Teams Meeting

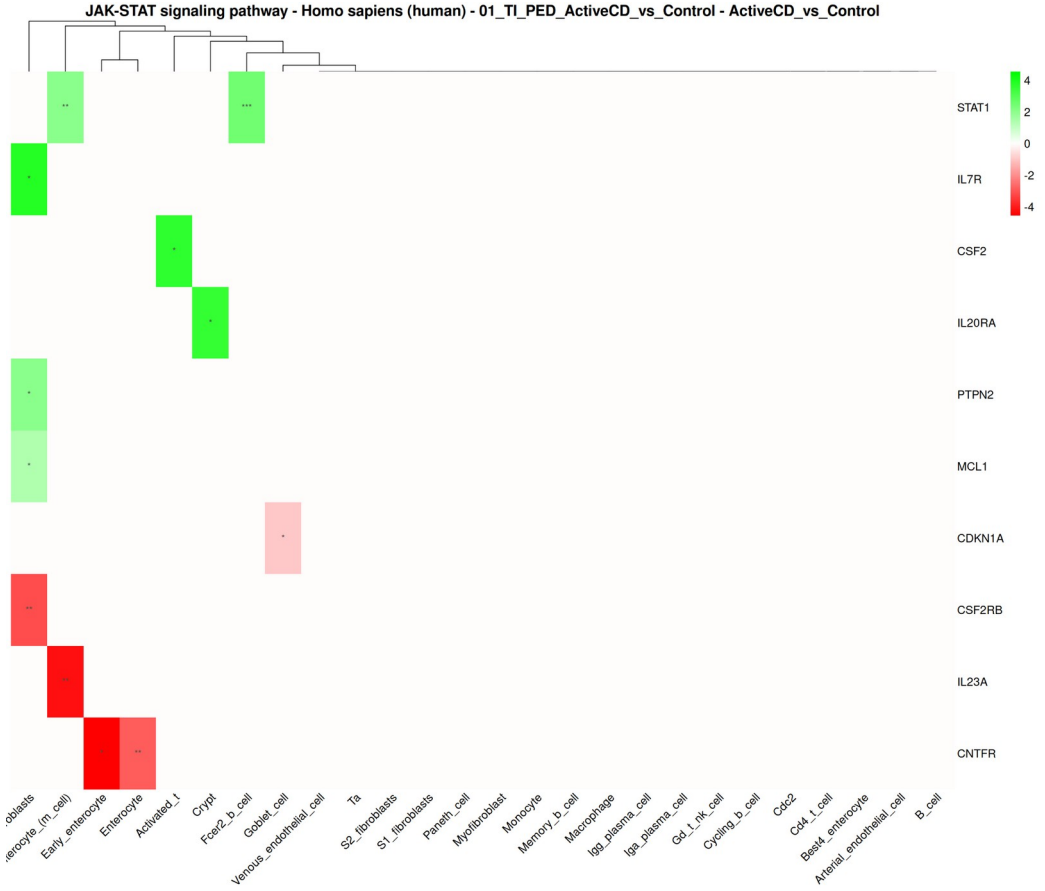
13-06-25

Goals

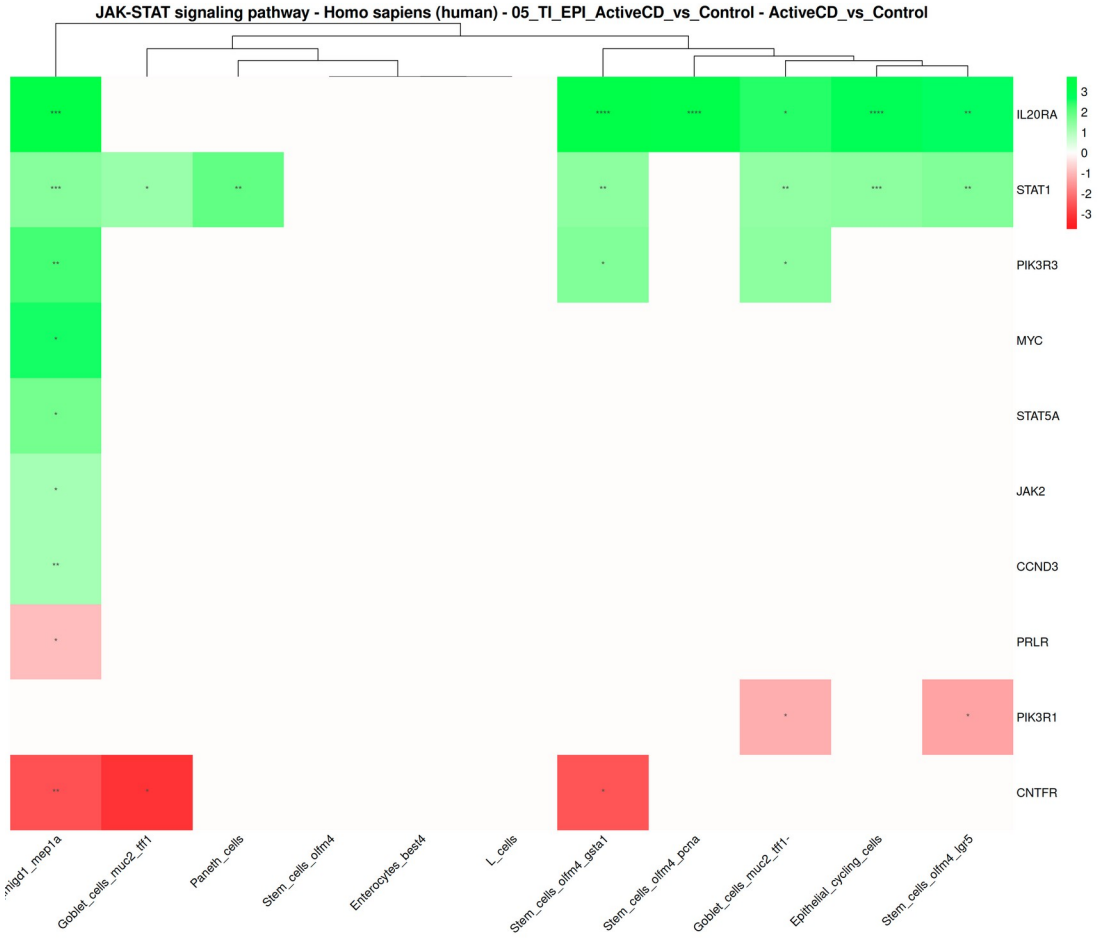
- Create heatmaps for KEGG pathways of interest ✅
- Filter GO enrichment to JAK1/2, STAT1, SOCS1 genes ⏳
    - Pre-filter GO terms: Query the GO database to find all GO terms containing JAK1/2, STAT1, or SOCS1, then cache these filtered term lists ✅
