

Figure 1 displays a multi-panel plot showing gene expression data for the "cluser4" gene set. The x-axis represents the Gene List Index, ranging from 0 to 17,346 (total number of genes in the list) and 253 (number of genes in the gene set).

The top panel shows a blue line plot representing the gene expression signal. The signal starts at a baseline, dips to a minimum at index 13,085 (labeled "Peak at 13085"), and crosses the baseline at index 9,190 (labeled "Zero crossing at 9190").

The middle panel shows a barcode plot representing the gene expression levels across the gene list index.

The bottom panel shows a green area plot representing the distribution of gene expression levels. The area is labeled "cluser4" on the left and "NON.cluser4" on the right.

The figure is a density plot showing the probability density function (PDF) 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 3. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks around -0.25 and 0.15. A vertical black line represents the 'Observed Gene Set ES value' at approximately -0.254. The area under the red curve to the left of this line is shaded in light blue. Text labels indicate 'Neg. ES "NON.clus4"' for the negative region and 'Pos. ES: "clus4"' for the positive region. At the bottom, summary statistics are provided: ES = -0.254, NES = -1.24, Nom. p-val = 0.272, FWER = 1, and FDR = 1.

Heatmap visualization showing gene expression data across 100 samples, categorized into two groups: **clus4** (left) and **NON.clus4** (right). The color scale ranges from -2 (blue) to 2 (red).

The genes listed on the y-axis are:

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