

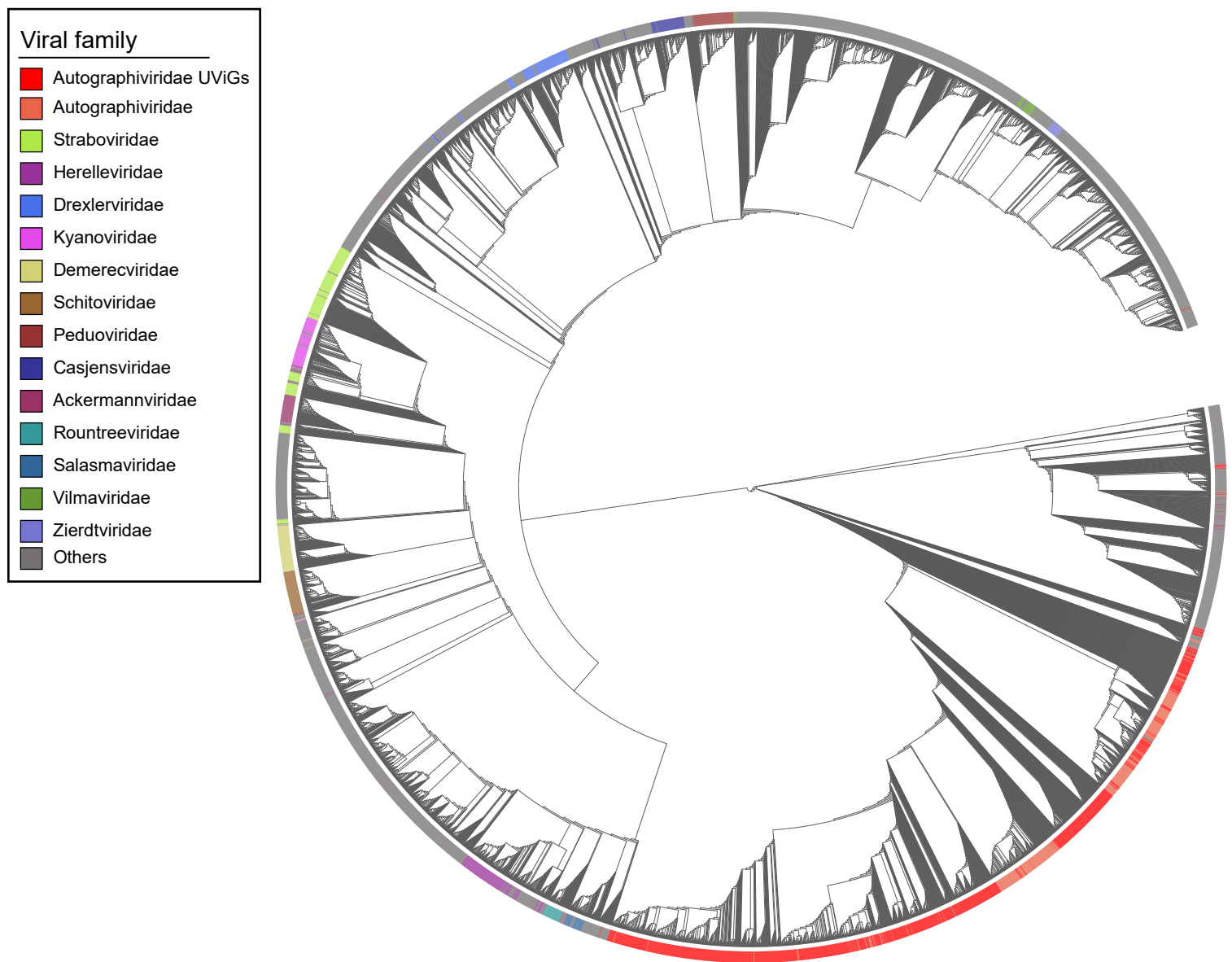


Fig. S1. The genome-wide proteomic tree was constructed using VipTree. The colored outer ring represents viral family classifications of the reference phage genomes and the UViGs recovered in this study.

