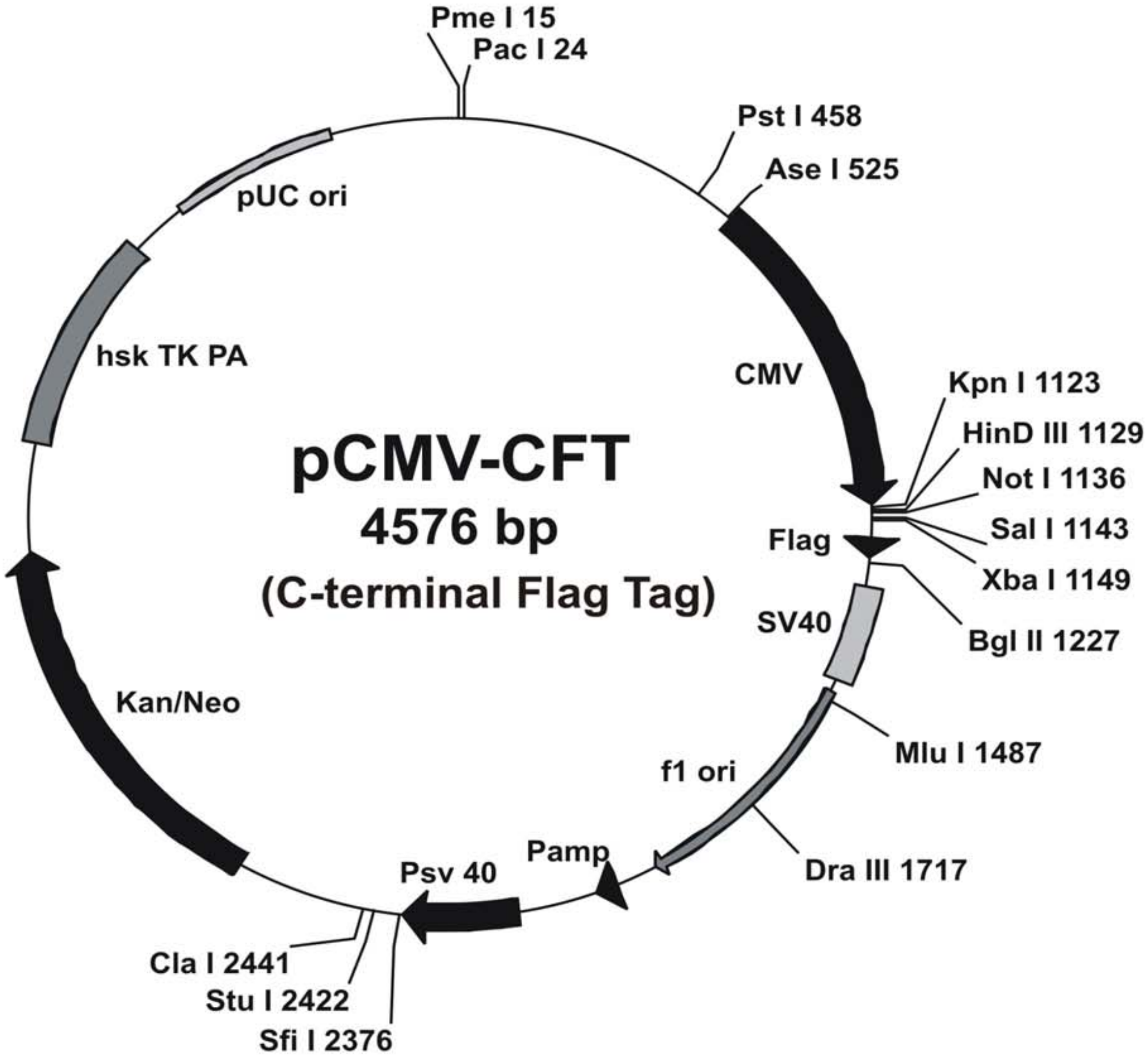
Name of Vector: pCMV-CFT
Antibiotic Selection: Kan
Created by: Wei Jiang and Qing Luo
(He Lab @ The University of Chicago)
Date of Creation: February 2004



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

                         Flag Tag                 Bgl II
GTC GAG GGA GAT TAC AAG GAT GAC GAC GAT AAG ATA TGAGATCT
 V   E   G   D   Y   K   D   D   D   D   K   I   -
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pCMV-CFT Full-length Sequence and Restriction Sites

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TAGTTATTATGTTTAAacttaattaagtgcacgagtgggttacatcgaactggatctcaa  60
cagcggtaagatccttgagagttttcgccccgaagaacgttttccaatgatgagcacttt  120
taaagttctgctatgtggcgcggtattatcccgtgttgacgccgggcaagagcaactcgg  180
tcgccgcatacactattctcagaatgacttggttgagtactcaccagtcacagaaaagca  240
tcttacggatggcatgacagtaagagaattatgcagtgctgccataaccatgagtgataa  300
cactgcggccaacttacttctgacaacgatcggaggaccgaaggagctaaccgcttttt  360
gcacaacatgggggatcatgtaactcgccttgatcgttgggaaccggagctgaatgaagc  420
cataccaaacgacgagcgtgacaccacgatgcctgcagcaatggcaacaacgttgcgcaa  480
actattaactggcgaactacttactctagcttcccggcaacaATTAATAGTAATCAATTA  540
CGGGGTCATTAGTTCATAGCCCATATATGGAGTTCCGCGTTACATAACTTACGGTAAATG  600
GCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAATAATGACGTATGTTC  660
CCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAA  720
CTGCCCACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCA  780
ATGACGGTAAATGGCCCGCCTGGCATTATGCCCAGTACATGACCTTATGGGACTTTCCTA  840
CTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGTGATGCGGTTTTGGCAGT  900
ACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTG  960
ACGTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACA  1020
ACTCCGCCCCATTGACGCAAATGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCA  1080
GAGCTGGTTTAGTGAACCGTCAGATCCgctagagatcggtaccATGGAAGCTTGCGGCCG  1140
CGTCGACTCTAGAGGAGGCGGCGGAGGTGTCGAGGGAGATTACAAGGATGACGACGATAA  1200
GATATGagatctatccgatccaccggannnnnnTAACTGATCATAATCAGCCATACCACA  1260
TTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACAT  1320
AAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAA  1380
AGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGT  1440
TTGTCCAAACTCATCAATGTATCTTAACGCGTAAATTGTAAGCGTTAATATTTTGTTAAA  1500
ATTCGCGTTAAATTTTTGTTAAATCAGCTCATTTTTTAACCAATAGGCCGAAATCGGCAA  1560
AATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTGGAA  1620
CAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTATCA  1680
GGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTGCCG  1740
TAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAAGCC  1800
GGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCTGGC  1860
AAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCTACA  1920
GGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTT  1980
CTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATA  2040
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TAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGC  2220
ATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCCCTA  2280
ACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTATGCA  2340
GAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTTGGA  2400
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ACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTATGA  2520
CTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCAGGG  2580
GCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGACGA  2640
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GTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCGGCT  2820
GCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGAGCG  2880
AGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCATCA  2940
GGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGAGGA  3000
TCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCGCTT  3060
TTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGCGTT  3120
GGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGTGCT  3180
TTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGAGTT  3240
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CTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCATCA  3300
CGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTCCGG  3360
GACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCACCCT  3420
AGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATGACG  3480
GCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGGGTT  3540
CGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATACGCC  3600
CGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTCGCA  3660
GCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAGATT  3720
GATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCTC  3780
ATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAAG  3840
ATCAAAGGATCTTCTTGAGATCCTTTTTTTCTGCGCGTAATCTGCTGCTTGCAAACAAAA  3900
AAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCCG  3960
AAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTAG  4020
TTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCTG  4080
TTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACGA  4140
TAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAGC  4200
TTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGCC  4260
ACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGGA  4320
GAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTTT  4380
CGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTATGG  4440
AAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCAC  4500
ATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT  4557
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Unique enzymes in CMVCFT

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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        1208
PflM I      CCAN,NNN`NTGG   1227
BstX I      CCAN,NNNN`NTGG  1228
Bcl I       T`GATC,A        1239
Mun I       C`AATT,G        1332
Hpa I       GTT|AAC         1345
Mlu I       A`CGCG,T        1468
Dra III     CAC,NNN`GTG     1698
Sfi I       GGCCN,NNN`NGGCC 2357
Stu I       AGG|CCT         2403
Cla I       AT`CG,AT        2422
Kas I       G`GCGC,C        2581
Nar I       GG`CG,CC        2582
Ehe I       GGC|GCC         2583
Bbe I       G,GCGC`C        2585
Msc I       TGG|CCA         2664
Tth111 I    GACN`N,NGTC     2700
Rsr II      CG`GWC,CG       3098
BsiC I      TT`CG,AA        3264
BstB I      TT`CG,AA        3264
Bsa I       GGTCTC 7/11     3571
EcoO109 I   RG`GNC,CY       3680
Number of enzymes = 41
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The following enzymes do not cut in CMVCFT

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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
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CMVCFT: sites sorted by name

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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    1842
                  1869    1897    1900    1914
                  1957    2004    2067    2252
                  2264    2273    2285    2295
                  2306    2352    2491    2554
                  2648    2712    2813    2816
                  3056    3096    3101    3151
                  3167    3193    3249    3318
                  3321    3387    3469    3534
                  3601    3674    3908    3917
                  4052    4162    4283    4302
                  4429    4457    4548
Afl III     (2)   1468    4500
Aha II      (8)   160     640     693     776
                  962     2582    3284    3363
Alu I       (16)  347     410     510     1084
                  1131    1361    1528    1785
                  2080    2368    2688    3146
                  3943    4200    4246    4336
Alw I       (16)  60      66      381     1099
                  1213    2449    2760    2827
                  3006    3371    3398    3757
                  3758    3855    3855    3941
AlwN I      (2)   3683    4091
ApaL I      (2)   28      4186
Apo I       (3)   1396    1500    1511
Ase I       (1)   525
Asp718      (1)   1119
Ava II      (3)   336     3098    3543
Avr II      (2)   2404    3419
Ban I       (5)   983     1119    1735    2581
                  2616
Ban II      (3)   1773    2947    3657
Bbe I       (1)   2585
Bbv I       (7)   468     1370    2655    2697
                  3218    3671    4171
Bcl I       (1)   1239
