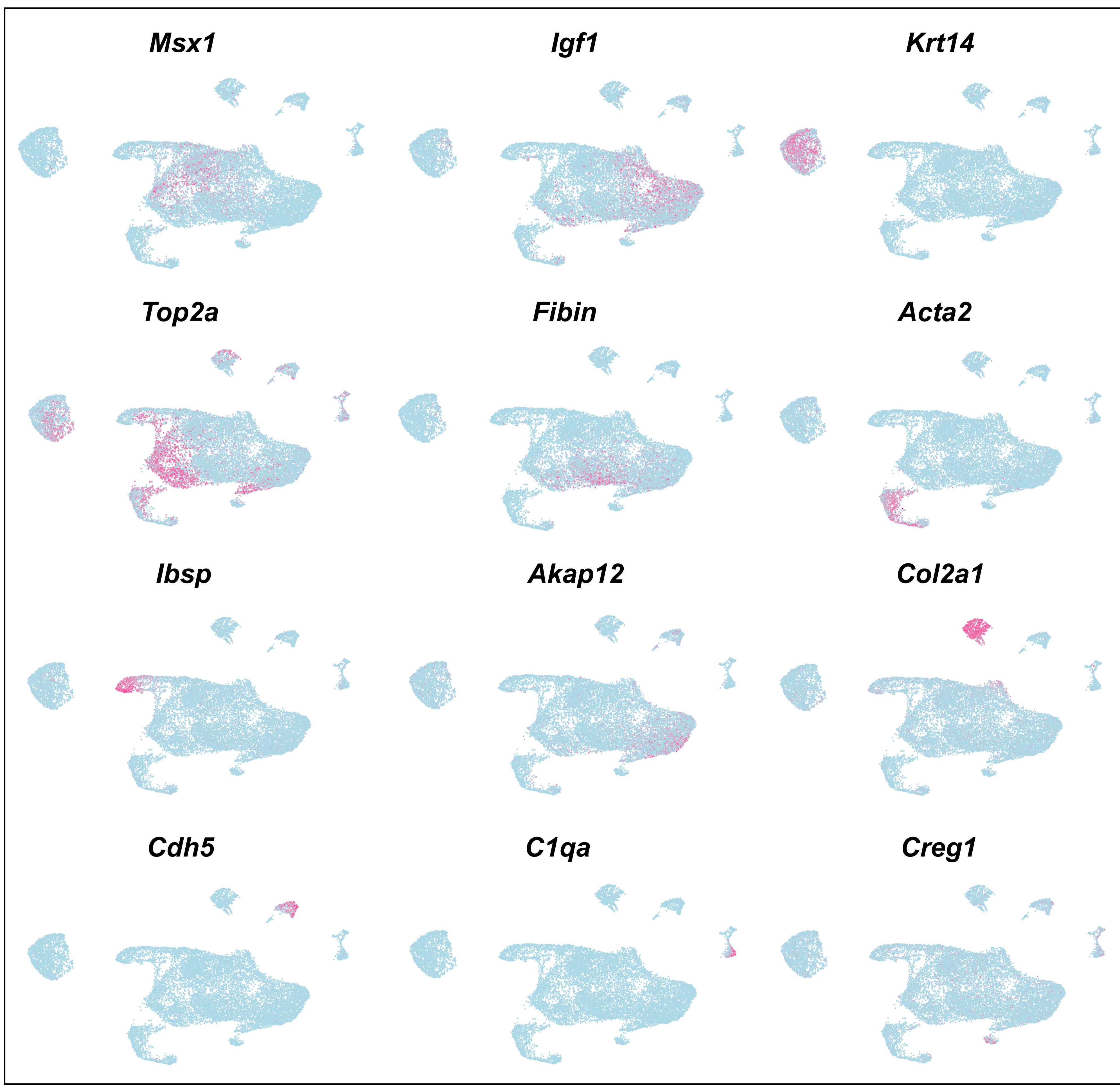
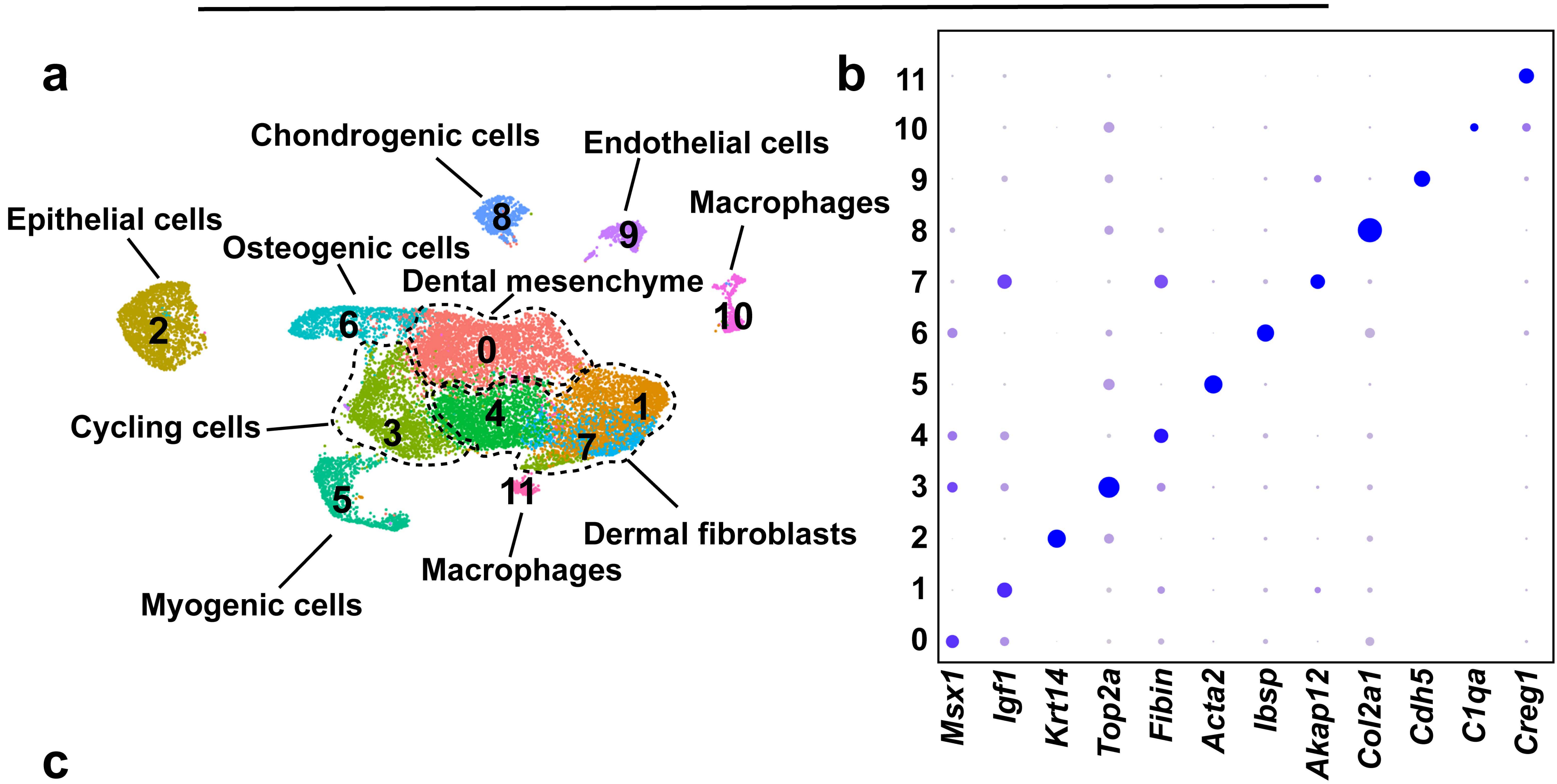


Spatiotemporal single-cell regulatory atlas reveals neural crest lineage diversification and cellular function during tooth morphogenesis

