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Corrigendum: Characterization and genomic analysis of a novel *Pseudomonas* phage vB_PaeM_M1, representing a new viral family, *Psaeviridae*

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A Corrigendum on

Characterization and genomic analysis of a novel *Pseudomonas* phage
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by Ren L, Liu Y, Liang Y, Liu B, McMinn A, Zheng K, Wang Z, Wang H, Shao H, Sung YY, Mok WJ,
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In the published article, there was an error. Due to an oversight, the newly isolated phage M1 was incorrectly named “vB_PsaP_M1” in the original article. To more accurately reflect its morphology and host specificity, the correct designation should be “vB_PaeM_M1”. All the instances of the incorrect name “vB_PsaP_M1” have been corrected with “vB_PaeM_M1” in the article title, in the legends for **Figures 1–7** (12 instances), in **Supplementary Tables 1, 3–5** and in **Supplementary Image 1**, in **Abstract** (4 instances), **Introduction** (3 instances), **Materials and methods** (9 instances), **Results and discussion** (36 instances), and **Conclusion** (2 instances). Please note that this naming correction does not affect any of the study’s results or conclusions, only the phage’s designation was incorrect. We sincerely apologize for this error.

In the published article, there was an error in **Figures 4–7** as published. “vB_PsaP_M1” should be changed with “vB_PaeM_M1”. The corrected **Figures 4–7** and their captions

appear below.

A correction has been made to **Data availability statement**. This sentence previously stated:

“The datasets presented in this study can be found in online repositories. The names of the repository/repositories and accession number(s) can be found in the article/Supplementary Material.”

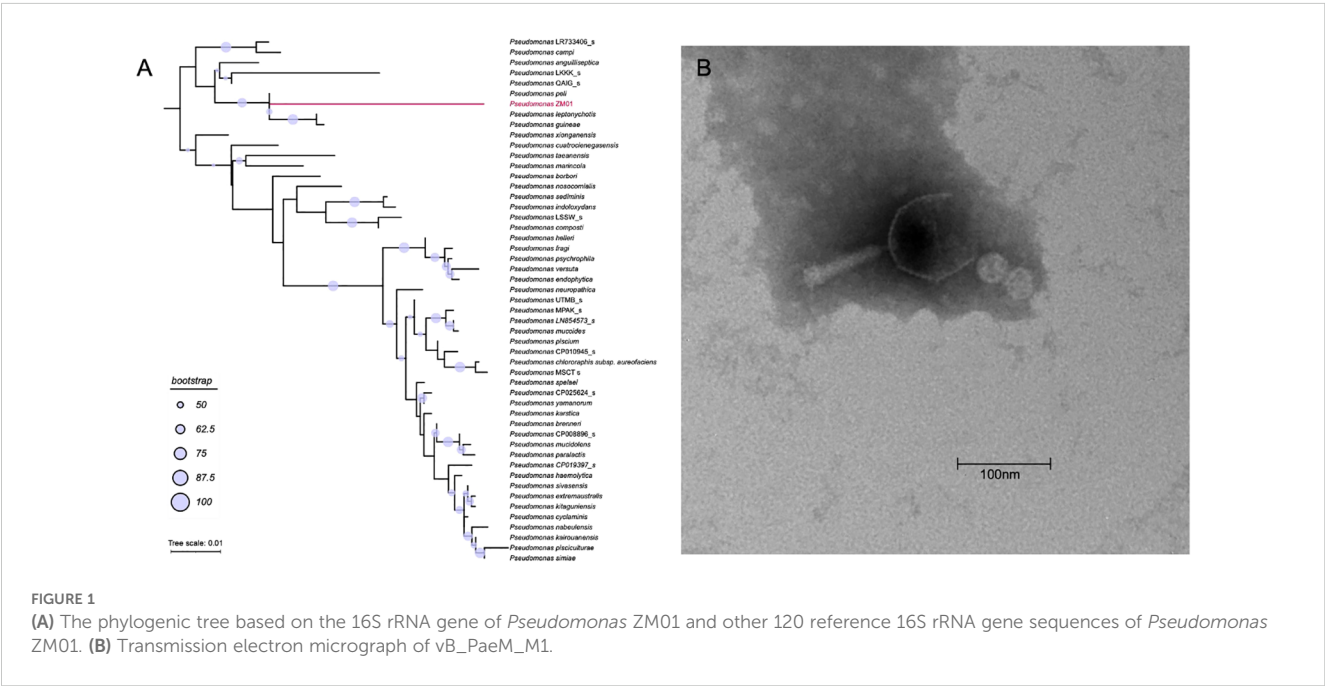
The corrected **Data availability statement** appears below:

“The complete genome sequence of *Pseudomonas* phage vB_PaeM_M1 is available in the GenBank database under accession number OP714164. In addition, the 16S rRNA gene sequence of *Pseudomonas* ZM01 has also been deposited in NCBI under accession number OP788125.”

