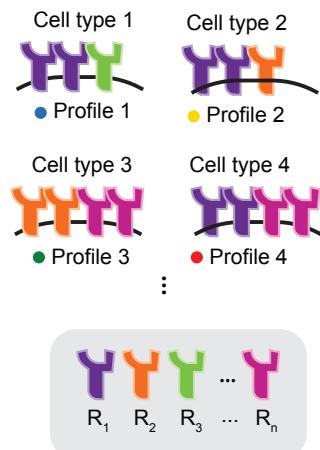


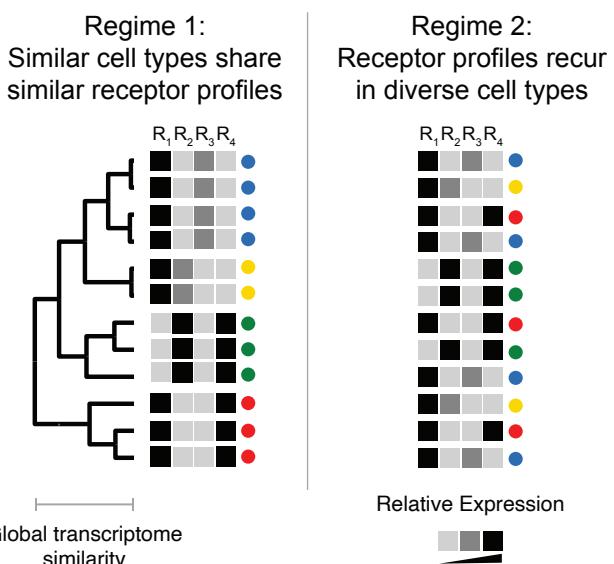
Figure 1: Pathway expression profiles could recur across diverse cell types

A

Receptor expression profiles

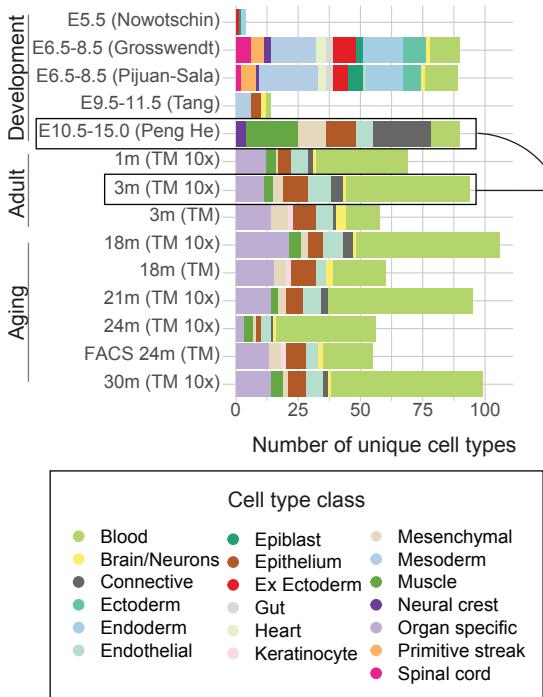


B



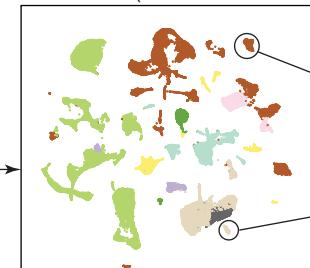
C

Multiple mouse cell atlas datasets

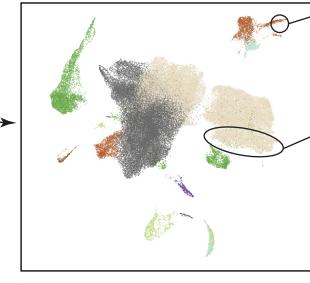


D Individual cell atlases
Single-cell transcriptome profiles
1 dot = 1 cell

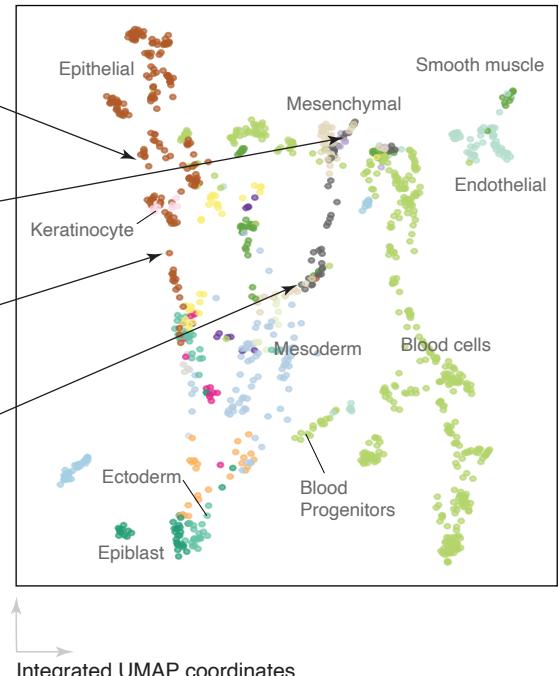
Tabula muris (3 month old mouse)



Forelimb (Days E10.5 - E15.0)



