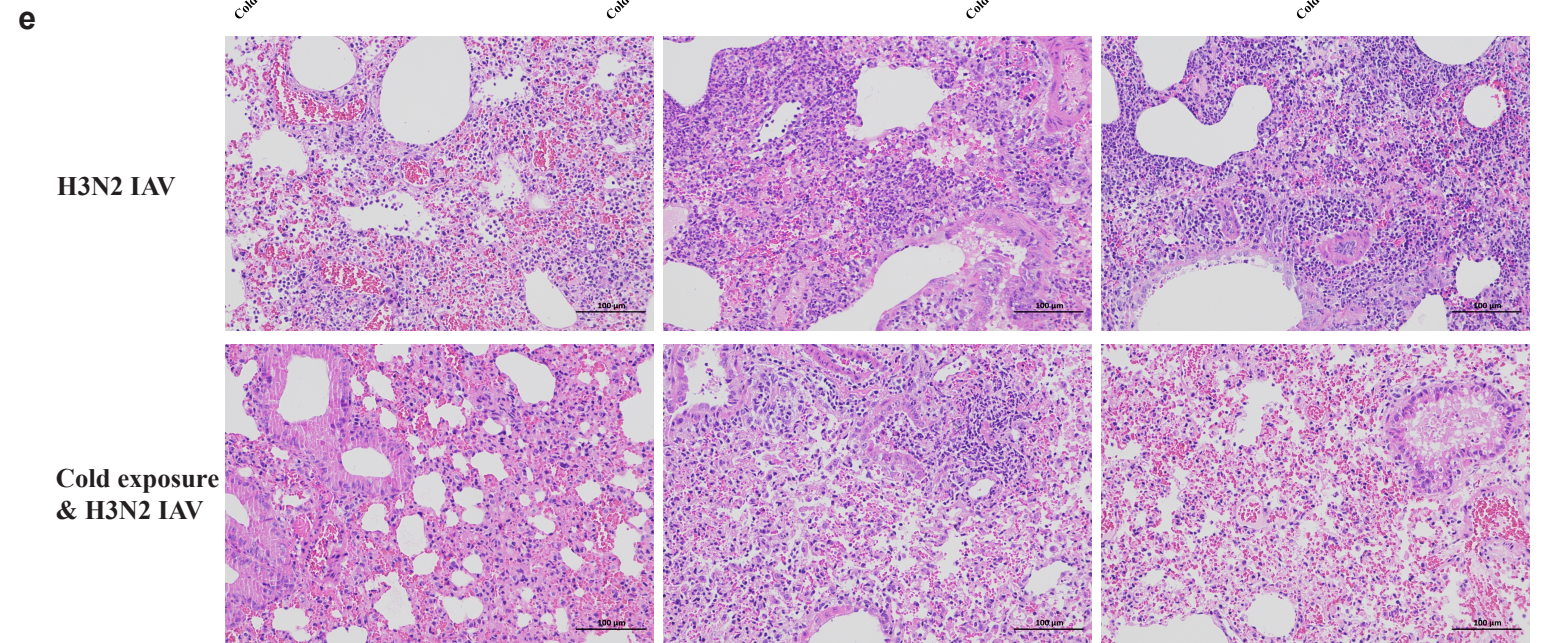
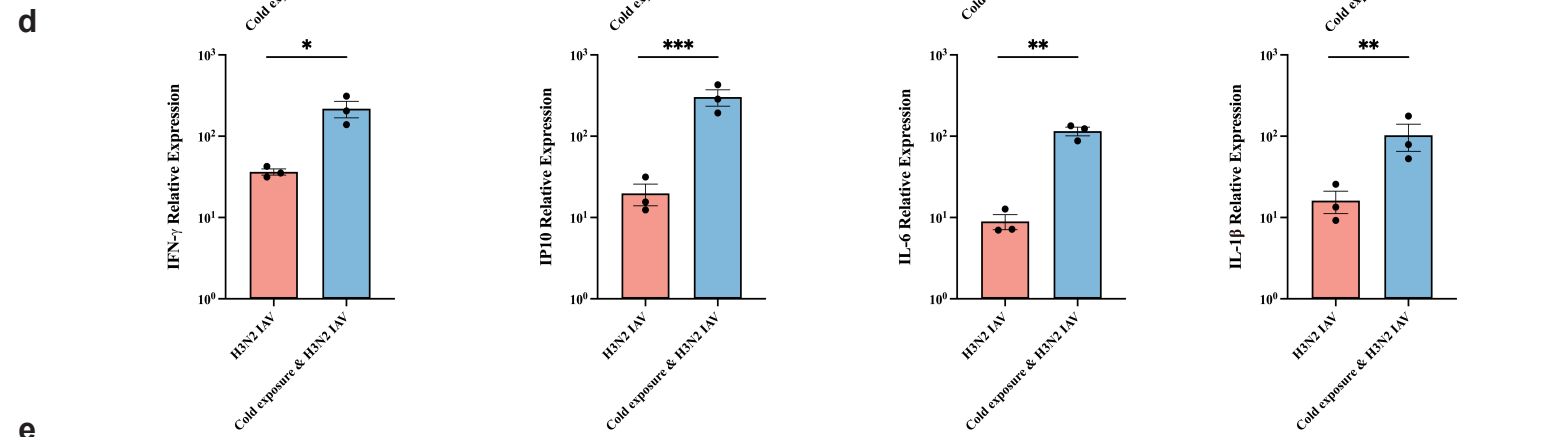
