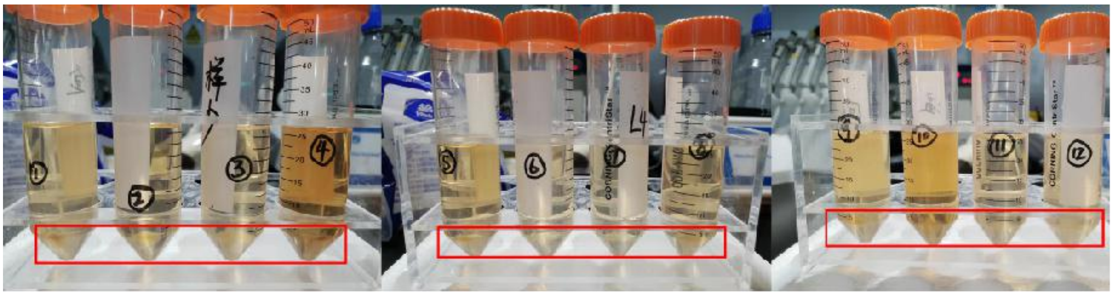

Figure S1. Image of partial enrichment of pig fecal virus-like particles.

Circled in red are pig virus-like particles.

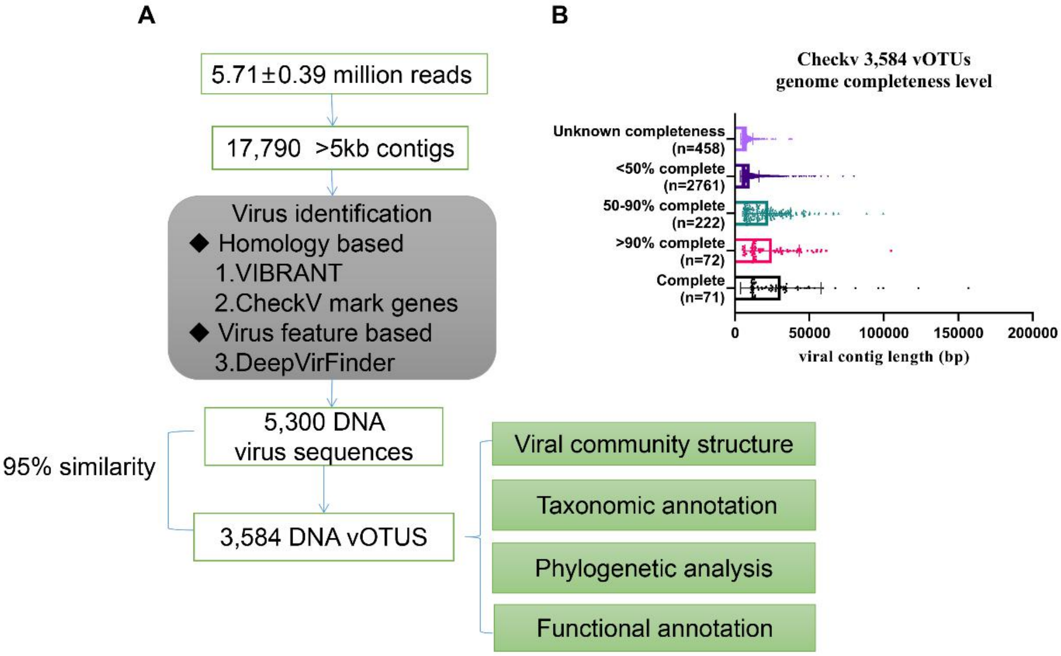

Figure S2. Analysis process and genomic quality assessment of pig gut virome.

(A) Bioinformatics process for pig gut virome analysis.

(B) Statistics of viral genome completeness and size.

