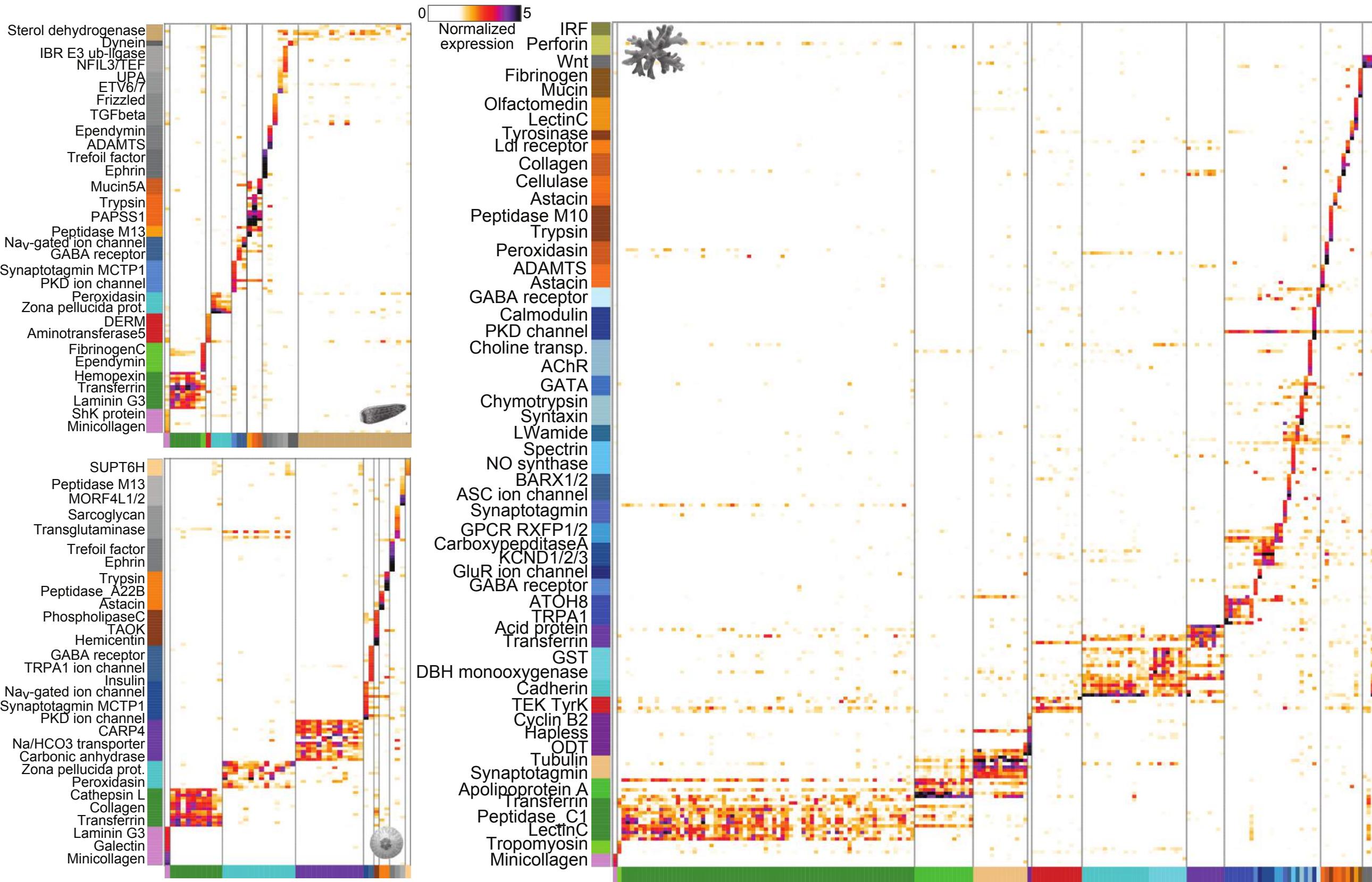
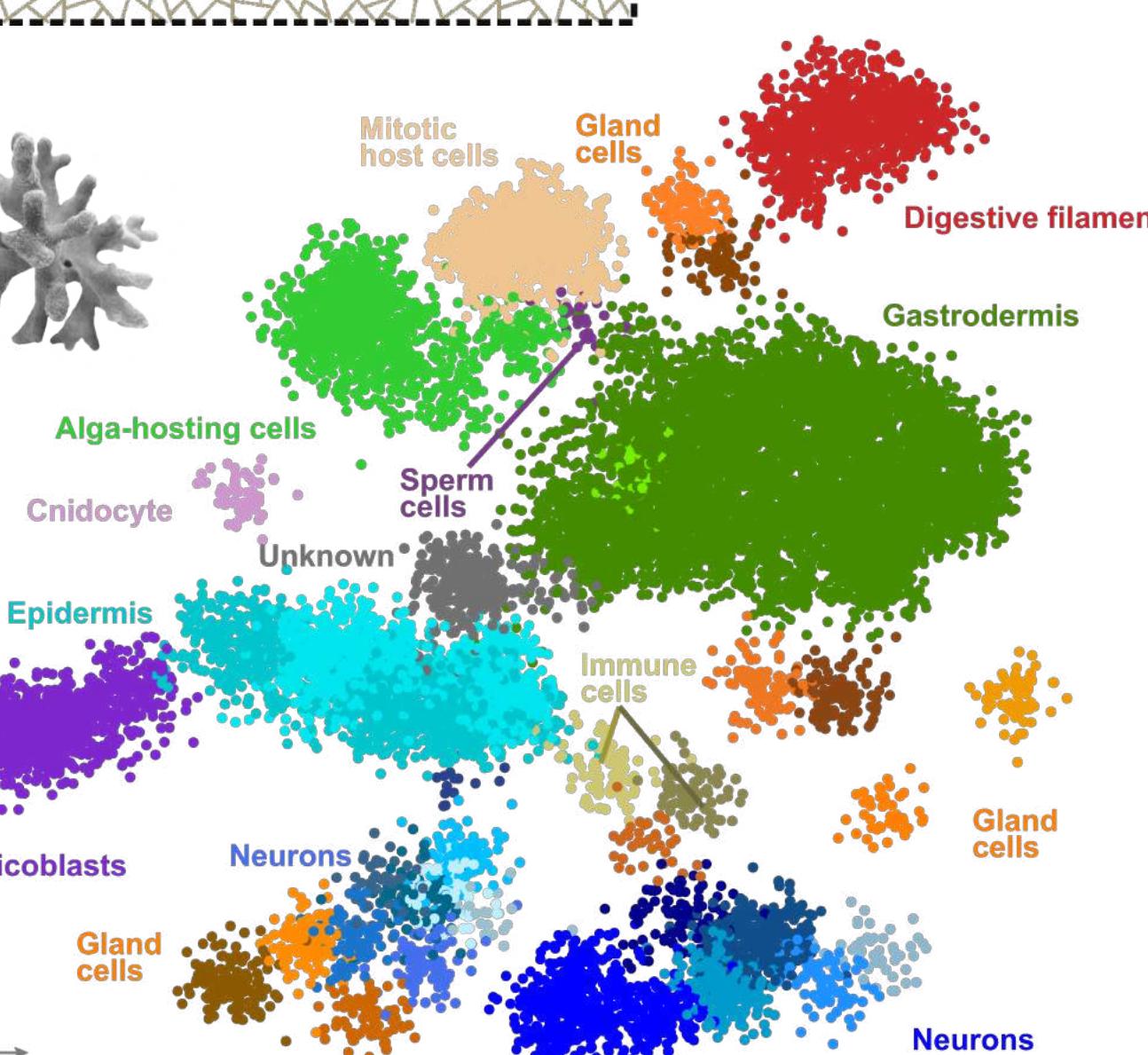
