

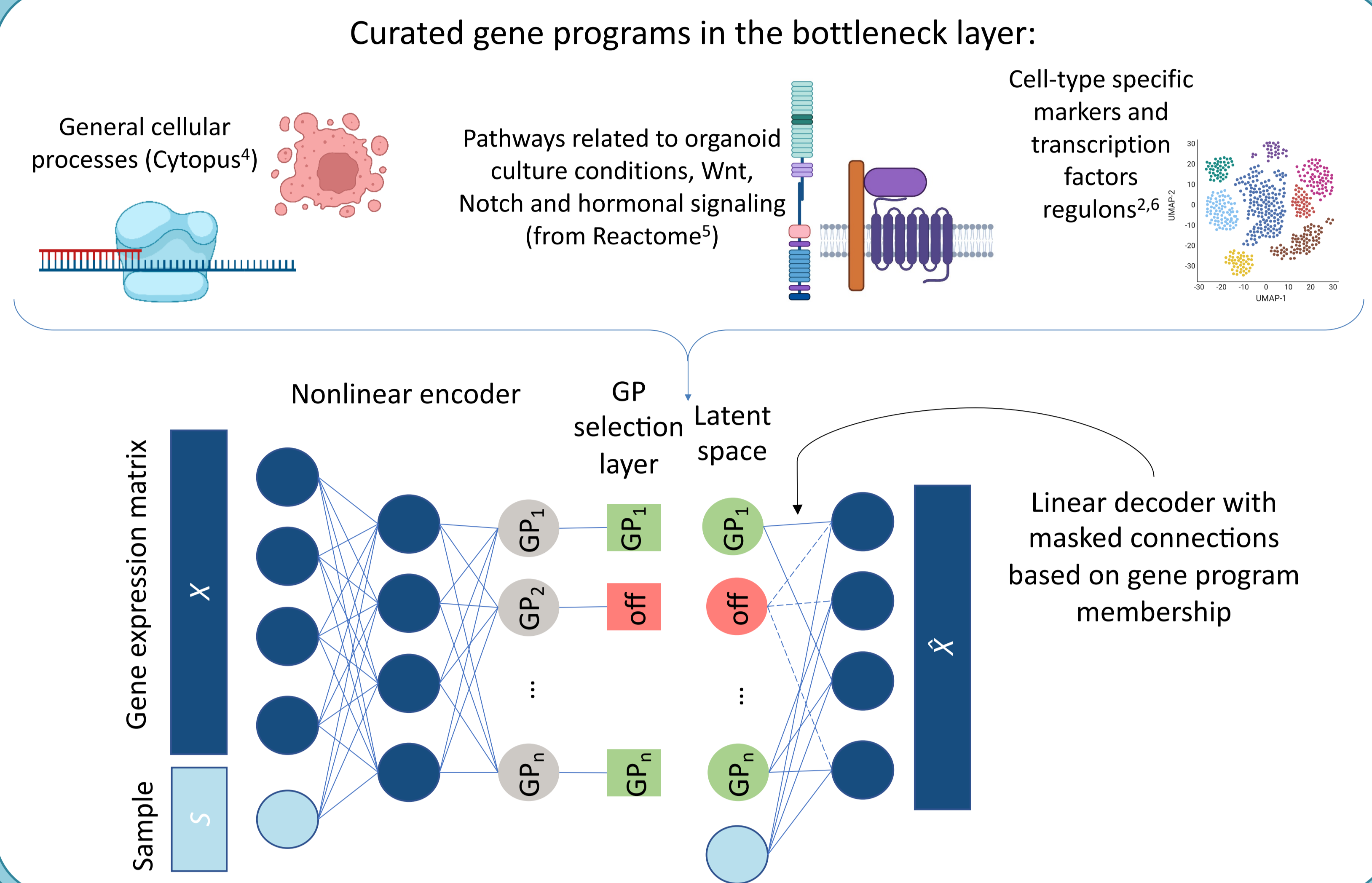
Learning interpretable embeddings for *in vivo/in vitro* comparison of endometrial epithelium

