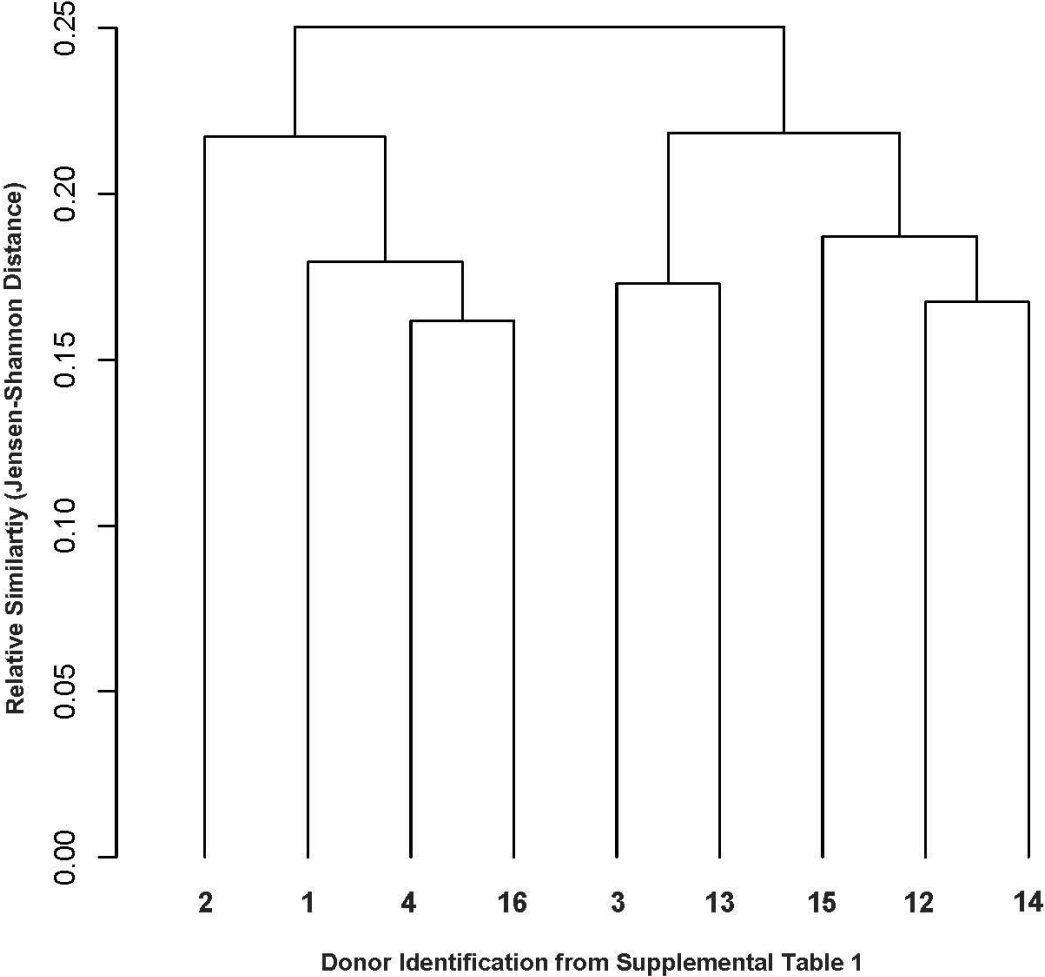
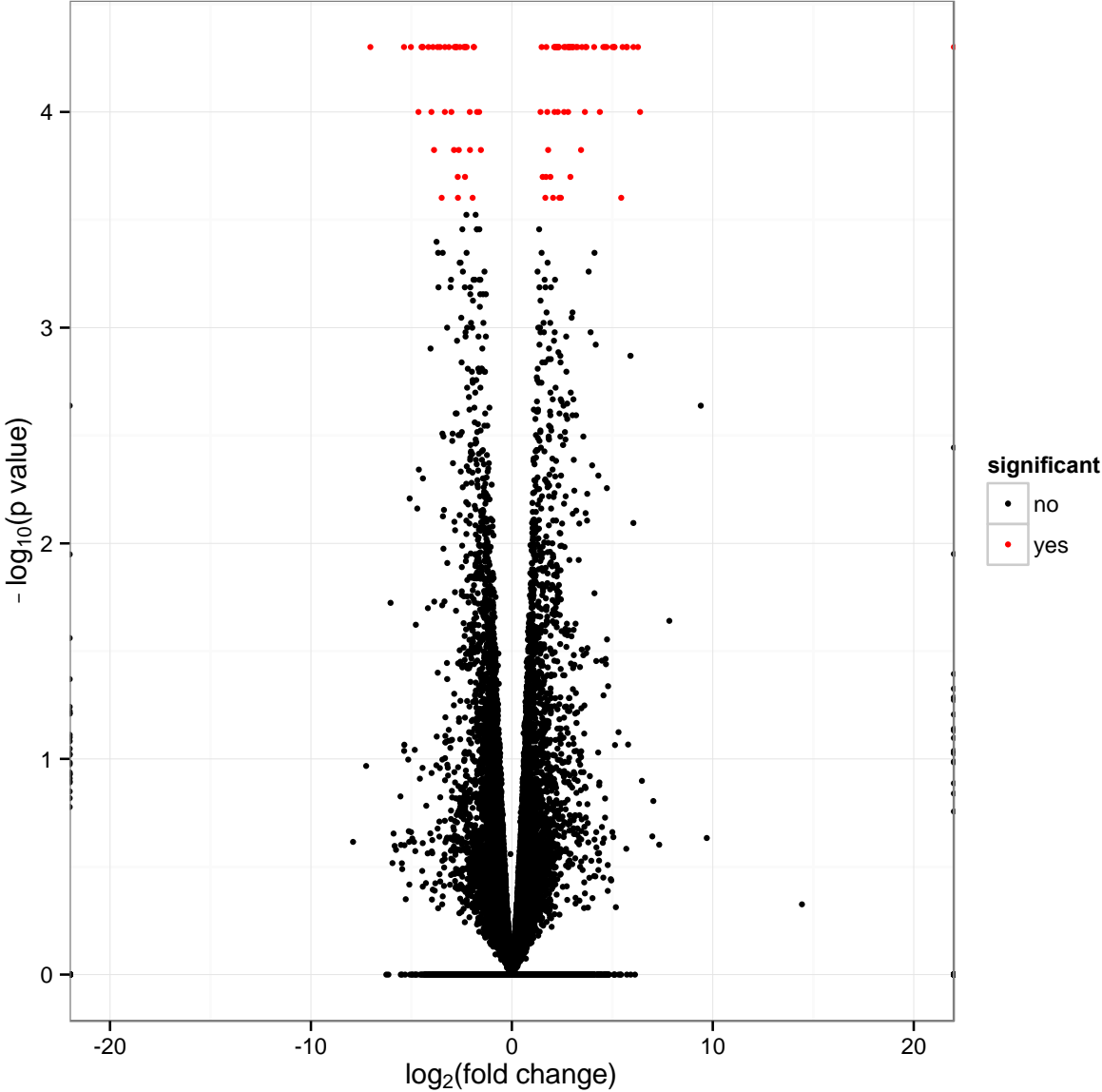


Figure S1: Dendrogram of the Gene Expression Similarity between RNAseq samples based on normalized gene expression.



The dendrogram visualizes the Jensen-Shannon distances between conditions based on normalized gene expression. Static cold storage (SCS) preservation samples cluster more similarly than partial or full persufflation (SCS+PSF) preservation samples. Identifiers correspond to Table 1; SCS samples are numbers 7,6,5,3 and SCS+PSF are numbers 18,15,17,15,16. The Jensen-Shannon divergence for one SCS and one SCS+PSF clustered more closely with the other group.

Figure S2: Volcano Plot of Global Gene Expression.



Gene transcripts that were detected in RNAseq analysis comparing islet mRNA from conditional groups are plotted as means for log₂ fold change (x-axis) and p value of the multiple testing correction analysis (y-axis). Differentially expressed genes ($P < 0.05$) between islets from persufflated and SCS organs are denoted in red, whereas nonsignificant genes are represented with black dots.