Bcn I       (6)   165     516     2587    2747
                  3360    4124
Bfa I       (9)   507     1110    1150    1431
                  1849    2405    3420    3754
                  4007
Bgl I       (4)   608     730     801     2357
Bgl II      (1)   1208
Bpm I       (2)   3365    3422
Bsa I       (1)   3571
BsaA I      (3)   858     1698    2886
BsaB I      (2)   1244    2441
BsaH I      (8)   160     640     693     776
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                 962     2582    3284    3363
BsaJ I     (16)  878     1123    2116    2188
                 2311    2346    2355    2404
                 2745    3014    3419    3546
                 3547    3649    3650    4340
BsaW I     (6)   404     1223    2613    3457
                 4147    4294
BseR I     (2)   1168    2400
BsiC I     (1)   3264
BsiE I     (5)   182     331     1139    2491
                 4166
BsiHKA I   (5)   32      117     2695    2885
                 4190
Bsm I      (2)   1333    1426
BsmA I     (5)   951     2007    2425    3444
                 3572
BsmF I     (10)  693     844     1012    2098
                 2170    2234    2733    3265
                 3374    3529
BsoF I     (35)  185     280     307     457
                 1136    1139    1160    1359
                 1878    1900    1914    2352
                 2491    2543    2554    2644
                 2649    2686    2727    2814
                 2817    2820    3056    3152
                 3193    3207    3321    3660
                 3675    3886    4092    4095
                 4160    4303    4458
Bsp1286 I  (2)   117     2885
BspH I     (2)   2008    3780
BspM I     (3)   2469    2850    3300
Bsr I      (11)  54      226     493     814
                 1612    2290    2525    2726
                 3972    4086    4099
BsrB I     (4)   1842    2006    3195    3249
BsrD I     (2)   466     2815
BssS I     (4)   31      3174    3300    4327
BstB I     (1)   3264
BstN I     (11)  608     801     2118    2173
                 2190    2969    3548    3651
                 4341    4354    4475
BstU I     (17)  141     578     1141    1470
                 1506    1882    1902    1926
                 1957    2648    2949    3387
                 3471    3534    3603    3876
                 4457
BstX I     (1)   1228
BstY I     (11)  53      70      1103    1208
                 2753    2999    3391    3750
                 3762    3848    3859
Bsu36 I    (2)   2062    3694
Cac8 I     (29)  454     604     797     1133
                 1801    1844    1858    2131
                 2150    2203    2222    2476
                 2662    2881    2947    2953
                 2981    2985    3026    3030
                 3084    3367    3554    3601
                 3657    3679    3890    4450
                 4487
Cfr10 I    (4)   1799    2901    3082    3365
Cla I      (1)   2422
Csp6 I     (9)   218     736     761     816
                 849     900     1057    1120
                 2887
Dde I      (7)   199     2062    2364    3245
                 3694    3817    4226
Dpn I      (26)  55      72      330     376
                 394     1105    1116    1210
                 1219    1241    2421    2425
                 2444    2755    2833    2914
                 2923    3001    3377    3393
                 3752    3764    3842    3850
                 3861    3936
DpnII      (26)  53      70      328     374
                 392     1103    1114    1208
                 1217    1239    2419    2423
                 2442    2753    2831    2912
                 2921    2999    3375    3391
                 3750    3762    3840    3848
                 3859    3934
Dra I      (5)   15      122     1284    3726
                 3745
Dra III    (1)   1698
Drd I      (3)   1653    2609    4398
Dsa I      (4)   878     1123    2311    3014
Eae I      (6)   307     1136    2488    2662
                 3053    3080
Eag I      (2)   1136    2488
Ear I      (3)   2049    2926    3136
Eco57 I    (3)   2727    3159    3959
EcoN I     (1)   339
EcoO109 I  (1)   3680
EcoR II    (11)  606     799     2116    2171