Integrated cell state atlas
Global cluster-averaged profiles
All data sets in (C)
1 dot = 1 cell cluster



E

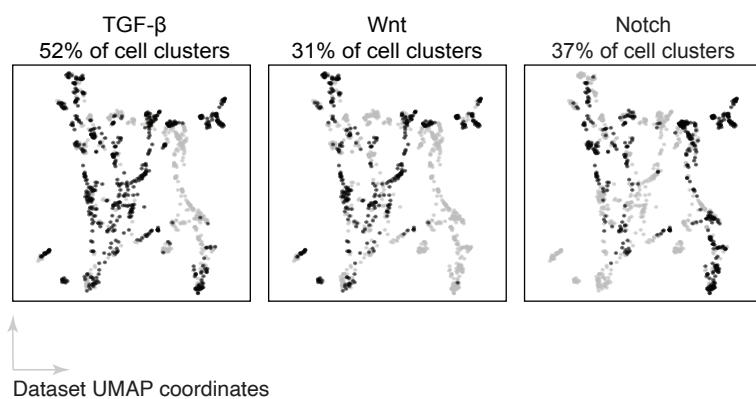
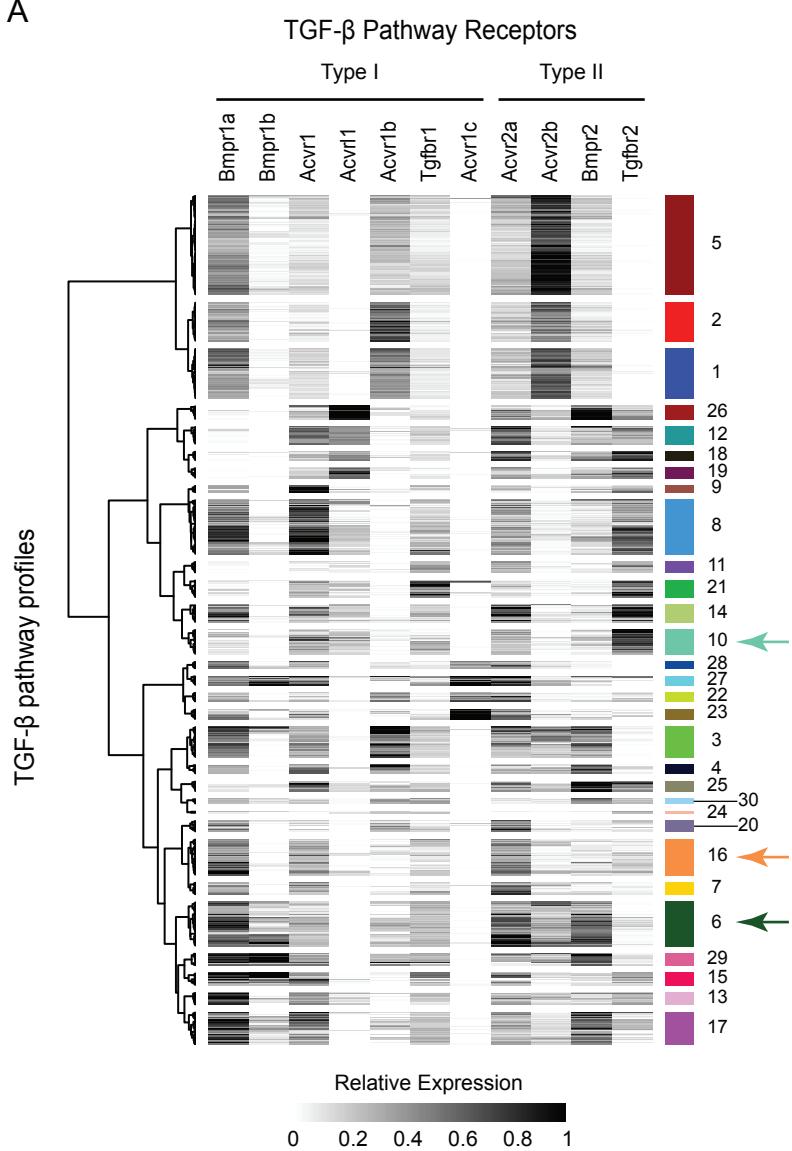
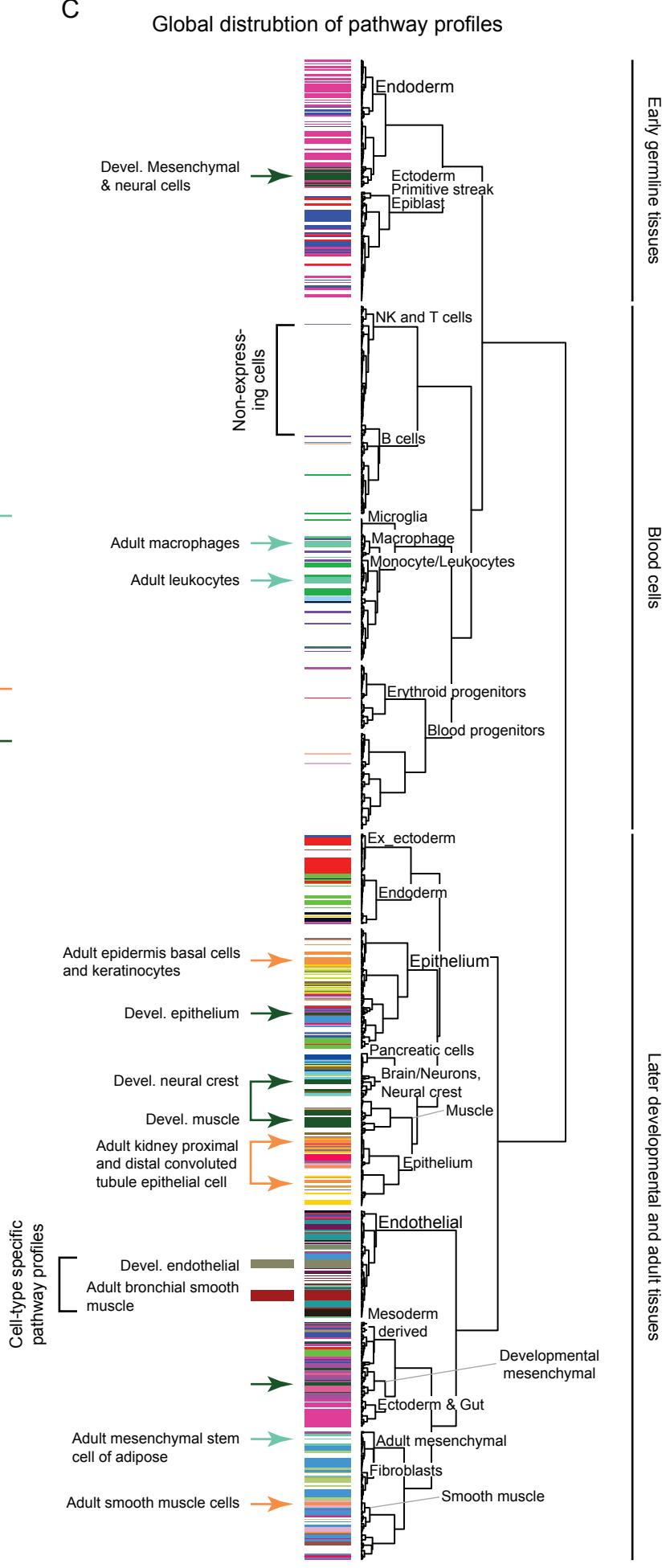


