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      CMV promoter
      |-----|
721  AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG
      |-----|
      CMV forward priming site
      |-----|
781  GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA
      |-----|
      TATA
      |-----|
      3' end of CMV promoter
      |-----|
      putative transcriptional start
      |-----|
      CAAT
      |-----|
841  CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
      |-----|
      T7 promoter/priming site
      |-----|
      Nhe I
      |-----|
901  GTTTAAACTT AAGCTTGGTA CCGAGCTCGG ATCCACTAGT CCAGTGTGGT GGAATTCTGC
      |-----|
      Pme I*  Afl II  Hind III  Asp718 I  Kpn I      Bam H I
      |-----|
      Bst X I*
      |-----|
961  AGATATCCAG CACAGTGGCG GCCGCTCGAG TCTAGAGGGC CCGTTTAAAC CCGCTGATCA
      |-----|
      Eco R V      Bst X I*  Not I      Xho I      Apa I  Pme I*
      |-----|
      BGH reverse priming site
      |-----|
1021 GCCTCGACTG TGCCTTCTAG TTGCCAGCCA TCTGTTGTTT GCCCCTCCCC CGTGCCTTCC
  
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pcDNA5/FRT DNA Sequence

1 GACGGATCGG GAGATCTCCC GATCCCCTAT GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAGTAT CTGCTCCCTG CTTGTGTGTT
101 GGAGGTTCGCT GAGTAGTGCG CGAGCAAAAT TTAAGCTACA ACAAGGCAAG GCTTGACCGA CAATTGCATG AAGAATCTGC TTAGGGTTAG GCGTTTTGCG
201 CTGCTTCGCG ATGTACGGGC CAGATATACG CGTTGACATT GATTATTGAC TAGTTATTAA TAGTAATCAA TTACGGGGTC ATTAGTTCAT AGCCCATATA
301 TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCCGC TGGCTGACCG CCCAACGACC CCCGCCATT GACGTCAATA ATGACGTATG TTCCCATAGT
401 AACGCCAATA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT AAACCTGCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCCC
501 CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCCAGTA CATGACCTTA TGGGACTTTC CTACTTGGCA GTACATCTAC GTATTAGTCA
601 TCGCTATTAC CATGGTGATG CCGTTTTGGC AGTACATCAA TGGGCGTGGG TAGCGGTTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA
701 TGGGAGTTTG TTTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA ACAACTCCGC CCCATTGACG CAAATGGGCG GTAGGCGTGT ACGGTGGGAG
801 GTCTATATAA GCAGAGCTCT CTGGCTAACT AGAGAACCCA CTGCTTACTG GCTTATCGAA ATTAATACGA CTCACTATAG GGAGACCCAA GCTGGCTAGC
901 GTTTAAACTT AAGCTTGGTA CCGAGCTCGG ATCCACTAGT CCAGTGTGGT GGAATTCTGC AGATATCCAG CACAGTGGCG GCCGCTCGAG TCTAGAGGGC
1001 CCGTTTAAAC CCGCTGATCA GCCTCGACTG TGCCTTCTAG TTGCCAGCCA TCTGTTGTTT GCCCTCCCC CGTGCCCTCC TTGACCCTGG AAGGTGCCAC
1101 TCCCCTGTC CTTTCCTAAT AAAATGAGGA AATTGCATCG CATTGTCTGA GTAGGTGTCA TTCTATTCTG GGGGGTGGGG TGGGGCAGGA CAGCAAGGGG
1201 GAGGATTGGG AAGACAATAG CAGGCATGCT GGGGATGCGG TGGGCTCTAT GGCTTCTGAG CCGGAAAGAA CCAGCTGGGG CTCTAGGGGG TATCCCCACG
1301 CCCTCTGTAG CCGCGCATA AGCGCGCGG GTGTGGTGGT TACGCGCGAT GTGACCTGCG CACTTGCCAG CGCCCTAGCG CCCCTCCTT TCGCTTTCTT
1401 CCCTTCTTTT CTCGCCACGT TCGCGGCTT TCCCGTCAA GCTCTAAATC GGGGGCTCCC TTTAGGGTTC CGATTTAGTG CTTTACGGCA CCTCGACCCC
1501 AAAAACTTG ATTAGGGTGA TGGTTCACGT ACCTAGAAGT TCCTATTCCG AAGTTCCTAT TCTCTAGAAA GTATAGGAAC TTCCTTGCC AAAAAGCCTG
1601 AACTCACCGC GACGTCTGTC GAGAAGTTTC TGATCGAAAA GTTCGACAGC GTCTCCGACC TGATGCAGCT CTCGGAGGGC GAAGAATCTC GTGCTTTCAG
1701 CTTCGATGTA GGAGGGCGTG GATATGTCTT GCGGGTAAAT AGCTGCGCCG ATGGTTTTCTA CAAAGATCGT TATGTTTTATC GGCACTTTGC ATCGGCCCGC
1801 CTCCCGATTC CGGAAGTGTG TGACATTGGG GAATTCAGCG AGAGCCTGAC CTATTGCATC TCCCGCCGTG CACAGGGTGT CACGTTGCAA GACCTGCCTG