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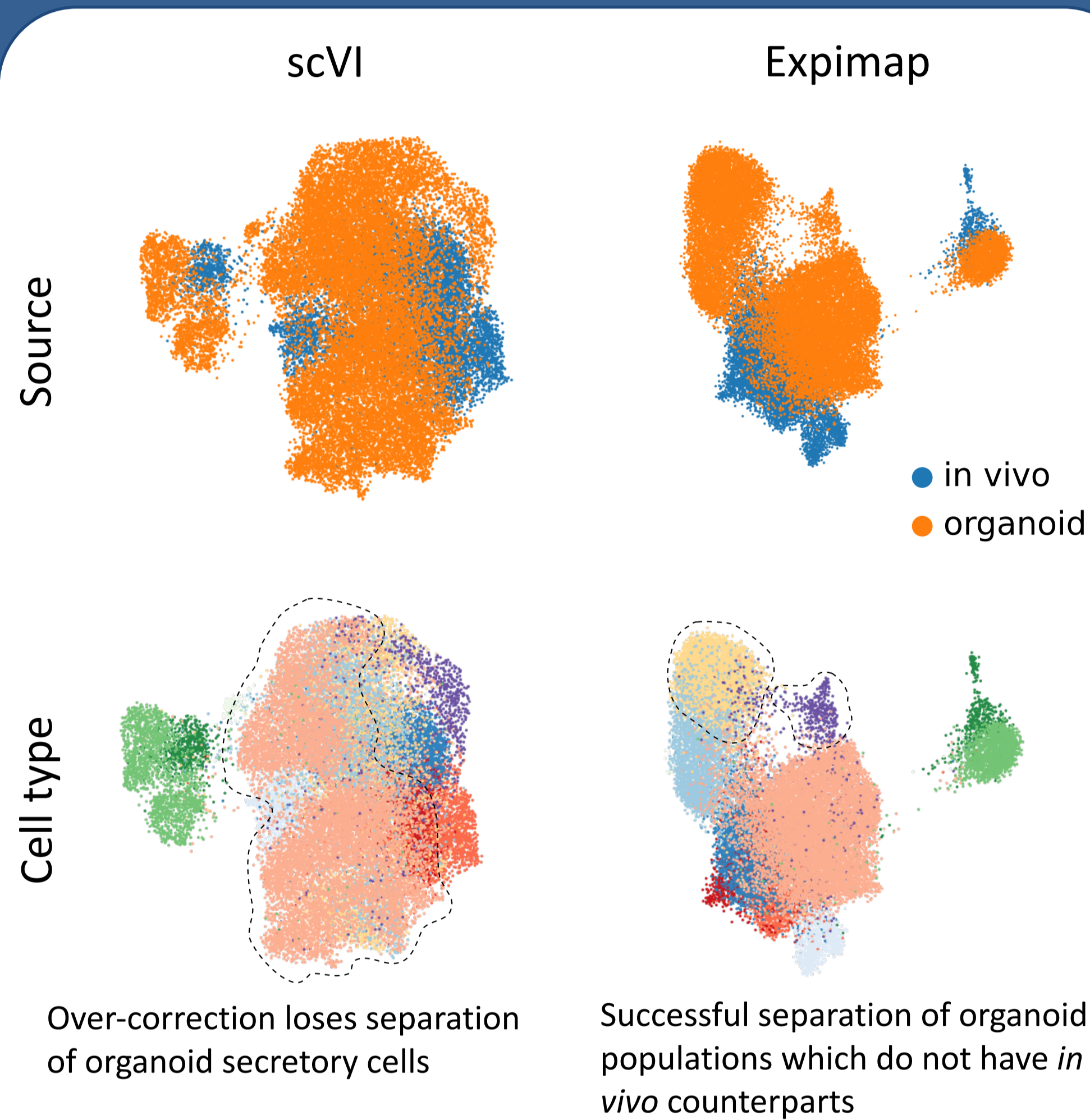
Background

- The endometrium is the mucosal lining of the uterus. It plays a key role in female reproductive health and disease.
- Endometrial organoids derived from glandular tissue reproduce key features of endometrial biology *in vitro*.^{1,2}
- Deep learning models can be used to learn low dimensional representations of single cell omic data. Expimap³ learns interpretable embeddings by mapping the gene expression matrix to known gene programs (GP).

