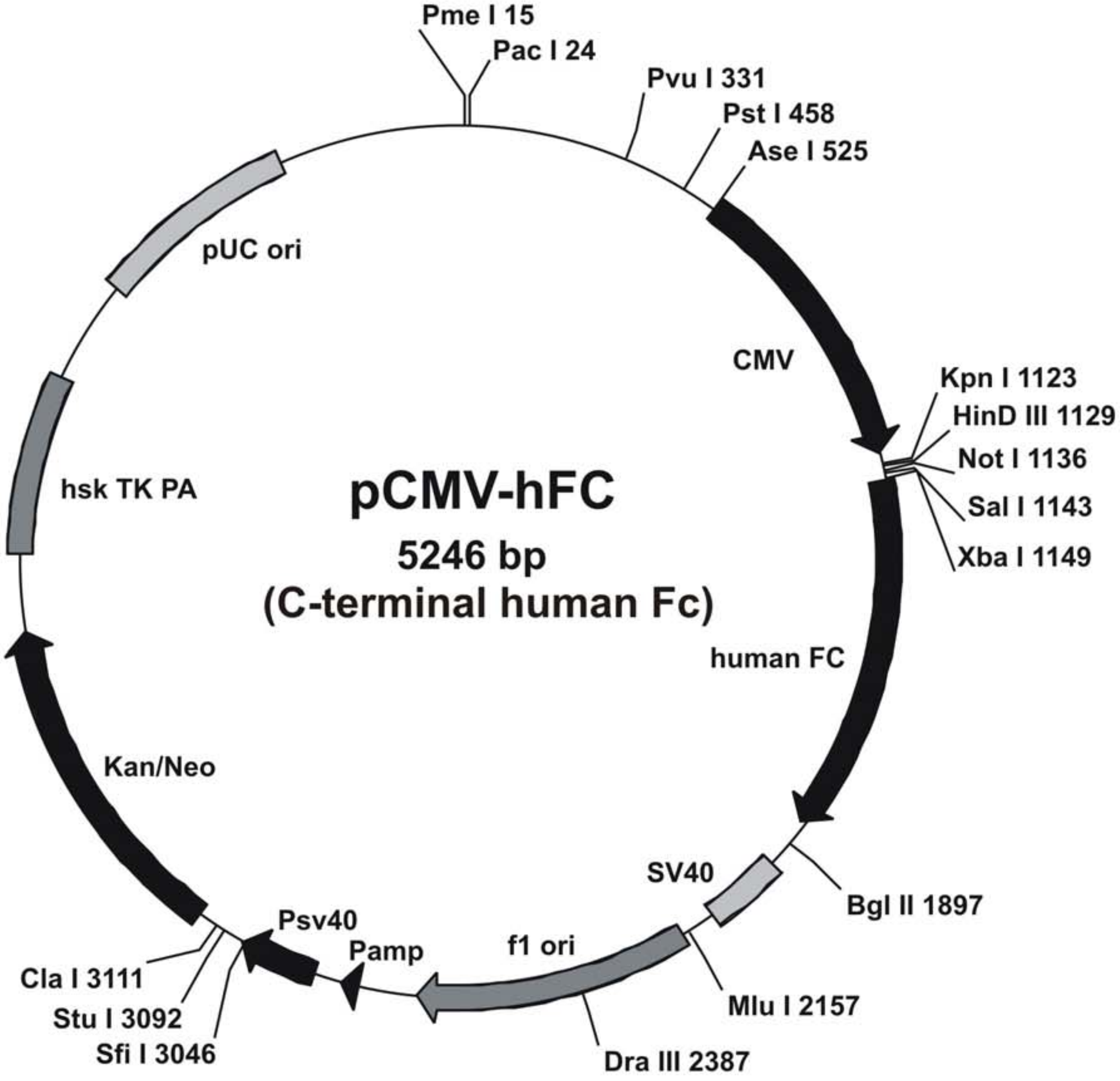
Name of Vector: pCMV-hFc
Antibiotic Selection: Kan
Created by: Jae Yoon Park, Wei Jiang, and Qing Luo
(He Lab @ The University of Chicago)
Date of Creation: February 2004



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
                  Human Fc fragment                 Bgl II
GTC GAG GGA ATG.....human IgG gamma 1 Fc Fragment..TGAGATCT
 V   E   G   M.....human IgG gamma 1 Fc Fragment... -
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pCMV-hFc 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
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GAGCTGGTTTAGTGAACCGTCAGATCCgctagagatcggtaccatggaagcttgcggccg  1140
cgtcgactctagaggaggcggcggaggtgtcgagcccaaatcttgtgacaaaactcacac  1200
atgcccaccgtgcccagcacctgaactcctggggggaccgtcagtcttcctcttcccccc  1260
aaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtgga  1320
cgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgca  1380
taatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgt  1440
cctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaa  1500
caaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgaga  1560
accacaggtgtacaccctgcccccatcccgggatgagctgaccaagaaccaggtcagcct  1620
gacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgg  1680
gcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttctt  1740
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ctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctcc  1860
gggtaaatgagatctatccgatccaccggannnnnnTAACTGATCATAATCAGCCATACC  1920
ACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAA  1980
CATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAA  2040
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CAAAATCCCTTATAAATCAAAAGAATAGACCGAGATAGGGTTGAGTGTTGTTCCAGTTTG  2280
GAACAAGAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAGGGCGAAAAACCGTCTA  2340
TCAGGGCGATGGCCCACTACGTGAACCATCACCCTAATCAAGTTTTTTGGGGTCGAGGTG  2400
CCGTAAAGCACTAAATCGGAACCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAA  2460
GCCGGCGAACGTGGCGAGAAAGGAAGGGAAGAAAGCGAAAGGAGCGGGCGCTAGGGCGCT  2520
GGCAAGTGTAGCGGTCACGCTGCGCGTAACCACCACACCCGCCGCGCTTAATGCGCCGCT  2580
ACAGGGCGCGTCAGGTGGCACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATT  2640
TTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCA  2700
ATAATATTGAAAAAGGAAGAGTCCTGAGGCGGAAAGAACCAGCTGTGGAATGTGTGTCAG  2760
TTAGGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAAAGCATGCATCTC  2820
AATTAGTCAGCAACCAGGTGTGGAAAGTCCCCAGGCTCCCCAGCAGGCAGAAGTATGCAA  2880
AGCATGCATCTCAATTAGTCAGCAACCATAGTCCCGCCCCTAACTCCGCCCATCCCGCCC  2940
CTAACTCCGCCCAGTTCCGCCCATTCTCCGCCCCATGGCTGACTAATTTTTTTTATTTAT  3000
GCAGAGGCCGAGGCCGCCTCGGCCTCTGAGCTATTCCAGAAGTAGTGAGGAGGCTTTTTT  3060
GGAGGCCTAGGCTTTTGCAAAGATCGATCAAGAGACAGGATGAGGATCGTTTCGCATGAT  3120
TGAACAAGATGGATTGCACGCAGGTTCTCCGGCCGCTTGGGTGGAGAGGCTATTCGGCTA  3180
TGACTGGGCACAACAGACAATCGGCTGCTCTGATGCCGCCGTGTTCCGGCTGTCAGCGCA  3240
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GGGGCGCCCGGTTCTTTTTGTCAAGACCGACCTGTCCGGTGCCCTGAATGAACTGCAAGA  3300
CGAGGCAGCGCGGCTATCGTGGCTGGCCACGACGGGCGTTCCTTGCGCAGCTGTGCTCGA  3360
CGTTGTCACTGAAGCGGGAAGGGACTGGCTGCTATTGGGCGAAGTGCCGGGGCAGGATCT  3420
CCTGTCATCTCACCTTGCTCCTGCCGAGAAAGTATCCATCATGGCTGATGCAATGCGGCG  3480
GCTGCATACGCTTGATCCGGCTACCTGCCCATTCGACCACCAAGCGAAACATCGCATCGA  3540
GCGAGCACGTACTCGGATGGAAGCCGGTCTTGTCGATCAGGATGATCTGGACGAAGAGCA  3600
TCAGGGGCTCGCGCCAGCCGAACTGTTCGCCAGGCTCAAGGCGAGCATGCCCGACGGCGA  3660
GGATCTCGTCGTGACCCATGGCGATGCCTGCTTGCCGAATATCATGGTGGAAAATGGCCG  3720
CTTTTCTGGATTCATCGACTGTGGCCGGCTGGGTGTGGCGGACCGCTATCAGGACATAGC  3780
GTTGGCTACCCGTGATATTGCTGAAGAGCTTGGCGGCGAATGGGCTGACCGCTTCCTCGT  3840
GCTTTACGGTATCGCCGCTCCCGATTCGCAGCGCATCGCCTTCTATCGCCTTCTTGACGA  3900
GTTCTTCTGAGCGGGACTCTGGGGTTCGAAATGACCGACCAAGCGACGCCCAACCTGCCA  3960