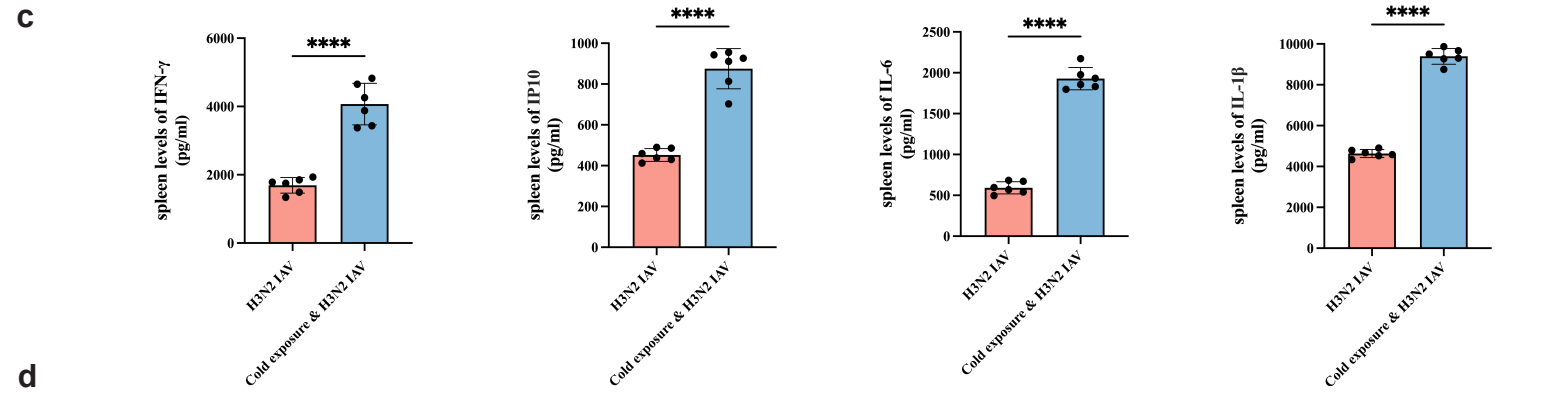
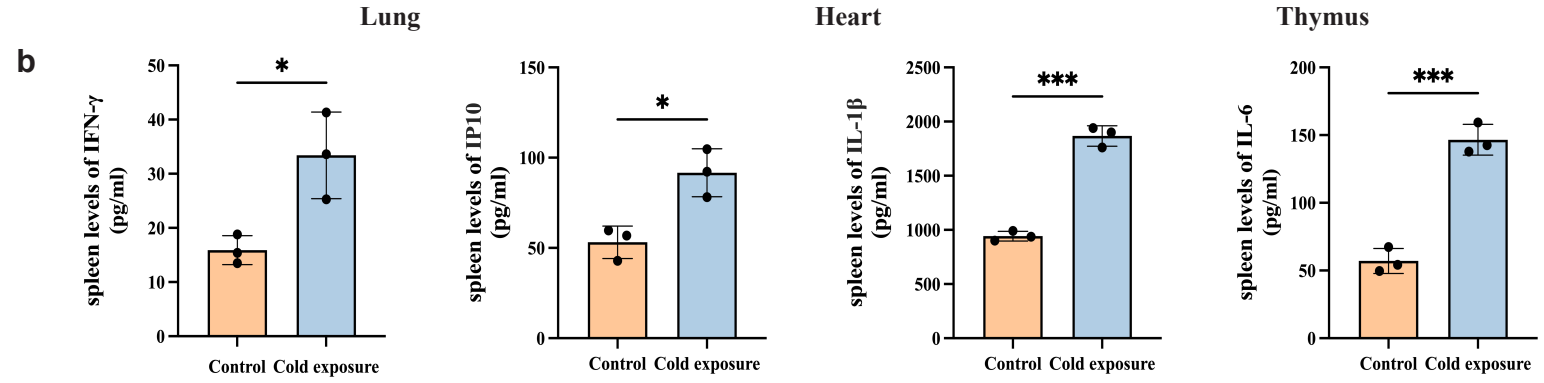
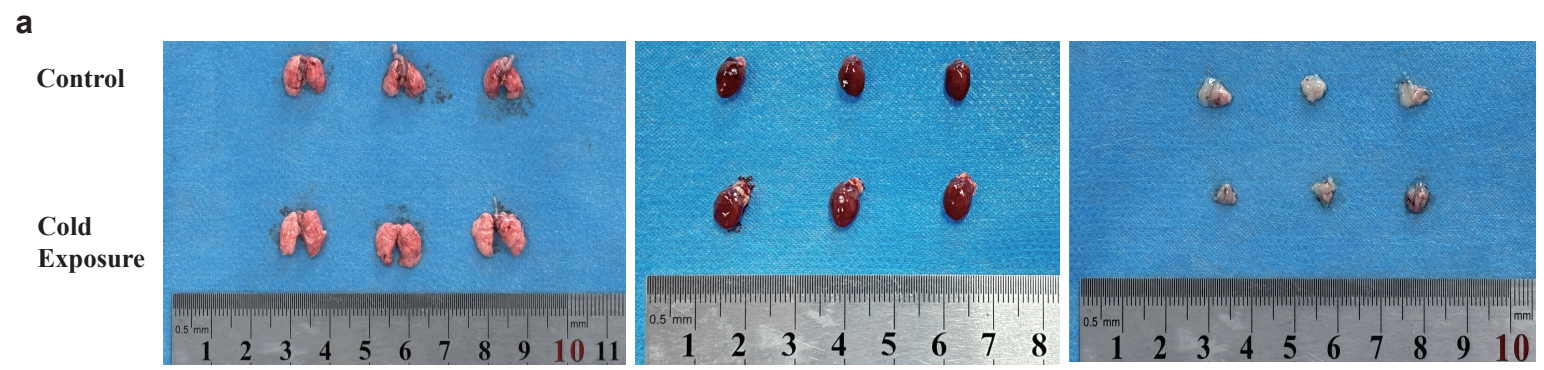
