

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

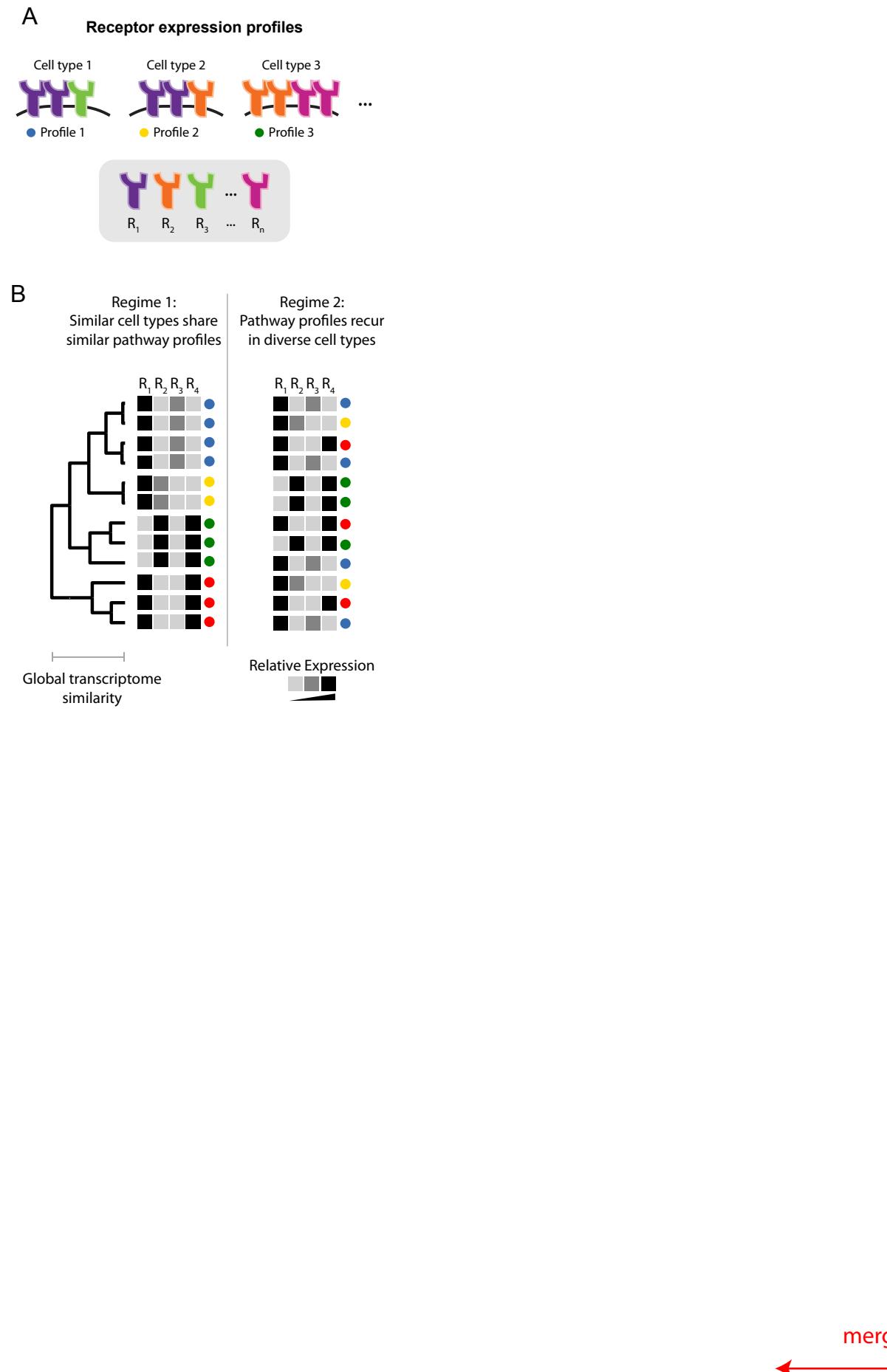
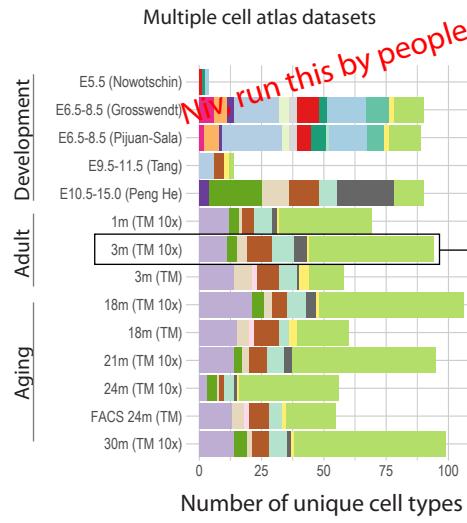


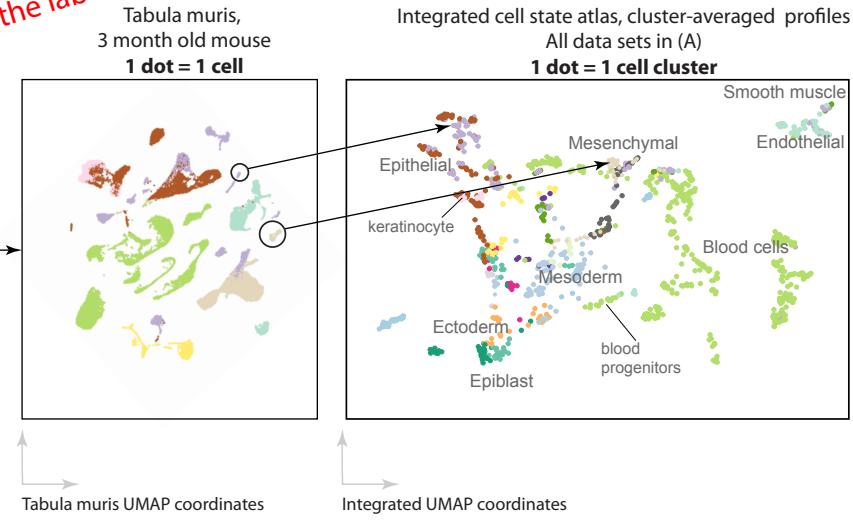
Figure 2: Multi-atlas integration provides a cell type expression profiles across developmental stage, tissue, and age

