

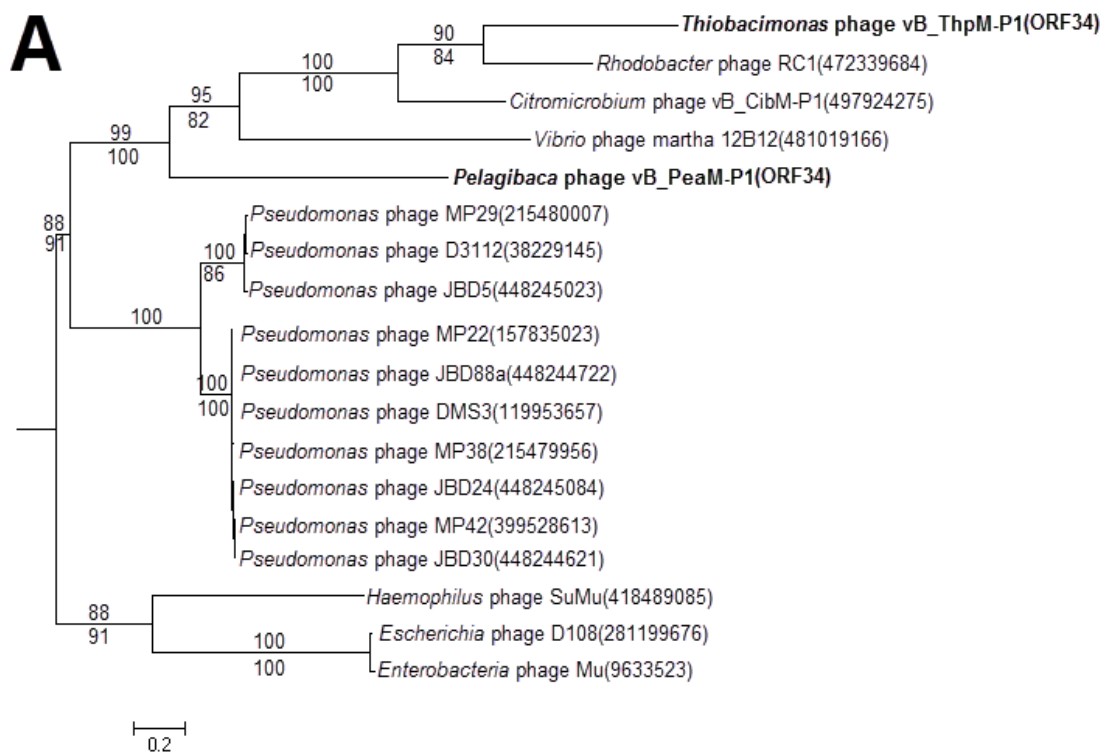
Supplementary Figures

Genomic, Proteomic and Bioinformatic Analysis of Two Temperate Phages in *Roseobacter* Clade Bacteria Isolated from the Deep-sea Water

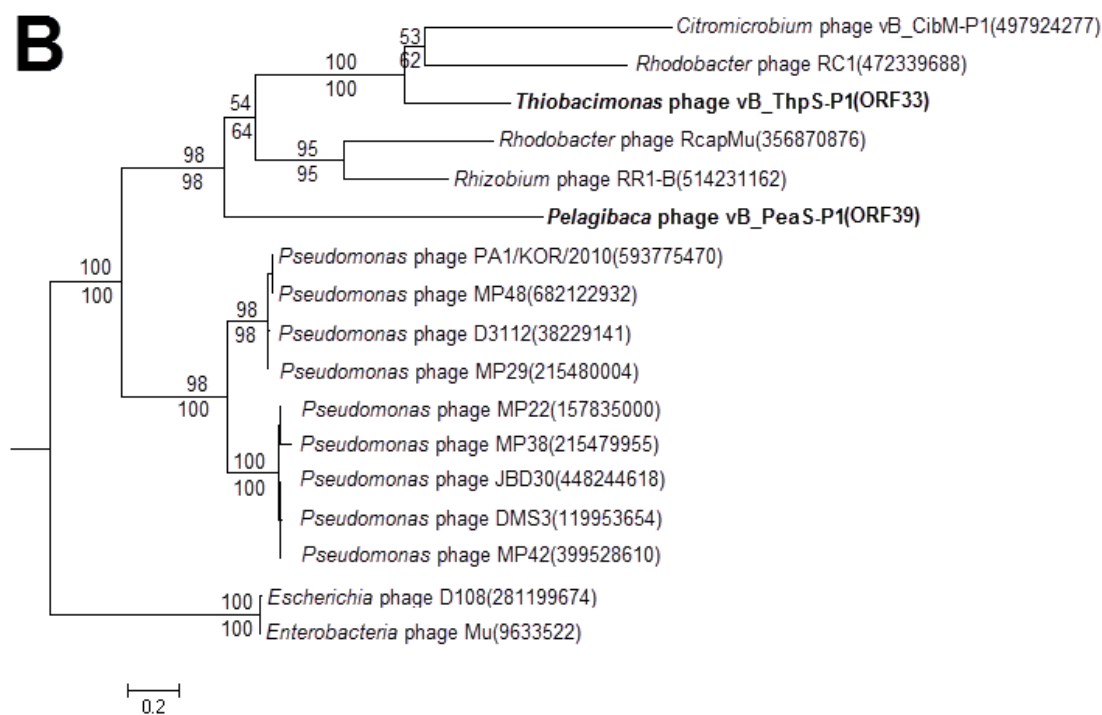
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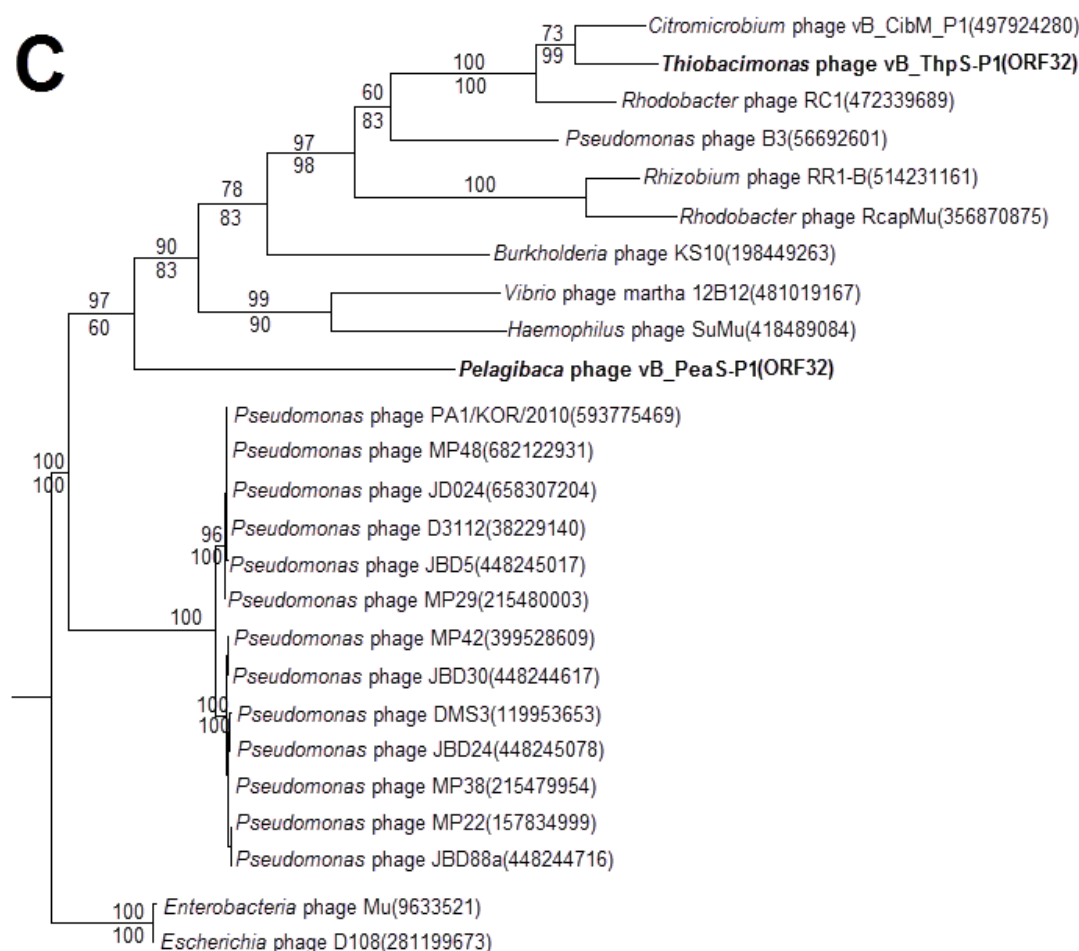


