Supplementary Fig. 1. Nucleotide sequence alignment of Hebe copies depicted in Fig. 1. Dots indicate identity to the consensus sequence. Internal deletions are highlighted in yellow, and 3’ terminal deletions in light gray. Additional copies of the 72-bp tandem repeat in the 3’ UTR are highlighted in green and dark gray. The ATG codon and polyadenylation signal are underlined. Copies with deletions are marked by ∆.