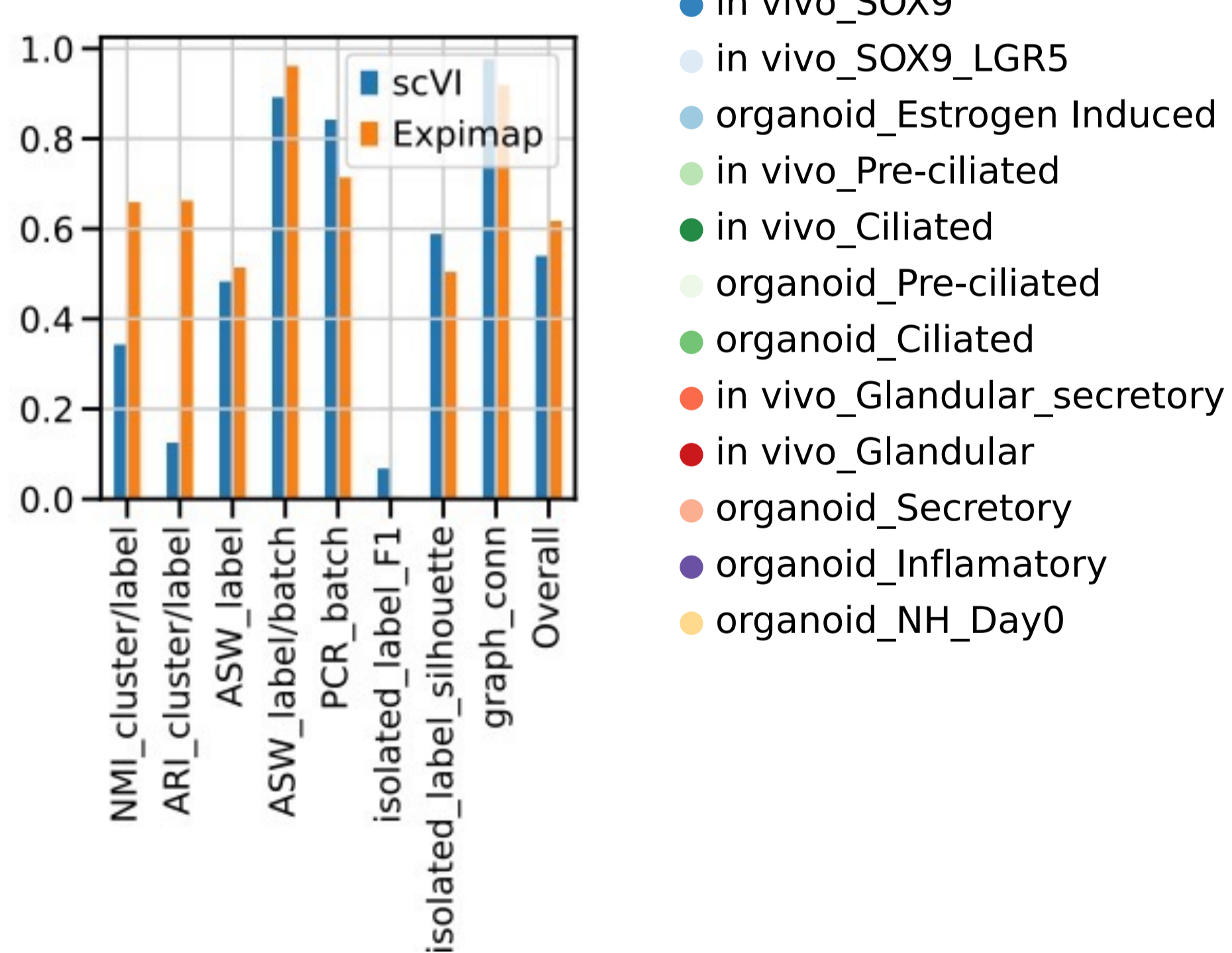
Building the Expimap model



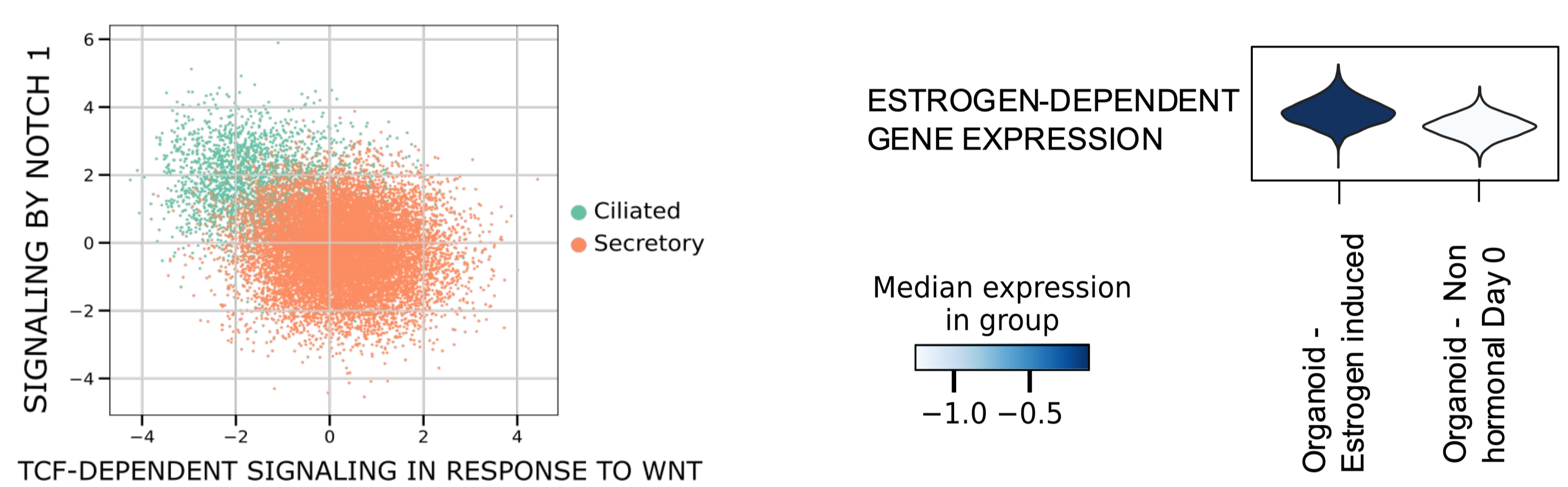
Expimap outperforms