

Figure S3. Alignment and genetic comparison of the SH proteins from sunrhaviruses and tupaviruses. Multiple amino acid sequences alignment of the SH 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). Due to the high genetic diversity, the 3 tupaviruses DUV, KLAV and TUPV compared to the 14 sunrhaviruses, they were aligned separately. 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: cysteine).

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BBOV_SH -MLVLILLAICFLAFKPRYVEWILFYILGHIHFGNTVLGTVNFFLWYVFNLPKQFMSKMFIDYQEFQSNSENLDILE-----
BEAV_SH MITLFLLLISLIVLLVRPRYVEWILFYMLGHYNVGATALYNTNFLFWYLFCDIPSRFLQNIQFQDMIEKYYQE-----
DURV_SH -MYVELLVLGFLFLCGQRIFLFGVLVLLGRFNLLWFVFDAIMFCMLWVFCKNLPSEVLRLTGDWLKPWSWESFQEEMYS-----
GARV_SH MIALFLLLTLVMVLRPRYVEWILFYMLGHYNVGLNALYNVNFVFWYLFCDIPSRFLNNVFGDMIEKYYQD-----
HDV_SH -MIIIFLILISLFLSKRIGALIAMYTLGYNAFGNIINYLTFFGWYIGVNLPHYKYLQHWSELVSEYQNSKRE-----
KLAV_SH -MLGEILIAIGICYLLGRRFFWGYLAYIAGQYNLLHYPLMIQFLLWLLFYNAPYQLWGLIWSTFQSSFDEFNPNPGEAAISPLDLPIYRRLGQK-
KOLV_SH -MLALILLSVCLLAFRPRYVEWILFYILGHIHFGETVPQTINFFLWYFFVNIPRQFMSNMFPVDYQSFYAQDQIFDYTE-----
MTYV_SH MIALFLLIILLILIIIRPRYVEWILFYMLGHYNVGMTALYNVNFVFWYLFCDIPSRFMHNAFGDMIEKYYQE-----
NASV_SH -MIALLVILLIVTIIKPRFVEWVIFYGLGHYQFGNLLLYNLFGLWYLFPHLPKQISERWFGDLIEQYYAME-----
OUAV_SH MIVGIIILALLCLVFKPRVAEWILFYSLGHLQFGTAILQNFSSFFLWYVFFYHLPTKVITNIFGDVVEQYYMTE-----
SNAV_SH -MIALLVILLIVTVVKPRFVEWVIFYGLGHYQFGNLLLYNLFALWYLFPHLPKTWSDRWFGDIMEQYYSTE-----
SUNV_SH -MILLVVLILFFGMLYKRLSFLMMAYLLGYNVFVGSVITYGSFFIWLFFYLLPSKWMGAGFAAIVESYNKEYAEWVSIE-----
TUPV_SH -MITTLIIIGAFLVGPRTFKFVLAAYLLGYNAFGPPLQIVQFMVWLIIIYFPKKFFSLGWYFCHDAFSSYFGDPNGGQLPVSTKPHSLTDMID
WCV_SH -MIVVIIIVLLALIIISKRLSAFIAMTYTLGYNAFGSLIINYLTFFGWYVGVNLPYKYLQHWSELVAEYRNSQ-----

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DDV_SH MGFQLNEKKTEVTMSAFWKVFFALVLFVSYWNNPEVASKTATTLFDMII-----GVMRYILAYIFPKGSPPCPPEVKSPYP
KWAV_SH -----MAGWKLLFVLLIVLYWHNPEGVTSLMKSSLNIMETILAEPKRVVS--FFTTPPCPPCPQCLVKTP
OVRV_SH -----MFWKVFFALVLFVSYWNNPDVASRTATTIFDMGL-----LATRYIASYILPASACPPCPPEVHAPLP

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