A

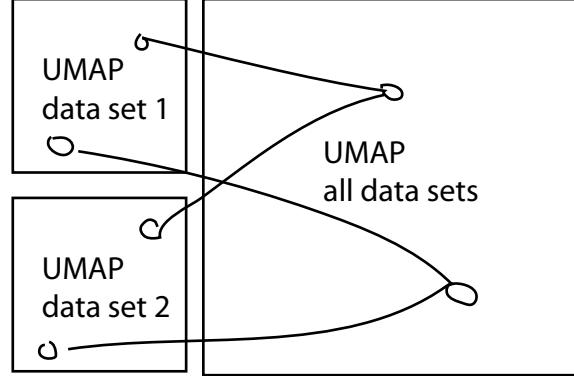
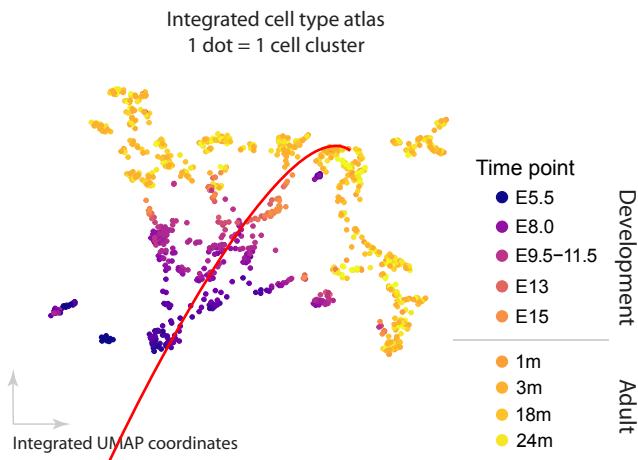
- Cell type class
- Blood
 - Brain/Neurons
 - Connective
 - Ectoderm
 - Endoderm
 - Endothelial
 - Epiblast
 - Epithelium
 - Ex Ectoderm
 - Gut
 - Heart
 - Keratinocyte
 - Mesenchymal
 - Mesoderm
 - Muscle
 - Neural crest
 - Organ specific
 - Primitive streak
 - Spinal cord



B



C



supplementary

Add Alejandro's analysis that cell types of the same class are more similar to each other than to other cell types --> matrix + dendrogram
- what genes should this be based on?

to figure 1

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

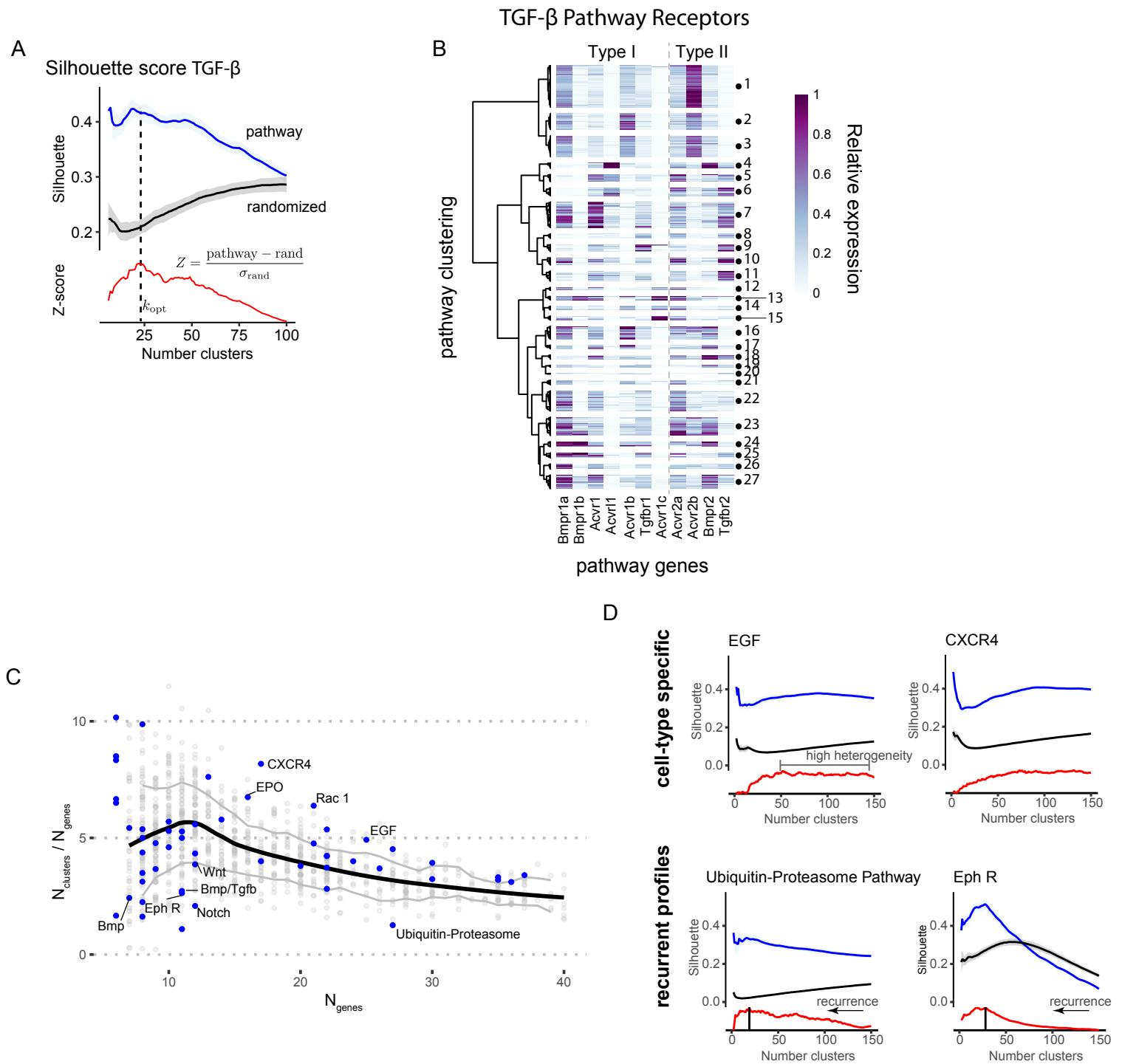
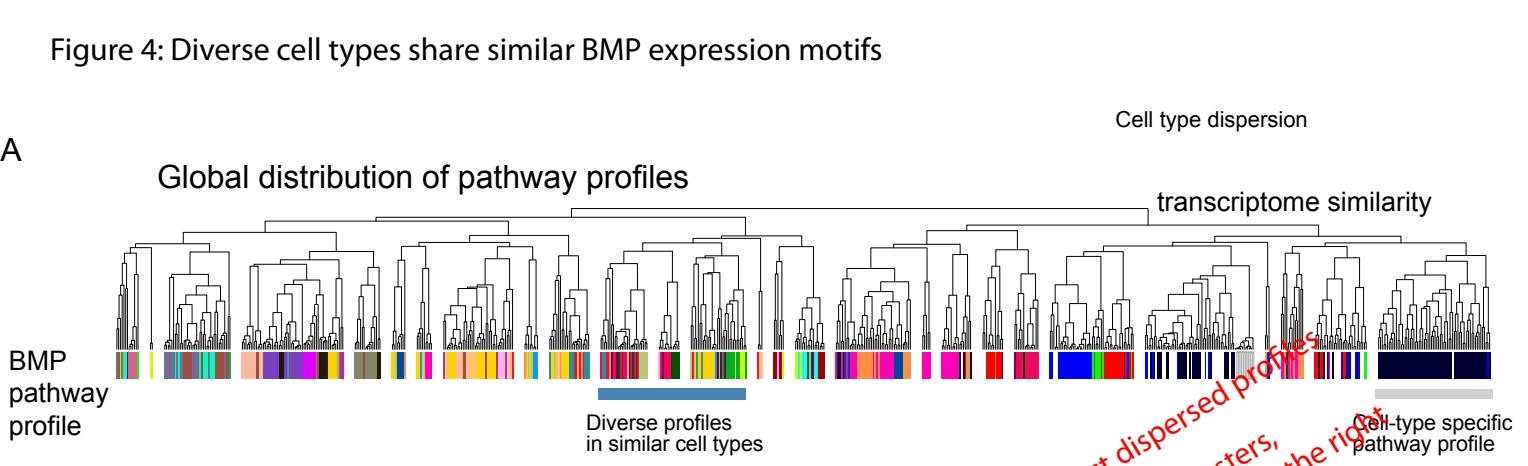
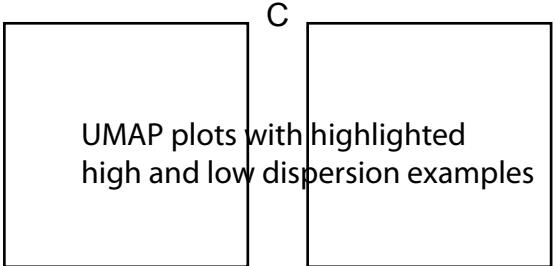