                 2188    2967    3546    3649
                 4339    4352    4473
Ehe I      (1)   2583
Fnu4H I    (35)  185     280     307     457
                 1136    1139    1160    1359
                 1878    1900    1914    2352
                 2491    2543    2554    2644
                 2649    2686    2727    2814
                 2817    2820    3056    3152
                 3193    3207    3321    3660
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                 3675    3886    4092    4095
                 4160    4303    4458
Fok I      (7)   261     1200    2255    2449
                 2906    2931    3385
Fsp I      (2)   477     2684
Gdi II     (7)   308     1135    1137    2487
                 2489    3052    3079
Gsu I      (2)   3366    3421
Hae I      (5)   2403    2664    4026    4478
                 4489
Hae II     (4)   1849    1857    2585    4260
Hae III    (21)  309     602     795     1138
                 1548    1690    2345    2351
                 2360    2403    2490    2664
                 3055    3082    3591    3648
                 3681    4026    4460    4478
                 4489
Hga I      (8)   167     1043    1131    1916
                 3291    3370    3811    4389
HgiA I     (5)   32      117     2695    2885
                 4190
HgiE II    (2)   1221    3911
Hha I      (22)  141     478     1848    1856
                 1882    1904    1913    1926
                 1957    2576    2584    2648
                 2685    2951    3211    3387
                 3473    3876    3985    4159
                 4259    4326
HinC II    (3)   158     1145    1345
Hind II    (3)   158     1145    1345
HinD III   (1)   1129
Hinf I     (12)  928     1146    1625    1647
                 2057    3067    3201    3253
                 3311    3348    4130    4526
HinI I     (8)   160     640     693     776
                 962     2582    3284    3363
HinP I     (22)  139     476     1846    1854
                 1880    1902    1911    1924
                 1955    2574    2582    2646
                 2683    2949    3209    3385
                 3471    3874    3983    4157
                 4257    4324
Hpa I      (1)   1345
Hpa II     (20)  163     405     515     1224
                 1800    2487    2564    2586
                 2614    2745    2835    2902
                 3083    3358    3366    3458
                 3932    4122    4148    4295
Hph I      (6)   215     893     1700    2761
                 3652    3768
Kas I      (1)   2581
Kpn I      (1)   1123
Mae I      (9)   507     1110    1150    1431
                 1849    2405    3420    3754
                 4007
Mae II     (16)  98      471     640     652
                 693     776     857     962
                 1642    1654    1697    1807
                 2698    2885    3666    3799
Mae III    (16)  39      227     380     438
                 579     666     1015    1370
                 1871    1883    2702    3008
                 3698    3964    4080    4143
Mbo I      (26)  53      70      328     374
                 392     1103    1114    1208
                 1217    1239    2419    2423
                 2442    2753    2831    2912
                 2921    2999    3375    3391
                 3750    3762    3840    3848
                 3859    3934
Mbo II     (10)  104     1837    2065    2942
                 3152    3234    3401    3601
                 3771    3844
Mlu I      (1)   1468
Mme I      (3)   1674    4108    4292
Mnl I      (29)  327     1059    1146    1149
                 1158    1166    1261    1300
                 1309    1726    2057    2335
                 2341    2364    2370    2378
                 2381    2393    2433    2497
                 2633    2990    3182    3388
                 3420    3702    4072    4323
                 4396
Msc I      (1)   2664
Mse I      (20)  14      20      24      121
                 486     525     1283    1344
                 1465    1486    1497    1509
                 1520    1537    1635    1906
                 3725    3739    3744    3796
Msl I      (4)   288     883     1228    3019