    - Modify enrichment function: Update code to accept the pre-filtered GO term list and use custom mappings instead of the full GO database ⏳
- Separate Epithelial cells, Immune cells, and Stromal cells ⏳
- Normalise dotplot scales across datasets ⏳

JAKSTAT Pathway – Ileum – Active Crohn’s

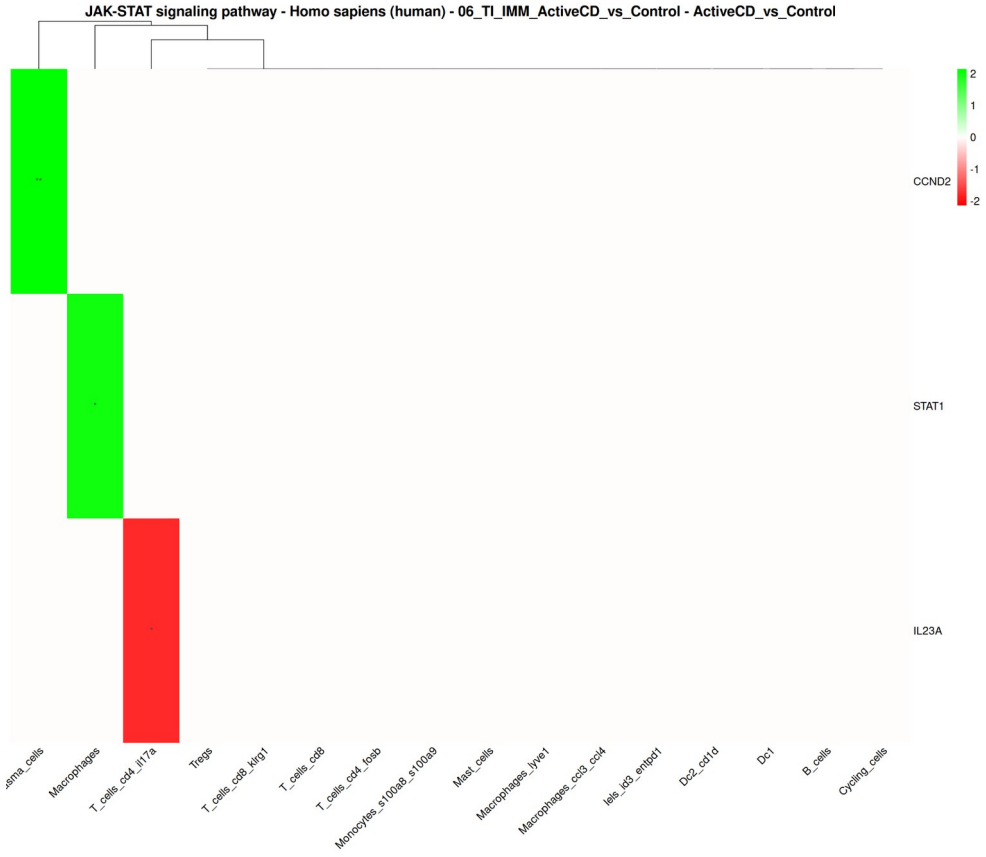
Dataset 1 - JAKSTAT Pathway (Ileum)



