

The figure is a density plot showing the probability density function (PDF) of ES values. The x-axis is labeled 'ES' and ranges from approximately -1.0 to 0.8, with major ticks at -0.5, 0.0, and 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.0, with major ticks at 0.0, 0.5, 1.0, 1.5, and 2.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 (height ~1.4) and 0.3 (height ~1.4). A vertical black line at ES = -0.651 represents the 'Observed Gene Set ES value'. Below the x-axis, the text 'Neg. ES "NON.clus1"' is positioned to the left of the observed value, and 'Pos. ES: "clus1"' is positioned to the right. At the bottom of the plot, the following statistics are listed: ES = -0.651, NES = -1.88, Nom. p-val= 0.00967, FWER= 0.189, and FDR= 0.154.

Heatmap visualization showing the expression of 100 genes across 100 samples. The samples are grouped into two clusters: **clus1** (red background) and **NON.clus1** (blue background). The genes are listed on the y-axis, and the expression levels are represented by a color scale from blue (low) to red (high).

Genes listed on the y-axis (from top to bottom):

- GWA3
- WAP1
- WAP2
- WAP3
- WAP4
- WAP5
- WAP6
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- WAP97
- WAP98
- WAP99
- WAP100