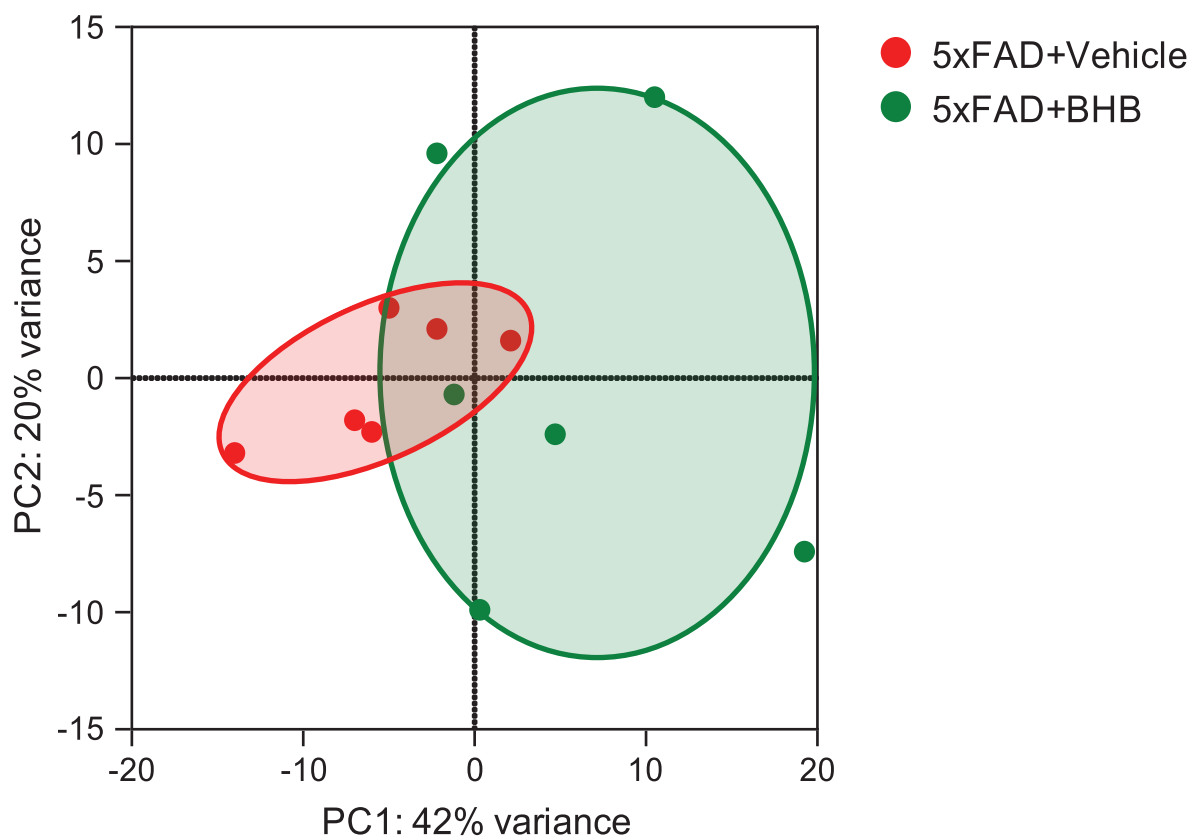
