

Figure 1 displays a multi-panel plot illustrating gene expression data for the "NON.clus1" gene set, showing the relationship between the Gene List Index (X-axis, 0 to 15,000) and log₂(RPKM) (Y-axis).

The top panel shows the log₂(RPKM) expression profile (red line). The expression starts low, rises sharply to a peak at index 2601, and then gradually decreases, crossing the zero line at index 8581. A dashed horizontal line indicates the zero baseline.

The middle panel displays a barcode visualization of gene expression, where vertical lines represent individual genes. The density of lines is highest near the peak at index 2601 and lowest near the zero crossing at index 8581.

The bottom panel shows the distribution of gene expression across the gene list index, represented by a green area plot. The area is labeled "clus1" on the left and "NON.clus1" on the right, indicating the distribution of genes within the cluster.

Key annotations include:

- Peak at 2601
- Zero crossing at 8581

Gene List Index

Number of genes: 18258 (in list), 84 (in gene set)

A density plot showing the distribution of ES values. The x-axis is labeled 'ES' and ranges from -0.5 to 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 3.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.3 and 0.3. A vertical black line at ES = 0.494 represents the 'Observed Gene Set ES value'. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for negative values and 'Pos. ES: "clus1"' for positive values. At the bottom, statistical results are provided: ES = 0.494, NES = 1.36, Nom. p-val = 0.103, FWER = 0.967, and FDR = 0.793.

Heatmap visualization showing gene expression patterns across two clusters: **clus1** (red) and **NON.clus1** (blue). The y-axis lists 100 genes, and the x-axis represents individual samples. The heatmap is color-coded by cluster, with clus1 in red and NON.clus1 in blue. The genes are grouped into two main clusters, clus1 and NON.clus1, with clus1 genes showing high expression in the clus1 cluster and low expression in the NON.clus1 cluster, and vice versa for NON.clus1 genes.

Genes listed on the y-axis (from top to bottom):

- CH2A2
- LAMA2
- CACNA2D2
- TNNC1
- ACTC1
- TES
- SGCD
- ADCY1
- CACNB4
- TNNI2
- ITGA11
- IGF1
- ADRB1
- CACNG4
- ITGB8
- CACNA1S
- TGFB2
- CACNB2
- SGCA
- CACNB3
- ITGA9
- DMO
- CACNG8
- CACNA1D
- DAG1
- MYH7
- TGFB3
- SGCG
- TNN3
- PLN
- ITGA2
- TNNI2
- ITGA2
- ITGA8
- ITGB3
- ITGA7
- CACNG6
- GNAS
- ADG1
- CACNA1C
- PRKRA
- MYL3
- PRKRL
- ITGB8
- TPM
- ACTG1
- CACNB1
- ITGB1
- CACNA3D
- EMO
- ACTB
- ITGA9
- ITGB9
- PRKX
- LAMA
- ATP2A2
- ITGA1
- ADCY4
- ADCY8
- TPM3
- CACNB5
- ADCY9
- ITGA10
- ITGA5
- TPM1
- TGFB1
- ITGA20
- INF
- ADCY2
- SGCB
- CACNA1D1
- SILCB1A1
- ITGB4
- ITGB8
- ITGA3
- MYL2
- ITGA4
- ADCY7
- MYBPC1
- RYR2
- ITGB7
- TPN
- CACNA1F
- CACNA2D4
- CACNG5