

Figure 1 displays a multi-panel plot illustrating the relationship between the Gene List Index (X-axis, ranging from 0 to 18,315) and various metrics.

The top panel shows a red line graph representing the number of genes in the gene set. The curve starts at 0, rises sharply to a peak at index 2826, and then gradually declines, crossing the zero line at index 7868. A horizontal dashed line is present at the zero level.

The middle panel shows a barcode representation of the gene sets. The red vertical line marks the peak at index 2826, and the green vertical line marks the zero crossing at index 7868.

The bottom panel shows a green area graph representing the number of genes in the gene set. The area is shaded green, and the curve starts at a high value and decreases towards zero. The red vertical line marks the peak at index 2826, and the green vertical line marks the zero crossing at index 7868.

Labels on the plot include:

- Peak at 2826
- Zero crossing at 7868
- "clus4"
- "NON.clus4"

The X-axis is labeled "Gene List Index" and "Number of genes: 18315 (in list), 99 (in gene set)".

ES = 0.537 NES = 1.67 Nom. p-val= 0.00211 FWER= 0.813 FDR= 0.111

Heatmap visualization showing gene expression patterns across two clusters: **clus4** (red) and **NON.clus4** (blue). The y-axis lists 100 genes, and the x-axis shows expression levels for each gene across the two clusters. The heatmap is color-coded by cluster, with clus4 in red and NON.clus4 in blue. The genes are grouped into two main sections: the top 50 genes (clis8, WNT10B, CAMK2A, etc.) and the bottom 50 genes (MAP2K1, P-CBL, CAMK2G, etc.). The expression patterns are highly variable across the two clusters, with many genes showing high expression in clus4 and low expression in NON.clus4, and vice versa.