

Figure 1: Pathway expression profiles could recur across diverse cell types

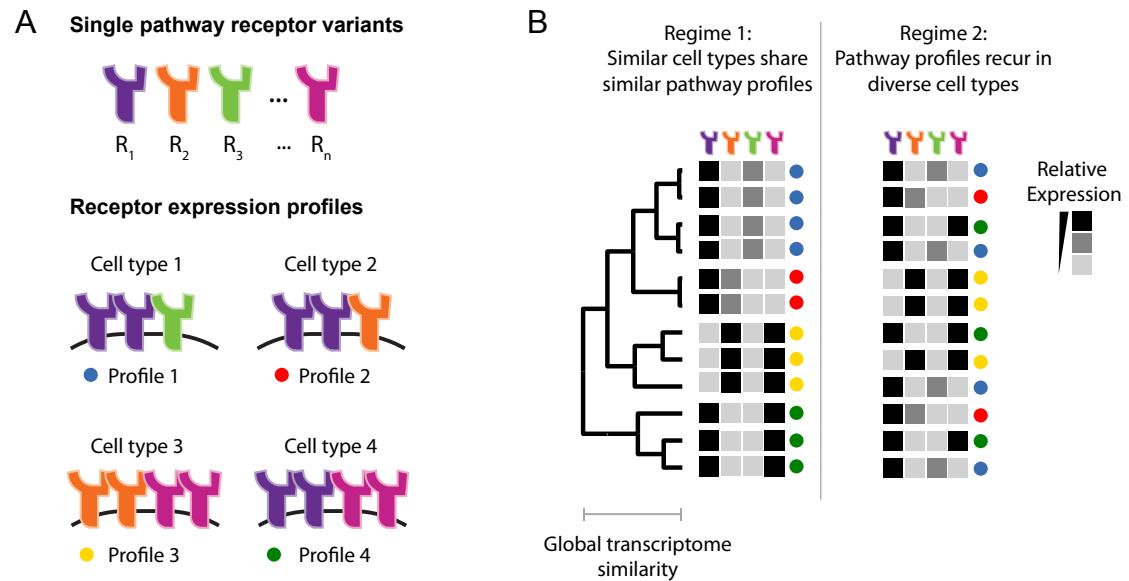
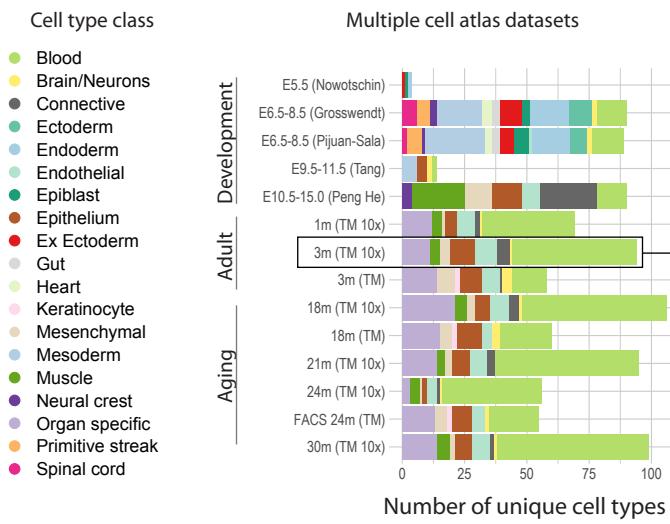
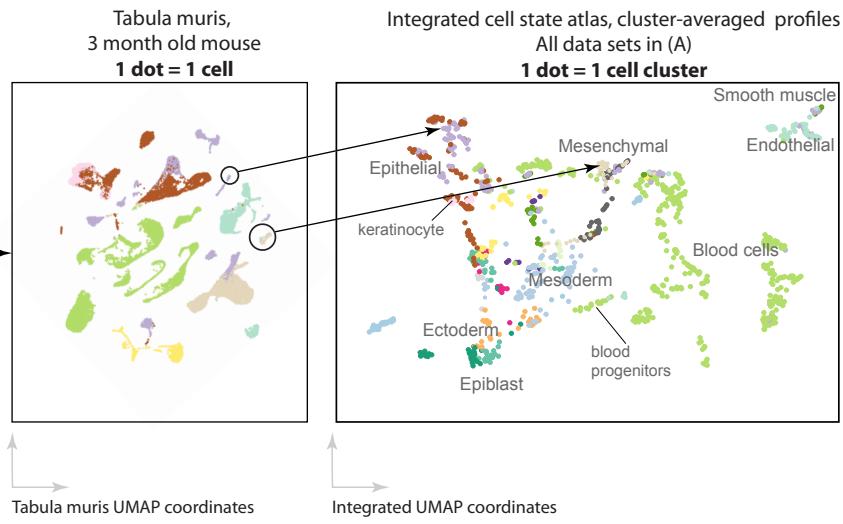