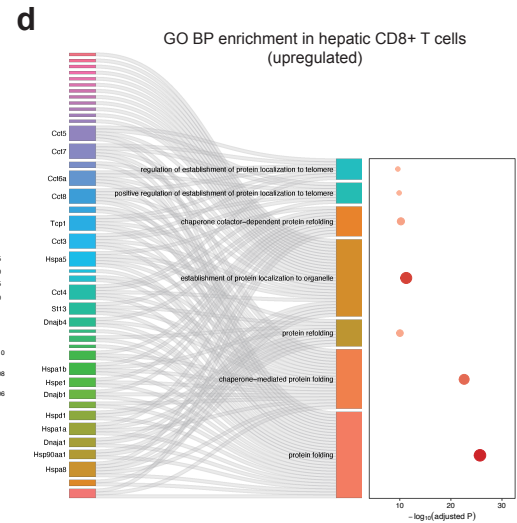
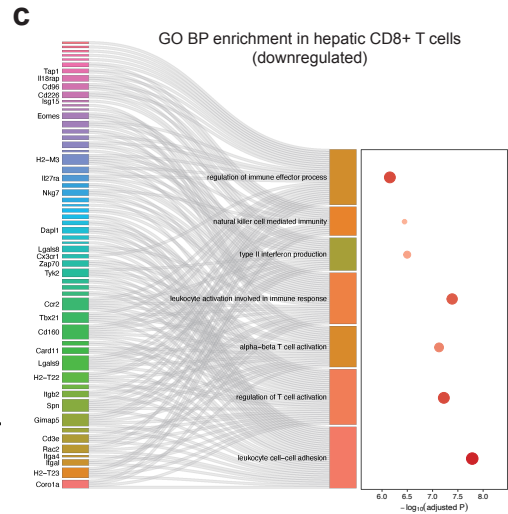
