

Figure 1 displays the distribution of genes across a gene list index, showing the number of genes (y-axis) versus the Gene List Index (x-axis, 0 to 18,169).

The plot illustrates the distribution of genes across the gene list index, highlighting the peak at 3,572 and the zero crossing at 8,081. The distribution is characterized by a sharp peak at the beginning of the index, followed by a gradual decline.

The plot is divided into two main regions: "clus1" (left) and "NON.clus1" (right), separated by a vertical dashed line at index 8,081. The "clus1" region shows a high density of genes, while the "NON.clus1" region shows a lower density.

Key features of the distribution include:

- Peak at 3,572:** The maximum number of genes is observed at this index.
- Zero crossing at 8,081:** The distribution crosses the zero line at this index, indicating a change in the number of genes.

The plot also shows the number of genes in the list (18,169) and the number of genes in the gene set (114).

A density plot showing the distribution of ES values 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 0.0 to 2.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.2 and 0.25. A vertical black line at ES = 0.544 represents the 'Observed Gene Set ES value'. The area to the left of this line is labeled 'Neg. ES "NON.clus1"' and the area to the right is labeled 'Pos. ES: "clus1"'. Below the x-axis, the following statistics are provided: ES = 0.544, NES = 1.81, Nom. p-val = 0.00589, FWER = 0.579, and FDR = 0.146.

[illegible]