TCACGAGATTTCGATTCCACCGCCGCCTTCTATGAAAGGTTGGGCTTCGGAATCGTTTTC  4020
CGGGACGCCGGCTGGATGATCCTCCAGCGCGGGGATCTCATGCTGGAGTTCTTCGCCCAC  4080
CCTAGGGGGAGGCTAACTGAAACACGGAAGGAGACAATACCGGAAGGAACCCGCGCTATG  4140
ACGGCAATAAAAAGACAGAATAAAACGCACGGTGTTGGGTCGTTTGTTCATAAACGCGGG  4200
GTTCGGTCCCAGGGCTGGCACTCTGTCGATACCCCACCGAGACCCCATTGGGGCCAATAC  4260
GCCCGCGTTTCTTCCTTTTCCCCACCCCACCCCCCAAGTTCGGGTGAAGGCCCAGGGCTC  4320
GCAGCCAACGTCGGGGCGGCAGGCCCTGCCATAGCCTCAGGTTACTCATATATACTTTAG  4380
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CTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAA  4500
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AAAAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTT  4620
CCGAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCG  4680
TAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATC  4740
CTGTTACCAGTGGCTGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGA  4800
CGATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCC  4860
AGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGC  4920
GCCACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACA  4980
GGAGAGCGCACGAGGGAGCTTCCAGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGG  5040
TTTCGCCACCTCTGACTTGAGCGTCGATTTTTGTGATGCTCGTCAGGGGGGCGGAGCCTA  5100
TGGAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCT  5160
CACATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCATGCAT  5220
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Unique enzymes in PCMV-HFC

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Pme I       CTTT|AAAC       15
Pac I       TTA,AT`TAA      24
Sca I       AGT|ACT         219
Pvu I       CG,AT`CG        331
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   1242
Sac II      CC,GC`GG        1401
BsrG I      T`GTAC,A        1570
PspA I      C`CCGG,G        1588
Xma I       C`CCGG,G        1588
Sma I       CCC|GGG         1590
Bgl II      A`GATC,T        1871
PflM I      CCAN,NNN`NTGG   1890
BstX I      CCAN,NNNN`NTGG  1891
Bcl I       T`GATC,A        1902
Mun I       C`AATT,G        1995
Hpa I       GTT|AAC         2008
Mlu I       A`CGCG,T        2131
Dra III     CAC,NNN`GTG     2361
Sfi I       GGCCN,NNN`NGGCC 3020
Stu I       AGG|CCT         3066
Cla I       AT`CG,AT        3085
Kas I       G`GCGC,C        3244
Nar I       GG`CG,CC        3245
Ehe I       GGC|GCC         3246
Bbe I       G,GCGC`C        3248
Msc I       TGG|CCA         3327
Tth111 I    GACN`N,NGTC     3363
Rsr II      CG`GWC,CG       3761
BsiC I      TT`CG,AA        3927
BstB I      TT`CG,AA        3927
EcoO109 I   RG`GNC,CY       4343
Number of enzymes = 43
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The following enzymes do not cut in PCMV-HFC

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Afl II      Age I       Apa I       Asc I       BamH I
Blp I       BsiW I      BsmB I      Bsp120 I    BspM II
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      Sac I
Spe I       Spl I       Srf I       Xca I       Xcm I
```

PCMV-HFC: sites sorted by name:

```
Aat II      (4)   643      696      779      965
Acc I       (1)   1144
Acc65 I     (1)   1119
Aci I       (65)  64       141      185      306
                  352      576      604      616
                  630      797      888      921
                  1025     1046     1107     1135
                  1139     1159     1162     1398
                  1400     2505     2532     2560
                  2563     2577     2620     2667
                  2730     2915     2927     2936
                  2948     2958     2969     3015
                  3154     3217     3311     3375
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                  3476     3479     3719     3759
                  3764     3814     3830     3856
                  3912     3981     3984     4050