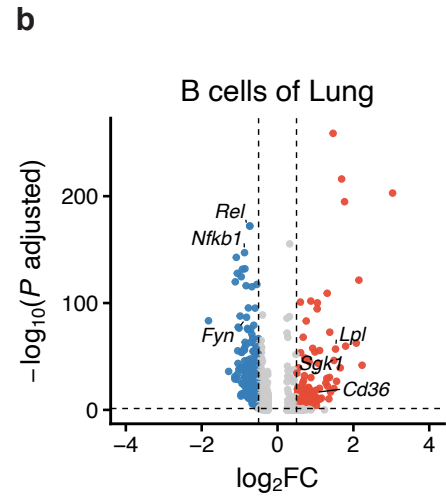
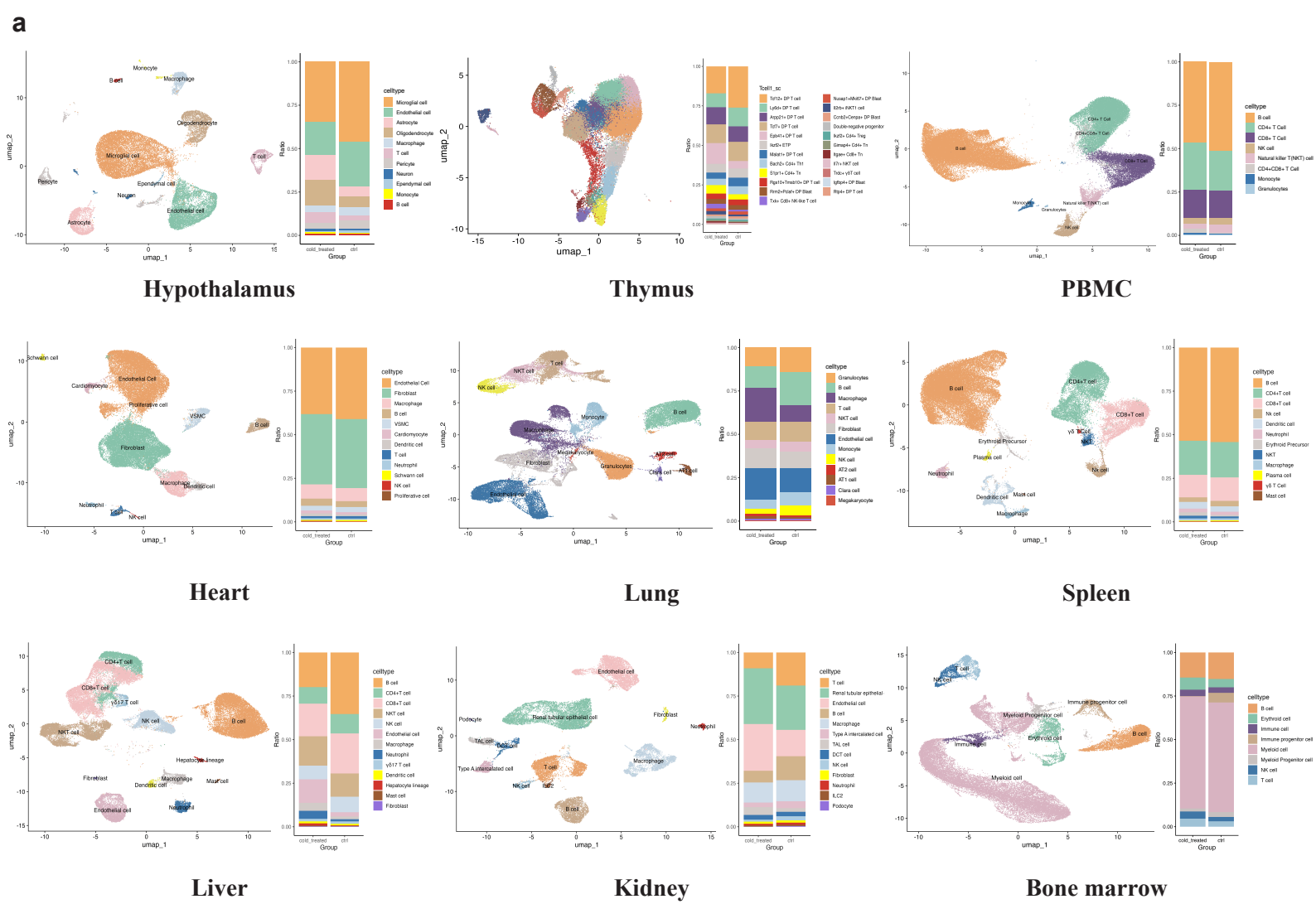