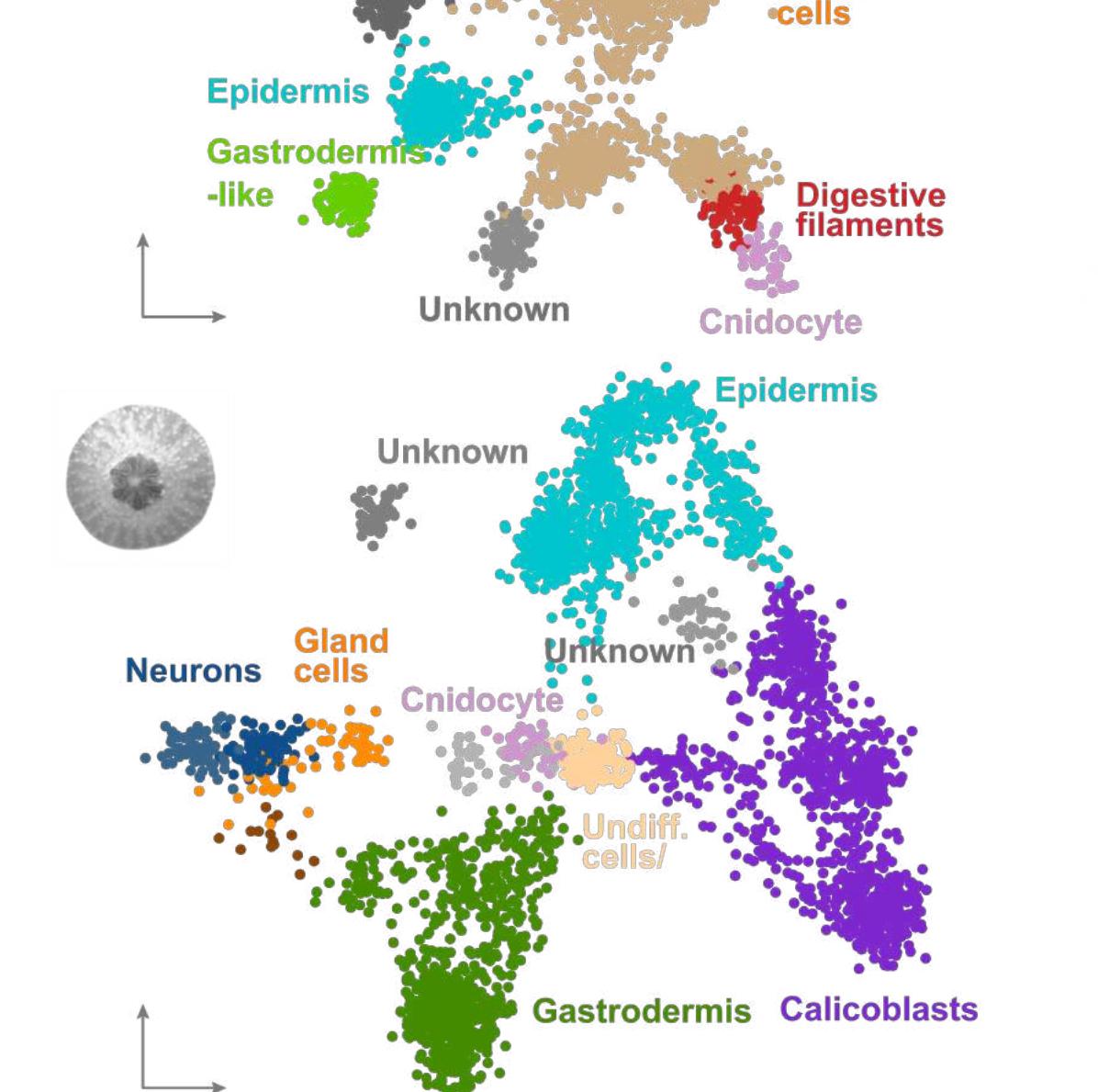
