SUPPLEMENTARY MATERIAL

A metagenomic collection of 19,778 viruses reveals the diverse virome of the chicken gut

Johan S. Sáenz[1,2], Timur Yergaliyev[1,2], Bibiana Rios-Galicia[1,2], Jana Seifert[1,2] & Amelia Camarinha-Silva[1,2]

[1]Institute of Animal Science, University of Hohenheim, Emil-Wolff-Str. 6-10, 70599 Stuttgart, Germany

[2]HoLMiR—Hohenheim Center for Livestock Microbiome Research, University of Hohenheim, Leonore-Blosser-Reisen Weg 3, 70599 Stuttgart, Germany

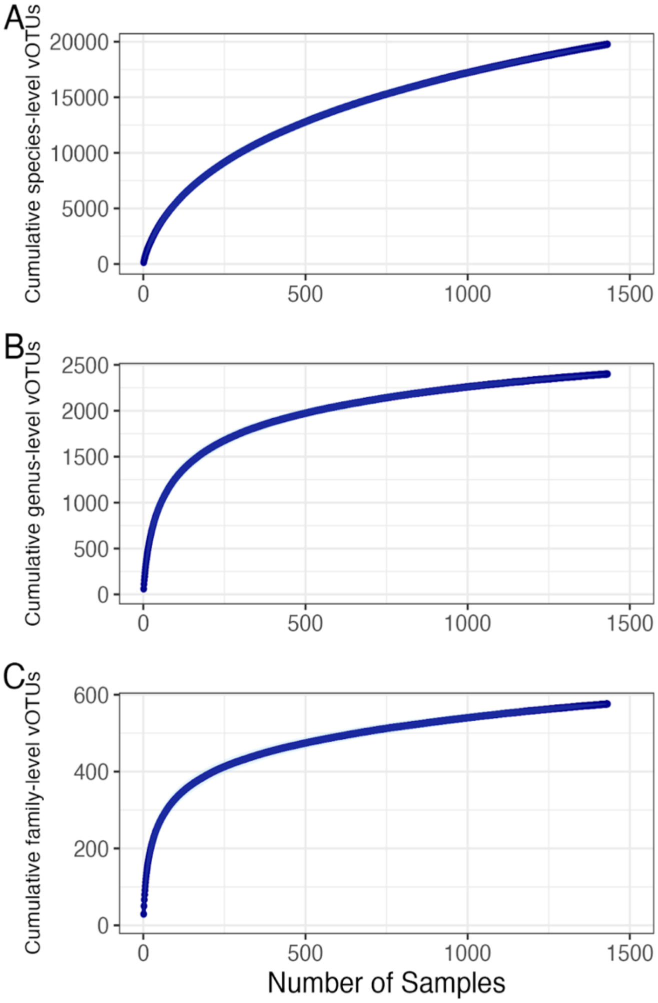

Figure S1. Saturation curves of viral diversity across taxonomic levels. Accumulation curves show the cumulative number of viral operational taxonomic units (vOTUs) detected at the species (A), genus (B), and family (C) levels as a function of the number of metagenomic samples analyzed.

