

Figure 1: A multi-panel plot showing the relationship between the number of genes in a set and the number of genes in the list. The top panel shows a red line representing the relationship, peaking at 3158 genes and crossing zero at 10828 genes. The middle panel shows a barcode of genes, with a green shaded area indicating the number of genes in the set. The bottom panel shows a green shaded area representing the number of genes in the set, with a red line indicating the number of genes in the list. The x-axis is labeled 'Gene List Index' and ranges from 0 to 15000. The y-axis is labeled 'Number of genes: 18113 (in list), 126 (in gene set)'.

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 -0.75 to 0.75, with major ticks at -0.5, 0.0, and 0.5. The y-axis is labeled 'P(ES)' and ranges from 0.0 to 2.5, with major ticks at 0.0, 0.5, 1.0, 1.5, 2.0, and 2.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately ES = -0.25 (P ≈ 1.8) and ES = 0.35 (P ≈ 1.5). A vertical black line represents the 'Observed Gene Set ES value' at ES = 0.551. The area under the red curve to the right of this line is shaded in light blue. Text labels on the x-axis indicate 'Neg. ES "NON.clus1"' for negative values and 'Pos. ES: "clus1"' for positive values. At the bottom, statistical results are provided: ES = 0.551, NES = 1.53, Nom. p-val = 0.0397, FWER = 0.813, and FDR = 0.217.

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