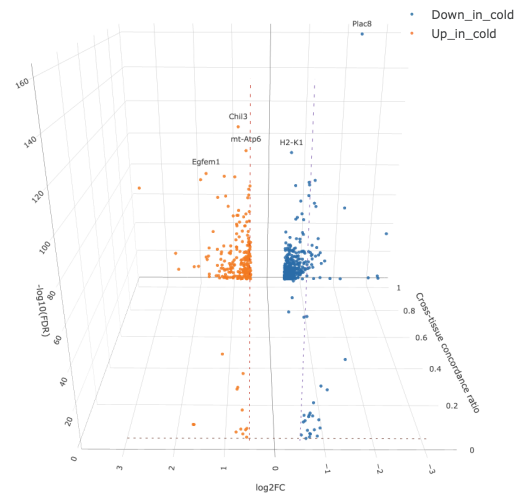


average log2FC

Cell type

● adjusted P-val < 0.01
● adjusted P-val >= 0.01

Cell types: B cell, T cell, Neutrophil, Microglia, NK cell, Macrophage, Monocyte, Dendritic cell



GO BP enrichment of upregulated genes

Y-axis (from top to bottom): fatty acid beta-oxidation, fatty acid oxidation, lipid oxidation, cellular lipid catabolic process, fatty acid metabolic process, monocarboxylic acid metabolic process, carboxylic acid metabolic process, oxoacid metabolic process, organic acid metabolic process, cellular lipid metabolic process.

X-axis: $\log_2(\text{Fold enrichment})$

Legend: Gene count (25, 50, 75, 100, 125); $-\log_{10}(P \text{ value})$ (6.0, 6.5, 7.0, 7.5).

KEGG enrichment of upregulated genes

Y-axis (from top to bottom): Propanoate metabolism, Fatty acid degradation, PPAR signaling pathway, Fatty acid metabolism, Carbon metabolism, Huntington disease, Parkinson disease, Prion disease, Alzheimer disease, Metabolic pathways.

X-axis: $\log_2(\text{Fold enrichment})$

Legend: Gene count (50, 100, 150); $-\log_{10}(P \text{ value})$ (4.0, 4.5, 5.0, 5.5, 6.0).

WikiPathways enrichment of upregulated genes

Y-axis (from top to bottom): TCA cycle and deficiency of pyruvate dehydrogenase complex (PDH), Enterocyte cholesterol metabolism, Cholesterol metabolism.

X-axis: $\log_2(\text{Fold enrichment})$

Legend: Gene count (10, 12, 14, 16, 18); $-\log_{10}(P \text{ value})$ (4.05, 4.10, 4.15, 4.20, 4.25).

GO BP enrichment of downregulated genes

Y-axis (from top to bottom): inflammatory response, cytokine production, positive regulation of immune response, regulation of cytokine production, leukocyte activation, lymphocyte activation, regulation of response to external stimulus, regulation of immune response, defense response to symbiont, cell adhesion.