unconstrained models



scIB⁷ benchmarking



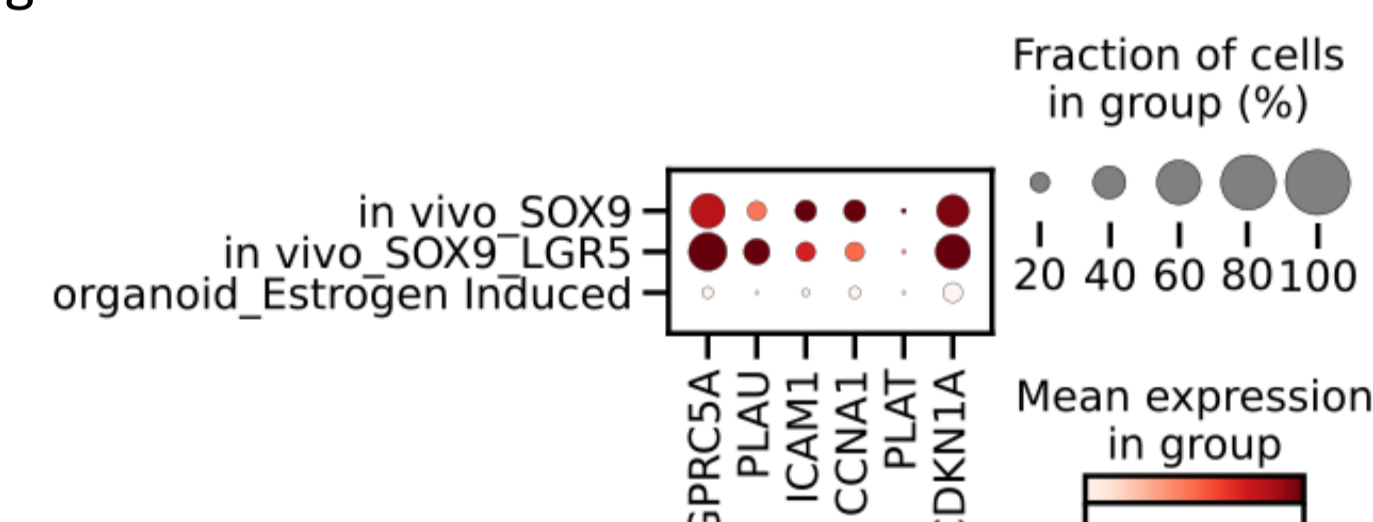
Expimap recovers expected biological patterns