The authors apologize for the errors and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

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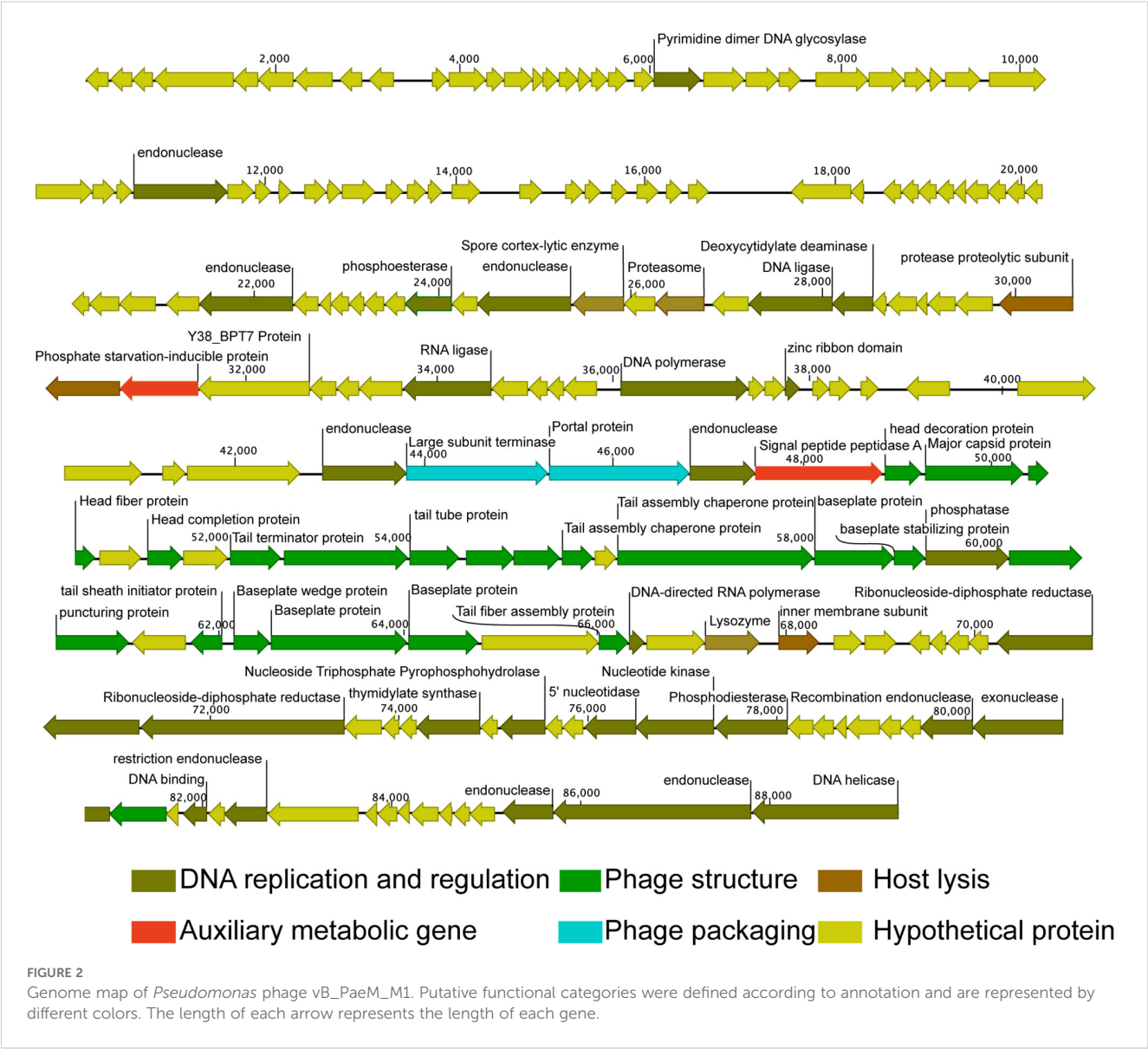


FIGURE 2
Genome map of *Pseudomonas* phage vB_PaeM_M1. Putative functional categories were defined according to annotation and are represented by different colors. The length of each arrow represents the length of each gene.

