**Report**

The summary Statistics for A\_vs\_B: There are 60 significantly upregulated genes and 42 significantly downregulated genes. P-values range from 0 to 1, with a median of 0.19 and a mean of 0.31. Log2 fold changes range from -25.53 to 20.89, with a median of -0.01 and a mean of -0.07.

The summary Statistics for A\_vs\_F: There are 627 significantly upregulated genes and 821 significantly downregulated genes. P-values range from 0 to 1, with a median of 0.06 and a mean of 0.23. Log2 fold changes range from -25.22 to 22.27, with a median of -0.005 and a mean of -0.11.

These results demonstrate significant differences in the number of upregulated and downregulated genes between the comparisons. The distribution of p-values and log2 fold changes highlights notable variations in gene expression across the conditions. The substantial number of differentially expressed genes suggests that critical biological processes may be involved. Likely pathways affected include stress response and immune regulation, as genes with significant upregulation or downregulation could be part of pathways activated under different environmental or experimental conditions. Metabolic pathways may also be impacted, as changes in gene expression could reflect shifts in metabolic activities caused by the treatments.

Additionally, the heatmap shows distinct clusters of upregulated and downregulated genes, suggesting that certain genes respond similarly across conditions. This clustering indicates coordinated regulation of gene expression, and genes in the same cluster may belong to shared functional categories or pathways, reflecting synchronized biological responses.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Comparison** | **Significance** | **Count** | **P- value summary** | **Log2 Fold Change Summary** |
| A\_vs\_B | Upregulated | 60 | Min: 0.00, Max: 1.00 | Min: -25.53, Max: 20.89 |
|  | Downregulated | 42 | Median: 0.19, Mean: 0.31 | Median: -0.01, Mean: -0.07 |
| A\_vs\_F | Upregulated | 627 | Min: 0.00, Max: 1.00 | Min: -25.22, Max: 22.27 |
|  | Downregulated | 821 | Median: 0.06, Mean: 0.23 | Median: -0.005, Mean: -0.11 |

**Volcano plots**

图表

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**Figure 1: Volcano plot for A\_vs\_B comparison** showing log2 fold changes against -log10(p-values). Upregulated genes are in red, downregulated genes in blue, and non-significant genes in grey.

图示

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**Figure 2: Volcano plot for A\_vs\_F comparison** showing log2 fold changes (x-axis) against -log10(p-values) (y-axis). Upregulated genes are represented in red, downregulated genes in blue, and non-significant genes in grey.

**MA plot**

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**Figure 3: MA plot for A\_vs\_B comparison** illustrating the relationship between mean expression (x-axis) and log2 fold change (y-axis). The color indicates the significance of genes.

图示

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**Figure 4: MA plot for A\_vs\_F comparison** illustrating the relationship between mean expression levels (x-axis, log10 scale) and log2 fold changes (y-axis). Genes are colored to indicate significance, with red representing upregulated genes, blue for downregulated genes, and gray for non-significant genes.

**Histogram of p-values**

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**Figure 5: Histogram of p-values for A\_vs\_B comparison,** showing the distribution of statistical significance across all genes.

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**Figure 6: Histogram of p-values for the A\_vs\_F comparison,** showing the distribution of statistical significance across all genes. A peak at low p-values suggests a notable number of significantly expressed genes.

**Heatmap of the top differentiall**

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**Figure 7: Heatmap of the top 50 differentially expressed genes for A\_vs\_B comparison**. Rows represent genes, and columns represent conditions.

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**Figure 4: Heatmap of the top 50 differentially expressed genes for A\_vs\_F comparison.** Rows correspond to individual genes, and columns represent experimental conditions. The color scale reflects expression levels, with hierarchical clustering highlighting patterns of gene co-expression.