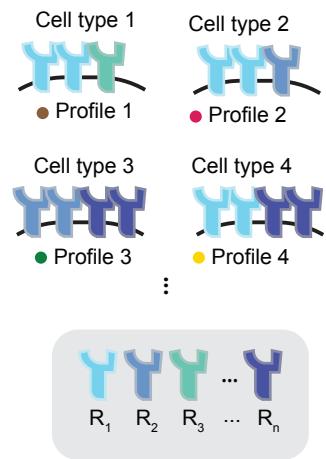


Figure 1: Pathway expression profiles could be distributed across cell types in different ways.

A

Receptor expression profiles



B

Pathway profiles could be...

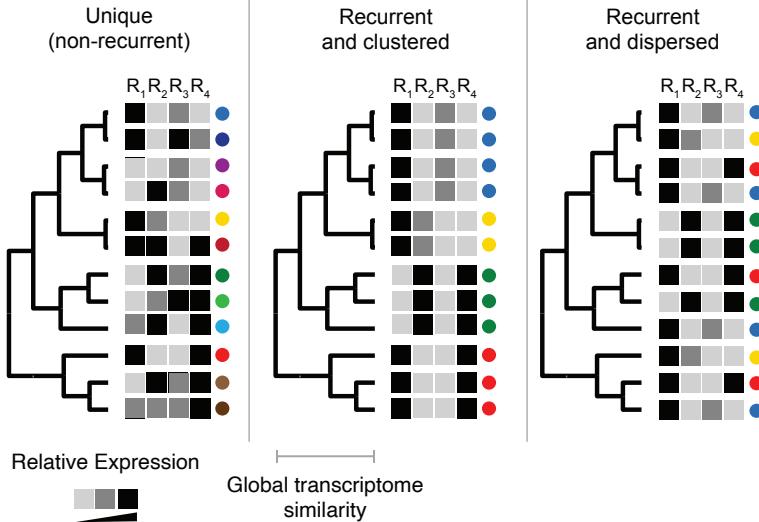
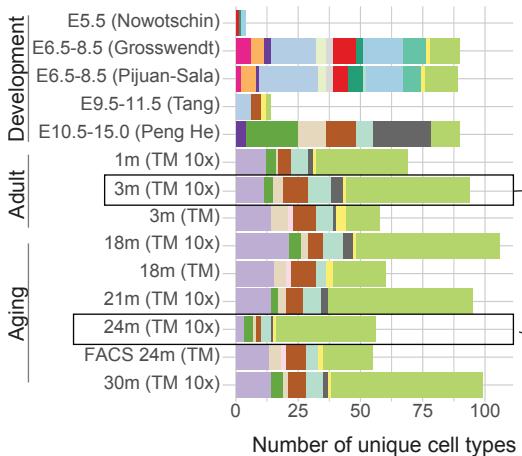


Figure 2: Integration of scRNA-seq atlas data reveals widespread expression of signaling pathway components.

A

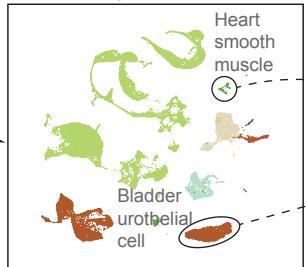
Multiple mouse cell atlas datasets



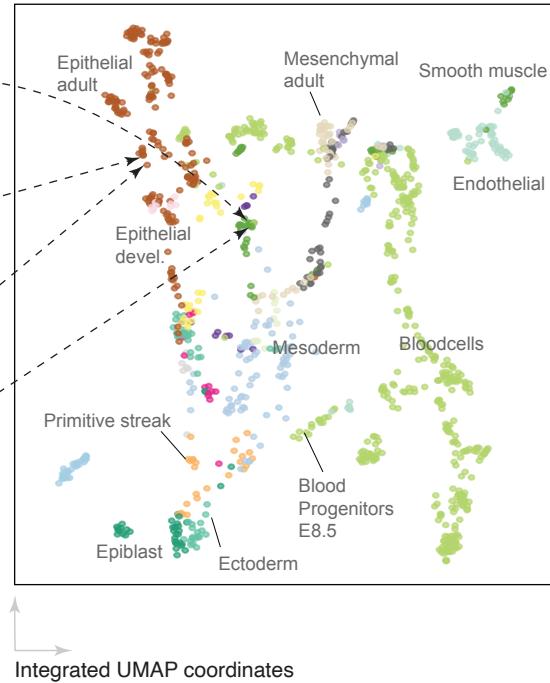
B

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

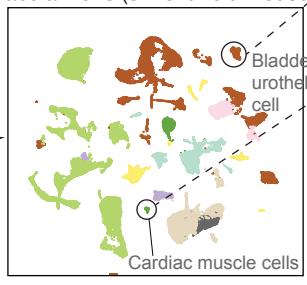
Tabula senis (24 month old mouse)



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



Tabula muris (3 month old mouse)

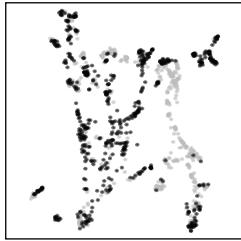


Dataset UMAP coordinates

Integrated UMAP coordinates

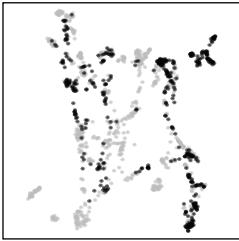
C

TGF- β
52% of cell states



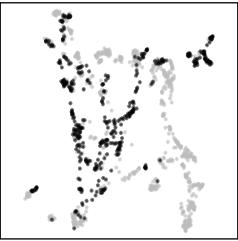
Min. # of genes exp: 2
Threshold for exp.: 0.2

Notch
37% of cell states



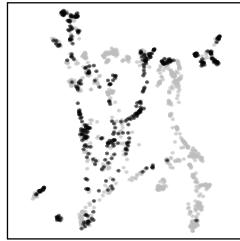
Min. # of genes exp: 2
Threshold for exp.: 0.2

Eph-ephrin
36% of cell states



Min. # of genes exp: 2
Threshold for exp.: 0.3

Wnt
31% of cell states



Min. # of genes exp: 2
Threshold for exp.: 0.3

Dataset UMAP coordinates

Figure 3: TGF- β receptors exhibit recurrent and dispersed pathway expression profiles.

