

Figure 1 displays a multi-panel plot showing gene expression data across a gene list index (0 to 17,824).

The top panel shows the $\log_2(\text{RPKM})$ expression level (blue line) versus the Gene List Index. A dashed horizontal line indicates a threshold at $\log_2(\text{RPKM}) = 1.5$. The expression level decreases from approximately 1.5 at index 0 to a minimum around index 12,366, then increases sharply towards index 17,824.

The middle panel shows the expression level (black vertical bars) versus the Gene List Index. The bars represent the expression level of individual genes, showing a similar trend to the blue line in the top panel.

The bottom panel shows the expression level (green area) versus the Gene List Index. The area represents the cumulative expression level, showing a sharp increase starting around index 12,366, reaching a plateau around index 17,824.

Key features marked on the plot include:

- Zero crossing at 9125 (indicated by a green vertical dashed line).
- Peak at 12366 (indicated by a blue vertical dashed line).

The x-axis is labeled "Gene List Index" and "Number of genes: 17824 (in list), 113 (in gene set)". The y-axis is labeled " $\log_2(\text{RPKM})$ ".

A density plot showing the distribution of ES values for two gene sets. The x-axis is labeled 'ES' and ranges from -0.5 to 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.0. A red curve represents the 'Gene Set Null Density'. A vertical black line at ES = -0.428 represents the 'Observed Gene Set ES value'. The area to the left of this line is labeled 'Neg. ES "NON.clus4"' and the area to the right is labeled 'Pos. ES: "clus4"'. Below the x-axis, the following text is displayed: ES = -0.428 NES = -1.46 Nom. p-val= 0.205 FWER= 0.921 FDR= 1

[illegible]