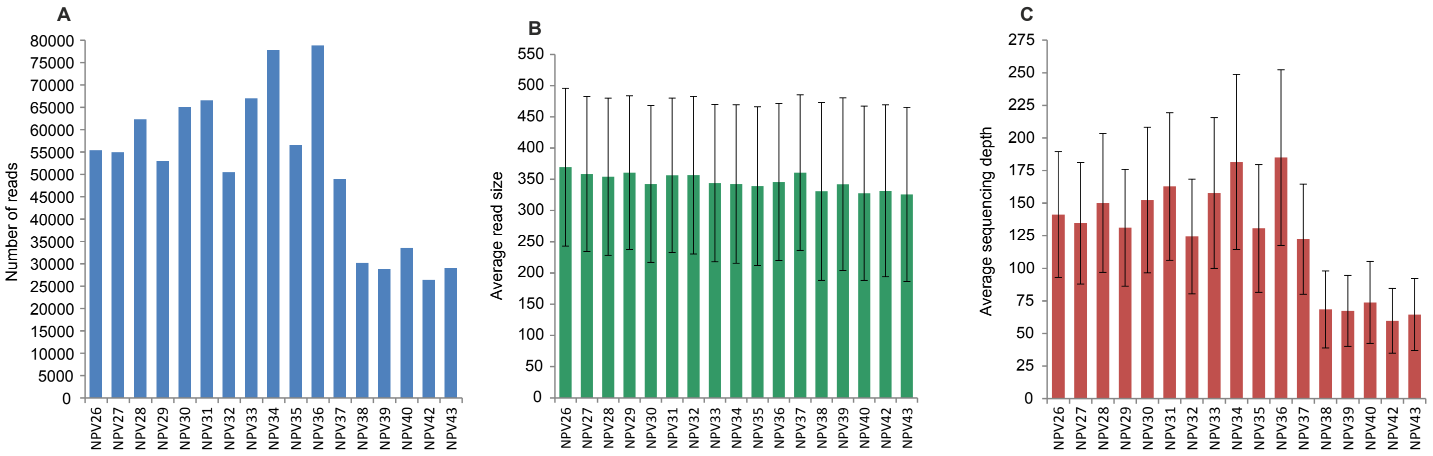
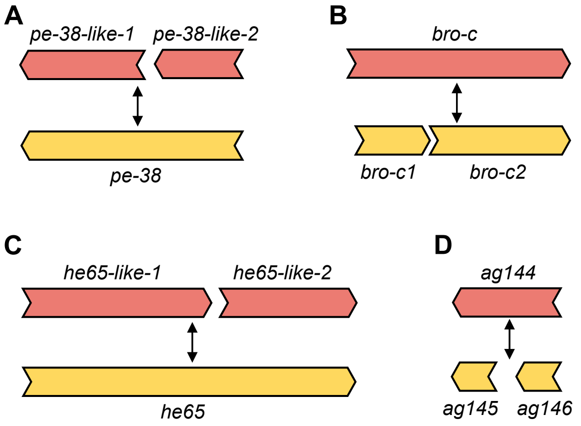
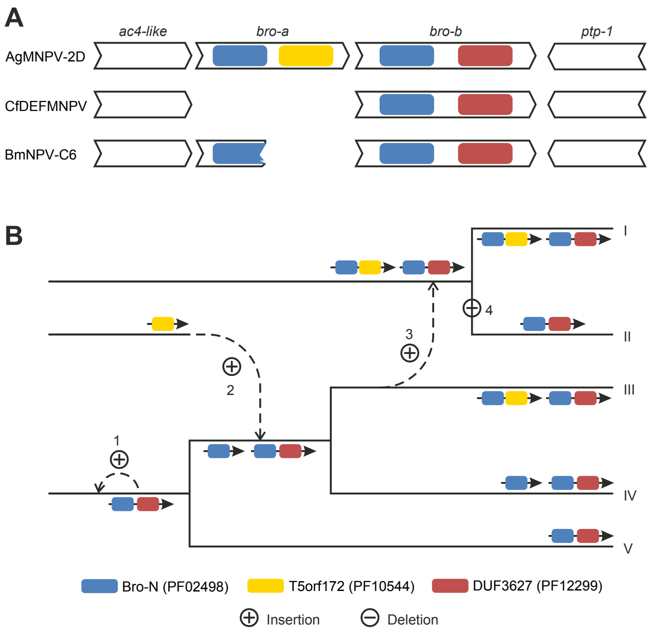
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Features of sequence datasets of AgMNPV. A) Total number of reads per sample. B) Average read sizes. C) Average sequencing depth.



Supplementary Figure 2. Examples of AgMNPV genes that evolve via gene fission/fusion: A) pe-38; B) bro-c; C) he65; and D) ag144. Red arrows represent ORFs previously annotated in the genome of AgMNPV-2D, and yellow ones are new ORFs derived from events of fission/fusion.



Supplementary Figure 3. Structural variations and hypothetical mechanisms outlining the evolution of the haplotype of bro-a. A) Homologs of the haplotype bro-a/bro-b and its neighbouring genes. B) Hypothetical evolutionary relationships among different haplotypes containing bro genes. Events of partial duplication (+), horizontal transfer (+), and deletion (-), numbered from 1 to 4 depict those hypotheses discussed in the text. Taxa I and III have the same gene content as the haplotype bro-a/bro-b, and their evolutionary history could explain the origin of this haplotype in AgMNPV-2D. The taxon V illustrates a haplotype that never had homologs of bro-a and bro-b next to each in the genome, while taxon II illustrates a haplotype that lost a homolog of bro-a, similarly to what likely happened with some AgMNPV genotypes. Taxon IV has a haplotype similar to that one observed in BmNPV-C6. The scenario in IV could represent both a haplotype that has two DUF3627 domains as result of duplication, or a haplotype that lost a T5orf172 domain.