                  4132     4197     4264     4337
                  4571     4580     4715     4825
                  4946     4965     5092     5120
                  5211
Afl III     (2)   2131     5163
Aha II      (8)   160      640      693      776
                  962      3245     3947     4026
Ahd I       (1)   1242
Alu I       (18)  347      410      510      1084
                  1131     1598     1754     2024
                  2191     2448     2743     3031
                  3351     3809     4606     4863
                  4909     4999
Alw I       (16)  60       66       381      1099
                  1876     3112     3423     3490
                  3669     4034     4061     4420
                  4421     4518     4518     4604
AlwN I      (3)   1221     4346     4754
ApaL I      (2)   28       4849
Apo I       (3)   2059     2163     2174
Ase I       (1)   525
Asp718      (1)   1119
Ava I       (2)   1555     1588
Ava II      (5)   336      1236     1291     3761
                  4206
Avr II      (2)   3067     4082
Ban I       (5)   983      1119     2398     3244
                  3279
Ban II      (4)   1177     2436     3610     4320
Bbe I       (1)   3248
Bbs I       (3)   1238     1339     1784
Bbv I       (10)  468      1562     1694     1790
                  2033     3318     3360     3881
                  4334     4834
Bbv II      (3)   1239     1338     1785
Bcl I       (1)   1902
Bcn I       (10)  165      516      1290     1590
                  1591     1862     3250     3410
                  4023     4787
Bfa I       (9)   507      1110     1150     2094
                  2512     3068     4083     4417
                  4670
Bgl I       (4)   608      730      801      3020
Bgl II      (1)   1871
Bpm I       (2)   4028     4085
Bsa I       (2)   1499     4234
BsaA I      (5)   858      1361     1423     2361
                  3549
BsaB I      (2)   1907     3104
BsaH I      (8)   160      640      693      776
                  962      3245     3947     4026
BsaJ I      (22)  878      1123     1229     1267
                  1398     1588     1660     1759
                  2779     2851     2974     3009
                  3018     3067     3408     3677
                  4082     4209     4210     4312
                  4313     5003
BsaW I      (6)   404      1886     3276     4120
                  4810     4957
BseR I      (3)   1168     1419     3063
Bsg I       (2)   1437     1806
BsiC I      (1)   3927
BsiE I      (5)   182      331      1139     3154
                  4829
BsiHKA I    (5)   32       117      3358     3548
                  4853
Bsm I       (2)   1996     2089
BsmA I      (7)   951      1498     1860     2670
                  3088     4107     4235
BsmF I      (11)  693      844      1012     1249
                  2761     2833     2897     3396
                  3928     4037     4192
BsoF I      (39)  185      280      307      457
                  1136     1139     1160     1398
                  1551     1683     1779     2022
                  2541     2563     2577     3015
                  3154     3206     3217     3307
                  3312     3349     3390     3477
                  3480     3483     3719     3815
                  3856     3870     3984     4323
                  4338     4549     4755     4758
                  4823     4966     5121
Bsp1286 I   (2)   117      3548
BspH I      (3)   1279     2671     4443
BspM I      (5)   1632     1762     3132     3513
                  3963
Bsr I       (13)  54       226      493      814
                  1358     1466     2275     2953
                  3188     3389     4635     4749
                  4762
BsrB I      (4)   2505     2669     3858     3912
BsrD I      (3)   466      1682     3478