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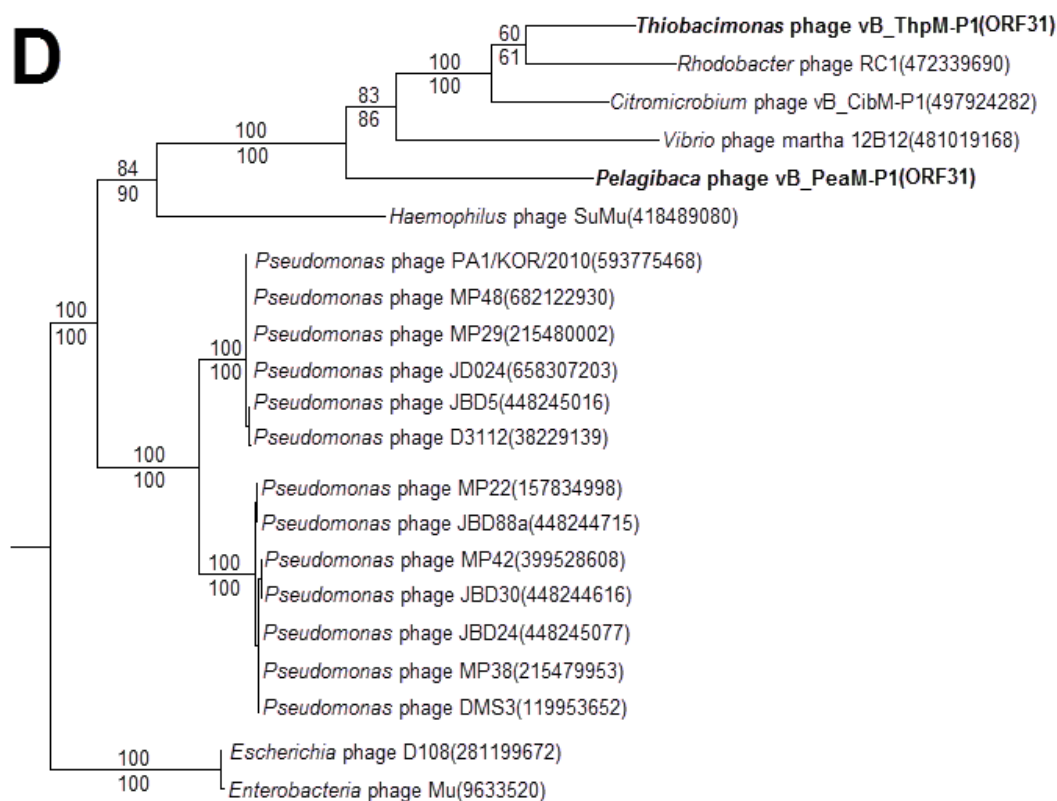
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D



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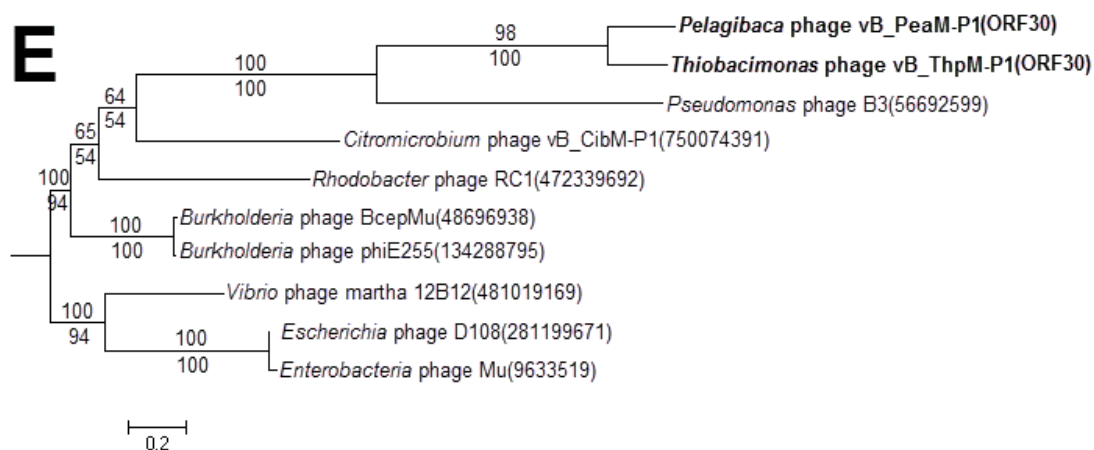