Figure 4: Diverse cell types share similar BMP expression motifs

A

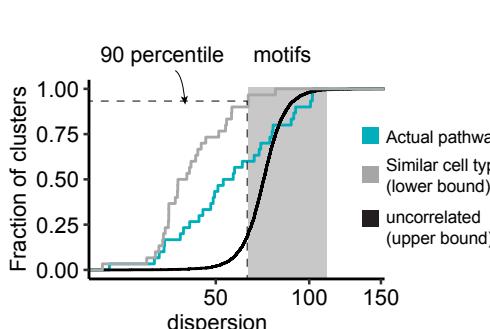
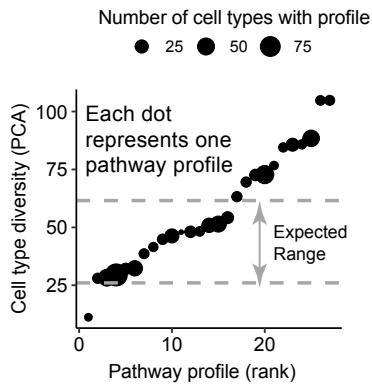


B

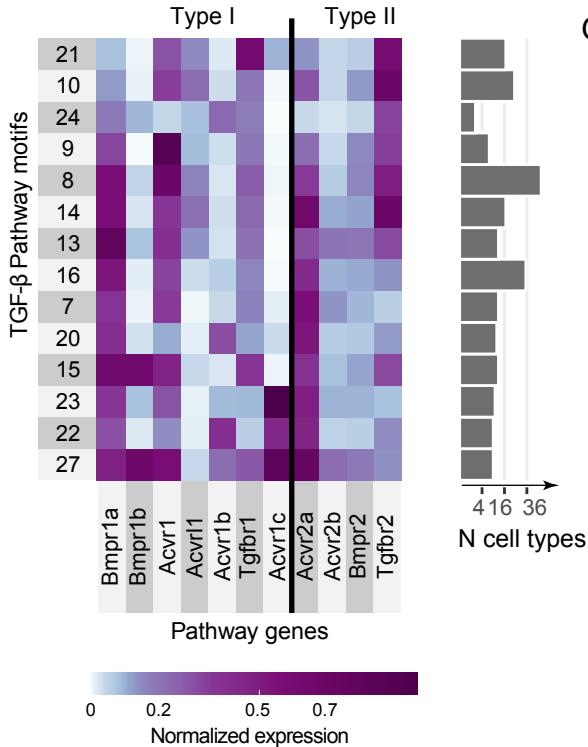


C

E



F



G

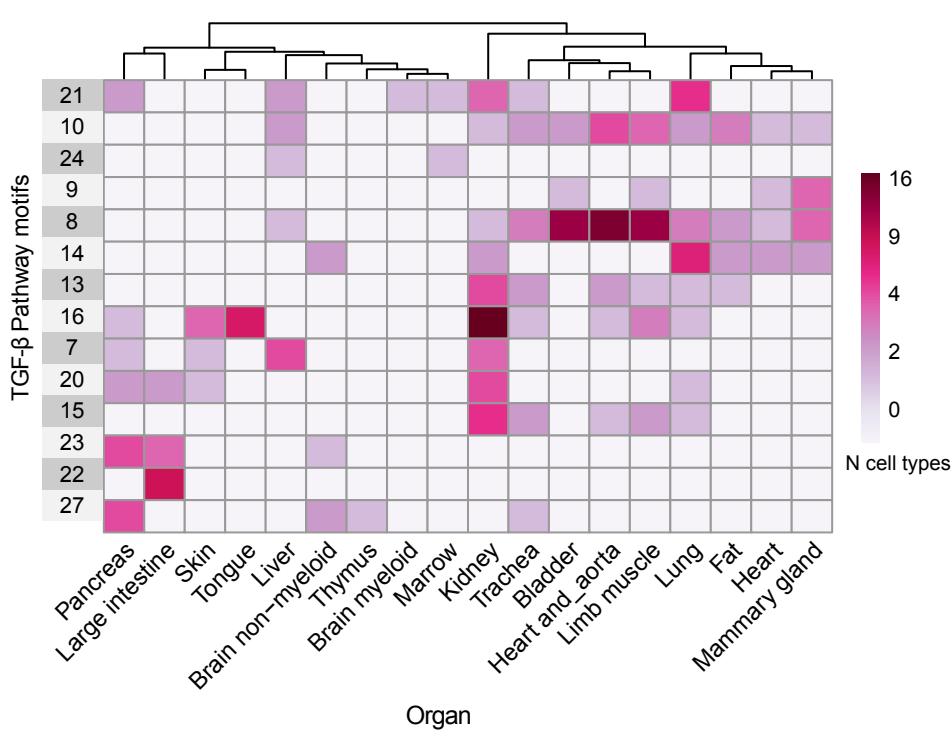
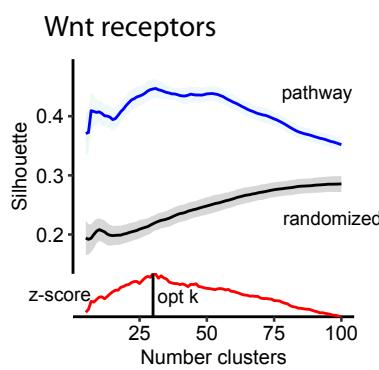
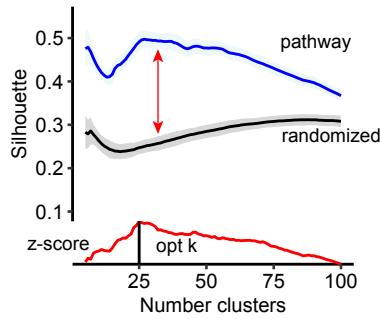


