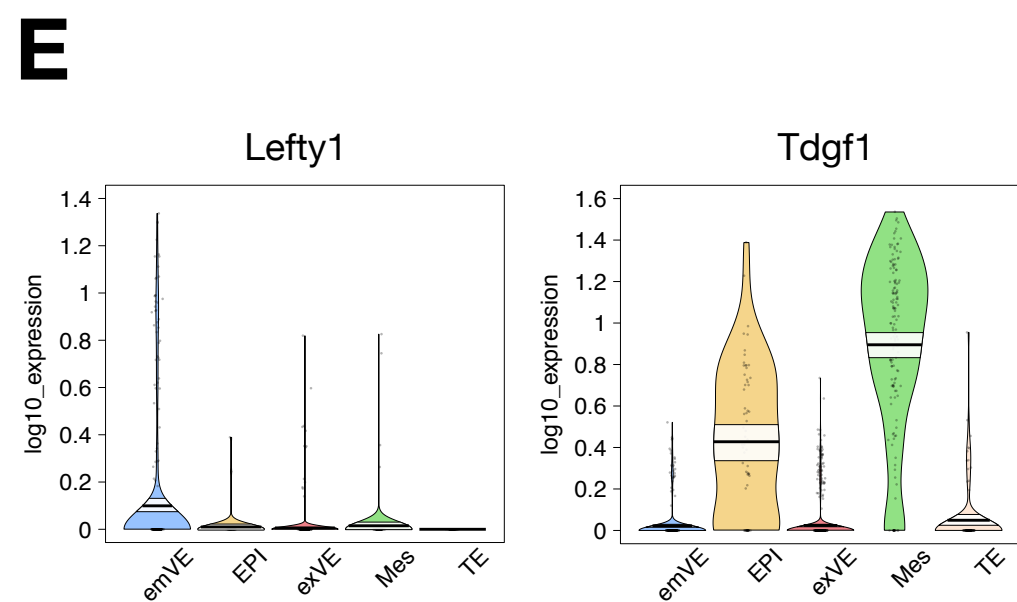
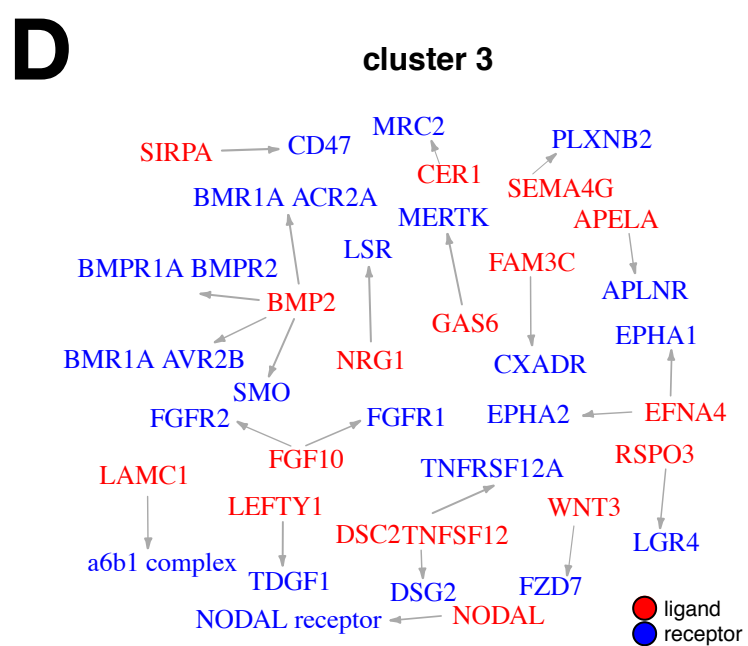
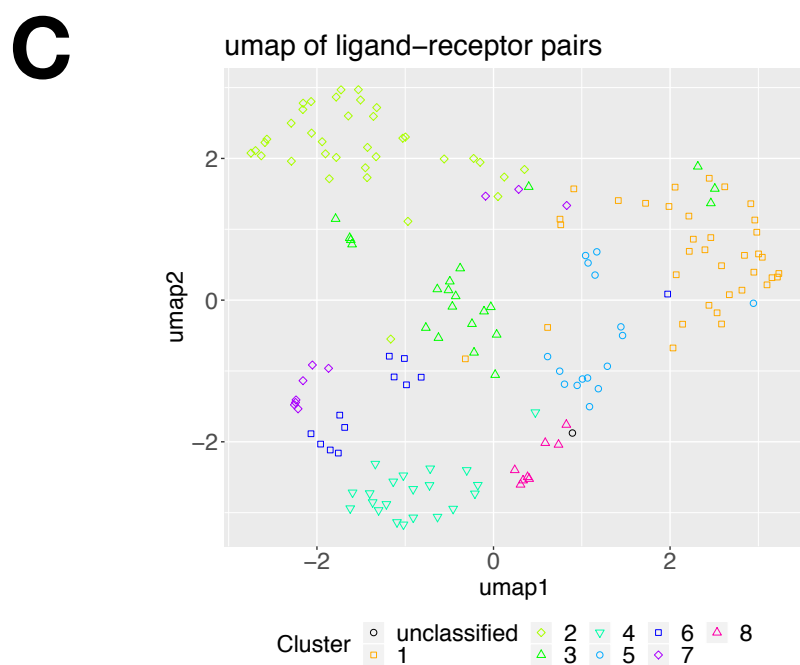
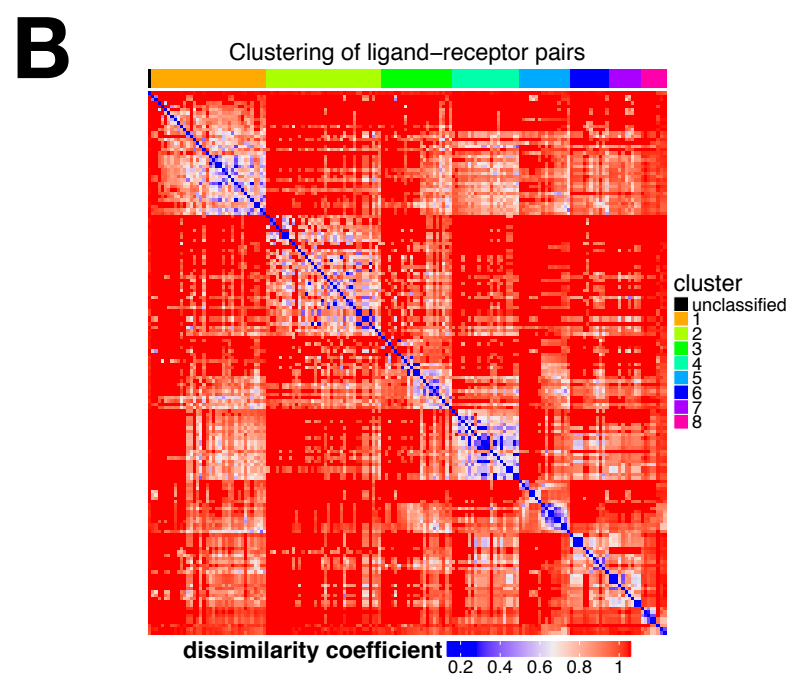
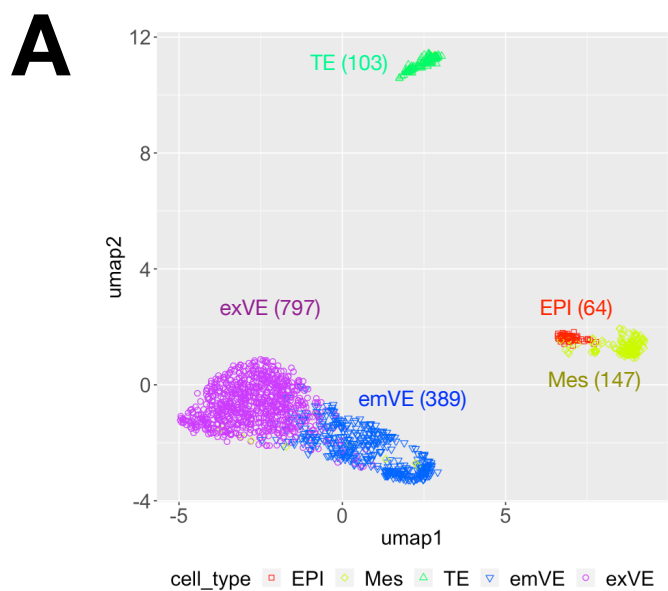
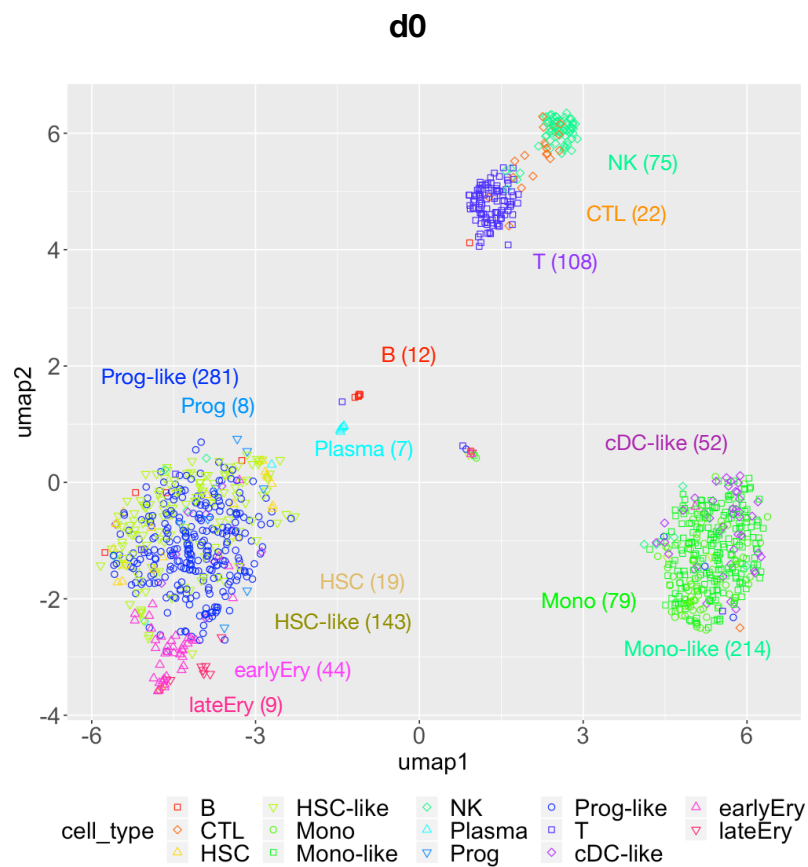
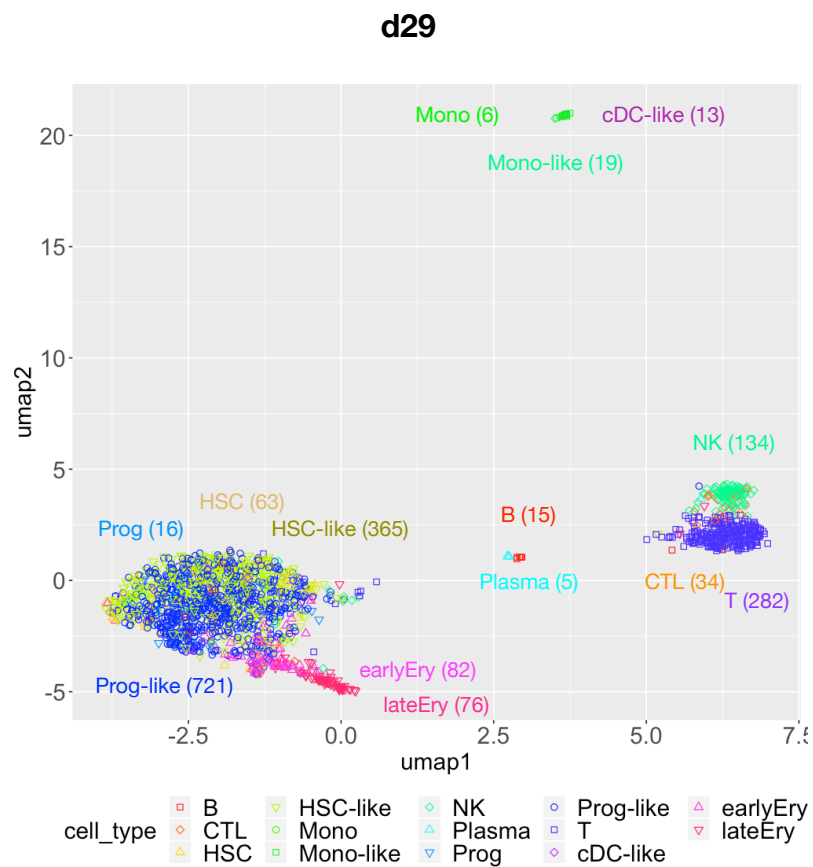
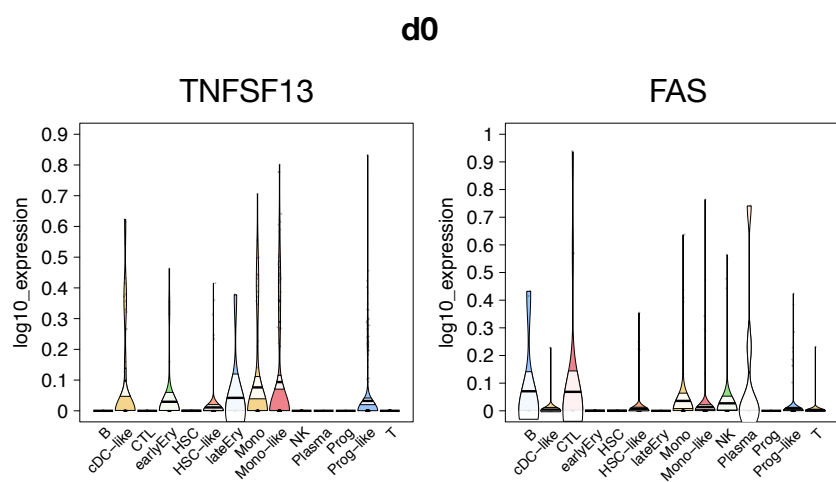