Figure S1. Phylogenetic trees of the head modules proteins of (pro)phages. Maximum likelihood tree and neighbor-joining tree methods and bootstrap analysis (100 replicates) based on the alignment of the amino acid sequence of the I protein (A), the virion morphogenesis protein (B), the Mu-like phage F protein (C), the Mu-like phage gp29 protein (D), and the Mu-like phage gp28 protein (E) of (pro)phages. The numbers at the nodes indicate bootstrap probabilities of that particular branch of the maximum likelihood (above) and neighbor-joining (below) trees.

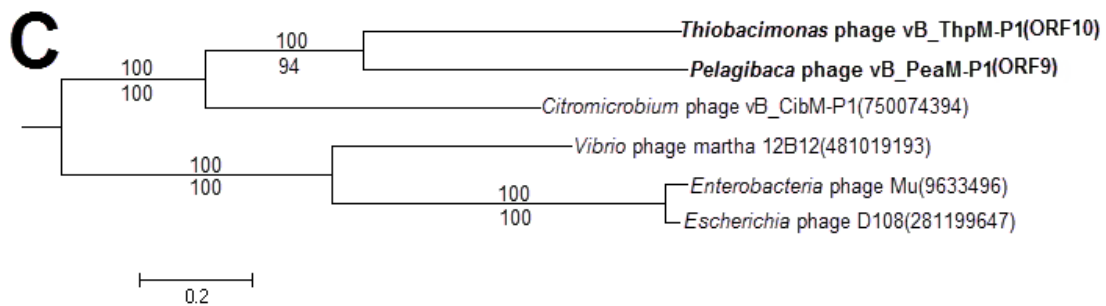
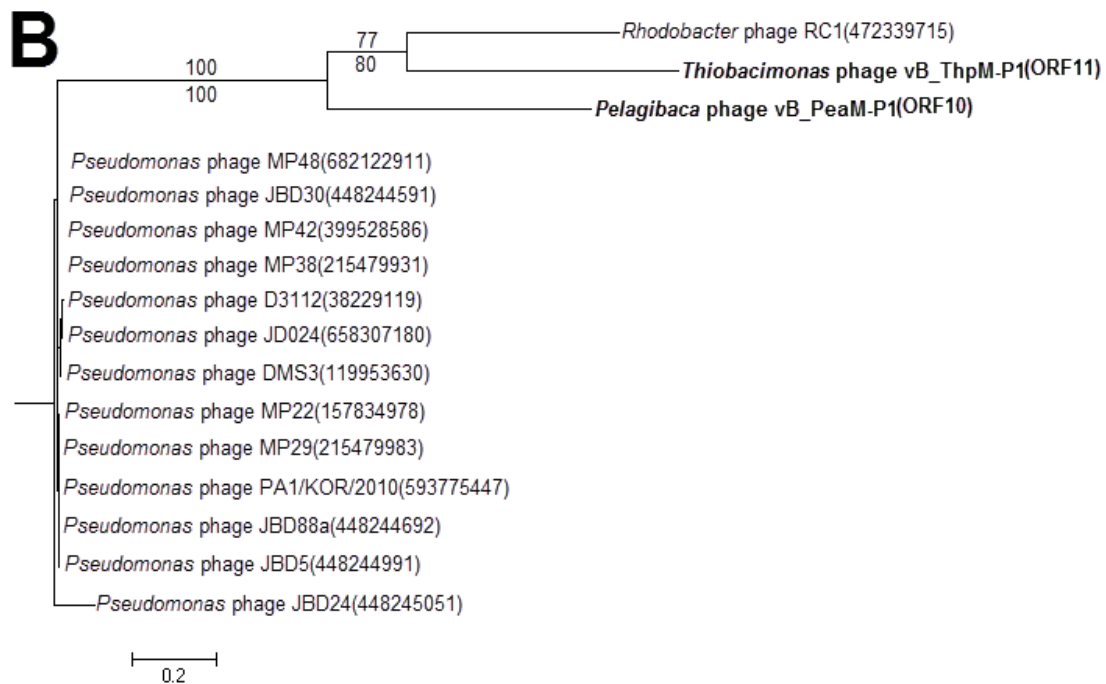