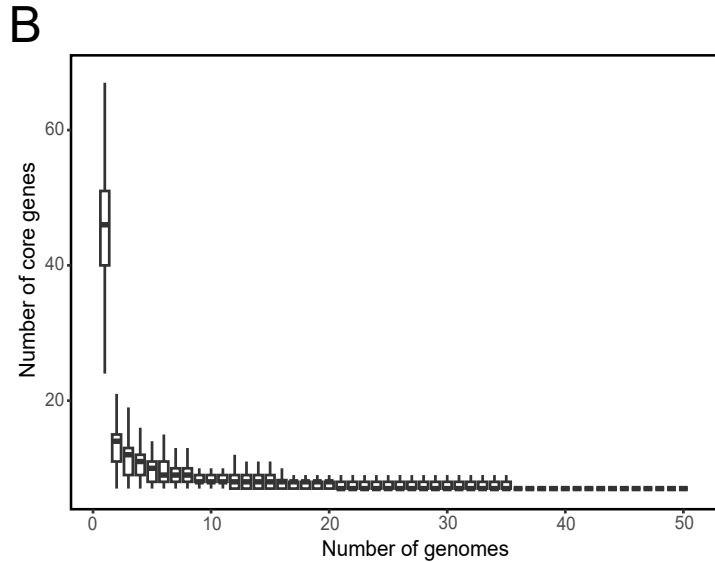
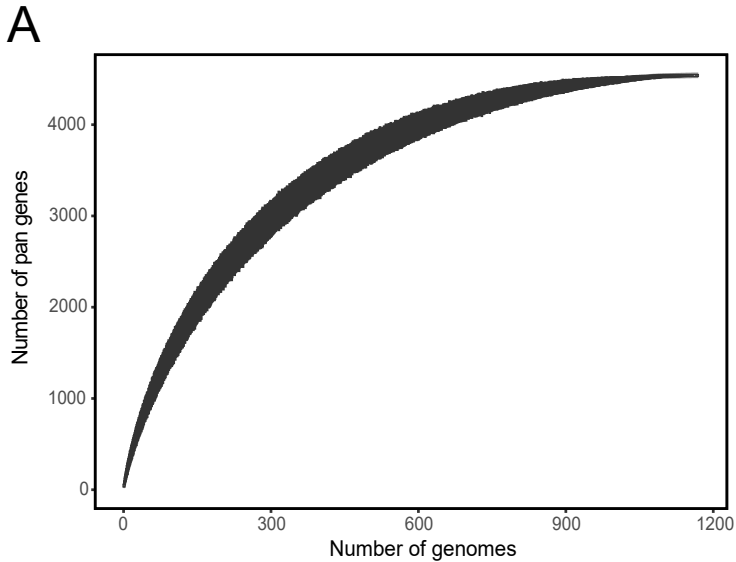


Fig. S2. Accumulation curves of the marine *Autographiviridae* pan-genome and core genome as a function of analyzed *Autographiviridae* phages. (A) pan-genome, (B) core-genome.

