

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" ranging from 0 to 18169. The top panel shows a blue line representing the "Number of genes in the set" (y-axis, 0 to 18169). The line starts at (0, 18169), decreases to a minimum at index 15374 (labeled "Peak at 15374"), and then increases. A vertical green dotted line marks the "Zero crossing at 10414". The middle panel shows a barcode of vertical black lines representing the "Number of genes in the list" (y-axis, 0 to 18169) against the "Gene List Index" (x-axis, 0 to 18169). The bottom panel shows a green area representing the "Number of genes in the set" (y-axis, 0 to 18169) against the "Gene List Index" (x-axis, 0 to 18169). The area is labeled "clus3" and "NON.clus3".

A density plot showing the probability density function (P(ES)) of ES values. The x-axis is labeled 'ES' and ranges from approximately -0.8 to 0.8, 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 around -0.3 and 0.3. A vertical black line at ES = -0.635 represents the 'Observed Gene Set ES value'. 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.clus3"' for the left side and 'Pos. ES: "clus3"' for the right side. At the bottom, a summary line provides the following values: ES = -0.635, NES = -1.89, Nom. p-val = 0.00794, FWER = 0.348, and FDR = 1.

[illegible]