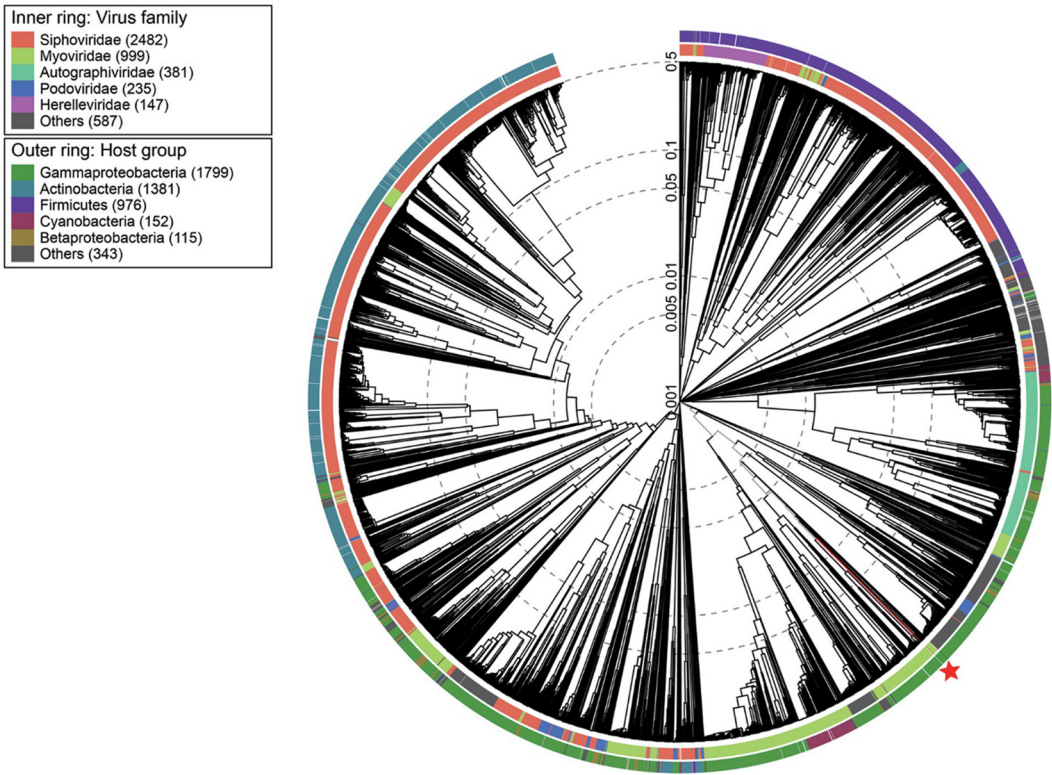


FIGURE 3
Viral phylogenetic tree of whole phage vB_PaeM_M1 genomes represented in the circular view. The colored rings represent the host groups (outer ring) and virus families (inner ring). These trees are calculated by BIONJ according to the genome distance matrix and take the midpoint as the root.

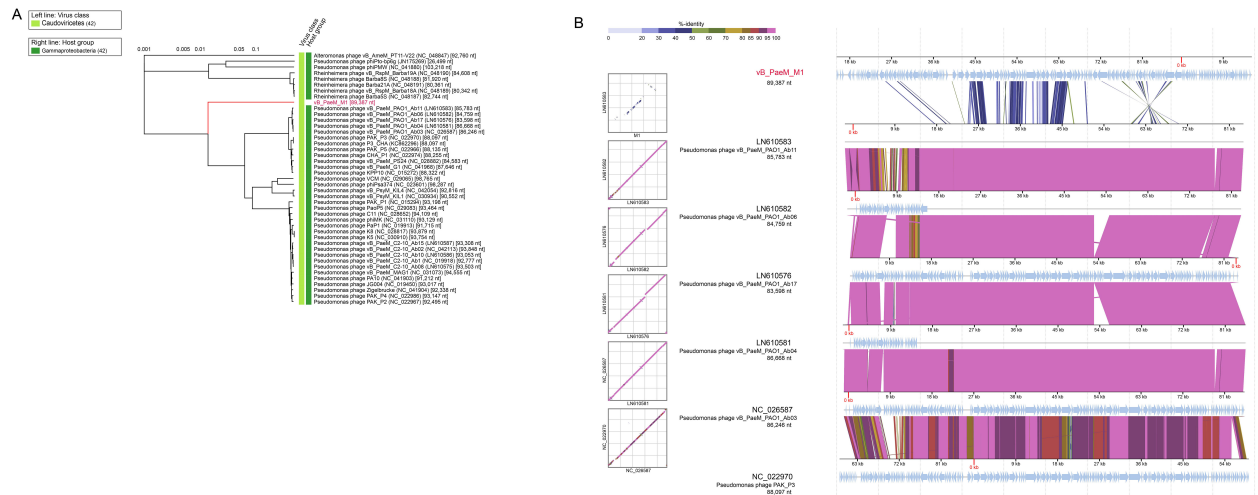


FIGURE 4
Phylogenetic and comparative genomic analyses of *Pseudomonas* phage vB_PaeM_M1. **(A)** Phylogenetic tree of *Pseudomonas* phage vB_PaeM_M1 and the 36 closest virus genomes. **(B)** Genomic comparisons between *Pseudomonas* phage vB_PaeM_M1 and vB_PaeM_M1-like viruses. The shading below each genome indicates sequence similarities between the genomes, with different colors representing the levels of similarity.

