

Figure 1: Genome-wide diversity in the SfMNPV ARG-M isolate. (a) Distribution of synonymous (yellow), nonsynonymous (violet) and intergenic (orange) iSNVs across the genome. (b) Number of iSNVs detected for each category. (c) Boxplot showing the allele frequency for each iSNV category.

Figure 2: Genetic diversity present in SfMNPV isolates. (a) Maximum likelihood phylogeny reconstructed from a whole-genome sequence alignment. Support values were computed using 1000 Ultra-Fast Bootstrap replicates. *Spodoptera exigua* nucleopolyhedrovirus (SeMNPV) was selected as outgroup. (b) Histogram showing the number of SNPs per bin detected within the sequence alignment. The alignment was splitted into 13 bins, which correspond to 10.38 Kbp per bin. (c) Barplot showing the number of SNPs detected for each isolate and the combinations detected.

Figure 3: Proteome diversity within SfMNPV. For each coding region in SfMNPV the number of nonsynonymous variants was computed. The inner circle represents SNPs derived from isolates whole-genome sequence alignment, while the outer ring corresponds to the iSNVs detected within SfMNPV ARG-M.

Figure 4: Sf29 Molecular Evolution. (a) Maximum likelihood phylogeny of *sf29* orthologs. Support values were computed using 1000 UltraFast Bootstrap replicates. *E. canis* and *C. Rickettsiella* were included as outgroups. Branches experiencing positive selection, as detected by aBSREL, are colored in orange. (b) Sequence analysis of *sf29*. Sites under positive selection are marked in blue, while iSNV are depicted in orange. The peptidase M9 domain is colored violet and the disordered region is in green. (c) Sequence conservation of the peptidase activate site motif (HEXXH), extracted from the *sf29* sequence alignment.

Supplementary Tables

Supplementary Table 1: Annotated coding sequences for SfMNPV ARG-M.

Supplementary Table 2: Intrahost single nucleotide variants (iSNVs) detected with Lofreq.

Supplementary Table 3: Structural variants detected with both Delly and Lumpy.

Supplementary Table 4: Single nucleotide polymorphisms (SNPs) present in SfMNPV isolates.