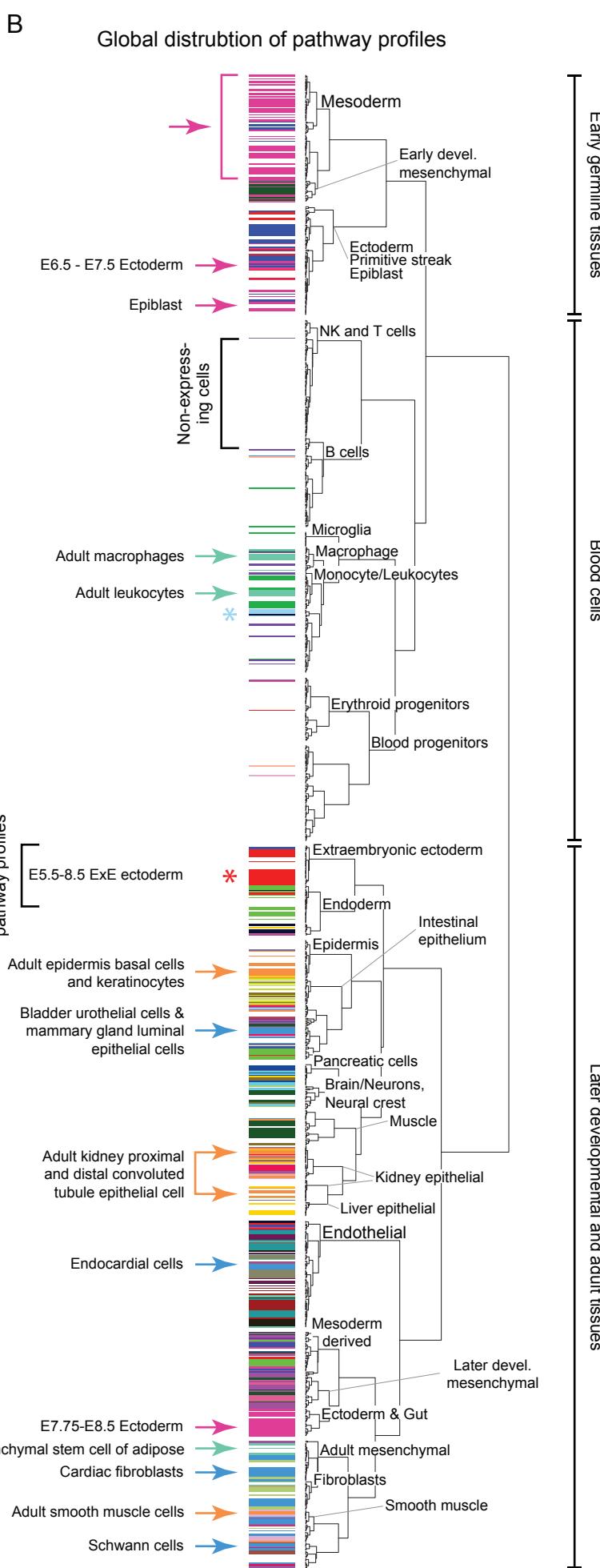
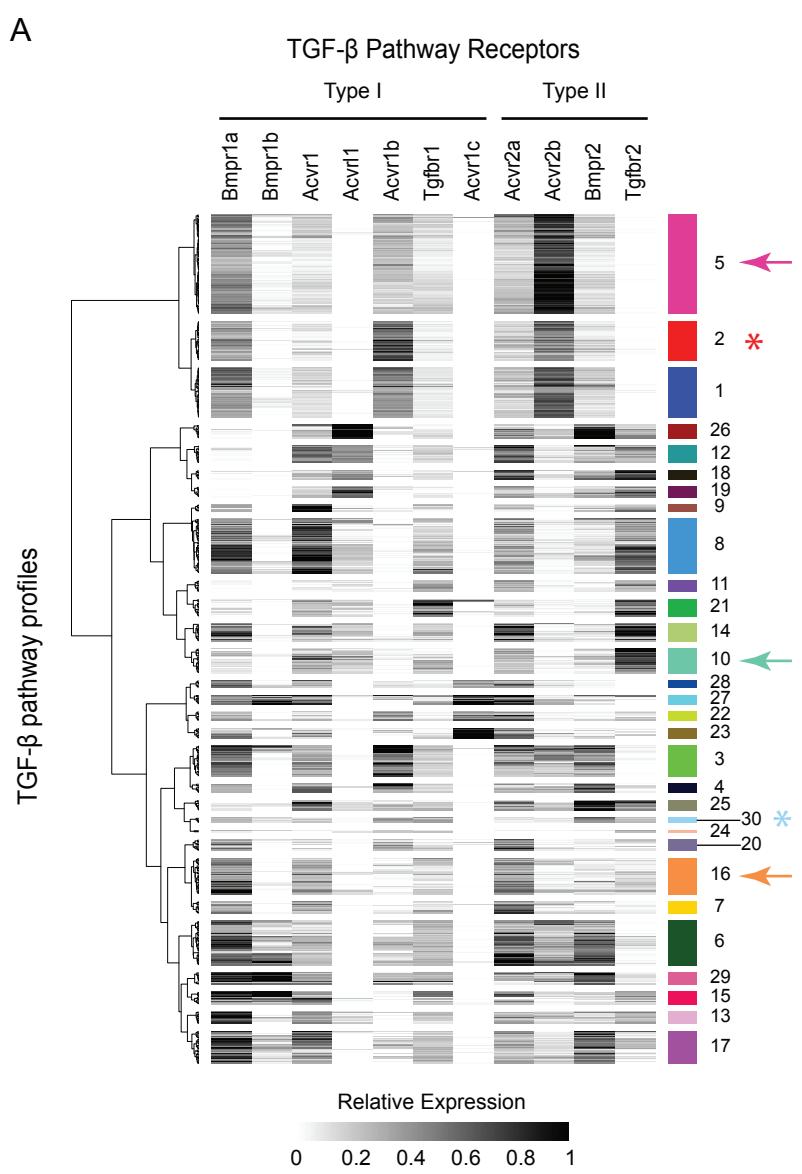


Figure 4: TGF- β expression motifs are dispersed across cell types and organs.