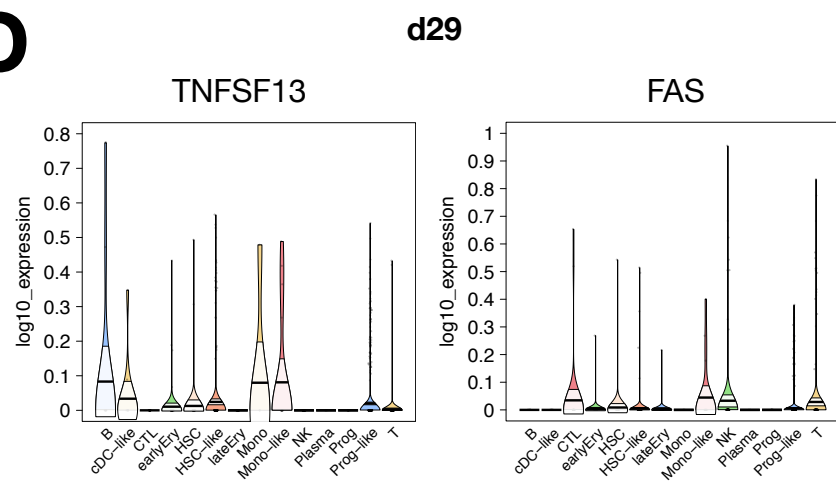
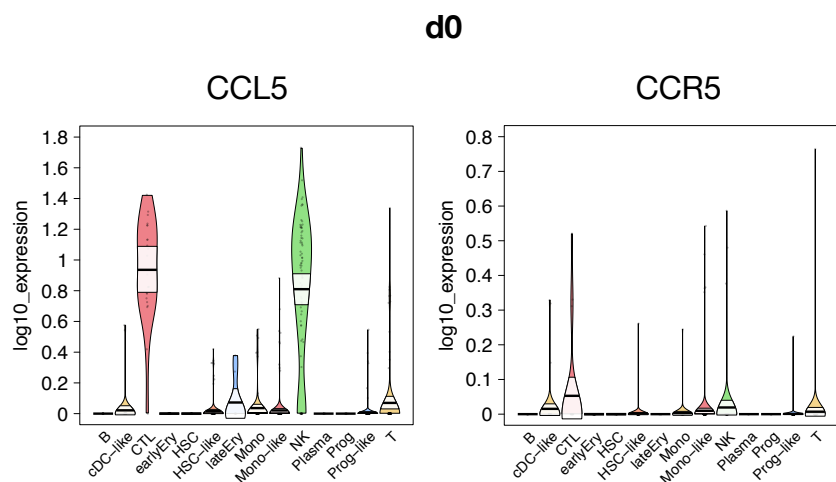
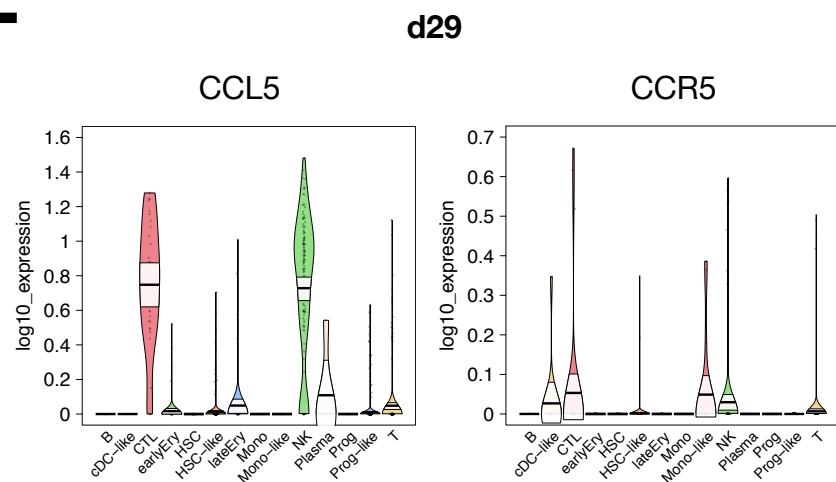




Supplemental Figure 1 - E6.5 mouse embryo data

- A. UMAP of the E6.5 mouse embryo scRNA-seq data (subset to 1500 cells). Cell types are: embryonic visceral endoderm (emVE), epiblast (EPI), extraembryonic visceral endoderm (exVE), mesoderm (Mes), and trophoctoderm (TE).
- B. Heatmap showing the dissimilarity of **interacting partners** in the scRNA-seq data from E6.5 mouse embryo (subset to 1500 cells). Rows and columns are sorted by cluster number, the color represents dissimilarity between two pairs with 0 for identical pattern (blue), 1 for completely different pattern (red).
- C. UMAP of **interacting partners** colored by cluster.
- D. **interacting partners** in cluster 3. Ligands are represented in red, receptors in blue; arrows go from the ligand to the associated receptor.
- E. Log10 expression levels of Lefty1 and Tdgf1.

A**B****C****D****E****F**

Supplemental Figure 2 - AML patient data

A-B. UMAP of bone marrow of AML patient at d0 (panel A) and d29 (panel B). Number of cells in each population is represented in brackets.

C-D. Log10 expression levels of TNFSF13 and FAS at d0 (panel C) and d29 (panel D).

E-F. Log10 expression levels of CCL5 and CCR5 at d0 (panel E) and d29 (panel F).