Figure 2: Multi-atlas integration provides cell type expression profiles across developmental stage, tissue, and age

A



B



C

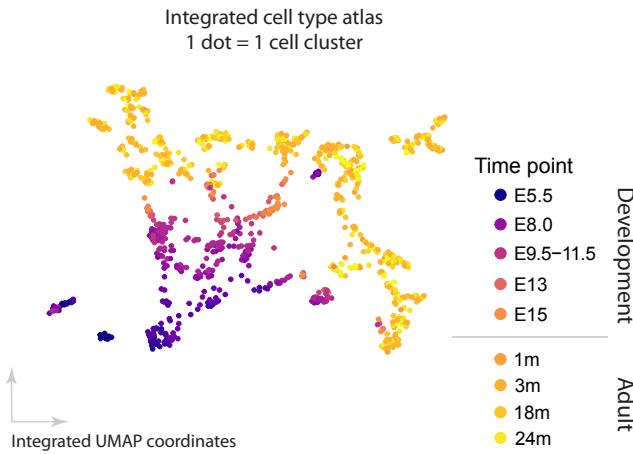
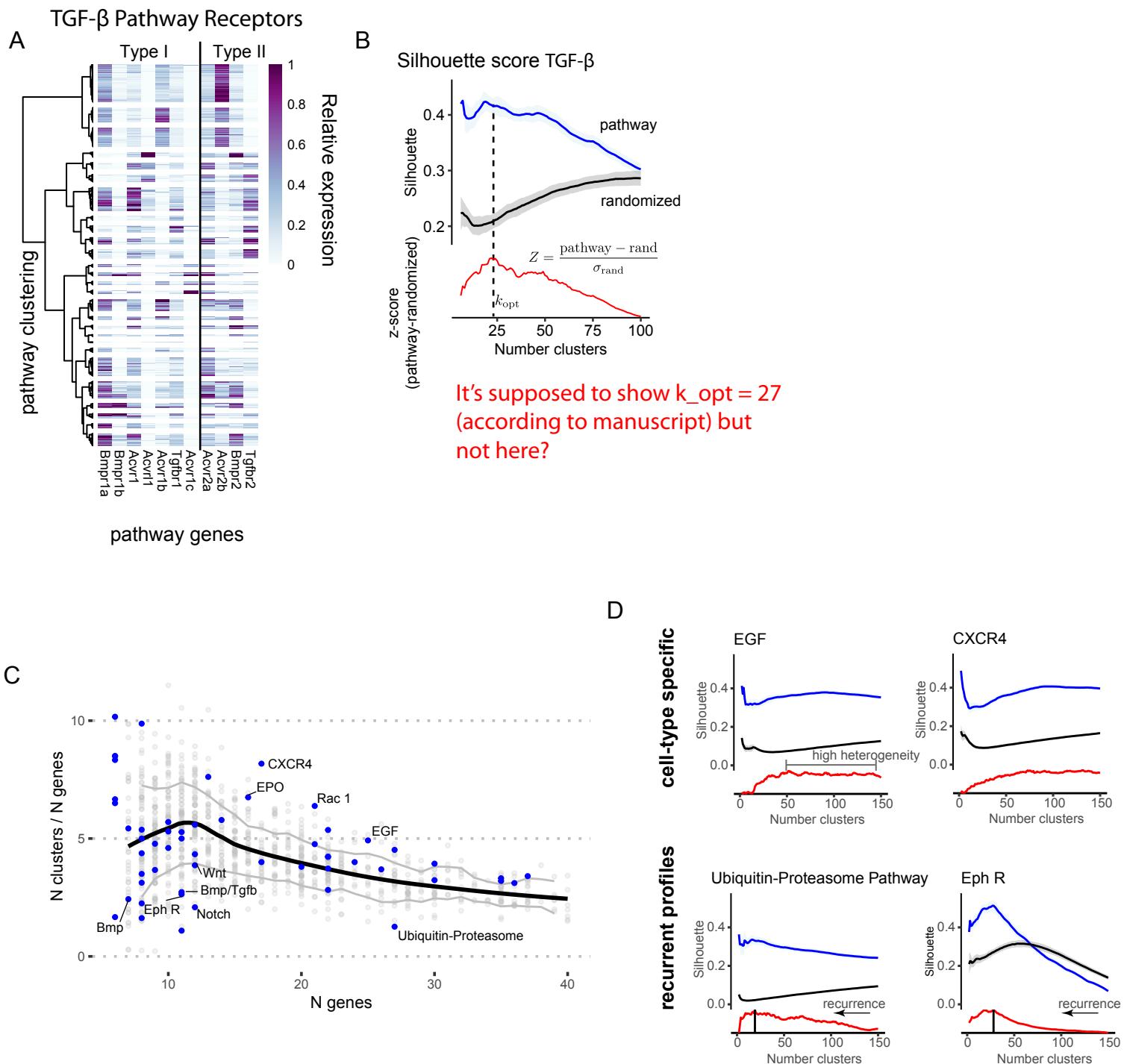