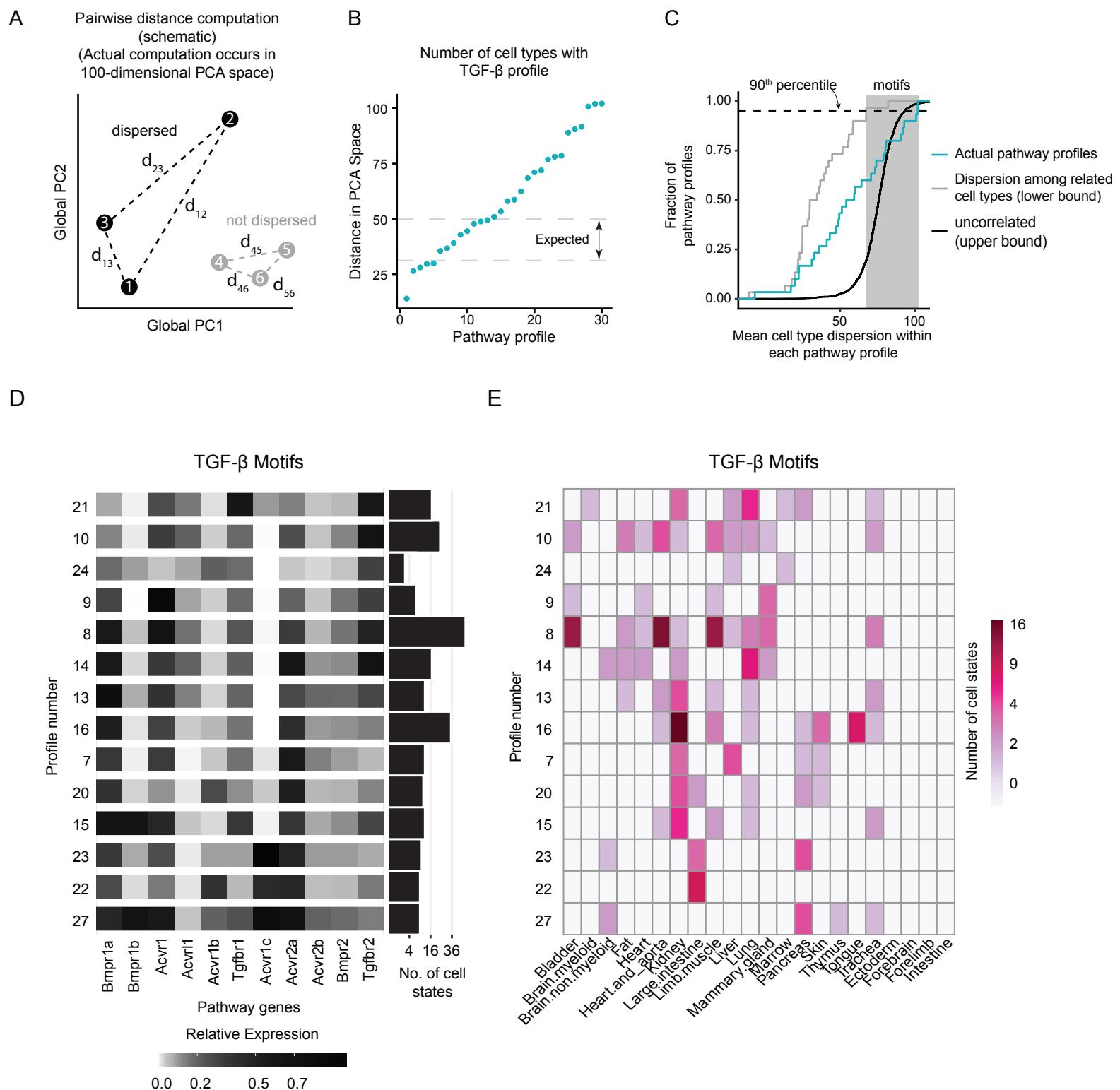


Figure 5: Expression motifs occur in multiple pathways.

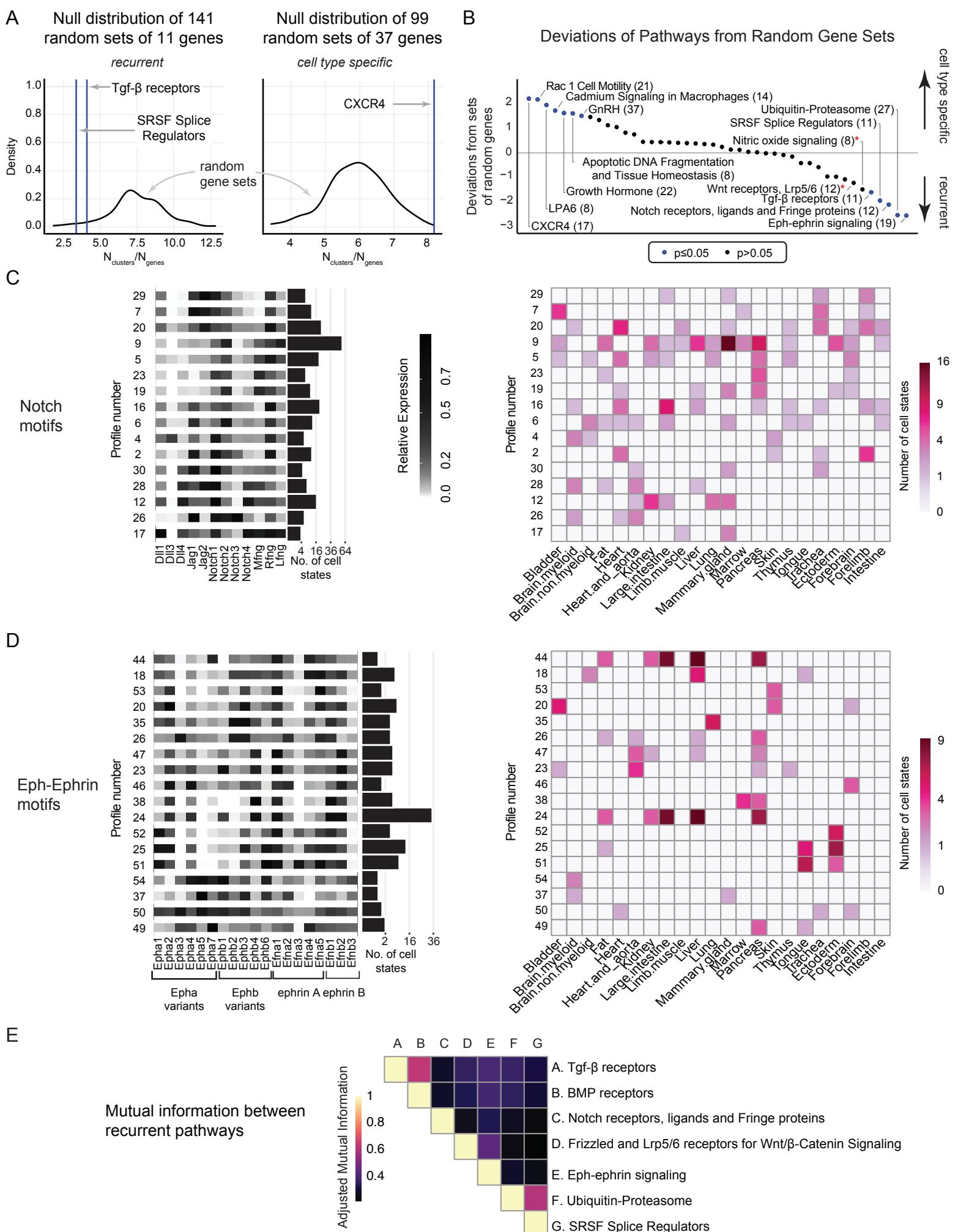


Figure 6:

