

Figure 1: A plot showing the number of genes in the top 50 clusters versus the Gene List Index. The x-axis ranges from 0 to 18,646. The y-axis ranges from 0 to 18,646. A blue line represents the number of genes in the top 50 clusters, which starts at 18,646 at index 0, decreases to a minimum of 58 at index 13,422, and then increases back to 18,646 at index 18,646. A green shaded area represents the number of genes in the top 50 clusters for the 'clus4' cluster, which is 18,646 for the first 8,788 genes and 58 for the remaining 9,858 genes. A red shaded area represents the number of genes in the top 50 clusters for the 'NON.clus4' cluster, which is 58 for the first 8,788 genes and 18,646 for the remaining 9,858 genes. Vertical dashed lines indicate the zero crossing at 8,788 and the peak at 13,422.

A density plot showing the distribution of ES values. The x-axis is labeled 'ES' and ranges from -1.0 to 0.75. 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 -0.25 (height ~1.9) and 0.35 (height ~1.7). A vertical black line at ES = -0.586 represents the 'Observed Gene Set ES value'. 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.clus4"' for the left side and 'Pos. ES: "clus4"' for the right side. At the bottom, a summary line reads: 'ES = -0.586 NES = -1.58 Nom. p-val= 0.0107 FWER= 0.947 FDR= 1'.

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