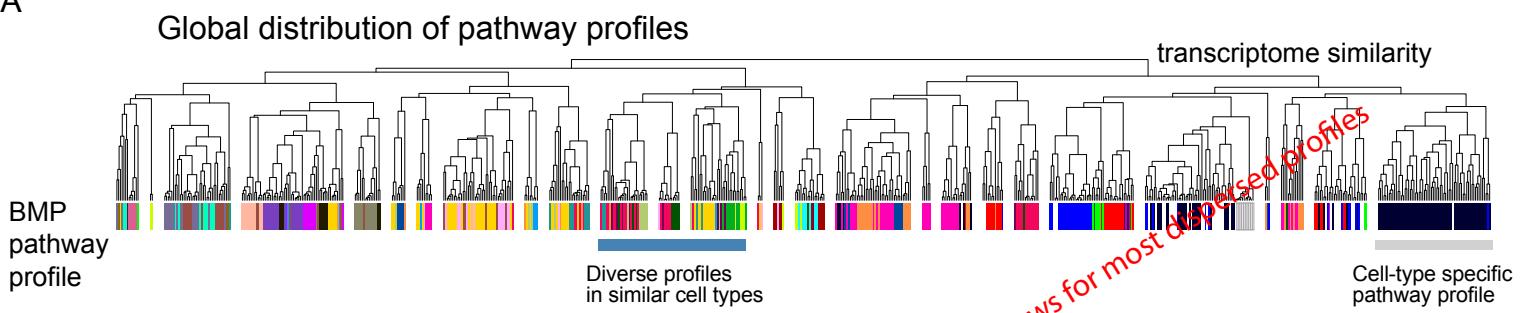
Figure 3: Silhouette analysis identifies recurrent profiles for BMP and other pathways