Figure 2: TGF- β Receptors exhibit distinct and recurrent pathway expression profiles

A



C



B

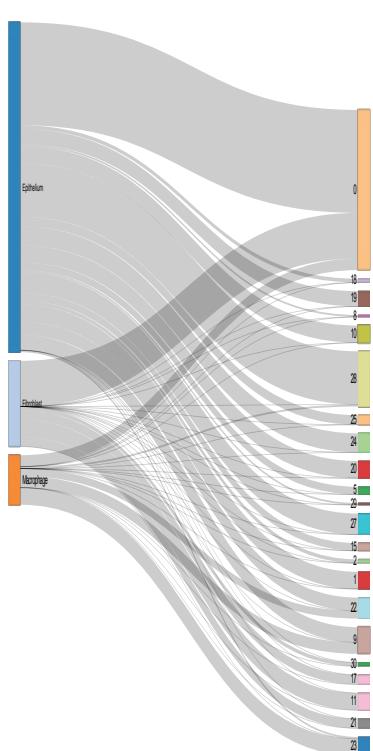
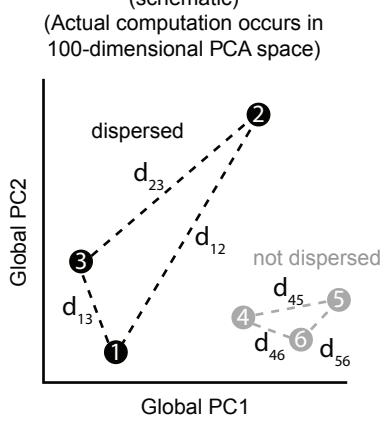
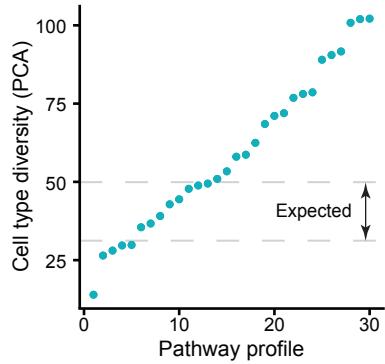


Figure 3: TGF- β expression motifs are dispersed across cell types and organs

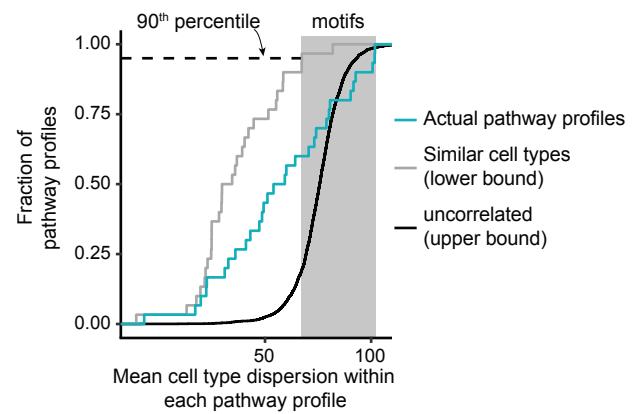
A Pairwise distance computation (schematic)
(Actual computation occurs in 100-dimensional PCA space)