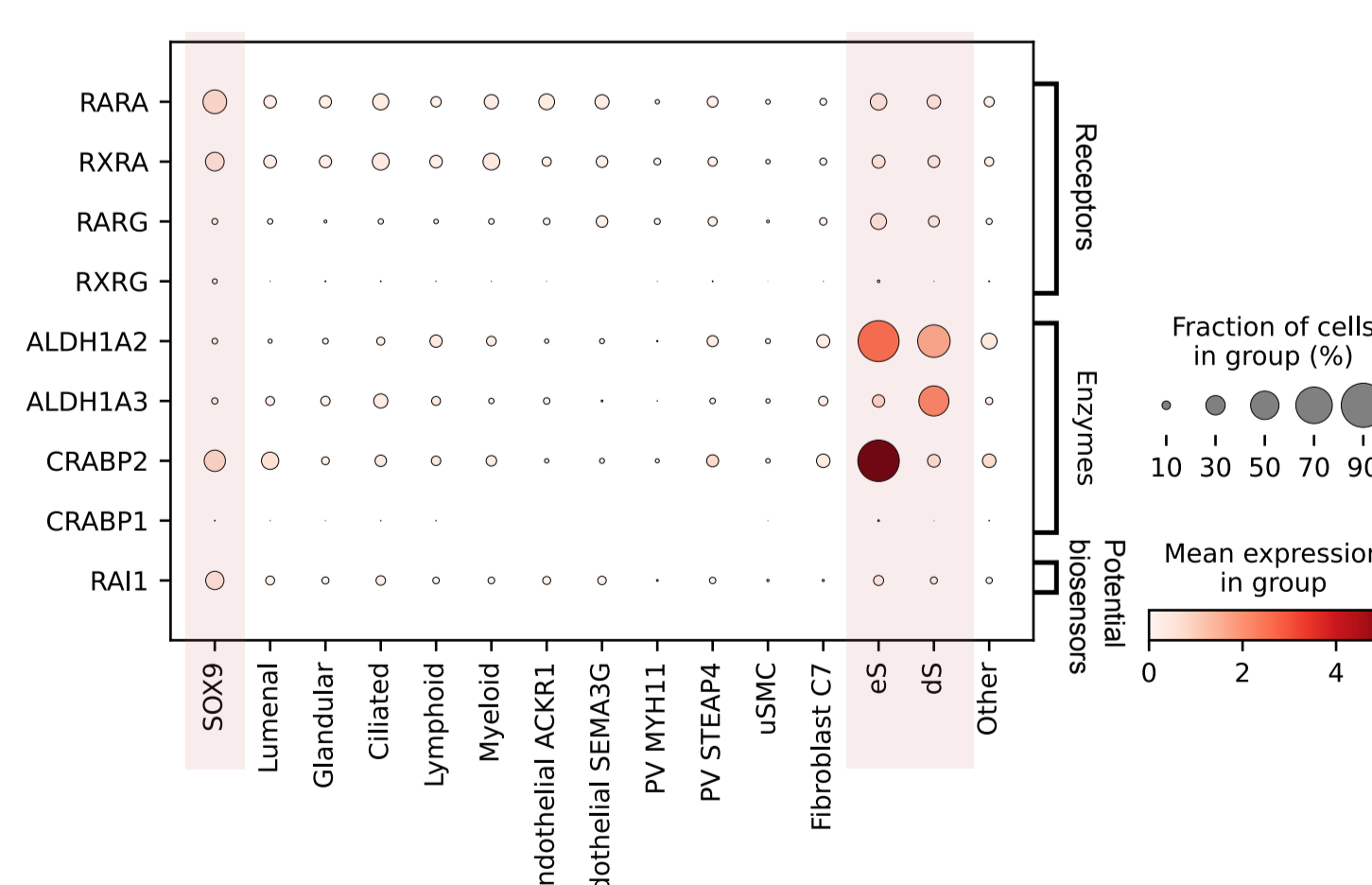
Expimap identifies *in vivo/in vitro* differences

Differentially active GP are linked to cell division and proliferation, as well as organoid culture conditions and absence of stromal cell interactions