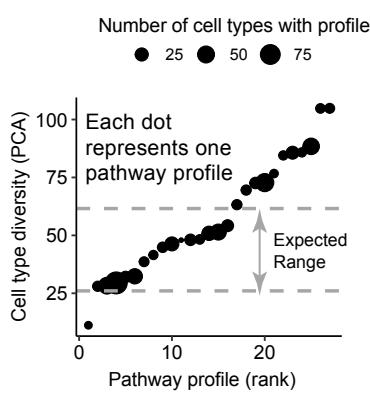
dispersion

Figure 4: Diverse cell types share similar BMP expression motifs

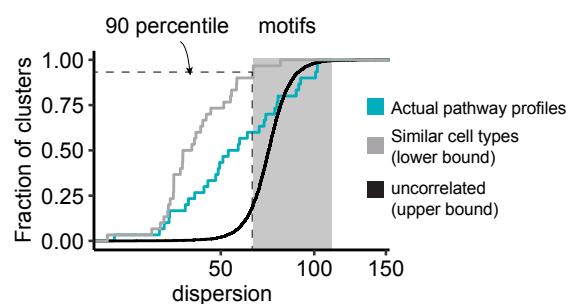
A



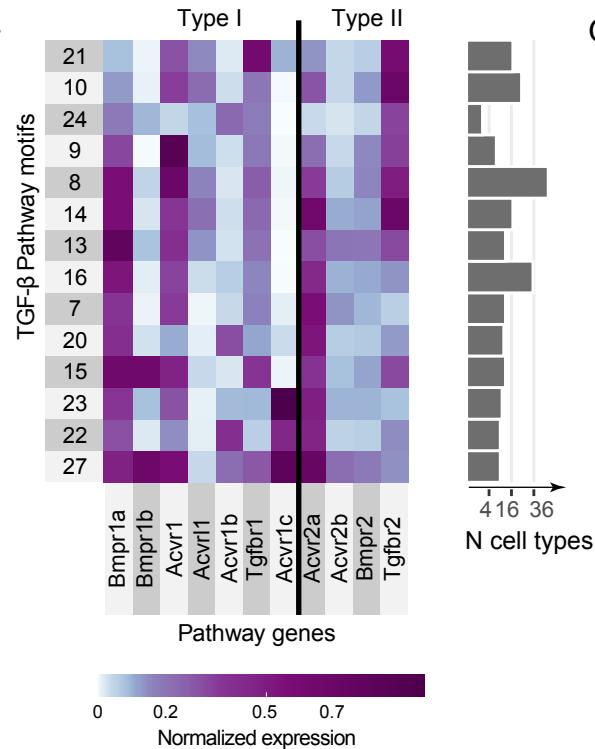
D



E



F



G

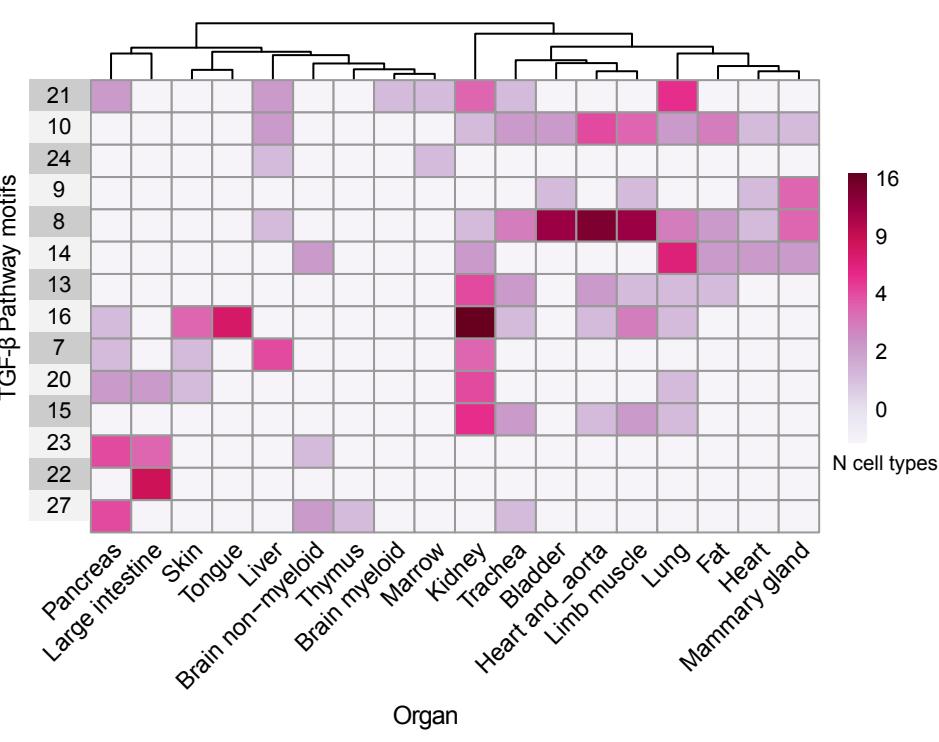
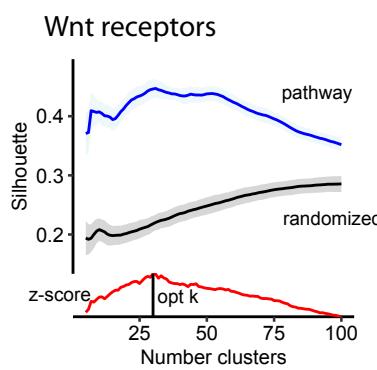
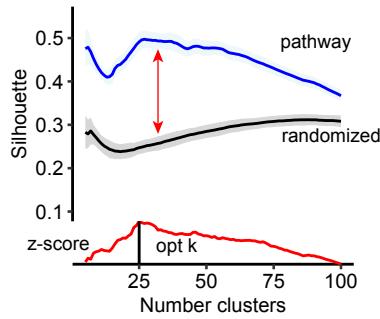


