TB Analysis

1. Intro
   1. TB is bad
   2. Latent vs progressors to disease
   3. Need for biomarkers
   4. Need for mechanism
   5. Brazil study
2. Methods
   1. SingleCellTK
      1. Log CPM
      2. Limma
      3. Differential Analysis
      4. EnrichR database search
3. Results
   1. Genes are differentially regulated between progressors and latents
      1. Heatmap
      2. enrichR tables
   2. Genes are differentially regulated between progessors and middle group latents
      1. Heatmap
      2. enrichR tables
   3. GVAS Analysis
      1. Pathways chart?
      2. Violin map?
4. Conclusion
   1. 136 potentially relevant pathways
      1. Involved in Immune system function
      2. Involved in oxidation
      3. Involved in proteasome degradation pathway
   2. SingleCellTK makes it easy to analyze data
   3. Things to change
      1. Way to analyze middle group by function, not by hand
      2. Maybe clustering data separate
      3. Top 500 gene list names? Instead of the overlay, adjustable font size
      4. Welcome feedback on code, might be hints as where things could be more clear for beginners/non-R users
5. References