

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 = -0.385. 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 side and 'Pos. ES: "clus1"' for the right side. At the bottom, a summary line provides the following values: ES = -0.385, NES = -1.32, Nom. p-val = 0.121, FWER = 0.996, and FDR = 1.

Heatmap visualization showing gene expression data across 100 samples. The samples are grouped into two main clusters: **clus1** (left, red header) and **NON.clus1** (right, blue header). The genes are listed on the y-axis, with some grouped into clusters like **CLUS1** and **NON.clus1**. The color scale ranges from -2 (blue) to 2 (red), with 0 being white. The heatmap shows a clear separation between the two sample groups, with **clus1** samples generally having higher expression of genes in the **CLUS1** cluster and lower expression of genes in the **NON.clus1** cluster, and vice versa for **NON.clus1** samples.