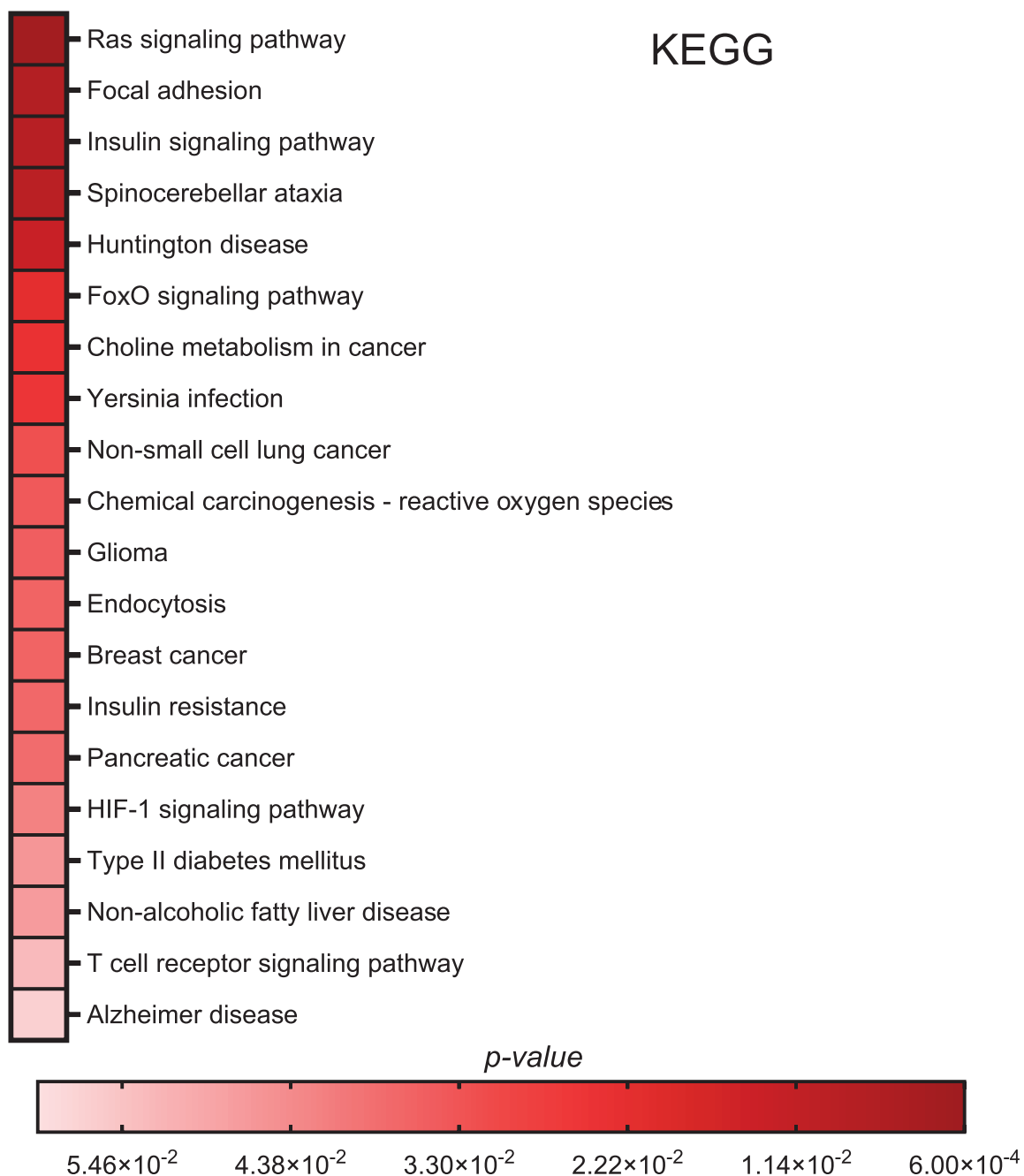


