

Figure 1: A plot showing the number of genes in the "cluser" set as a function of the gene list index. The x-axis is "Gene List Index" (0 to 18646) and the y-axis is "Number of genes" (0 to 28). A blue line represents the "cluser" set, which starts at 28 genes and decreases to 0 at index 9167. A green vertical line marks the "Zero crossing at 9167". A blue vertical line marks the "Peak at 14027". A green shaded area at the bottom represents the "NON.cluser" set, which is 0 for indices 0 to 9167 and increases to 28 for indices 14027 to 18646. The plot is labeled "cluser" and "NON.cluser".

A density plot showing the distribution 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 to 3. 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 ES = -0.414. 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 negative region and 'Pos. ES: "clus1"' for the positive region. At the bottom, a summary line provides the following values: ES = -0.414, NES = -1.56, Nom. p-val= 0.0536, FWER= 0.782, FDR= 1.

[illegible]