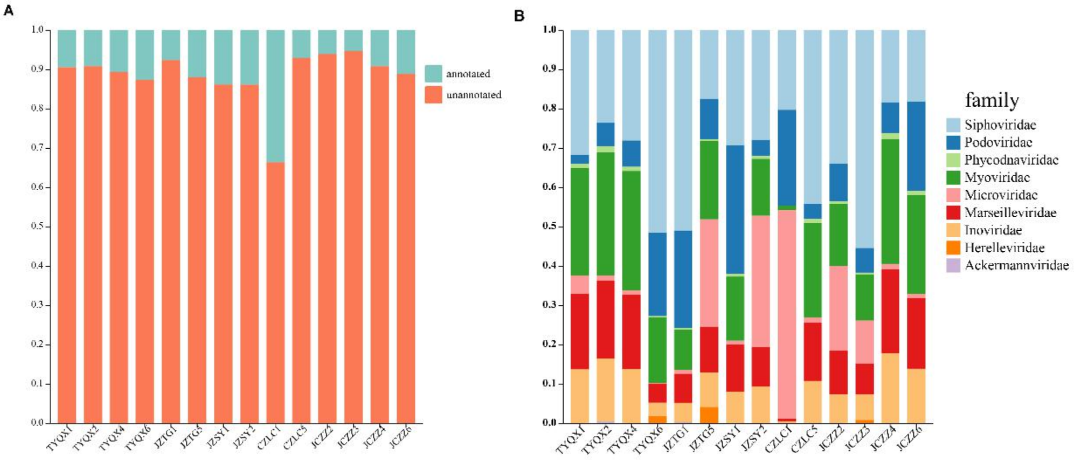

Figure S3. Annotation of 14 pig gut viromes at the family level.

(A) Proportion of 14 pig gut viromes annotated and unannotated at the family level.

(B) Composition of gut virome at the family level based on annotated vOTUs in 14 pigs from five farms.

