

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" ranging from 0 to 15,000. The top panel is a red line graph showing the number of genes per cluster, with a peak at 2449 and a zero crossing at 9196. The middle panel is a barcode of vertical lines representing gene lists. The bottom panel is a green area chart showing the cumulative distribution of gene lists, with "clus1" on the left and "NON.clus1" on the right.

A density plot showing the distribution of ES values. The x-axis is labeled 'ES' and ranges from -0.6 to 0.6. The y-axis is labeled 'P(ES)' and ranges from 0 to 4. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 and 0.25. A vertical black line represents the 'Observed Gene Set ES value' at ES = 0.316. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for negative values and 'Pos. ES: "clus1"' for positive values. At the bottom, statistical results are provided: ES = 0.316, NES = 1.23, Nom. p-val = 0.188, FWER = 0.997, and FDR = 0.981.

Heatmap visualization showing the expression of 100 genes across 100 samples. The color scale ranges from 0 (blue) to 100 (red). The genes are listed on the y-axis, and the samples are listed on the x-axis. The heatmap shows a clear pattern of gene expression across the samples, with some genes showing high expression (red) and others showing low expression (blue).