Timothy Liu

Comparing IGF1 Treatment of Developing Mouse Molar

Dataset GSE218338 utilizes high throughput sequencing to investigate the developmental and evolutionary scaling of mammalian molar teeth, and specifically examines the effects of insulin-like growth factor 1 (IGF1) treatment. The dataset includes a comparison between five mice that received IGF1-containing media and five mice that were untreated, serving as controls.

DESeq was utilized to identify genes exhibiting significant differential expression between the control and treatment groups. ENSMUSG00000061615 displayed the most significant correlation with an adjusted p-value of 9.83x10^-5, indicating that the observed difference is significant for that gene. This particular gene encodes the Thy-1 Cell Surface Antigen, a protein that promotes cell adhesion and facilitates the growth of nerve fibers. The control group had significantly higher counts per million (cpm) than the treatment group with no overlaps(Figure 2). Given the complex nature of tooth development, which requires coordination among diverse cell types and signaling molecules, ENSMUSG00000061615 possibly has an association with determining tooth scaling. The IGF1 treatment may have coincided with a change in tooth scaling process by reducing the expression of this gene, which could potentially impact cell adhesion and communication during tooth development. Another gene found to be highly correlated was ENSMUSG00000064368, which corresponds to the murine gene called "Stathmin 1" or STMN1. The control group showed lower cpm overall, ranging from 350-470 cpm with 4 of the 5 control samples being above 400 cpm while the treatment group had cpm ranging from 480-1,000 cpm with one of the samples showing a cpm of just under 500(Figure 3). ENSMUSG00000064368 is involved in the regulation of the microtubule filament system by destabilizing microtubules. It prevents assembly and promotes disassembly of microtubules, which are components of the cell's cytoskeleton and play vital roles in cell division, cell movement, and the maintenance of cell shape. There is a possibility that the changes observed in the IGF1 treatment group could be linked to the dynamics of the microtubule system during tooth development. Since microtubules play crucial roles in cell division and movement, changes in Stathmin 1 levels might be coincident with changes in the rate of cell division, cell positioning, and overall tissue shape during tooth development, which could affect tooth size. On the other hand, ENSMUSG00000000001 exhibited the weakest correlation, as indicated by an adjusted p-value of 0.96. A scatter plot was done on Sample Control 3 and Sample Treatment 5 with Pearson's correlation coefficient being 0.96, indicating a strong positive correlation between those two samples (Figure 4).

Data:

GSE218338

https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE218338

Figures:

