

Figure 1 displays a multi-panel plot showing gene expression data for 18,113 genes. The x-axis represents the Gene List Index (0 to 18,113).

The top panel shows the log₂(RPKM) expression values (red line). The expression peaks at 1900 (labeled "Peak at 1900") and crosses zero at 10828 (labeled "Zero crossing at 10828").

The middle panel shows a barcode representation of gene expression, with vertical lines indicating the presence of genes. The genes are grouped into two clusters: "clus1" (left) and "NON.clus1" (right).

The bottom panel shows the distribution of genes, with a green area plot. The area is divided into two regions: "clus1" (left) and "NON.clus1" (right).

Number of genes: 18113 (in list), 72 (in gene set)

The figure is a density plot showing the probability density function (PDF) of ES values. The x-axis is labeled 'ES' and ranges from approximately -0.75 to 0.75, with major ticks at -0.5, 0.0, and 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 3.0, with major ticks every 0.5 units. A red curve represents the 'Gene Set Null Density', which is a bimodal distribution with peaks at approximately ES = -0.25 (P ≈ 2.0) and ES = 0.3 (P ≈ 1.7). A vertical black line represents the 'Observed Gene Set ES value' at ES = 0.474. The area under the red curve to the left of the observed value is shaded light blue and labeled 'Neg. ES "NON.clus1"'. The area under the red curve to the right of the observed value is shaded light red and labeled 'Pos. ES: "clus1"'. Below the x-axis, the following text is displayed: 'ES = 0.474 NES = 1.43 Nom. p-val= 0.0998 FWER= 0.929 FDR= 0.233'.