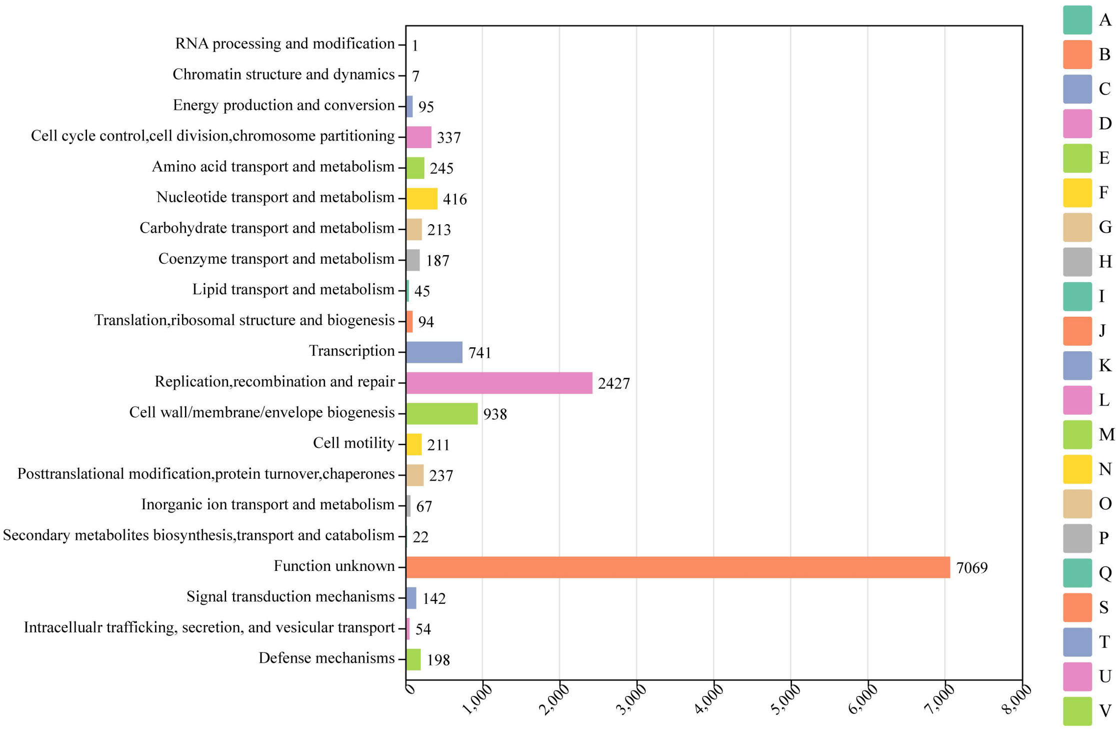

Figure S4. Functional annotation of the clusters of orthologous groups(COGs) information for pig gut viromes.

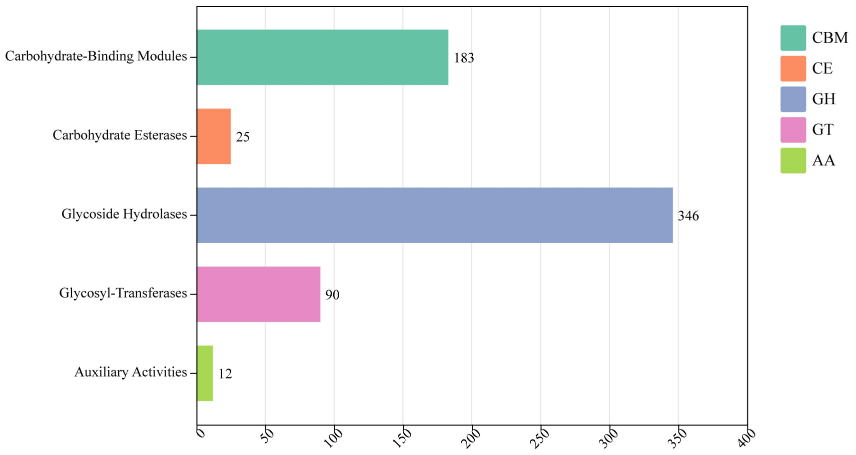

Figure S5. Annotation of pig gut viral carbohydrate–metabolism-related ORFs based on dbCAN database.

