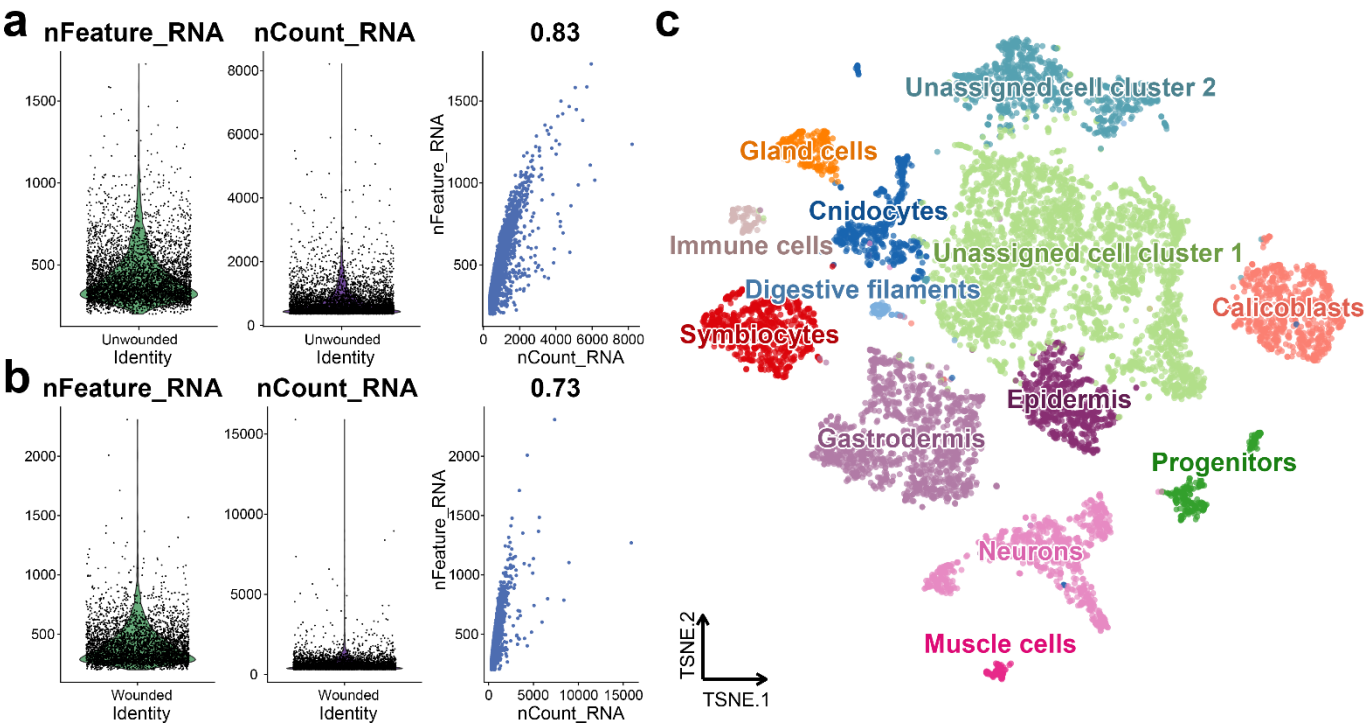
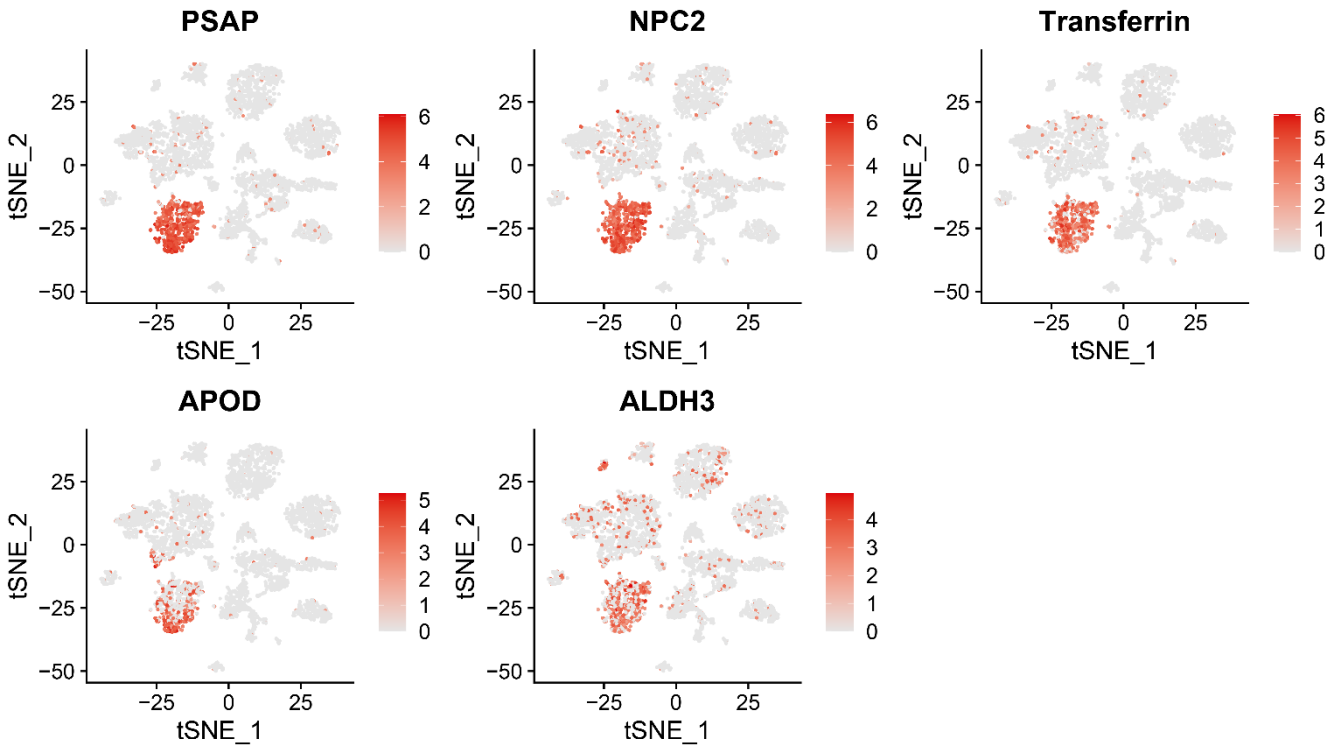
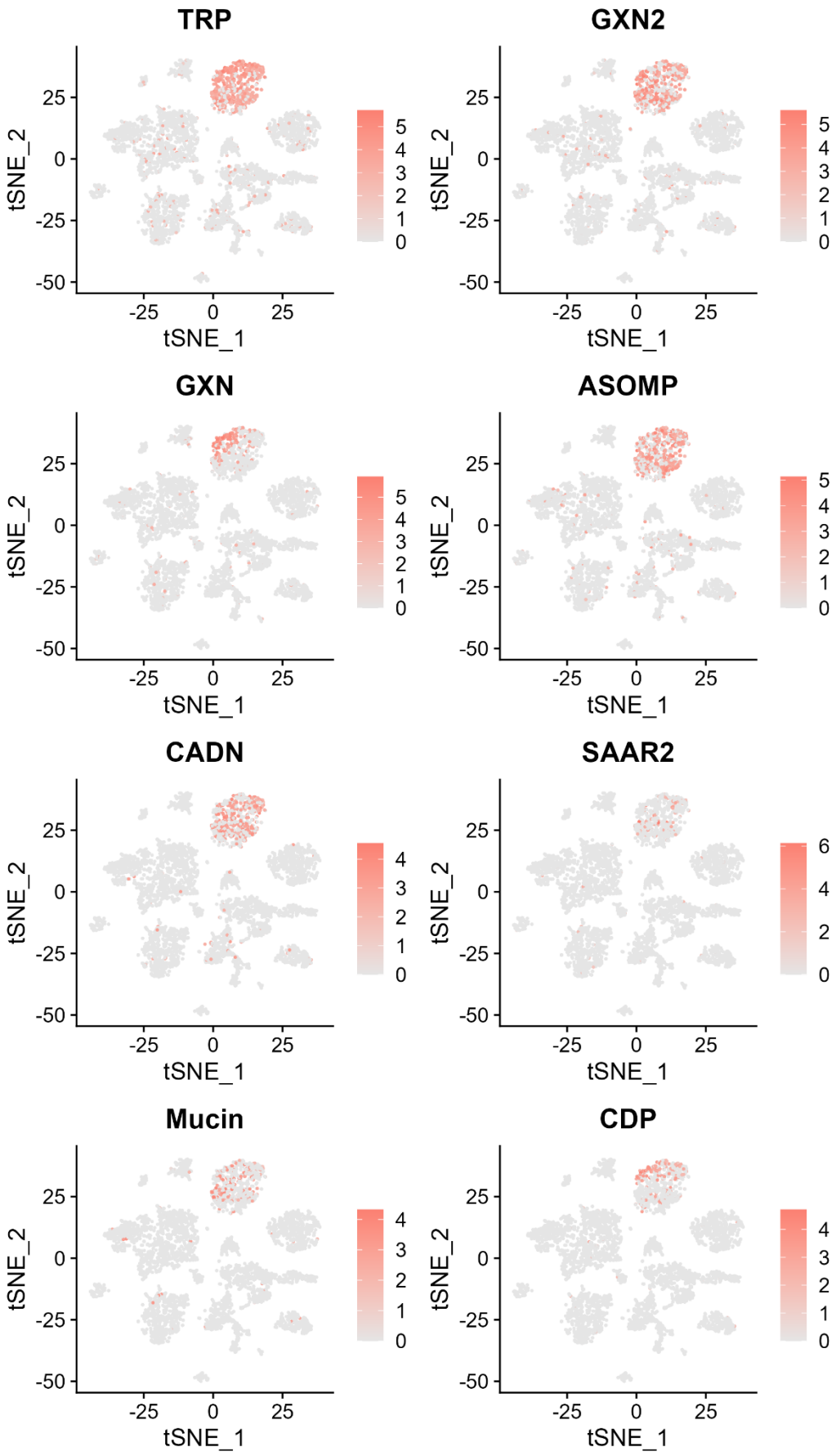


