

Expanded View Figures

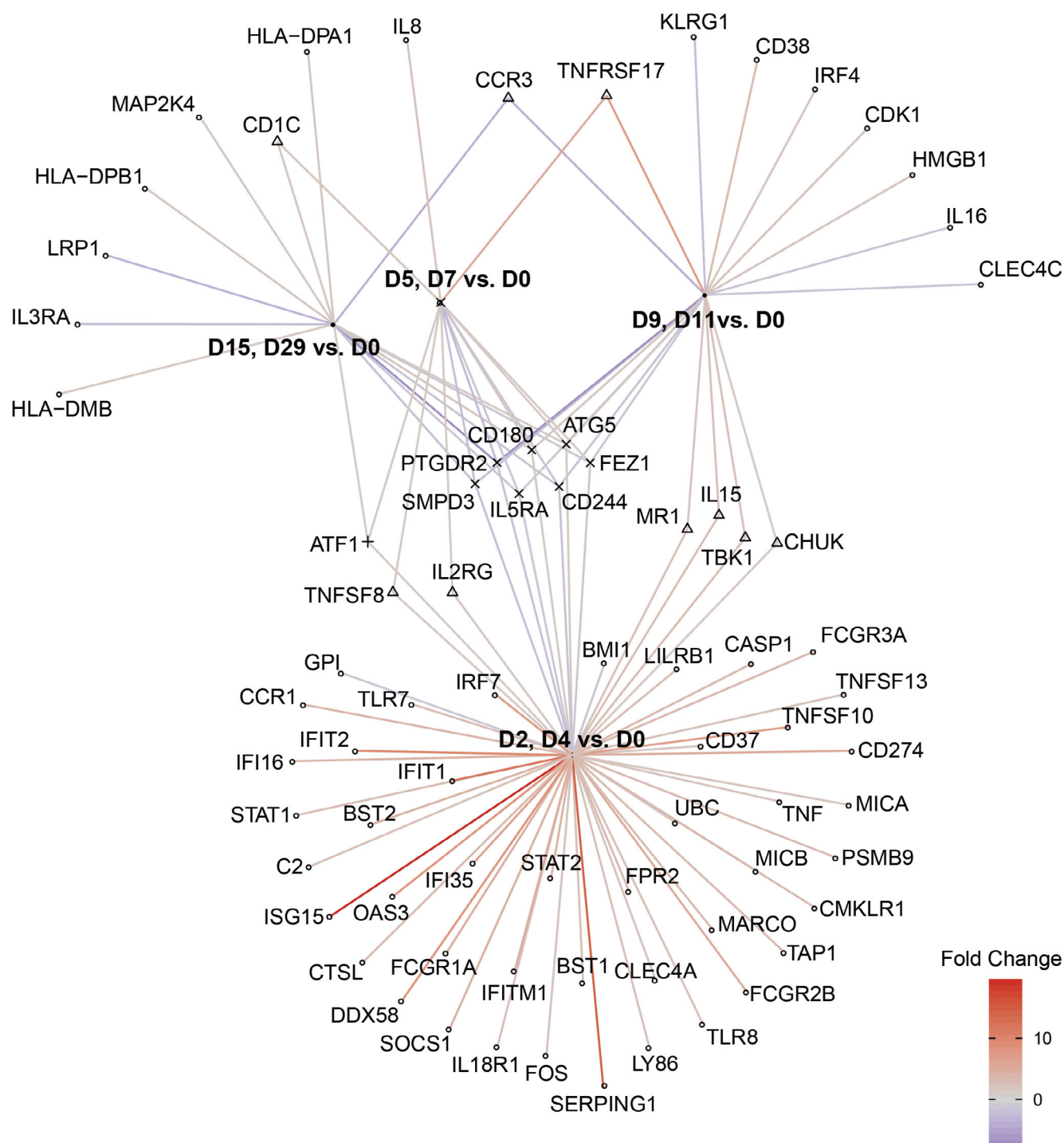


Figure EV1. Gene network visualisation of significant differentially expressed immune response over 2 weeks of intravenous anti-pseudomonal adjunctive phage therapy with 2 weeks of follow-up.

D0: pre-phage, D2–D11: during phage administration, D15: one day post-adjunctive phage therapy, D29: 15 days post-adjunctive phage therapy. The gene network highlights the significant gene expression changes at the beginning of adjunctive phage therapy (D2–4), and the overlaps of common genes for the duration of adjunctive phage therapy.