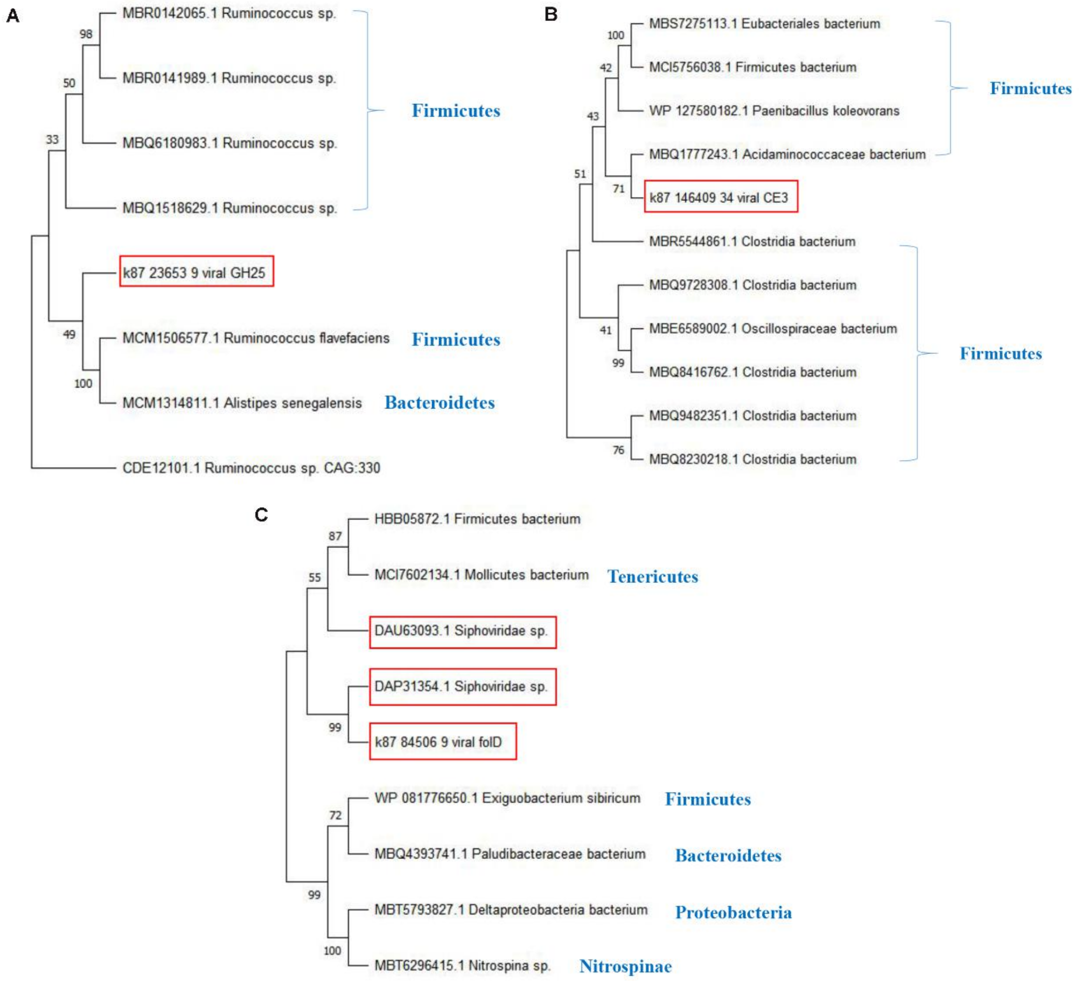

Figure S6. Phylogenetic tree of viral AMGs associated with carbon metabolism.

(A) Phylogenetic tree of the viral GH25 gene.

(B) Phylogenetic tree of the viral CE3 gene.

(C) Phylogenetic tree of the viral folD gene.

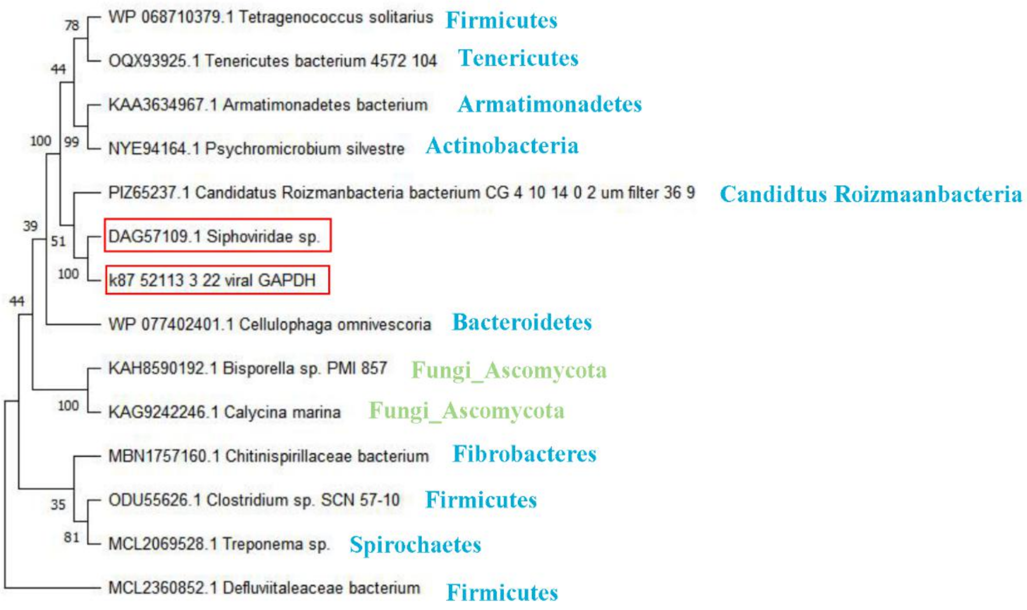

Figure S7 Phylogenetic tree of viral AMGs associated with carbon metabolism.
Phylogenetic tree of the viral GAPDH gene.

