Project update

J. Shah chimeric mouse collaboration

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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 (FDR < 0.3) in contrasts model
    - Resulted in 18 modules + 399 genes in module 0
4. Contrasts model of modules
    - All modules significant at 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?