

Figure 1: A plot showing the number of genes in the *clus5* cluster as a function of the gene list index. The x-axis is 'Gene List Index' (0 to 17824) and the y-axis is 'Number of genes' (0 to 17824). A blue line represents the number of genes in the *clus5* cluster, which starts at 17824 and decreases to a minimum of 37 at index 11581, then increases back to 17824. A green shaded area represents the number of genes in the NON.*clus5* cluster, which starts at 0 and increases to 17824 at index 11581. Vertical dashed lines mark the 'Zero crossing at 8945' and the 'Peak at 11581'. The plot is divided into two regions: '*clus5*' (left) and 'NON.*clus5*' (right).

A density plot showing the probability density function (P(ES)) of ES values. The x-axis is labeled 'ES' and ranges from -0.6 to 0.6. 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 -0.25 and 0.25. A vertical black line represents the 'Observed Gene Set ES value' at approximately -0.446. 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.clus5"' for the left side and 'Pos. ES: "clus5"' for the right side. At the bottom, a summary of statistics is provided: ES = -0.446, NES = -1.63, Nom. p-val = 0.0277, FWER = 0.874, and FDR = 1.

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