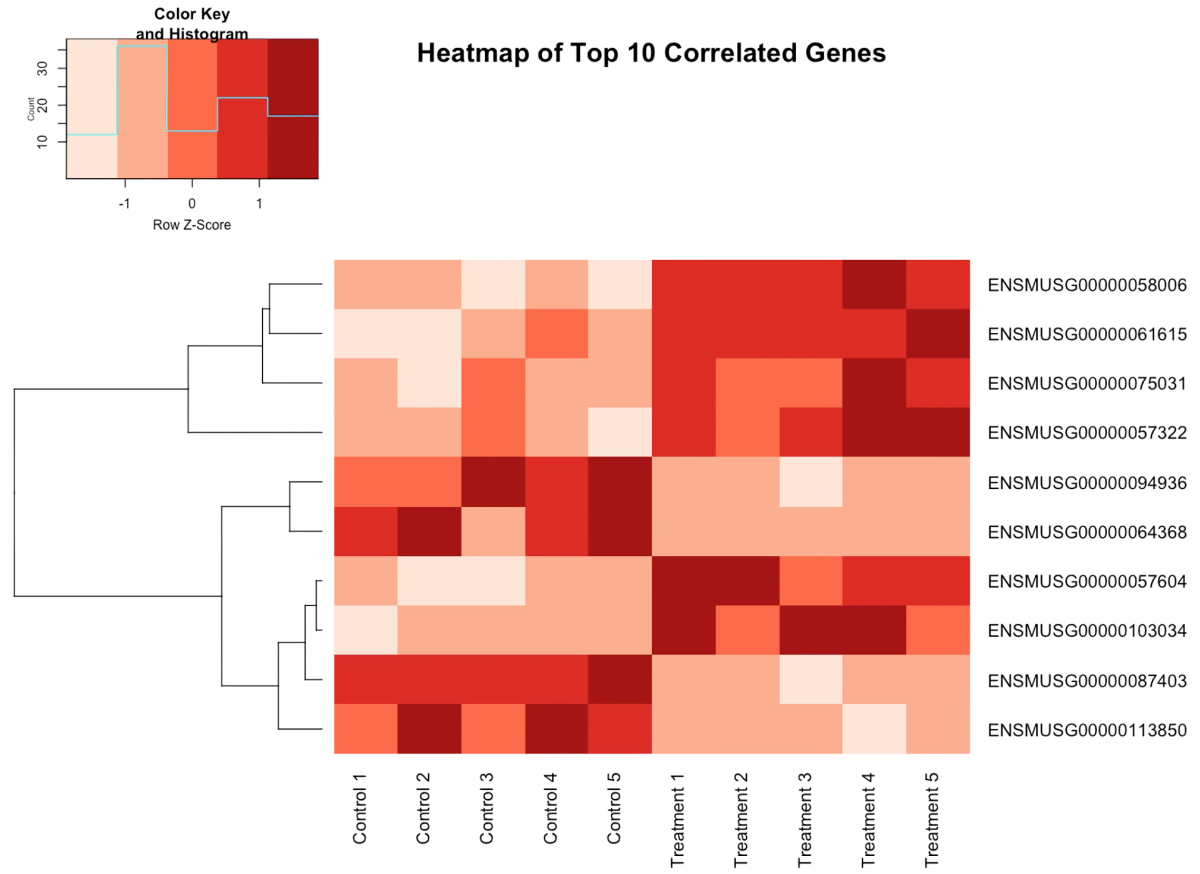

Figure 1: Heatmap of the top 10 correlated genes between the control group and treatment group, made with ggbeeswarm. Gene expression levels are displayed as colors ranging from light red to dark red, with cluster reordering disabled. Darker shades of red indicate larger Z-scores, while lighter shades indicate smaller Z-scores. The top left legend presents a histogram depicting the distribution of Z-scores.

