

Figure 3–figure supplement 1

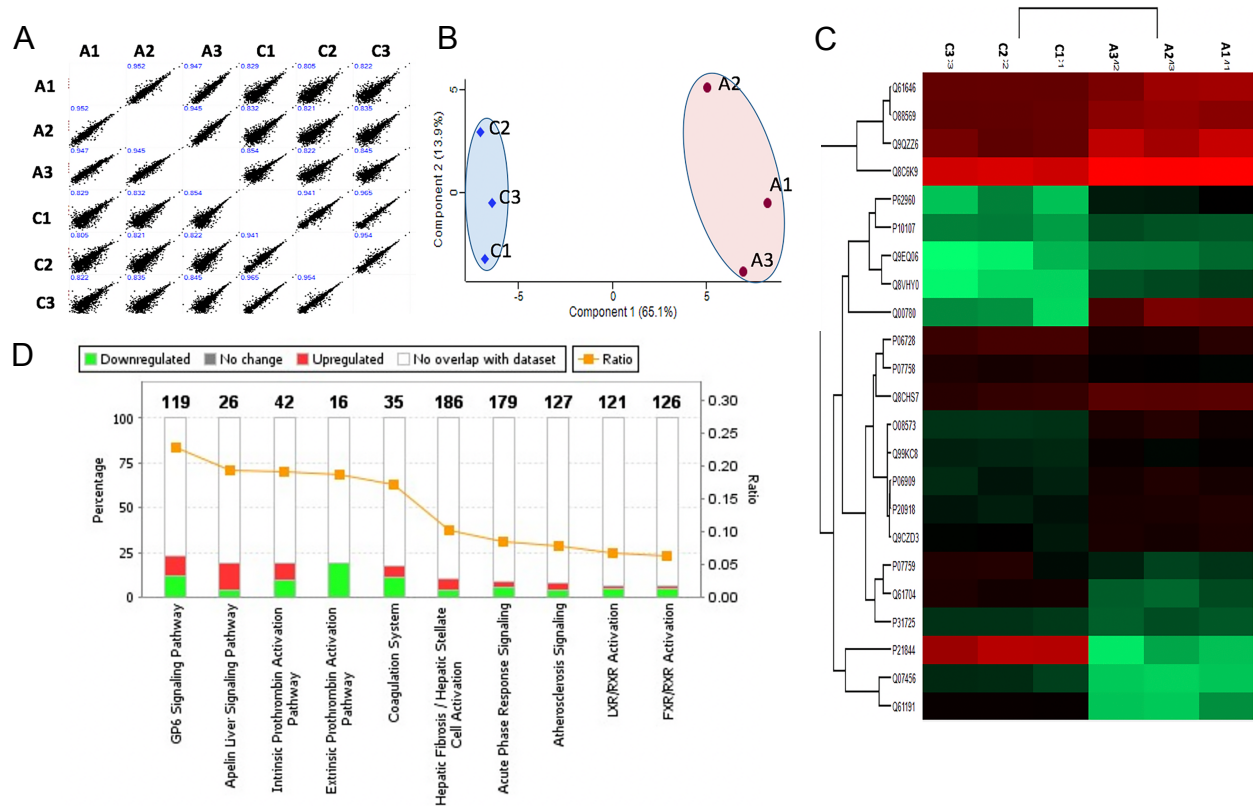


Figure 3–figure supplement 1. Shotgun proteomics of decellularized heart tissue. (A) Multi-sample scatter plots with Pearson's correlation coefficient value (blue text) showing strong correlation between individual samples. (B) Principal component analysis (PCA) of decellularized ventricular proteomes from control (C1, C2, C3) and ablated samples (A1, A2, A3). The first and second component segregation account for 65.1 % and 13.9% of the differences between the two clusters, respectively. (C) Heat map of differentially abundant ECM proteins after unsupervised hierarchical clustering. (D) Top ten canonical pathways from secreted/ECM proteins showing statistically significant differential abundance. Control: n=4; ablated: n=4.