

Proteomic analysis reveals a protective role of specific macrophage subsets in liver repair

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Figure S1

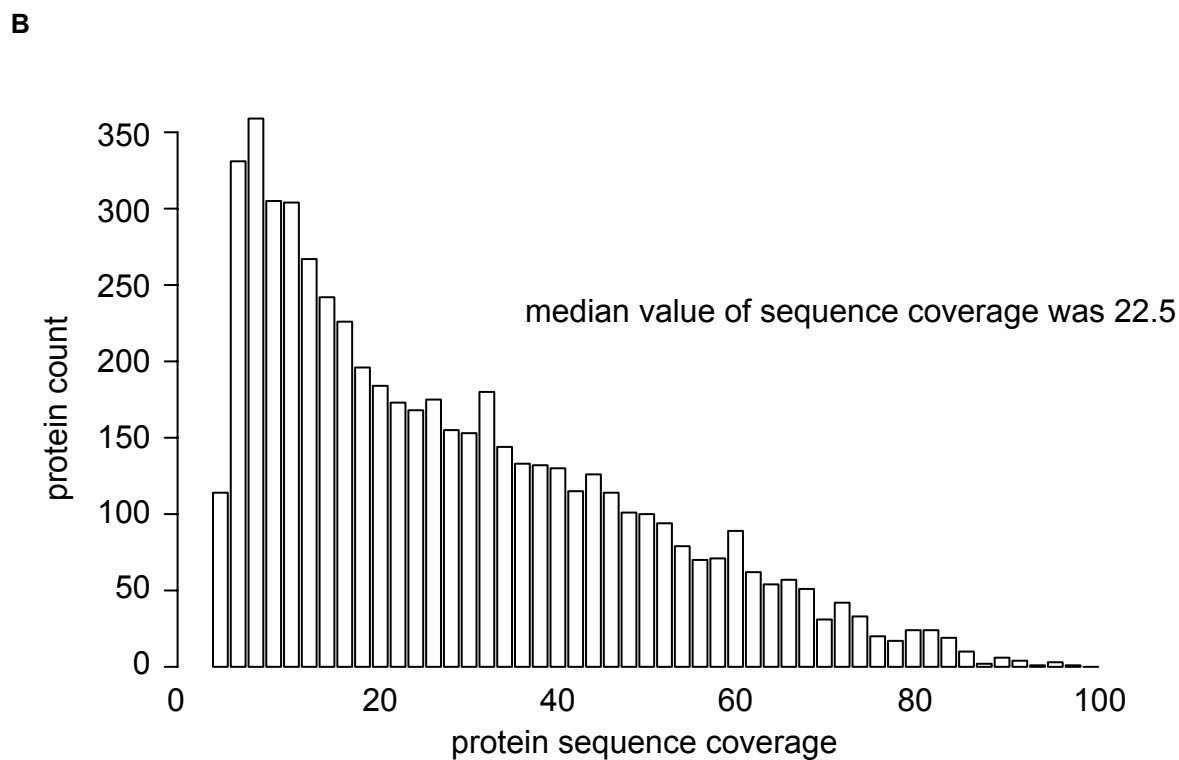
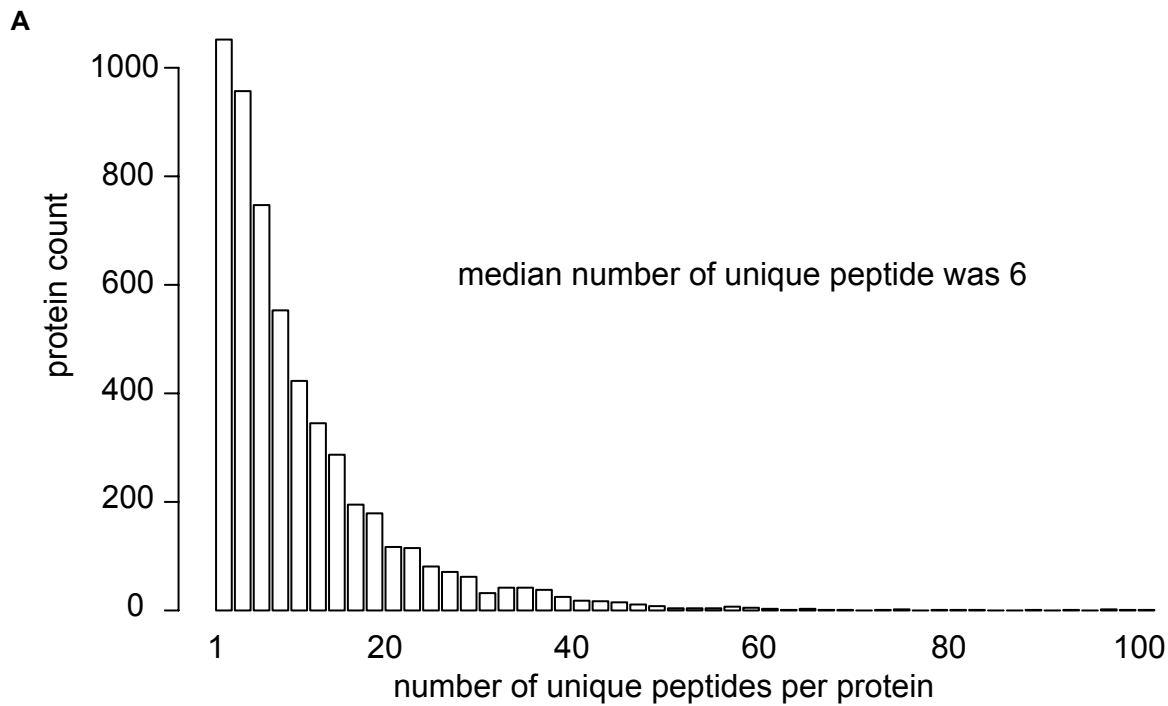


