

Figure 1 displays a multi-panel plot illustrating gene set enrichment analysis results. The x-axis represents the Gene List Index, ranging from 0 to 22,748 (total genes in list) and 126 (genes in the set).

The top panel shows the Enrichment Score (ES) curve (blue line). The curve starts at a baseline, dips to a minimum around index 17,175, and then rises sharply. A horizontal dashed line indicates the zero crossing at index 10,010. A vertical green dotted line marks the zero crossing, and a vertical blue dotted line marks the peak at index 17,175.

The middle panel shows a barcode plot representing the distribution of genes in the gene set across the gene list index. The bottom panel shows a green area plot representing the distribution of genes in the gene set across the gene list index. The area is labeled "clus1" on the left and "NON.clus1" on the right.

Number of genes: 22748 (in list), 126 (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 to 3. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 and 0.25. A vertical black line at ES = -0.415 represents the 'Observed Gene Set ES value'. The area to the left of this line is labeled 'Neg. ES "NON.clus1"' and the area to the right is labeled 'Pos. ES: "clus1"'. Below the x-axis, the following text is displayed: ES = -0.415 NES = -1.46 Nom. p-val= 0.0611 FWER= 0.825 FDR= 0.387.

[illegible]