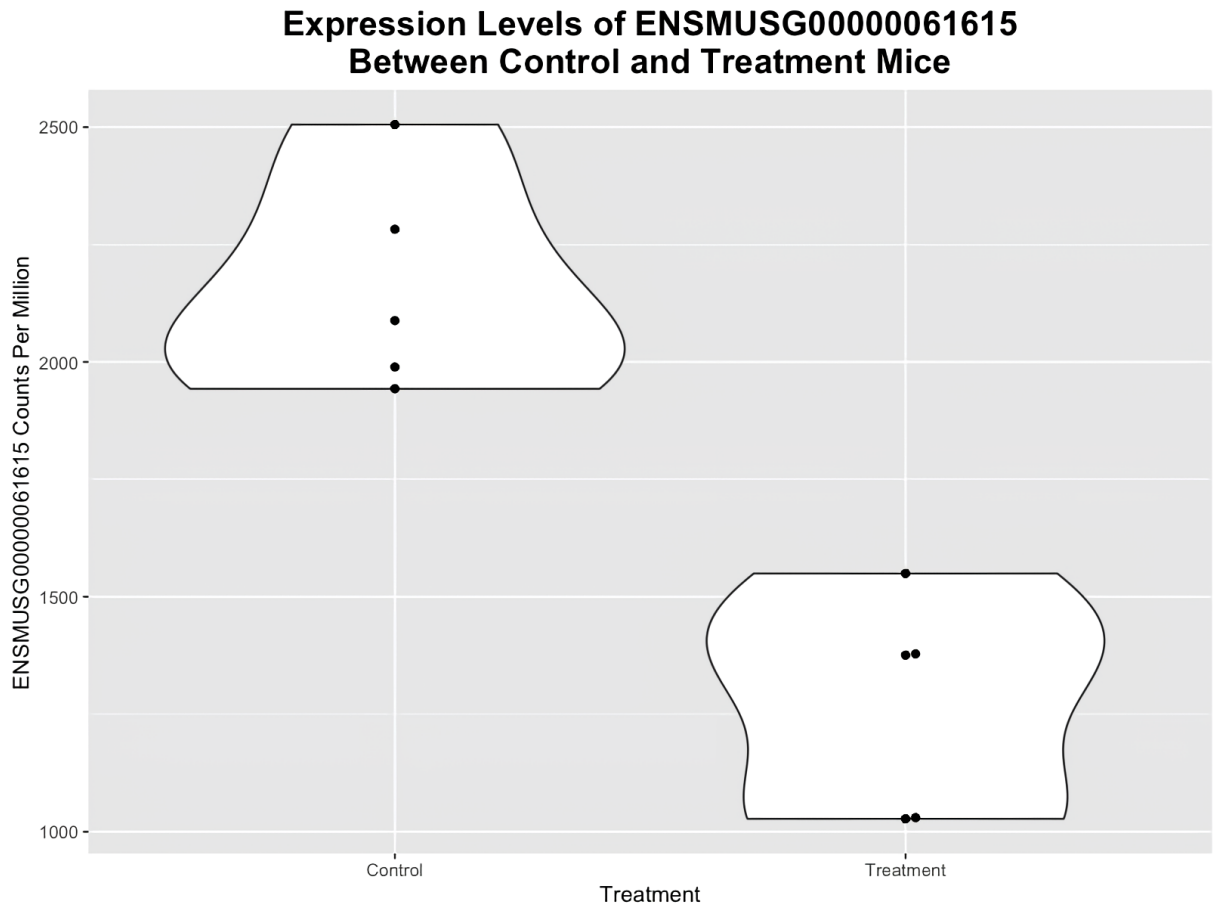

Figure 2: Beeswarm and violin plot illustrating the normalized counts of the highly correlated gene, ENSMUSG00000061615, for the control and treatment groups. No data points overlapped, indicating distinct expression patterns. The control group displayed a range of approximately 2000-2500 counts per million, while the treatment group exhibited a range of approximately 1000-1500 counts per million.

