

Figure 1 displays a multi-panel plot showing gene expression data for cluster 1. The x-axis represents the Gene List Index, ranging from 0 to 17,346 (total genes in list) and 85 (genes in gene set).

The top panel shows the log₂(RPKM) expression level (blue line) across the gene list index. The expression level decreases from approximately 1.5 at index 0 to a minimum around index 11,750, then increases sharply to approximately 1.5 at index 17,346. A dashed horizontal line indicates the zero crossing point at index 9,217. A vertical dotted line marks the peak at index 11,750.

The middle panel shows the distribution of genes across the gene list index, represented by vertical black lines. The density of genes is highest between index 11,750 and 15,000.

The bottom panel shows the density of genes in cluster 1 (green area). The density is highest at the beginning of the gene list (index 0) and decreases as the index increases, reaching a minimum around index 11,750. The area is labeled "clus1" on the left and "NON.clus1" on the right.

Number of genes: 17346 (in list), 85 (in gene set)

A density plot showing the probability density function $P(ES)$ on the y-axis (ranging from 0.0 to 1.5) against the ES value on the x-axis (ranging from -1.0 to 1.0). The plot features a red curve representing the 'Gene Set Null Density' and a vertical black line at $ES = -0.591$ representing the 'Observed Gene Set ES value'. The null density curve is bimodal, with peaks around $ES = -0.3$ and $ES = 0.25$. The observed value is located in the left tail of the distribution. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for negative values and 'Pos. ES: "clus1"' for positive values. At the bottom, a summary of statistics is provided: $ES = -0.591$, $NES = -1.48$, $Nom. p\text{-val} = 0.16$, $FWER = 0.845$, and $FDR = 1$.

[illegible]