Figure 5: Wnt and Notch also exhibit pathway expression motifs

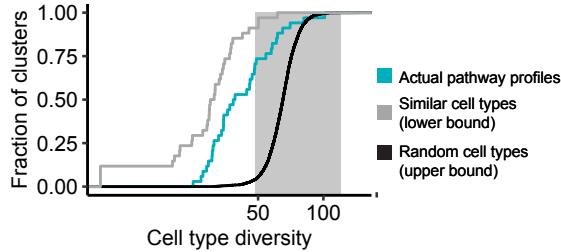
A



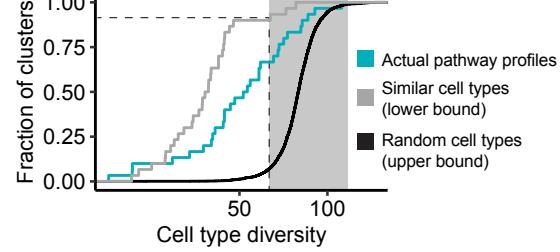
D Notch Receptors + ligands



B



E



Wnt receptors

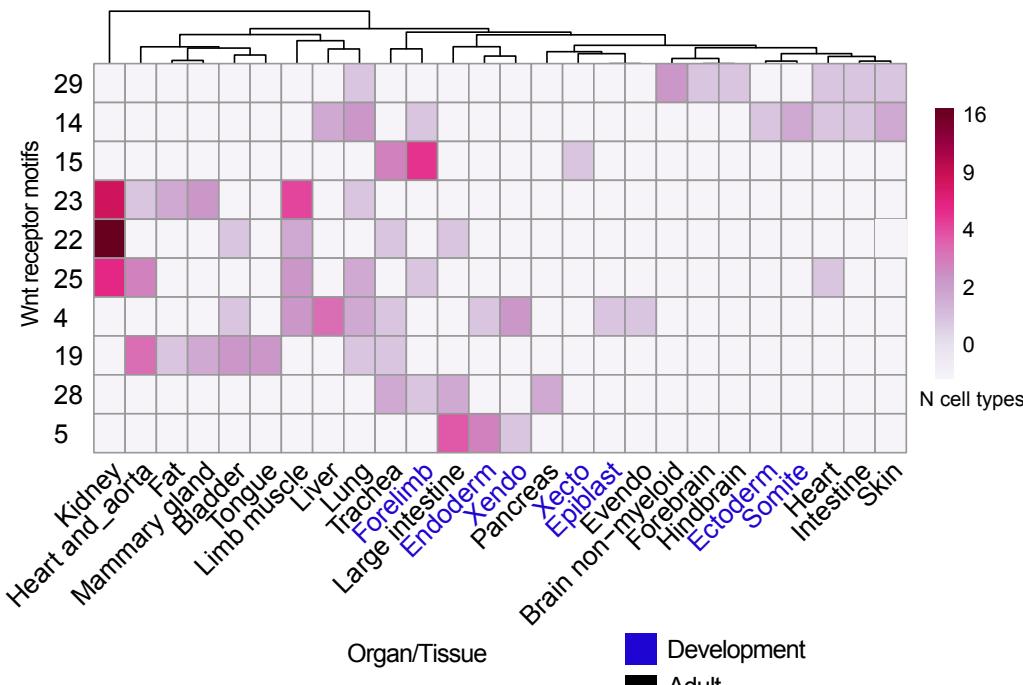
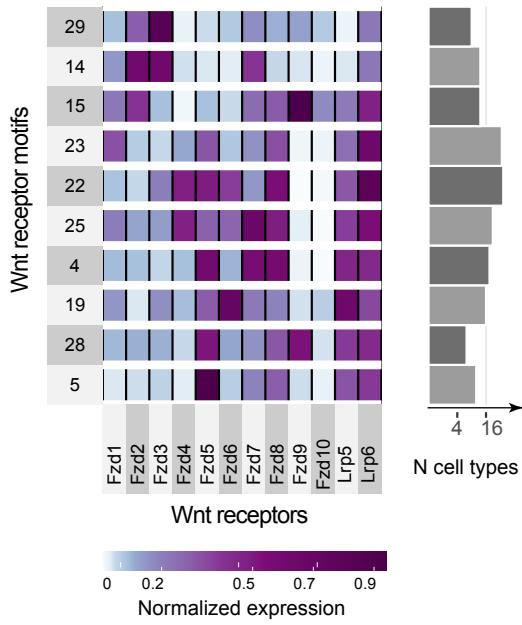
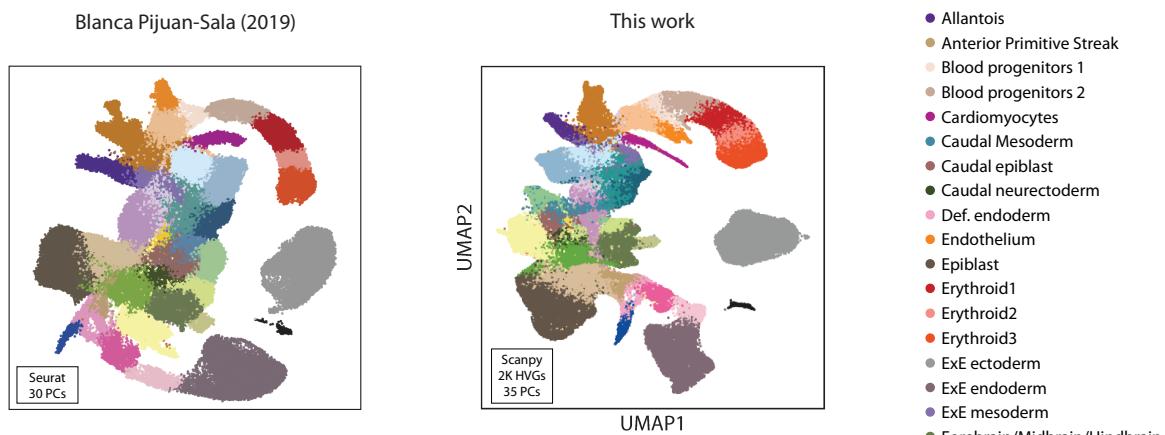