Number of cell types with TGF- β profile

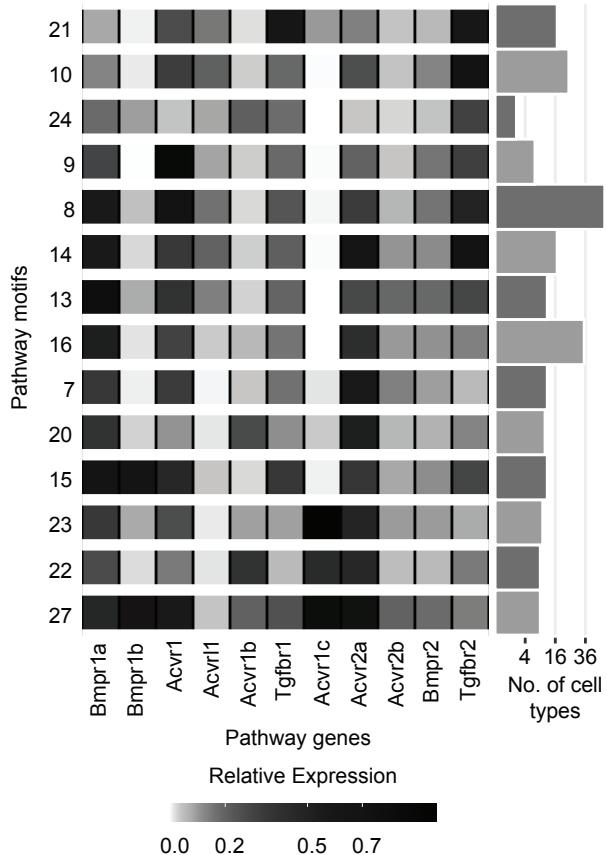


B



D

Broadly Dispersed TGF- β Motifs



E

Broadly Dispersed TGF- β Motifs

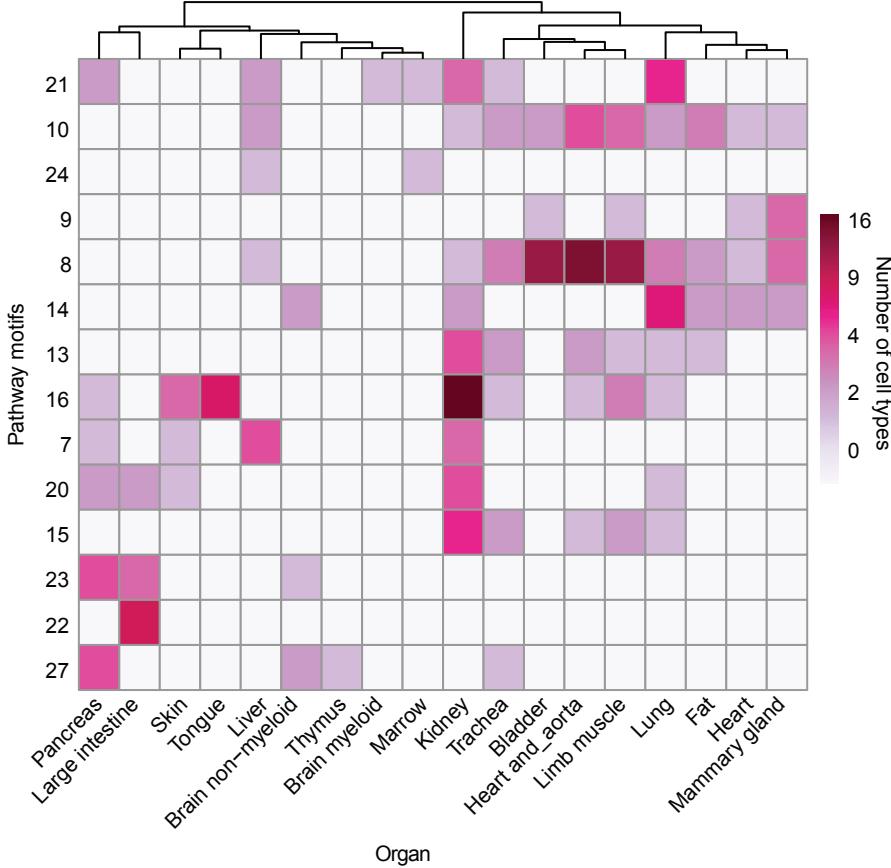
