Supplemental Material to:
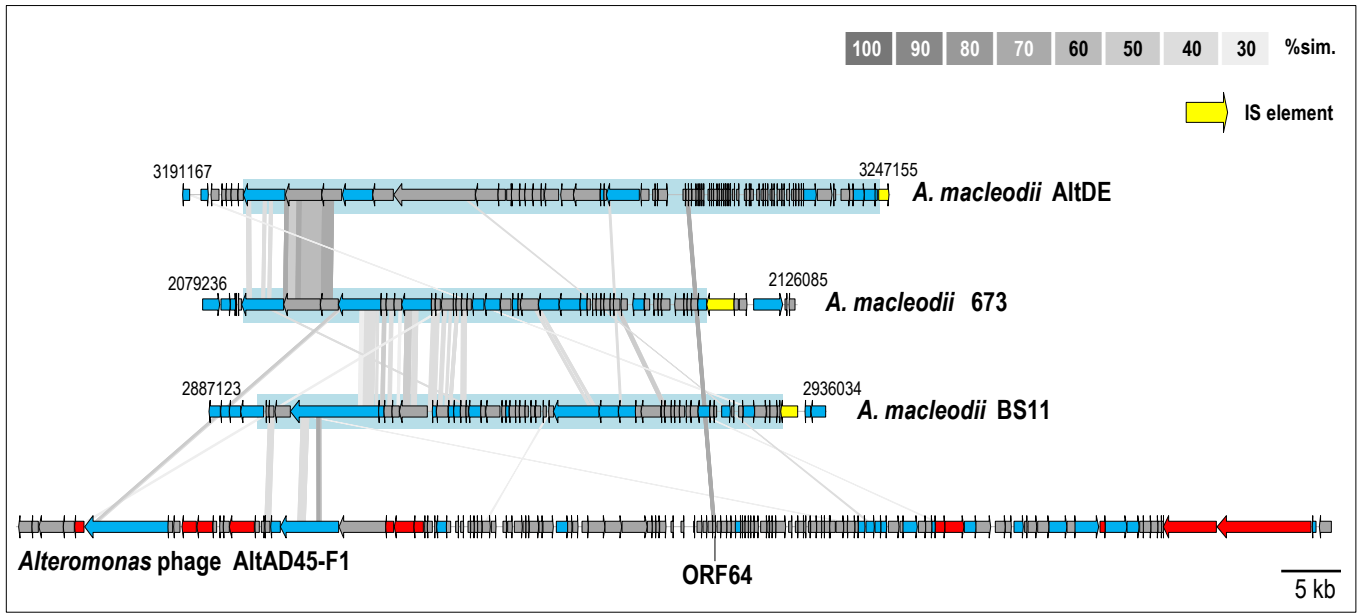
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## Novel group of podovirus infecting the marine bacterium *Alteromonas macleodii*