Figure S1. Histogram of the unique peptides and sequence coverage for the quantified proteins.

(A) Histogram of the unique peptides for the quantified proteins. The median number of unique peptide was 6.

(B) Histogram of the sequence coverage (%) for the quantified proteins. The median value of protein sequence coverage was 22.5.

Figure S2

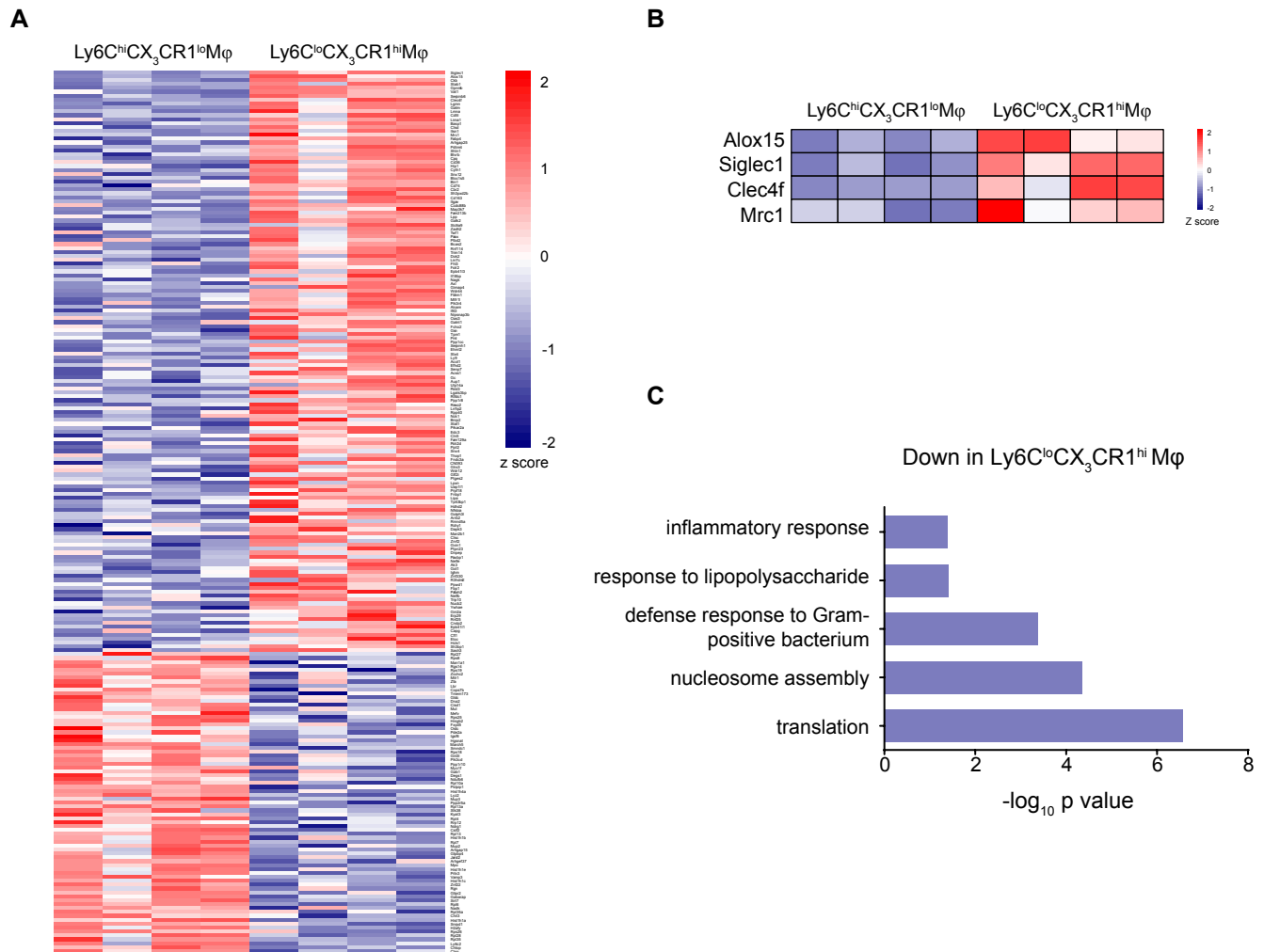


Figure S2. Proteomic analysis of distinct macrophage subsets from distinct phases in APAP-induced liver injury.