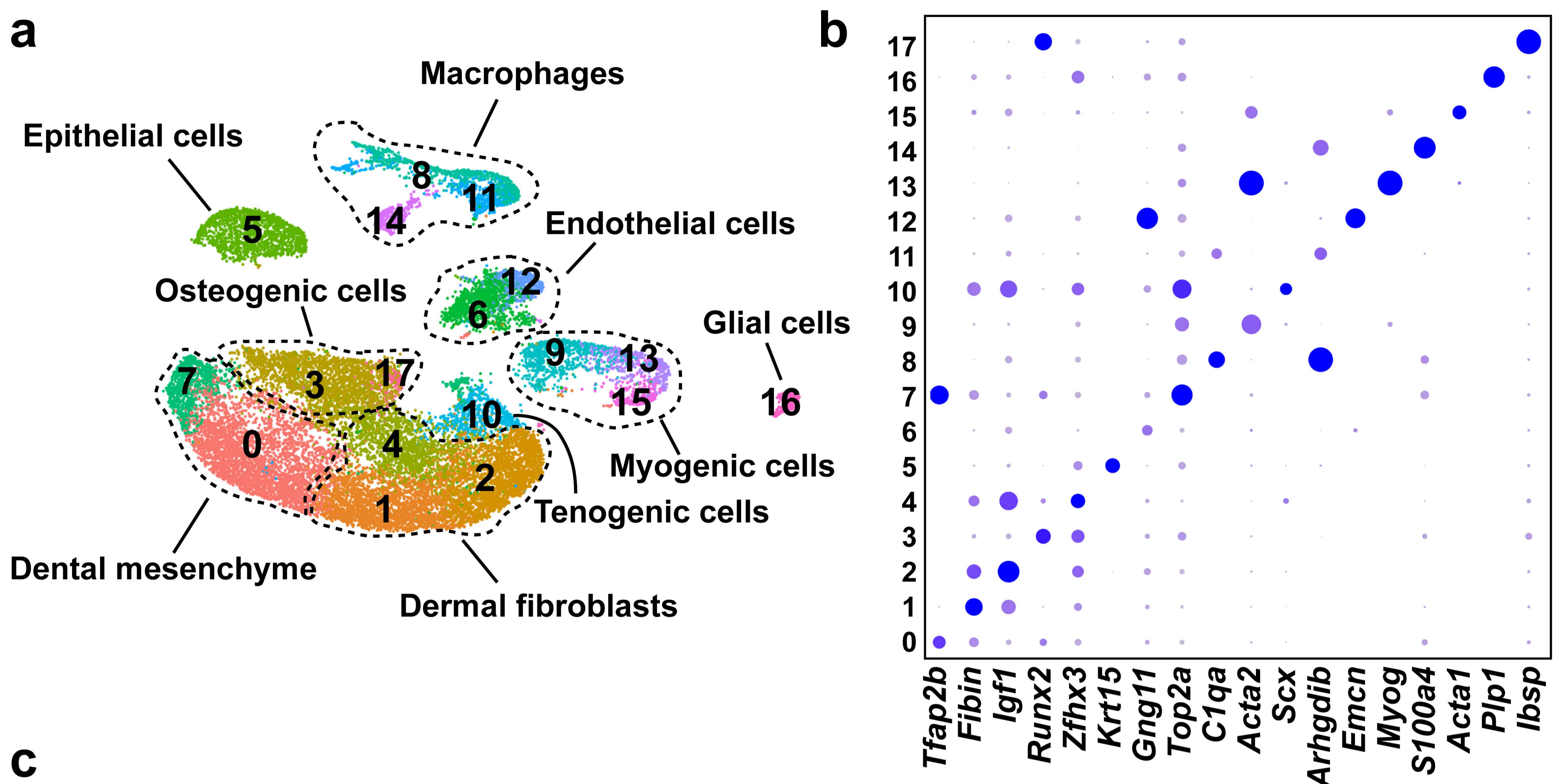
This document includes:

Supplementary Fig. 1 to Supplementary Fig. 12

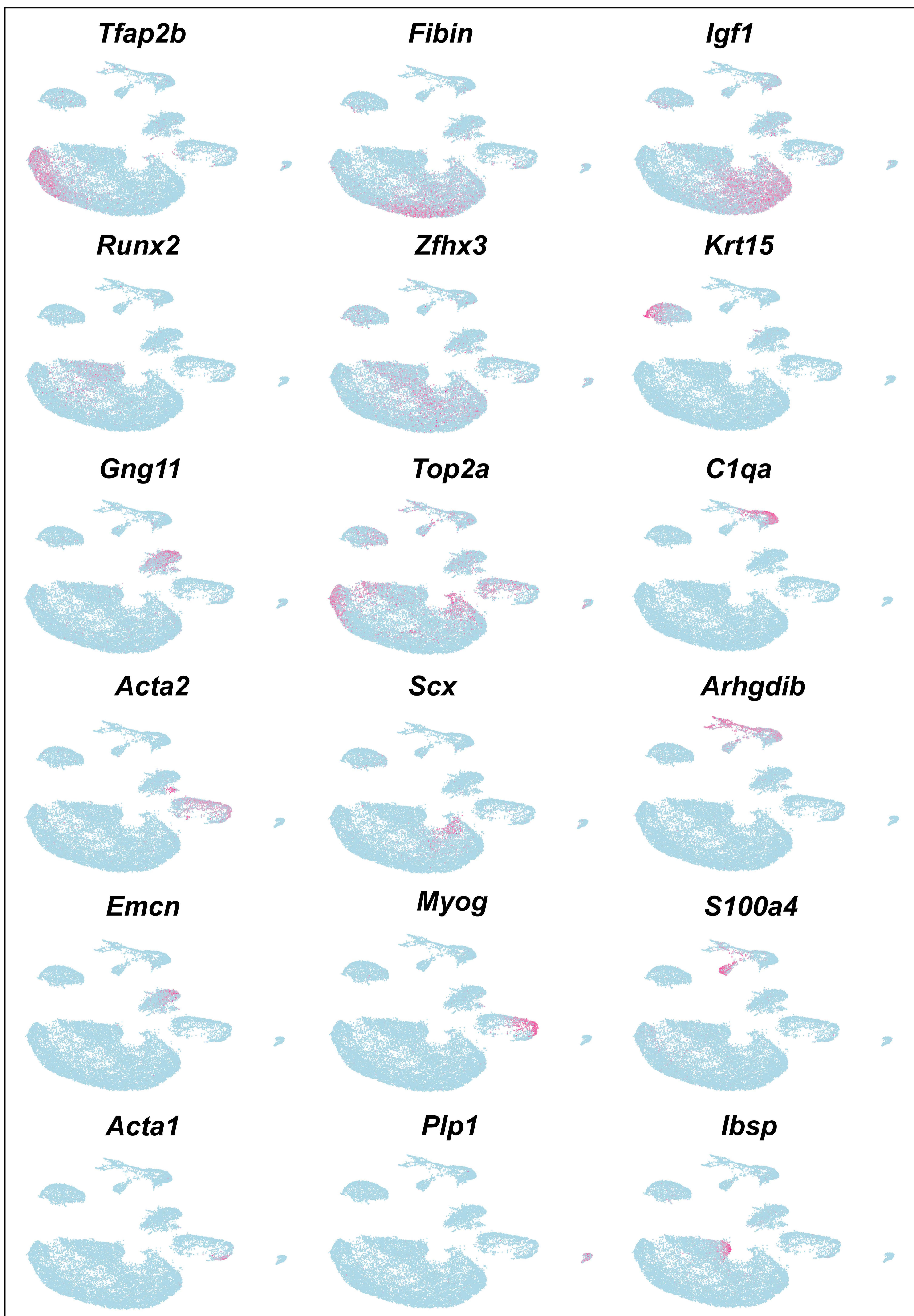
E13.5



Supplementary Fig. 1 Cell populations in the mouse molar and its surrounding tissue at E13.5. **a** UMAP plot of cell types in the mouse molar and its surrounding tissue at E13.5. Cell types were annotated based on their expression of cell type-specific marker genes; **b** Dotplot of signature genes in the cell populations shown in **a**. **c** Feature plot of markers genes shown in **b**.

