

Figure 1 displays the distribution of gene lists by the number of genes in the gene set, showing the number of gene lists (Y-axis) versus the number of genes (X-axis, ranging from 0 to 18,748).

The plot illustrates the distribution of gene lists across the number of genes, highlighting the peak at 3127 genes and the zero crossing at 10,241 genes. The distribution is characterized by a sharp increase in the number of gene lists as the number of genes increases, peaking at 3127 genes, followed by a gradual decline.

The distribution is further characterized by the proportion of gene lists in the "clus4" cluster (dark green area) and the "NON.clus4" cluster (light green area). The "clus4" cluster shows a high proportion of gene lists for low gene counts, while the "NON.clus4" cluster shows a high proportion of gene lists for high gene counts.

Key features of the distribution include:

- Peak at 3127:** The number of gene lists reaches its maximum at 3127 genes.
- Zero crossing at 10,241:** The distribution crosses the zero line at 10,241 genes, indicating a transition point in the distribution.
- Gene List Index:** The X-axis represents the Gene List Index, ranging from 0 to 18,748.
- Number of genes:** The total number of genes in the list is 18,748, and the number of genes in the gene set is 79.

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 2.0, with major ticks at 0.0, 0.5, 1.0, 1.5, and 2.0. The plot features a red curve representing the 'Gene Set Null Density', which is bimodal with peaks at approximately ES = -0.4 (P ≈ 1.2) and ES = 0.4 (P ≈ 1.3). A vertical black line represents the 'Observed Gene Set ES value' at ES = 0.652. The area under the red curve to the right of this line is shaded in light blue. Text labels on the x-axis indicate 'Neg. ES "NON.clus4"' for negative values and 'Pos. ES: "clus4"' for positive values. At the bottom of the plot, the following statistics are displayed: ES = 0.652, NES = 1.48, Nom. p-val= 0.0466, FWER= 0.928, and FDR= 0.187.

clus4 **NON.clus4**

Gene list (y-axis):

- CD44
- CD1E
- CD1E
- FLT3
- PD0
- CD1D
- GP1BA
- MSHA1
- CD1B
- CD33
- CR1
- CD22
- CSF3RA
- NTF
- CD37
- CD2A
- CD2
- ITGAM
- CD35
- CD5
- CD8B
- IL2RA
- CD3E
- IL11RA
- CSF1R
- FCER2
- ITGB3
- CD4
- CD1D
- CD1B
- IL3RA
- FCGR1A
- FLT3L
- IL7R
- CD1A
- ITGA4
- CSF3R
- CD38
- GP5
- CD35
- THPO
- IL5
- CD34
- CD5
- IL2RA
- CD7
- ITGA1
- CSF1
- HLA-DRA
- HLA-DRA
- IL1R1
- HLA-DRB5
- IL6
- CD14
- IL7
- IL6R
- ITGA2B
- CD44
- CD59
- CD9
- ITGA3
- IL4R
- ITGA5
- EPOR
- KITL
- TNF
- MME
- ITGA6
- EPOR
- TTRC
- GP9
- CD55
- CSF3
- IL1R2
- ITGA3
- ANPEP
- CSF2
- IL1A
- IL10
- IL1T