

Figure 1 displays a multi-panel plot showing gene expression data for the "cluser1" gene set, which contains 86 genes. The x-axis for all panels is the "Gene List Index" (0 to 18,748).

The top panel shows the $\log_2(\text{RPKM})$ expression level (blue line). A dashed horizontal line indicates the baseline. A vertical green dotted line marks the "Zero crossing at 8853". A vertical blue dotted line marks the "Peak at 13790".

The middle panel shows the barcode plot, representing the number of genes (black vertical lines) across the gene list index.

The bottom panel shows the probability distribution (green area). The region to the left of the zero crossing is labeled "clus1", and the region to the right is labeled "NON.clus1".

Number of genes: 18748 (in list), 86 (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 -0.5 to 0.5. 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 -0.18 (height ~2.9) and 0.18 (height ~3.1). A vertical black line represents the 'Observed Gene Set ES value' at ES = -0.329. The area under the red curve to the left of this line is shaded in light blue. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for the left tail and 'Pos. ES: "clus1"' for the right tail. Below the x-axis, the following statistics are provided: ES = -0.329, NES = -1.58, Nom. p-val = 0.0738, FWER = 0.798, and FDR = 1.

[illegible]