Figure 5: Wnt and Notch also exhibit pathway expression motifs

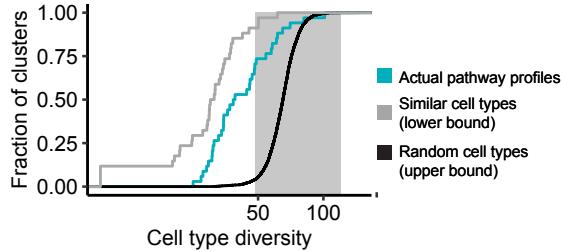
A



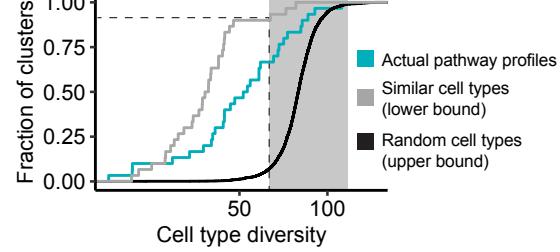
D Notch Receptors + ligands



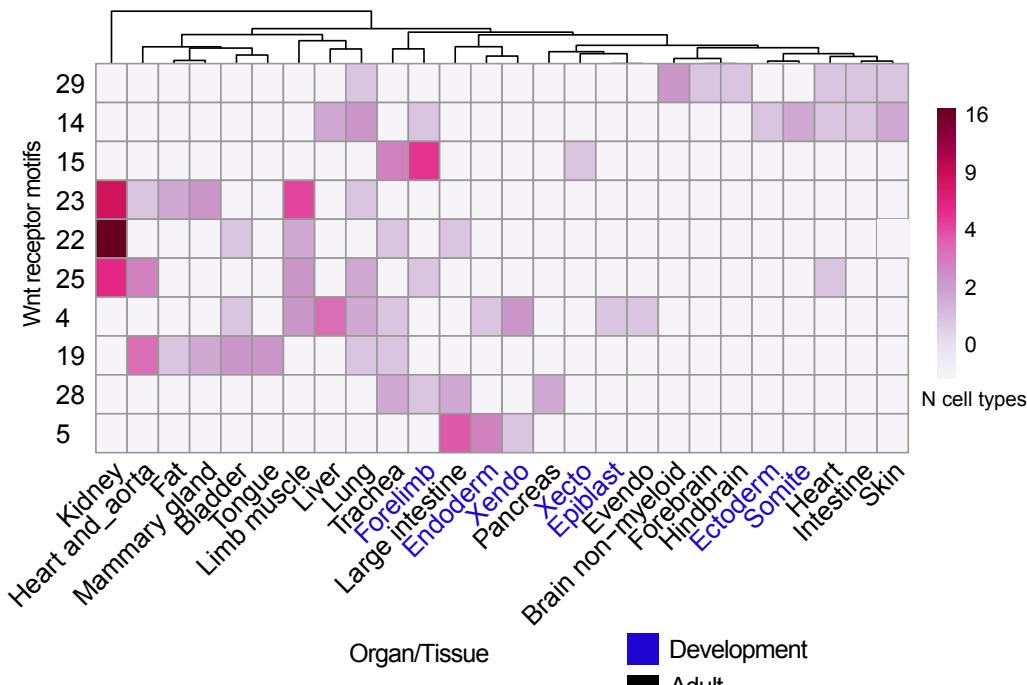
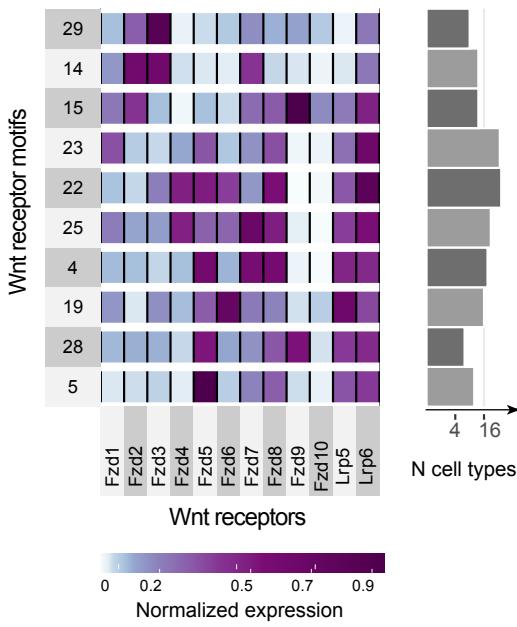
B

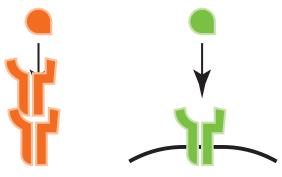


E



Wnt receptors





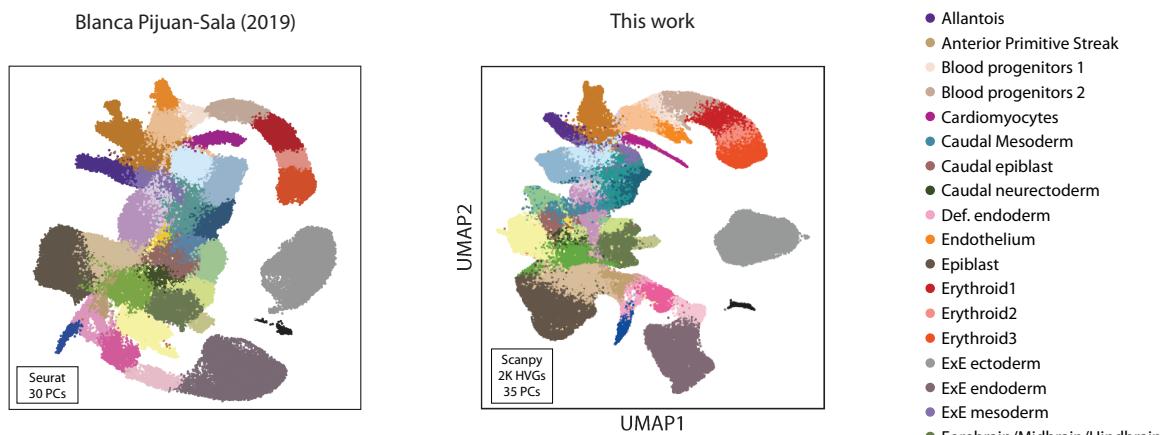
Are we including any supplementary figure for Fig. 1?
I don't think we need to?