BsrG I      (1)   1570
BssS I      (4)   31       3837     3963     4990
BstB I      (1)   3927
BstN I      (15)  608      801      1230     1458
                  1611     1629     2781     2836
                  2853     3632     4211     4314
                  5004     5017     5138
BstU I      (18)  141      578      1141     1400
                  2133     2169     2545     2565
                  2589     2620     3311     3612
                  4050     4134     4197     4266
                  4539     5120
BstX I      (1)   1891
BstY I      (11)  53       70       1103     1871
                  3416     3662     4054     4413
                  4425     4511     4522
Bsu36 I     (4)   1297     1339     2725     4357
Cac8 I      (30)  454      604      797      1133
                  1752     2464     2507     2521
                  2794     2813     2866     2885
                  3139     3325     3544     3610
                  3616     3644     3648     3689
                  3693     3747     4030     4217
                  4264     4320     4342     4553
                  5113     5150
Cfr10 I     (4)   2462     3564     3745     4028
Cla I       (1)   3085
Csp6 I      (14)  218      736      761      816
                  849      900      1057     1120
                  1358     1412     1424     1481
                  1571     3550
Dde I       (9)   199      1297     1339     2725
                  3027     3908     4357     4480
                  4889
Dpn I       (27)  55       72       330      376
                  394      1105     1116     1284
                  1873     1882     1904     3084
                  3088     3107     3418     3496
                  3577     3586     3664     4040
                  4056     4415     4427     4505
                  4513     4524     4599
DpnII       (27)  53       70       328      374
                  392      1103     1114     1282
                  1871     1880     1902     3082
                  3086     3105     3416     3494
                  3575     3584     3662     4038
                  4054     4413     4425     4503
                  4511     4522     4597
Dra I       (5)   15       122      1947     4389
                  4408
Dra III     (1)   2361
Drd I       (4)   1341     2316     3272     5061
Dsa I       (7)   878      1123     1398     1660
                  1759     2974     3677
Eae I       (6)   307      1136     3151     3325
                  3716     3743
Eag I       (2)   1136     3151
Ear I       (5)   1257     1836     2712     3589
                  3799
Eco57 I     (3)   3390     3822     4622
EcoN I      (2)   339      1455
EcoO109 I   (1)   4343
EcoR II     (15)  606      799      1228     1456
                  1609     1627     2779     2834
                  2851     3630     4209     4312
                  5002     5015     5136
Ehe I       (1)   3246
Fnu4H I     (39)  185      280      307      457
                  1136     1139     1160     1398
                  1551     1683     1779     2022
                  2541     2563     2577     3015
                  3154     3206     3217     3307
                  3312     3349     3390     3477
                  3480     3483     3719     3815
                  3856     3870     3984     4323
                  4338     4549     4755     4758
                  4823     4966     5121
Fok I       (8)   261      1571     1605     2918
                  3112     3569     3594     4048
Fsp I       (2)   477      3347
Gdi II      (7)   308      1135     1137     3150
                  3152     3715     3742
Gsu I       (2)   4029     4084
Hae I       (5)   3066     3327     4689     5141
                  5152
Hae II      (4)   2512     2520     3248     4923