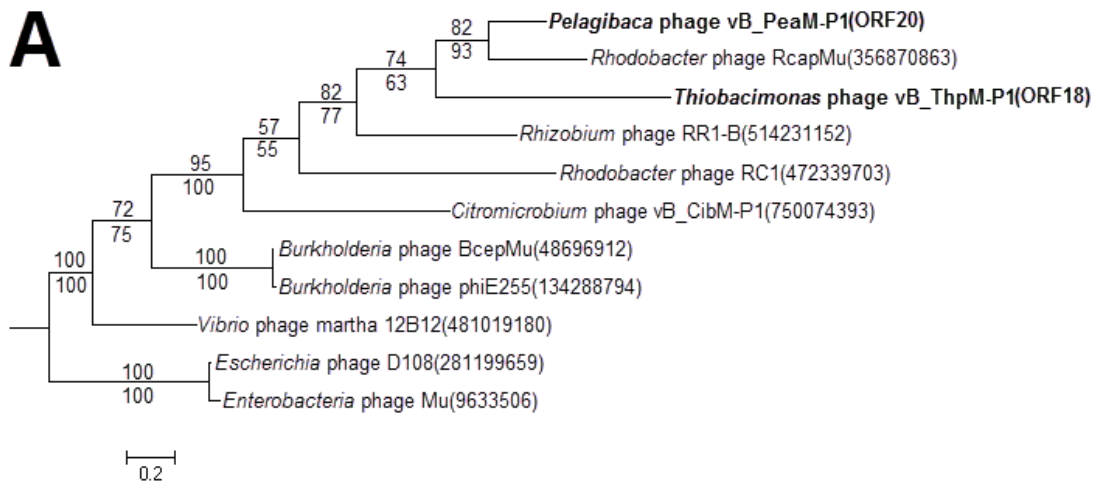


Figure S2. Phylogenetic trees of the transcriptional regulator (A), transposase B (B), and transposase A (C) of the (pro)phages. The numbers at the nodes indicate the bootstrap probabilities of that particular branch of the maximum likelihood (above) and neighbor joining (below) trees.