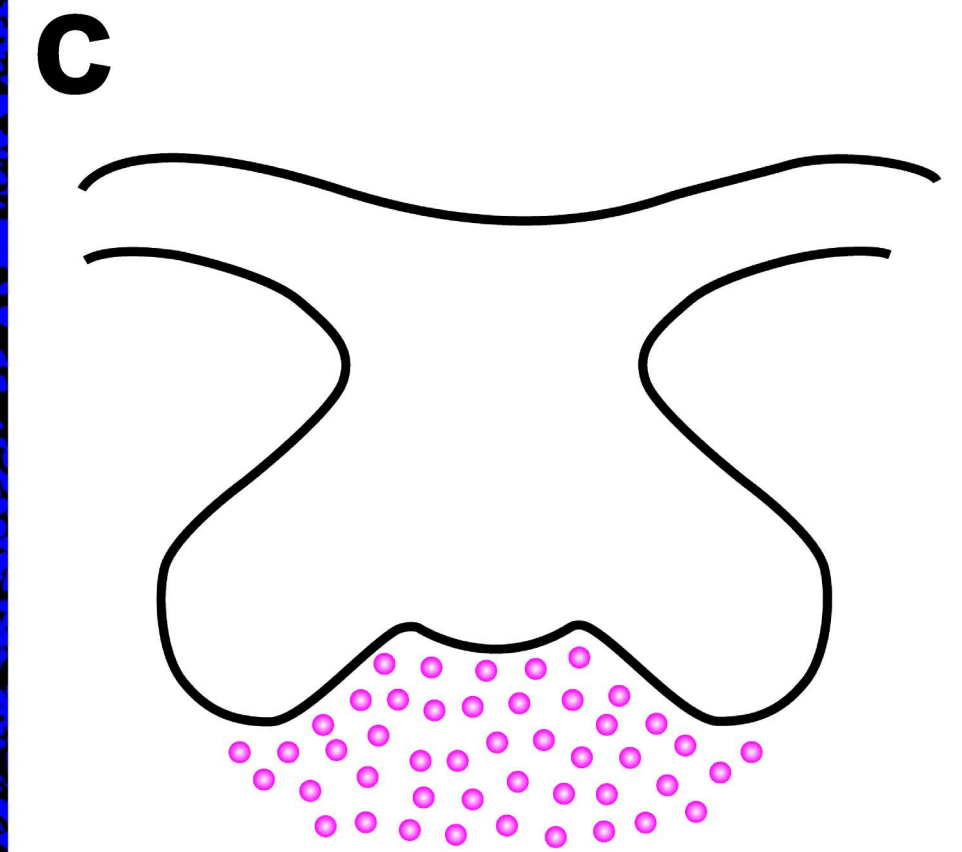
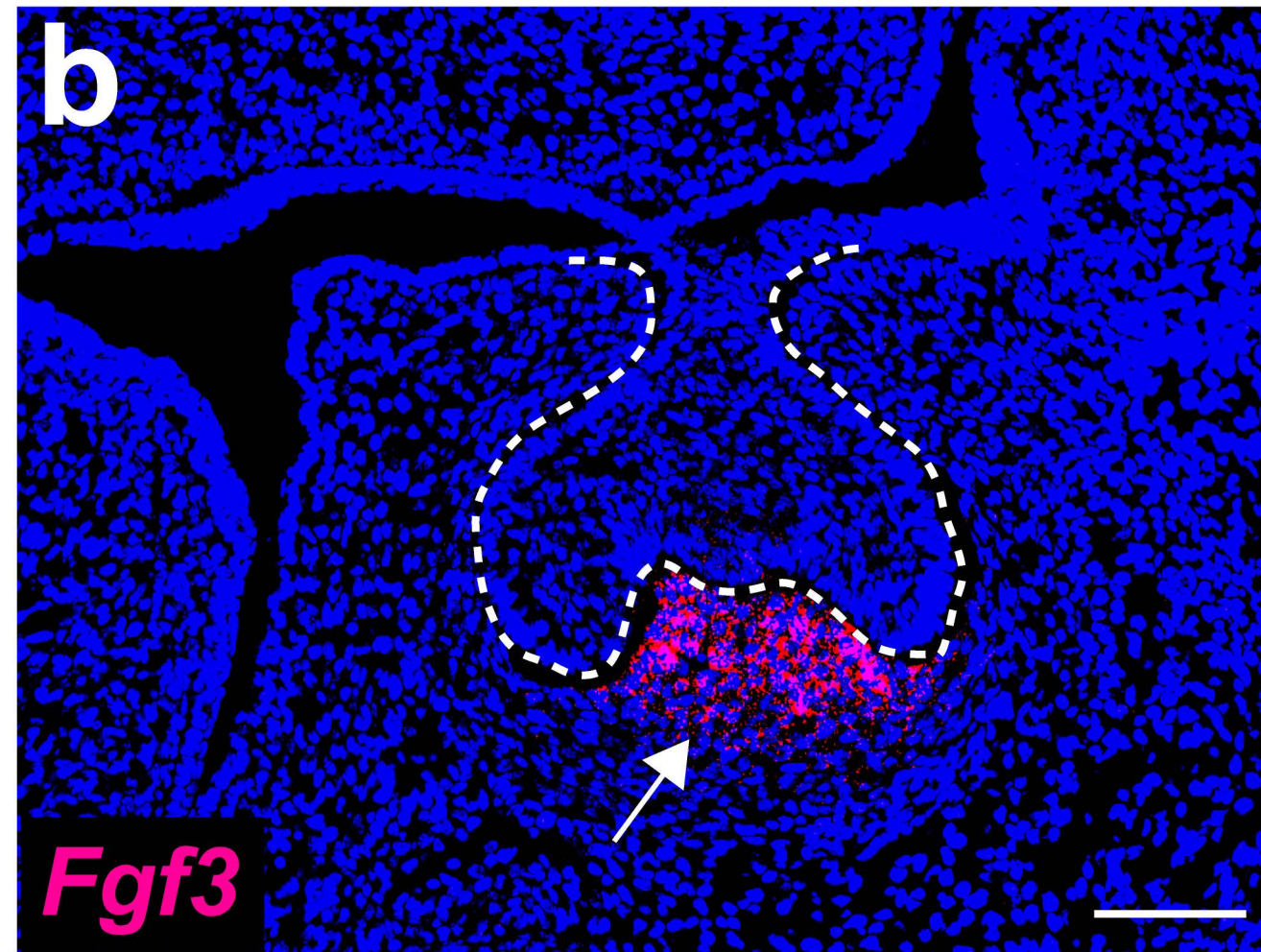