Msp I      (20)  163     405     515     1224
                 1800    2487    2564    2586
                 2614    2745    2835    2902
                 3083    3358    3366    3458
                 3932    4122    4148    4295
MspA1 I    (5)   64      2080    2688    3917
                 4162
Mun I      (1)   1332
Nae I      (3)   1801    3084    3367
Nar I      (1)   2582
Nci I      (6)   164     515     2586    2746
                 3359    4123
Nco I      (4)   878     1123    2311    3014
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Nde I       (1)   752
NgoM I      (3)   1799     3082     3365
Nla III     (20)  257      293      371      381
                  822      882      1127     2012
                  2152     2224     2315     2456
                  2801     2987     3018     3044
                  3400     3784     4504     4555
Nla IV      (16)  403      985      1121     1737
                  1758     1770     1961     2122
                  2194     2583     2618     3466
                  3545     3590     4433     4472
Not I       (1)   1136
Nsi I       (3)   2154     2226     4557
Nsp7524 I   (4)   2148     2220     2983     4500
NspB II     (5)   64       2080     2688     3917
                  4162
NspH I      (4)   2152     2224     2987     4504
Pac I       (1)   24
Pal I       (21)  309      602      795      1138
                  1548     1690     2345     2351
                  2360     2403     2490     2664
                  3055     3082     3591     3648
                  3681     4026     4460     4478
                  4489
PflM I      (1)   1227
Ple I       (2)   1633     2065
Pme I       (1)   15
Psp1406 I   (2)   98       471
Pst I       (1)   458
Pvu I       (1)   331
Pvu II      (2)   2080     2688
Rsa I       (9)   219      737      762      817
                  850      901      1058     1121
                  2888
Rsr II      (1)   3098
Sal I       (1)   1143
Sap I       (2)   2926     3136
Sau3A I     (26)  53       70       328      374
                  392      1103     1114     1208
                  1217     1239     2419     2423
                  2442     2753     2831     2912
                  2921     2999     3375     3391
                  3750     3762     3840     3848
                  3859     3934
Sau96 I     (9)   336      601      794      1689
                  3098     3543     3589     3647
                  3680
Sca I       (1)   219
ScrF I      (17)  164      515      608      801
                  2118     2173     2190     2586
                  2746     2969     3359     3548
                  3651     4123     4341     4354
                  4475
Sec I       (16)  878      1123     2116     2188
                  2311     2346     2355     2404
                  2745     3014     3419     3546
                  3547     3649     3650     4340
SfaN I      (13)  247      440      876      1397
                  2160     2232     2541     2796
                  2880     2944     3012     3219
                  4404
Sfc I       (4)   454      1917     4044     4235
Sfi I       (1)   2357
SnaB I      (1)   858
Sph I       (3)   2152     2224     2987
Ssp I       (2)   1490     2043
Stu I       (1)   2403
Sty I       (6)   878      1123     2311     2404
                  3014     3419
Taq I       (14)  46       1144     1171     1731
                  2422     2695     2851     2875
                  2911     3073     3264     3309
                  3564     4402
Tfi I       (5)   3067     3201     3311     3348
                  4526
Tsp45 I     (5)   227      438      1871     2702
                  3008
Tth111 I    (1)   2700
Tth111 II   (4)   3018     3878     3908     3917
Vsp I       (1)   525
Xba I       (1)   1149
Xho II      (11)  53       70       1103     1208
                  2753     2999     3391     3750
                  3762     3848     3859
Xma III     (2)   1136     2488
Xmn I       (1)   100

Site usage in CMVCFT.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         16     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
Bbe I      G,GCGC`C          1      Bbs I      GAAGAC 8/12       -
