

Figure 1 displays a multi-panel plot illustrating gene set analysis results. The x-axis for all panels is the Gene List Index, ranging from 0 to 18,113 (total number of genes in the list) and 83 (number of genes in the gene set).

The top panel shows the 'clus2' statistic (blue line) plotted against the Gene List Index. The statistic starts high, decreases, and then increases, forming a U-shape. Key features are marked: 'Zero crossing at 7260' and 'Peak at 11954'. A dashed horizontal line indicates a threshold.

The middle panel is a barcode plot showing the distribution of gene set sizes. The vertical lines represent the number of genes in each set, with a dense cluster of lines around the peak at 11,954.

The bottom panel is a green area plot showing the distribution of gene set sizes. The area is labeled 'clus2' on the left and 'NON.clus2' on the right, indicating the distribution of gene sets that are or are not in the 'clus2' 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 -0.6 to 0.6. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 3.0. 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 = -0.434 represents the 'Observed Gene Set ES value'. 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.clus2"' for the left side and 'Pos. ES: "clus2"' for the right side. At the bottom, statistical values are provided: ES = -0.434, NES = -1.54, Norm. p-val = 0.0558, FWER = 0.819, and FDR = 0.169.

[illegible]