

Supplementary Figure S1

Midpoint-rooted phylogenetic tree of $n = 269$ *S. aureus* phages based on protein distances between genomes.

The three external rings indicate the family, subfamily and genus rank, respectively. Genomes with available ICTV taxonomy are shown as dots on tip ends.

(1) Taxonomy source

● ICTV

(2) Family

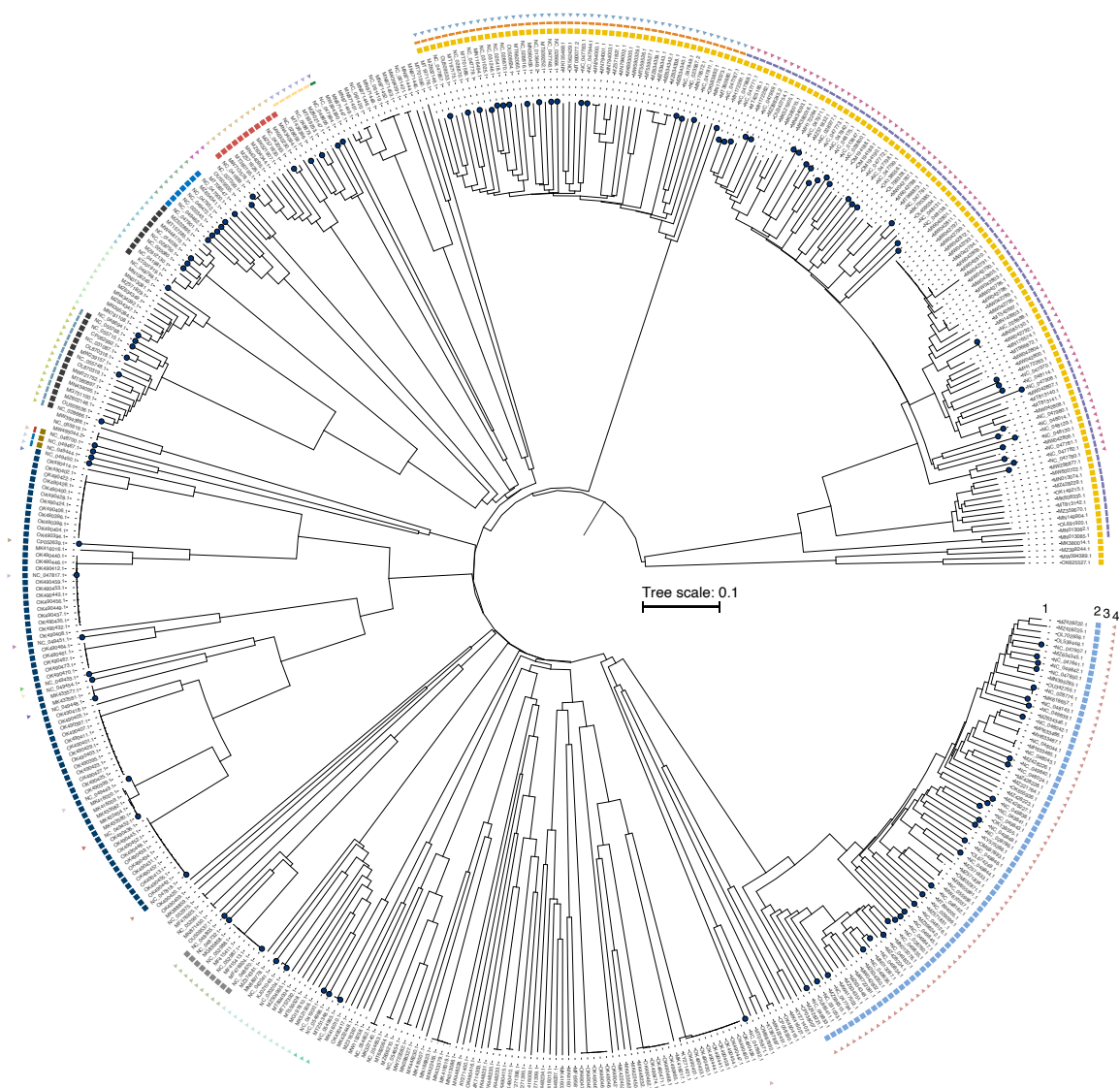
Ackermannviridae
 Autographiviridae
 Casjensviridae
 Demereciviridae
 Drexelviridae
 Peduoviridae
 Schitoviridae
 Straboviridae

(3) Subfamily

Enquatrovirinae
 Humphriesvirinae
 Slopekvirinae
 Stephanstirmvirinae
 Studiervirinae
 Tevenvirinae
 Vequintavirinae