Hae III     (21)  309      602      795      1138
                  2211     2353     3008     3014
                  3023     3066     3153     3327
                  3718     3745     4254     4311
                  4344     4689     5123     5141
                  5152
Hga I       (9)   167      1043     1131     1428
                  2579     3954     4033     4474
                  5052
HgiA I      (5)   32       117      3358     3548
                  4853
HgiE II     (2)   1884     4574
Hha I       (22)  141      478      2511     2519
                  2545     2567     2576     2589
                  2620     3239     3247     3311
                  3348     3614     3874     4050
                  4136     4539     4648     4822
                  4922     4989
HinC II     (3)   158      1145     2008
Hind II     (3)   158      1145     2008
HinD III    (1)   1129
Hinf I      (13)  928      1146     1722     2288
                  2310     2720     3730     3864
                  3916     3974     4011     4793
                  5189
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HinI I      (8)   160      640      693      776
                  962      3245     3947     4026
HinP I      (22)  139      476      2509     2517
                  2543     2565     2574     2587
                  2618     3237     3245     3309
                  3346     3612     3872     4048
                  4134     4537     4646     4820
                  4920     4987
Hpa I       (1)   2008
Hpa II      (24)  163      405      515      1289
                  1589     1686     1860     1887
                  2463     3150     3227     3249
                  3277     3408     3498     3565
                  3746     4021     4029     4121
                  4595     4785     4811     4958
Hph I       (8)   215      893      1437     1749
                  2363     3424     4315     4431
Kas I       (1)   3244
Kpn I       (1)   1123
Mae I       (9)   507      1110     1150     2094
                  2512     3068     4083     4417
                  4670
Mae II      (20)  98       471      640      652
                  693      776      857      962
                  1321     1360     1422     1789
                  2305     2317     2360     2470
                  3361     3548     4329     4462
Mae III     (18)  39       227      380      438
                  579      666      1015     1185
                  1301     2033     2534     2546
                  3365     3671     4361     4627
                  4743     4806
Mbo I       (27)  53       70       328      374
                  392      1103     1114     1282
                  1871     1880     1902     3082
                  3086     3105     3416     3494
                  3575     3584     3662     4038
                  4054     4413     4425     4503
                  4511     4522     4597
Mbo II      (16)  104      1239     1245     1343
                  1731     1785     1852     2500
                  2728     3605     3815     3897
                  4064     4264     4434     4507
Mlu I       (1)   2131
Mme I       (5)   1521     1749     2337     4771
                  4955
Mnl I       (40)  327      1059     1146     1149
                  1158     1259     1286     1292
                  1334     1367     1397     1451
                  1517     1719     1751     1808
                  1856     1924     1963     1972
                  2389     2720     2998     3004
                  3027     3033     3041     3044
                  3056     3096     3160     3296
                  3653     3845     4051     4083
                  4365     4735     4986     5059
Msc I       (1)   3327
Mse I       (20)  14       20       24       121