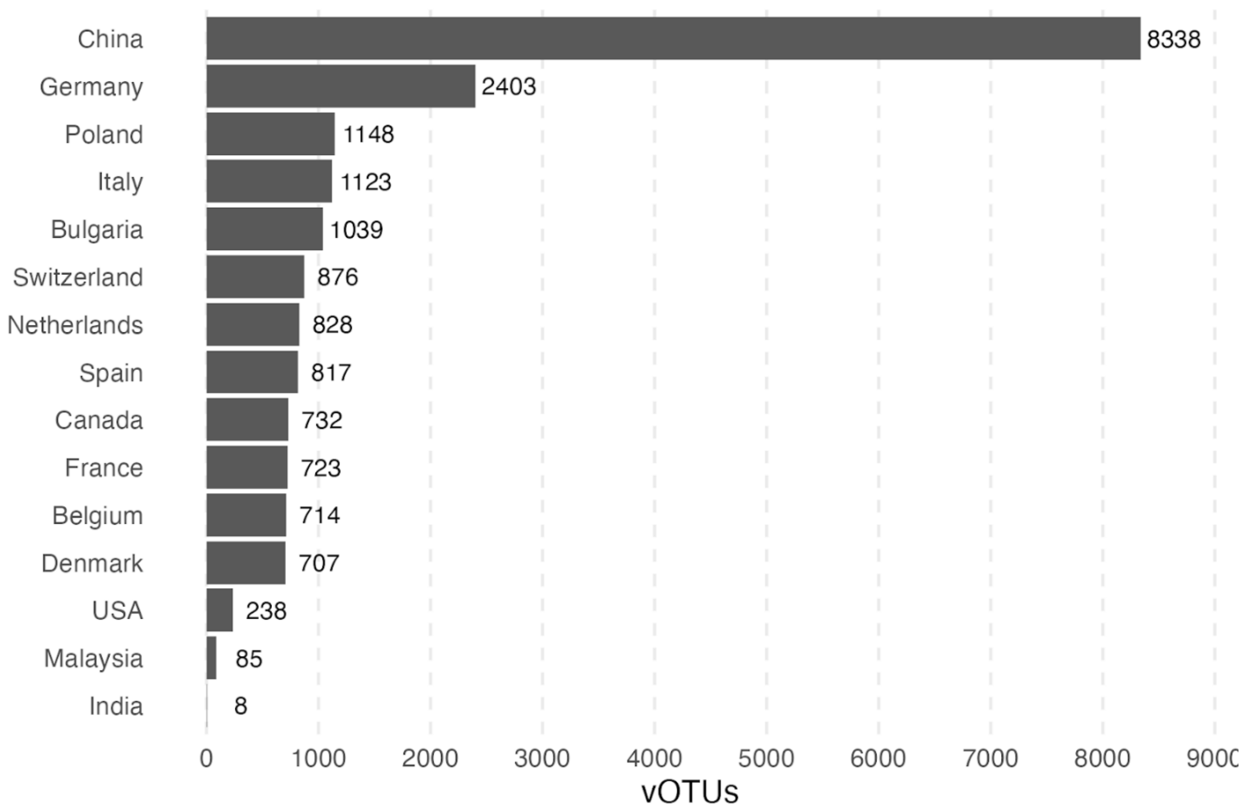

Figure S2. Number of species-level vOTUs (n=19778) mined per country of sample origin.