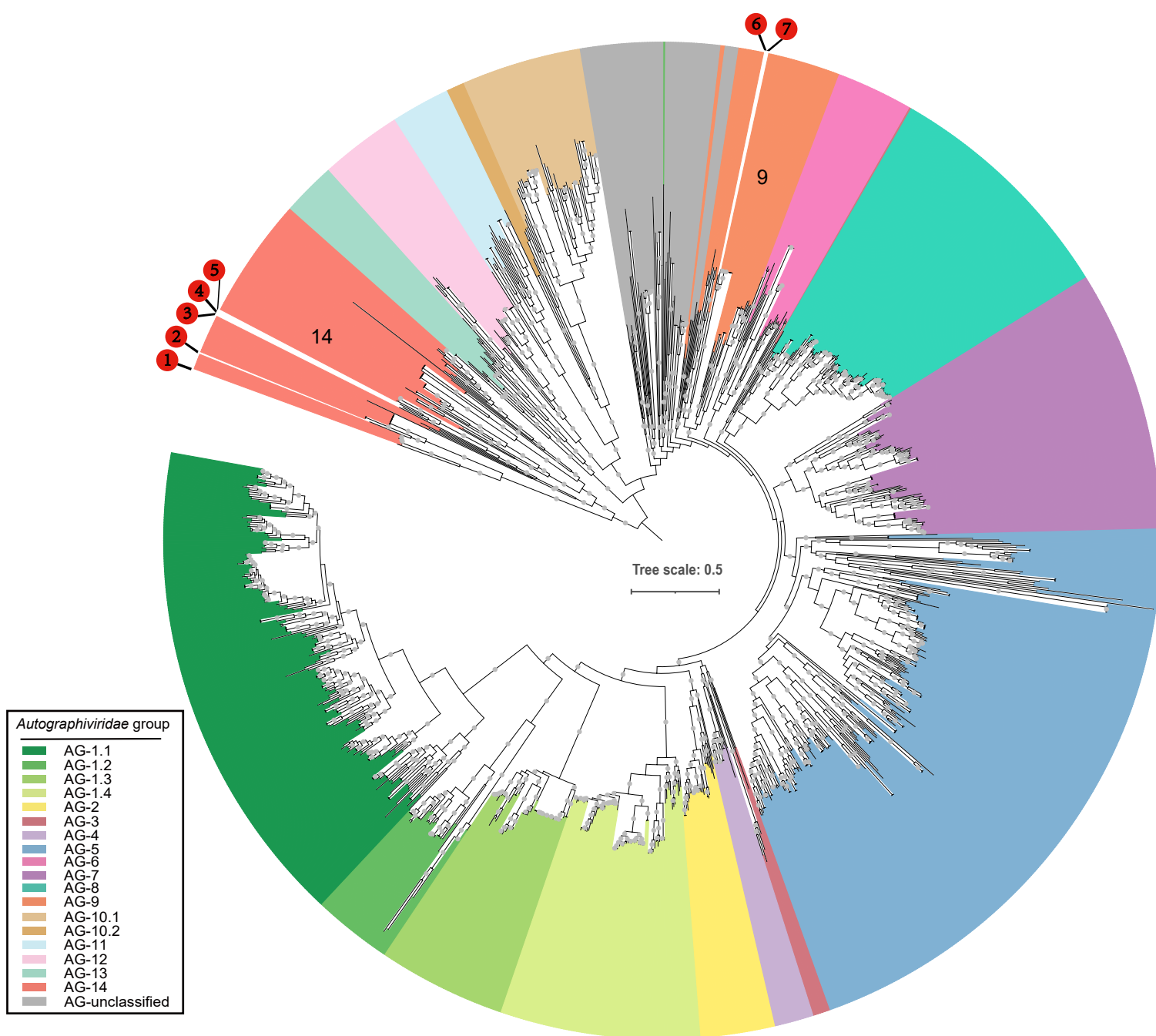
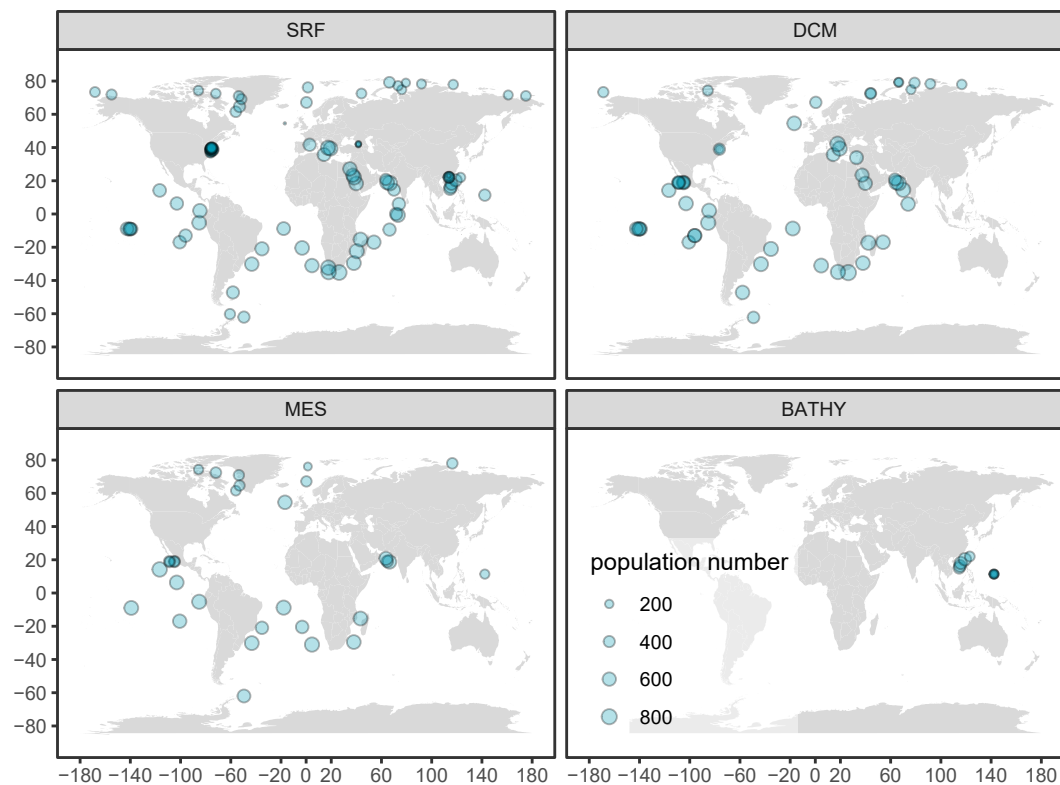
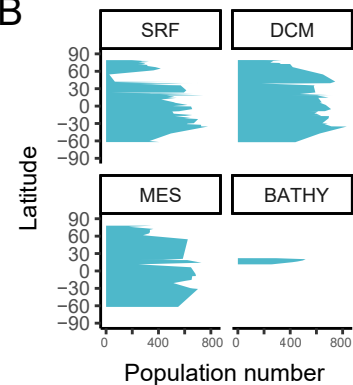


