

Heatmap visualization of gene expression data across various conditions and samples. The heatmap is organized into a grid with columns representing different samples (e.g., CRR125939, CRR125943, etc.) and rows representing different genes or conditions (e.g., GO:0, GO:1, GO:0, etc.). A dendrogram at the top shows hierarchical clustering of the samples. A color scale on the left indicates the intensity of expression, ranging from blue (low) to red (high). The heatmap is divided into several sections by vertical lines, and the rows are labeled with GO terms on the right side.

