

Figure 1 displays a multi-panel plot showing the distribution of gene lists. The x-axis represents the Gene List Index, ranging from 0 to 17728. The y-axis represents density, ranging from -1.0 to 0.4.

The top panel shows a red curve representing the density function. The curve starts near 0, rises to a peak at 7217 (labeled "Peak at 7217"), and then decreases, crossing the zero line at 10017 (labeled "Zero crossing at 10017").

The middle panel shows a barcode of vertical black lines representing gene lists. A red vertical line marks the peak at 7217, and a green vertical line marks the zero crossing at 10017.

The bottom panel shows a stacked area plot. The area is divided into two regions: "clus4" (green) and "NON.clus4" (dark green). The "clus4" region is the upper part of the distribution, and the "NON.clus4" region is the lower part. The total area under the curve is approximately 1.0.

A density plot showing the probability distribution of ES values. The x-axis is labeled 'ES' and ranges from -0.5 to 0.5. The y-axis is labeled 'P(ES)' and ranges from 0 to 3. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.2 and 0.2. A vertical black line at ES = 0.372 represents the 'Observed Gene Set ES value'. The area under the red curve to the left of the observed value is shaded light blue, and the area to the right is shaded light red. The observed value is in the right tail of the null distribution.

ES = 0.372 NES = 1.68 Nom. p-val= 0.0124 FWER= 0.799 FDR= 0.0708

[illegible]