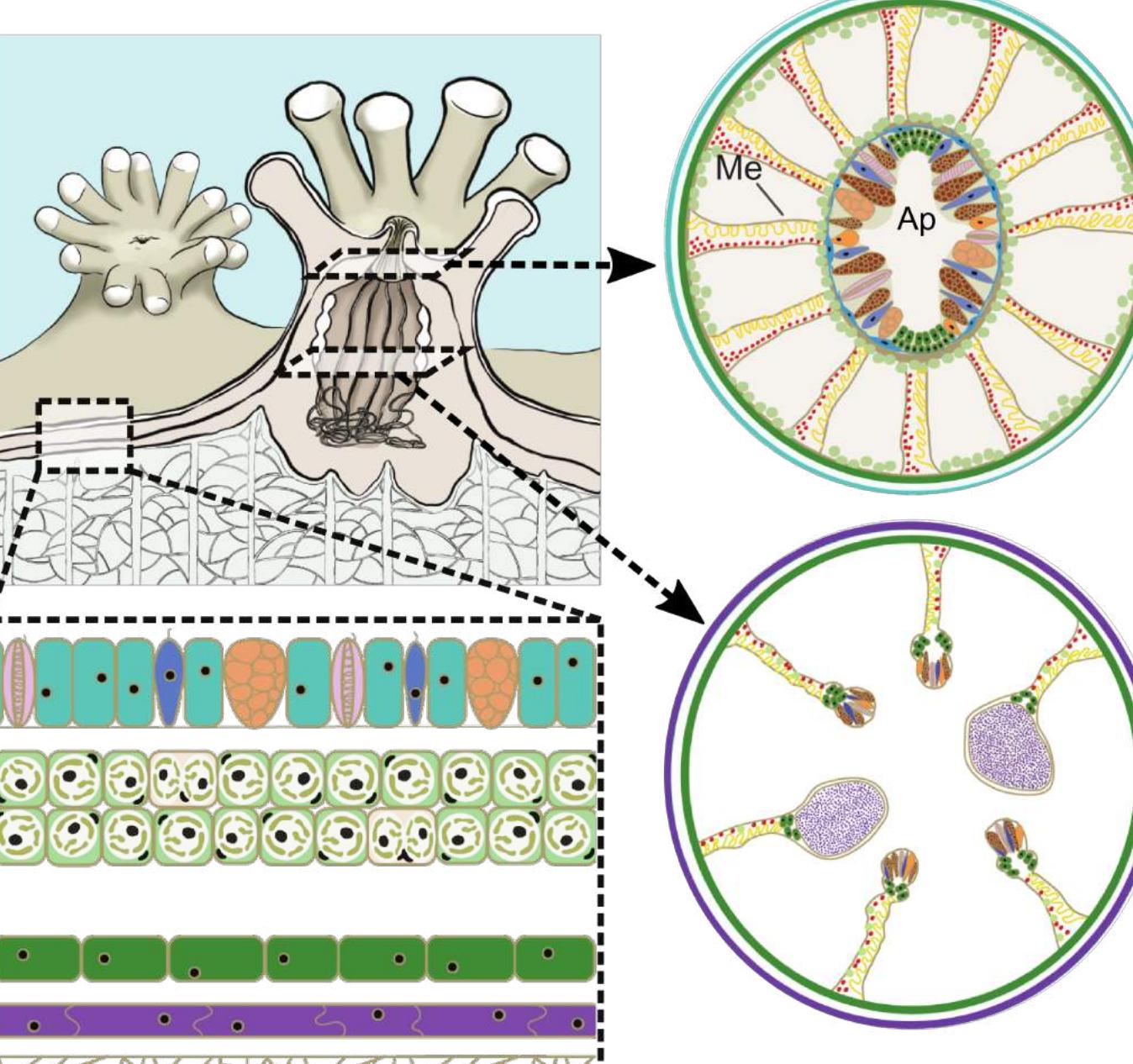
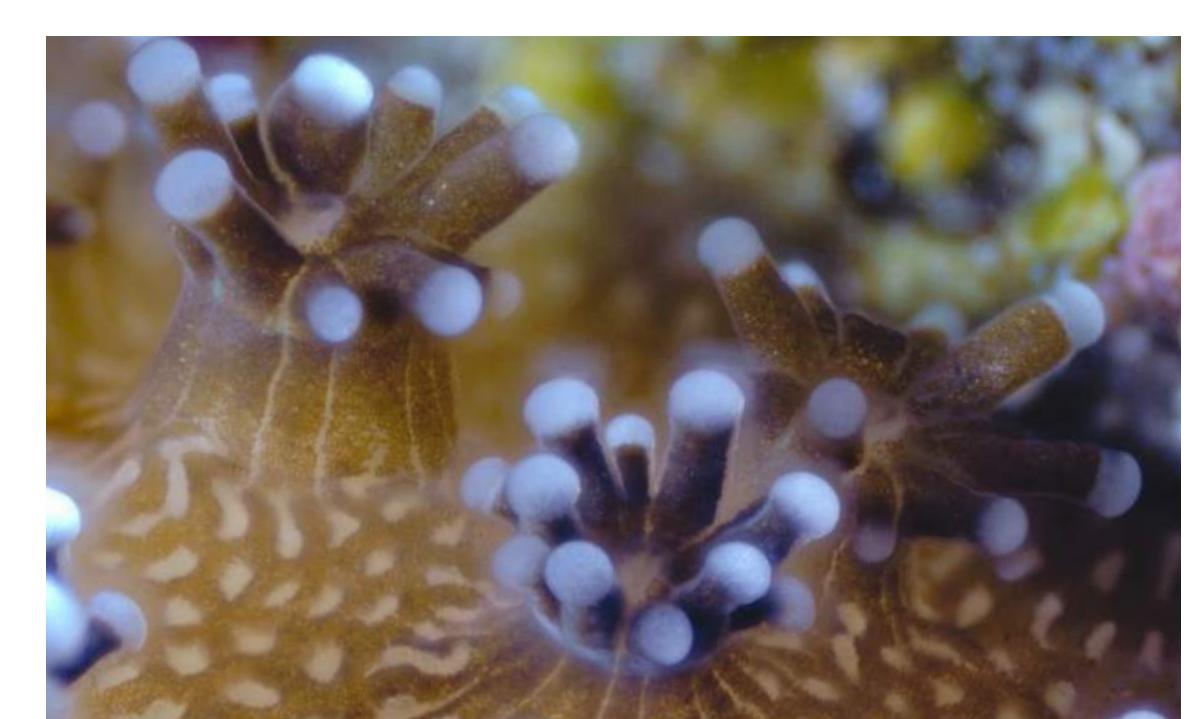