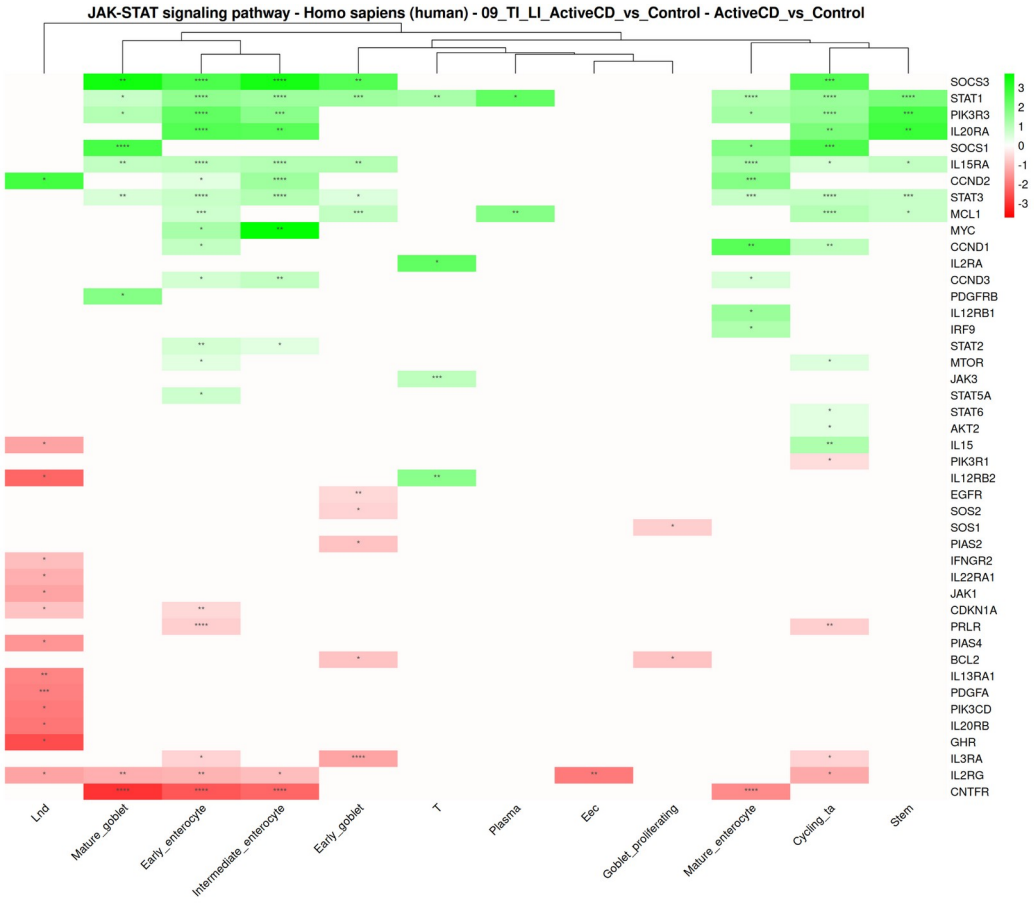
Dataset 2 - JAKSTAT Pathway (EPI - Ileum)



