

Figure 1 displays a multi-panel plot showing the distribution of gene sets across a gene list index. The x-axis represents the Gene List Index, ranging from 0 to 18,646 (total number of genes in the list) and 38 (number of genes in the gene set). The y-axis represents the number of gene sets, ranging from 0 to 100.

The top panel shows a red line plot representing the number of gene sets (y-axis) versus the Gene List Index (x-axis). The line starts at 0, rises sharply to a peak of approximately 100 at index 2840, and then gradually decreases, crossing the zero line at index 8614. A horizontal dashed line is drawn at y=0.

The middle panel shows a series of vertical black bars representing the number of gene sets at each index. The bars are concentrated at the beginning of the index, with a prominent peak at index 2840. The bars extend to the right, indicating the presence of gene sets at higher indices.

The bottom panel shows a green area plot representing the cumulative distribution of gene sets. The area is highest at the beginning of the index (near index 0) and decreases as the index increases, reaching zero at index 8614. The area is labeled "clus2" on the left and "NON.clus2" on the right.

Key annotations include:

- Peak at 2840
- Zero crossing at 8614
- "clus2"
- "NON.clus2"

Gene List Index
Number of genes: 18646 (in list), 38 (in gene set)

A density plot showing the probability density function (P(ES)) of ES values. The x-axis is labeled 'ES' and ranges from -1.0 to 1.0. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 1.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks around -0.5 and 0.5. A vertical black line at ES = 0.759 represents the 'Observed Gene Set ES value'. The plot is divided into two regions: 'Neg. ES "NON.clus2"' on the left and 'Pos. ES: "clus2"' on the right. Below the x-axis, the following statistics are provided: ES = 0.759, NES = 1.56, Nom. p-val= 0.0325, FWER= 0.76, and FDR= 0.255.

[illegible]