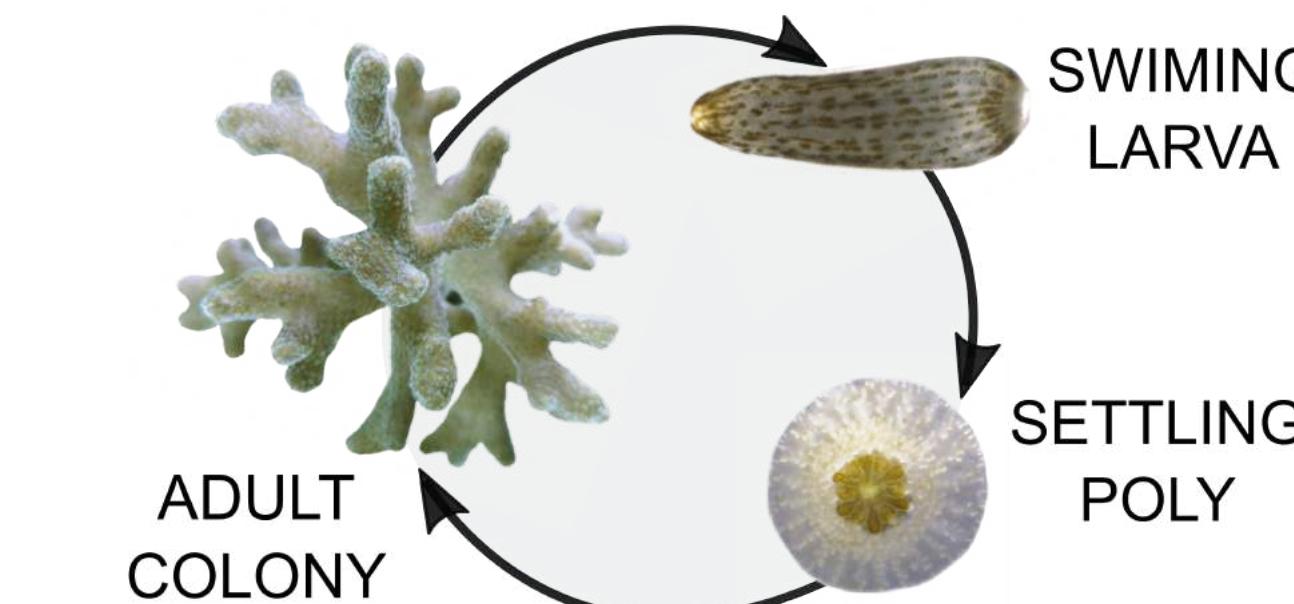