(4) Genus

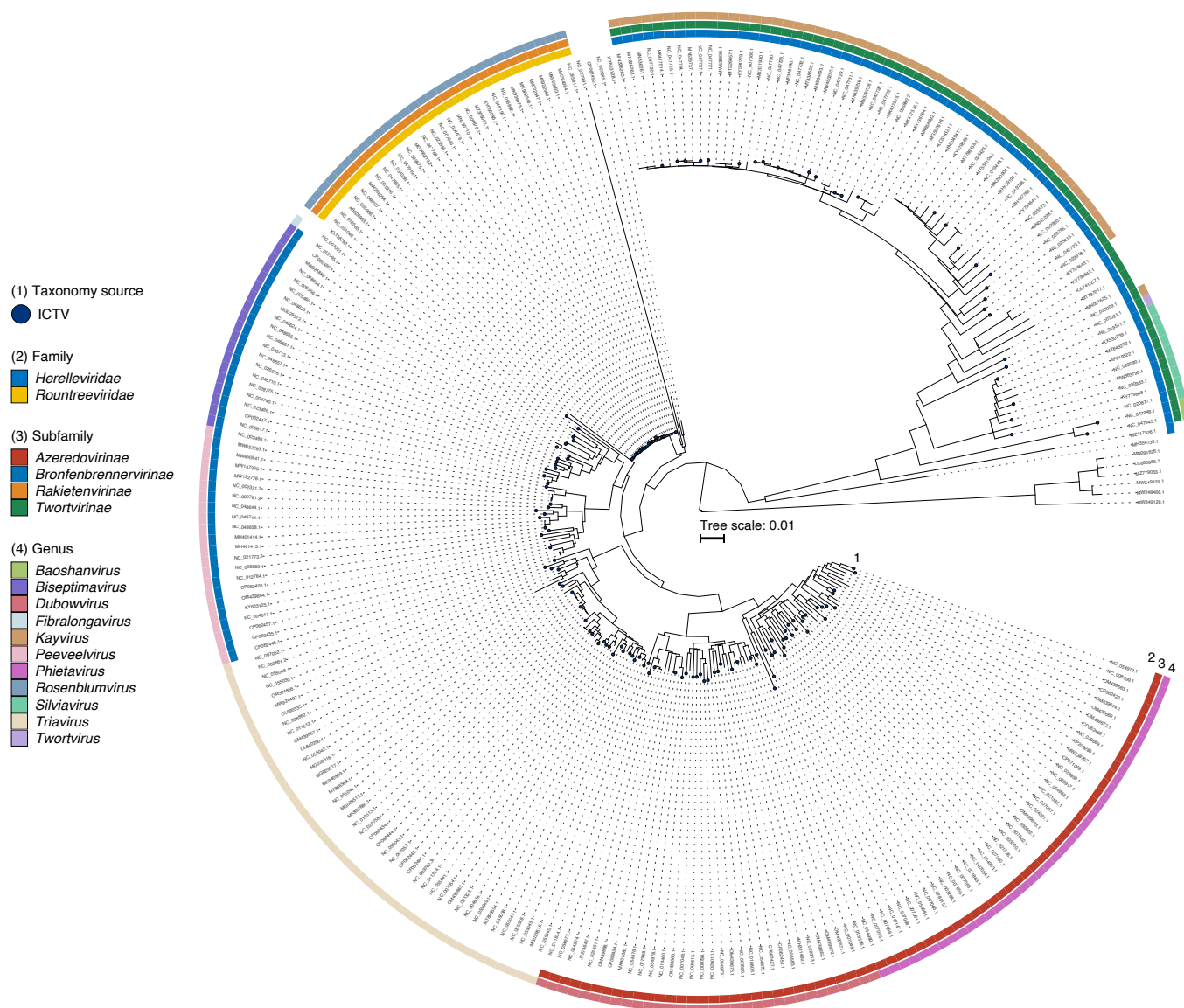
Alcyoneusvirus
 Dagavirus
 Drulisvirus
 Elveevirus
 Felsduovirus
 Gegavirus
 Gegevirus
 Jedunavirus
 Jiaodavirus
 Kapieceevirus
 Kaypocavirus
 Lastavirus
 Marfavirus
 Mydovirus
 Phapecocravirus
 Przondovirus
 Pylasvirus
 Reginaelenavirus
 Reipivirus
 Slopekvirus
 Sortsnevirus
 Sugarlandvirus
 Taipeivirus
 Vimunumvirus
 Webervirus
 Yonseivirus
 Yulgyerivirus



Supplementary Figure S2

Midpoint-rooted phylogenetic tree of $n = 480$ *K. pneumoniae* phages based on protein distances between genomes.

