

Figure 1 displays a multi-panel plot showing the relationship between Gene List Index (X-axis, 0 to 18,258) and various metrics.

The top panel shows a blue line representing a metric (likely a score or density) that decreases from approximately 0.3 at index 0 to a minimum around index 14,306, then increases sharply back to approximately 0.3. A horizontal dashed line is drawn at y=0.3. A green vertical line marks the "Zero crossing at 8581", and a blue vertical line marks the "Peak at 14306".

The middle panel shows a barcode representation of gene sets, with vertical lines indicating the presence of specific genes. The density of lines increases significantly after the peak at 14,306.

The bottom panel shows a green area plot representing the proportion of genes in "clus1" (left) and "NON.clus1" (right) clusters. The proportion of genes in "clus1" decreases sharply after the peak at 14,306, while the proportion in "NON.clus1" increases sharply.

Number of genes: 18258 (in list), 112 (in gene set)

A density plot showing the distribution of ES values. The x-axis is labeled 'ES' and ranges from approximately -1.0 to 1.0, with major ticks at -0.5, 0.0, and 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.0, with major ticks at 0.0, 0.5, 1.0, 1.5, and 2.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.3 (height ~1.5) and 0.3 (height ~1.4). A vertical black line represents the 'Observed Gene Set ES value' at ES = -0.622. 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.clus1"' for the left side and 'Pos. ES: "clus1"' for the right side. Below the x-axis, the following statistics are provided: ES = -0.622, NES = -1.51, Nom. p-val= 0.0267, FWER= 0.88, and FDR= 0.229.

[illegible]