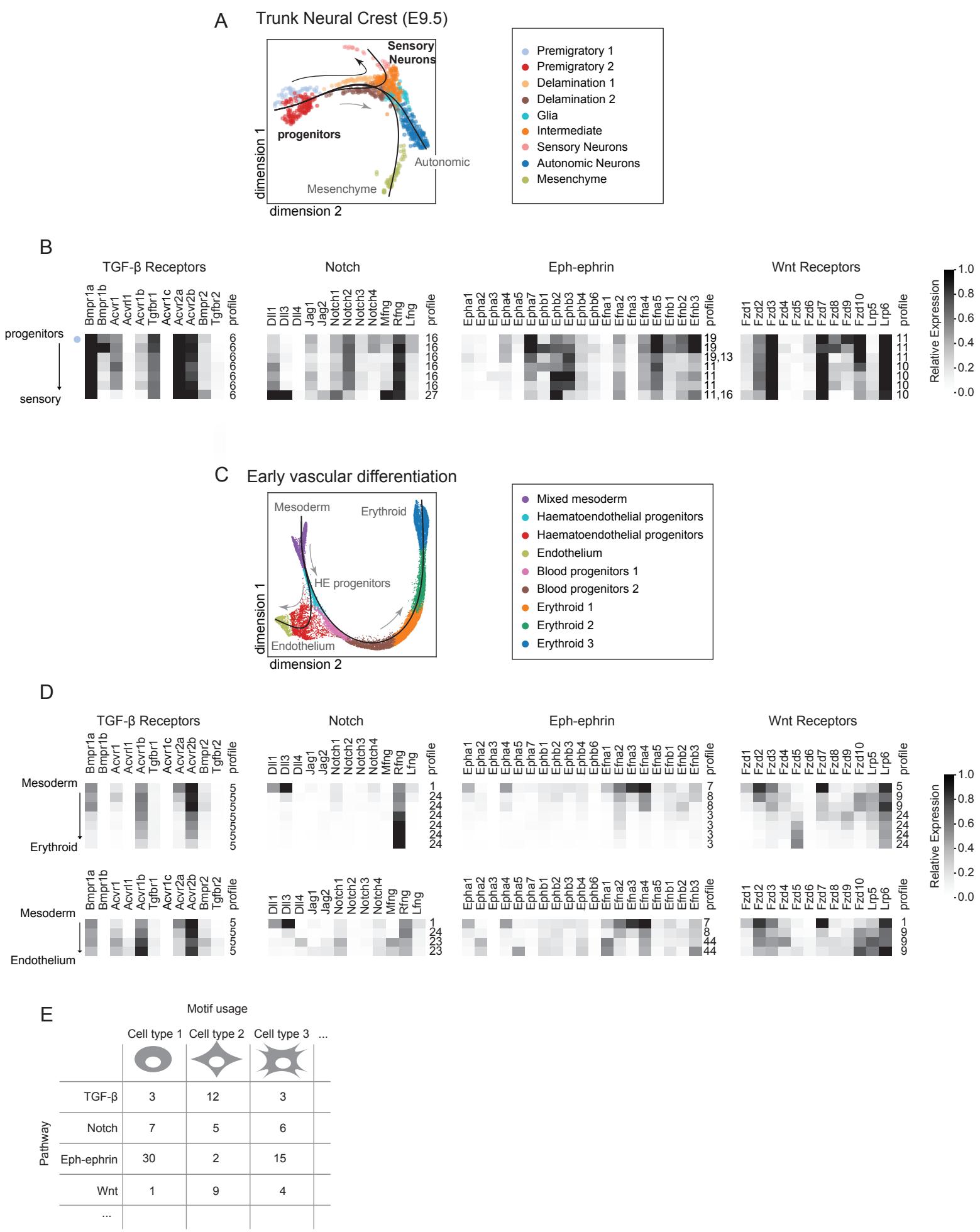
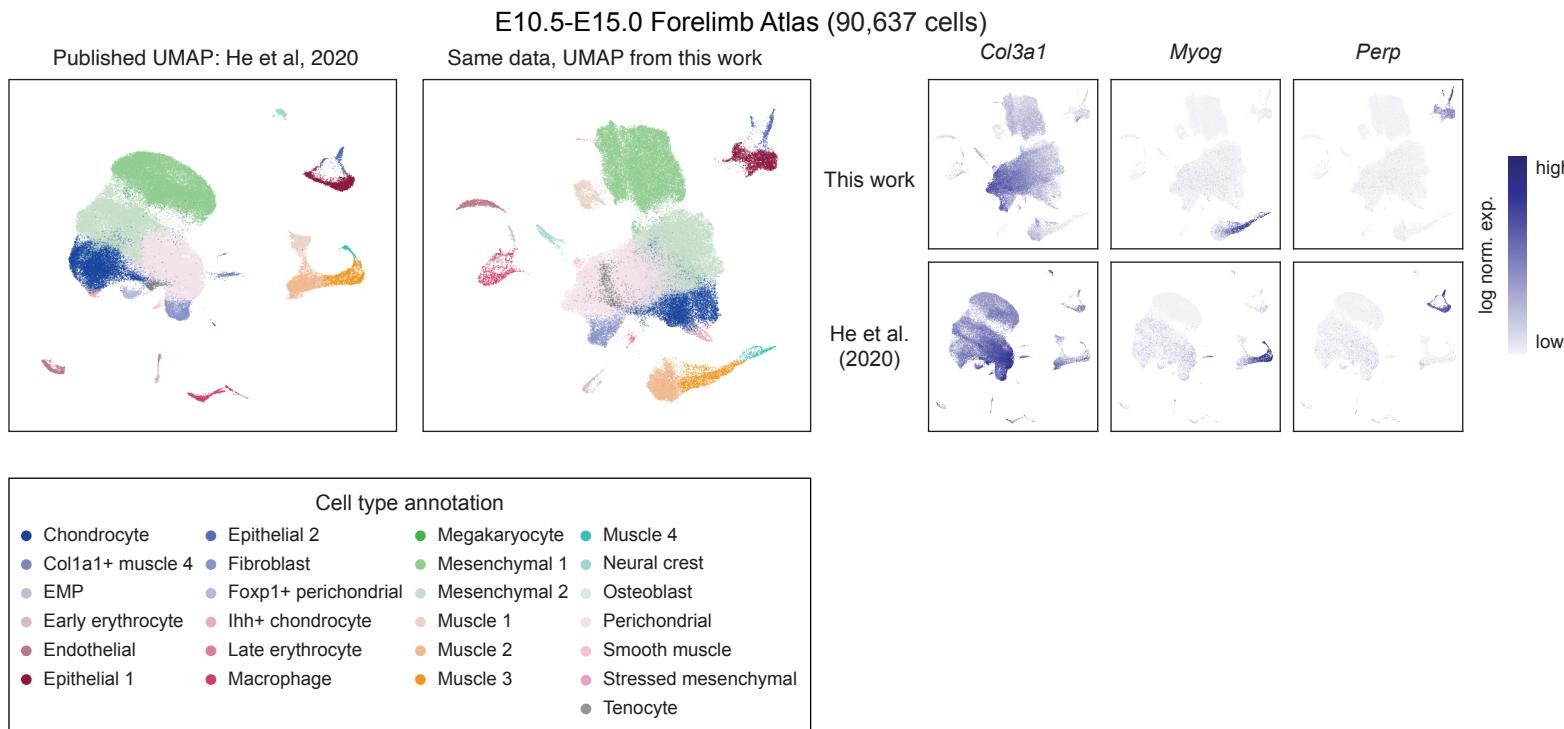
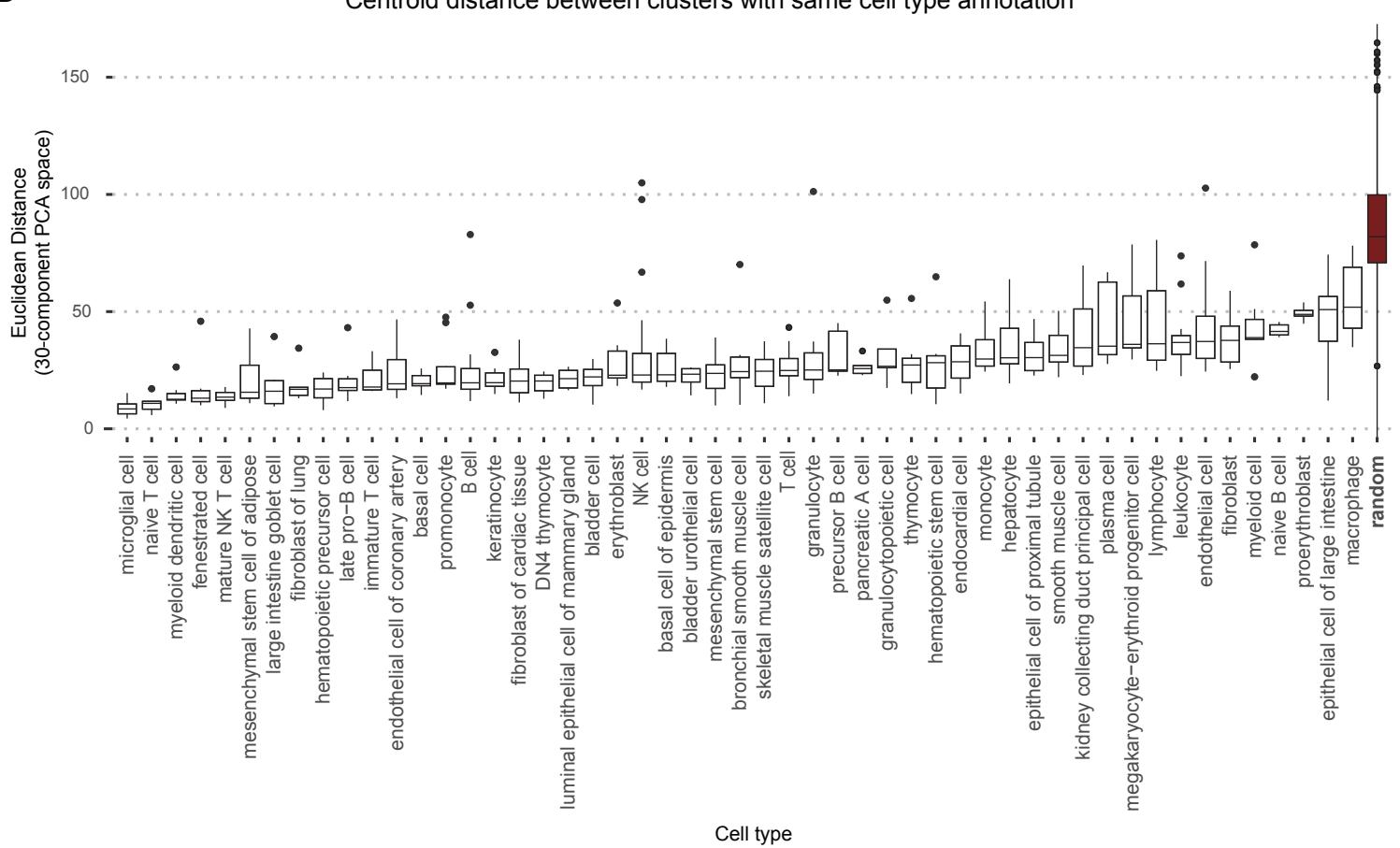