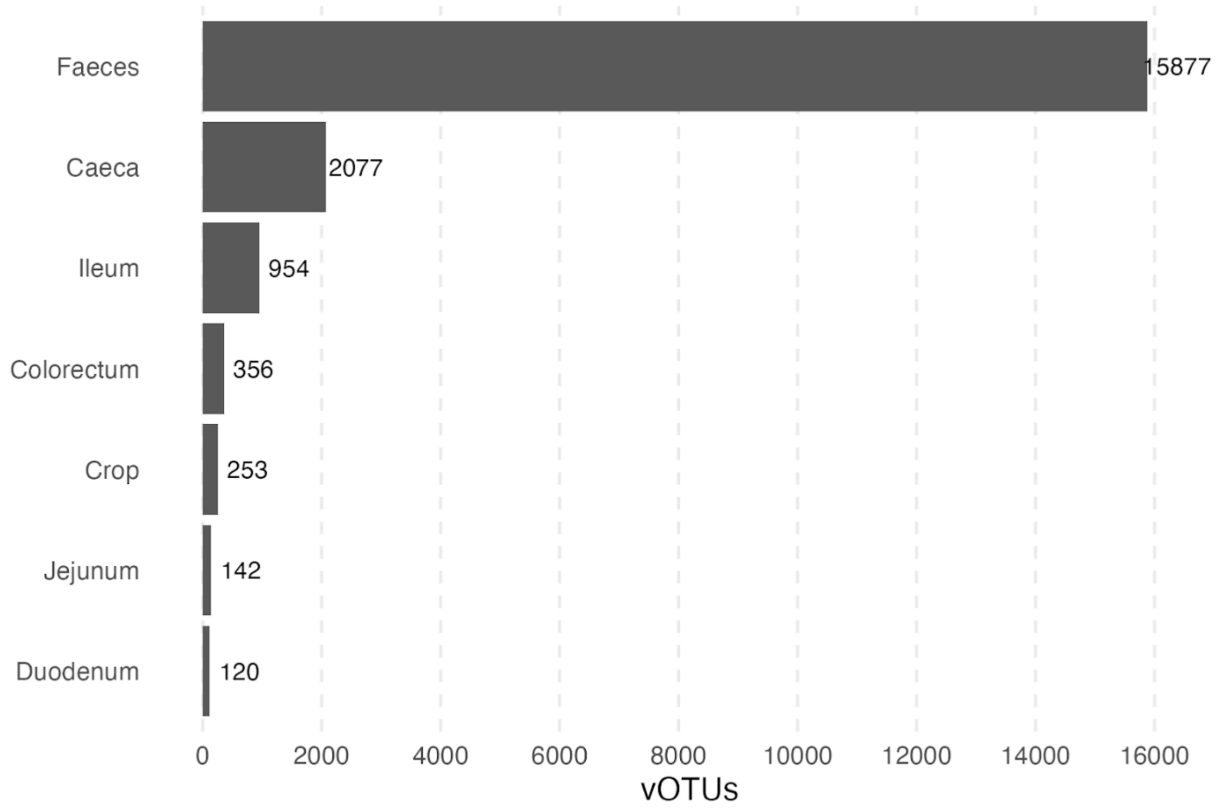

Figure S3. Number of species-level vOTUs (n=19778) mined per gastrointestinal region.