Fig S3. Phylogenomic analyses of marine *Autographiviridae* phages and non-marine representative *Autographiviridae* phages. A maximum-likelihood tree was constructed using concatenated sequences of seven core genes. Maximum-likelihood analysis was performed using IQ-TREE. The numbers within the red circles indicate non-marine genomes. The numbered red circles indicate non-marine viral genomes with their corresponding subfamilies: 1. *Slopekvirinae* (Klebsiella phage KpV71); 2. *Beijerinckvirinae* (Acinetobacter phage APK09); 3. *Molineuxvirinae* (Salmonella phage SP6); 4. *Colwellvirinae* (Vibrio phage VEN); 5. *Colwellvirinae* (Vibrio phage Vp670); 6. *Studiervirinae* (Kluyvera phage Kvp1); 7. *Studiervirinae* (Escherichia phage T7).

A



B



C

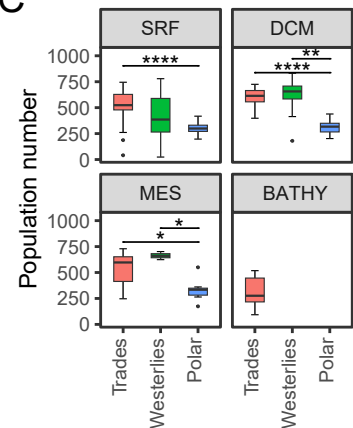


Fig. S4. (A) Map of the number of *Autographiviridae* populations detected in viromes of different depths. The size of the dots represents the number of *Autographiviridae* populations. (B) Area plot of the population number with latitude on the y-axis in different depths. (C) Boxplot of the number of *Autographiviridae* populations detected in viromes of different depth and climate zones. The significance of pairwise comparisons calculated using *t*-test was shown with the asterisk corresponding to the *p*-value (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$).