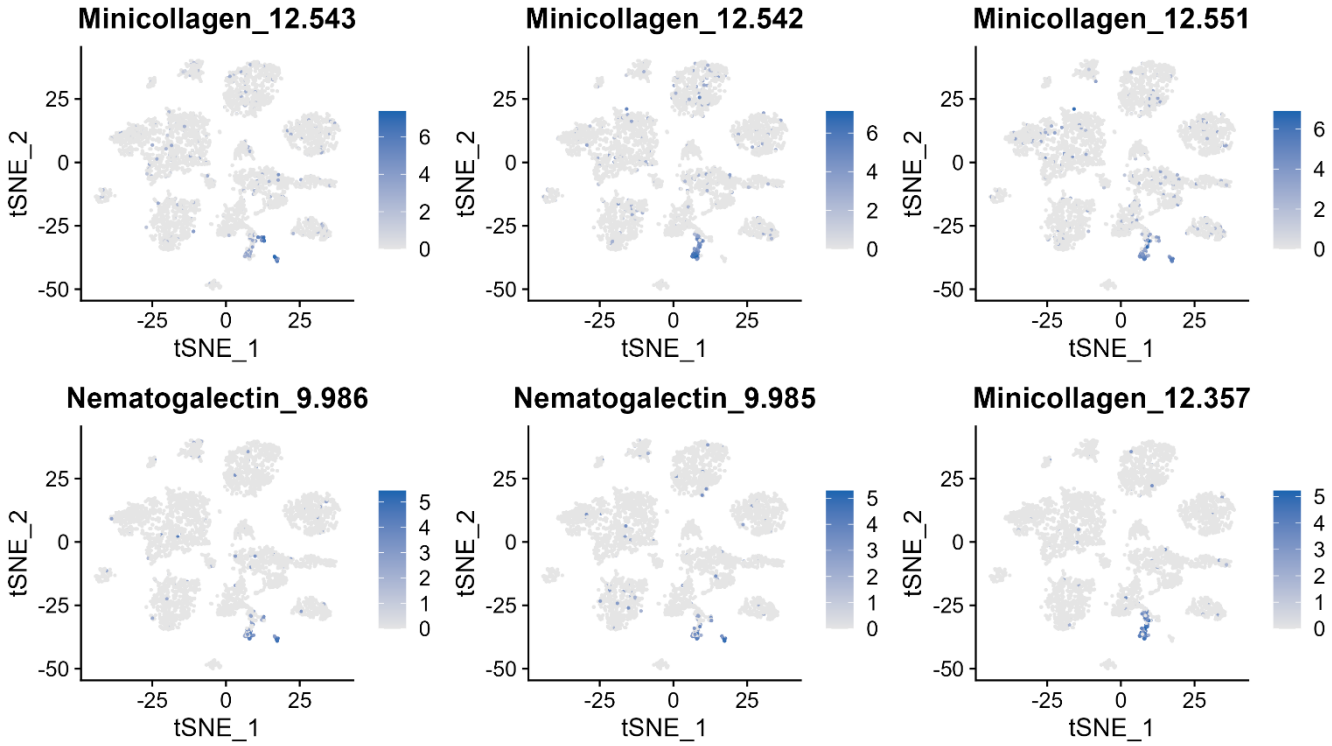
Supplementary Fig. 1. Details of *A. muricata* cell atlas construction. a, Visualization of QC metrics for the unwounded treatment (referred to as 'Unwounded'). **b**, Visualization of QC metrics for the healing treatment with peak biomineralization (referred to as 'Wounded'). **c**, t-SNE map of *A. muricata*, where individual cells are depicted and distinguished by different colors based on their respective cell-type clusters.



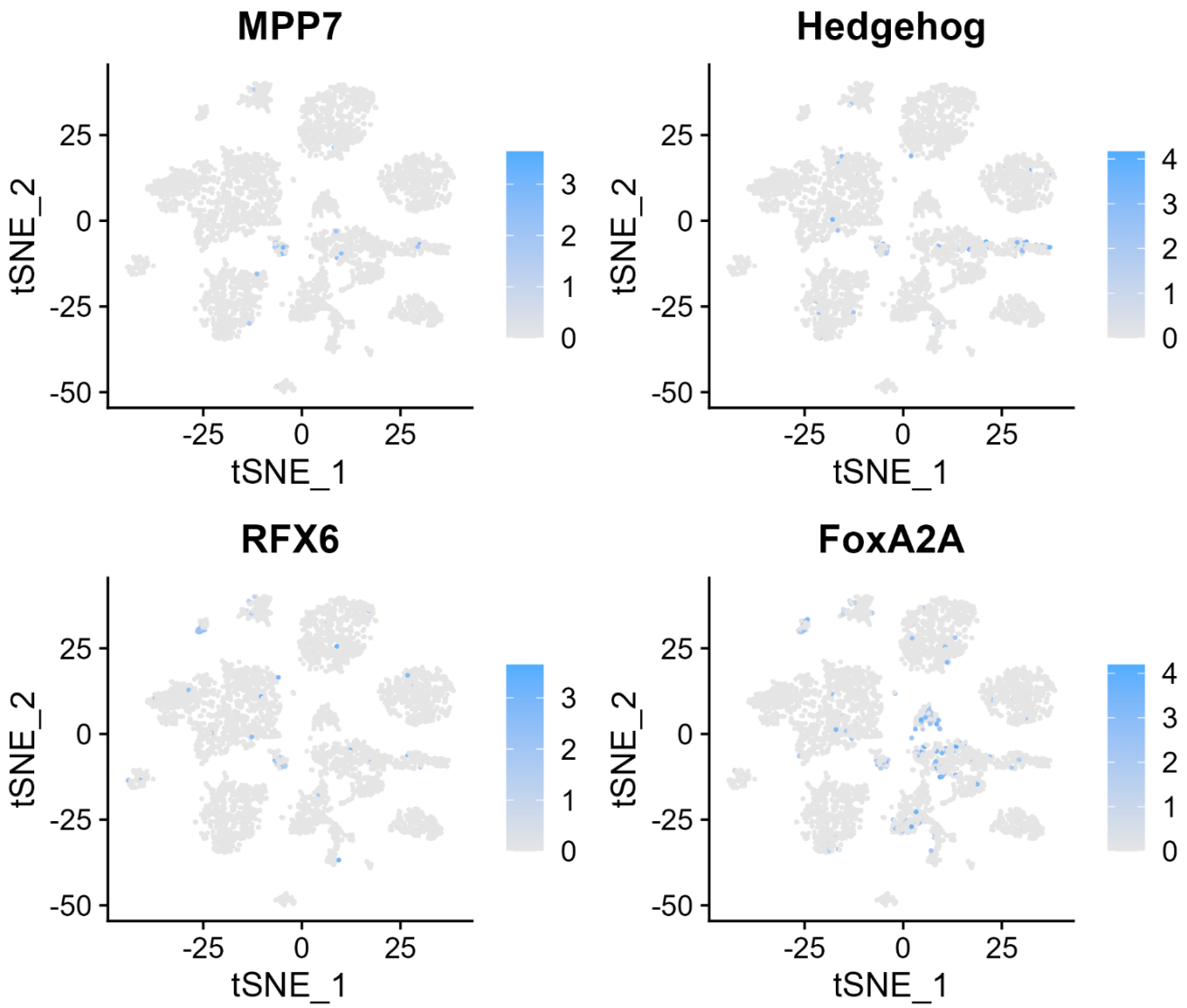
Supplementary Fig. 2. t-SNE visualization of the expression of marker genes in symbiocytes.