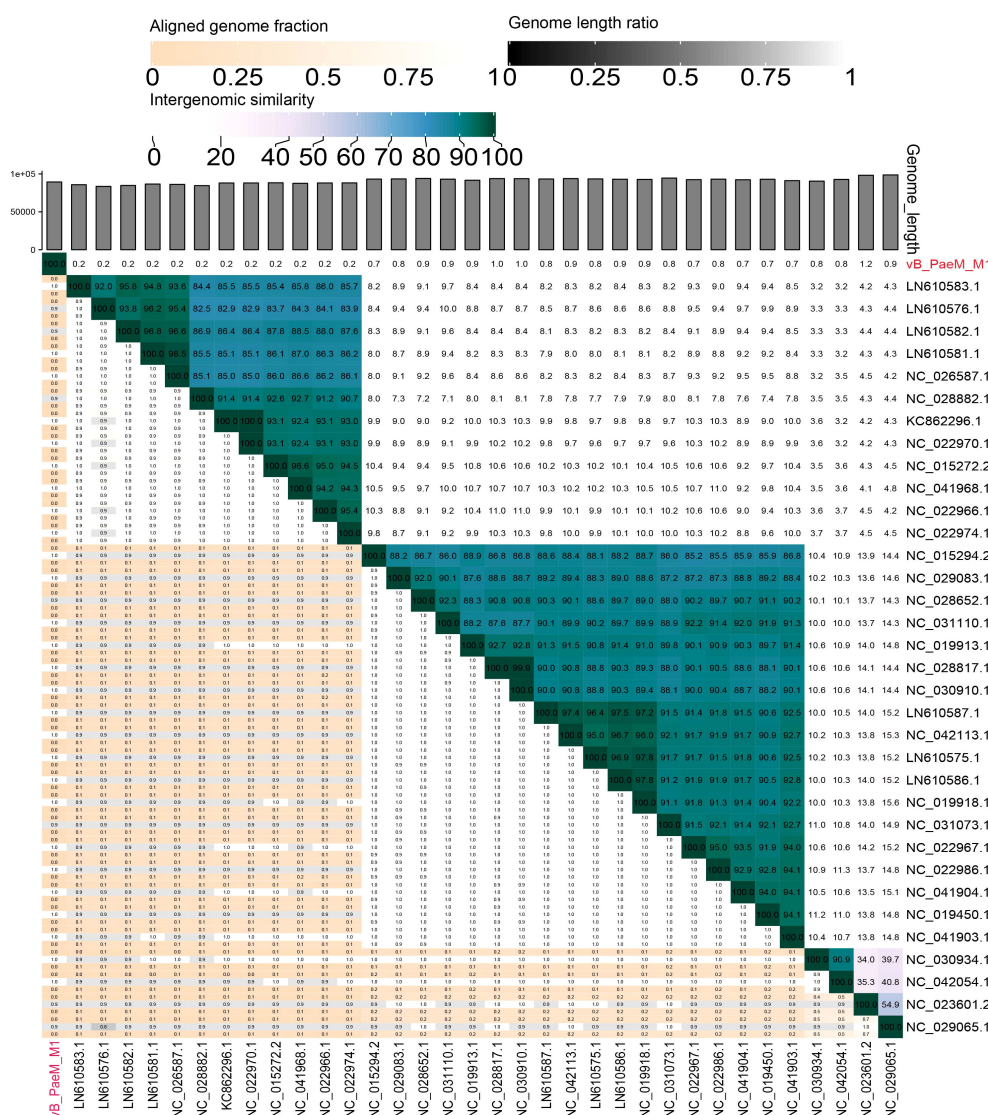


FIGURE 5

Shared gene heat map of vB_PaeM_M1 and vB_PaeM_M1 like virus in rectangular phylogenetic tree. In the right half, color coding allows rapid visualization of phage genome clustering based on intergenic similarity: the closer the relationship between genomes, the darker the color. These numbers represent the similarity values of each genome pair. In the left half, the three indicator values of each genome pair are expressed in order from top to bottom: aligned partial genome 1 (for the genome found in this row), genome length ratio (for two genomes in this pair), and aligned partial genome 2 (for the genome found in this column). Darker colors emphasize lower values, indicating that there is only a small number of genome aligned genome pairs (orange to white gradient), or there is a large difference in the length of the two genomes (black to white gradient). As the distance between phages increases, the aligned genomic fragments are expected to decrease.

