Supplementary figures

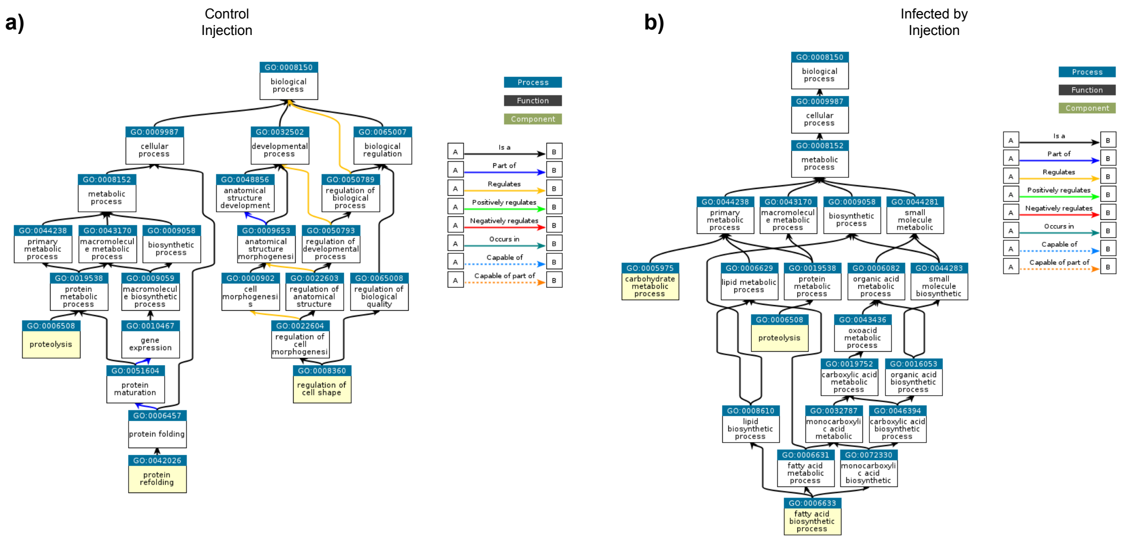

Figure 1S. Functional analysis of microbial-derived peptides under injection-based conditions. **a)** Gene Ontology (GO) biological processes enriched in microbiota peptides from larvae injected with PBS (control). Detected processes relate primarily to general metabolism and protein folding. **b)** Functional network from larvae injected with *P. aeruginosa* reveals expanded enrichment of processes including lipid, organic acid, and small molecule metabolism, as well as proteolysis and biosynthetic activity. Diagrams reflect increased metabolic diversity and microbial activation under systemic infection.

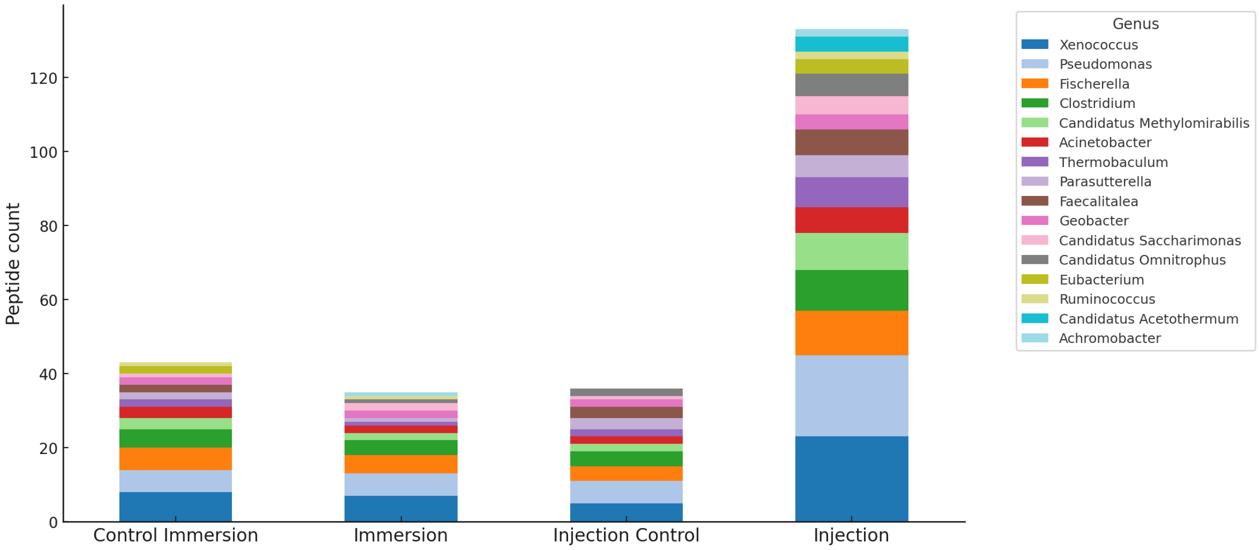

Figure 2S. Genus-level peptide distribution across experimental conditions. Stacked bar plot showing the number of microbial-derived peptides assigned to selected genera in each condition: control immersion, infected immersion, control injection, and infected injection. Each color represents a different genus, with height proportional to peptide count. A notable increase in both genus richness and peptide abundance is observed in the injection-infected group, reflecting taxonomic expansion of the microbiota under systemic infection.