X-axis: $\log_2(\text{Fold enrichment})$

Legend: Gene count (100, 110, 120, 130); $-\log_{10}(P \text{ value})$ (13, 14, 15, 16).

KEGG enrichment of downregulated genes

Y-axis (from top to bottom): Staphylococcus aureus infection, Hematopoietic cell lineage, Cell adhesion molecule (CAM) interaction, Inflammatory bowel disease, Th1 and Th2 cell differentiation, Cytokine-cytokine receptor interaction, Leishmaniasis, JAK-STAT signaling pathway, Osteoclast differentiation, Herpes simplex virus 1 infection.

X-axis: $\log_2(\text{Fold enrichment})$

Legend: Gene count (15, 20, 25, 30); $-\log_{10}(P \text{ value})$ (5, 6, 7).

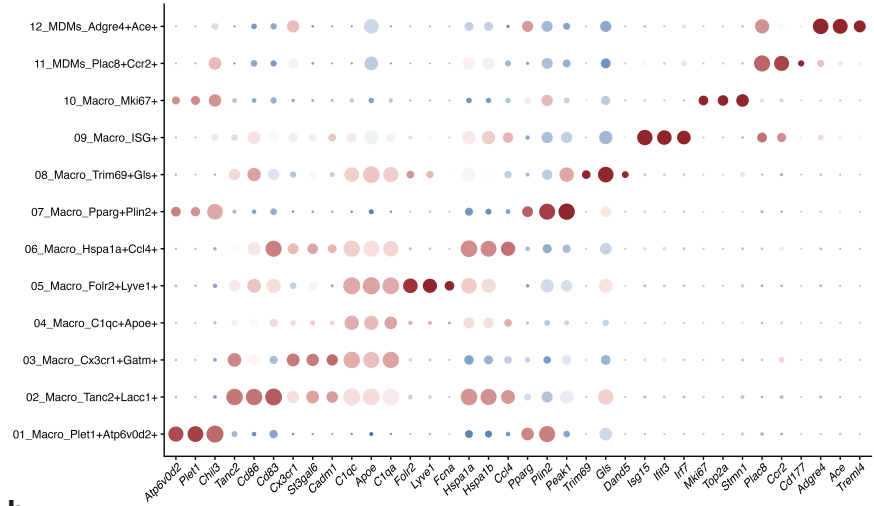
WikiPathways enrichment of downregulated genes

Y-axis (from top to bottom): IL10 anti-inflammatory signaling, Interferon signaling in tuberculosis, GPCRs, class A rhodopsin-like, Hair follicle development, cytodifferentiation - stage 3 of 3, Type II interferon signaling, Allograft rejection, Regulatory circuits of STAT3 signaling, Vitamin D receptor pathway, Cytokine-cytokine receptor interaction, Spinal cord injury.

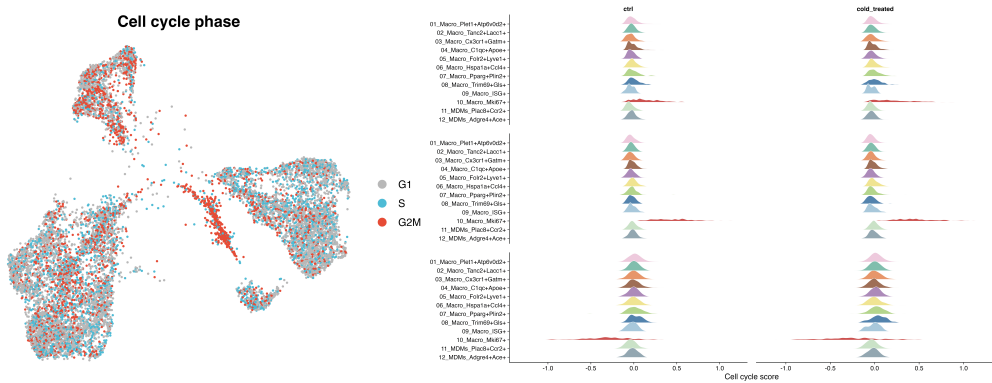
X-axis: $\log_2(\text{Fold enrichment})$

Legend: Gene count (10, 15, 20); $-\log_{10}(P \text{ value})$ (4.0, 4.5, 5.0, 5.5).