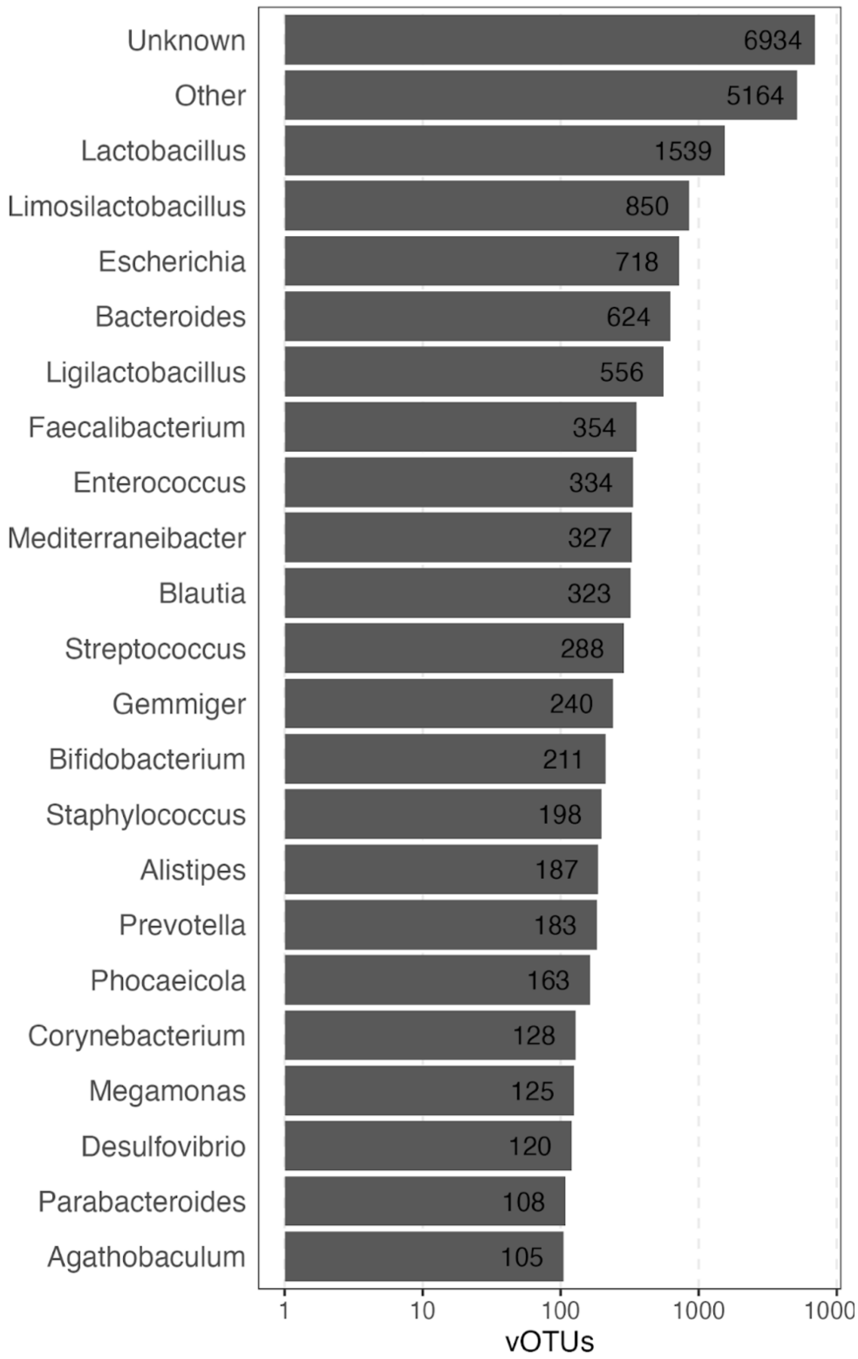

Figure S4. Number of species-level vOTUs linked to a host, at genus levels, using Integrated Phage HOst Prediction (iPHoP).

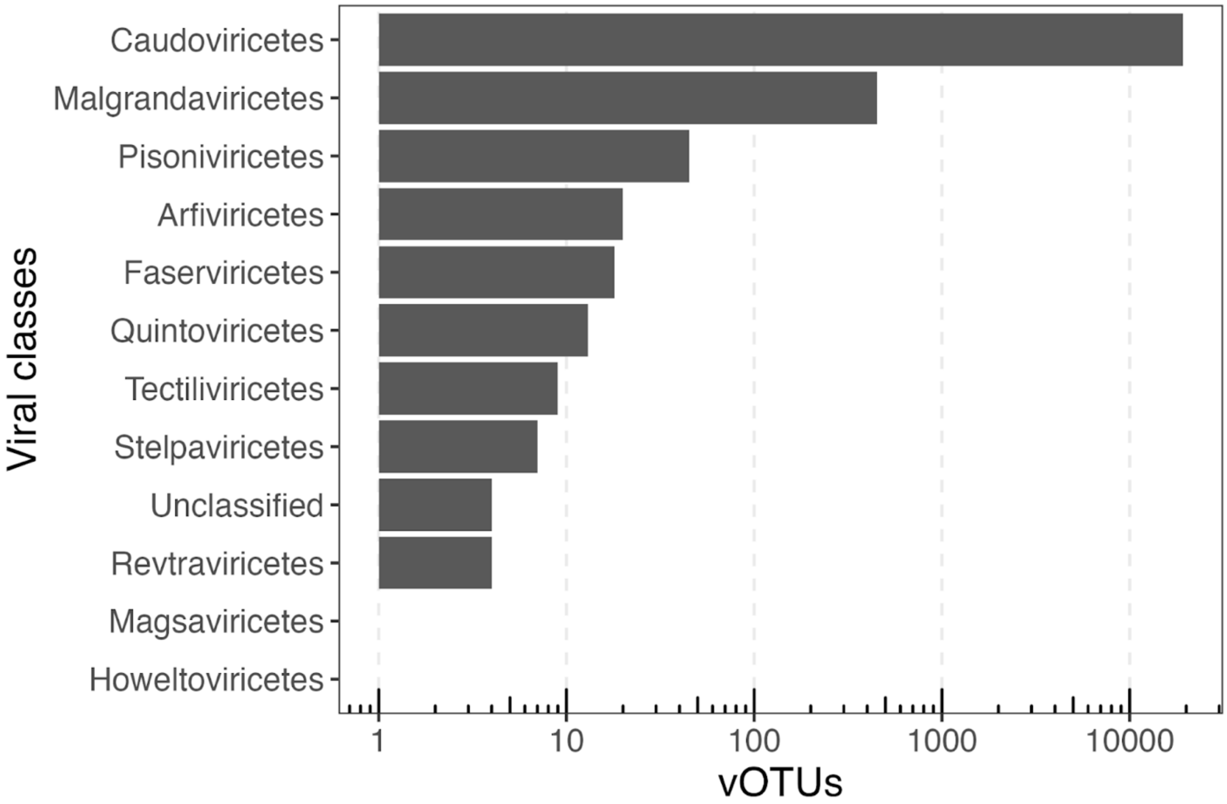

Figure S5. Number of species-level vOTUs by predicted viral class. X-axis is depicted in logarithmic scale.