Figure 2—figure supplement 1

A



B



C

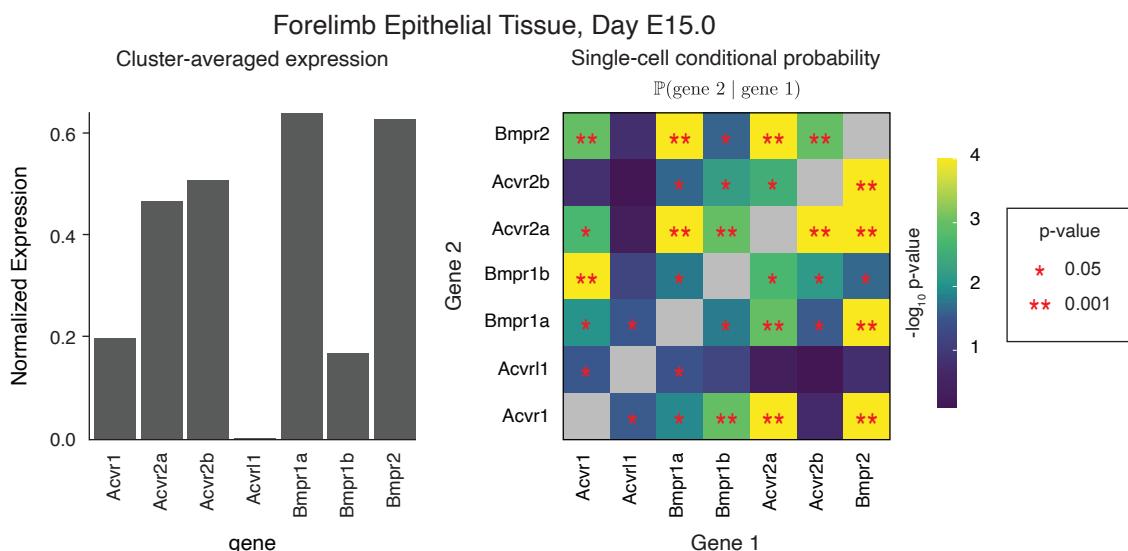
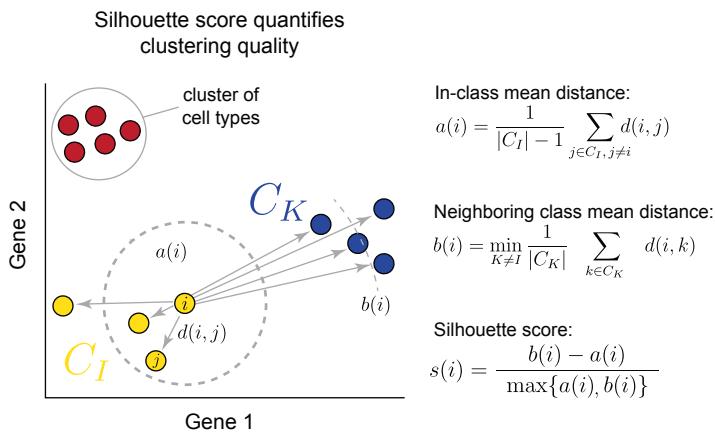