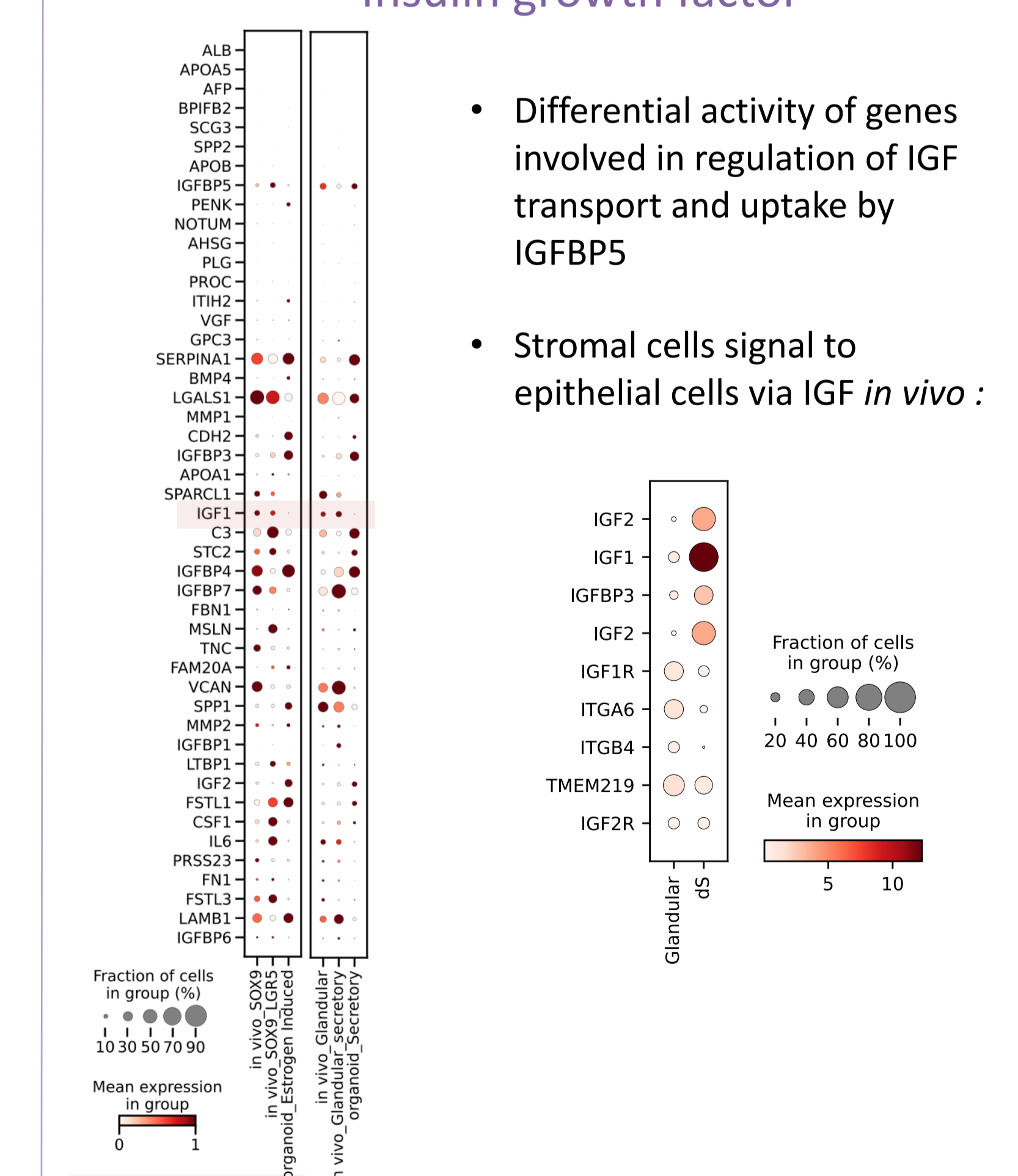
- Increased expression of retinoic acid receptor α target genes *in vivo*



- In vivo*, stromal cells signal to epithelial cells via RA



Insulin growth factor



➤ Do these differences remain in organoids cultured with media containing vitamin A and insulin?

Future directions

- Extension to scRNA-seq datasets from organoids cultured according to different protocols
- Extension to multiple modalities (eg chromatin accessibility)
- Comparison to attention-based methods
- Perturbing differentially active pathways *in silico* and experimentally

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