

A density plot showing the distribution 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 ES = -0.48. 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.clus1"' for the left side and 'Pos. ES: "clus1"' for the right side. Below the x-axis, summary statistics are provided: ES = -0.48, NES = -1.67, Nom. p-val = 0.0275, FWER = 0.592, and FDR = 0.0692.

Heatmap visualization showing the relationship between 1000 samples (columns) and 1000 genes (rows). The genes are grouped into two clusters: **clus1** (bottom 500 genes) and **NON.clus1** (top 500 genes). The heatmap displays a clear separation between the two gene clusters, with **clus1** genes showing high expression in the first 500 samples and **NON.clus1** genes showing high expression in the last 500 samples.