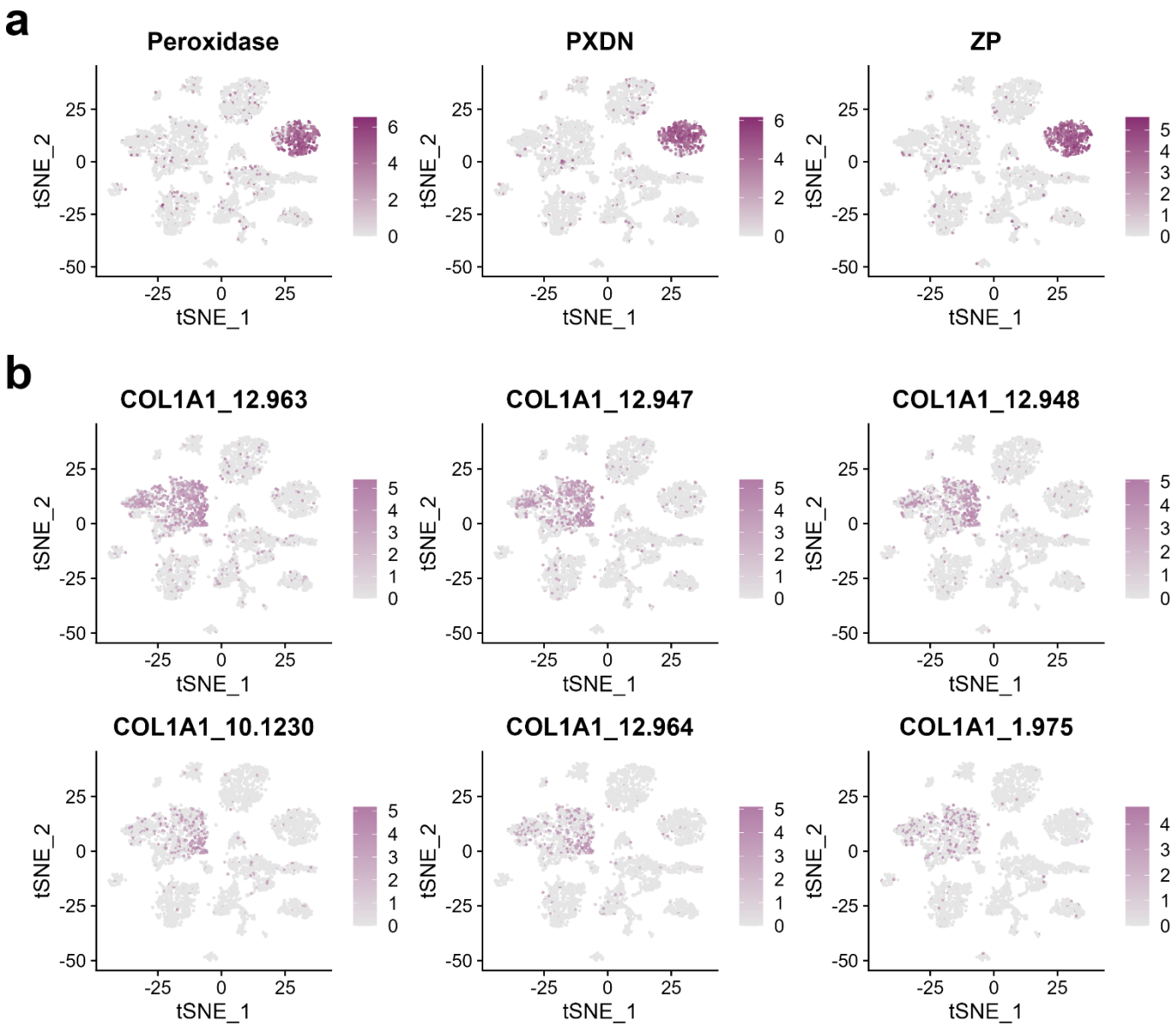
Supplementary Fig. 3. t-SNE visualization of the expression of marker genes in calicoblasts.



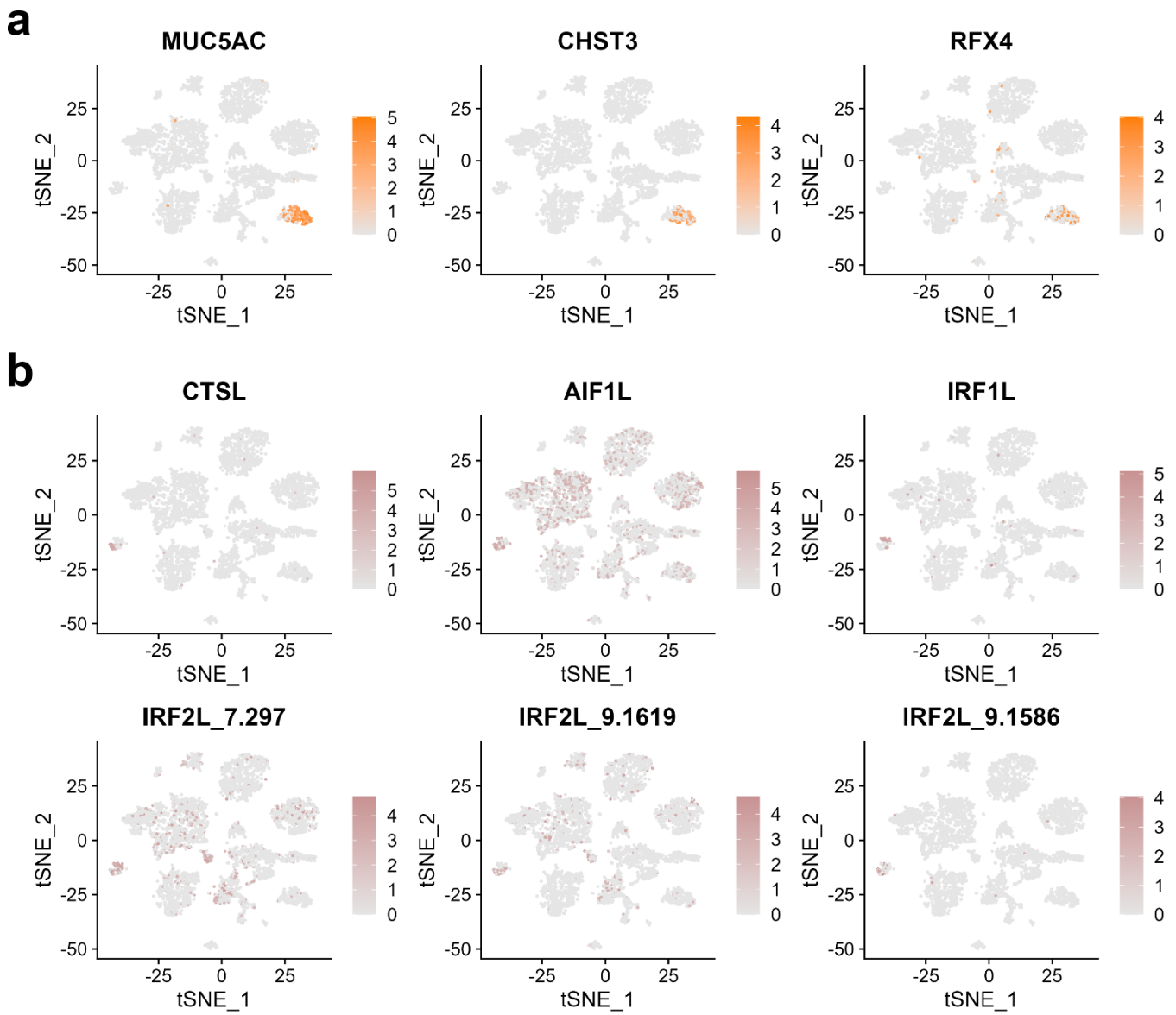
Supplementary Fig. 4. t-SNE visualization of the expression of marker genes in cnidocytes.



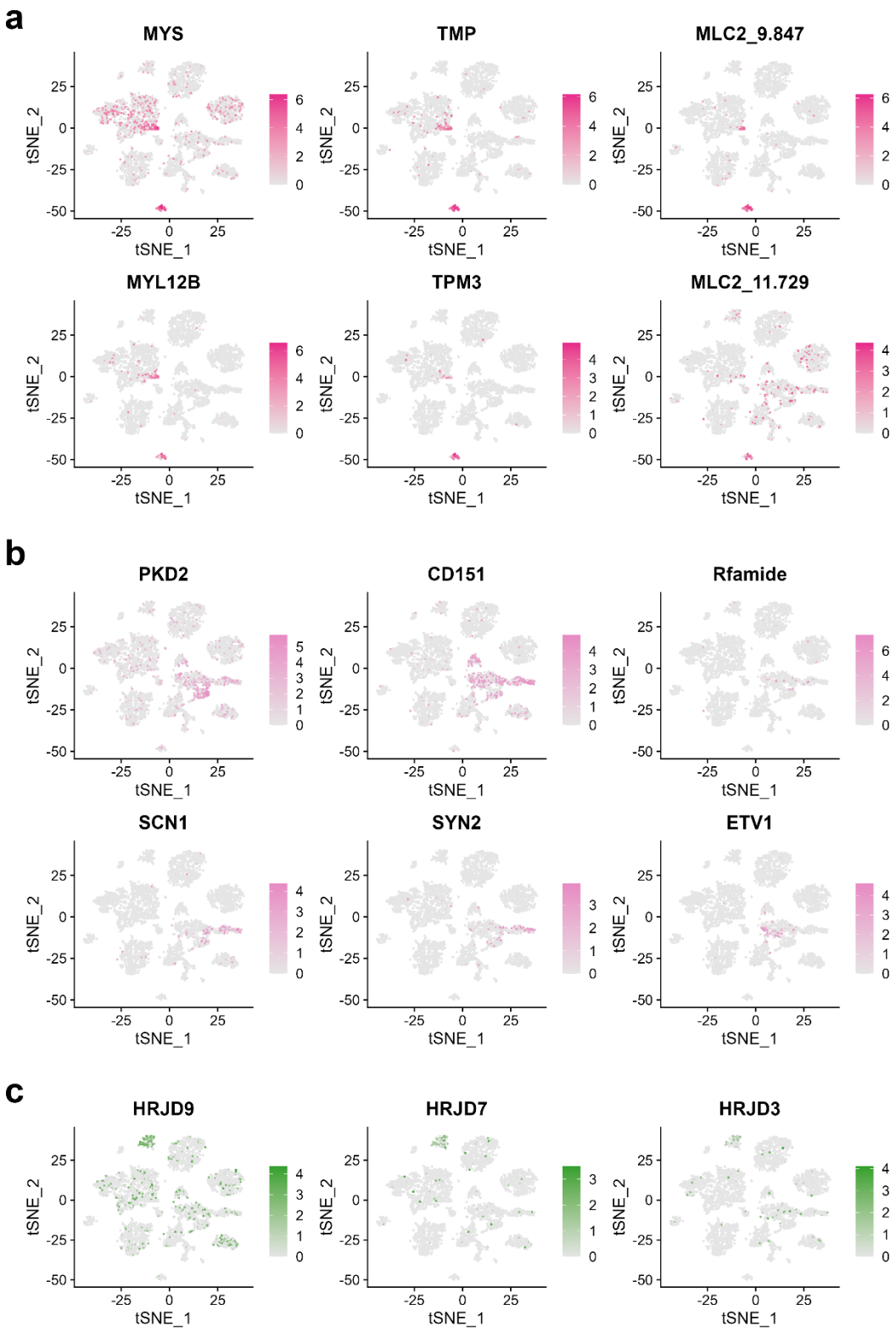
Supplementary Fig. 5. t-SNE visualization of the expression of marker genes in digestive filament cells.