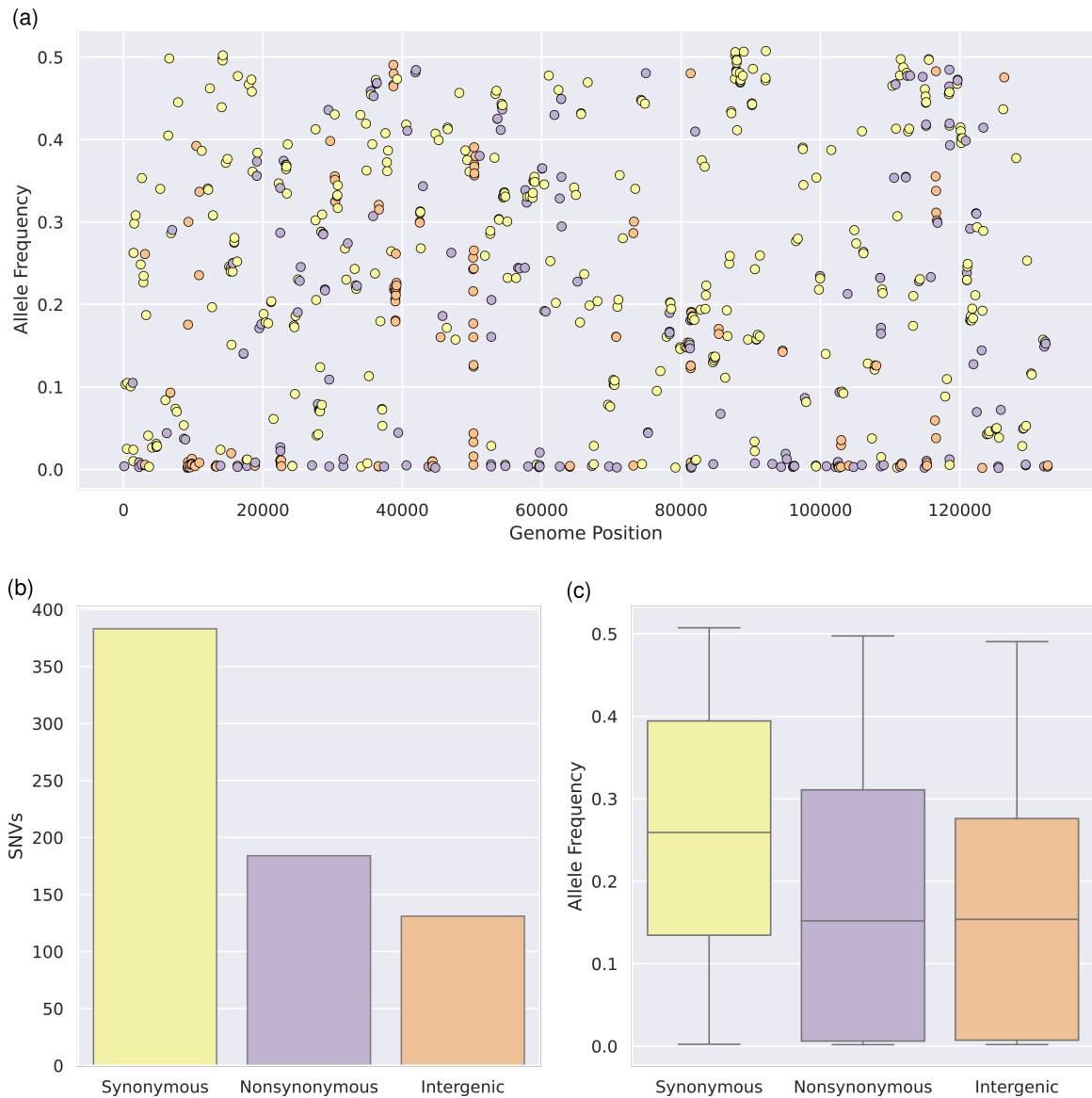


Figure 1