                  486      525      1946     2007
                  2128     2149     2160     2172
                  2183     2200     2298     2569
                  4388     4402     4407     4459
Msl I       (5)   288      883      1659     1891
                  3682
Msp I       (24)  163      405      515      1289
                  1589     1686     1860     1887
                  2463     3150     3227     3249
                  3277     3408     3498     3565
                  3746     4021     4029     4121
                  4595     4785     4811     4958
MspA1 I     (6)   64       1400     2743     3351
                  4580     4825
Mun I       (1)   1995
Nae I       (3)   2464     3747     4030
Nar I       (1)   3245
Nci I       (10)  164      515      1289     1589
                  1590     1861     3249     3409
                  4022     4786

Nco I       (4)   878      1123     2974     3677
Nde I       (1)   752
NgoM I      (3)   2462     3745     4028
Nla III     (25)  257      293      371      381
                  822      882      1127     1204
                  1283     1309     1801     1815
                  2675     2815     2887     2978
                  3119     3464     3650     3681
                  3707     4063     4447     5167
                  5218
Nla IV      (19)  403      985      1121     1237
                  1293     1733     2400     2421
                  2433     2624     2785     2857
                  3246     3281     4129     4208
                  4253     5096     5135
Not I       (1)   1136
Nsi I       (4)   1813     2817     2889     5220
Nsp7524 I   (6)   1200     1305     2811     2883
                  3646     5163

NspB II     (6)   64       1400     2743     3351
                  4580     4825

NspH I      (6)   1204     1309     2815     2887
                  3650     5167

Pal I       (21)  309      602      795      1138
                  2211     2353     3008     3014
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                  3023     3066     3153     3327
                  3718     3745     4254     4311
                  4344     4689     5123     5141
                  5152
PflM I      (1)   1890
Ple I       (2)   2296     2728
Pme I       (1)   15
Psp1406 I   (2)   98       471
PspA I      (1)   1588
Pst I       (1)   458
Pvu I       (1)   331
Pvu II      (2)   2743     3351
Rsa I       (14)  219      737      762      817
                  850      901      1058     1121
                  1359     1413     1425     1482
                  1572     3551
Rsr II      (1)   3761
Sac II      (1)   1401
Sal I       (1)   1143
Sap I       (3)   1836     3589     3799
Sau3A I     (27)  53       70       328      374
                  392      1103     1114     1282
                  1871     1880     1902     3082
                  3086     3105     3416     3494
                  3575     3584     3662     4038
                  4054     4413     4425     4503
                  4511     4522     4597
Sau96 I     (11)  336      601      794      1236
                  1291     2352     3761     4206
                  4252     4310     4343
Sca I       (1)   219
ScrF I      (25)  164      515      608      801
                  1230     1289     1458     1589
                  1590     1611     1629     1861
                  2781     2836     2853     3249
                  3409     3632     4022     4211
                  4314     4786     5004     5017
                  5138
Sec I       (22)  878      1123     1229     1267
                  1398     1588     1660     1759
                  2779     2851     2974     3009
                  3018     3067     3408     3677
                  4082     4209     4210     4312
                  4313     5003
