

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" ranging from 0 to 15,000. The top panel shows a red line plot representing a function that starts at a baseline, rises to a peak at index 6089, and then declines, crossing the baseline at index 9679. The middle panel is a barcode plot showing the density of genes across the index, with vertical black lines representing individual genes. The bottom panel is a density plot showing the distribution of gene list indices. A green shaded area represents the "clus2" set, which is concentrated at low indices. The white area represents the "NON.clus2" set, which is distributed across the entire range of indices.

The figure is a density plot showing the probability density function (PDF) of ES values for two gene sets. 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 1.5, with major ticks at 0.0, 0.5, 1.0, and 1.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks around -0.3 and 0.3. A black vertical line at ES = 0.554 represents the 'Observed Gene Set ES value'. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus2"' for negative values and 'Pos. ES: "clus2"' for positive values. Below the x-axis, the following statistics are provided: ES = 0.554, NES = 1.57, Nom. p-val = 0.0947, FWER = 0.949, and FDR = 0.208.

Gene Set Null Density

Observed Gene Set ES value

P(ES)

Neg. ES "NON.clus2"

Pos. ES: "clus2"

ES

ES = 0.554 NES = 1.57 Nom. p-val = 0.0947 FWER = 0.949 FDR = 0.208