

Figure 1 consists of three vertically stacked panels sharing a common x-axis labeled "Gene List Index" ranging from 0 to 17,728. The top panel is a red line graph showing the number of genes in the clus4 cluster. It starts at 0, rises to a peak of 46 at index 3135, and then gradually declines, crossing the zero line at index 10017. A horizontal dashed line is at y=0. The middle panel shows vertical tick marks for each gene in the clus4 cluster, with a dense cluster of ticks around index 3135. The bottom panel is a green area plot showing the distribution of genes in clus4. The area is labeled "clus4" on the left and "NON.clus4" on the right. The area is highest at index 3135 and tapers off towards the right. Text labels indicate "Peak at 3135" and "Zero crossing at 10017".

ES = 0.501 NES = 1.64 Nom. p-val = 0.0182 FWER = 0.872 FDR = 0.0763

Heatmap visualization showing gene expression patterns across two clusters: **clus4** and **NON.clus4**. The y-axis lists 40 genes, and the x-axis represents individual samples. The color scale ranges from blue (low expression) to red (high expression).

**Gene List (Y-axis):**

- Class
- LAMA2
- LAMC2
- LAMC3
- PMP22
- LAMA1
- ITGB4
- MST1R
- COL17A1
- LAMB1
- CDH1
- LAMA5
- CD9
- LAMA4
- EGF
- ERBB2
- YWHAZ
- ITGB1
- EGFR
- LAMC1
- LAMB3
- CASP7
- SHC1
- YWHAH
- YWHA8
- LAMB2
- RAC1
- AKT1
- PIK3CA
- YWHA6
- LAMA3
- YWHA3
- IL1A
- HRAS
- SFN
- YWHAQ
- RXRG
- GRB2
- ITGA6
- RXRA
- PIK3R1
- RPS6KB1
- RXRB
- MET
- ERBB3
- PRKCA
- MST1