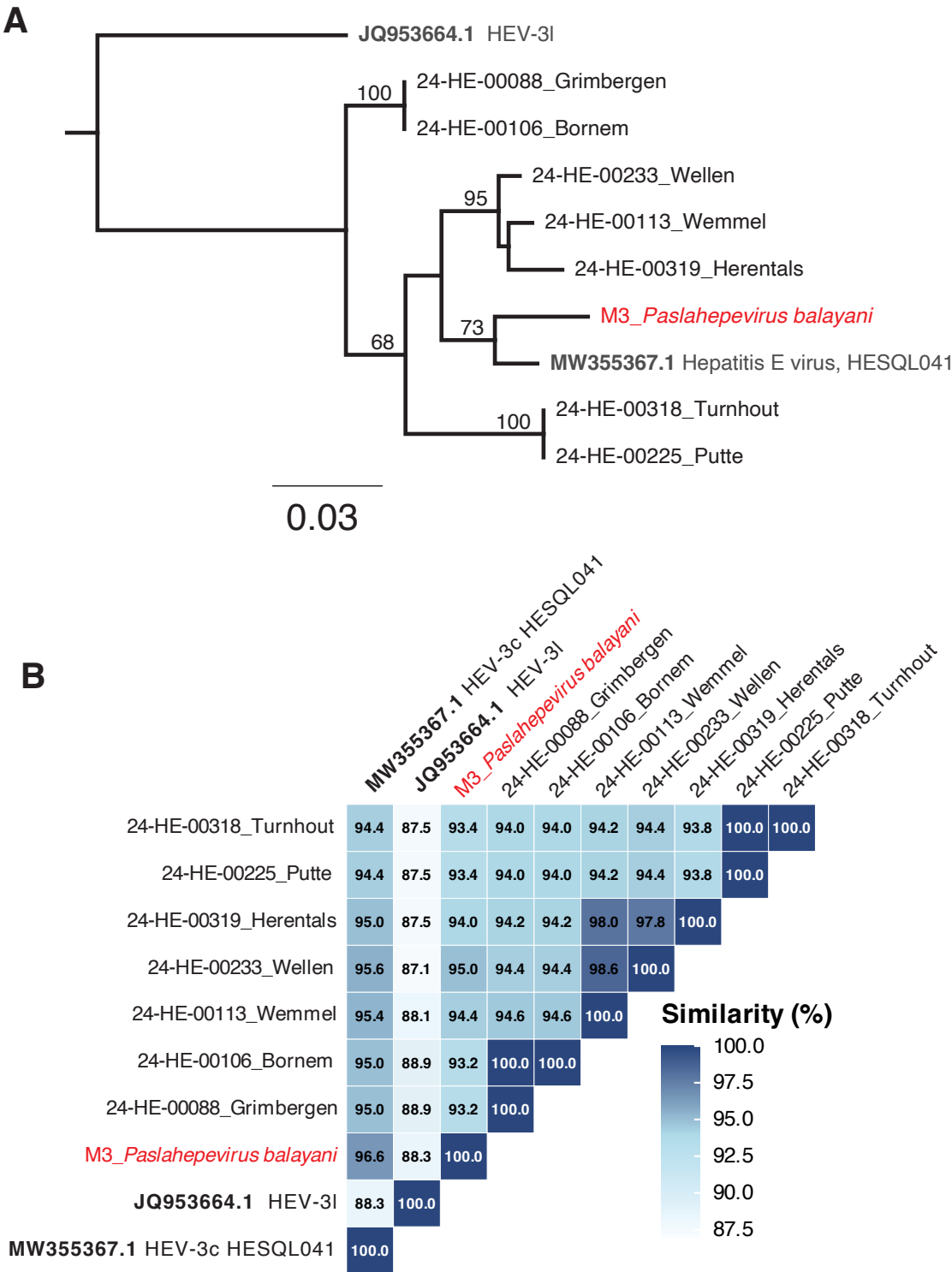


**Supplementary information Figure 1.** Insect-associated viruses identified in wastewater samples, on species level.

Supplementary information



**Supplementary information Figure 2. A.** Maximum-likelihood phylogenetic tree of 497 nucleotide long region of HEV genomes. Tree was constructed using Geneious 2025.0.3 PHYML with 100 bootstraps. Sequences originating from wastewater (*M3\_Paslahepevirus balayani*), human HEV-3c cases from Belgium in January 2024 (24-HE-xxxxx-Location) and sequences from GenBank (JQ953664 and MW355367) were used for analyses. **B.** Nucleotide similarity matrix of sequences used for phylogenetics analyses use for panel A.