1901 AAACCGAATC GCCCGCTGTT CTGCAGCCGG TCGCGGAGGC CATGGATGCG ATCGCTGCGG CCGATCTTAG CCAGACGAGC GGGTTCGGCG CATTGGGACC
2001 GCAAGGAATC GGTCAATACA CTACATGGCG TGATTTTATA TCGCGGATTG CTGATCCCCA TGTGTATCAC TGGCAAAC TGATGGACGA CACCGTCAGT
2101 GCGTCCGTCG CGCAGGCTCT CGATGAGCTG ATGCTTTGGG CCGAGGACTG CCCCAGAGTC CGGCACCTCG TGCACGCGGA TTTCCGGCTCC ACAAATGTCC
2201 TGACGGACAA TGGCCGATA ACAGCGGTCA TTGACTGGAG CGAGGCGATG TTCGGGGATT CCCAATACGA GGTCCGCAAC ATCTTCTTCT GGAGGCCGTG
2301 GTTGGCTTGT ATGGAGCAGC AGACGCGCTA CTTGAGCGG AGGCATCCGG AGCTTGCAGG ATCGCCGCGG CTCGGGGCGT ATATGCTCCG CATTGGTCTT
2401 GACCAACTCT ATCAGAGCTT GGTGACGGC AATTTGATG ATGCAGCTTG GCGCGAGGGT CGATGCGACG CAATCGTCCG ATCCGGAGCC GGGACTGTCC
2501 GGCGTACACA AATCGCCCGC AGAAGCGCGG CCGTCTGGAC CGATGGCTGT GTAGAAGTAC TCGCCGATG TGGAACC CGCCCCAGCA CTCGTCCGAG
2601 GGCAAGGAA TAGCACGTAC TACGAGATT CGATTCACC GCCGCCTTCT ATGAAAGGTT GGGCTTCGGA ATCGTTTTCC GGGACGCCCG CTGGATGATC
2701 CTCCAGCGCG GGGATCTCAT CTTGGAGTTT TCCGCCACC CCAACTTGT TATTGCAGCT TATAATGGTT ACAAAATAAG CAATAGCATC ACAAATTTCA
2801 CAAATAAAGC ATTTTFTTCA CTGCATTCTA GTTGTGGTTT GTCCAAACTC ATCAATGTAT CTTATCATGT CTGTATACCG TCGACCTCTA GCTAGAGCTT
2901 GGCGTAATCA TGGTCATAGC TGTTTCTGT GTGAAATTGT TATCCGCTCA CAATTCCACA CAACATACGA GCCGGAAGCA TAAAGTGTAA AGCCTGGGGT
3001 GCCTAATGAG TGAGCTAACT CACATTAATT GCGTTCGCT CACTGCCCGC TTFCCAGTCG GGAAACCTGT CGTGCCAGCT GCATTAATGA ATCGGCCAAC
3101 GCGCGGGGAG AGGCGGTTTG CGTATTGGGC GCTCTTCCGC TTCTCGCTC ACTGACTCGC TGCGCTCGGT CGTTCCGGCTG CCGCGAGCCG TATCAGTCA
3201 CTCAAAGGCG GTAATACGGT TATCCACAGA ATCAGGGGAT AACGCAGGAA AGAACATGTG AGCAAAAGGC CAGCAAAAGG CCAGGAACCG TAAAAGGCC
3301 GCGTGTCTGG CTTTTTCCA TAGGCTCCG CCCCCTGACG AGCATCAGAA AAATCGAGC TCAAGTCAGA CCCGACAGGA CCGTATAAGAT
3401 ACCAGGCGTT TCCCCTGGA AGCTCCCTCG TCGCTCTCC TGTCCGACC CTGCCGCTTA CCGGATACCT GTCCGCTTTT CTCCCTTCGG GAAGCGTGGC
3501 GCTTCTCAT AGCTCACGCT GTAGGTATCT CAGTTCGGTG TAGGTCGTTT GCTCCAAGCT GGGCTGTGTG CACGAACCCC CCGTTCAGCC CGACCGCTGC
3601 GCCTTATCCG GTAACATCG TCTTGAGTCC AACCCGTAA GACACGACTT ATCGCCACTG GCAGCAGCCA CTGGTAACAG GATTAGCAGA GCGAGGTATG
3701 TAGGCGGTGC TACAGAGTTC TTGAAGTGGT GGCCTAACTA CGCTACACT AGAAGGACAG TATTTGGTAT CTGCGCTCTG CTGAAGCCAG TTACCTTCGG
3801 AAAAAAGATT GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT
3901 CAAGAAGATC CTTTGATCTT TTCTACGGGG TCTGACGCTC AGTGGACGTA AAATCAAGT TAAGGGATTT TGGTCATGAG ATTATAAAA AGGATCTTCA
4001 CCTAGATCCT TTTAAATTAA AAATGAAGT TTTAAATCAAT CTAAAGTATA TATGAGTAAA CTGTGCTGTA CAGTTACCAA TGCTTAATCA GTGAGGACC
4101 TATCTCAGCG ATCTGTCTAT TTCGTTTCAT CATAGTTGCC TGAATCCCCG TCGTGTAGAT AACTACGATA CGGGAGGGCT TACCATCTGG CCCCAGTGCT
4201 GCAATGATAC CGCGAGACCC ACGCTCACCG GCTCCAGATT TATCAGCAAT AAACCAGCCA GCCGGAAGGG CCGAGCGCAG AAGTGGTCTT GCAACTTTAT
4301 CCGCCTCCAT CCAGTCTATT AATTGTTGCC GGGAAAGCTAG AGTAAGTAGT TCGCCAGTTA ATAGTTTGGC CAACGTTGTT GCCATTGCTA CAGGCATCGT
4401 GGTGTACGC TCGTCGTTTG GTATGGCTTC ATTCAGCTCC GGTTCCTAAC GATCAAGGCG AGTTACATGA TCCCCATGT TGTGCAAAAA AGCGGTTAGC
4501 TCCTTCGGTC CTCCGATCGT TGTCAGAAGT AAGTTGGCCG CAGTGTATTAC ACTCATGGTT ATGGCAGCAC TGCATAATTC TCTTACTGTC ATGCCATCCG
4601 TAAGTAGCTT TTCTGTGACT GGTGAGTACT CAACCAAGTC ATTCGTAGAA TAGTGTATGC GGGCAGCCAG TTGCTCTTGC CCGGCTTAC TACGGGATAA
4701 TACCGCGCCA CATAGCAGAA CTTTAAAGT GCTCAACTATT GGAAAACGTT TCTCGGGGCG AAAACTCTCA AGGATCTTAC CGTGTTGAG ATCCAGTTCG
4801 ATGTAACCCA CTCGTGCACC CAACTGATCT TCAGCATCTT TTACTTTTAC CAGCGTTTCT GGGTGAGCAA AAACAGGAAG GCAAAATGCC GCAAAAAAGG