(A) Heatmap showing the differentially expressed genes in 24 h Ly6C^{hi}CX₃CR1^{lo} macrophages as compared to 72 h Ly6C^{lo}CX₃CR1^{hi} macrophages. Row-based Z score normalized.

(B) Heatmap showing differential expression of the indicated genes in 24 h Ly6C^{hi}CX₃CR1^{lo} macrophages as compared to 72 h Ly6C^{lo}CX₃CR1^{hi} macrophages.

(C) Gene Ontology (GO) enrichment analysis of down-regulated genes in 72 h Ly6C^{lo}CX₃CR1^{hi} macrophages was classified by their biological functions.

Figure S3

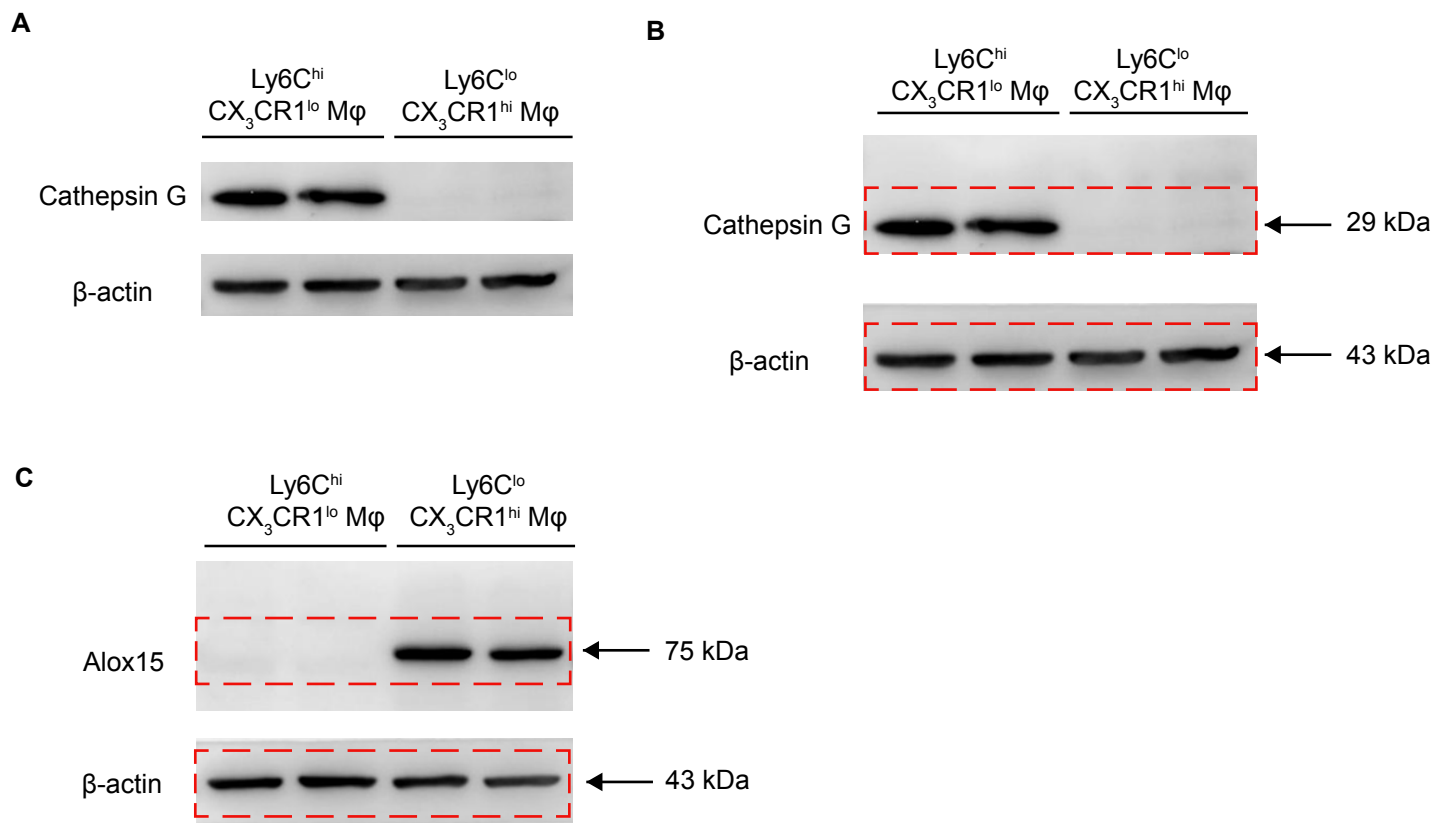


Figure S3. Western blot analysis for the differentially expressed proteins.

(A) Western blot analysis for the indicated down-regulated proteins.

(B) Full-length western blots of **Figure S3A**. The Red dotted lines show the cropping locations.

(C) Full-length western blots of **Figure 4A**.