

Figure 1 displays a multi-panel plot showing gene expression data for 18,283 genes. The x-axis represents the Gene List Index (0 to 18,283). The top panel shows a blue line graph of log₂(RPKM) values, which decreases from approximately 10 to a minimum near index 15,000 and then increases sharply. A vertical green dashed line marks the "Zero crossing at 9486", and a vertical blue dashed line marks the "Peak at 14991". The middle panel shows a barcode of vertical lines representing gene expression. The bottom panel shows a green area plot representing the distribution of genes across the index, with labels "clus1" and "NON.clus1".

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. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks around -0.4 and 0.4. A vertical black line at ES = -0.618 represents the 'Observed Gene Set ES value'. The area to the left of this line is labeled 'Neg. ES "NON.clus1"' and the area to the right is labeled 'Pos. ES: "clus1"'. Below the plot, the following statistics are provided: ES = -0.618, NES = -1.57, Nom. p-val= 0.00398, FWER= 0.738, FDR= 0.615.

Heatmap visualization showing gene expression patterns across samples, clustered by gene (Y-axis) and sample (X-axis). The Y-axis is labeled 'clus1' and 'NON.clus1'. The X-axis is labeled 'clus1' and 'NON.clus1'. The heatmap shows a dense grid of red and blue squares, indicating high and low expression levels respectively. The 'clus1' group on the Y-axis is highlighted with a red background, and the 'NON.clus1' group is highlighted with a blue background. The X-axis labels are also present at the top of the heatmap.