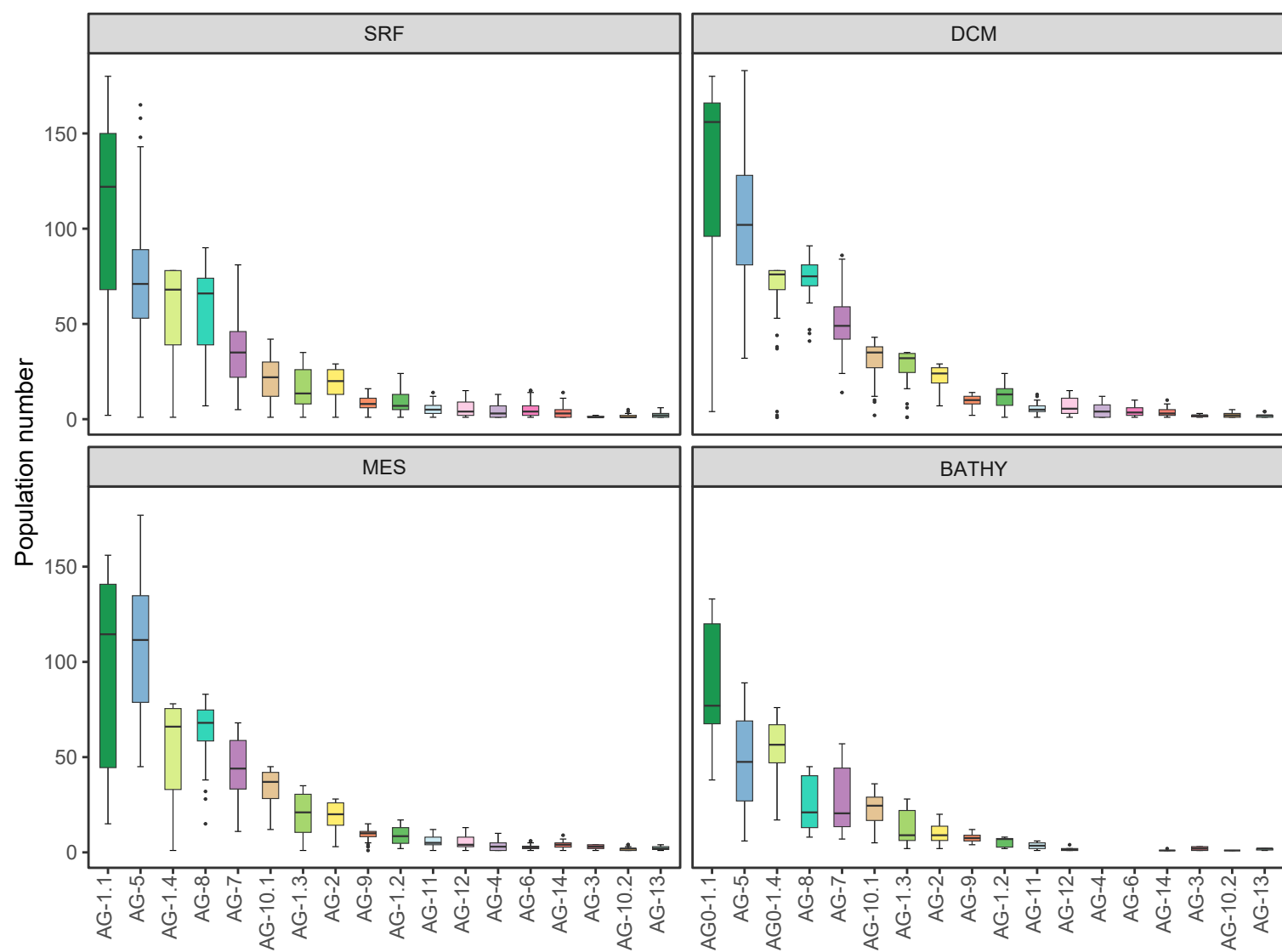


Fig. S5. Boxplot showing the number of populations of each *Autographiviridae* group in different ocean layers. (A) SRF; (B) DCM; (C) MES; (D) BATHY.

