

Figure 1 displays a multi-panel plot showing gene expression data for the "NON.clus1" gene set. The x-axis represents the Gene List Index, ranging from 0 to 15,000 (with data extending to 18,256 genes).

The top panel shows a red line graph representing the expression level (Y-axis) across the gene list. The curve starts low, rises sharply to a peak at index 4,812, and then gradually declines, crossing the zero line at index 10,356. A dashed horizontal line indicates the zero baseline.

The middle panel is a barcode plot showing the distribution of genes in the set. The plot consists of vertical black bars of varying heights, representing the frequency of genes. The distribution is skewed towards the left, with a peak around index 4,812.

The bottom panel is a green area plot showing the distribution of genes in the set. The area is shaded green, and the curve starts high on the left and decreases towards the right. The plot is labeled "clus1" on the left and "NON.clus1" on the right.

Number of genes: 18256 (in list), 128 (in gene set)

ES = 0.55 NES = 1.6 Nom. p-val= 0.0062 FWER= 0.712 FDR= 0.204

Heatmap visualization showing the expression of 100 genes across 100 samples. The samples are grouped into two clusters: **clus1** (left, red header) and **NON.clus1** (right, blue header). The genes are listed on the y-axis, with the first 50 genes labeled on the left and the remaining 50 genes labeled on the right. The color scale ranges from 0 (blue) to 100 (red), indicating gene expression levels. The heatmap shows a clear separation between the two clusters, with clus1 samples generally showing higher expression of the first 50 genes and lower expression of the last 50 genes, while NON.clus1 samples show the opposite pattern.