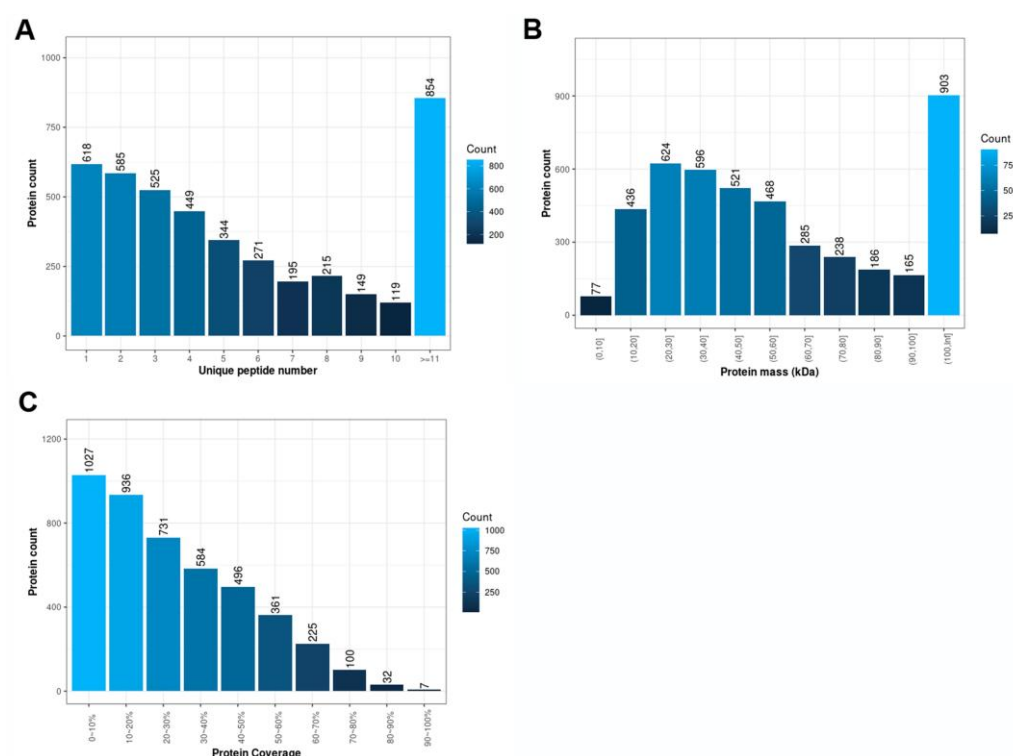
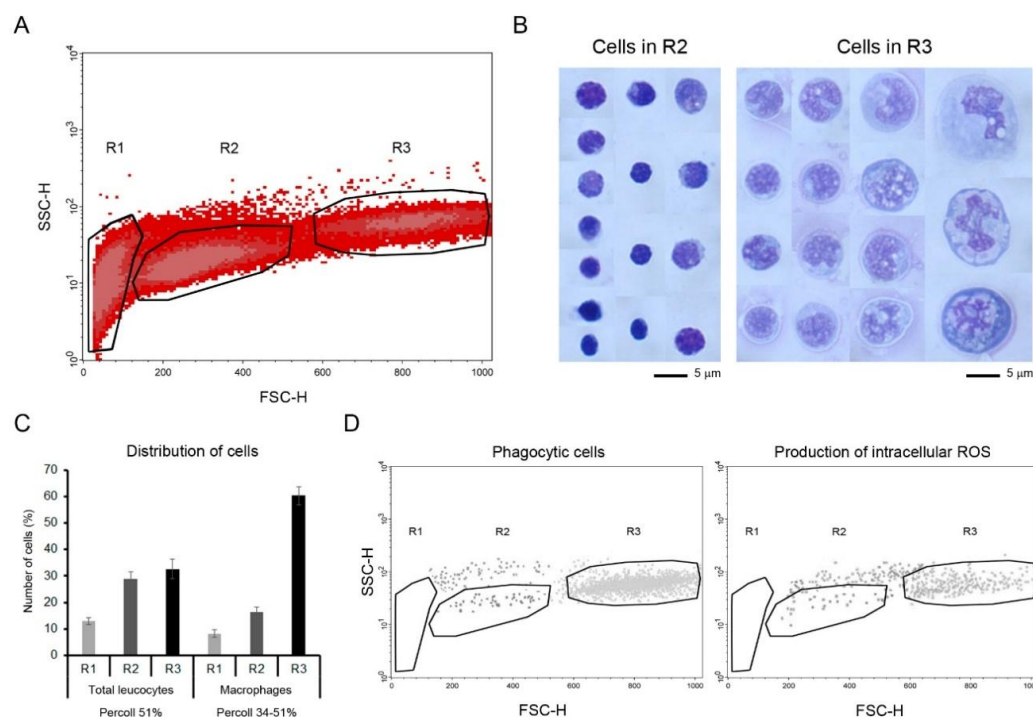




Supplementary Figure S1. Overview of library identification metrics. The figure presents key distributions obtained from the proteomic library analysis: (a) Distribution of unique peptides across the dataset, highlighting the diversity of peptide identifications; (b) Protein mass distribution, showing the range and prevalence of proteins identified according to their molecular weight; (c) Protein coverage distribution, representing the percentage of sequence coverage achieved for the identified proteins.



Supplementary Figure S2. Characterization of cells isolated from the head kidney: (a) Three distinct cell populations were identified in head kidney samples using a Percoll gradient; (b) The R1 region consisted mainly of cell debris and small lymphocytes, while the R2 region was predominantly enriched in lymphocytes, with a small number of neutrophils also present. The R3 region contained macrophages and neutrophils larger than 5 μm in diameter; (c) Total leukocytes was obtained from four head kidneys using a 51% Percoll gradient, and enrichment in macrophages and neutrophils was achieved using a 34-51% gradient; (d) Functional assays showed that the higher phagocytic activity (fluorescent latex bead uptake) and ROS production occurred in the R3 region, supporting the predominance of macrophages and neutrophils in this population.