

Figure 1 displays a multi-panel plot illustrating the distribution of gene lists, showing the relationship between the Gene List Index (X-axis) and various metrics.

The X-axis represents the Gene List Index, ranging from 0 to 17824 (total number of genes in the list) and 47 (number of genes in the gene set).

The top panel shows a blue line plot representing a function, likely the cumulative distribution function (CDF) or a related metric. The function starts near 1, peaks around index 1000, then decreases, crossing the zero line (indicated by a dashed horizontal line) at index 9125 (labeled "Zero crossing at 9125"). The function reaches a minimum around index 16186 (labeled "Peak at 16186") and then sharply increases towards the end of the list (index 17824).

The middle panel displays vertical tick marks representing the distribution of gene lists, showing a dense cluster of lists between index 10000 and 17824.

The bottom panel shows a green area plot, likely representing the probability density function (PDF) or a related metric. The area is concentrated near the end of the list (index 17824), labeled "clus4". The area near the beginning of the list (index 0) is labeled "NON.clus4".

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 -0.7 to 0.7, with major ticks at -0.5, 0.0, and 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 3.0, with major ticks every 0.5 units. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately ES = -0.4 (height ~2.2) and ES = 0.4 (height ~1.6). A vertical black line represents the 'Observed Gene Set ES value' at ES = -0.445. The area under the red curve to the left of this line is shaded in light blue. Text labels on the x-axis indicate 'Neg. ES "NON.clus4"' for the left tail and 'Pos. ES: "clus4"' for the right tail. At the bottom, a summary line provides the following statistics: ES = -0.445, NES = -1.1, Norm. p-val = 0.306, FWER = 0.999, and FDR = 1.

Heatmap visualization showing gene expression levels (color scale: blue = low, red = high) across 40 genes (rows) and 40 samples (columns). The top row is labeled 'clus4' and the top column is labeled 'NON.clus4'. The genes listed on the left are: Class, DGAT2, UGT1A6, ADH1B, UGT1A9, BCMO1, UGT2A3, UGT2B7, CYP2B1, UGT2B10, DHRS9, CYP2C18, CYP2C9, CYP2C8, ADH1A, CYP3A5, ADH5, RETSAT, ALDH1A1, ADH7, RDH10, DGAT1, RDH5, UGT2B4, DHRS4, PNPLA4, RDH16, DHRS4L2, ADH6, CYP4A11, RDH11, DHRS3, UGT2A1, RPE65, UGT2B11, CYP3A43, ALDH1A2, CYP2A6, ADH4, RDH12, CYP26A1, ADH1C, CYP1A1, CYP26C1, UGT2B28, CYP3A7, CYP1A2, and LRAT. The heatmap shows a strong pattern of high expression (red) in the top-left corner, indicating that the genes in the 'clus4' cluster are highly expressed in the 'NON.clus4' samples. The rest of the heatmap shows a mix of low (blue) and high (red) expression levels.