1. Table 1.1 Basic descriptive statistics and t-test of the genes



**Table legends:** Gene names, genotypes, number of observations, mean and standard deviation were presented in Table 1.1. Values of the gene expression were log-transformed with base 2 to improve interpretability and appearance of graphs for each gene. Mean ± SDa were calculated by original data and Mean ± SDb were calculated with log-transformed data (log2(x+1)). Two sample t-test was performed to detect difference between wild-type (Altered = 0) and the altered (Altered = 1) for selected genes. The significant level was set at 0.05. p-values less than 0.05 indicated significant difference between wild-type and altered groups.

1. Boxplots for significant genes

Diagram

Description automatically generated

**Figure legends:** Statistical analysis was conducted using R software version 4.0.3. Gene expression values were log transformed with base 2 due to large variability. Boxplots were presented for genes with p-values less than 0.05 in independent t-test. Outliers were also presented as scatter points.