

Figure 1 displays a multi-panel plot showing gene expression data across a gene list index (0 to 18,090).

The top panel shows the  $\log_2(\text{RPKM})$  expression level (red line) versus the Gene List Index. The expression peaks at index 4685 (labeled "Peak at 4685") and crosses the zero line at index 10263 (labeled "Zero crossing at 10263"). A dashed horizontal line indicates the zero expression level.

The middle panel shows a barcode representation of the gene list, with vertical lines indicating the presence of genes at specific indices.

The bottom panel shows the distribution of genes, with the area under the curve shaded green. The distribution is labeled "clus1" on the left and "NON.clus1" on the right, indicating the separation of genes into two clusters.

The x-axis is labeled "Gene List Index" and "Number of genes: 18090 (in list), 94 (in gene set)".

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 approximately 0.381. 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 = 0.381, NES = 1.43, Nom. p-val = 0.0455, FWER = 0.993, and FDR = 0.204.

Gene Set Null Density

Observed Gene Set ES value

Neg. ES "NON.clus1"

Pos. ES: "clus1"

ES

ES = 0.381 NES = 1.43 Nom. p-val = 0.0455 FWER = 0.993 FDR = 0.204

[illegible]