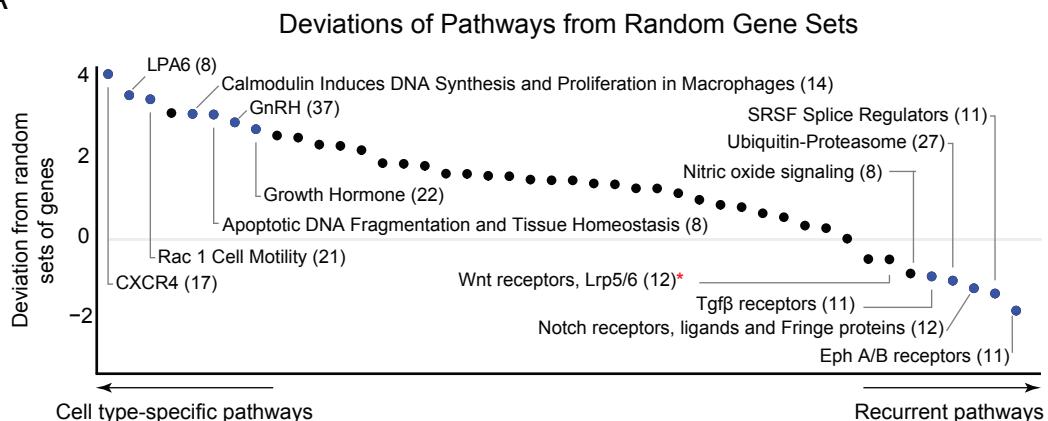
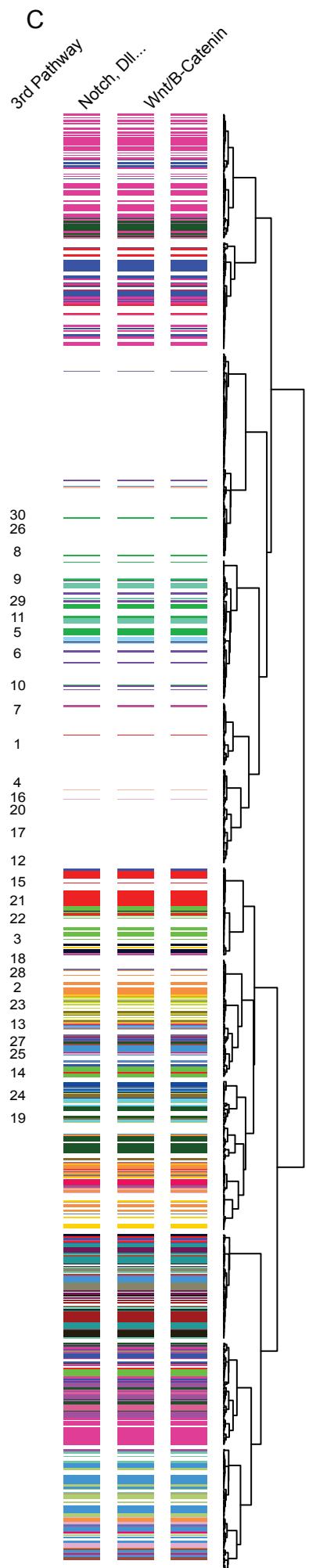
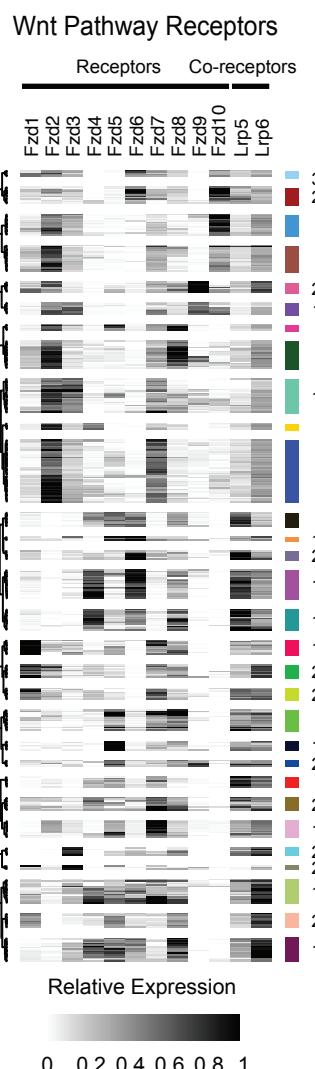
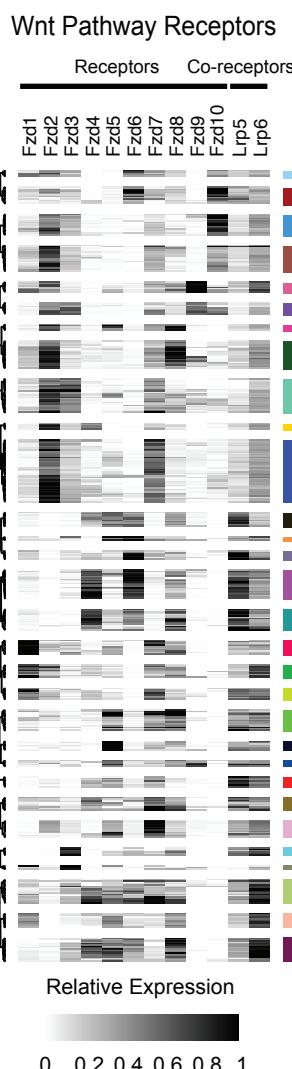
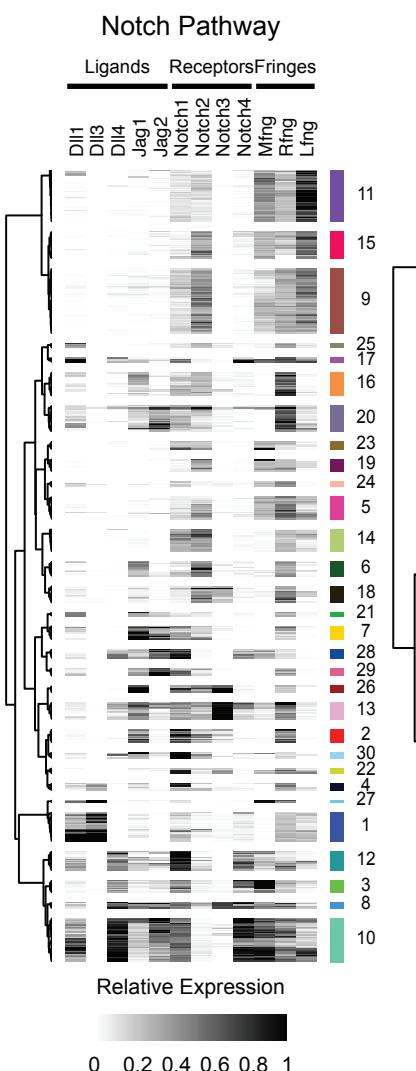


