

Figure S2. Alignment and genetic comparison of the C proteins from sunrhaviruses and tupaviruses. Multiple amino acid sequences alignment of the C proteins from the 14 sunrhaviruses (including the 7 newly bird-related viruses) or the 3 tupaviruses (with DUV, KLAV and TUPV), performed using Clustal Omega (default parameters, SnapGene, v. 5.3.2) and three different datasets (a = 11 sequences with BBOV, BEAV, GARV, HDV, KOLV, MTYV, NASV, OUAV, SJAV, SUNV and WCV; b = 3 sequences with DDV, KWA V and OVRV; c = 3 sequences with DURV, KLAV and TUPV). Aligned sequences were edited using MView (<https://www.ebi.ac.uk/Tools/msa/mview/>), with the corresponding amino acid color code (bright green: hydrophobic, dark green: large hydrophobic, purple: polar, bright blue: negative charge, dull blue: small alcohol, red: positive charge, yellow: cystein).