Figure 3—figure supplement 2

A



B

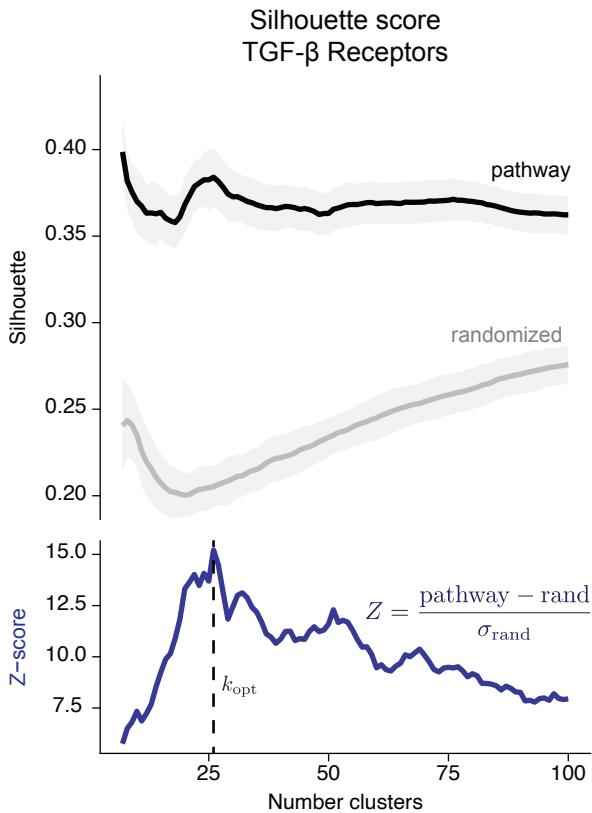
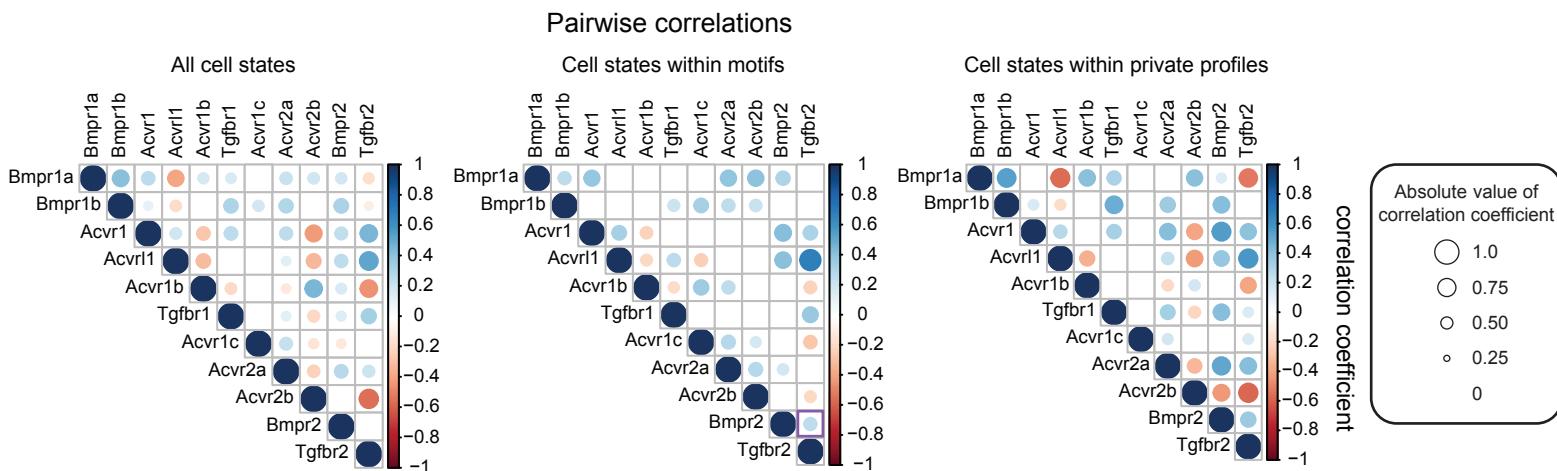


Figure 4—figure supplement 1

A



B

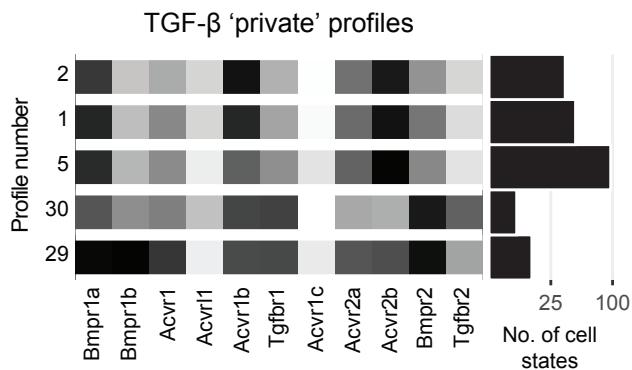
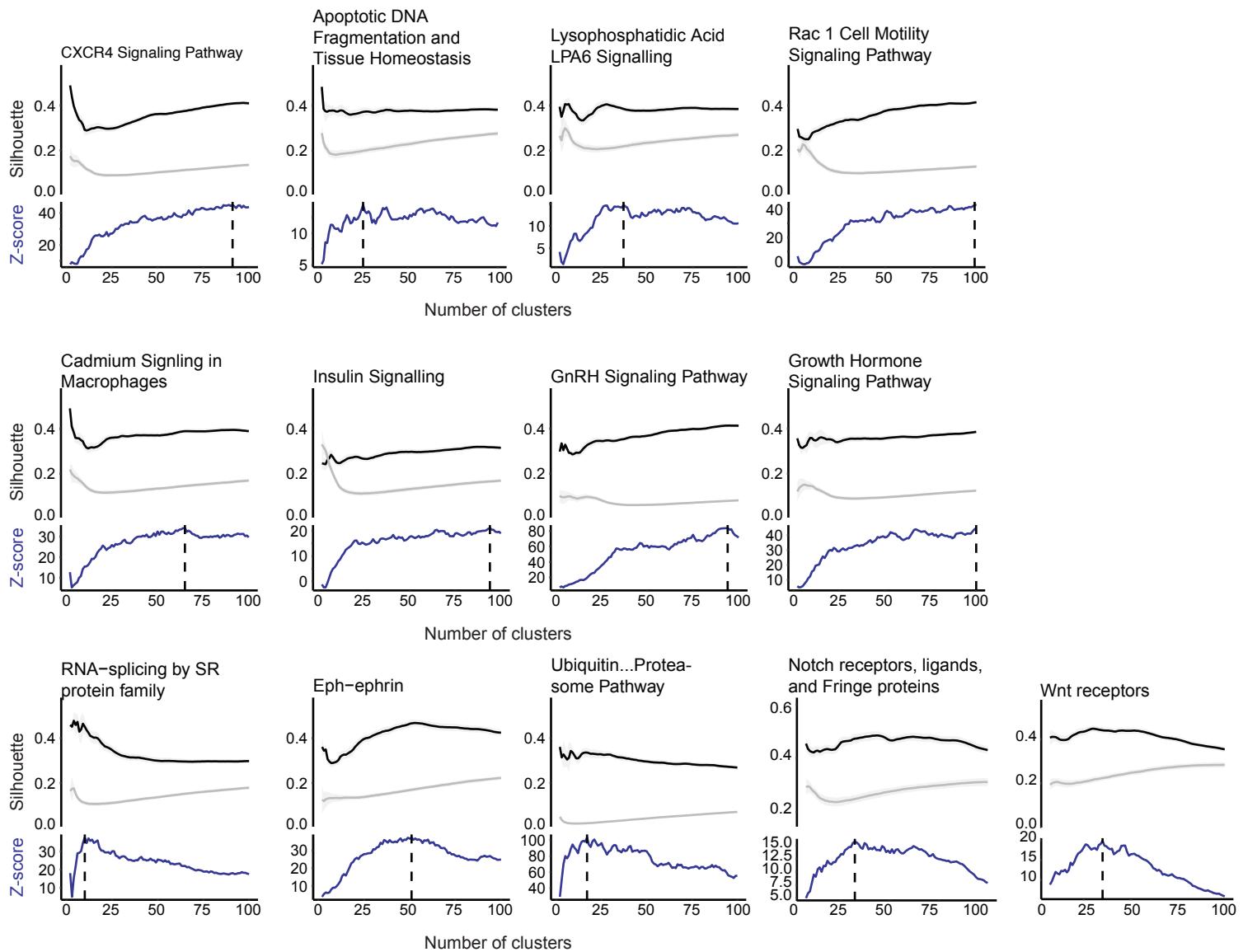


