

Figure 1 displays the distribution of gene list indices for two clusters, "clus6" and "NON.clus6", based on the number of genes in the list (x-axis, 0 to 15,000) and the number of genes in the gene set (y-axis, 0 to 42).

The top panel shows the difference in the number of genes between the two clusters (red line). The difference starts near zero, peaks at 6620 (labeled "Peak at 6620"), and crosses zero at 8586 (labeled "Zero crossing at 8586").

The middle panel shows the number of genes in the list (vertical bars) for each cluster. The distribution is highly skewed, with most genes having a low index (below 5,000).

The bottom panel shows the distribution of gene list indices for "clus6" (green area) and "NON.clus6" (white area). The "clus6" distribution is highly skewed towards low indices, while the "NON.clus6" distribution is more uniform across the range of indices.

Gene Set Null Density

Observed Gene Set ES value

Neg. ES "NON.clus6"

Pos. ES: "clus6"

ES

ES = 0.435 NES = 1.51 Nom. p-val= 0.0811 FWER= 0.961 FDR= 1

[illegible]