

Figure 1 displays a multi-panel plot showing gene expression data across a gene list index (0 to 18,197).

The top panel shows the $\log_2(\text{RPKM})$ expression level (Y-axis, ranging from -0.5 to 0.5) versus the Gene List Index (X-axis, ranging from 0 to 18,197). A red line represents the expression profile. A vertical red dotted line marks the "Peak at 3888", and a vertical green dotted line marks the "Zero crossing at 9694". A horizontal dashed line is drawn at $\log_2(\text{RPKM}) = 0$.

The middle panel is a barcode plot showing the presence (black vertical lines) of genes across the gene list index. The Y-axis ranges from -0.5 to 0.5.

The bottom panel is a density plot showing the distribution of genes. The Y-axis ranges from -1.0 to 0.0. The area under the curve is shaded green, labeled "clus1", and the area above the curve is white, labeled "NON.clus1".

Gene List Index
Number of genes: 18197 (in list), 94 (in gene set)

A density plot showing the distribution of ES values for two gene sets. The x-axis is labeled 'ES' and ranges from -0.6 to 0.6. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 and 0.25. A black vertical line at ES = 0.563 represents the 'Observed Gene Set ES value'. The area to the left of the line is labeled 'Neg. ES "NON.clus1"' and the area to the right is labeled 'Pos. ES: "clus1"'. Below the plot, the following statistics are provided: ES = 0.563, NES = 1.78, Nom. p-val = 0.00197, FWER = 0.347, and FDR = 0.0727.

[illegible]