Preliminary results

# Methods

## Data processing

Raw data was processed using Rsubread v2.16.0. Gene read counts from the four segments were summed to get the reads for each sample. Then, read counts from the five different guide-RNAs were summed to get the final read counts for each gene (except negative control genes). Total count normalization was used to normalize the data (it makes the total number of counts in each sample the same). For each gene, the ratios of counts for each sample pair (Het vs WT) were calculated. Fifty random genes were selected to check whether there is an overall trend of gene counts change as oxidization activity phenotype change.

A graph of a number of reads

Description automatically generatedA graph of a number of reads

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Figure 1. Total number of counts in each sample. Left: original scale Right: Log10 scale

A screenshot of a graph

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A screenshot of a graph

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Figure 2. Heatmap of the normalized counts. Upper: without clustering. Lower: with row and column clustering.

A blue and white striped graph

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Figure 3. Heatmap of ratio for each paired sample (Het vs WT)

A graph with colorful lines

Description automatically generated

Figure 4. The trend of ratios for the six oxidize-level phenotypes. No general trend observed for a randomly selected 50 genes. Maybe only a specific subset of genes close to oxidization activity is expected to show such a trend.