Supplementary Figure 1



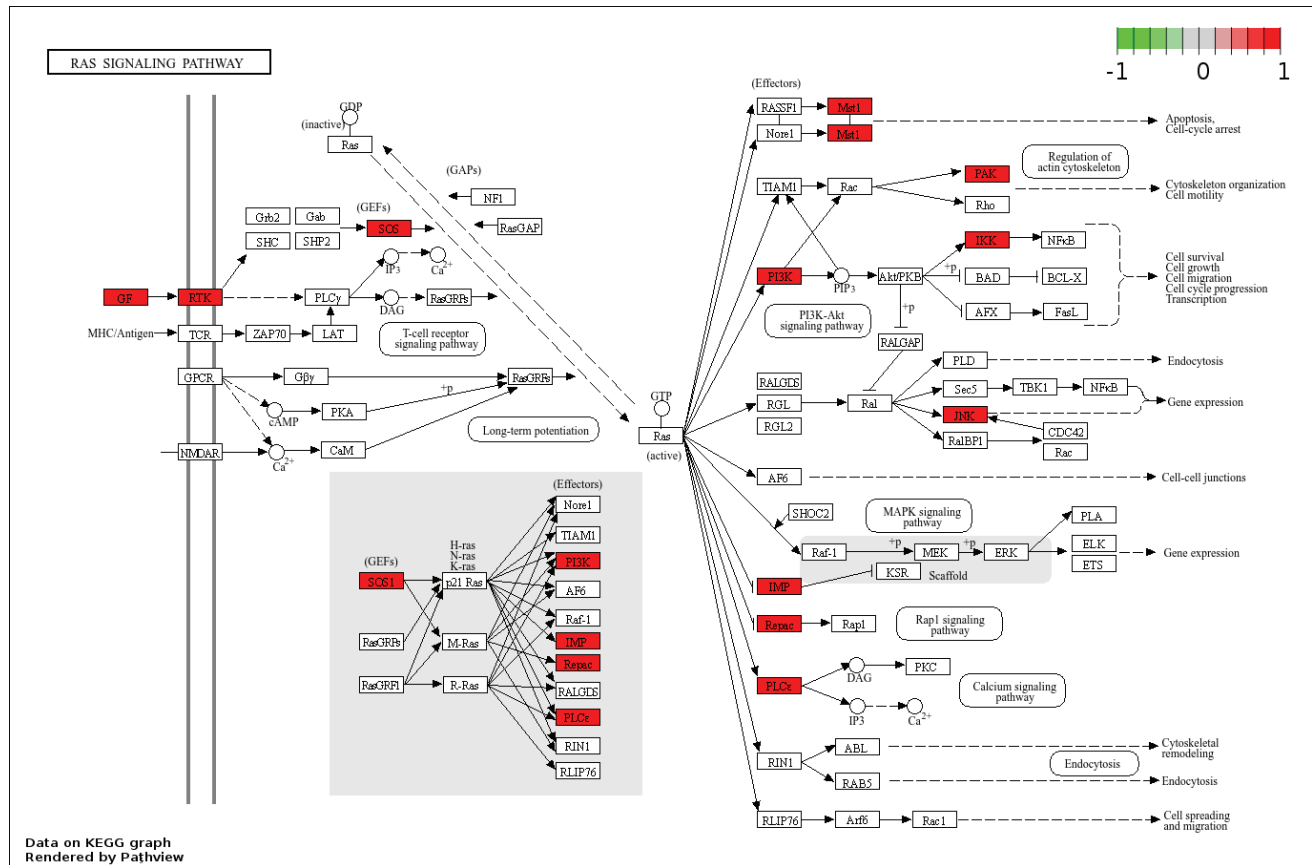
Supplementary Figure 1. Plot of principal component analysis (PCA) of gene expression revealed by RNA-seq, showing a clear separation between 5xFAD+vehicle and 5xFAD+BHB groups.