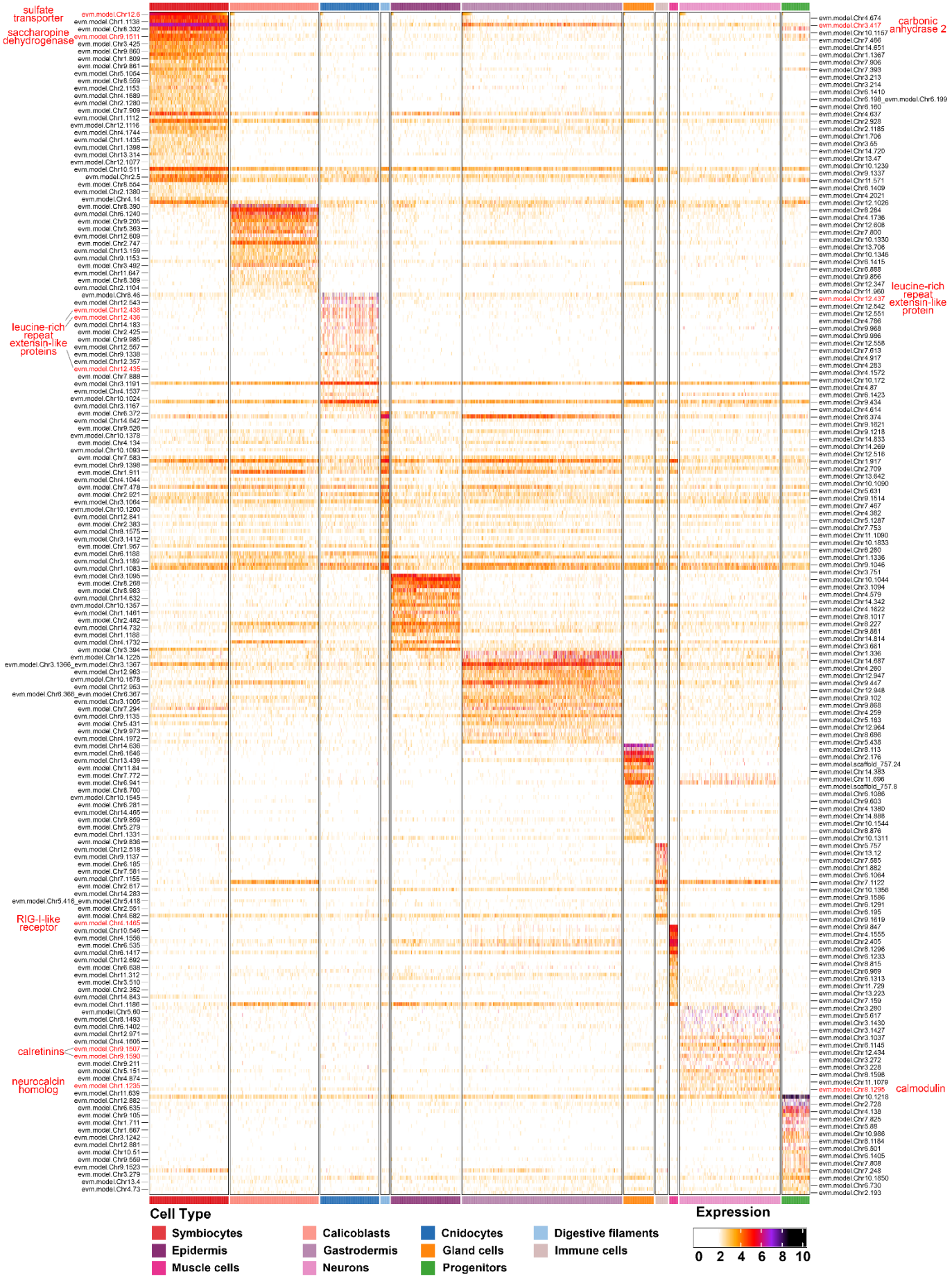
Supplementary Fig. 6. a, t-SNE visualization of the expression of marker genes in epidermal cells. **b**, t-SNE visualization of the expression of marker genes in gastrodermal cells.



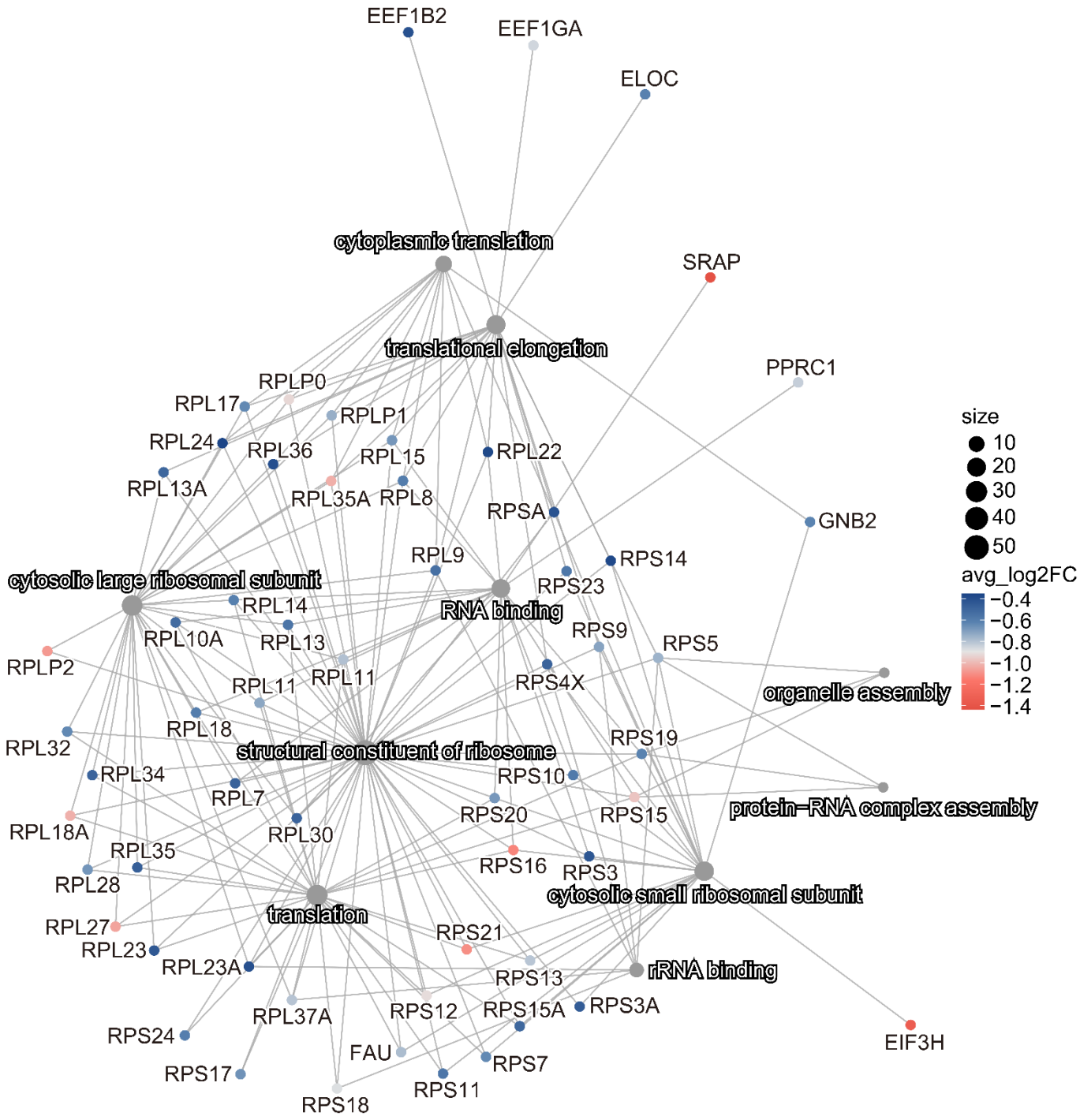
Supplementary Fig. 7. a, t-SNE visualization of the expression of marker genes in gland cells. **b**, t-SNE visualization of the expression of marker genes in immune cells.