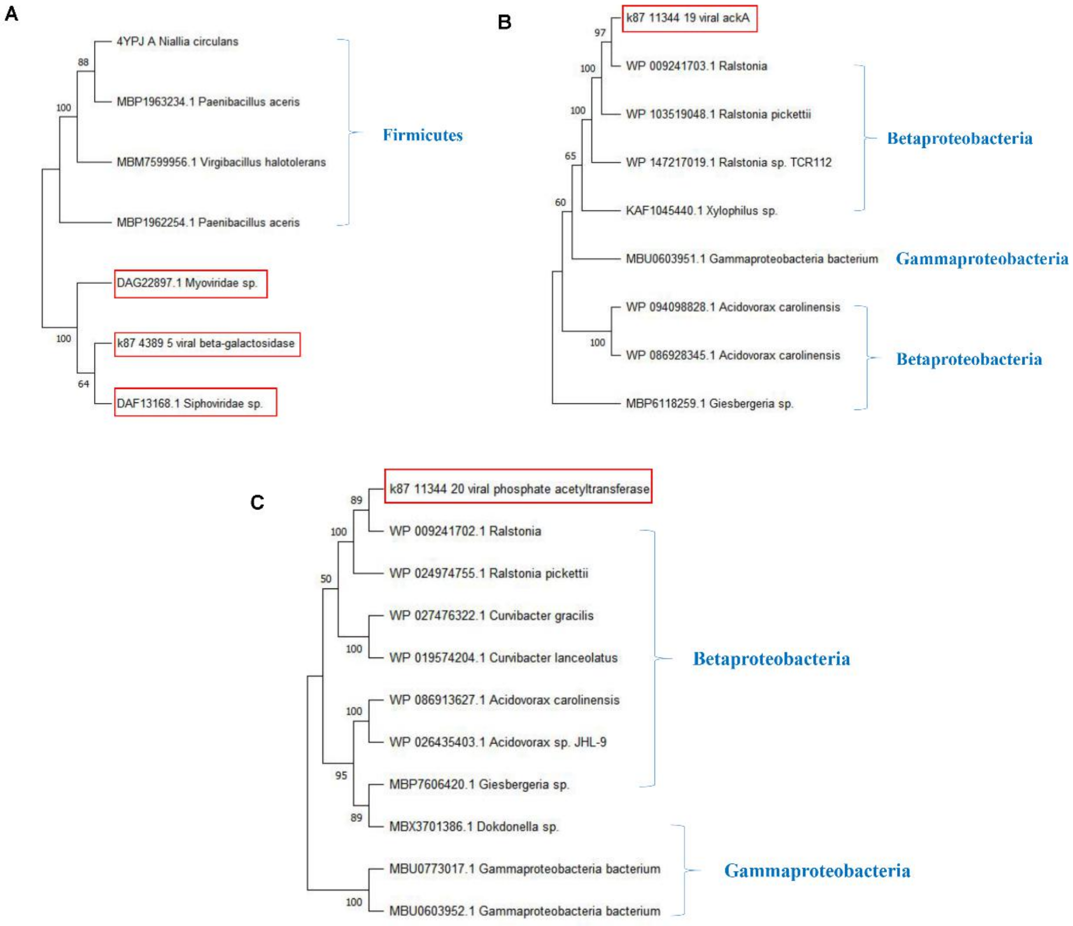

Figure S8. Phylogenetic tree of viral AMGs associated with carbon metabolism.

(A) Phylogenetic tree of the viral beta-galactosidase gene.

(B) Phylogenetic tree of the viral ackA gene.

(C) Phylogenetic tree of the viral phosphate acetyltransferase gene.