

Figure 1 displays a plot of the distribution of the number of clusters ( $N$ ) for two groups: "clus2" and "NON.clus2". The x-axis represents the number of clusters ( $N$ ), ranging from 0 to 15,000. The y-axis represents the density.

The "clus2" distribution (green area) is highly concentrated near  $N=0$ . The "NON.clus2" distribution (blue line) is broader, peaking around  $N=11,954$ . A vertical green dotted line marks the zero crossing at  $N=7,260$ , and a vertical blue dotted line marks the peak at  $N=11,954$ . A horizontal dashed line is at the top of the plot.

A density plot showing the probability density function (PDF) of ES values for two gene sets. The x-axis represents the ES value, ranging from approximately -0.7 to 0.7, with major ticks at -0.5, 0.0, and 0.5. The y-axis represents the probability density, P(ES), ranging from 0.0 to 2.0, with major ticks at 0.0, 0.5, 1.0, 1.5, and 2.0. The plot features two curves: a red curve labeled 'Gene Set Null Density' and a black vertical line labeled 'Observed Gene Set ES value'. The red curve is bimodal, with peaks at approximately -0.25 (P ≈ 1.45) and 0.25 (P ≈ 1.45), and a local minimum at 0.0 (P ≈ 0.05). The black vertical line is positioned at approximately -0.4, labeled 'Neg. ES "NON.clus2"'. The area under the red curve to the right of this line is shaded in light red, representing the null distribution for the 'clus2' gene set. The label 'Pos. ES: "clus2"' is placed at the bottom right of the plot.

[illegible]