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A novel *Saclayvirus Acinetobacter baumannii* phage genomic analysis and effectiveness in preventing pneumonia

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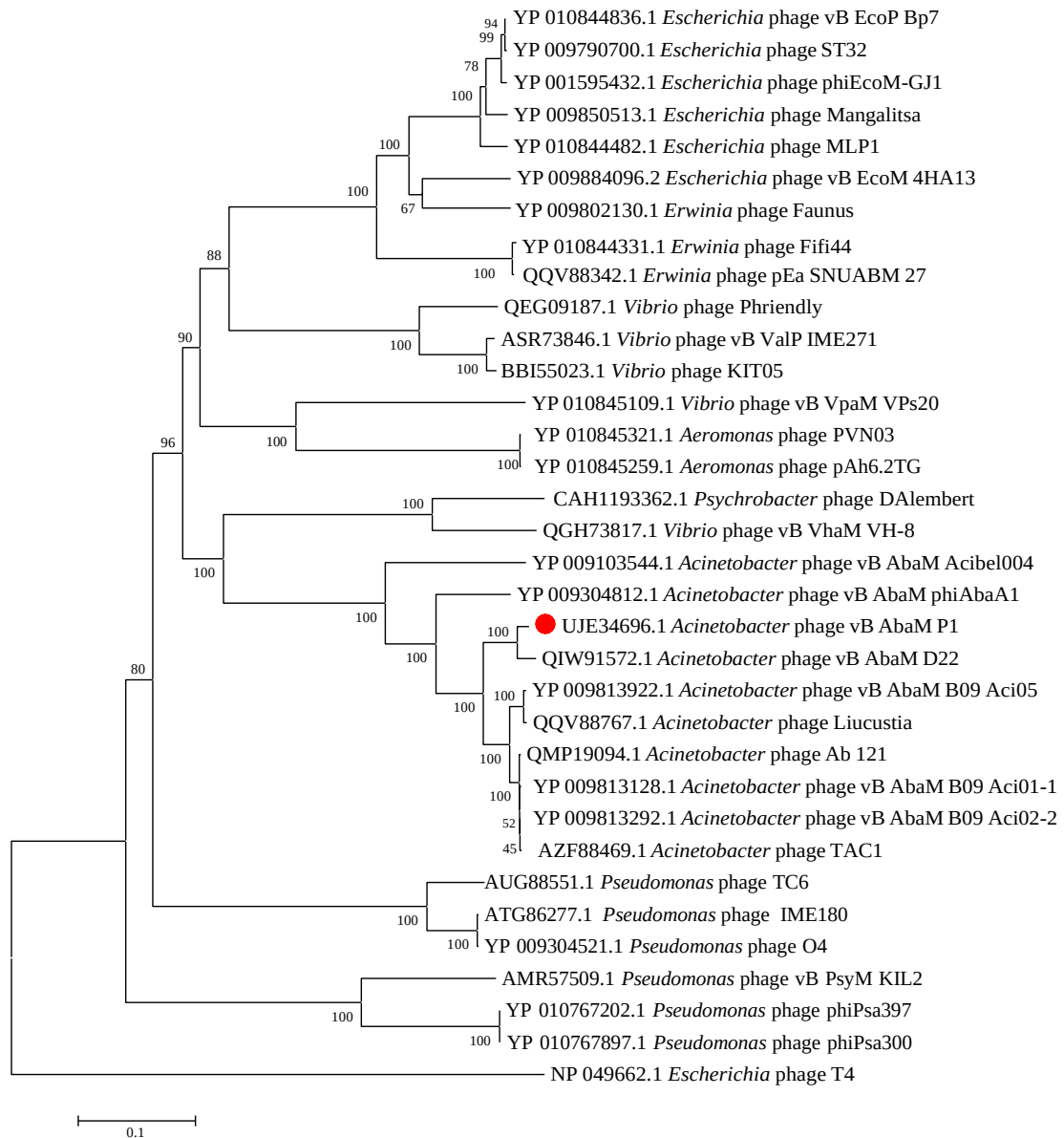


