

CAAT
 641 CAAATGGGCG GTAGGCGTGT ACGGTGGGAG GTCTATATAA GCAGAGCTCG TTTAGTGAAC
 TATA
 701 CGTCAGATCG CCTGGAGACG CCATCCACGC TGTTTTGACC TCATAGAAGA CACCGGGACC
 3' end of CMV promoter Putative transcriptional start
 761 GATCCAGCCT CCGGACTCTA GAGGATCCCT ACCGGTGATA TCCTCGAGACCC -----
 EmGFP or YFP

1552 attB1
 1527 AAG GGC TCG AGC CCA TCA ACA AGT TTG TAC AAA AAA GCA GGC TNN - - NAC
 TTC CCG AGC TCG GGT AGT TGT TCA AAC ATG TTT TTT CGT CCG ANN -GENE- NTG
 Lys Gly Ser Ser Pro Ser Thr Ser Leu Tyr Lys Lys Ala Glu ... - - ...

attB2 3235 V5 epitope
 3227 CCA GCT TTC TTG TAC AAA GTG GTT GAT AAC GGG AAG CCT ATC CCT AAC CCT CTC
 GGT CGA AAG AAC ATG TTT CAC CAA CTA TTG CCC TTC GGA TAG GGA TTG GGA GAG
 Pro Ala Phe Leu Tyr Lys Val Val Asp Asn Gly Lys Pro Ile Pro Asn Pro Leu

3281 CTC GGT CTC GAT TCT ACG CGT ACC GGT TAG TAA TGA GTTTAAACGG GGGAGGCTGAA
 GAG CCA GAG CTA AGA TGC GCA TGG CCA ATC GTT ACT
 Leu Gly Leu Asp Ser Thr Arg Thr Gly *** *** ***

TK polyA Reverse priming site
 3358 ACACGGAAGG AGACAATAC