SfaN I      (14)  247      440      876      1799
                  2060     2823     2895     3204
                  3459     3543     3607     3675
                  3882     5067
Sfc I       (5)   454      1745     2580     4707
                  4898
Sfi I       (1)   3020
Sma I       (1)   1590
SnaB I      (1)   858
Sph I       (3)   2815     2887     3650
Ssp I       (2)   2153     2706
Stu I       (1)   3066
Sty I       (7)   878      1123     1267     2974
                  3067     3677     4082
Taq I       (15)  46       1144     1171     1522
                  2394     3085     3358     3514
                  3538     3574     3736     3927
                  3972     4227     5065
Tfi I       (5)   3730     3864     3974     4011
                  5189
Tsp45 I     (7)   227      438      1185     1301
                  2534     3365     3671
Tth111 I    (1)   3363
Tth111 II   (4)   3681     4541     4571     4580
Vsp I       (1)   525
Xba I       (1)   1149
Xho II      (11)  53       70       1103     1871
                  3416     3662     4054     4413
                  4425     4511     4522
Xma I       (1)   1588
Xma III     (2)   1136     3151
Xmn I       (2)   100      1791
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Site usage in PCMV-HFC

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Aat II     G,ACGT`C          4     Acc I      GT`MK,AC          1
Acc65 I    G`GTAC,C          1     Aci I      C`CG,C            65
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     1     Alu I      AG|CT             18
Alw I      GGATC 8/9         16    AlwN I     CAG,NNN`CTG       3
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          2     Ava II     G`GWC,C           5
Avr II     C`CTAG,G          2     BamH I     G`GATC,C          -
Ban I      G`GYRC,C          5     Ban II     G,RGCY`C          4
Bbe I      G,GCGC`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            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       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**	**7**	**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**	**-**
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**	**18**
BstX I	**CCAN,NNNN`NTGG**	**1**	**BstY I**	**R`GATC,Y**	**11**
Bsu36 I	**CC`TNA,GG**	**4**	**Cac8 I**	**GCN|NGC**	**30**
Cfr10 I	**R`CCGG,Y**	**4**	**Cla I**	**AT`CG,AT**	**1**
Csp6 I	**G`TA,C**	**14**	**Dde I**	**C`TNA,G**	**9**
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**	**7**
Eae I	**Y`GGCC,R**	**6**	**Eag I**	**C`GGCC,G**	**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,NNAGG**	**2**	**EcoO109 I**	**RG`GNC,CY**	**1**
EcoR I	**G`AATT,C**	**-**	**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,GCGC`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**	**22**
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**	**22**
Hpa I	**GTT|AAC**	**1**	**Hpa II**	**C`CG,G**	**24**
Hph I	**GGTGA 12/11**	**8**	**Kas I**	**G`GCGC,C**	**1**
Kpn I	**G,GTAC`C**	**1**	**Mae I**	**C`TA,G**	**9**
Mae II	**A`CG,T**	**20**	**Mae III**	**`GTNAC,**	**18**
Mbo I	**`GATC,**	**27**	**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**	**24**	**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**	**-**
Nla III	**,CATG`**	**25**	**Nla IV**	**GGN|NCC**	**19**
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**
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**	**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**	**GCTCTTC 8/11**	**3**
Sau3A I	**`GATC,**	**27**	**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**	**-**	**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**	**7**	**Taq I**	**T`CG,A**	**15**
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**	**-**	**Xho II**	**R`GATC,Y**	**11**
Xma I	**C`CCGG,G**	**1**	**Xma III**	**C`GGCC,G**	**2**