

enhancer region (3' end)

689 CATTGACGTC AATGGGAGTT TGTTTTGGCA CCAAATCAA CGGGACTTTC CAAAATGTCG

CAAT TATA

749 TAACAACCTCC GCCCCATTGA CGCAAATGGG CGGTAGGCGT GTACGGTGGG AGGTCTATAT

3' end of hCMV putative transcriptional start

809 AAGCAGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAC TGGCTTATCG AAATTAATAC

T7 promoter/primer binding site

Nhe I A Pme I Afl II Hind III Asp718 I Kpn I

869 GACTCACTAT AGGGAGACCC AAGCTGGCTA GCGTTTAAAC TTAAGCTTGG TACCGAGCTC

BamH I BstX I\* EcoR I EcoR V BstX I\* Not I Xho I

929 GGATCCACTA GTCCAGTGTG GTGGAATTCT GCAGATATCC AGCACAGTGG CGGCCGCTCG

Xba I Apa I Pme I B pcDNA3.1/BGH reverse priming site

989 AGTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC

1049 CATCTGTTGT TTGCCCTCC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCCTG

BGH poly (A) site

1109 TCCTTTCCTA ATAAAATGAG GAAATTGCAT