

Figure 1: A multi-panel plot showing the relationship between gene list index, gene set size, and cluster membership. The top panel is a red line graph of the number of genes in the gene set (y-axis, 0 to 18113) versus the gene list index (x-axis, 0 to 18113). The line starts at 0, rises to a peak of 18113 at index 5224, and then gradually decreases to 0 at index 10828. A horizontal dashed line is at y=18113. The middle panel shows a barcode of vertical black lines representing the number of genes in the gene set for each gene list index. The bottom panel is a green area plot showing the number of genes in the gene set (y-axis, 0 to 18113) versus the gene list index (x-axis, 0 to 18113). The area is green for indices 0 to 5224 and white for indices 5224 to 10828. The x-axis is labeled 'Gene List Index' and 'Number of genes: 18113 (in list), 83 (in gene set)'. The y-axis is labeled 'Number of genes in the gene set'.

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 = 0.426 represents the 'Observed Gene Set ES value'. The area to the left of this line is labeled 'Neg. ES "NON.clus1"' and the area to the right is labeled 'Pos. ES: "clus1"'. Below the x-axis, the following statistics are provided: ES = 0.426, NES = 1.49, Nom. p-val= 0.0825, FWER= 0.862, FDR= 0.213.

[illegible]