Figure 2 supplement

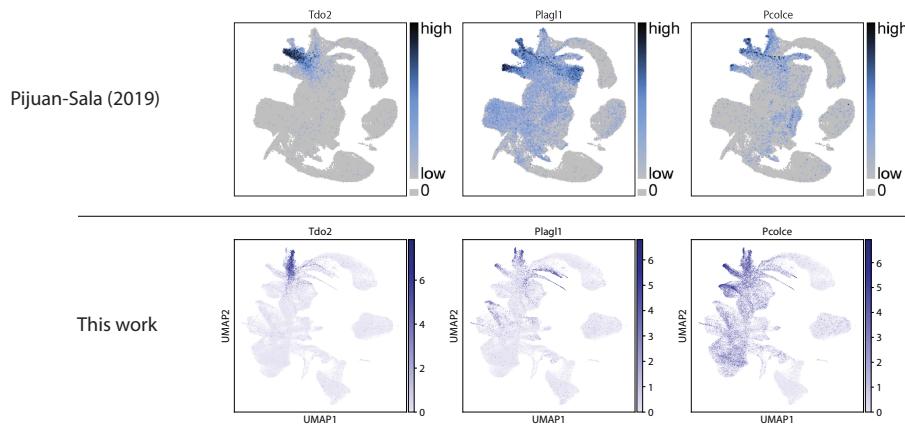
Are plots from both developmental datasets really necessary here?
Won't one suffice since we're showing the same thing from both?

