

Figure 1 displays a multi-panel plot illustrating gene expression data and cluster assignment for the 'NON.clus1' cluster.

The top panel shows the  $\log_2(\text{RPKM})$  expression level (Y-axis) versus the Gene List Index (X-axis, ranging from 0 to 17,824). The expression profile (blue line) shows a peak at 11,058 (labeled 'Peak at 11058') and a zero crossing at 9,077 (labeled 'Zero crossing at 9077').

The middle panel displays vertical black lines representing the expression patterns of individual genes across the gene list index.

The bottom panel shows the distribution of genes in the 'clus1' (green area) and 'NON.clus1' (white area) clusters. The X-axis is labeled 'Gene List Index' and 'Number of genes: 17824 (in list), 57 (in gene set)'. The Y-axis represents the density of genes.

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 -0.289 and 0.2. A vertical black line represents the 'Observed Gene Set ES value' at -0.289. The area under the red curve to the left of this line is shaded light blue. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for the left side and 'Pos. ES: "clus1"' for the right side. At the bottom, a summary line reads: 'ES = -0.289 NES = -1.18 Nom. p-val= 0.327 FWER= 0.993 FDR= 1'.

[illegible]