

**Fig. S1** Genome collinearity analysis between HycuNPV isolates and other baculovirus genomes using Mauve software. Each colored block is genetically similar, with the profile height inside each block showing the similarity percentages. A block above the center line indicates that the aligned region is in the forward orientation relative to the first genome, a block below the center line indicates regions that align in the reverse-complement (inverse) orientation. Using HycuNPV-N9 as the reference, two blocks were inverted between the HycuNPV-HB and HycuNPV-BJ genomes.