A

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

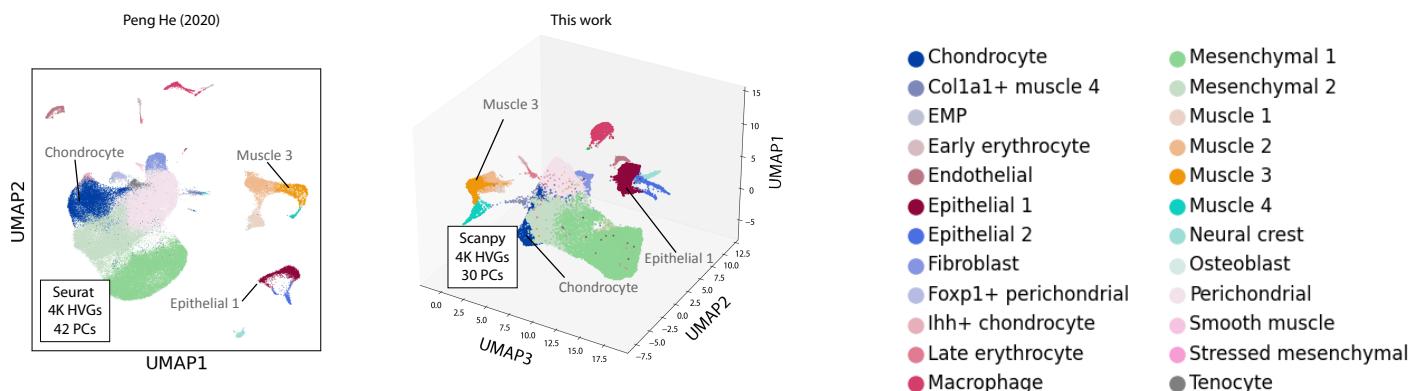


B



C

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



D

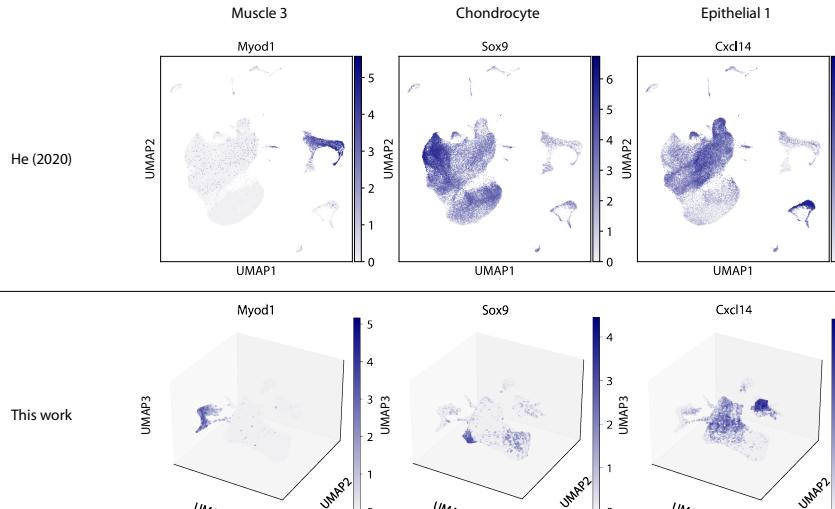


Figure 3 Supplement

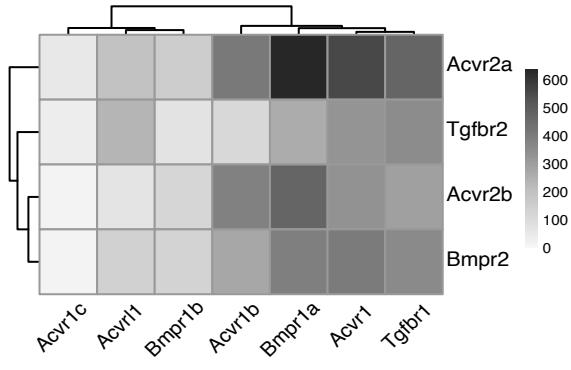
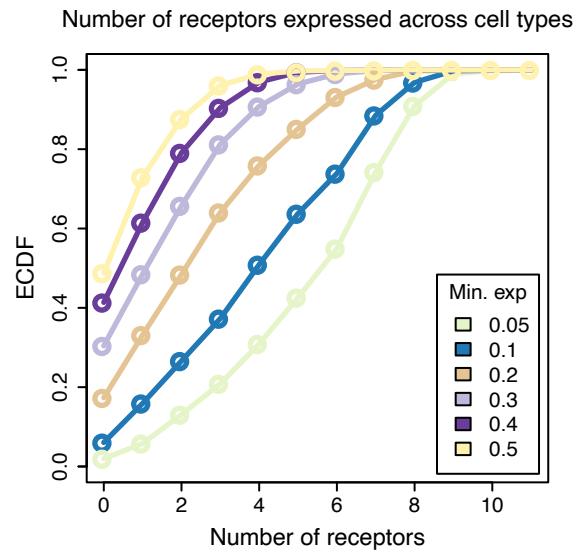
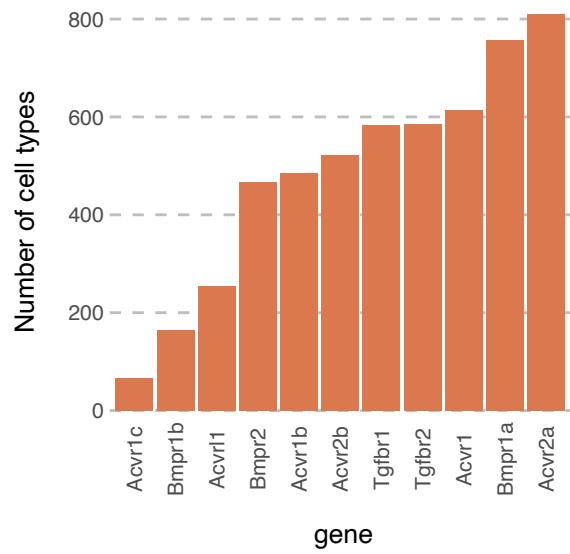
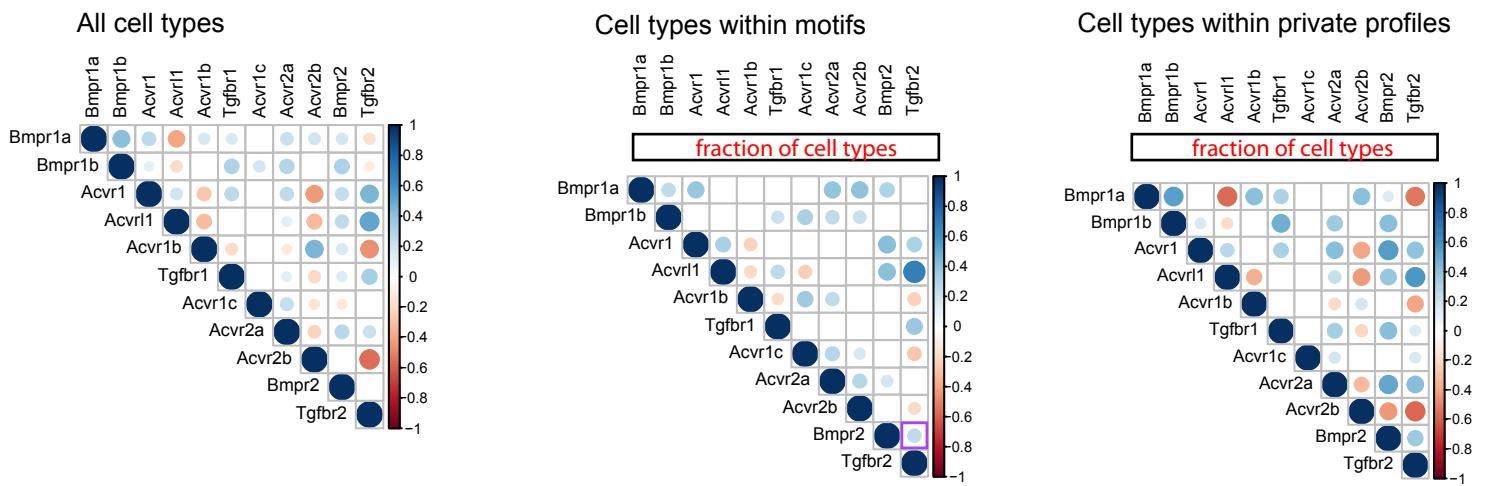


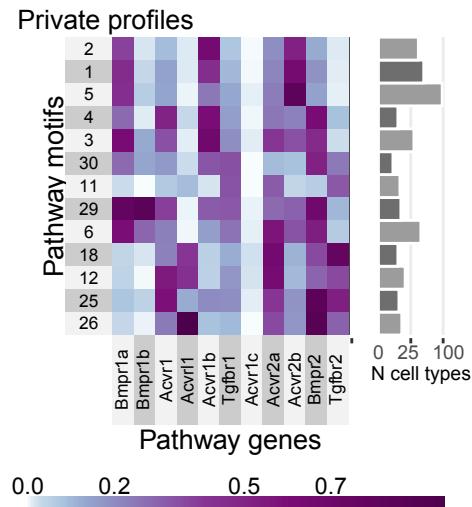
Figure 4 Supplement

How are we going to number this figure?

Pairwise correlations

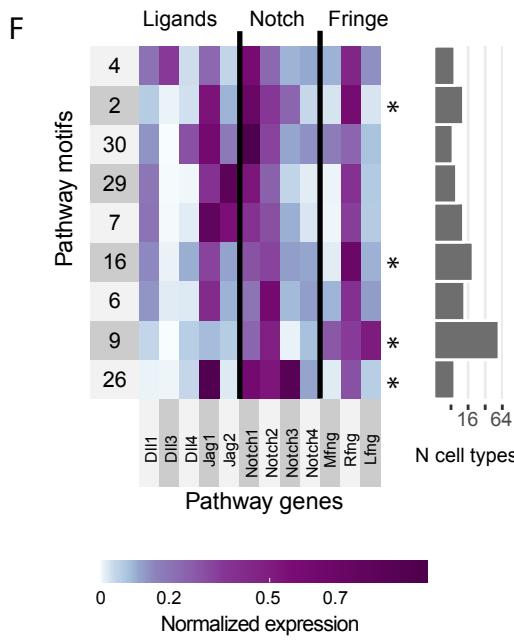


Need to add the Wnt and Notch correlation plots

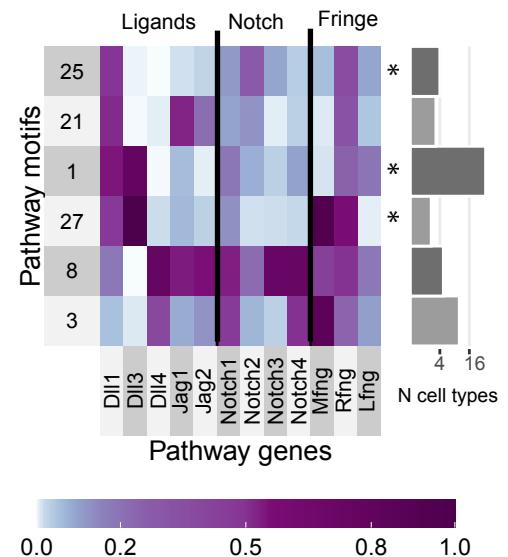


Which supp figure do these motif and private profile heatmaps belong to?

