Baseline Differential Expression Analysis Of Raw 264.7 Mouse Macrophage Cells

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Background

The mechanism of persistence in the environment of *Francisella tularensis*, an intracellular pathogen categorized as a tier 1 select agent due to its high virulence and capacity to cause severe disease, is poorly understood. To identify changes in gene expression of mammalian host cells in the presence of culturable and VBNC (viable but non culturable) *F. tularensis* (subspecies *holarctica* LVS), mouse RAW 264.7 macrophage cells were subjected to an infection assay.

While the primary objective of the infection assay was to identify whole transcriptome changes in gene expression of host macrophage cells, the bioinformatic methods presented here provide preliminary results about the baseline expression patterns of the cell lines used. RAW 264.7 macrophage cells are referred to by their intended treatment group (culturable, VBNC) but the sequences analyzed have been isolated from only the control time point (T0), prior to exposure to any pathogen.

Bioinformatic Objective: evaluate the baseline expression patterns of macrophage cells at timepoint 0, before the host cells were introduced to the VBNC/Culturable *F. tularensis* pathogen.

Methodology

Results

Conclusion

- The top 20 regulated genes expressed similar patterns in genetic expression between culturable and VBNC samples (Fig. 1). Suggesting that the macrophages at time point zero had analogous baseline conditions.

- Yet, when looking at the sample-to-sample count distances, the culturable and VBNC samples weren't as analogous. Although the genes themselves weren't necessarily changing, the magnitude of gene expression between the samples were revealed (Fig. 2).

- In the future, it would be advisable to look at the other macrophage time points and how *F. tularensis* affects them

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