Figure 2 supplement

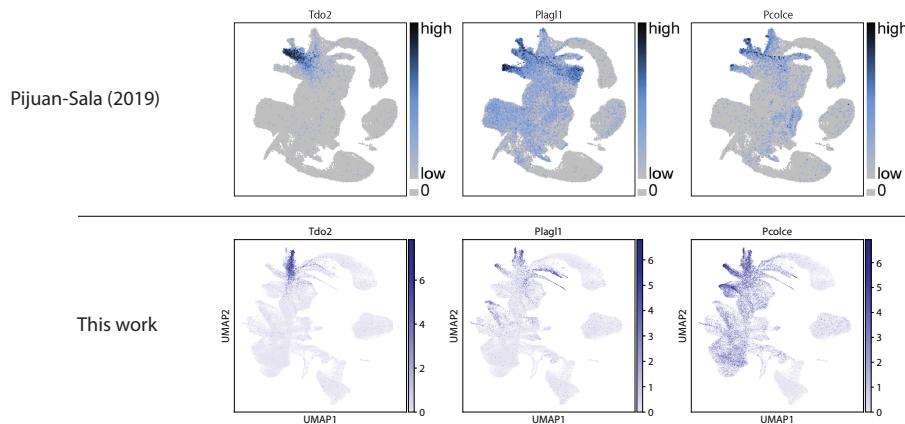
Are plots from both developmental datasets really necessary here?
Won't one suffice since we're showing the same thing from both?

A

E6.5-E8.5 Gastrulation and Early Organogenesis (114,781 cells)

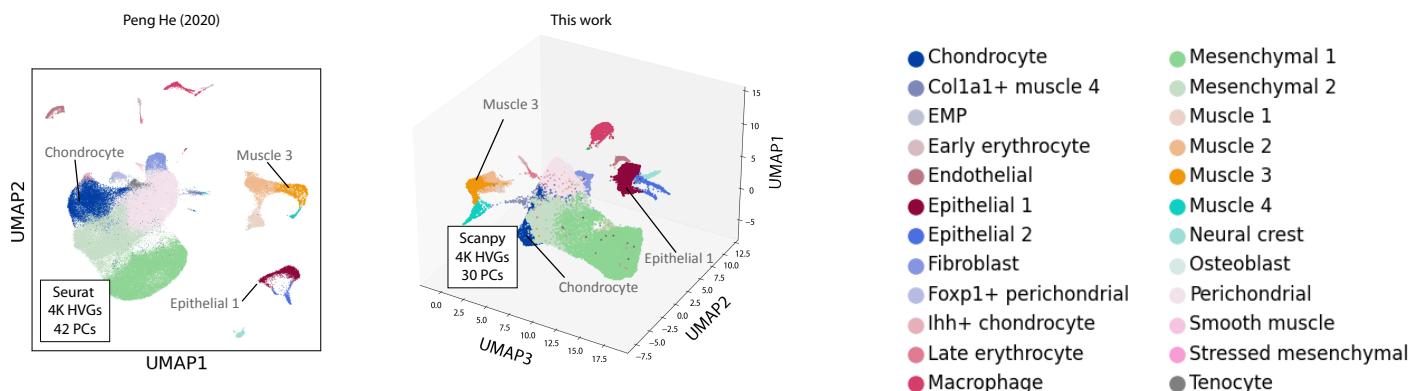


B



C

E10.5-E15.0 Forelimb (90,637 cells)



D

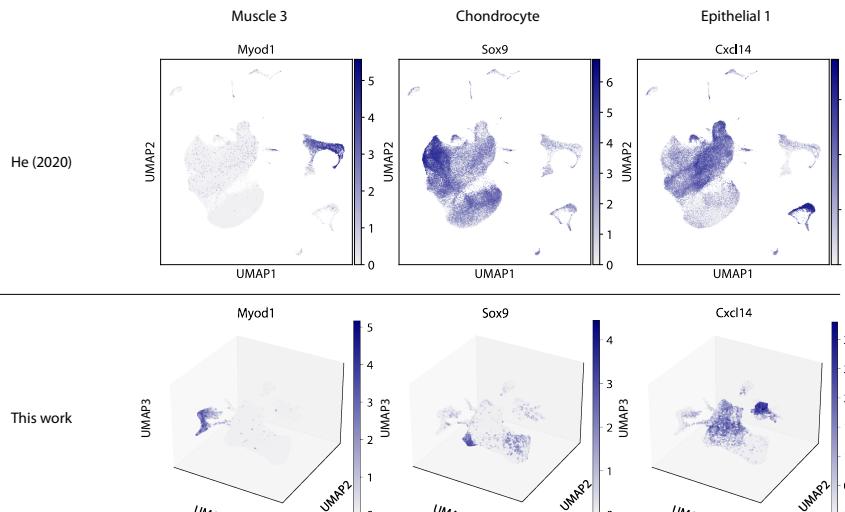


Figure 3 Supplement

Would **absolute cell type #'s** (out of 1206) OR **fraction of cell types** be easier to display?

