

Figure 1 displays a plot of the enrichment score (ES) across the gene list index (0 to 18113). The plot shows a blue line representing the ES, which starts at 0, decreases to a minimum at index 7260 (labeled "Zero crossing at 7260"), then increases to a peak at index 14842 (labeled "Peak at 14842"), and finally drops sharply. The bottom panel shows a green area plot representing the probability of a gene set being enriched, labeled "clus2" on the left and "NON.clus2" on the right. The x-axis is labeled "Gene List Index" and "Number of genes: 18113 (in list), 33 (in gene set)".

ES = -0.757 NES = -1.45 Nom. p-val = 0.0412 FWER = 0.924 FDR = 0.177

Heatmap showing gene expression profiles across various cell lines, categorized into two clusters: **clus2** and **NON.clus2**. The color scale ranges from -2 (blue) to 2 (red).

**Class**

**clus2**

**NON.clus2**

Class

RFXANK

BLNK

DCLRE1C

RFX5

RAG1

UNG

IGLL1

TAP1

IKBKG

TAP2

AIRE

CD40

RFXAP

ADA

JAK3

IL2RG

TNFRSF13C

CD4

CD3D

AICDA

CIITA

BTK

CD8B

ZAP70

CD3E

ICOS

LCK

CD40LG

PTPRC

TNFRSF13B

IL7R

CD19

CD79A

TCGA\_4G\_AA2Q\_01

TCGA\_4G\_AA2T\_01

TCGA\_W5\_AA2I\_01

TCGA\_W5\_AA2Q\_01

TCGA\_W5\_AA2T\_01

TCGA\_W5\_AA2W\_01

TCGA\_W5\_AA2Z\_01

TCGA\_W5\_AA34\_01

TCGA\_W5\_AA36\_01

TCGA\_W5\_AA38\_01

TCGA\_ZD\_A8I3\_01

TCGA\_ZH\_A8Y1\_01

TCGA\_ZH\_A8Y2\_01

TCGA\_ZH\_A8Y5\_01

TCGA\_ZH\_A8Y6\_01

TCGA\_3X\_AAIV\_01

TCGA\_3X\_AAVA\_01

TCGA\_3X\_AAVB\_01

TCGA\_3X\_AAVC\_01

TCGA\_3X\_AAVE\_01

TCGA\_W5\_AA2G\_01

TCGA\_W5\_AA2H\_01

TCGA\_W5\_AA2Q\_01

TCGA\_W5\_AA2R\_01

TCGA\_W5\_AA2U\_01

TCGA\_W5\_AA2X\_01

TCGA\_W5\_AA30\_01

TCGA\_W5\_AA31\_01

TCGA\_W5\_AA33\_01

TCGA\_W5\_AA39\_01

TCGA\_W6\_AA0S\_01

TCGA\_WD\_A7RX\_01

TCGA\_YR\_A95A\_01

TCGA\_ZH\_A8Y4\_01

TCGA\_ZH\_A8Y8\_01

TCGA\_ZU\_A8S4\_01