Fig. S1 A phylogenetic tree constructed with the DNA polymerase protein of phage vB_AbaM_P1. Comparison with corresponding proteins from other phages in the NCBI protein database were performed by BLASTp search (default parameters, but maximum target sequence set to 250). The tree was generated using the MEGA7 tool with the neighbor-joining method and 1000 bootstrap replicates. The *Escherichia* virus T4 protein was used as an outgroup to root the tree

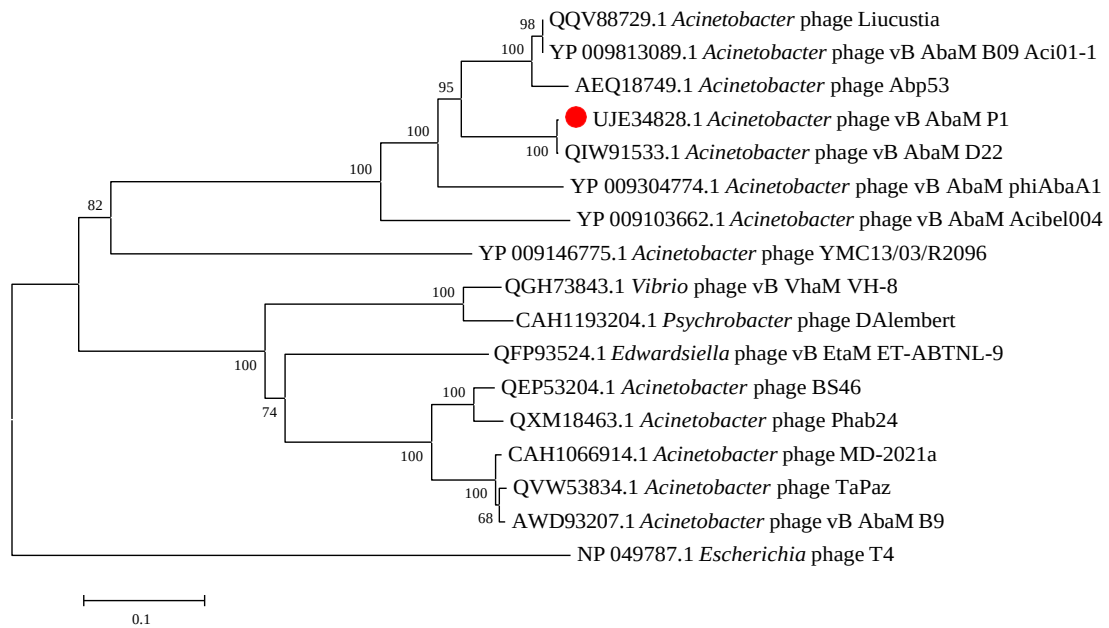


Fig. S2 A phylogenetic tree constructed with the major capsid protein of phage vB_AbaM_P1. Comparison with corresponding proteins from other phages in the NCBI protein database were performed by BLASTp search (default parameters, but maximum target sequence set to 250). The tree was generated using the MEGA7 tool with the neighbor-joining method and 1000 bootstrap replicates. The *Escherichia* virus T4 protein was used as an outgroup to root the tree