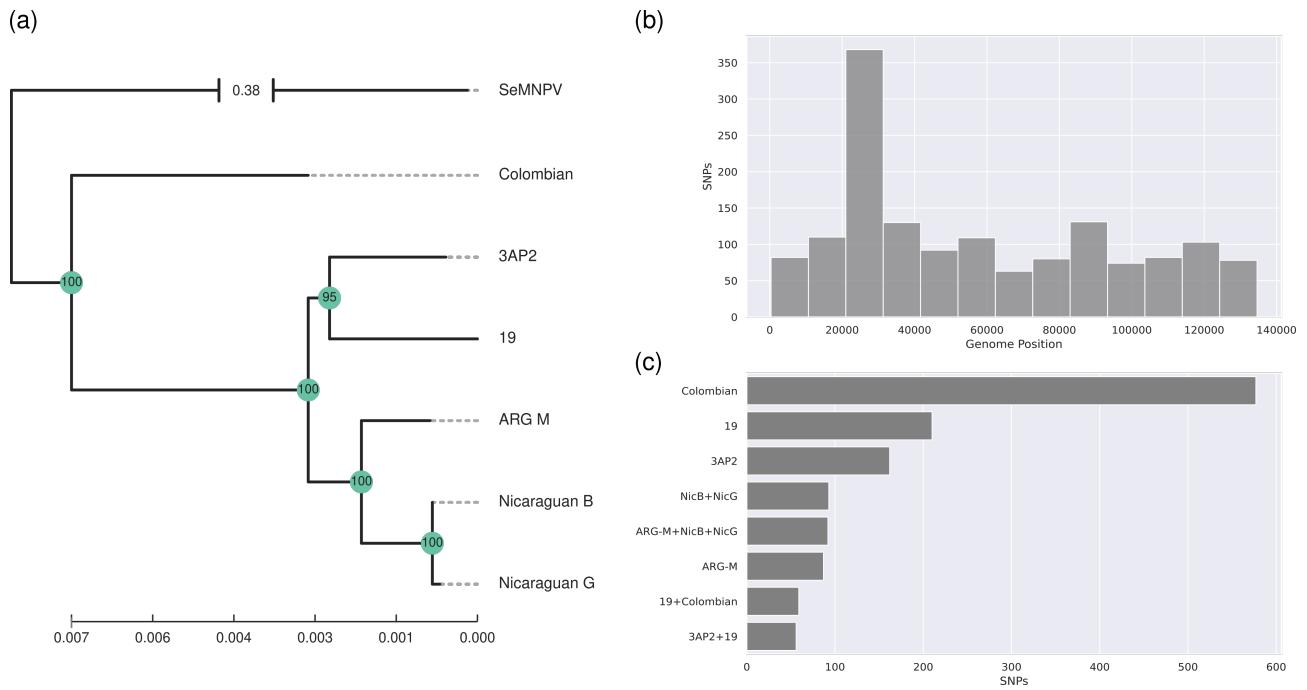
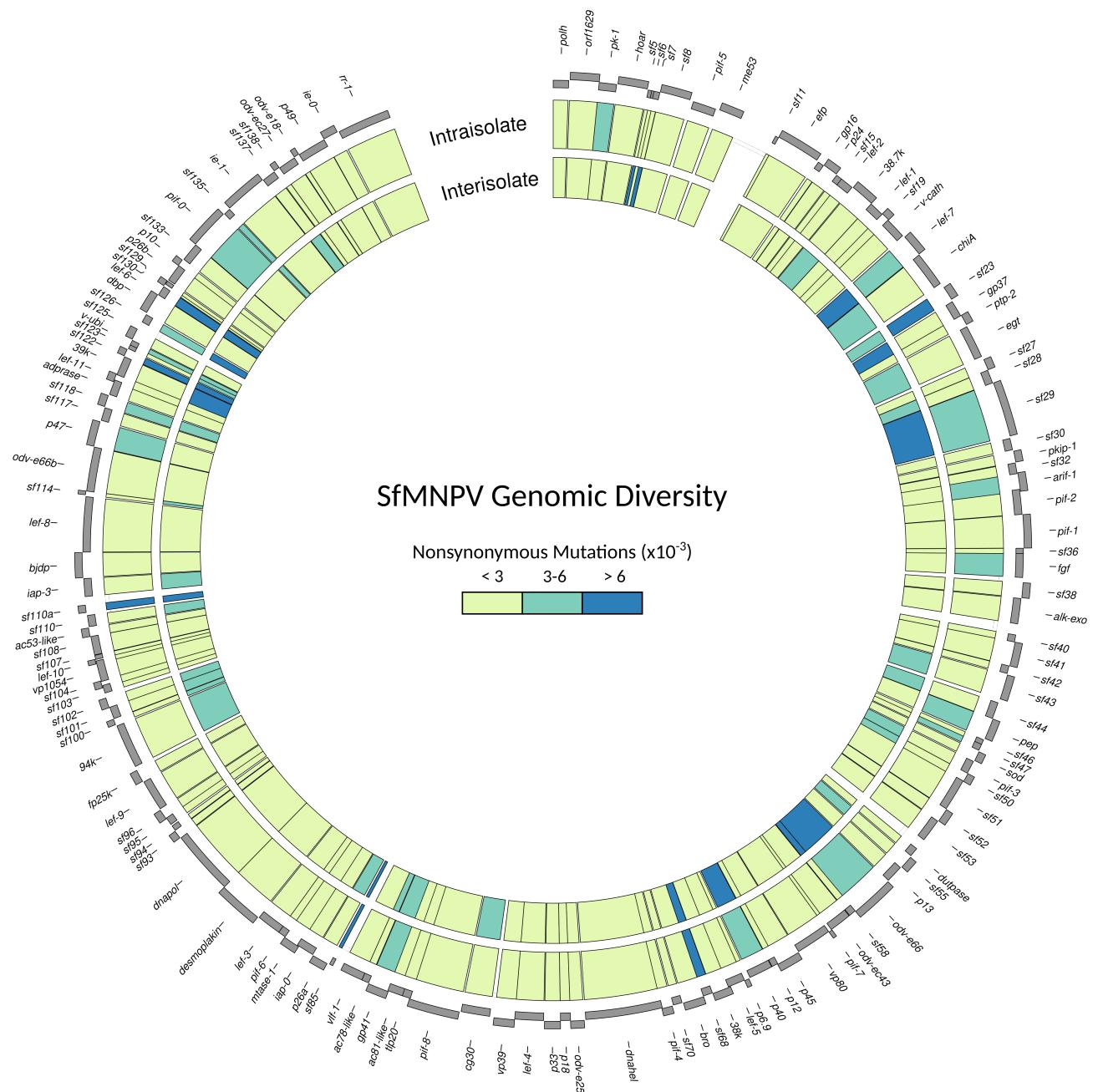