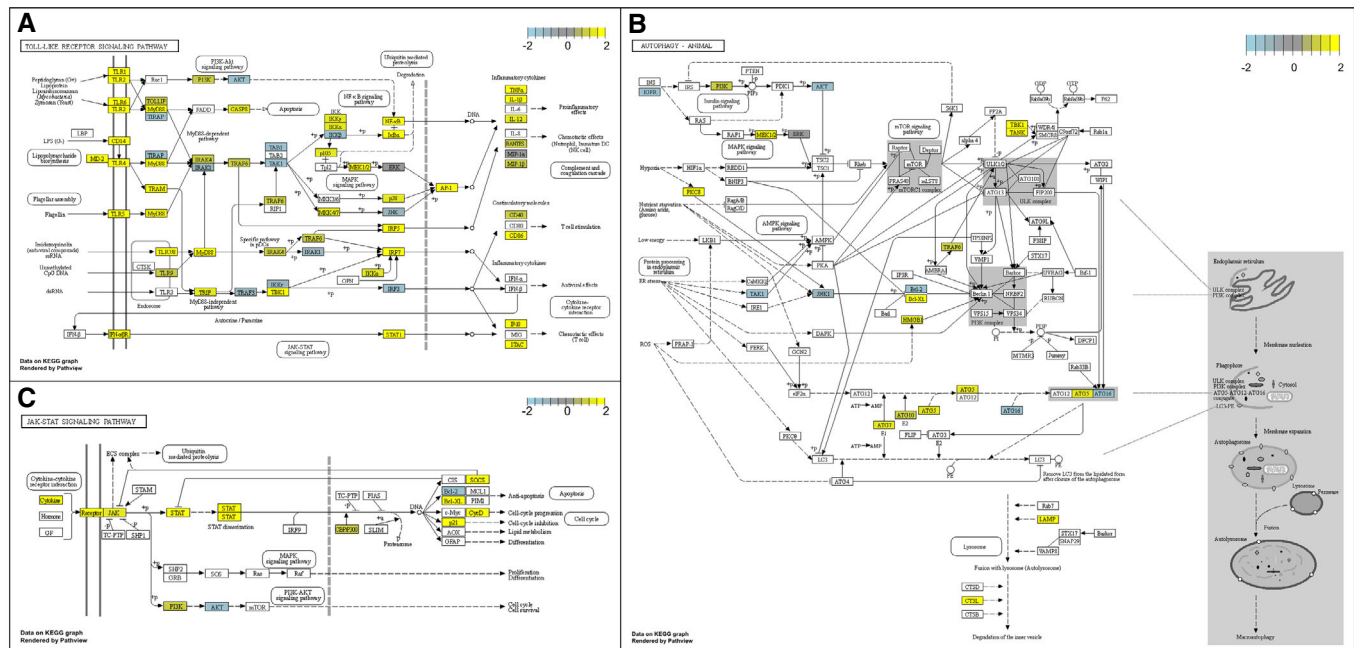


Figure EV2. Differentially expressed genes in major inflammation-associated pathways.

Visualisation using PathView following Gene Set Enrichment Analysis and Pathway enrichment analysis (KEGG, <https://www.genome.jp/kegg/>); genes with fold change > 2 and < -2 were integrated into KEGG pathways.

- A Toll-like receptor signalling pathway.
- B Autophagy.
- C JAK-STAT signalling pathway.

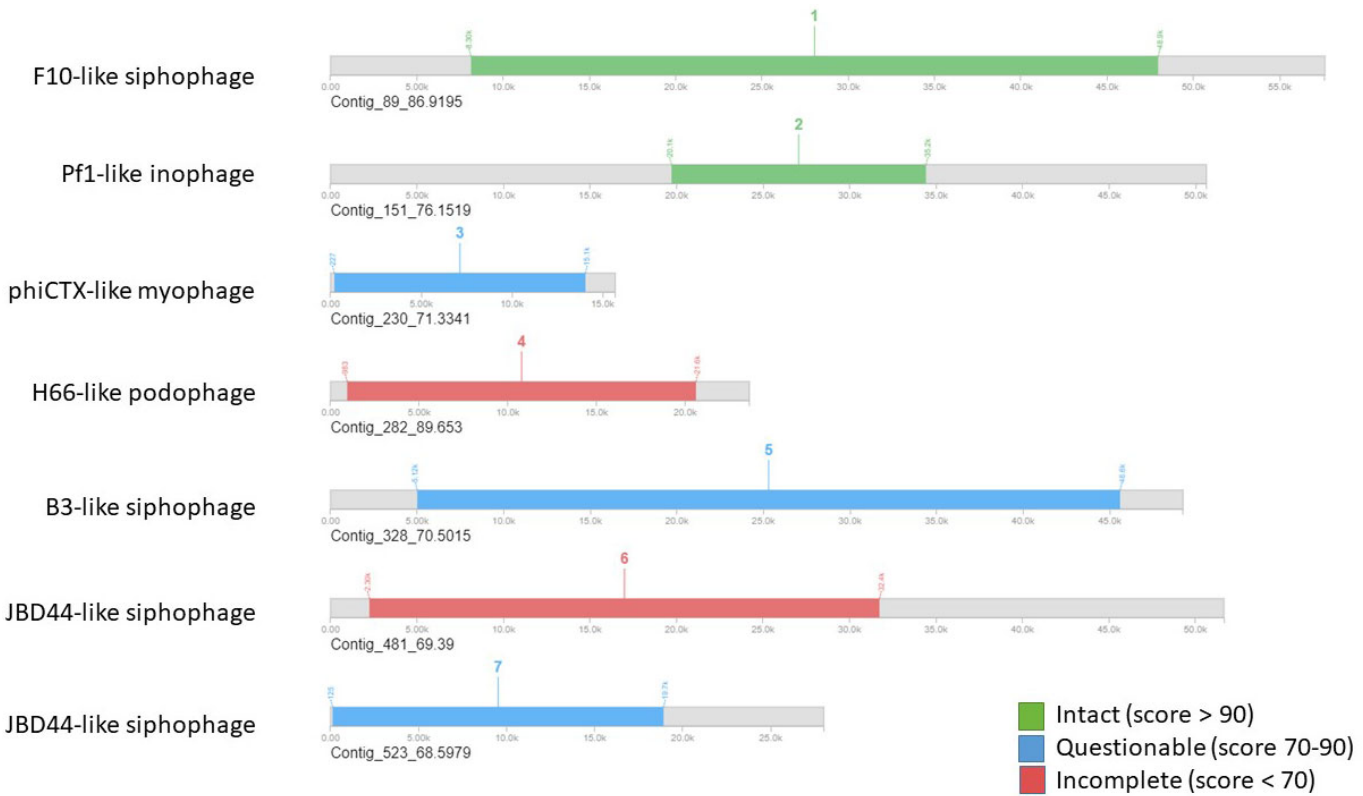


Figure EV3. Prophage sequences from PHAGE Search Tool Enhanced Release (PHASTER) for the clinical isolate of *Pseudomonas aeruginosa* (Ppa2.1).