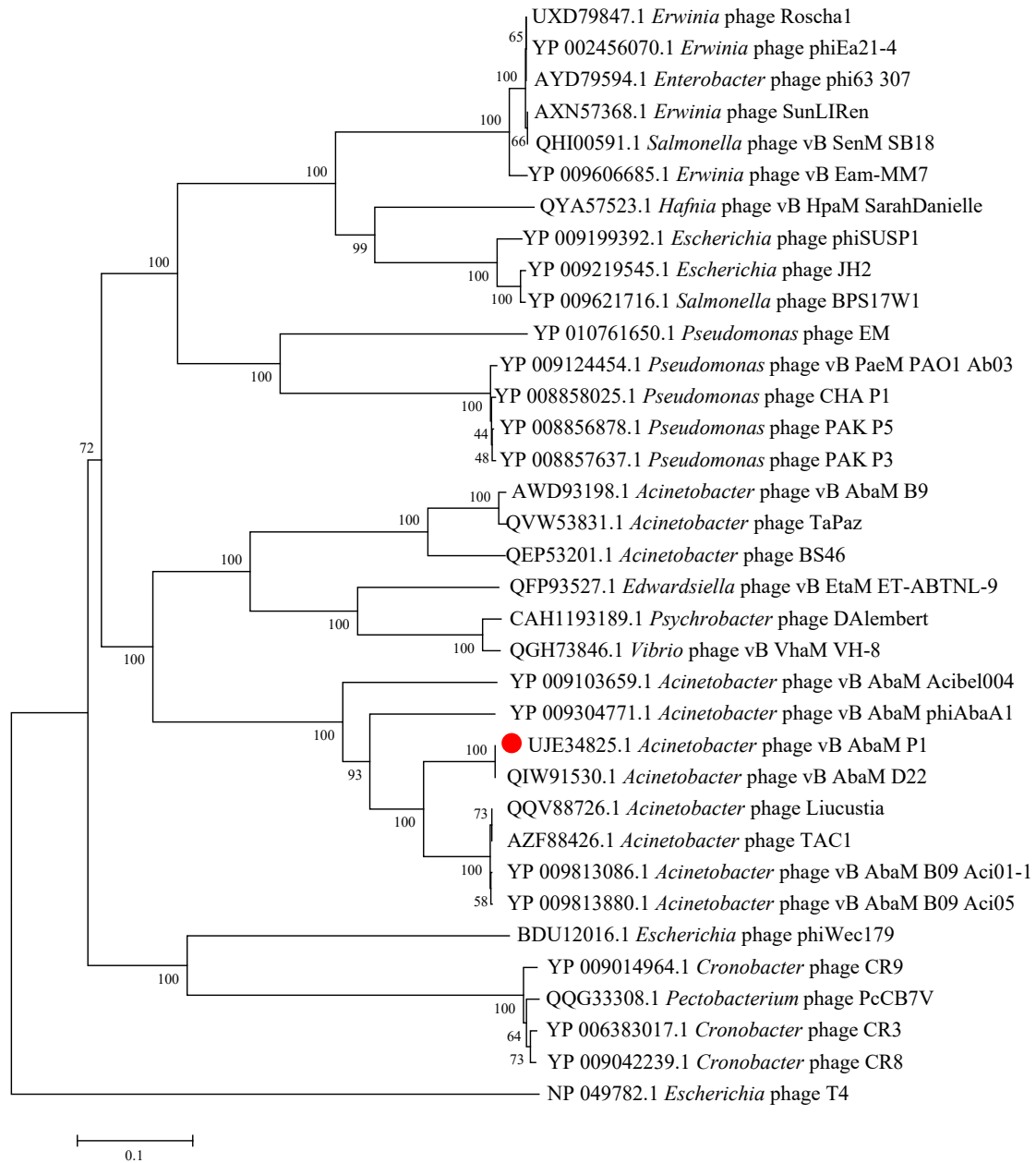


Fig. S3 A phylogenetic tree constructed with the portal protein of phage vB_AbaM_P1. Comparison with corresponding proteins from other phages in the NCBI protein database were performed by BLASTp search (default parameters, but maximum target sequence set to 250). The tree was generated using the MEGA7 tool with the neighbor-joining method and 1000 bootstrap replicates. The *Escherichia* virus T4 protein was used as an outgroup to root the tree

