

Figure 1 displays a multi-panel plot illustrating the distribution of gene lists. The x-axis represents the Gene List Index, ranging from 0 to 22,748 (with major ticks at 0, 5000, 10000, 15000, and 20000). The y-axis represents the number of genes in the list, ranging from 0 to 22,748 (with major ticks at 0, 5000, 10000, 15000, and 20000).

The top panel shows a red line graph representing the number of genes in the list versus the Gene List Index. The curve starts at 0, rises to a peak at 5313, and then decreases, crossing the zero line at 9754. A horizontal dashed line is drawn at the peak value of 5313. A vertical dotted red line marks the peak at 5313, and a vertical dotted green line marks the zero crossing at 9754.

The middle panel shows a barcode-like representation of the gene lists, with vertical lines indicating the presence of genes. The density of lines is highest at the beginning of the list and decreases towards the end.

The bottom panel shows a green area plot representing the distribution of gene lists. The area is labeled "clus3" on the left and "NON.clus3" on the right. The distribution is skewed towards the right, with a peak around 10,000.

Number of genes: 22748 (in list), 83 (in gene set)

The figure is a density plot showing the probability density function (PDF) of ES values. The x-axis is labeled 'ES' and ranges from approximately -0.8 to 0.8, with major ticks at -0.5, 0.0, and 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.5, with major ticks at 0.0, 0.5, 1.0, 1.5, 2.0, and 2.5. A red curve represents the 'Gene Set Null Density', which is a bimodal distribution with peaks at approximately -0.3 (P ≈ 1.6) and 0.3 (P ≈ 1.7). A vertical black line represents the 'Observed Gene Set ES value' at ES = 0.492. The area under the red curve to the left of the observed value is shaded light red and labeled 'Neg. ES "NON.clus3"'. The area under the red curve to the right of the observed value is shaded light blue and labeled 'Pos. ES: "clus3"'. Below the x-axis, the following statistics are displayed: ES = 0.492, NES = 1.42, Nom. p-val= 0.0979, FWER= 0.838, and FDR= 0.21.

Heatmap visualization showing gene expression data across two clusters: **clus3** (red background) and **NON.clus3** (blue background). The y-axis lists 100 genes, and the x-axis represents individual samples. The heatmap is divided into two vertical sections: a red section for clus3 and a blue section for NON.clus3. Each gene's expression profile is represented by a horizontal row of colored dots (red for high expression, blue for low expression) across the samples.

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

- Class1
- THBS5
- FNX3
- RELN
- SV2B
- THN1
- COL4A4
- THN
- ITGA8
- ITGA9
- GP5
- ITGA7
- COMP
- LAMA3
- SV2C
- CD36
- SV2A
- ITGA10
- ITGB3
- GP1B1
- ITGA1
- SDC2
- ITGA11
- SDC3
- THBS1
- THBS2
- COL6A2
- LAMA4
- ITGA4
- THN
- ITGB7
- COL4A6
- VWF
- COL3A3
- COL3A1
- THBS3
- LAMB2
- FN1
- ITGA5
- COL5A1
- COL5A2
- COL6A6
- COL4A2
- HSPG2
- GP1B3
- COL1A1
- LAMC1
- GP9
- COL4A1
- ITGB1
- COL5A2
- LAMB1
- ITGA9
- ITGB5
- DKF1
- CD44
- COL11A1
- GP6
- CHY
- SDC4
- LAMA5
- COL5A3
- CHAD
- COL11A2
- KDR
- SPR1
- LAMB4
- LAMA1
- ITGB8
- ITGA3
- ITGA2B
- ITGA6
- ITGA2
- ITGB4
- LAMA2
- COL2A1
- HMMR
- LAMB3
- SDC1
- LAMC2
- LAMC3
- ITGB6
- IRS1