

Figure 1 displays a multi-panel plot showing gene expression data across a gene list index (0 to 17824).

The top panel shows the  $\log_2(\text{RPKM})$  expression level (Y-axis, ranging from -2 to 2) versus the Gene List Index (X-axis, ranging from 0 to 17824). A blue line represents the expression profile. Key features are marked: a "Zero crossing at 8453" (indicated by a green vertical dotted line) and a "Peak at 12381" (indicated by a blue vertical dotted line). A horizontal dashed line is drawn at  $\log_2(\text{RPKM}) = 0$ .

The middle panel shows a barcode plot (Y-axis, ranging from 0 to 10) representing the presence of genes across the index. Vertical black lines indicate the presence of individual genes.

The bottom panel shows the proportion of genes in two clusters: "clus2" (green area) and "NON.clus2" (red area). The Y-axis represents the proportion (ranging from 0 to 1). The "clus2" cluster is dominant in the early part of the index (0 to approximately 8453), while the "NON.clus2" cluster is dominant in the later part (approximately 8453 to 17824).

Number of genes: 17824 (in list), 132 (in gene set)

A density plot showing the probability density function  $P(ES)$  on the y-axis (ranging from 0 to 6) against the ES value on the x-axis (ranging from -0.4 to 0.4). The plot features a red curve representing the 'Gene Set Null Density', which is bimodal with peaks at approximately  $ES = -0.15$  and  $ES = 0.15$ . A vertical black line at  $ES = -0.277$  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.clus2"' for negative values and 'Pos. ES: "clus2"' for positive values. Below the x-axis, the following statistics are provided:  $ES = -0.277$ ,  $NES = -1.64$ ,  $Nom. p\text{-val} = 0.0324$ ,  $FWER = 0.613$ , and  $FDR = 0.428$ .

Heatmap showing the correlation of gene expression between two clusters, **clus2** and **NON.clus2**. The color scale ranges from -0.2 (blue) to 0.2 (red). The heatmap displays a dense grid of correlation values for various genes, with the top row labeled **clus2** and the right column labeled **NON.clus2**. The genes are listed on the left side of the heatmap, grouped into several categories: **clust1** (top), **clust2** (middle), **clust3** (bottom), and **clust4** (bottom right). The heatmap shows a high degree of correlation within each cluster, with the **clust1** cluster showing the highest correlation values (red) and the **clust4** cluster showing the lowest correlation values (blue).