Supplementary Figure 2



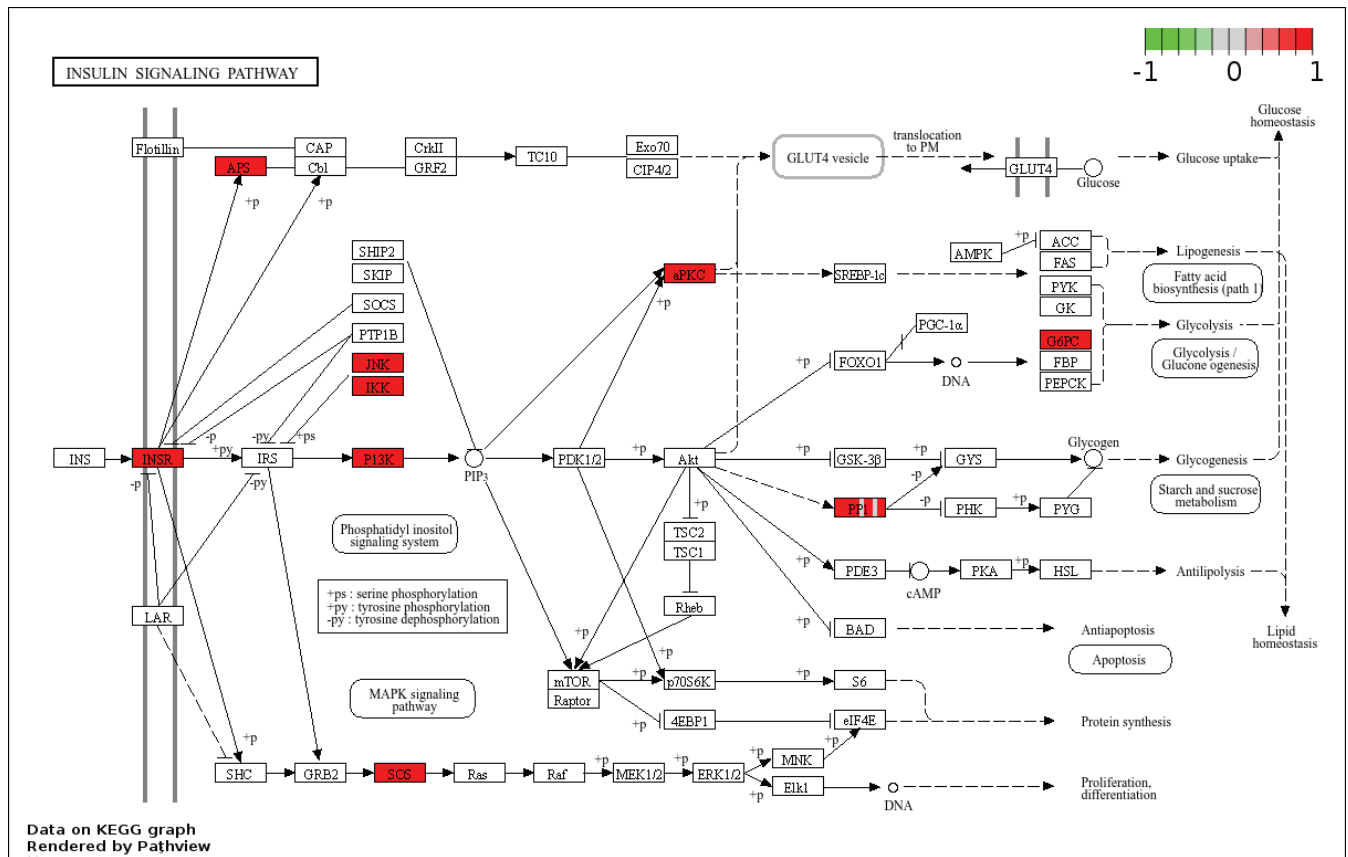
Supplementary Figure 2. Top KEGG pathways of DEGs in 5xFAD+BHB compared to 5xFAD+vehicle.