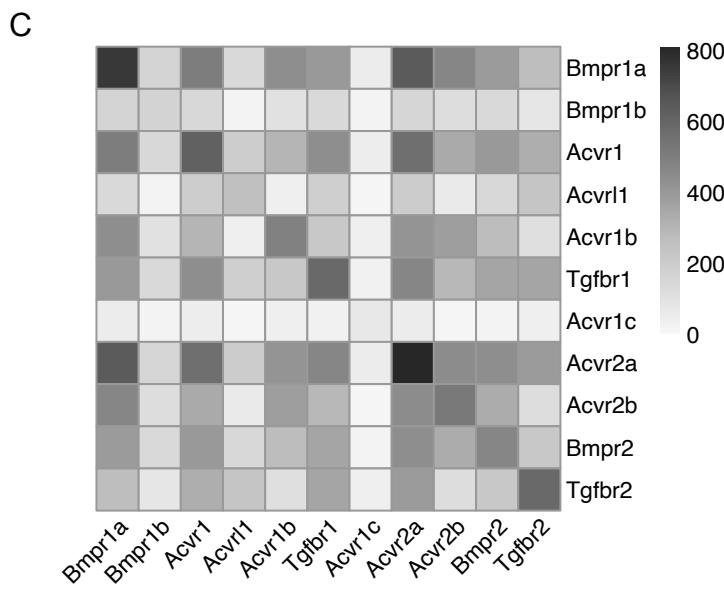
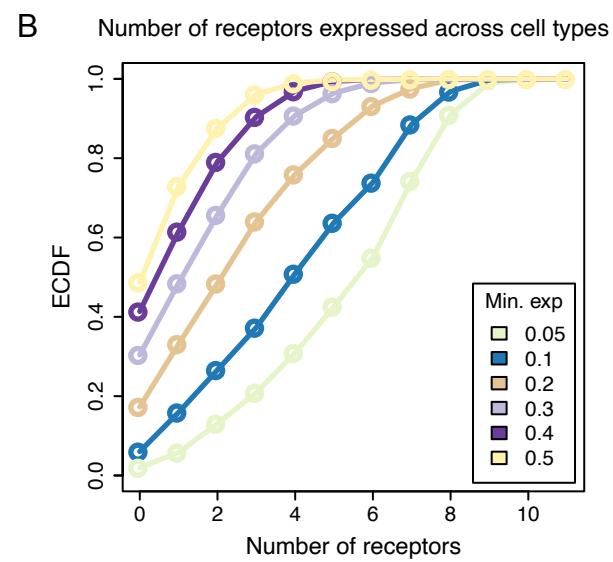
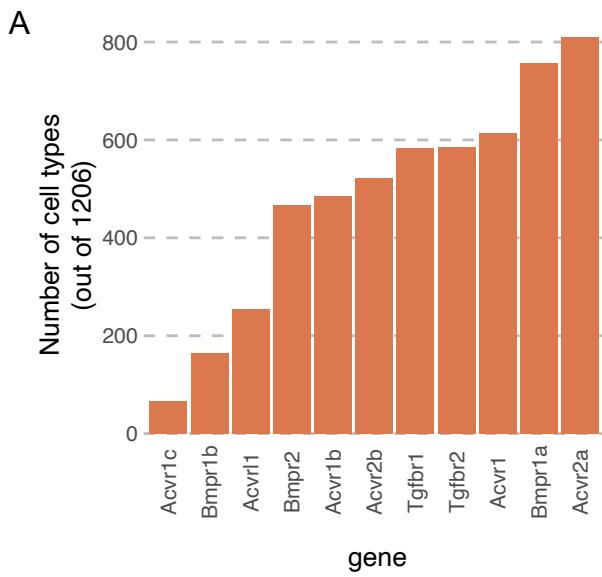
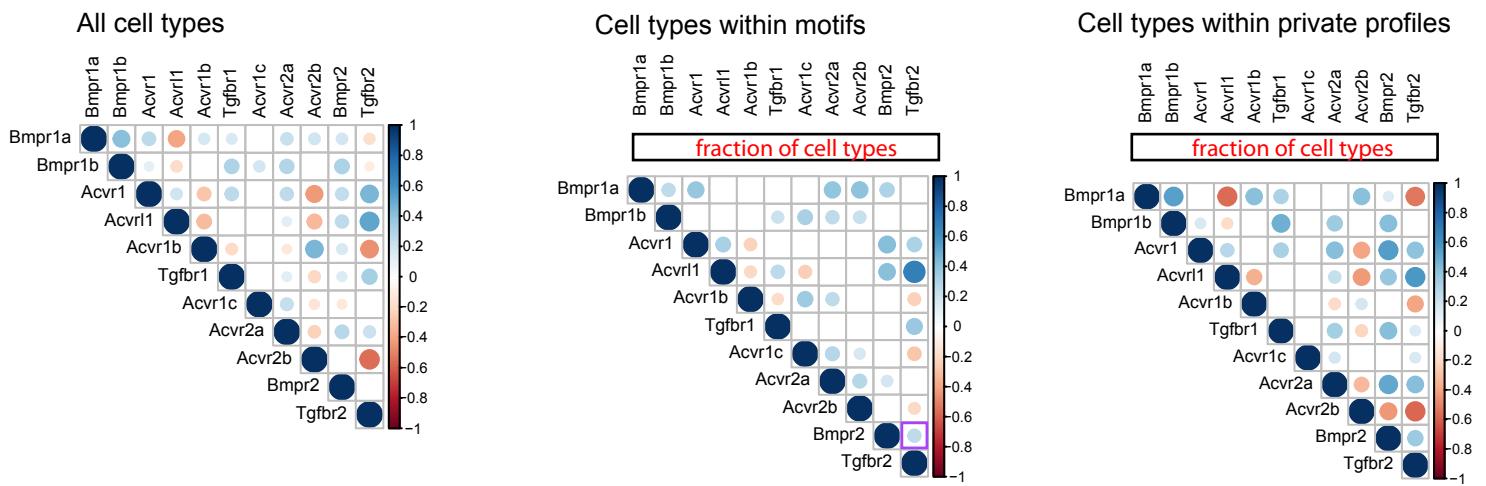


