



**Supplementary figure 5** Comparison of the longest viral MEGAHIT contigs obtained after implementation of ZWA2 versus the respective viral genomic sequences deposited in the NCBI GenBank database for the BioProject PRJNA806751. The examined sequences were annotated by BLASTn and their annotated regions are displayed here as colourful rectangles, which were drawn in scale and placed upon typically structured viral genomes (thick horizontal black lines) according to structural information sourced from top BLASTn hits during the annotation process of each virus. The diagonally shaded regions upon each viral genomic sequence depict areas which were not available in the GenBank sequences or in the assembled MEGAHIT contigs after ZWA2 compared to the typically structured viral genomes. The annotated names and lengths of the identified regions are displayed below each viral genomic sequence and expressed in nucleotides (nts), while their size and position were estimated according to their top BLASTn hits.