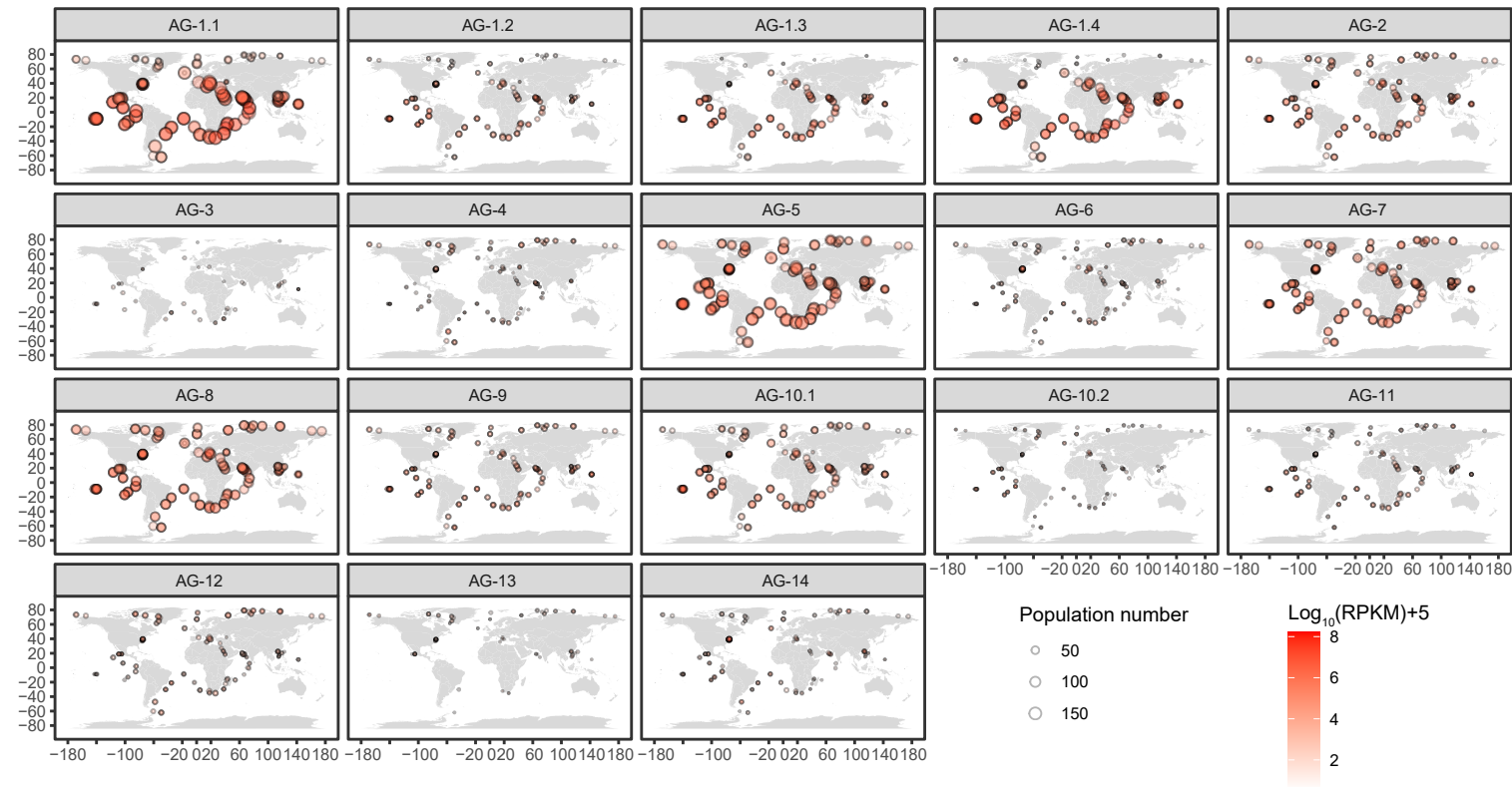


Fig. S6. Map of the number of populations of each *Autographiviridae* group detected in each virome. The size of the dots represents the number of *Autographiviridae* populations.

