Tree scale: 0.1

Family ICTV

- Ackermannviridae
- Aggregaviridae
- Assiduviridae
- Autographiviridae
- Autolykiviridae
- Casjensviridae
- Chaseviridae
- Corticoviridae
- Crevaviridae
- Demerecviridae
- Drexlerviridae
- Duneviridae
- Finnlakeviridae
- Forsetiviridae
- Guelinviridae
- Helgolandviridae
- Herelleviridae
- Intestiviridae
- Kwiatkowskiviridae
- Kyanoviridae
- Matshushitaviridae
- Mesyanzhinovviridae
- Molycolviridae
- Naomviridae
- Orlajensenviridae
- Pachyviridae
- Peduoviridae
- Pervagoviridae
- Rountreeviridae
- Salasmaviridae
- Schitoviridae
- Simuloviridae
- Steigviridae
- Straboviridae
- Suoliviridae
- Tectiviridae
- Vilmaviridae
- Winoviridae
- Zierdtviridae
- Zobellviridae

Order ICTV

- Crassvirales
- Halopanivirales
- Kalamavirales
- Lautamovirales
- Vinavirales
- unasig

Class ICTV

- Caudoviricetes
- Laserviricetes
- Tectiliviricetes
- Ainoaviricetes

Phylum ICTV

- Dividoviricota
- Preplasmiviricota
- Uroviricota

Kingdom ICTV

- Bamfordvirae
- Helvetiavirae
- Heunggongvirae

Realm ICTV

- Duplodnaviria
- Varidnaviria

Fig. S1: Circular representation of the PSC-based genome tree for the Fam_DB dataset. The annotation circles encode the ICTV taxonomy for each phage genome, as follows from inner to outer circles: family, order, class, phylum, kingdom, and realm. The tree was split using a distance threshold of 0.9 and the resulting VGCs are encoded by different branch colors

Fig. 5c: Rectangular representation of the PAC-based genome tree for the Fam_DB dataset. The tree was split using a distance threshold of 0.5 and the resulting OCLs are encoded by different branch colors.