# *Stylophora pistillata* cell atlas illuminates stony coral symbiosis, calcification and immunity

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## A multi-stage coral cell type atlas

Using single-cell RNA sequencing, we characterized over 40 cell types across the three life stages of a stony coral *Stylophora pistillata*.



## Calicoblasts have a metabolic and Ca skeleton producing role in polyp and more epidermal-like identity in adult coral

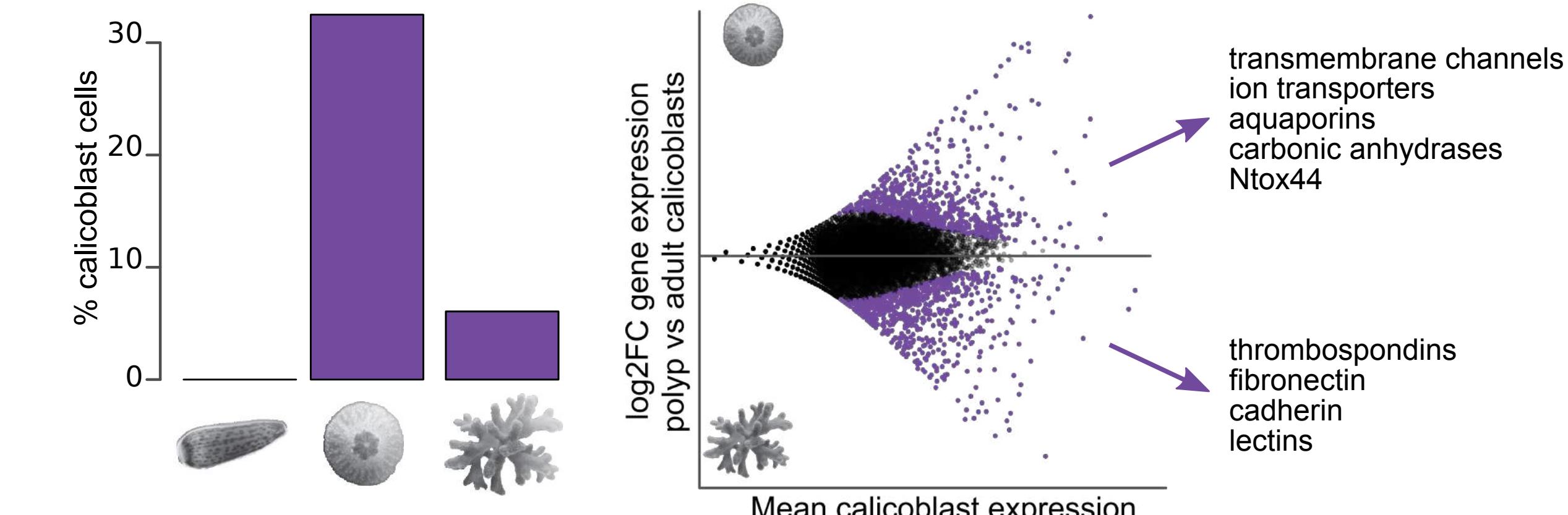


Figure 2. Fraction of calicoblast cells in each sampled life stage (left) and differential gene expression between primary polyp calicoblasts and adult colony calicoblasts (right).

