

Fig. S2 Overview of SNPs identified in two Chinese HycuNPV genomes. (A) SNP counts based on their exchange characteristics (transition or transversion), their genome position (coding or non-coding), their coding influence (synonymous or non-synonymous) and their codon position (first, second or third). (B) SNP counts based on their SNP class. (C) SNP counts based on their functional group.

