

Figure 1: A plot showing the number of genes in the top 100 clusters versus the Gene List Index. The x-axis is labeled "Gene List Index" and ranges from 0 to 18,000. The y-axis is labeled "Number of genes" and ranges from 0 to 18,000. A blue line represents the number of genes in the top 100 clusters, which starts at approximately 18,000, decreases to a minimum of about 800 at index 13,836, and then increases sharply to about 18,000 at index 18,187. A green vertical line marks the "Zero crossing at 7681". A blue vertical line marks the "Peak at 13836". A green shaded area at the bottom represents the number of genes in the top 100 clusters, which is mostly zero, with a small peak at index 13,836. The plot is divided into two regions: "clus1" (left of the green line) and "NON.clus1" (right of the blue line).

A density plot showing the distribution of ES values. The x-axis is labeled 'ES' and ranges from approximately -0.8 to 0.8. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.3 and 0.4. A vertical black line represents the 'Observed Gene Set ES value' at ES = -0.582. The area under the red curve to the left of this line is shaded in light blue. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for the left peak and 'Pos. ES: "clus1"' for the right peak. Below the x-axis, the following statistics are provided: ES = -0.582, NES = -1.51, Nom. p-val= 0.0444, FWER= 0.879, and FDR= 0.825.

The heatmap displays the expression levels of 100 genes across 100 samples. The samples are grouped into two main clusters: **clus1** (left, blue background) and **NON.clus1** (right, red background). The genes are listed on the y-axis, with the first 100 genes grouped under the **clus1** label and the remaining 100 genes grouped under the **NON.clus1** label. The color scale ranges from blue (low expression) to red (high expression). The heatmap shows a clear separation between the two clusters, with the **clus1** cluster generally showing lower expression levels for the genes in the **NON.clus1** group and higher expression levels for the genes in the **clus1** group.