Notch motif profiles

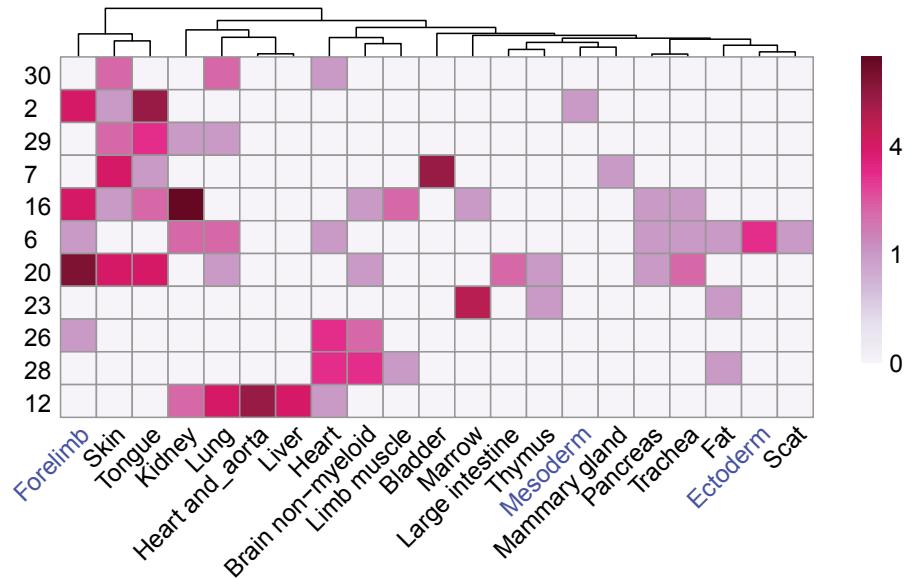
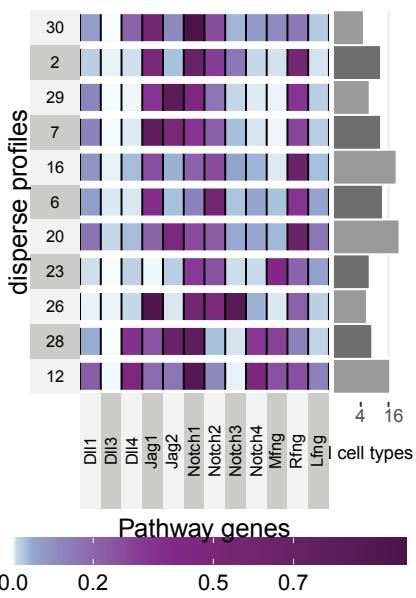


Notch private profiles

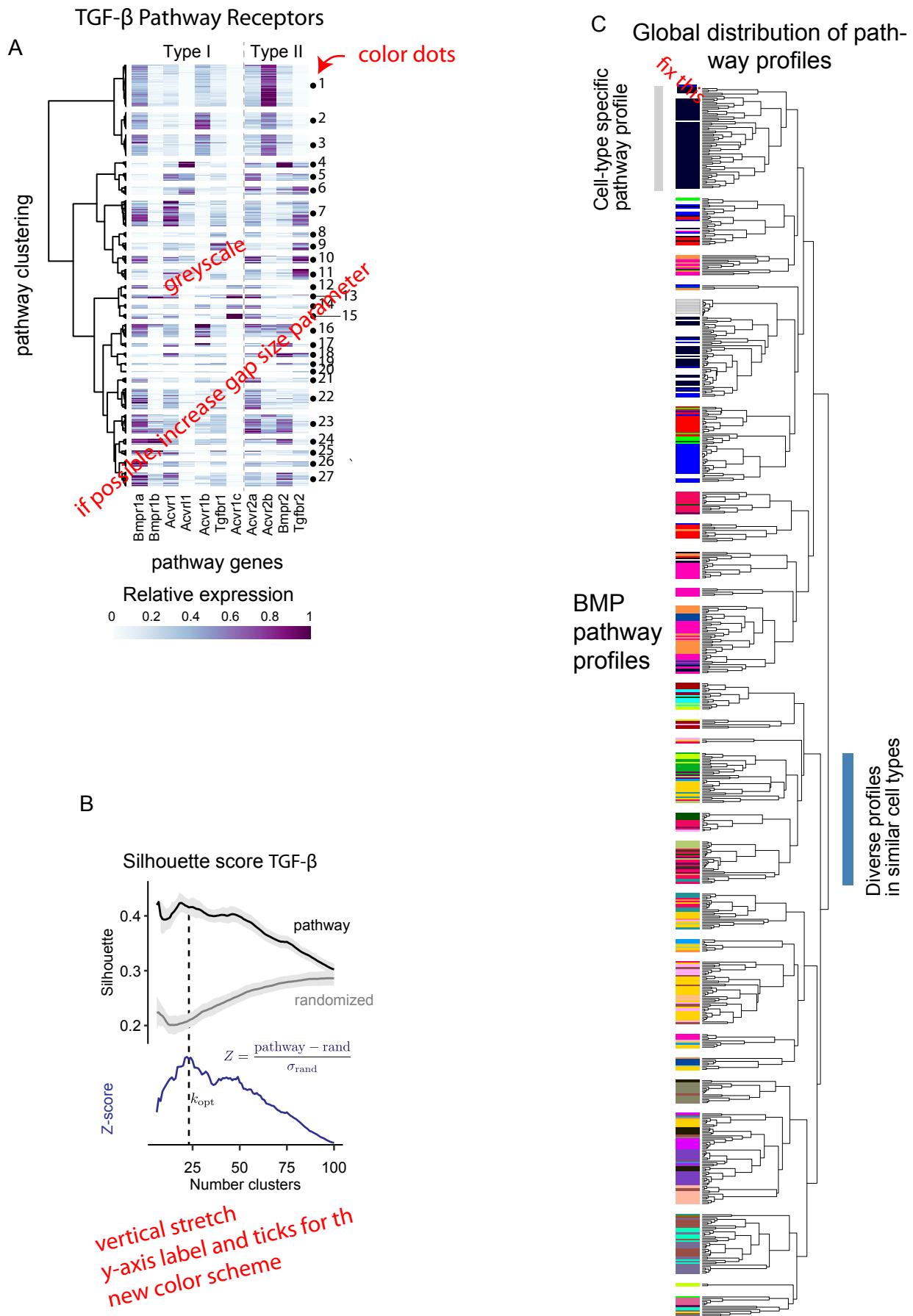


50% of cell types within motif or private

Is this a part of Fig. 5?



