

enhancer region (3' end)

689 CATTGACGTC AATGGGAGTT TGTTTTGGCA CCAAATCAA CGGGACTTTC CAAAATGTCTG

749 TAACAACTCC GCCCATTGA CAAT CGCAAATGGG CGGTAGGCGT GTACGGTGGG TATA AGGTCTATAT

3' end of hCMV

putative transcriptional start

809 AAGCAGAGCT CTCTGGCTAA CTAGAGAACC CACTGCTTAC TGGCTTATCG AAATTAATAC

T7 promoter/primer binding site

869 GACTCACTAT AGGGAGACCC AAGCTGGCTA GCGTTTAAAC TTAAGCTTGG TACCGAGCTC

Nhe I *Pme* I *Afl* II *Hind* III *Asp*718 I *Kpn* I

929 GGATCCACTA GTCCAGTGTG GTGGAATTCT GCAGATATCC AGCACAGTGG CGGCCGCTCG

*Bam*H I *Bst*X I* *Eco*R I *Eco*R V *Bst*X I* *Not* I *Xho* I

989 AGTCTAGAGG GCCCGTTTAA ACCCGCTGAT CAGCCTCGAC TGTGCCTTCT AGTTGCCAGC

Xba I *Dra* II *Apa* I *Pme* I pcDNA3.1/BGH reverse priming site

1049 CATCTGTTGT TTGCCCTCC CCCGTGCCTT CCTTGACCCT GGAAGGTGCC ACTCCCACTG

BGH poly (A) site

1109 TCCTTTCCTA ATAAAATGAG GAAATTGCAT