

Figure 1: A plot showing the distribution of genes in the "clus4" cluster. The x-axis is "Gene List Index" (0 to 17824) and the y-axis is "Number of genes: 17824 (in list), 28 (in gene set)". The plot features a blue line graph, a green shaded area, and a black line graph. A vertical green dashed line marks the "Zero crossing at 9125" and a vertical blue dotted line marks the "Peak at 15672". The green shaded area is labeled "clus4" and the black line graph is labeled "NON.clus4".

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 3.0. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 and 0.3. A vertical black line at ES = -0.353 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 peak and 'Pos. ES: "clus4"' for the right peak. At the bottom, a summary line provides the following values: ES = -0.353, NES = -1.14, Nom. p-val= 0.328, FWER= 0.998, FDR= 1.

Heatmap showing gene expression profiles across 48 samples, grouped into **clus4** and **NON.clus4** clusters. The y-axis lists 20 genes: Class, NTRK1, TPM3, NRAS, RXRB, TCF7L2, TP53, MYC, NCOA4, TPR, CCDC6, BRAF, CTNNB1, KRAS, RXRA, MAPK1, MAPK3, TCF7L1, MAP2K2, MAP2K1, PAX8, TFG, CCND1, PPARG, RXRG, TCF7, CDH1, LEF1, and RET. The x-axis shows 48 samples, with the first 12 labeled as **clus4** and the remaining 36 as **NON.clus4**. The color scale ranges from -2 (blue) to 2 (red).