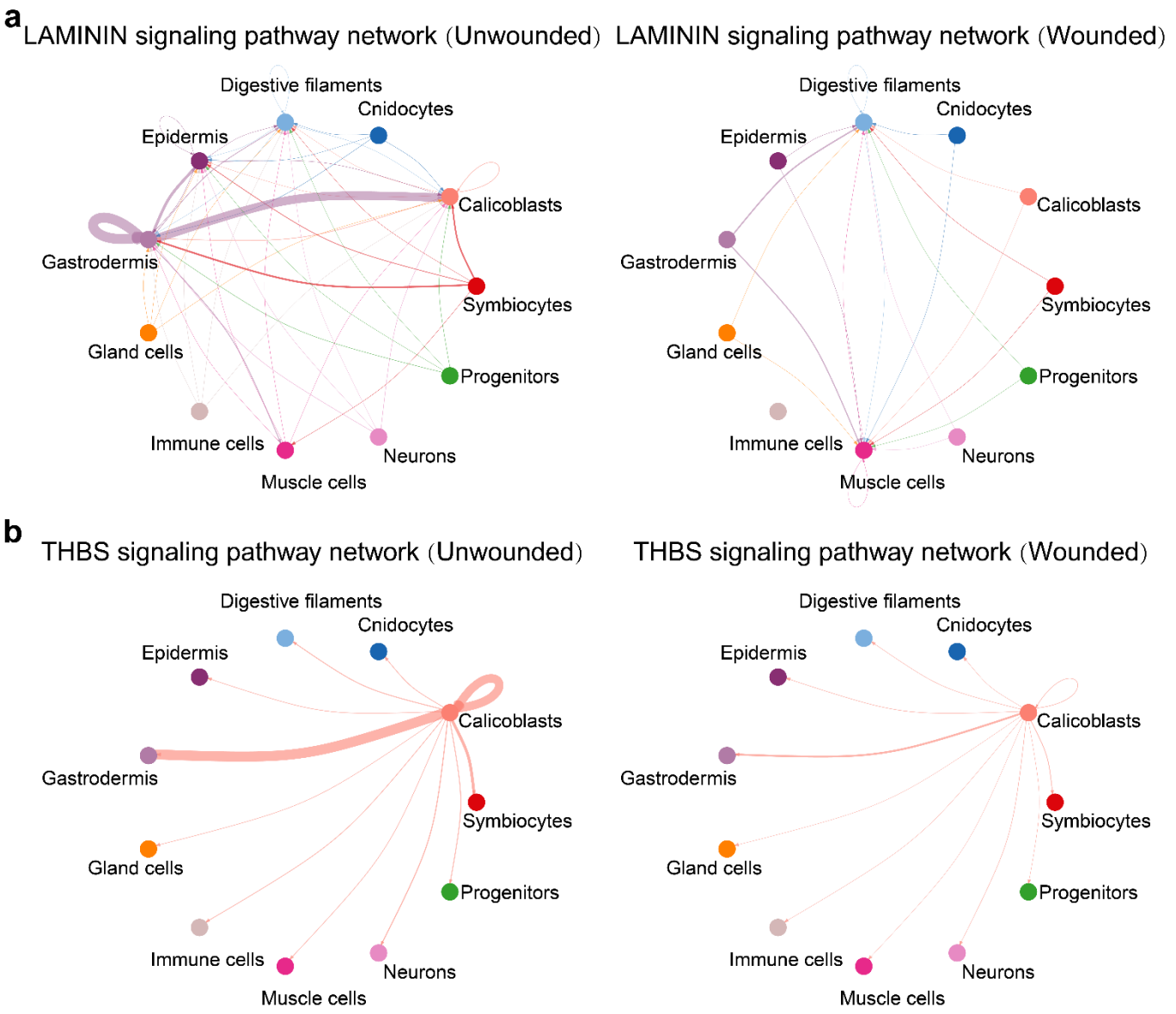
Supplementary Fig. 8. a, t-SNE visualization of the expression of marker genes in muscle cells. **b**, t-SNE visualization of the expression of marker genes in neurons. **c**, t-SNE visualization of the expression of marker genes in progenitor cells.



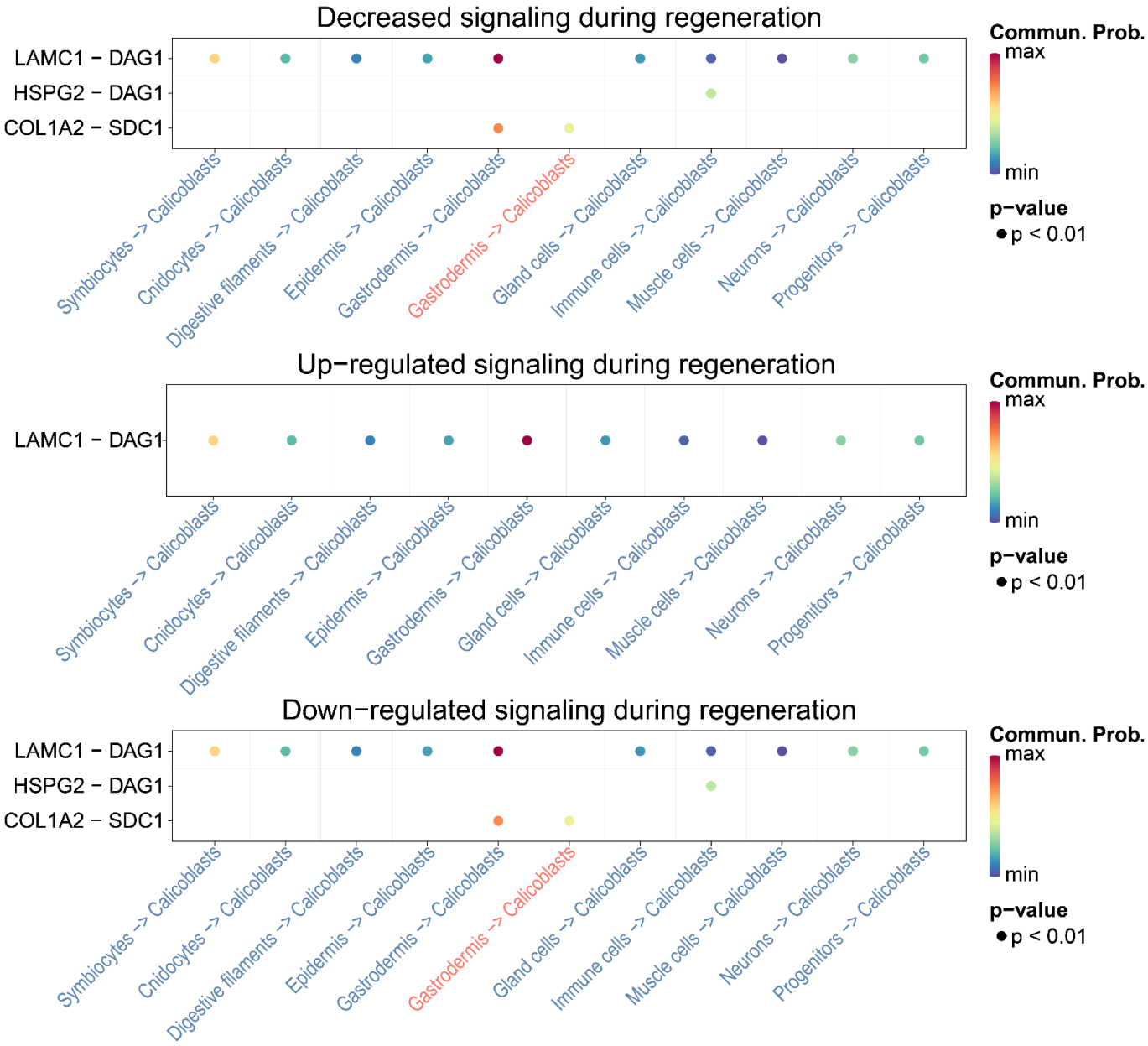
Supplementary Fig. 9. Candidate marker genes for different cell types.