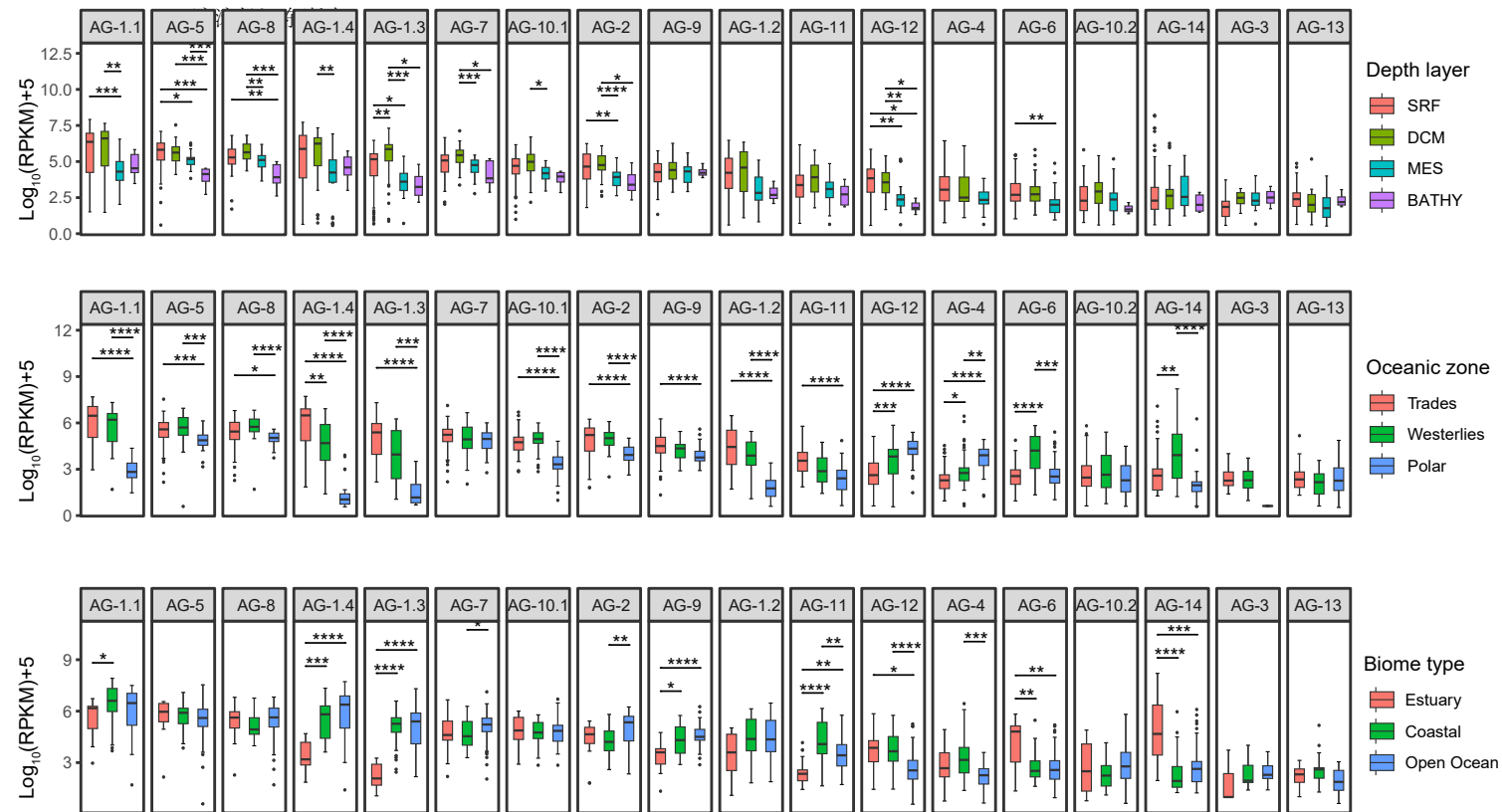


Fig. S7. Box plots of the relative abundance of each *Autographiviridae* group in different ecological zones. The significance of pairwise comparisons calculated using the two-tailed Mann–Whitney U test was shown with the asterisk corresponding to the p -value (* $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$, **** $p < 0.0001$).