## Gastrodermal cells hosting algal endosymbiont have a distinct expression program enriched in metabolic functions

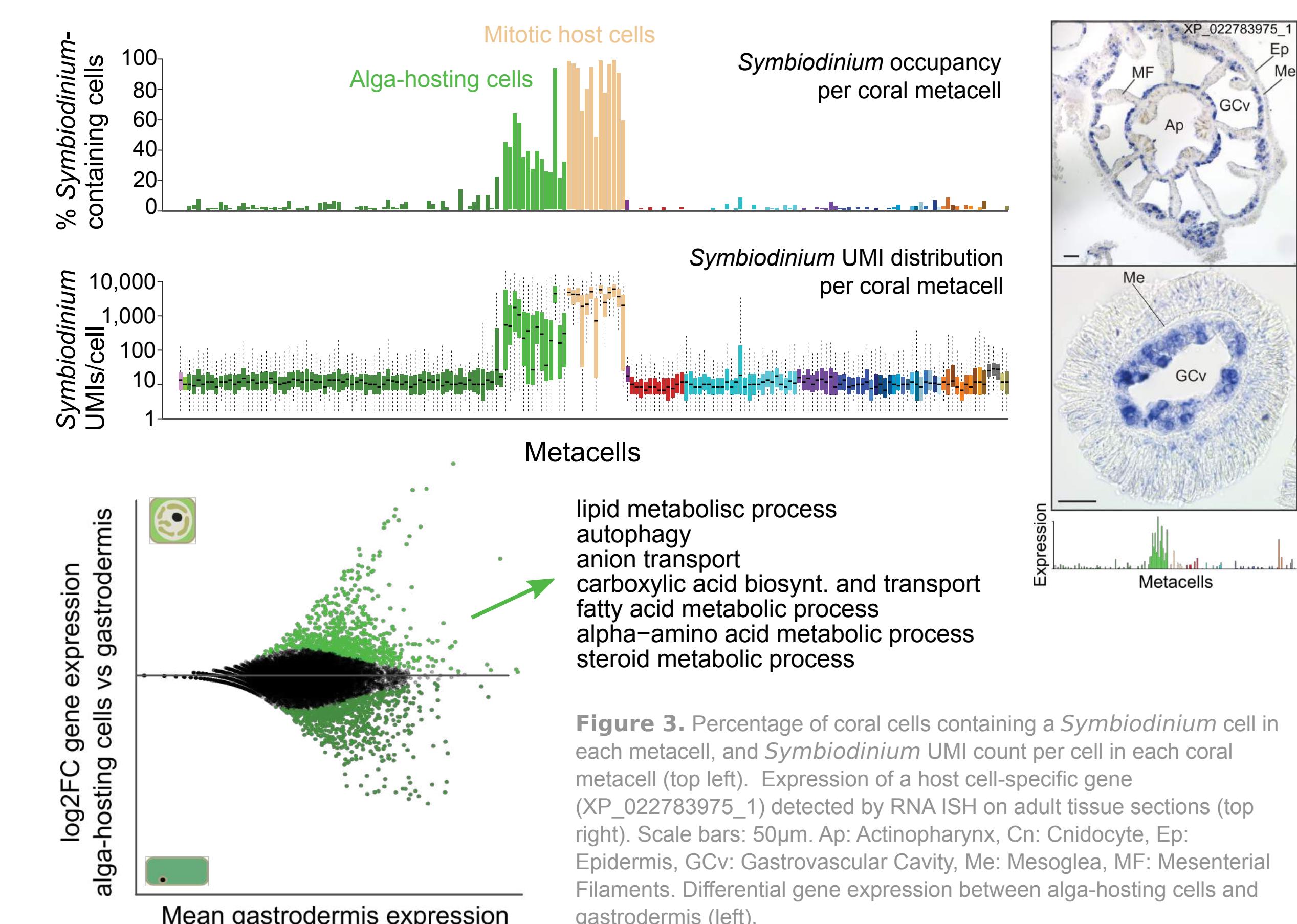


Figure 3. Percentage of coral cells containing a *Symbiodinium* cell in each metacell, and *Symbiodinium* UMI count per cell in each coral metacell (top left). Expression of a host cell-specific gene (XP\_022783975\_1) detected by RNA ISH on adult tissue sections (top right). Scale bars: 50 μm. Ap: Actinopharynx, Cn: Cnidocyte, Ep: Epidermis, Gcv: Gastrovascular Cavity, Me: Mesoglea, MF: Mesenterial Filaments. Differential gene expression between alga-hosting cells and gastrodermis (left).