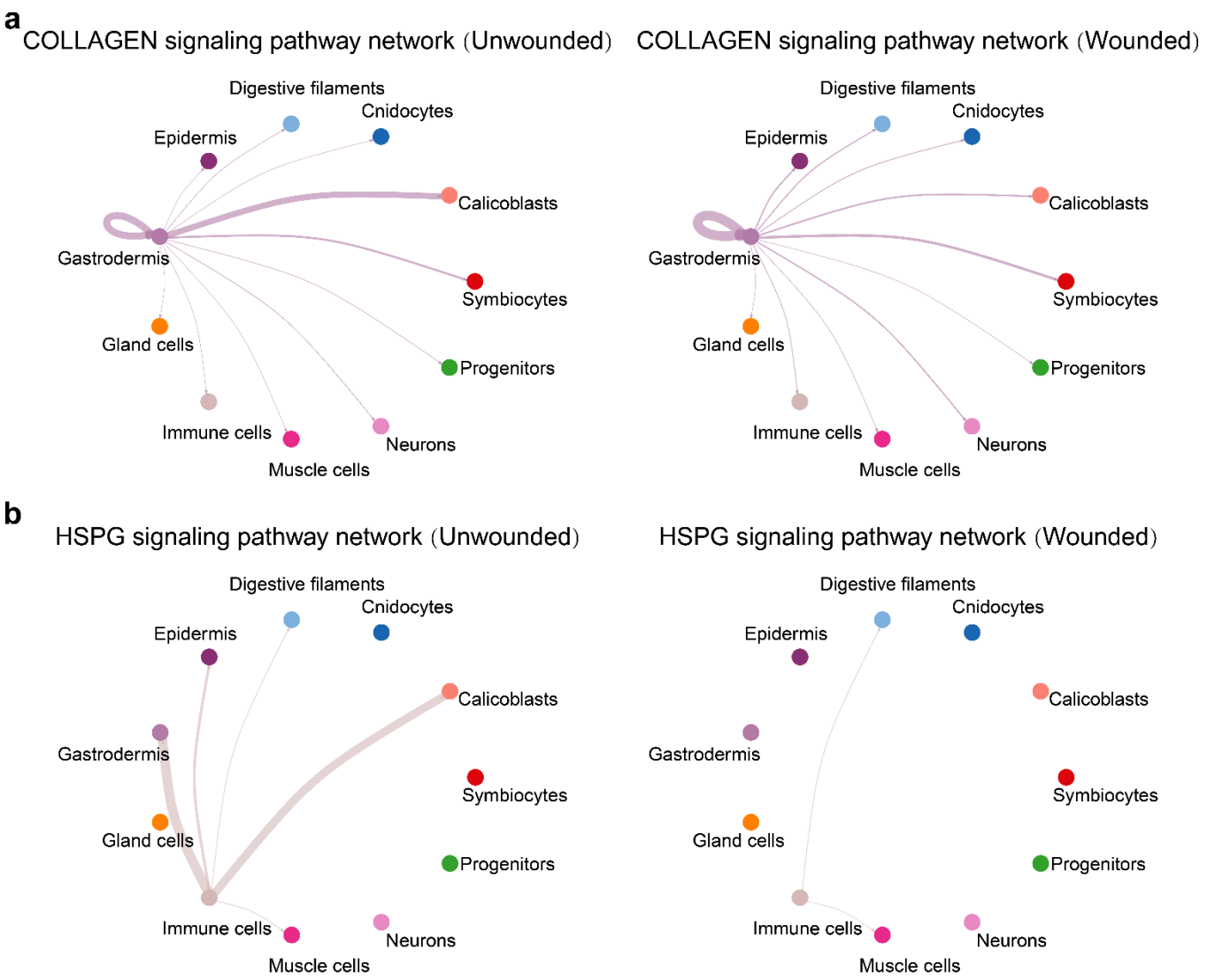
Supplementary Fig. 10. Cnetplot displays the remaining part of network linking significantly downregulated DEGs to enriched GO pathways.



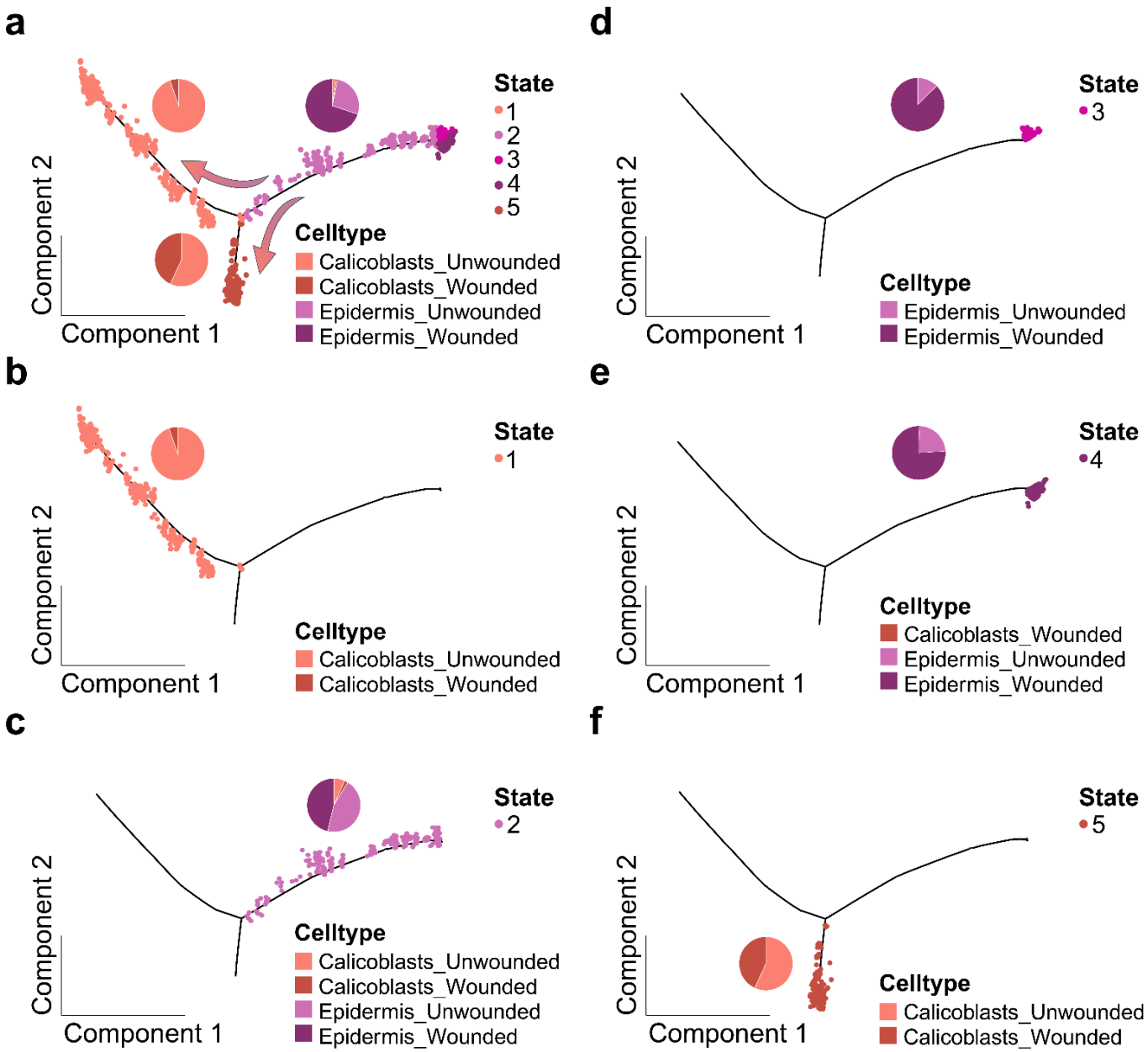
Supplementary Fig. 11. a, Pathway network of laminin signaling in different treatments. **b**, Pathway network of THBS signaling in different treatments. A thicker edge line indicates a stronger signal.



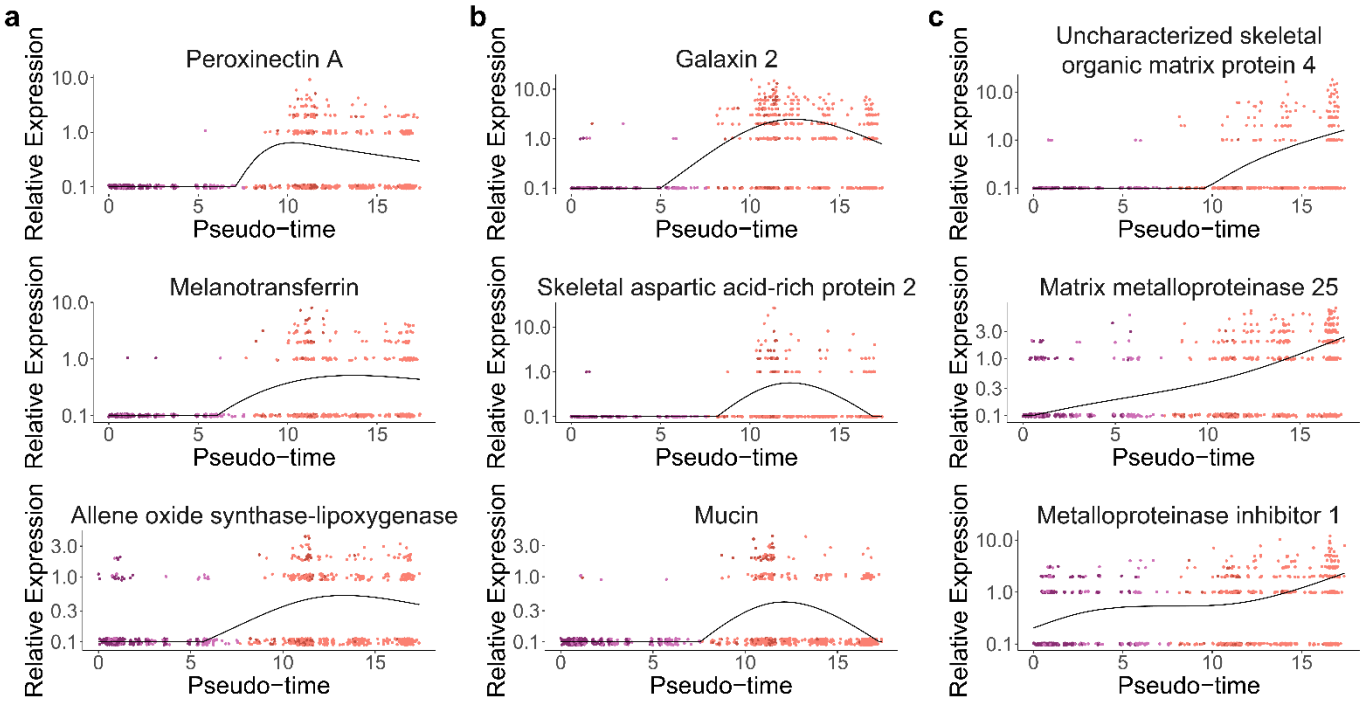
Supplementary Fig. 12. Increased (up-regulated) and decreased (down-regulated) in the communication probability of signaling ligand-receptor pairs from other cell types to calicoblasts in the wounded treatment compared to the unwounded treatment.