Supplementary Figure 3



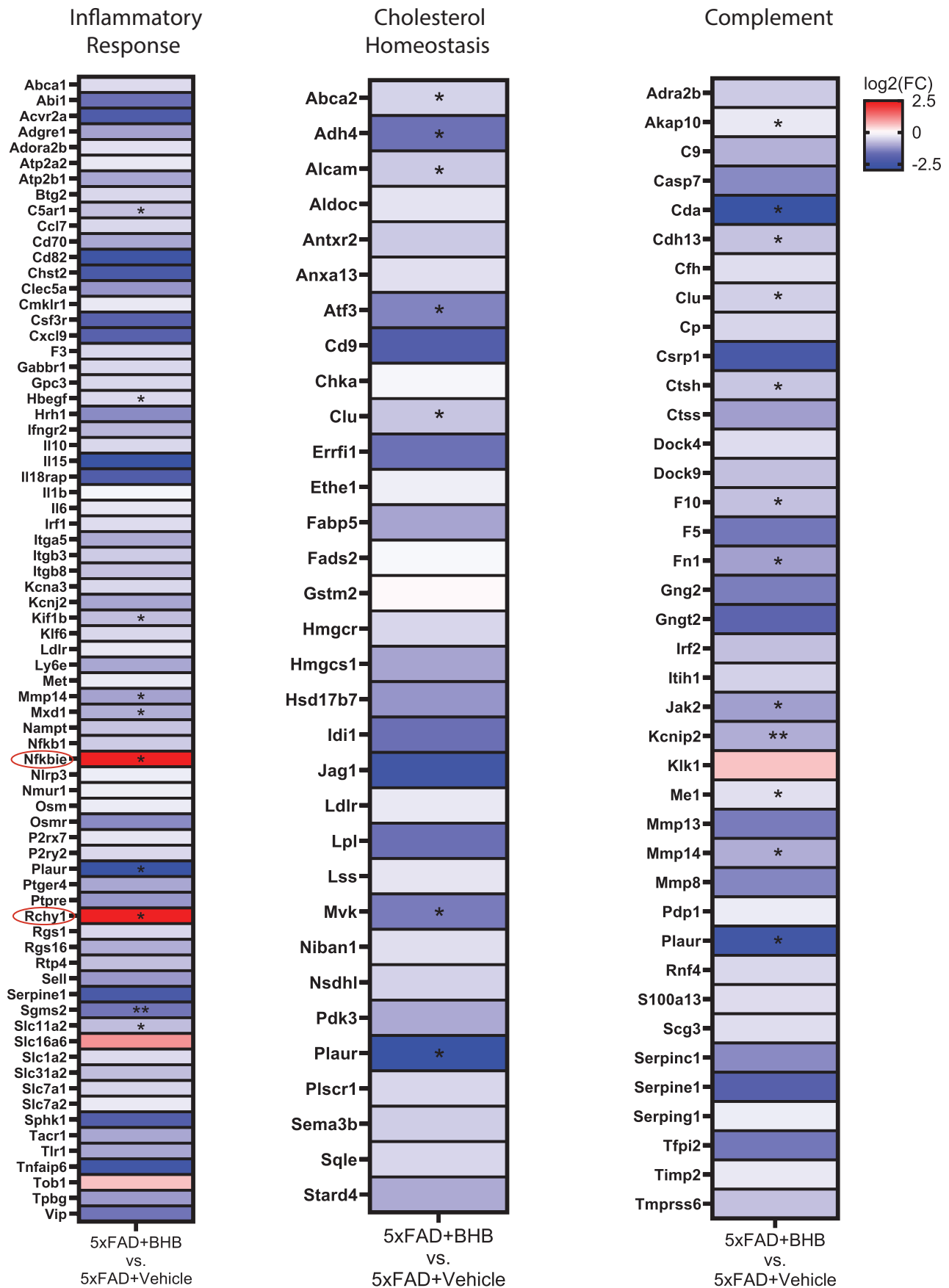
Supplementary Figure 3. RAS signaling pathway from KEGG analysis in 5xFAD+BHB compared to 5xFAD+Vehicle. Red highlights represent genes with increased relative expression in 5xFAD+BHB group.

