

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

The top panel shows a red line representing a metric (likely a correlation or enrichment score) that peaks at 4160 and crosses zero at 8936. The y-axis ranges from -0.2 to 0.0.

The middle panel shows a barcode of vertical black lines representing gene sets. The y-axis ranges from -0.4 to -0.6.

The bottom panel shows a green area plot representing the probability of a gene set being in "clus1" (dark green) or "NON.clus1" (light green). The y-axis ranges from -0.8 to -1.0.

Gene List Index: 0, 5000, 10000, 15000

Number of genes: 18361 (in list), 125 (in gene set)

Peak at 4160

Zero crossing at 8936

"clus1"

"NON.clus1"

A density plot showing the distribution of ES values. 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 vertical black line represents the 'Observed Gene Set ES value' at approximately 0.357. 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.

[illegible]