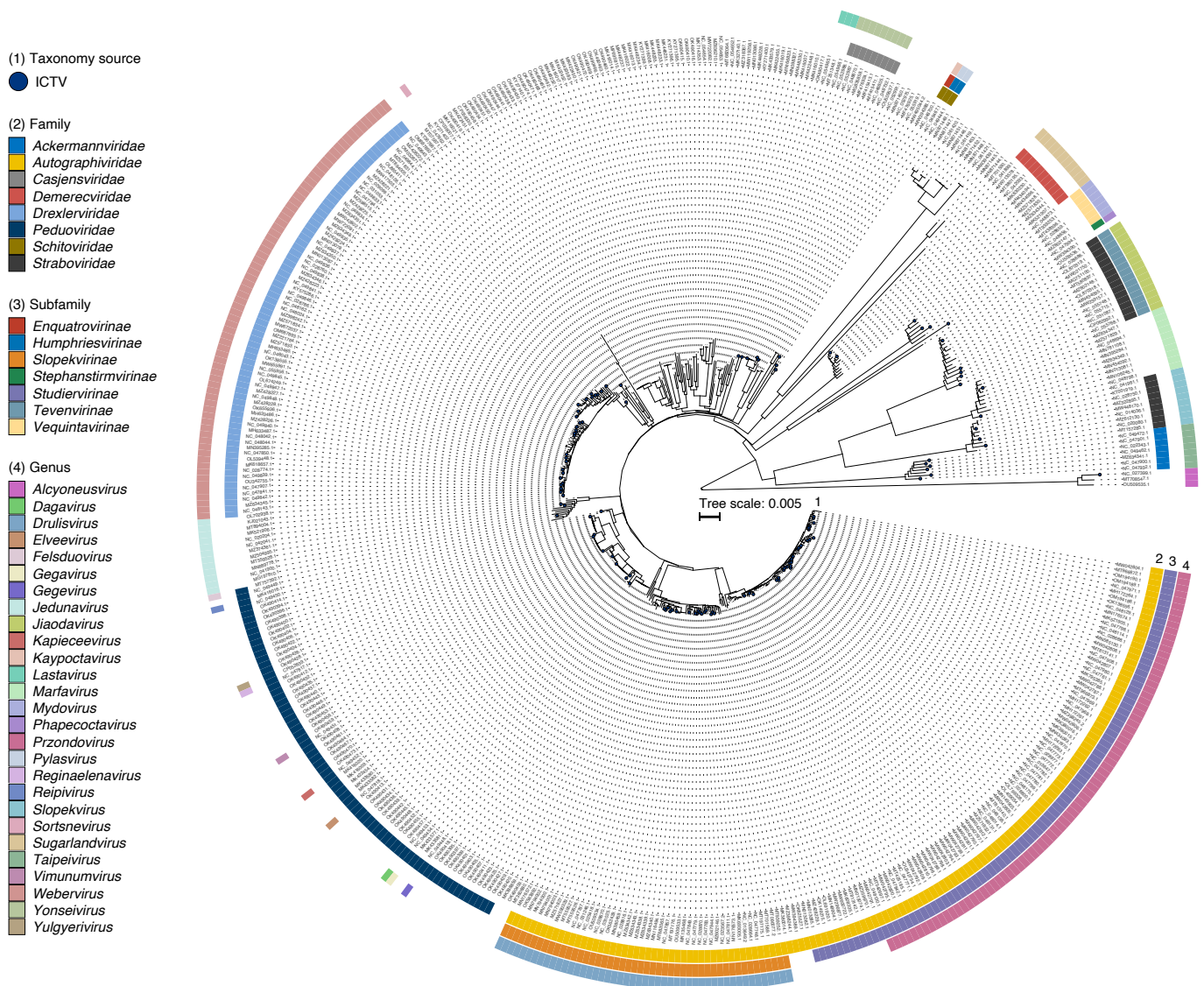
The three external rings indicate the family, subfamily and genus rank, respectively. Genomes with available ICTV taxonomy are shown as dots on tip ends.



Supplementary Figure S3

Midpoint-rooted phylogenetic tree of $n = 269$ *S. aureus* phages based on pairwise distance matrix from gene presence/absence data.

The three external rings indicate the family, subfamily and genus rank, respectively. Genomes with available ICTV taxonomy are shown as dots on tip ends.



Supplementary Figure S4

Midpoint-rooted phylogenetic tree of $n = 480$ *K. pneumoniae* phages based on pairwise distance matrix from gene presence/absence data.

The three external rings indicate the family, subfamily and genus rank, respectively. Genomes with available ICTV taxonomy are shown as dots on tip ends.