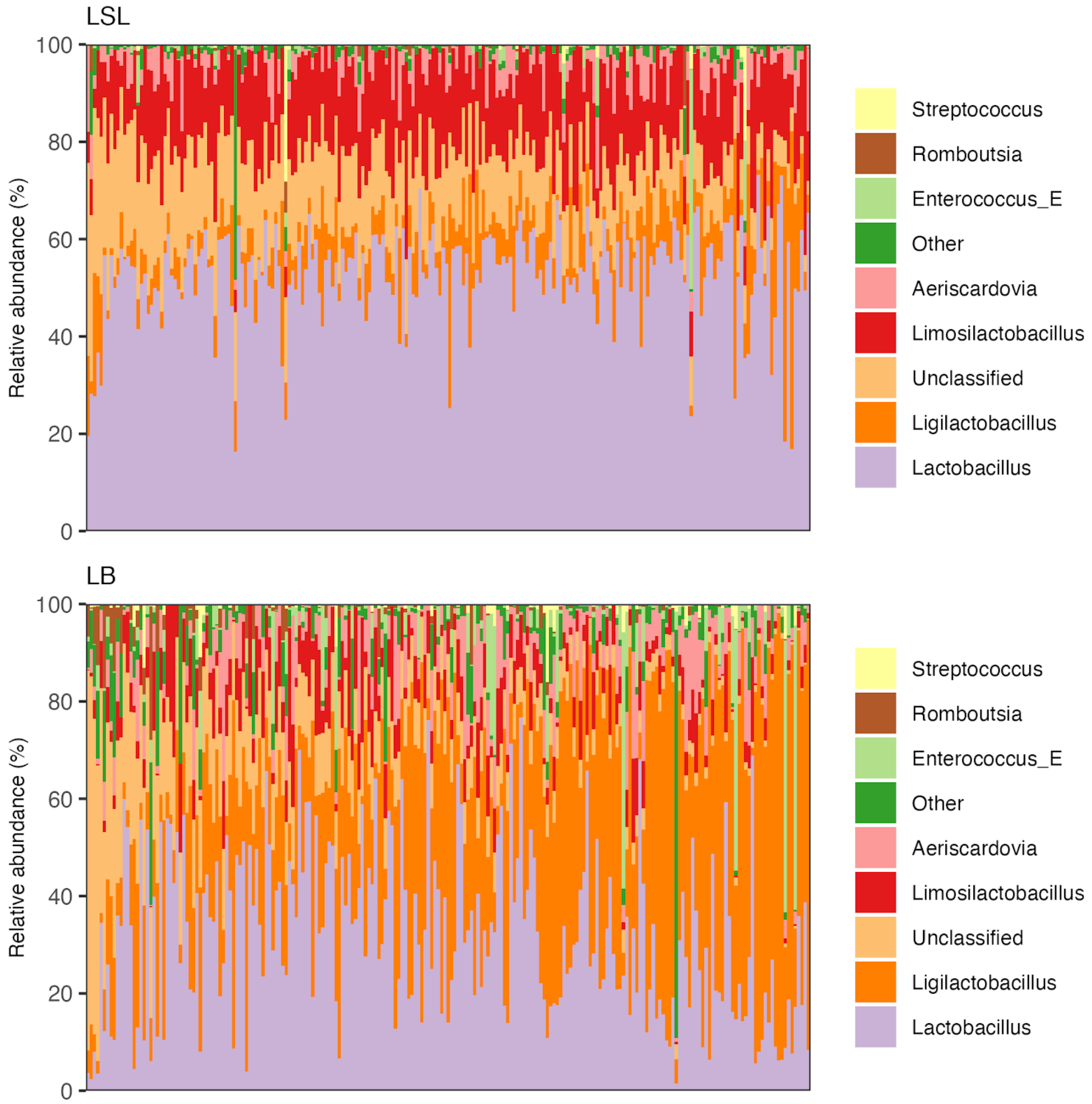

Figure S6. Abundance of vOTUs by host across 435 samples of two distinct chicken breeds, LSL (n=216) and LB (n=219).