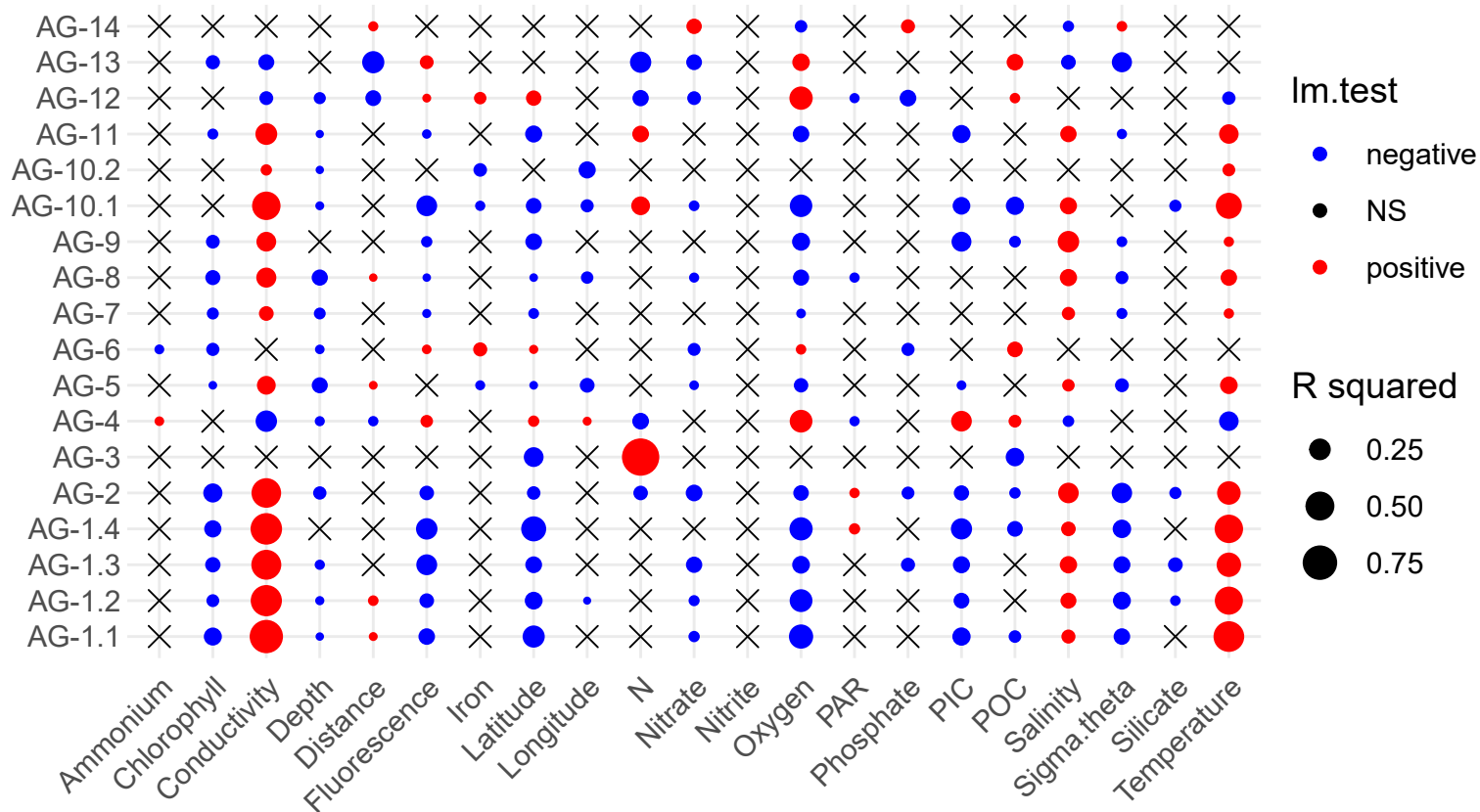


Fig. S8. Environmental drivers of *Autographiviridae* group distribution. The correlation of phage group distribution with environmental factors was calculated using linear regression. The size of the circle corresponds to the R-squared coefficient of the linear regression. The red and blue circles represent statistically significant positive and negative correlations ($p < 0.05$), respectively.