## Cellular immune system in corals implies existence of conserved immune transcriptional response across animals

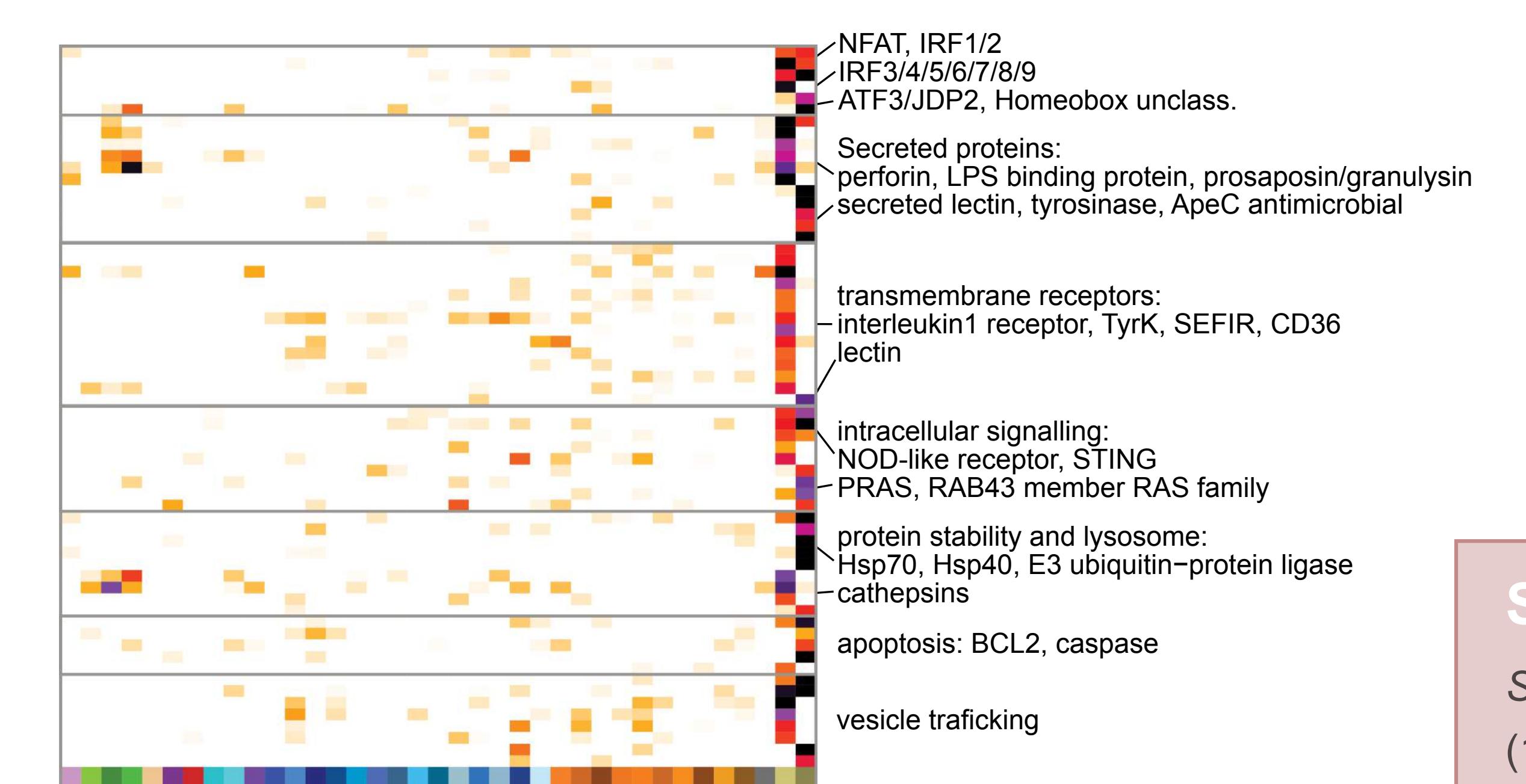


Figure 4. Gene expression for selected immune-related genes across *S. pistillata* cell types.

Figure 1. Life cycle of *Stylophora pistillata* with schematic representation of the coral anatomy and tissue architecture. Ap: Actinopharynx, Me: Mesoglea, MF: Mesenterial Filaments. Per-stage single cells 2D projections and selected marker genes heatmaps.

## Cross-species cell type comparison

We show a strong conservation of broad cell types across three major cnidarian lineages that diverged from a common ancestor 500 million years ago.

At the level of specific cell types we observe many-to-many similarities across species, suggesting a subsequent rapid evolutionary diversification.