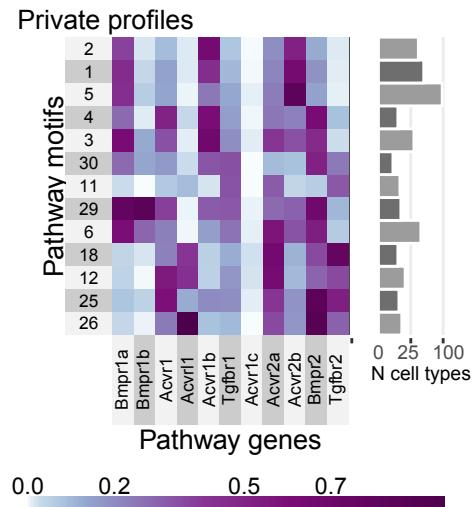
Figure 4 Supplement

How are we going to number this figure?

Pairwise correlations

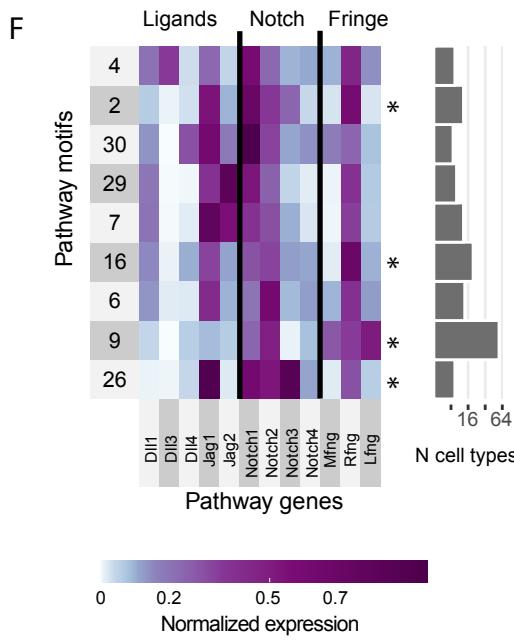


Need to add the Wnt and Notch correlation plots

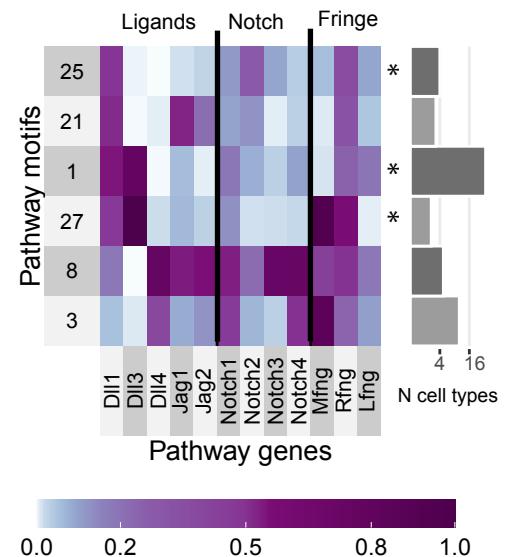


Which supp figure do these motif and private profile heatmaps belong to?

Notch motif profiles



Notch private profiles



50% of cell types within motif or private

Is this a part of Fig. 5?

