

Figure 1: A plot showing the distribution of gene lists by the number of genes in the set. The x-axis is 'Gene List Index' (0 to 17346) and the y-axis is 'Number of genes' (0 to 119). A blue line represents the distribution, which is mostly flat but has a sharp peak at index 15452. A green shaded area under the line represents the distribution of gene lists. A vertical green dashed line is at index 9190, labeled 'Zero crossing at 9190'. A vertical blue dashed line is at index 15452, labeled 'Peak at 15452'. The plot is divided into two regions: 'clus4' (left of 9190) and 'NON.clus4' (right of 15452).

The heatmap displays gene expression data for 100 genes across 100 samples. The genes are grouped into two clusters: **clus4** (top) and **NON.clus4** (bottom). The samples are grouped into two clusters: **clus4** (left) and **NON.clus4** (right). The heatmap shows a clear pattern of gene expression, with genes in **clus4** showing higher expression in **clus4** samples and genes in **NON.clus4** showing higher expression in **NON.clus4** samples.

**clus4**

**NON.clus4**

**clus4**

**NON.clus4**