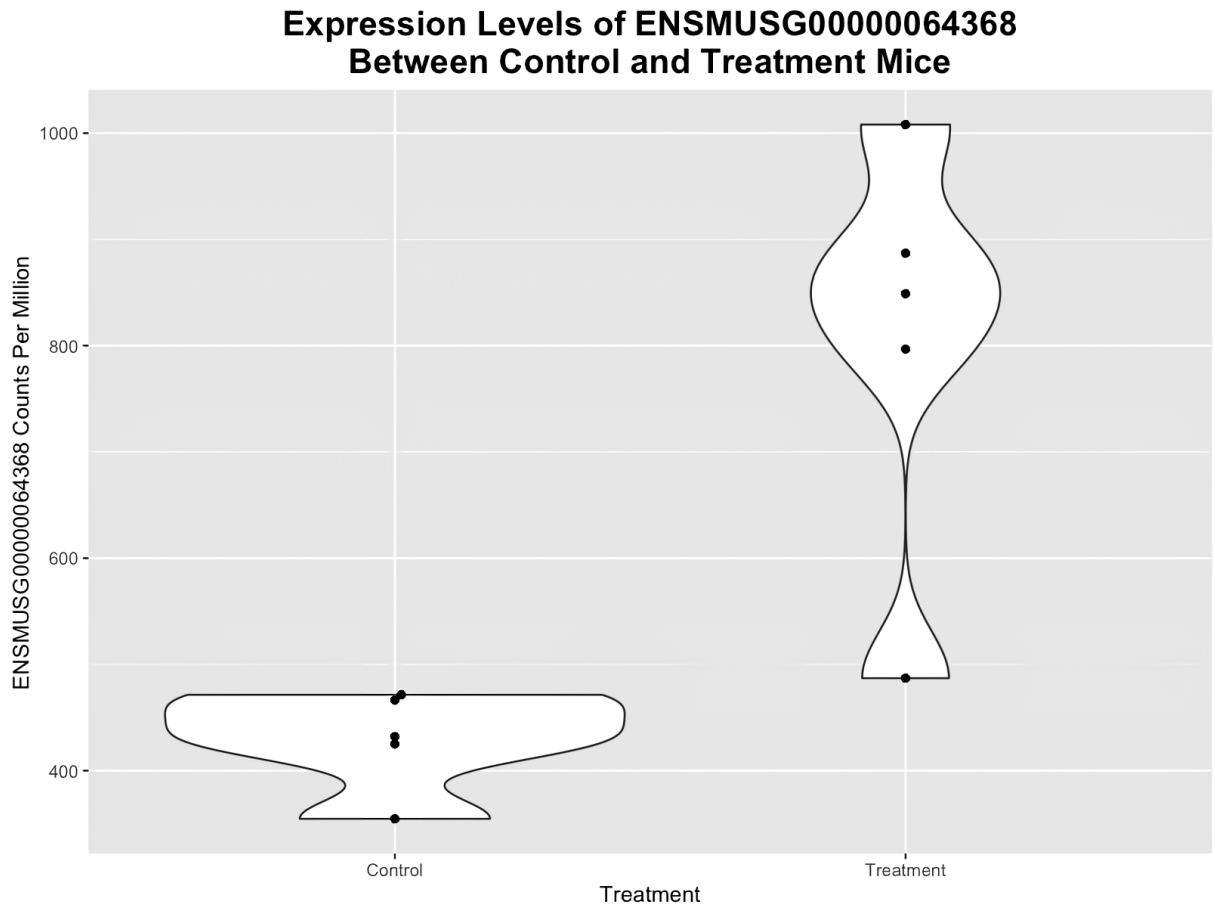

Figure 3: Beeswarm and violin plot illustrating the normalized counts of the highly correlated gene, ENSMUSG00000064368, for the control and treatment groups. No data points overlapped, indicating distinct expression patterns. The control group displayed a range of approximately 350-470 counts per million, while the treatment group exhibited a range of approximately 490-1000 counts per million.