a

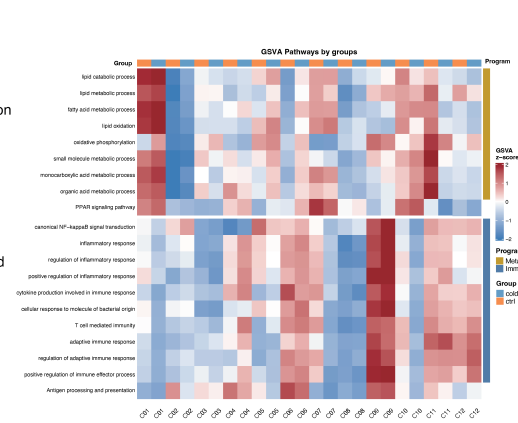


b

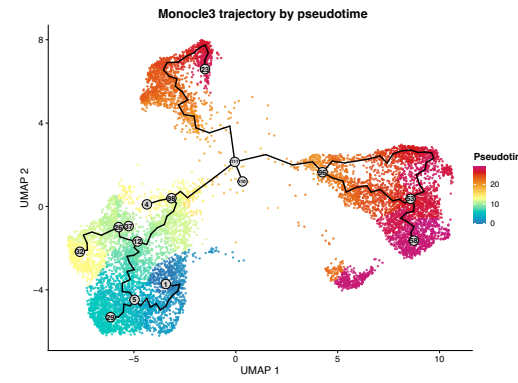


c

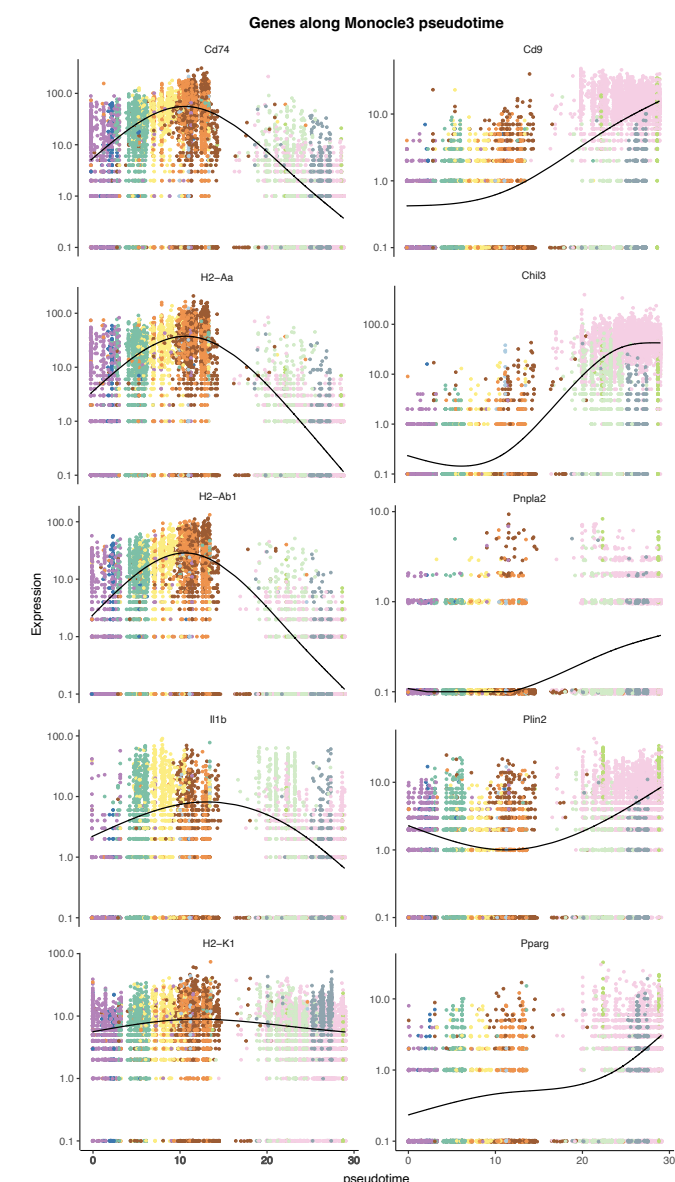
c



d



e



f