Figure 5—figure supplement 1

A



B

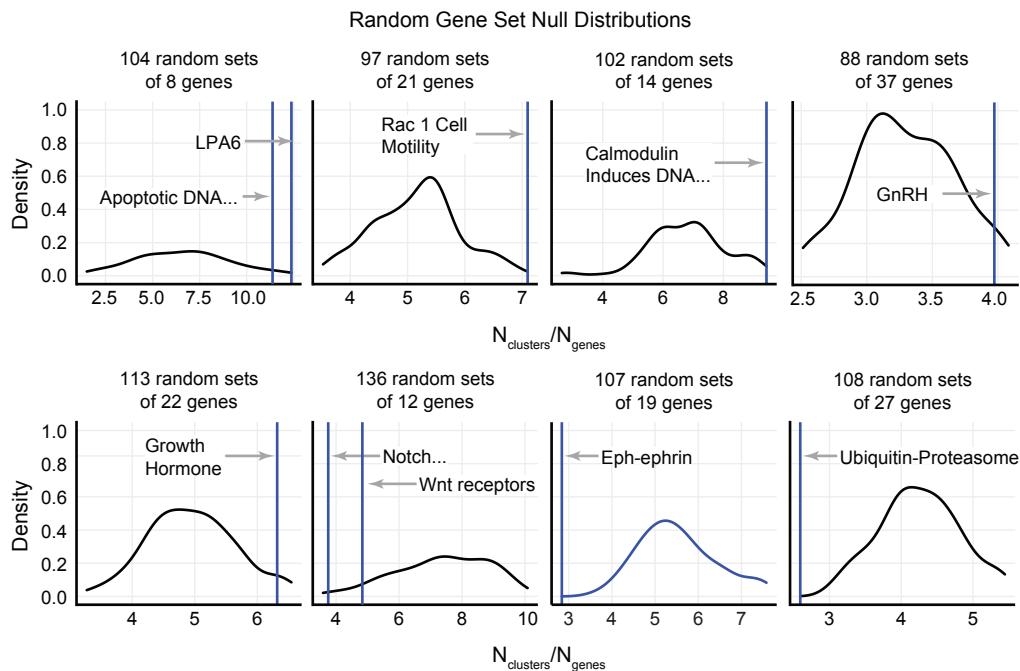


Figure 5—figure supplement 3

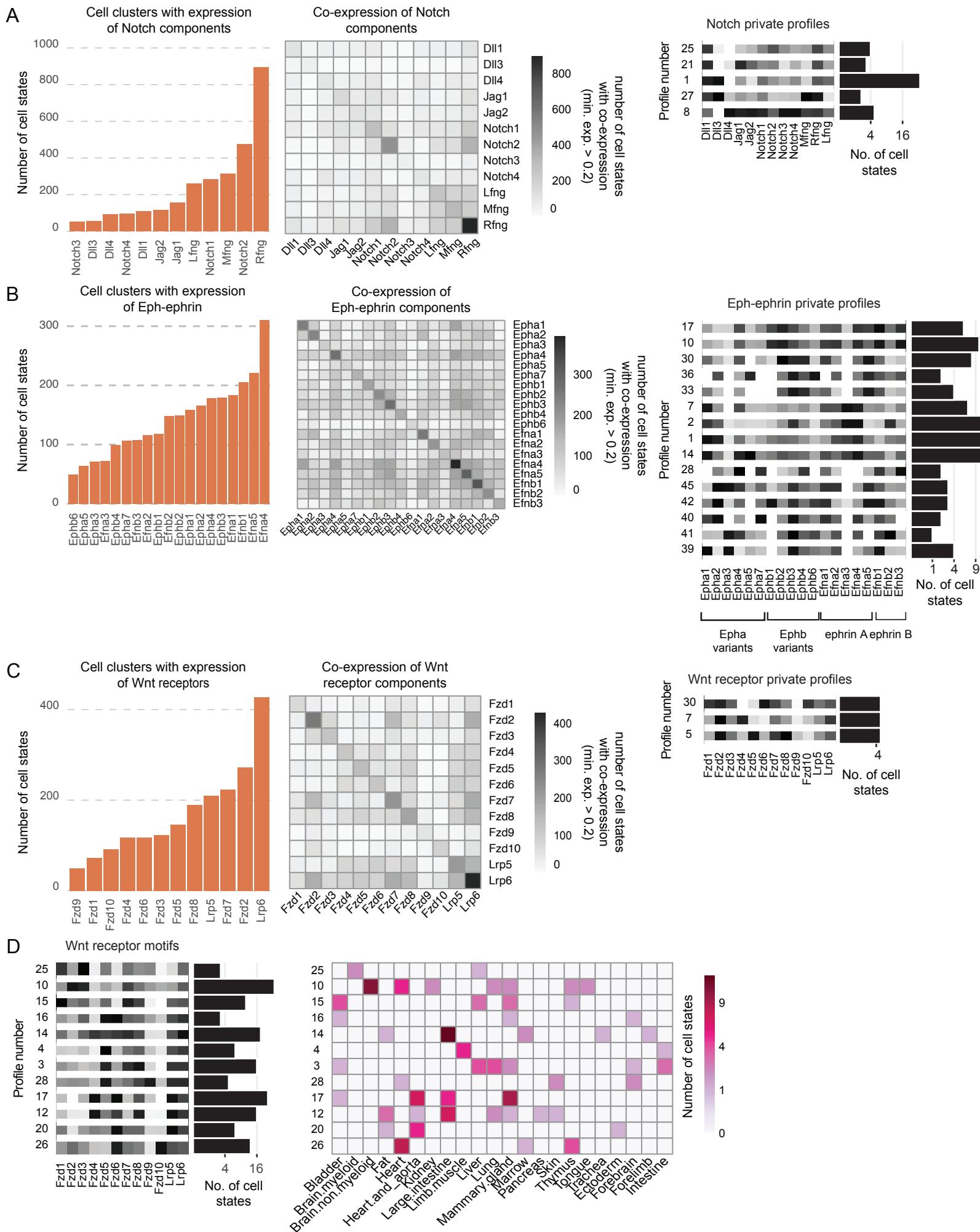


Figure 3–figure supplement 1