Supplementary Figure 1. Genomic comparison of AltAD45-P1 phage with specific regions (see main text) of *A. macleodii* 673, BS11 and AltDE strains. The arrows represent the predicted ORFs. Conserved genomic regions are indicated by grey shaded areas. Conserved ORFs with N4-like viruses are red coloured and in blue, ORFs with assigned functions.
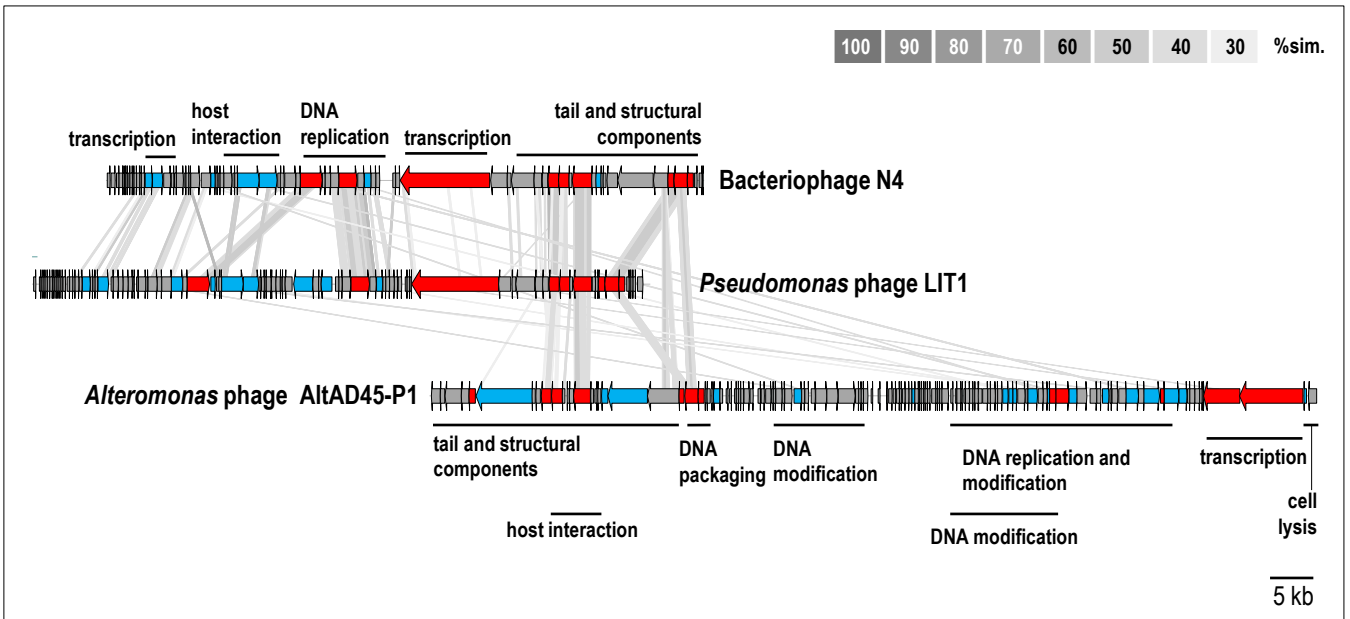
Supplementary Figure 2. Genomic comparison of Enterobacter phage N4, *Pseudomonas* phage LIT1 and AltAD45-P1. The arrows represent the predicted ORFs. Conserved genomic regions are indicated by grey shaded areas. Conserved ORFs with N4-like viruses are red coloured and in blue ORFs with assigned functions.
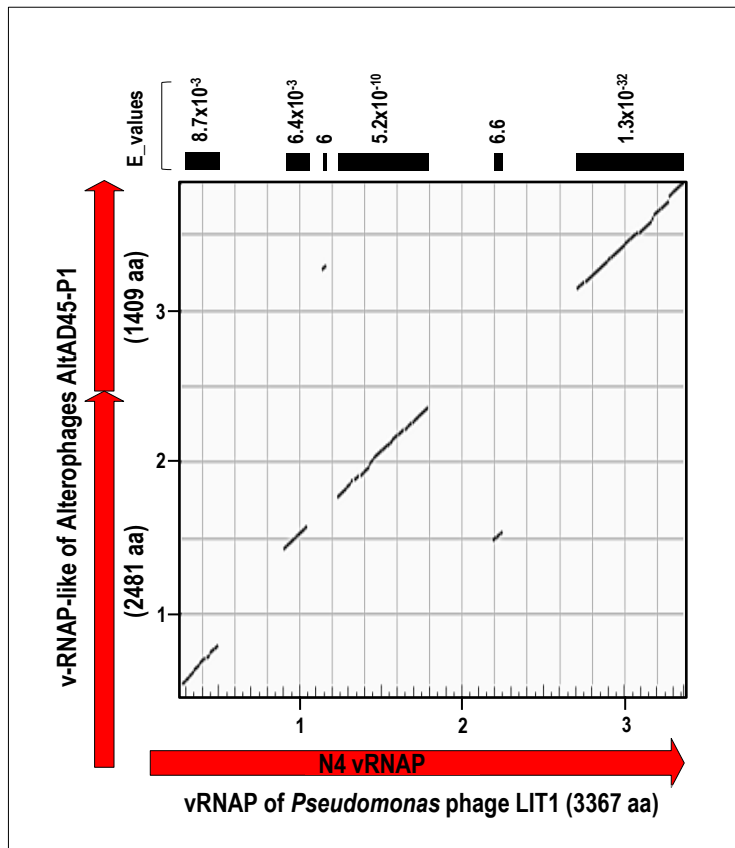
Supplementary Figure 3. Dot matrix view showing the regions of similarity based upon BLASTP results between the vRNAP protein of *Pseudomonas* phage LIT1 (X-axis) and the N4-gp50-like proteins present in Alterophage AltAD45-P1 (Y-axis). Alignments are shown in the plot as lines. E_values are indicated in the upper panel.

1 **SUPPLEMENTARY MATERIAL**

2

3 **SUPPLEMENTARY TABLES**

4

5 **Supplementary Table 1. Details of the AltAD45-phages sequencing.**

phage	Platform	# reads	Average read length (pb)	Coverage (X-fold)	# contigs assembled
AltAD45-P1	454, GS-FLX system	11910	717.9	82.28	1
AltAD45-P2	454, GS-FLX system	8153	709.7	55.62	1
AltAD45-P3	454, GS-FLX system	20748	443.45	90.45	1
AltAD45-P4	454, GS-FLX system	16590	676.19	111.49	1

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