4901 GAATAAGGGC GACACGGAAA TGTGAATAC TCATACTCTT CCTTTTCAA TATTATTGAA GCATTTATCA GGGTTATTGT CTCATGAGCG GATACATATT
 5001 TGAATGTATT TAGAAAAATA AACAAATAGG GGTTCGCGC ACATTTCCCC GAAAAGTGCC ACCTGACGTC

pcDNA5/FRT Restriction Map

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Enzyme      Cuts    [ ----- Base 5' to Cleave Sites ----- ]
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AatII       6       375  428  511  697  1615  5069
AccI        2       2874 2881
AclI        2       4373 4746
AcyI        9       372  425  508  694  1612  2580  2684  4684  5066
AflII       1       908
AflIII      2       228 3254
AgeI        0
AhaIII      5       904 1006 4013 4032 4724
AluI        28      135  816  891  913  925 1274 1441 1668
           1700 1742 2127 2352 2417 2446 2758 2891
           2897 2919 3014 3078 3196 3422 3512 3558
           3815 4336 4436 4499
AlwNI       2       80 3670
ApaBI       2       1894 2170
ApaI        1       1001
ApaLI       5       32 1868 2170 3568 4814
ApoI        4       127 952 1831 2793
AscI        0
AsuI        13      217 333 526 997 998 1987 1996 2138
           2537 4189 4268 4285 4507
AsuII       0
AvaI        1       985
AvaII       4       1996 2537 4285 4507
  