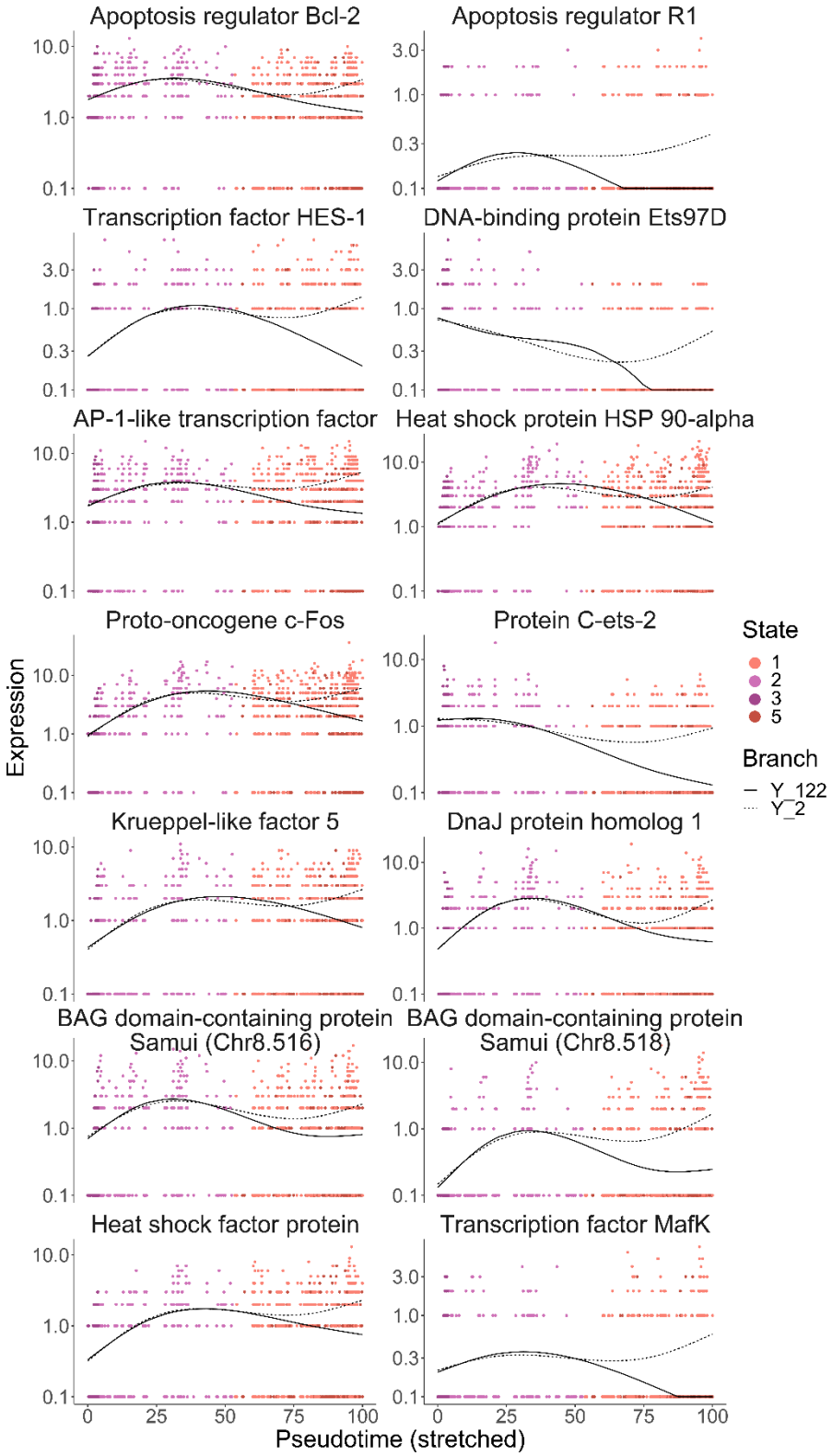
Supplementary Fig. 13. a, Pathway network of collagen signaling in different treatments. **b**, Pathway network of HSPG signaling in different treatments. A thicker edge line indicates a stronger signal.



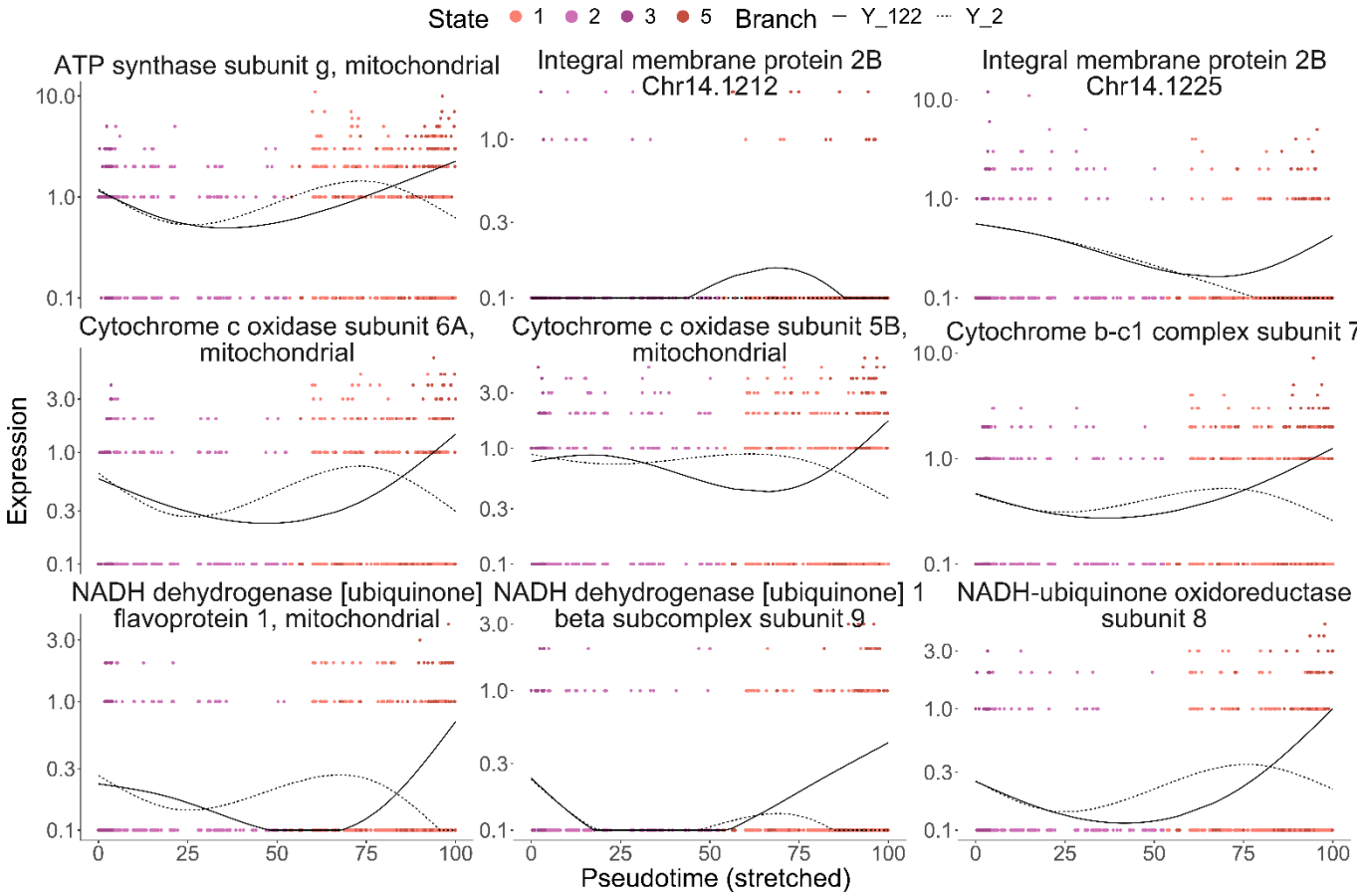
Supplementary Fig. 14. Pseudotime trajectory showing different states. Points along the trajectory are color-coded to represent cells belonging to different states. Pie charts depict the distribution of cells based on treatments and cell types along different branches of the trajectory. **a**, All states. **b-f**, State 1-5.