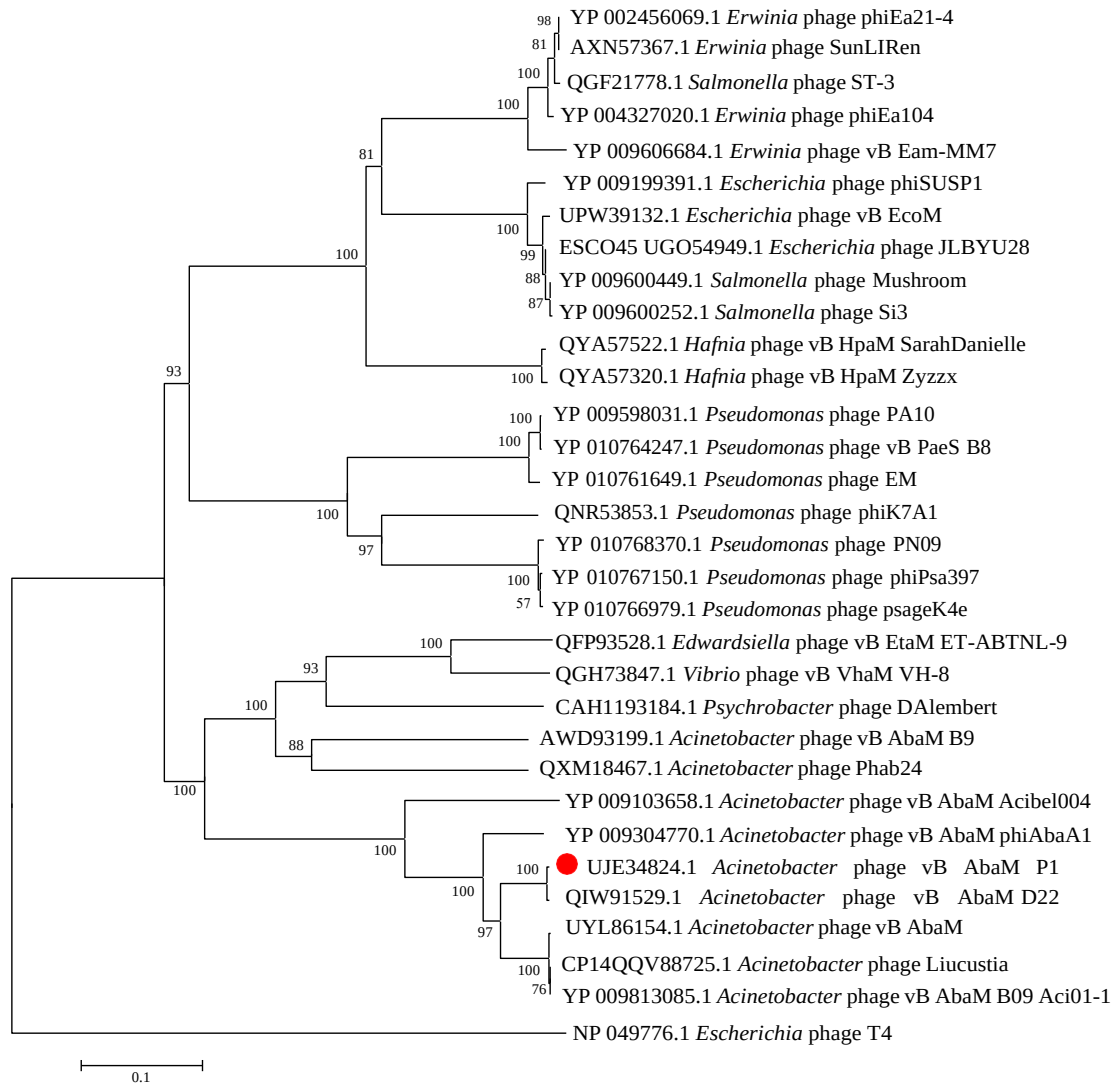


Fig. S4 A phylogenetic tree constructed with the terminase large subunit of phage vB_AbaM_P1. Comparison with corresponding proteins from other phages in the NCBI protein database were performed by BLASTp search (default parameters, but maximum target sequence set to 250). The tree was generated using the MEGA7 tool with the neighbor-joining method and 1000 bootstrap replicates. The *Escherichia virus T4* protein was used as an outgroup to root the tree