

Figure 1 displays a multi-panel plot showing gene expression data for clus1 and NON.clus1. The x-axis represents the Gene List Index (0 to 18258) and the Number of genes (18258 in list, 106 in gene set).

The top panel shows the log2(RPKM) expression level (y-axis, ranging from -1.0 to 0.0) across the Gene List Index. A blue line represents the expression profile. A green vertical dashed line marks the Zero crossing at 8581. A blue vertical dashed line marks the Peak at 15967.

The middle panel shows the barcode plot, representing the number of genes (y-axis, ranging from 0 to 10) across the Gene List Index. The plot shows a dense distribution of genes, with a peak around the Zero crossing at 8581.

The bottom panel shows the density plot of the Gene List Index (y-axis, ranging from 0.0 to 1.0). The plot is divided into two regions: "clus1" (left, green area) and "NON.clus1" (right, green area). The density is highest in the "clus1" region and decreases towards the "NON.clus1" region.

A density plot showing the distribution of ES values for two gene sets. The x-axis is labeled 'ES' and ranges from approximately -1.0 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 around -0.2 and 0.3. A vertical black line at ES = -0.54 represents the 'Observed Gene Set ES value'. The area to the left of this line is labeled 'Neg. ES "NON.clus1"' and the area to the right is labeled 'Pos. ES: "clus1"'. Below the x-axis, the following statistics are provided: ES = -0.54, NES = -1.56, Nom. p-val = 0.0732, FWER = 0.795, and FDR = 0.234.

Heatmap visualization showing the distribution of 1000 genes across two conditions: **clus1** and **NON.clus1**. The y-axis lists the genes, and the x-axis shows the two conditions. The heatmap displays a dense pattern of red and blue vertical stripes, indicating high variability in gene expression across the samples.

Gene list (Y-axis):

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