

Figure 1 displays a multi-panel plot showing gene expression data for the "cluser1" gene set. The x-axis represents the Gene List Index, ranging from 0 to 18,113 (total genes in list) and 69 (genes in gene set). The y-axis represents expression levels.

The top panel shows a red line plot representing the expression profile across the gene list. A peak is identified at index 5,241, and a zero crossing is identified at index 10,828. A dashed horizontal line indicates the baseline expression level.

The middle panel shows vertical black bars representing the expression profiles of individual genes. The bars are clustered around the peak and zero crossing points.

The bottom panel shows a green area plot representing the distribution of gene expression levels. The area is labeled "cluser1" on the left and "NON.cluser1" on the right, indicating the distribution of genes within and outside the cluster.

The figure is a density plot showing the probability density function (PDF) of Enrichment Scores (ES) for two gene sets. 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 4. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 and 0.25. A black vertical line at ES = 0.428 represents the 'Observed Gene Set ES value'. The area under the red curve to the left of the observed value is shaded light blue and labeled 'Neg. ES "NON.clus1"'. The area under the red curve to the right of the observed value is shaded light red and labeled 'Pos. ES: "clus1"'. Below the x-axis, the following statistics are provided: ES = 0.428, NES = 1.68, Nom. p-val = 0.0116, FWER = 0.523, and FDR = 0.223.

Gene Set	ES	NES	Nom. p-val	FWER	FDR
NON.clus1	-0.25	-1.68	0.0116	0.523	0.223
clus1	0.428	1.68	0.0116	0.523	0.223

[illegible]