Figure 4: Wnt and Notch also show broadly dispersed recurrent pathway expression motifs

A



B



D

Mutual information between recurrent pathways

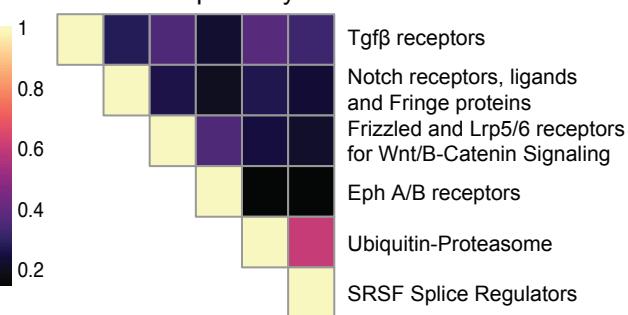
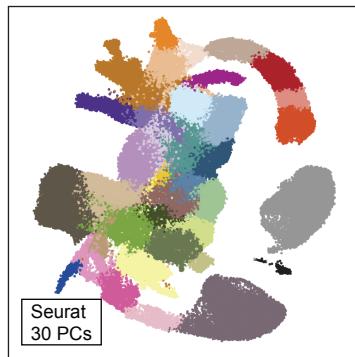


Figure 1, Supplement 1

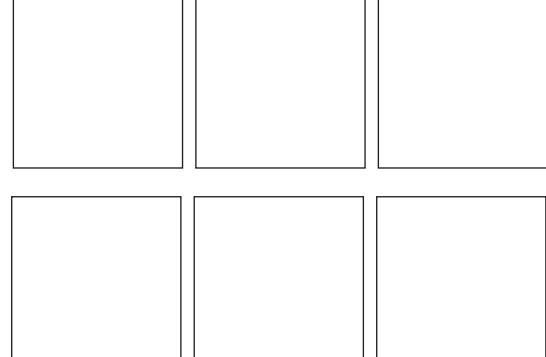
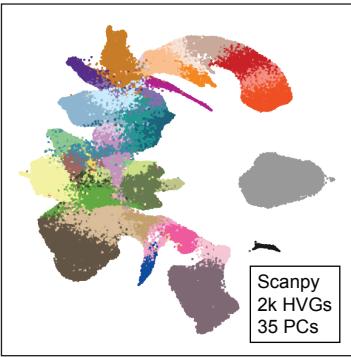
A

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

Blanca Pijuan-Sala (2019)



This work



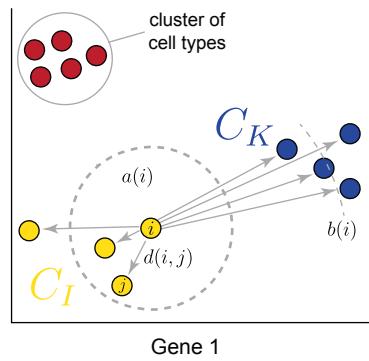
Cell type annotation

● Allantois	● Caudal epiblast	● Erythroid2	● Gut	● Nascent mesoderm	● Pharyngeal mesoderm
● Anterior Primitive Streak	● Caudal neurectoderm	● Erythroid3	● Haematoendothelial progenitors	● Neural crest	● Primitive Streak
● Blood progenitors 1	● Def. endoderm	● ExE ectoderm	● Intermediate mesoderm	● Notochord	● Rostral neurectoderm
● Blood progenitors 2	● Endothelium	● ExE endoderm	● Mesenchyme	● PGC	● Somitic mesoderm
● Cardiomyocytes	● Epiblast	● ExE mesoderm	● Mixed mesoderm	● Paraxial mesoderm	● Spinal cord
● Caudal Mesoderm	● Erythroid1	● Forebrain/Midbrain/Hindbrain	● NMP	● Parietal endoderm	● Surface ectoderm
					● Visceral endoderm

