

Figure 1: A plot showing the relationship between the Gene List Index and the number of genes in a set. The top panel shows a red line representing the number of genes in a set, which peaks at 2568 and then decreases. The bottom panel shows a green area representing the number of genes in a set, which is zero for the first 2568 genes and then increases. The x-axis is labeled 'Gene List Index' and ranges from 0 to 15,000. The y-axis ranges from -1.0 to 0.5. A vertical red dotted line marks the peak at 2568, and a vertical green dotted line marks the zero crossing at 11274. The plot is divided into two regions: 'clus1' (left) and 'NON.clus1' (right).

A density plot showing the 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 0.0 to 2.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks around -0.3 and 0.3. A vertical black line at ES = 0.532 represents the 'Observed Gene Set ES value'. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' on the left and 'Pos. ES: "clus1"' on the right. At the bottom, a summary of statistics is provided: ES = 0.532, NES = 1.58, Nom. p-val = 0.0589, FWER = 0.667, and FDR = 0.199.

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