



**Figure 7. Analysis of common and unique genes and biological process found in the sulcus**

Using the genes that were found to be significantly altered in the sulcus compared to the crest, we compared which genes were common to all groups and which were unique to each condition. A stringent criteria was used to avoid including any genes that were significant in one group but also had p values close to significant others suggesting they could be common genes if power was increased. Therefore, only genes that had a  $p < 0.05$  in one group and a  $p > 0.25$  in all others were marked to be “uniquely” altered. A) A Venn diagram of the common and unique genes found among all three groups. B) A heatmap of the common genes showing similar directions of effect of the majority of genes. C) GO analysis of the common genes. D) A plot of the unique sulcal genes found in control cases. E) GO analysis of the unique control genes. F) A plot of the unique sulcal genes found in RHI cases. G) GO analysis of unique RHI genes. H) A plot of the unique sulcal genes found in CTE cases. I) GO analysis of unique CTE genes. In all plots, red dots denote genes that met FDR adjusted  $p < 0.1$ . GO analysis was performed using any gene that met nominal  $p < 0.05$  significance. The top 5 positive and negative genes for each group were annotated.