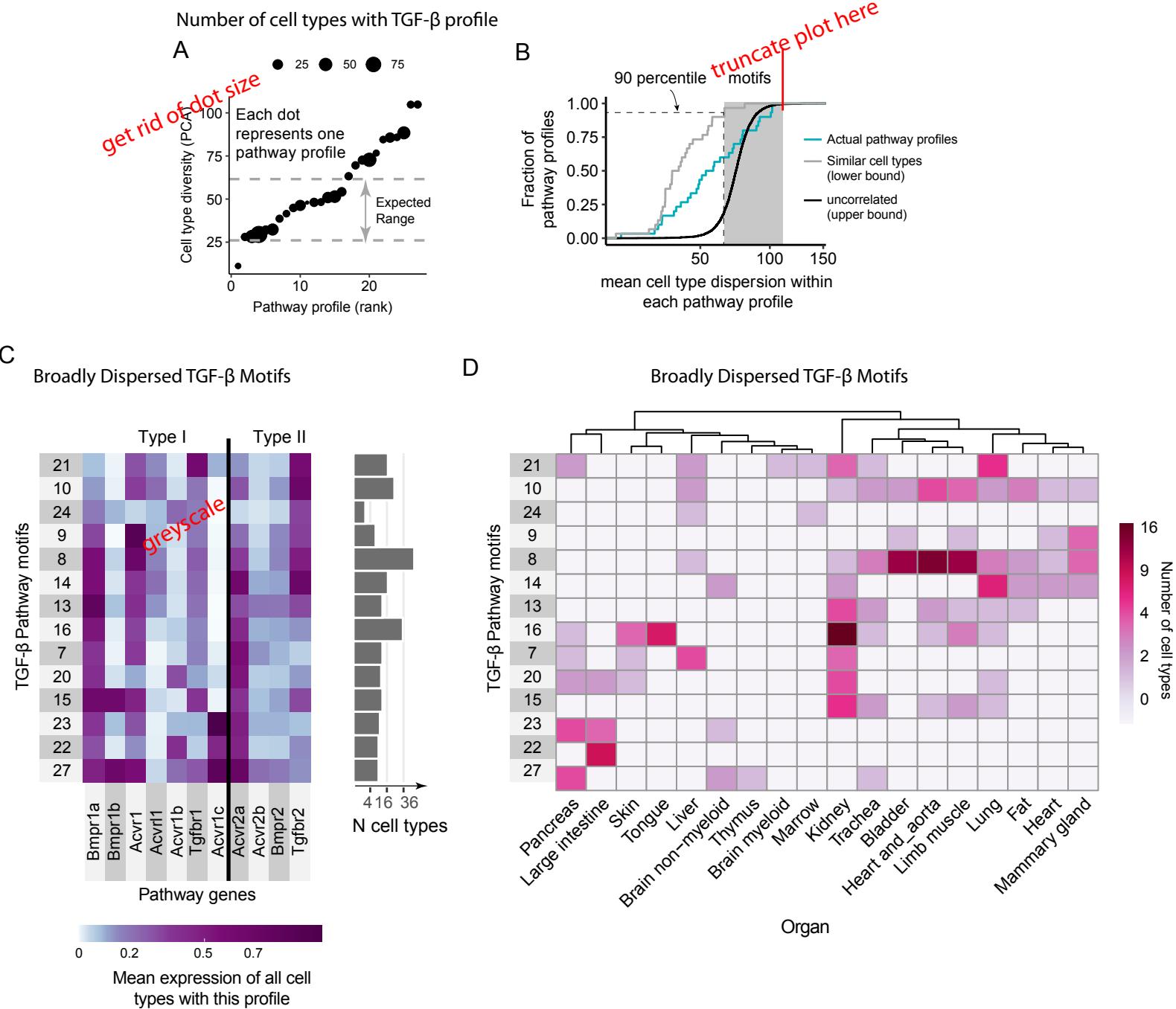
Alternate Figure 3



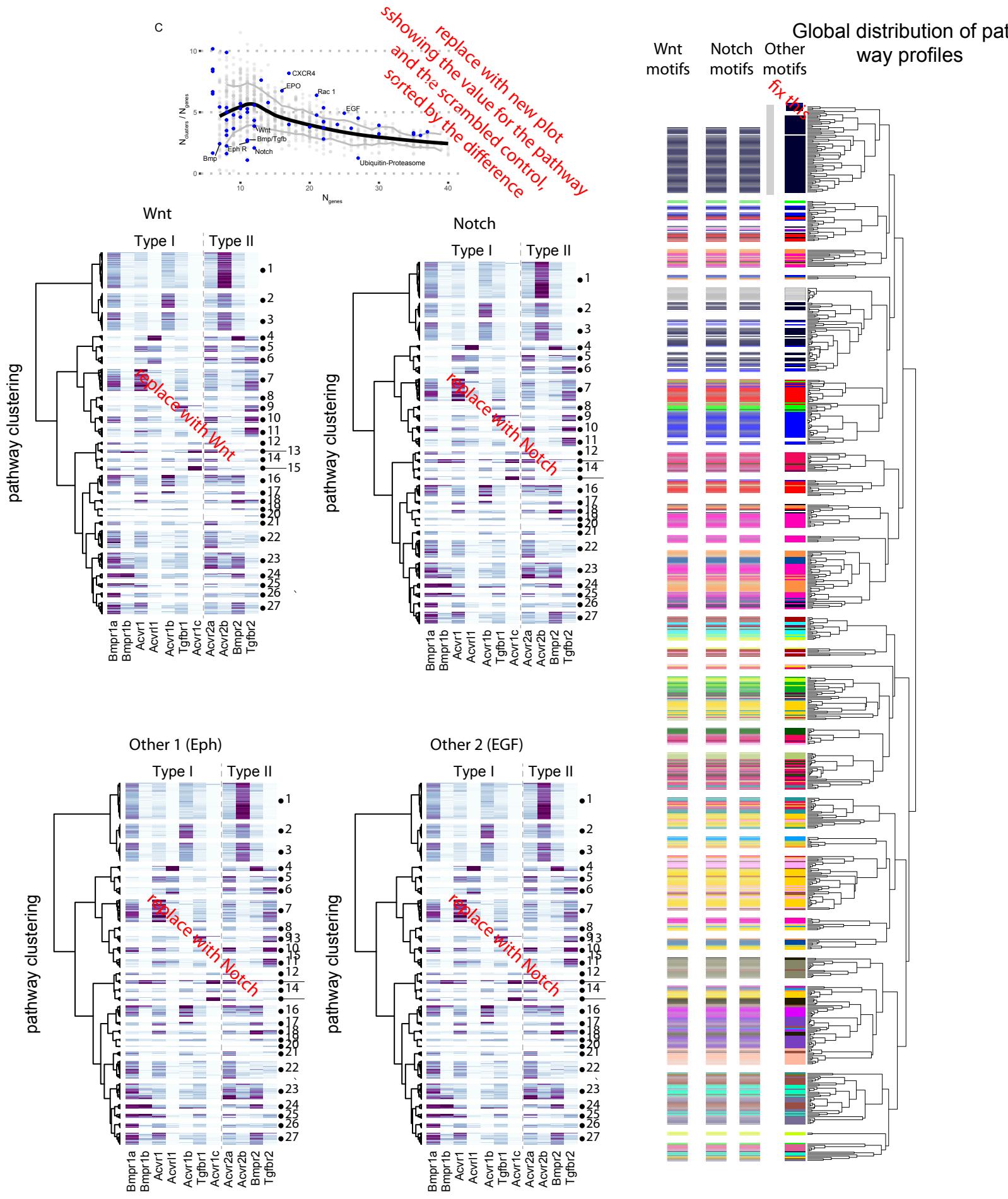
transcriptome similarity

vertical stretch
y-axis label and ticks for th
new color scheme

Alternate Figure 4: Some TGF- β motifs are expressed across diverse tissues and organs



Alternate Figure 5: Wnt and Notch also show broadly dispersed recurrent pathway expression motifs



Pathway-pathay correlations