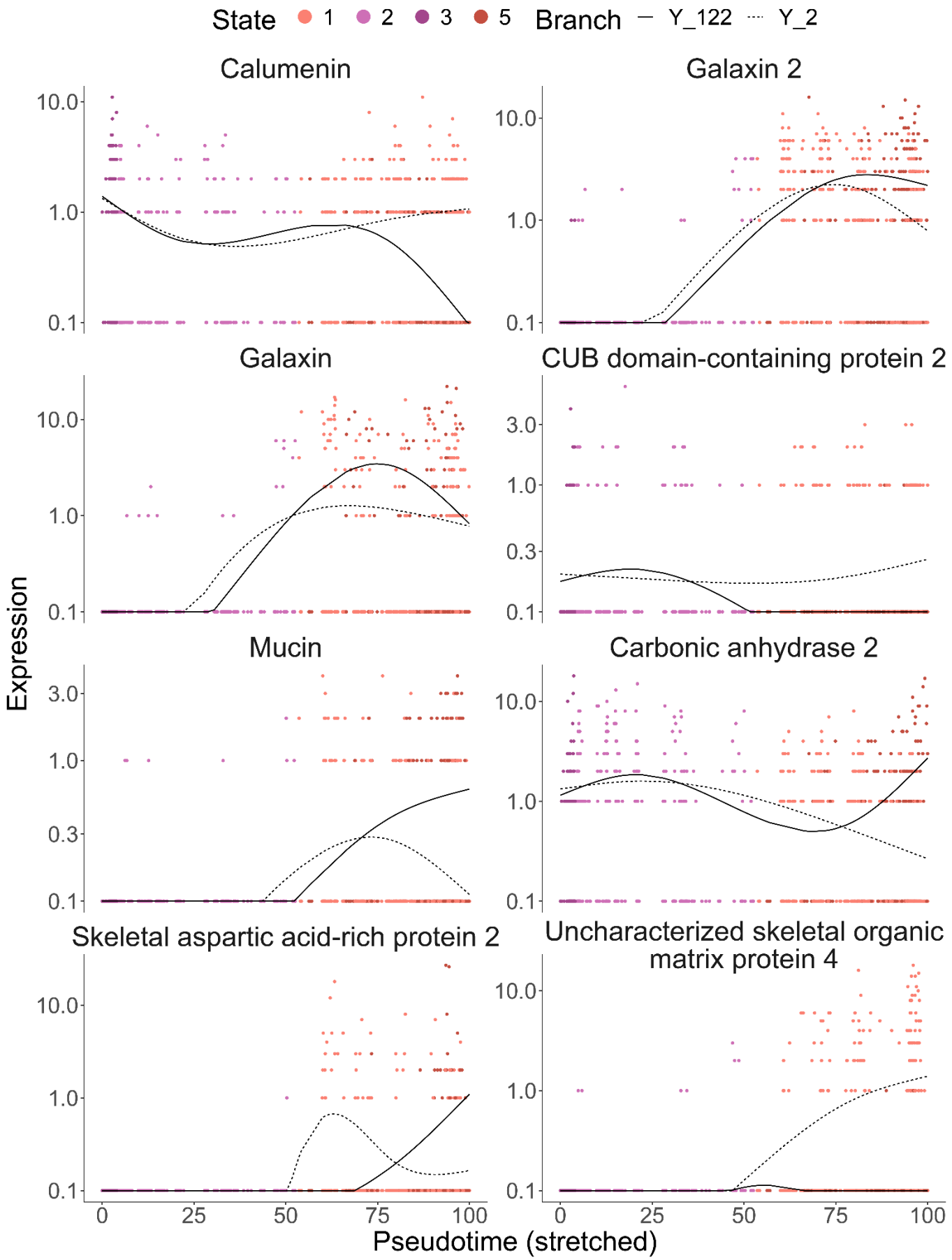
Supplementary Fig. 15. Pseudotime analysis of other important genes based on cell types in Fig. 5e. a, Genes associated with immune response in Cluster 1. **b**, Genes related to biomineralization in Cluster 3. **c**, Genes associated with biomineralization in Cluster 4.



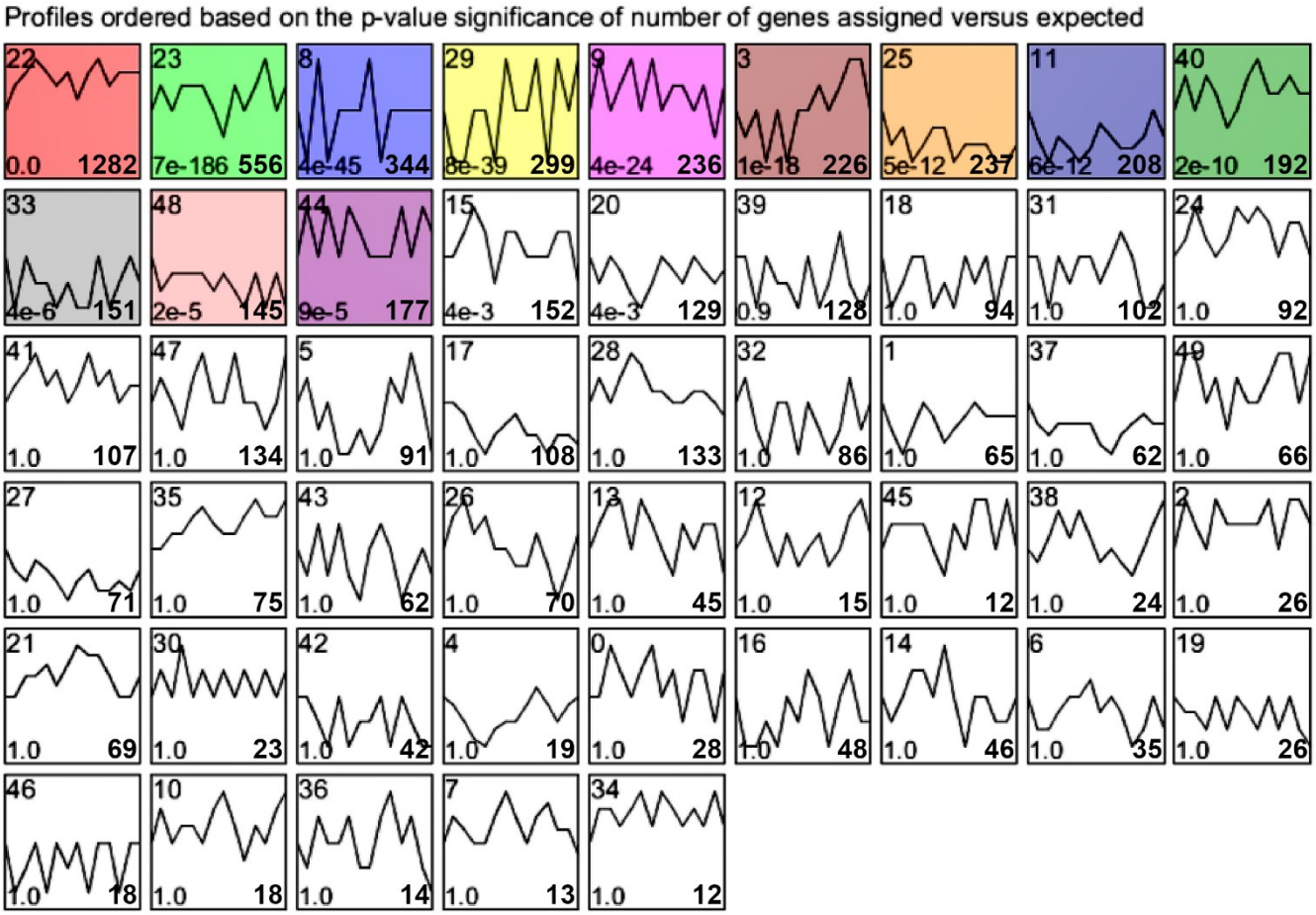
Supplementary Fig. 16. Differential expression analysis of genes enriched in two GO terms, protein stabilization, and apoptosis signaling pathways in Cluster 3 (labeled as "g" in Fig. 5), across different cell fates.



Supplementary Fig. 17. Differential expression analysis of genes enriched in three GO terms—proton motive force-driven ATP synthesis, transmembrane transporter complex, and regulation of cell population proliferation—in Cell fate 2 (labeled as "g" in Fig. 5), across various cell fates.



Supplementary Fig. 18. Differential expression analysis of genes related to biomineralization in different cell fates, as indicated in Fig. 5g.



Supplementary Fig. 19. Clustering results obtained from temporal expression patterns of DEGs in bulk RNA-seq data by STEM. For each cluster, the upper-left corner of each subplot indicates the cluster number, the lower-left corner shows the statistical significance (p-value), and the lower-right corner displays the number of DEGs included in each cluster.