

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" with values 0, 5000, 10000, and 15000. The top panel shows a red line representing the number of genes (y-axis, 0 to 18,197) as a function of the gene list index. The line starts at 0, rises to a peak of approximately 18,197 at index 5205, and then gradually declines. A horizontal dashed line is drawn at y = 110. The middle panel is a barcode plot showing the number of gene lists containing a given number of genes (y-axis, 0 to 18,197) as a function of the gene list index. The plot shows a dense collection of vertical black lines. The bottom panel is a green area plot showing the number of gene lists containing a given number of genes (y-axis, 0 to 18,197) as a function of the gene list index. The area is filled with green. The plot shows a sharp peak at index 0, followed by a rapid decay. Two vertical dotted lines are present: a red one at index 5205 labeled "Peak at 5205" and a green one at index 10533 labeled "Zero crossing at 10533". The x-axis is labeled "Gene List Index" and "Number of genes: 18197 (in list), 110 (in gene set)".

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 2.5. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.35 and 0.4. A vertical black line at ES = 0.587 represents the 'Observed Gene Set ES value'. The plot is divided into two regions: 'Neg. ES "NON.clus2"' on the left and 'Pos. ES: "clus2"' on the right. Below the plot, the following statistics are provided: ES = 0.587, NES = 1.43, Nom. p-val = 0.0691, FWER = 0.926, and FDR = 0.192.