

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" ranging from 0 to 15,000. The top panel shows a red line representing the number of genes in the clus2 cluster. It starts at 0, rises to a peak of 2888 at index 2888, and then gradually declines, crossing the zero line at index 8627. A horizontal dashed line is at y=0. The middle panel is a barcode plot showing the number of genes in clus2 for each gene in the list. The bars are black and their heights correspond to the values in the red line. The bottom panel is a green area plot showing the number of genes in clus2 for each gene in the list. The area is green and its height corresponds to the values in the red line. The area is labeled "clus2" on the left and "NON.clus2" on the right. The x-axis is labeled "Gene List Index" and "Number of genes: 18525 (in list), 95 (in gene set)".

A density plot showing the distribution of ES values. The x-axis is labeled 'ES' and ranges from -0.6 to 0.6. The y-axis is labeled 'P(ES)' and ranges from 0 to 4. A red curve represents the 'Gene Set Null Density', which is bimodal with peaks at approximately -0.25 and 0.25. A vertical black line represents the 'Observed Gene Set ES value' at approximately 0.414. The area under the red curve to the right of this line is shaded in light red. Text labels on the x-axis indicate 'Neg. ES "NON.clus2"' for the left peak and 'Pos. ES: "clus2"' for the right peak. At the bottom, a summary line reads: 'ES = 0.414 NES = 1.46 Nom. p-val= 0.0429 FWER= 0.923 FDR= 1'.

Heatmap visualization showing gene expression profiles across 100 samples. The samples are grouped into two clusters: **clus2** (left, red background) and **NON.clus2** (right, blue background). The genes are listed on the y-axis, grouped into two main categories: **clust1** (top, red background) and **clust2** (bottom, blue background). The color scale represents expression levels, ranging from low (blue) to high (red).

Gene List (Y-axis):

- clust1 (Red background):** C1orf103, PLAZ2A4, LML1, CACNA1B, CACNA1C, PLAZ2B1, CALML5, PRKCA, PRKCB, PLCB4, ITPR2, GPR108, MAP2K2, CACNA1D, PLCB3, PLAZ2B, CACNA1C, CACNA1E, PRKCB, PLCB1, ADCY4, GRIK1, CACNA2A, MAPK11, MAP2K4, JAK2, PRKACB, PLAZ2B1, PLAZ2B, MAPK7, ITPR1, PLCB, ITPR2, MAP2K2, PLAZ2B1, PLAZ2B, ITPR3, MAPK9, MAPK1, ITP4, GRIK1, HRAS, MAPK4, MAPK1, MAPK4, EGFR, PLCB, SRC, PLAZ2B, MAP2K7, JUN, PLAZ2B1, MAPK12, ITP2B, ADCY2, MAP1K2, E1, SOS2, KIF13B, PRKCB, CALML1, RAF1, PRKCA, GRIK2, MAPK14, MAP1K1, MAP1K1, PRKX, SOS1, PLAZ2B1, PLD1, PLAZ2A, MAPK3, PLCB3, CACNA1F, PRKCD, PLAZ2B, ITP2, CACNA2A, MAPK10, ADCY2.
- clust2 (Blue background):** (Same gene list as clust1, but with different expression profiles).