Figure 2



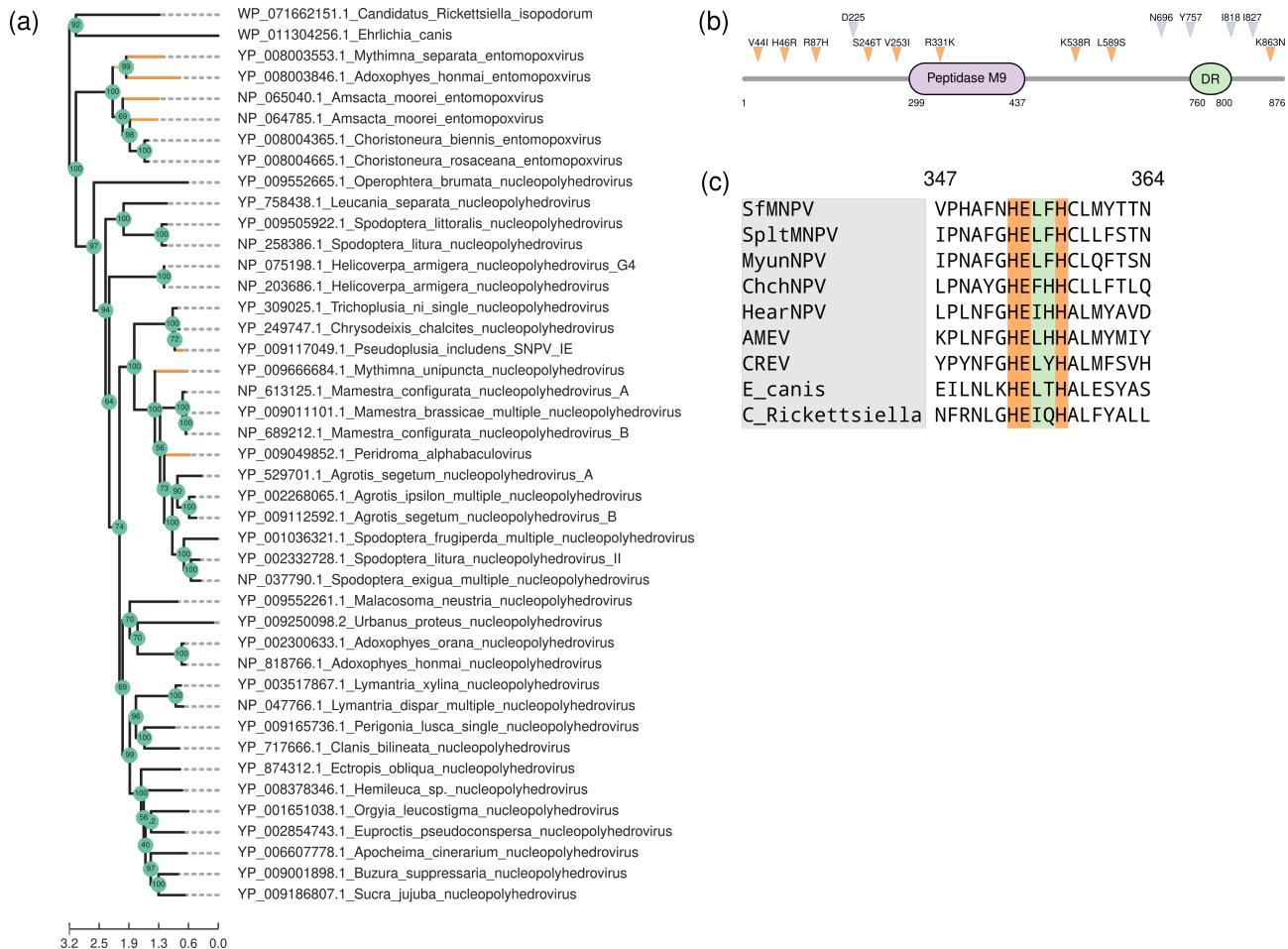


Figure 4