Dataset 2 - JAKSTAT Pathway (IMM - Ileum)



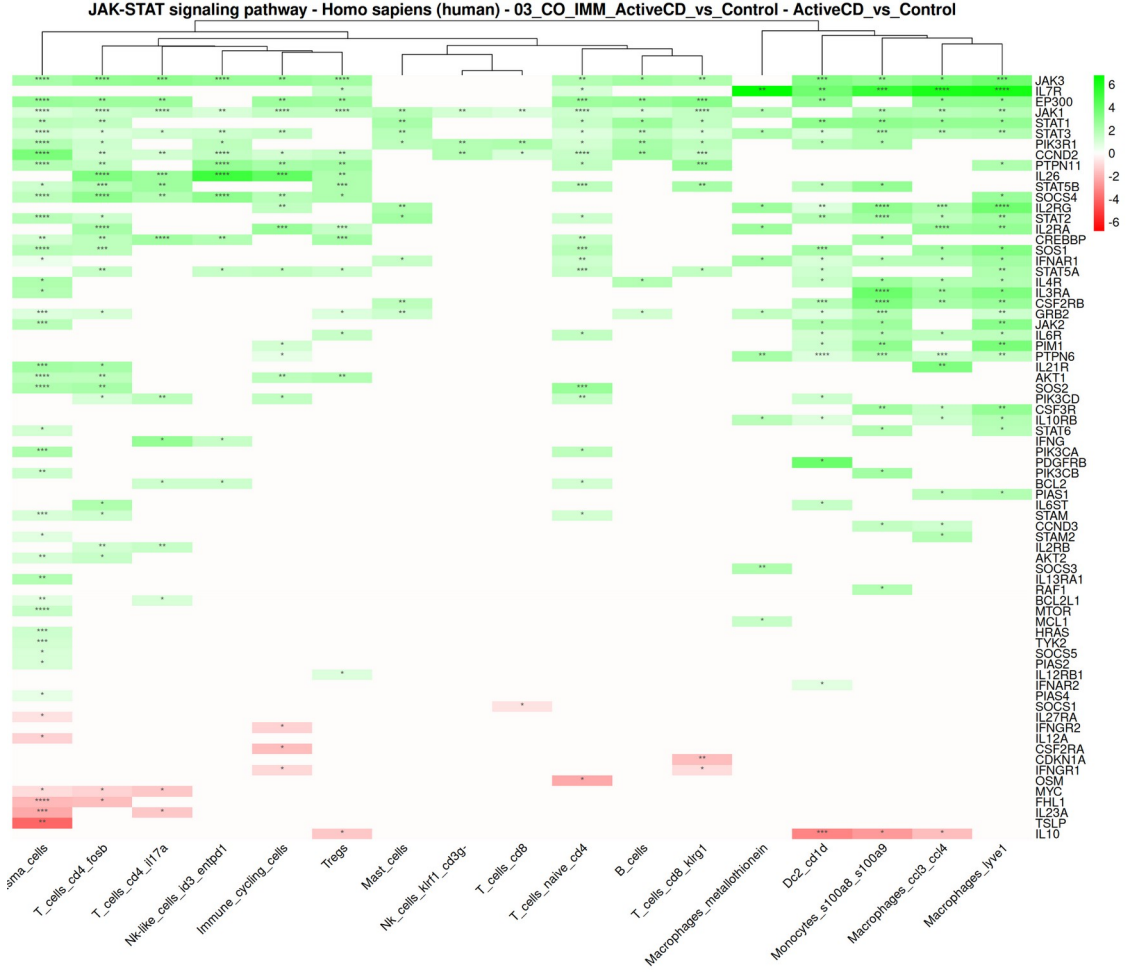
Dataset 3 - JAKSTAT Pathway (Ileum)



JAKSTAT Pathway – Colon – Active Crohn’s

Dataset 2 - JAKSTAT Pathway (EPI - Colon)

Dataset 2 - JAKSTAT Pathway (IMM - Colon)



Dataset 3 - JAKSTAT Pathway (Colon)

Other KEGG Pathways analysed

- Autophagy
- MAPK
- NFKB
- Tight Junction

(Will view these images from PC results repository)

Next goals

- Separate cell type groups for the first (pediatric) and third datasets
- Finish GO term script
- Update dotplots
- Order cell types in dotplots for comparability