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AvrII	0								
BalI	1	1588							
BamHI	1	929							
BclI	1	1015							
BetI	6	1809	2346	2482	3460	3607	4438		
BglI	4	340	462	533	4267				
BglII	1	12							
BsaAI	3	590	1528	2616					
BsaBI	0								
BseMII	4	53	3543	3952	4118				
BsePI	0								
BsiYI	13	299 3102	1309 3276	1809 3294	1872 3460	2159 3739	2268	2489	2709
BspI407I	0								
BspHI	2	3974	4982						
BspLU11I	1	3254							
BspMII	3	1809	2346	2482					
BstEII	0								
BstXI	2	948	974						
Cac8I	24	122 1368 2688	336 1382 3047	529 1425 3076	893 1913 3185	897 2114 3271	1045 2174 3308	1222 2354 3868	1226 2517 4259
CauII	6	2374	2490	2680	3634	4330	4681		
Cfr10I	4	1423	1926	2686	4227				
CfrI	8	979	1586	1793	1958	2211	2528	3093	4535
ClaI	0								
CviJI	90	73 816 999 1441 1844 2140	135 824 1021 1455 1926 2186	151 851 1047 1588 1939 2213	219 891 1244 1596 1960 2295	292 895 1252 1668 1970 2305	334 913 1274 1700 1988 2352	343 925 1280 1742 2116 2370	527 981 1427 1795 2127 2417

		2446	2488	2530	2546	2663	2690	2758	2891
		2897	2919	2971	2992	3014	3078	3095	3177
		3196	3269	3280	3298	3324	3422	3512	3558
		3563	3588	3667	3732	3743	3786	3815	4178
		4190	4231	4257	4261	4270	4336	4426	4436
		4499	4537						
CviRI	23	34	166	959	1135	1665	1789	1856	1870
		1887	1923	2172	2356	2443	2755	2823	3081
		3570	3866	4201	4291	4484	4572	4816	
DdeI	10	39	109	180	1147	1256	1966	3529	3938
		4104	4644						
DpnI	27	6	14	22	931	1017	1633	1766	1951
		1964	2054	2361	2481	2698	2714	3822	3897
		3908	3916	3994	4006	4111	4452	4470	4516
		4774	4791	4827					
DraII	1	997							
DraIII	2	1876	2169						
DrdI	3	2092	2473	3362					
DsaI	4	610	1940	2296	2365				
Eam1105I	1	4147							
Eco47III	0								
EcoNI	0								
EcoRI	2	952	1831						
EcoRII	7	338	531	1085	2992	3280	3401	3414	
EcoRV	1	964							
EspI	0								
Fnu4HI	36	61	201	979	982	1311	1325	1347	1666
		1743	1796	1924	1955	1958	2214	2317	2365
		2368	2444	2528	2642	2756	3079	3160	3178
		3181	3299	3454	3597	3662	3665	3871	4199
		4538	4565	4660	4889				
FnuDII	24	120	208	230	310	1300	1324	1344	1609
		1798	1933	2044	2110	2176	2325	2367	2527
		2708	3101	3103	3301	3882	4212	4705	5037
FseI	0								
HaeI	5	1588	1939	3269	3280	3732			

HaeII	4	1373	1381	3132	3502				
HaeIII	22	219	334	527	981	999	1588	1795	1939
		1960	1988	2140	2213	2295	2530	3095	3269
		3280	3298	3732	4190	4270	4537		
HgiAI	8	36	818	927	1872	2174	3572	4733	4818
HgiCI	7	715	917	1093	1487	2162	2998	4095	
HgiJII	6	818	927	1001	1246	1282	1457		
HhaI	29	120	200	1302	1315	1324	1346	1372	1380
		1747	1800	2044	2112	2327	2454	2527	2708
		3038	3103	3131	3164	3434	3501	3601	3775
		3884	4277	4370	4707	5039			
HincII	3	234	2424	2882					
HindIII	1	911							
HinfI	15	173	660	869	988	1684	1806	2006	2257
		2632	2669	3089	3154	3229	3625	4142	
HpaI	0								
HpaII	20	1424	1810	1927	2160	2347	2373	2483	2489
		2679	2687	2972	3461	3608	3634	3824	4228
		4262	4329	4439	4681				
KpnI	1	921							
MaeI	16	250	829	896	936	992	1037	1283	1375
		1533	1564	2828	2888	2892	3749	4002	4337
MaeII	15	372	384	425	508	589	694	1417	1527
		1612	1882	2615	3957	4373	4746	5066	
MaeIII	15	311	398	747	1338	1350	1878	2767	3610
		3673	3789	4072	4403	4461	4614	4802	
MboI	27	4	12	20	929	1015	1631	1764	1949
		1962	2052	2359	2479	2696	2712	3820	3895
		3906	3914	3992	4004	4109	4450	4468	4514
		4772	4789	4825					
McrI	10	982	1796	1931	1952	1961	2531	3170	3594
		4517	4666						
MfeI	1	161							
MluI	1	228							
MseI	18	69	131	257	862	903	909	1005	1318
		3025	3084	3960	4012	4017	4031	4084	4319