Bbv I      GCAGC 13/17       7      Bbv II     GAAGAC 7/11       -
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Bcl I      T`GATC,A         1      Bcn I      CC,S`GG          6
Bfa I      C`TA,G           9      Bgl I      GCCN,NNN`NGGC    4
Bgl II     A`GATC,T         1      Blp I      GC`TNA,GC        -
Bpm I      CTGGAG 22/20     2      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         16
BsaW I     W`CCGG,W         6      BseR I     GAGGAG 16/14     2
Bsg I      GTGCAG 22/20     -      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         5      BsmB I     CGTCTC 7/11      -
BsmF I     GGGAC 15/19      10     BsoF I     GC`N,GC          35
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`          11
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         1      BstE II    G`GTNAC,C        -
BstN I     CC`W,GG          11     BstU I     CG|CG            17
BstX I     CCAN,NNNN`NTGG   1      BstY I     R`GATC,Y         11
Bsu36 I    CC`TNA,GG        2      Cac8 I     GCN|NGC          29
Cfr10 I    R`CCGG,Y         4      Cla I      AT`CG,AT         1
Csp6 I     G`TA,C           9      Dde I      C`TNA,G          7
Dpn I      GA|TC            26     DpnII      `GATC,           26
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         6      Eag I      C`GGCC,G         2
Ear I      CTCTTC 7/10      3      Eco47 III  AGC|GCT          -
Eco57 I    CTGAAG 21/19     3      Eco72 I    CAC|GTG          -
EcoN I     CCTNN`N,NNAGG    1      EcoO109 I  RG`GNC,CY        1
EcoR I     G`AATT,C         -      EcoR II    `CCWGG,          11
EcoR V     GAT|ATC          -      Ehe I      GGC|GCC          1
Esp I      GC`TNA,GC        -      Fnu4H I    GC`N,GC          35
Fok I      GGATG 14/18      7      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,GCGC`Y         4      Hae III    GG|CC            21
Hga I      GACGC 9/14       8      HgiA I     G,WGCW`C         5
HgiE II    ACCNNNNNNGGT -1/132      Hha I       G,CG`C           22
HinC II    GTY|RAC          3      Hind II    GTY|RAC          3
HinD III   A`AGCT,T         1      Hinf I     G`ANT,C          12
HinI I     GR`CG,YC         8      HinP I     G`CG,C           22
Hpa I      GTT|AAC          1      Hpa II     C`CG,G           20
Hph I      GGTGA 12/11      6      Kas I      G`GCGC,C         1
Kpn I      G,GTAC`C         1      Mae I      C`TA,G           9
Mae II     A`CG,T           16     Mae III    `GTNAC,          16
Mbo I      `GATC,           26     Mbo II     GAAGA 12/11      10
Mlu I      A`CGCG,T         1      Mme I      TCCRAC 25/23     3
Mnl I      CCTC 10/10       29     Msc I      TGG|CCA          1
Mse I      T`TA,A           20     Msl I      CAYNN|NNRTG      4
Msp I      C`CG,G           20     MspA1 I    CMG|CKG          5
Mun I      C`AATT,G         1      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         -
Nla III    ,CATG`           20     Nla IV     GGN|NCC          16
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         -
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         -
Pst I      C,TGCA`G         1      Pvu I      CG,AT`CG         1
Pvu II     CAG|CTG          2      Rsa I      GT|AC            9
Rsr II     CG`GWC,CG        1      Sac I      G,AGCT`C         -
Sac II     CC,GC`GG         -      Sal I      G`TCGA,C         1
Sap I      GCTCTTC 8/11     2      Sau3A I    `GATC,           26
Sau96 I    G`GNC,C          9      Sca I      AGT|ACT          1
ScrF I     CC`N,GG          17     Sec I      C`CNNG,G         16
SfaN I     GCATC 9/13       13     Sfc I      C`TRYA,G         4
Sfi I      GGCCN,NNN`NGGCC  1      Sma I      CCC|GGG          -
SnaB I     TAC|GTA          1      Spe I      A`CTAG,T         -
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`CWWG,G         6
Taq I      T`CG,A           14     Tfi I      G`AWT,C          5
Tsp45 I    `GTSAC,          5      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         -
Xho II     R`GATC,Y         11     Xma I      C`CCGG,G         -
Xma III    C`GGCC,G         2      Xmn I      GAANN|NNTTC      1
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