Figures

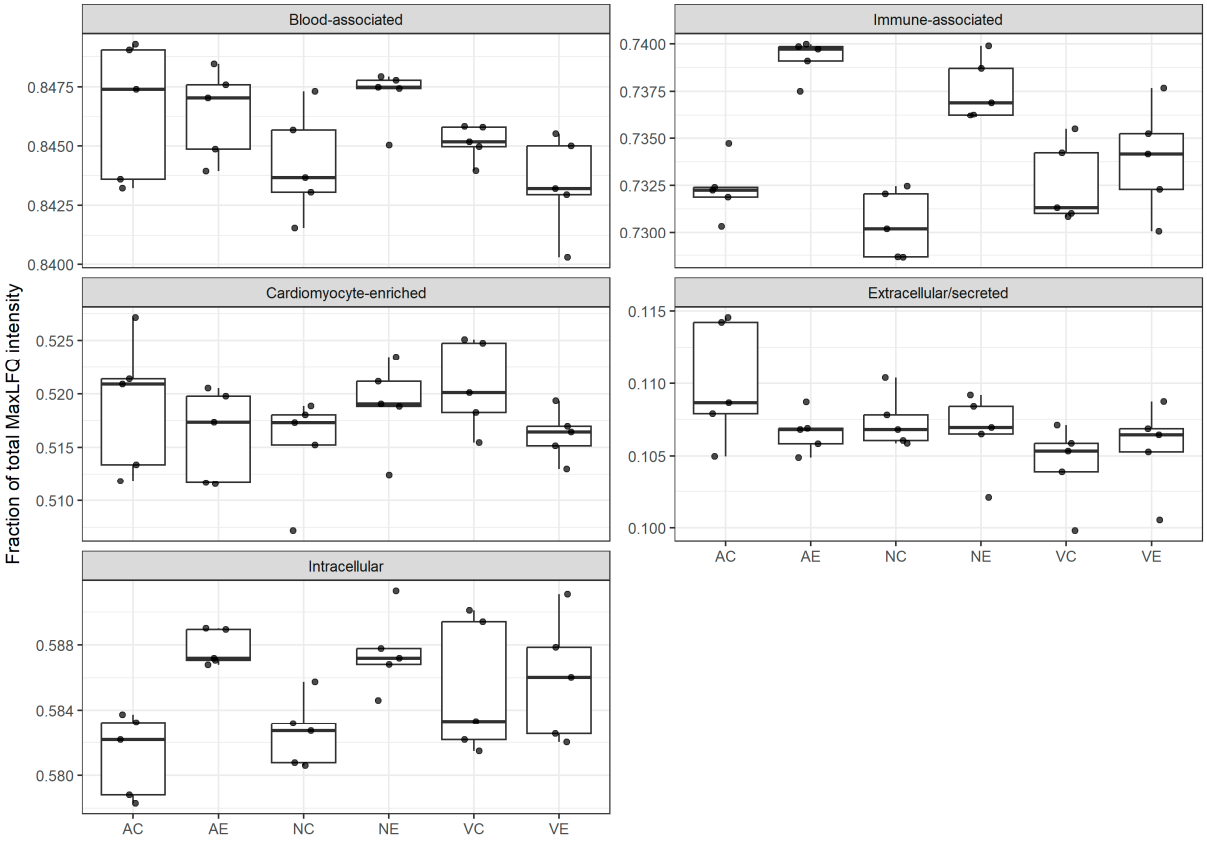


Figure S1. Composition of ventricular proteomes across experimental groups

Boxplots show the fraction of total MaxLFQ intensity attributable to each protein category (blood-associated, immune-associated, cardiomyocyte-enriched, extracellular/secreted, intracellular) across experimental groups. Individual points represent biological replicates. This figure indicates that there are no systematic differences in tissue or cellular composition across the observed proteomic profiles.

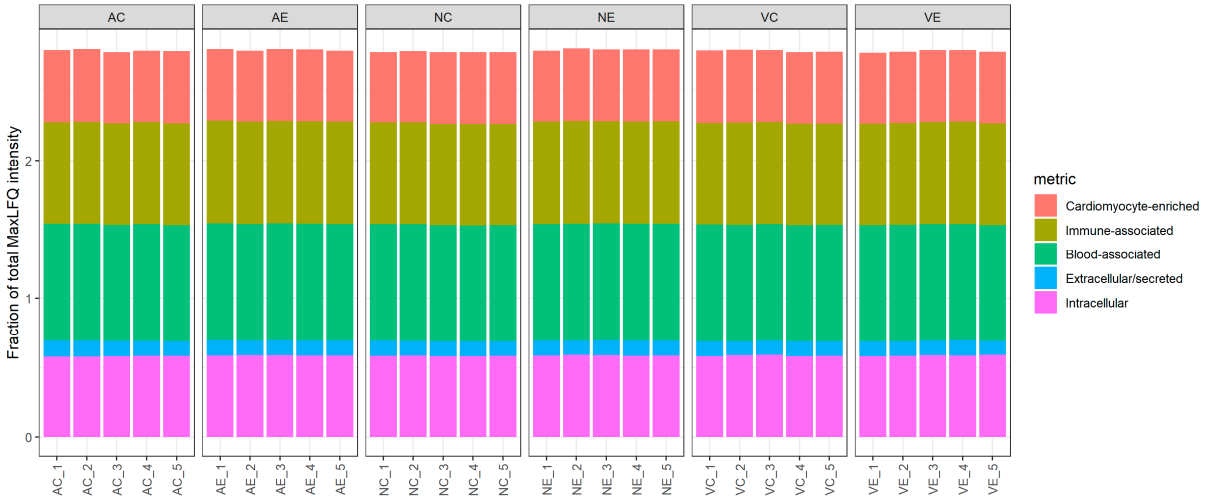


Figure S2. Sample-level composition profiles

Stacked bar plots display the relative contribution of each protein category to the total MaxLFQ signal for individual samples, grouped by experimental condition. This visualization highlights within-group consistency and confirms that no subset of samples is dominated by blood, immune, or non-cardiomyocyte proteins.