		4358	4723							
MslI	4	615	4399	4558	4917					
MstI	1	4369								
MwoI	33	197	340	462	494	533	626	650	1234	
		1258	1319	1321	1363	1390	1420	1795	1862	
		1893	1945	1954	1976	1985	2107	2169	2322	
		2349	2449	2998	3042	3126	3193	3307	3879	4267
NaeI	2	1425	2688							
NarI	0									
NcoI	2	610	1940							
NdeI	2	484	2038							
NheI	1	895								
NlaIII	17	170	554	614	1228	1944	2027	2062	2721	
		2869	2912	3258	3978	4469	4479	4557	4593	4986
NlaIV	20	717	919	931	999	1095	1456	1468	1489	
		2164	2187	2371	2487	3000	3286	3325	4097	
		4191	4232	4443	5033					
NotI	1	979								
NruI	1	208								
NspBII	9	1013	1274	1915	2224	2367	3078	3596	3841	4782
NspI	2	1228	3258							
PacI	0									
PflMI	0									
PmaCI	0									
PmeI	2	904	1006							
PpuMI	0									
PshAI	1	1615								
PstI	2	961	1925							
PvuI	2	1952	4517							
PvuII	2	1274	3078							
RsaI	14	44	214	469	494	549	582	633	790	

		919	1530	2505	2558	2618	4627		
RsrII	1	1996							
SacI	2	818	927						
SacII	1	2368							
SalI	1	2880							
SanDI	0								
SauI	0								
ScaI	2	2558	4627						
ScrFI	13	340	533	1087	2374	2490	2680	2994	3282
		3403	3416	3634	4330	4681			
SduI	12	36	818	927	1001	1246	1282	1457	1872
		2174	3572	4733	4818				
SecI	10	610	1085	1583	1940	2141	2296	2365	2596
		2993	3414						
SexAI	0								
SfeI	7	875	957	1305	1921	3519	3710	4388	
SfiI	0								
SgfI	1	1952							
SgrAI	0								
SmaI	0								
SmlI	6	908	985	3360	3622	3899	4767		
SnaBI	1	590							
SpeI	2	249	935						
SphI	1	1228							
SplI	0								
SrfI	0								
Sse8387I	0								
Sse8647I	0								
SspI	1	4951							

StuI	0									
StyI	3	610	1583	1940						
SwaI	0									
TaqI	16	856 2120	986 2333	1024 2435	1493 2460	1619 2630	1634 2881	1643 3354	1703 4798	
TatI	7	42	467	547	580	631	2556	4625		
TfiI	9	173	1684	1806	2006	2257	2632	2669	3089	3229
TseI	18	200 2755 4198	1346 3078 4564	1665 3159	1742 3177	1923 3596	1954 3661	2316 3664	2443 3870	
Tsp45I	4	1350	1878	4403	4614					
Tsp4CI	16	326 2094	448 2496	519 2879	793 3218	974 3289	1029 3759	1107 4072	2079 4587	
TspEI	15	127 2793	161 2934	268 2951	859 3026	952 4014	1130 4320	1831 4575	2430	
TspRI	16	845 3156	948 3662	979 3675	1110 3946	2074 4095	2103 4200	2825 4547	3047 4574	
Tth111I	2	1648	2092							
VspI	5	257	862	3025	3084	4319				
XbaI	2	991	1563							
XcmI	0									
XhoI	1	985								
XhoII	9	12	929	2712	3895	3906	3992	4004	4772	4789
XmaIII	4	979	1793	1958	2528					
XmnI	1	4746								

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