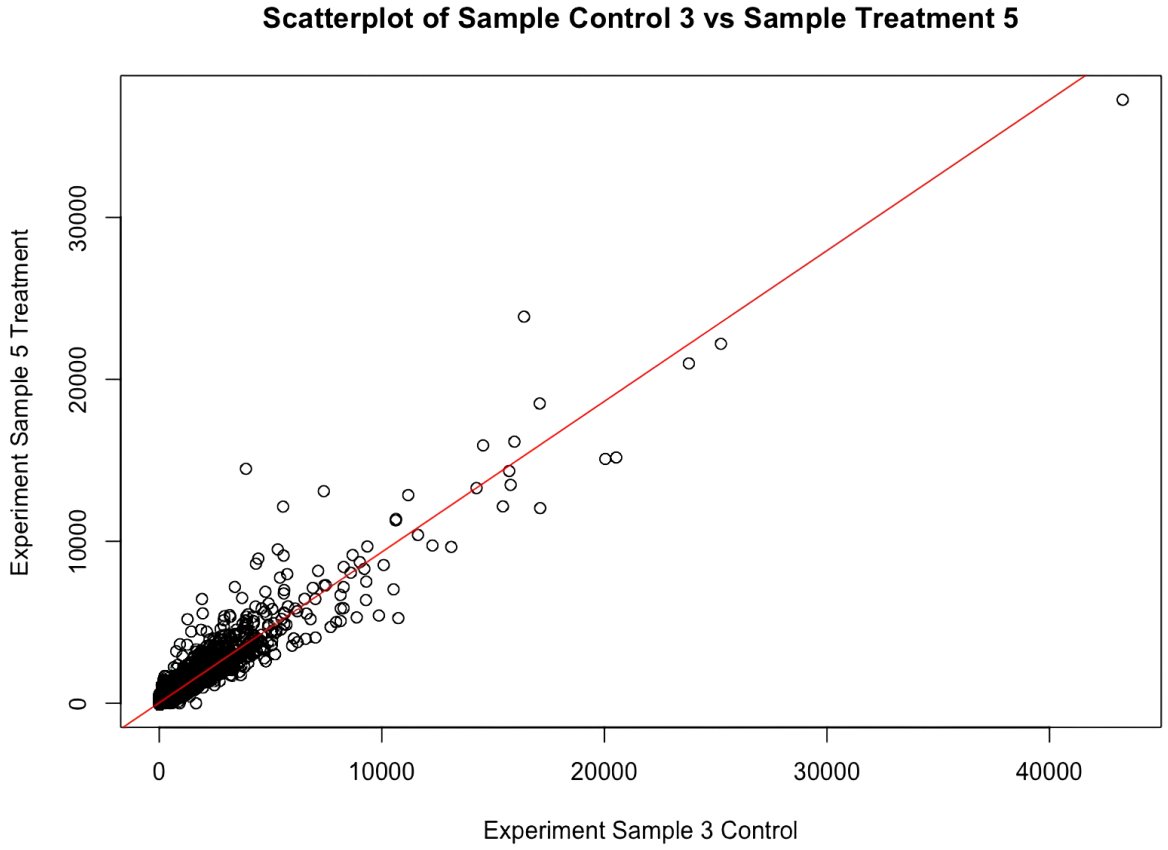

Figure 4: Scatter plot illustrating the relationship of gene expression between Sample 3 Control and Sample 5 Treatment. The solid red line represents the linear regression line, indicating the trend in the data. The Pearson's correlation coefficient (r) between the two variables is 0.96, indicating a strong positive correlation.

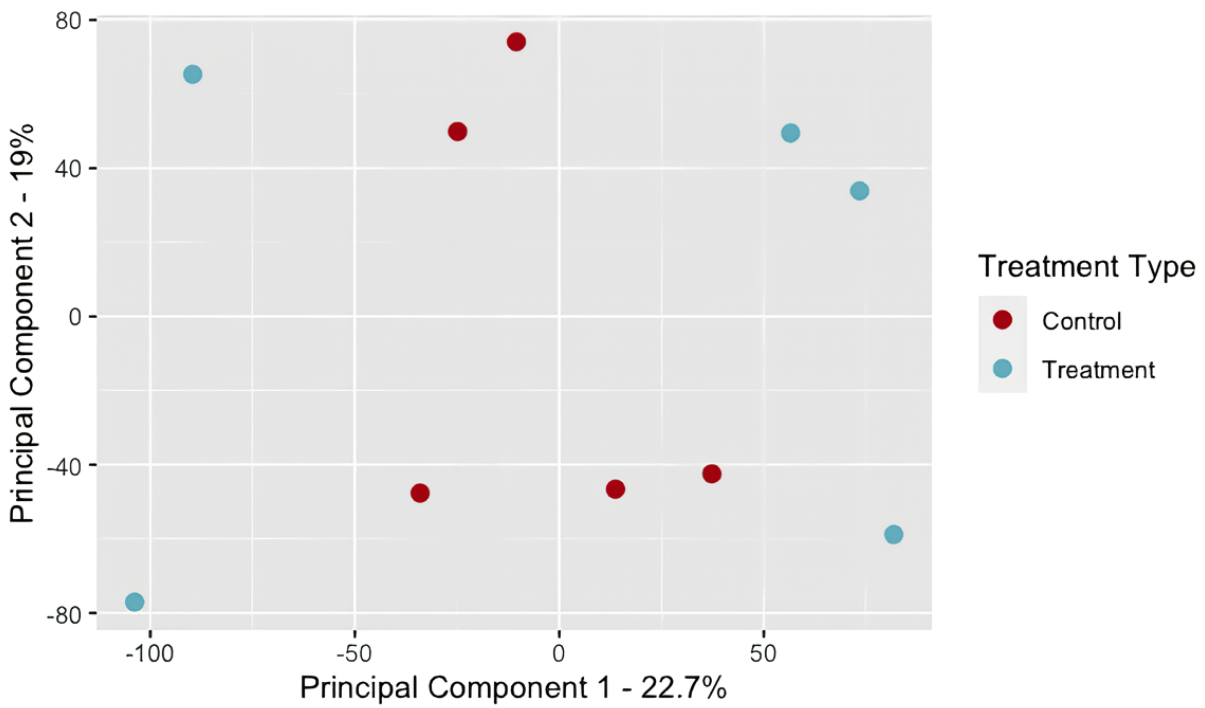

Figure 5: PCA plot of gene expression between treatment and control groups. Each point represents a sample, with treatment samples in blue and control samples in red. Principal Component 1 (PC1) captures 22.7% of the variance in the dataset, while Principal Component 2 (PC2) explains 19% of the variance. Other principal components (not shown) capture decreasing levels of variance. The spread of treatment samples to the four corners of the graph suggests the possibility of high degree of variability in the gene expression profiles within the treatment group.