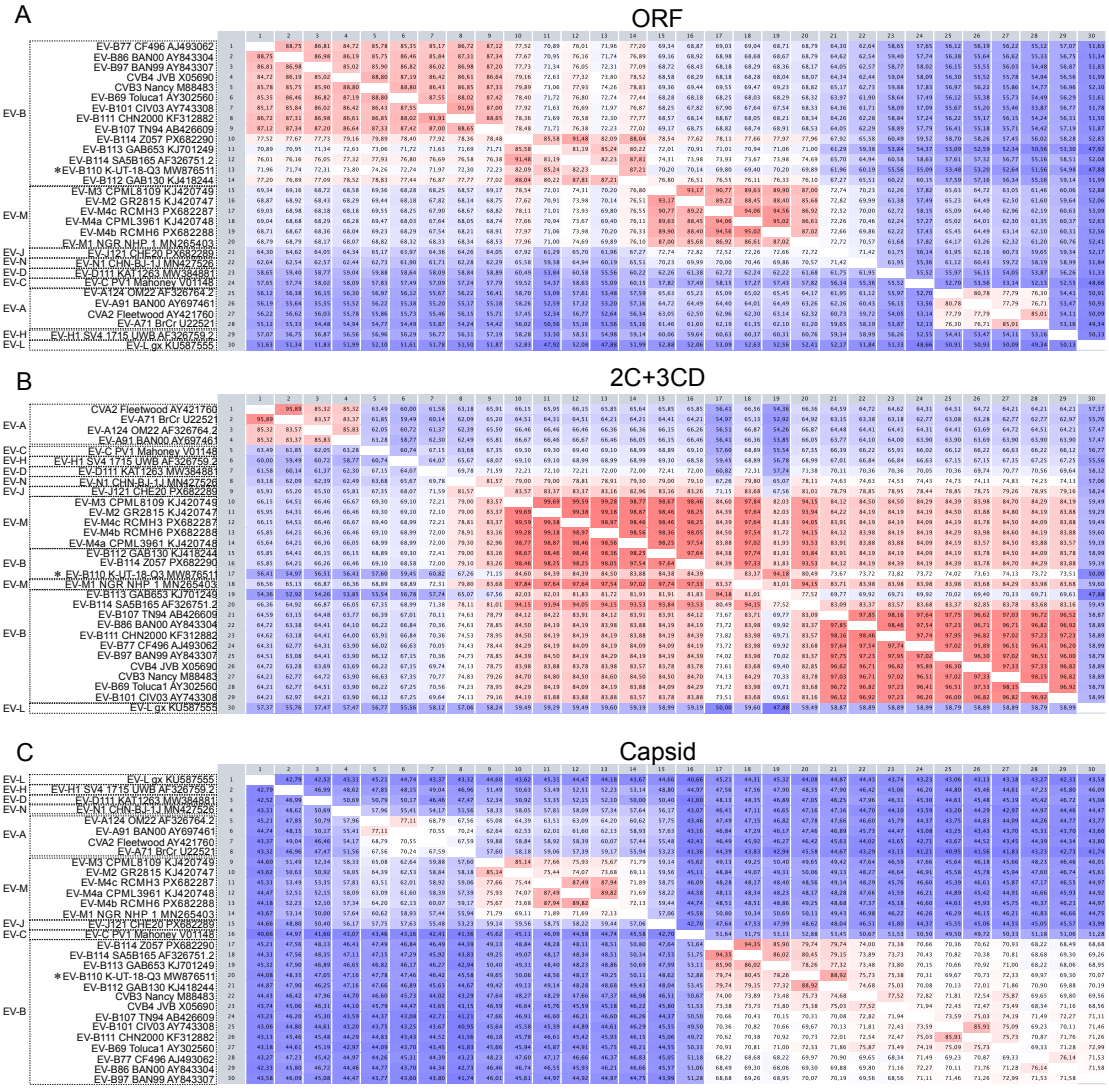


Species characterization of enterovirus M strains. Amino acid identity matrices of **(A)** the complete ORF, **(B)** the 2C+3CD and **(C)** the capsid sequences are shown. Multiple sequence alignments were done with MAFFT while translation of nucleotide sequences and identity matrices were computed using CLC Main Workbench v24. The asterisk (*) indicates the sequence where the last 399 nt are missing in the 3D gene.