Figure 2, Supplement 1

D

Silhouette score quantifies clustering quality



$$\text{In-class mean distance: } a(i) = \frac{1}{|C_I| - 1} \sum_{j \in C_I, j \neq i} d(i, j)$$

$$\text{Neighboring class mean distance: } b(i) = \min_{K \neq I} \frac{1}{|C_K|} \sum_{k \in C_K} d(i, k)$$

$$\text{Silhouette score: } s(i) = \frac{b(i) - a(i)}{\max\{a(i) - b(i)\}}$$

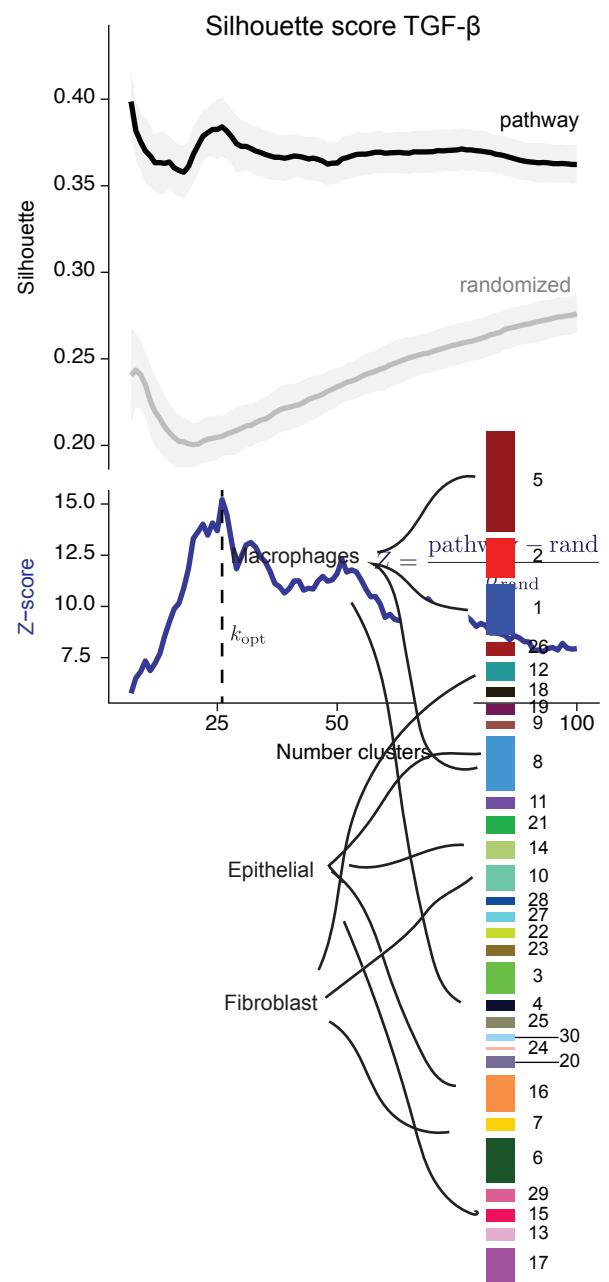
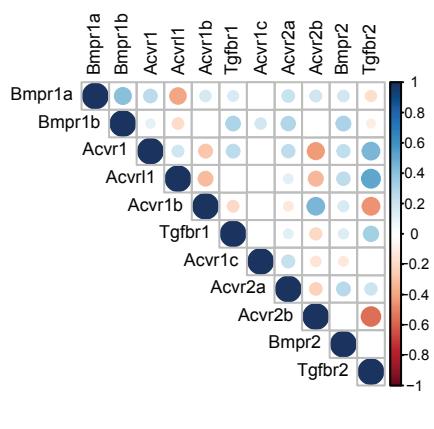


Figure 3 Supplement

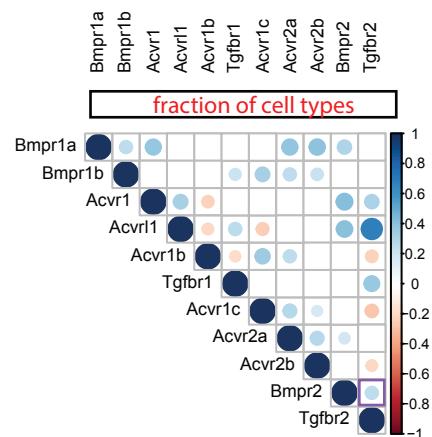
How are we going to number this figure?

