**Version original:**

Heatmaps are a graphical representation in which the values of a matrix are displayed using colors. Each entry in the matrix is assigned a color based on its value, allowing for easier visualization of variations, distribution, and intensity of a variable in a data matrix. It is common to sort either rows or columns to identify clusters and similarities among elements in order to detect trends between different variables.

If the data has a wide range and the goal is to highlight differences in small values, a logarithmic scale is used. In this case the $log2$ function is applied to the $EiMybs$ data frame, adding 1 to each value before performing the logarithmic transformation. This is often done to stabilize variance and handle data with large differences in scale.

The data was prepared to be in the correct format and free of missing values. In case of any missing data, the corresponding row was removed to ensure that no data was missing and thus generate the heatmap, also A boxplot is created using the boxplot()function to visualize the log-transformed data. Finally a Venn diagram is created using the venn function from the VennDiagram package to visualize the overlapping genes between the all the columns in the data matrix.

**Version final:**

Heatmaps are visual representations of a matrix using colors to display values. Sorting rows or columns helps identify clusters and similarities, showing relationships between variables. For data with a wide range, a logarithmic scale can highlight differences in small values. The log2 function is applied to the "EiMybs" data frame, adding 1 to each value before transformation to stabilize variance and handle data with a wide range of values. Missing data is removed to ensure a complete heatmap. A boxplot is created to visualize the log-transformed data, and a Venn diagram shows overlapping genes in the data matrix.

**CORRECCION 2:**

Heatmaps are a graphical representation of matrix data. Each entry is assigned a color based on its value. It can be used to identify clusters, trends, and variations in data. To highlight small values, a logarithmic scale can be used to stabilize variance and handle data with significant differences in scale. The log2 function is applied to the data frame and 1 is added to each value before performing the logarithmic transformation. The data was prepared to be in the correct format and free of missing values. A boxplot and Venn diagram were created using the boxplot() and venn() functions respectively.

**CORRECCION 4:**

Heatmaps are visual representations of a matrix using colors to display values. Sorting rows or columns helps identify clusters and similarities, showing relationships between variables. For data with a wide range, a logarithmic scale can highlight differences in small values. The log2 function is applied to the "EiMybs" data frame, adding 1 to each value before transformation to stabilize variance and handle data with wide range of values. Missing data is removed to ensure a complete heatmap. A boxplot is created to visualize the log-transformed data, and a Venn diagram shows overlapping genes in the data matrix.

**CORRECCION 1:**

Heatmaps are a graphical representation of the values of a matrix, where each entry in the matrix is assigned a color based on its value. This allows for easier visualization of variations, distribution, and intensity of a variable in a data matrix. It is common to sort either the rows or columns to identify clusters and similarities among elements, in order to detect trends between different variables.

If the data has a wide range and the goal is to highlight differences in small values, a logarithmic scale can be used. In this case, the log2 function is applied to the EiMybs data frame, adding 1 to each value before performing the logarithmic transformation. This is often done to stabilize variance and handle data with large differences in scale.

The data was prepared to be in the correct format and free of missing values. In case of any missing data, the corresponding row was removed to ensure that no data was missing and thus generate the heatmap. A boxplot was created using the boxplot() function to visualize the log-transformed data. Finally, a Venn diagram was created using the venn() function from the VennDiagram package to visualize the overlapping genes between all the columns in the data matrix.

**CORRECCION 3:**

Heatmaps are graphical representations that display the values of a matrix using colors. Each entry in the matrix is assigned a color based on its value, making it easier to visualize variations, distribution, and intensity of a variable in the data matrix. It is common to sort either the rows or columns to identify clusters and similarities among elements, which helps in detecting trends between different variables.

When the data has a wide range and the objective is to emphasize differences in small values, a logarithmic scale is employed. In this case, the $log2$ function is applied to the "EiMybs-clean" data frame, with 1 added to each value before performing the logarithmic transformation. This technique is often used to stabilize variance and handle data with significant differences in scale.

The data has been prepared in the correct format and is free of missing values. If any missing data were present, the corresponding row was removed to ensure that no data was missing. This step guarantees the generation of a complete heatmap. Additionally, a boxplot is created using the "boxplot()" function to visualize the log-transformed data. Finally, a Venn diagram is generated using the "venn" function from the VennDiagram package to visualize the overlapping genes among all the columns in the data matrix.