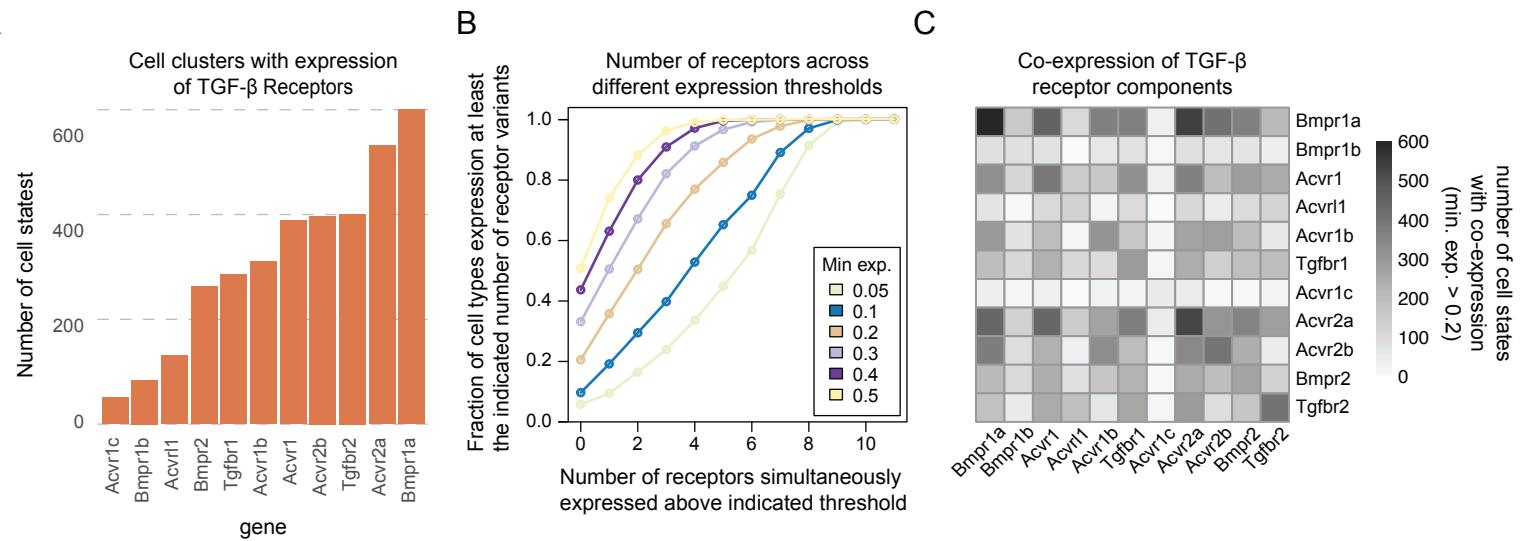
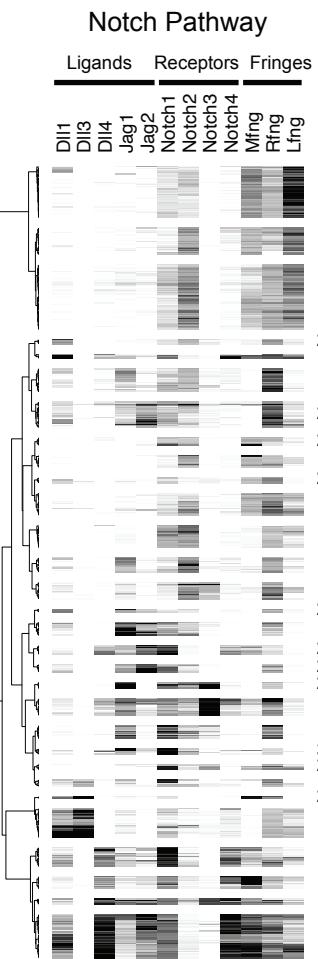
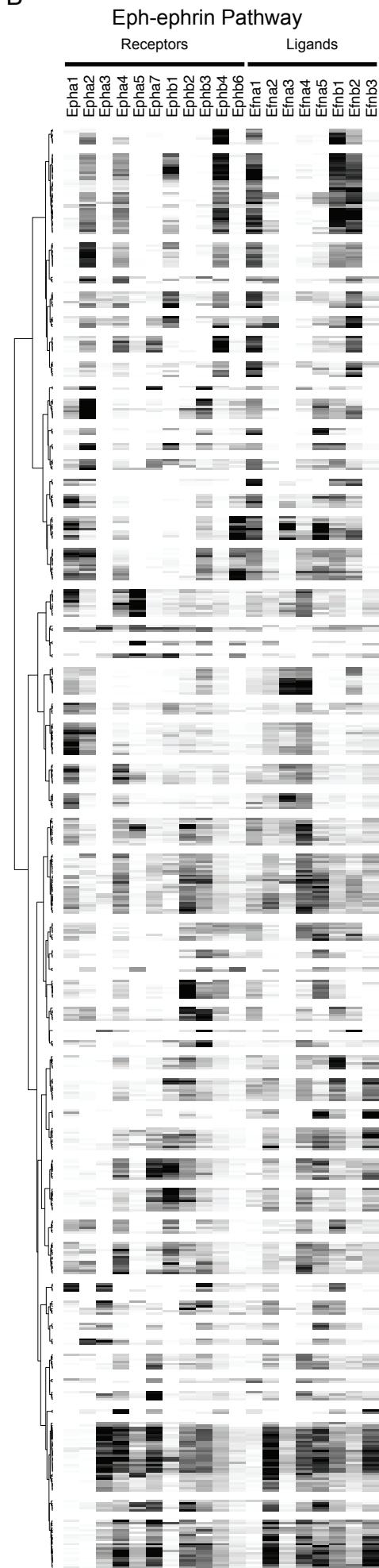


Figure 5—figure supplement 2

A



B



C