Supplementary Figure 4



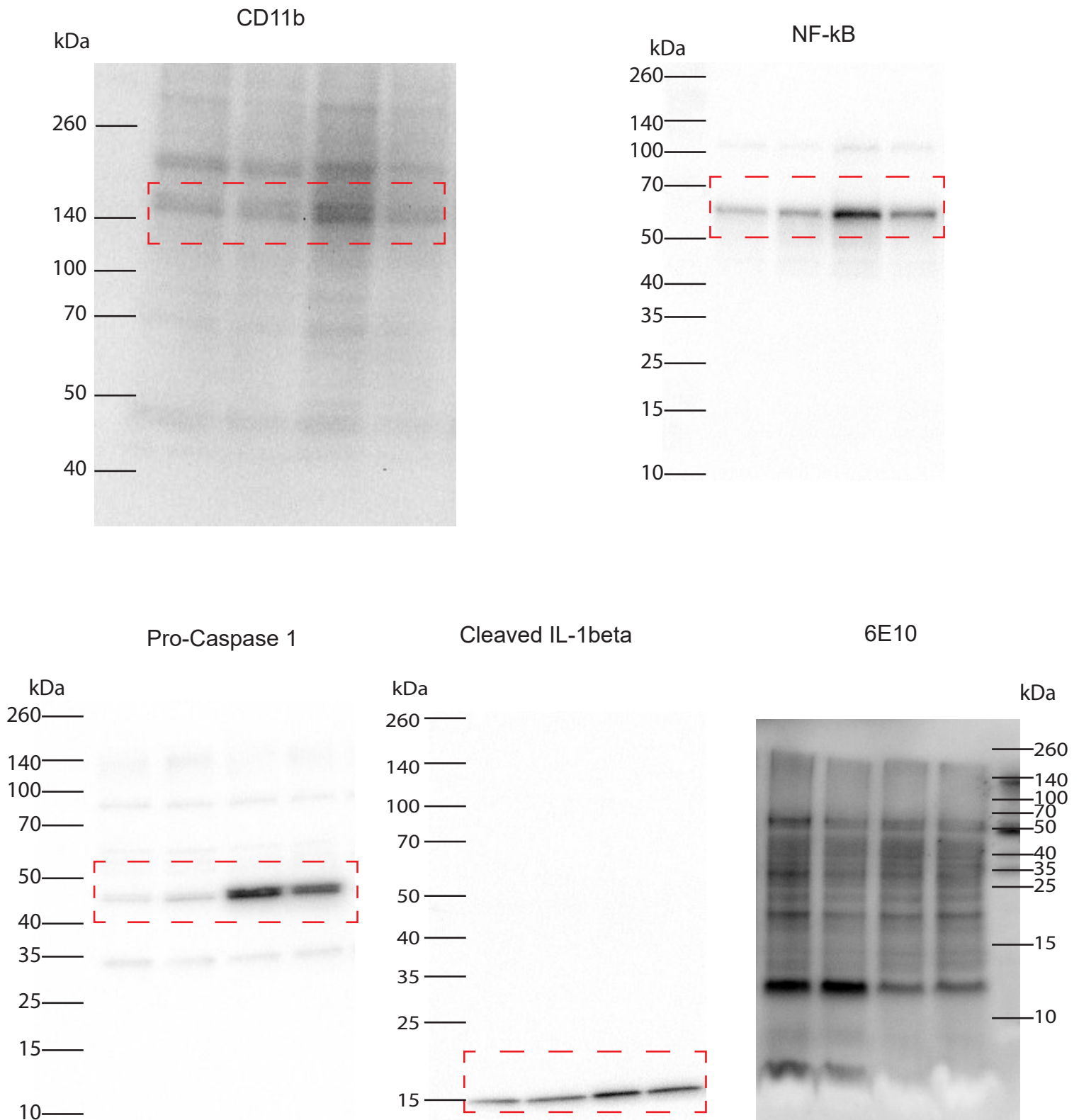
Supplementary Figure 4. Insulin signaling pathway from KEGG analysis in 5xFAD+BHB compared to 5xFAD+Vehicle. Red highlights represent genes with increased relative expression in 5xFAD+BHB group.

Supplementary Figure 5



Supplementary Figure 5. Heatmap showing the DEGs in the “Inflammatory response”, “Cholesterol homeostasis”, and “Complement” gene sets * p-value < 0.05 but FDR > 0.05, ** p-value < 0.05 and FDR < 0.05.

Supplementary Figure 6



Supplementary Figure 6. Uncropped blot