

Figure 1 displays a multi-panel plot illustrating the relationship between the Gene List Index (X-axis, ranging from 0 to 18,361) and various metrics.

The top panel shows a red line representing a metric (likely a correlation or enrichment score) that starts near 0, rises sharply to a peak of approximately 0.35 at index 4160, and then gradually declines, crossing the zero line at index 8936. A horizontal dashed line is drawn at y=0.0.

The middle panel shows a barcode plot where vertical lines represent the presence of specific genes in different gene sets. The lines are densely packed, indicating a high frequency of genes across the index range.

The bottom panel shows a green area plot representing the distribution of gene sets. The area is labeled "clus1" on the left and "NON.clus1" on the right, indicating the proportion of genes belonging to these two clusters. The distribution is skewed towards the left, with a peak near index 0.

Key annotations include:

- Peak at 4160 (marked by a red dotted line).
- Zero crossing at 8936 (marked by a green dotted line).

Number of genes: 18361 (in list), 125 (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 -0.4 to 0.4. The y-axis is labeled 'P(ES)' and ranges from 0 to 4. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.2 and 0.2. A black vertical line at ES = 0.357 represents the 'Observed Gene Set ES value'. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for negative values and 'Pos. ES: "clus1"' for positive values. Below the plot, the following statistics are provided: ES = 0.357, NES = 1.53, Nom. p-val = 0.0364, FWER = 0.859, and FDR = 0.119.

ES = 0.357 NES = 1.53 Nom. p-val = 0.0364 FWER = 0.859 FDR = 0.119

[illegible]