

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" ranging from 0 to 17,824. The top panel shows a red line graph representing the number of genes in the gene set (y-axis, 0 to 17,824). The line starts at 0, rises sharply to a peak of 17,824 at index 2724, and then gradually declines, crossing the x-axis at index 9125. A horizontal dashed line is drawn at y = 17,824. The middle panel shows a barcode of vertical lines representing gene lists. The bottom panel shows a green area plot representing the distribution of gene lists. The area is labeled "clus4" on the left and "NON.clus4" on the right. The x-axis is labeled "Gene List Index" and "Number of genes: 17824 (in list), 54 (in gene set)".

A density plot showing the probability density function (PDF) of ES values. The x-axis is labeled 'ES' and ranges from -0.5 to 0.5. 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 -0.35 (height ~2.2) and 0.35 (height ~1.6). A vertical black line at ES = 0.462 represents the 'Observed Gene Set ES value'. The plot is divided into two regions: 'Neg. ES "NON.clus4"' on the left and 'Pos. ES: "clus4"' on the right. Below the x-axis, the following statistics are displayed: ES = 0.462 NES = 1.19 Nom. p-val= 0.206 FWER= 0.986 FDR= 1.

[illegible]