

Project update

J. Shah chimeric mouse collaboration

Kim Dill-McFarland, kadm@uw.edu

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Completed

1. Change gene-level model to contrasts of WT:TKO within **uninfected** or **infected** samples
2. Compare above contrasts model to previous interaction term model (**~status*cell**)
 - Roughly half of genes identified as significant in either model are also significant in the other model.
 - Genes unique to the interaction model are only significant for infection status. Genes unique to the contrasts model were only significant for cell type within **infected** cells.
 - Thus, the contrasts model appears to be successfully removing much of the infection-only signal while amplifying cell type signal.
3. Modules made from 4950 genes significant ($\text{FDR} < 0.3$) in contrasts model
 - Resulted in 18 modules + 399 genes in module 0
4. Contrasts model of modules
 - All modules significant at $\text{FDR} < 0.05$
 - 3 modules significant in uninfected, 5 in infected (ignore module 0), and 10 for both
5. GSEA of significant genes and genes in each module

To discuss

- Other methods for assigning function to modules
- Additional analyses?

To-do

- GSEA of fold change module groups (*e.g.* up in uninfected, up in infected, up in both, etc)
 - Heatmap of module expression
 - Modify boxplots for publication
 - Point group to count files
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