Pairwise correlations

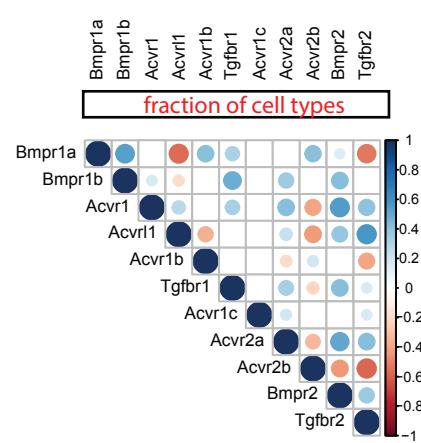
All cell types



Cell types within motifs



Cell types within private profiles



Need to add the Wnt and Notch correlation plots

TGF beta ligand-receptor mutual info

Private profiles

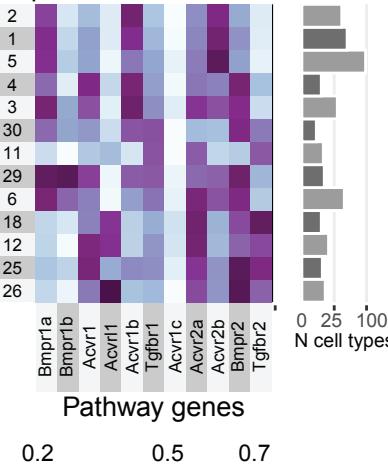
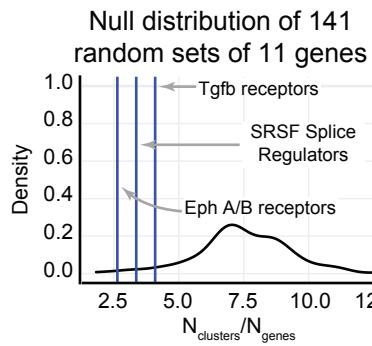


Figure 4 Supplement

B



A

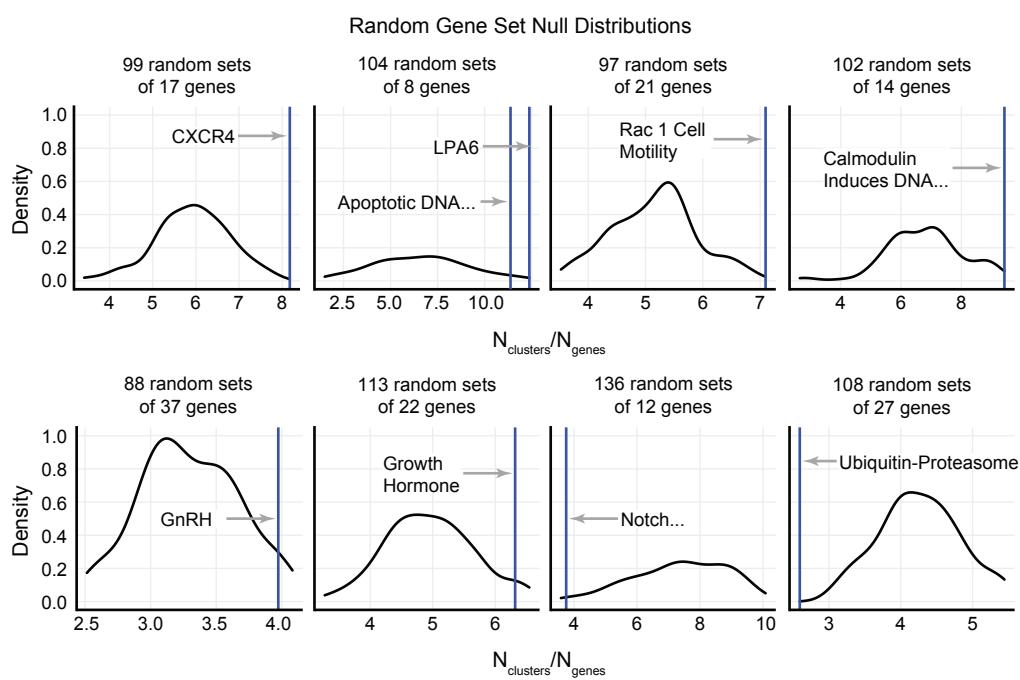
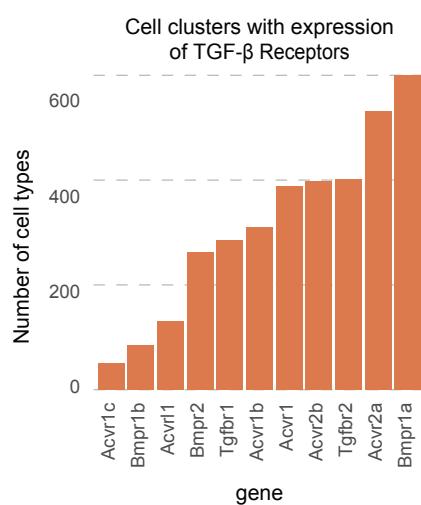
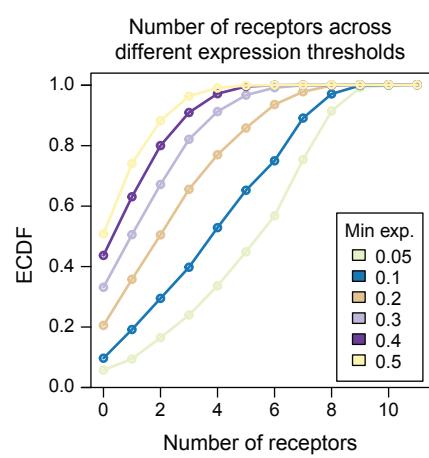


Figure 2, Supplement

A



B



C