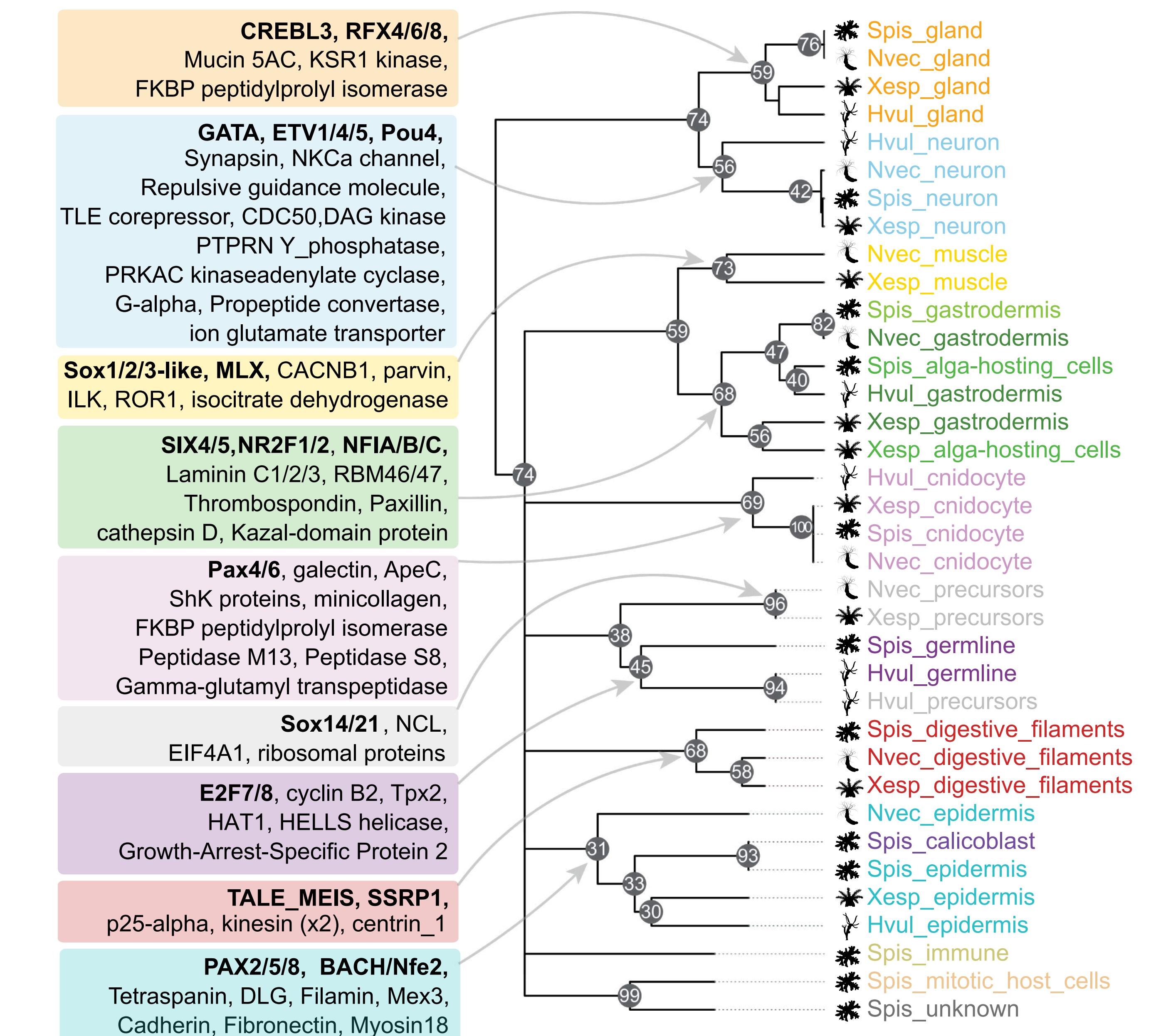


Figure 5. Cnidarian species tree and cell type tree for the four species in this study. Cell type tree is based on hierarchical clustering of 1,227 variably expressed one-to-one orthologs (max expression fold-change in any cell type > 1.8). Node values indicate percent jackknife support (with 75% downsampling). Selected genes supporting each node are indicated.

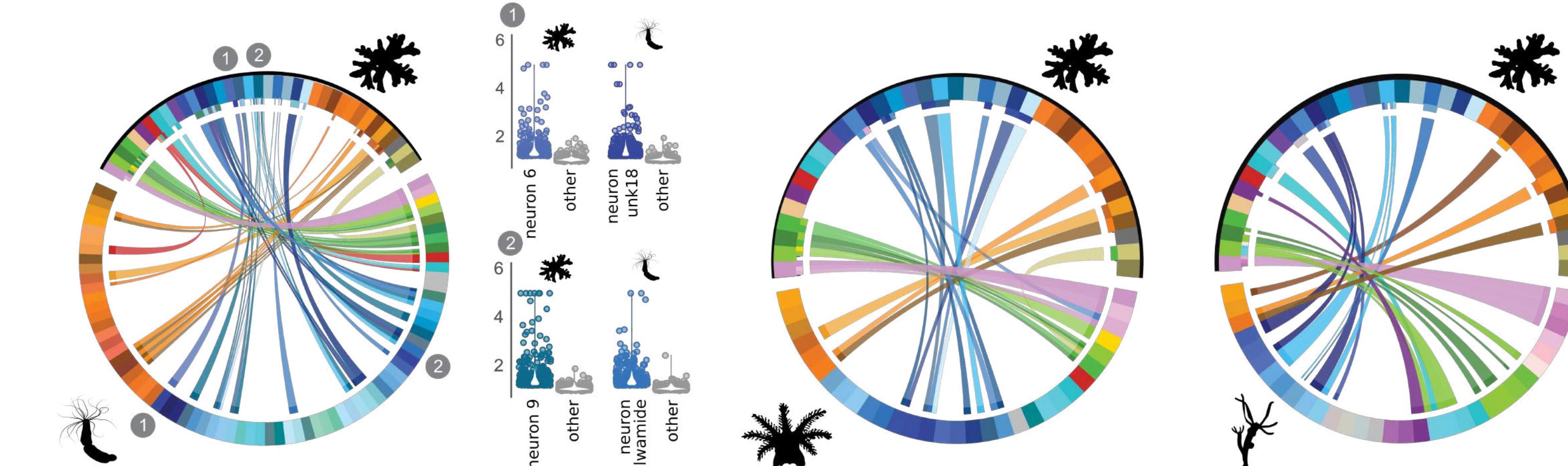


Figure 6. The top 2% cross-species pairwise cell type similarities, based on Kullback–Leibler divergence (KLD), shown as arches connecting cell types. The arch width is proportional to cell types' similarity. The normalized expression of the top shared orthologous genes (FC > 1.3) in two example cell types is shown, compared to the average expression of the same genes in all other cell types.

## Summary

### *Stylophora pistillata* cell atlas:

- (1) provides new insights into molecular pathways and gene regulatory programs involved in coral reef formation,
- (2) presents a valuable resource for the future functional coral studies, and
- (3) initiates phylogenetically informed comparative analysis of cnidarian cell types.

More information can be found in our manuscript:  
Levy et al. 2021 Cell 184 1–16  
<https://doi.org/10.1016/j.cell.2021.07.018>

The data can be explored in an interactive database at [sebe-lab.shinyapps.io/Stylophora\\_cell\\_atlas/](http://sebe-lab.shinyapps.io/Stylophora_cell_atlas/)

