

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" with values 0, 5000, 10000, and 15000. Below the x-axis, text indicates "Number of genes: 18113 (in list), 115 (in gene set)".

- Top Panel:** A red line plot showing a metric that starts at 0.0, rises to a peak of approximately 0.35 at index 2925 (marked by a red dotted vertical line), and then gradually declines, crossing 0.0 at index 8811 (marked by a green dotted vertical line).
- Middle Panel:** A barcode plot showing vertical black lines of varying heights, representing a distribution across the gene list index.
- Bottom Panel:** A green area plot showing a metric that starts at 1.0 and decreases rapidly to near 0.0 by index 2925, remaining near 0.0 until index 8811, where it slightly increases before returning to 0.0. The area is labeled "clus3" on the left and "NON.clus3" on the right.

A density plot showing the probability density function (PDF) 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 2.5, with major ticks at 0.0, 0.5, 1.0, 1.5, 2.0, and 2.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.3 (height ~1.85) and 0.35 (height ~1.4). A vertical black line at ES = 0.574 represents the 'Observed Gene Set ES value'. The area under the red curve to the left of this line is shaded light red, and the area to the right is shaded light blue. Text labels 'Neg. ES "NON.clus3"' and 'Pos. ES: "clus3"' are placed below the x-axis at approximately -0.5 and 0.574 respectively. At the bottom of the plot, the following statistics are listed: ES = 0.574 NES = 1.46 Nom. p-val= 0.0646 FWER= 0.895 FDR= 0.192.

[illegible]