c

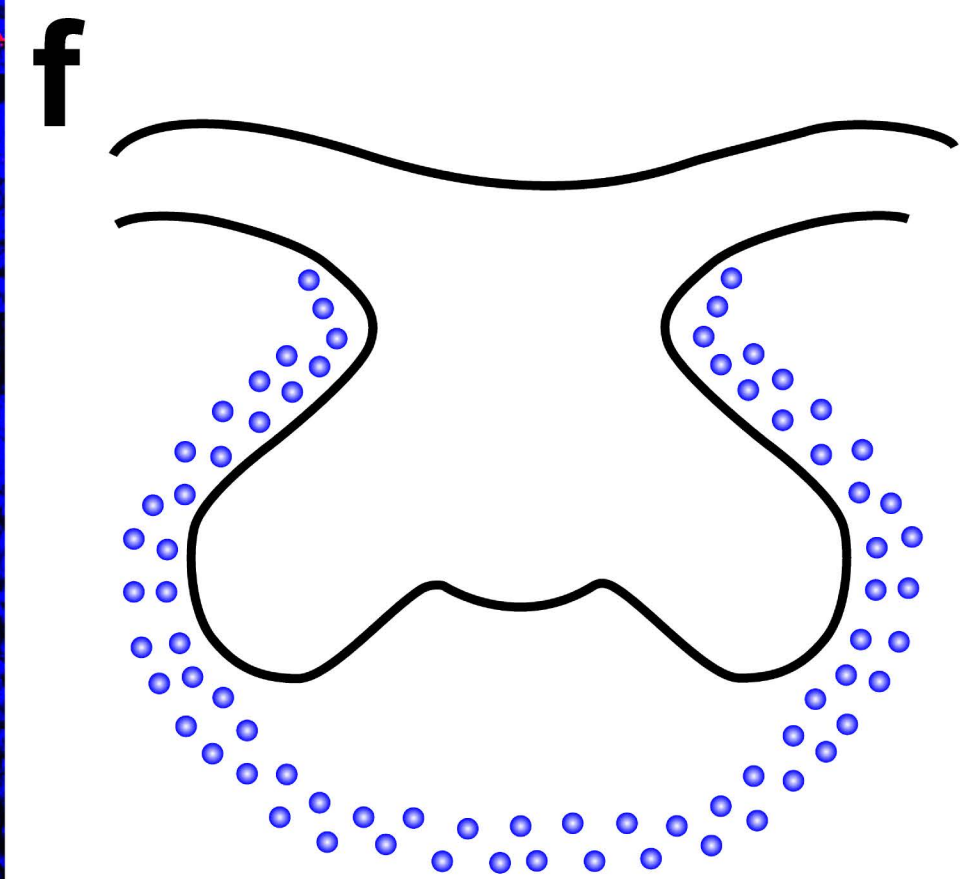
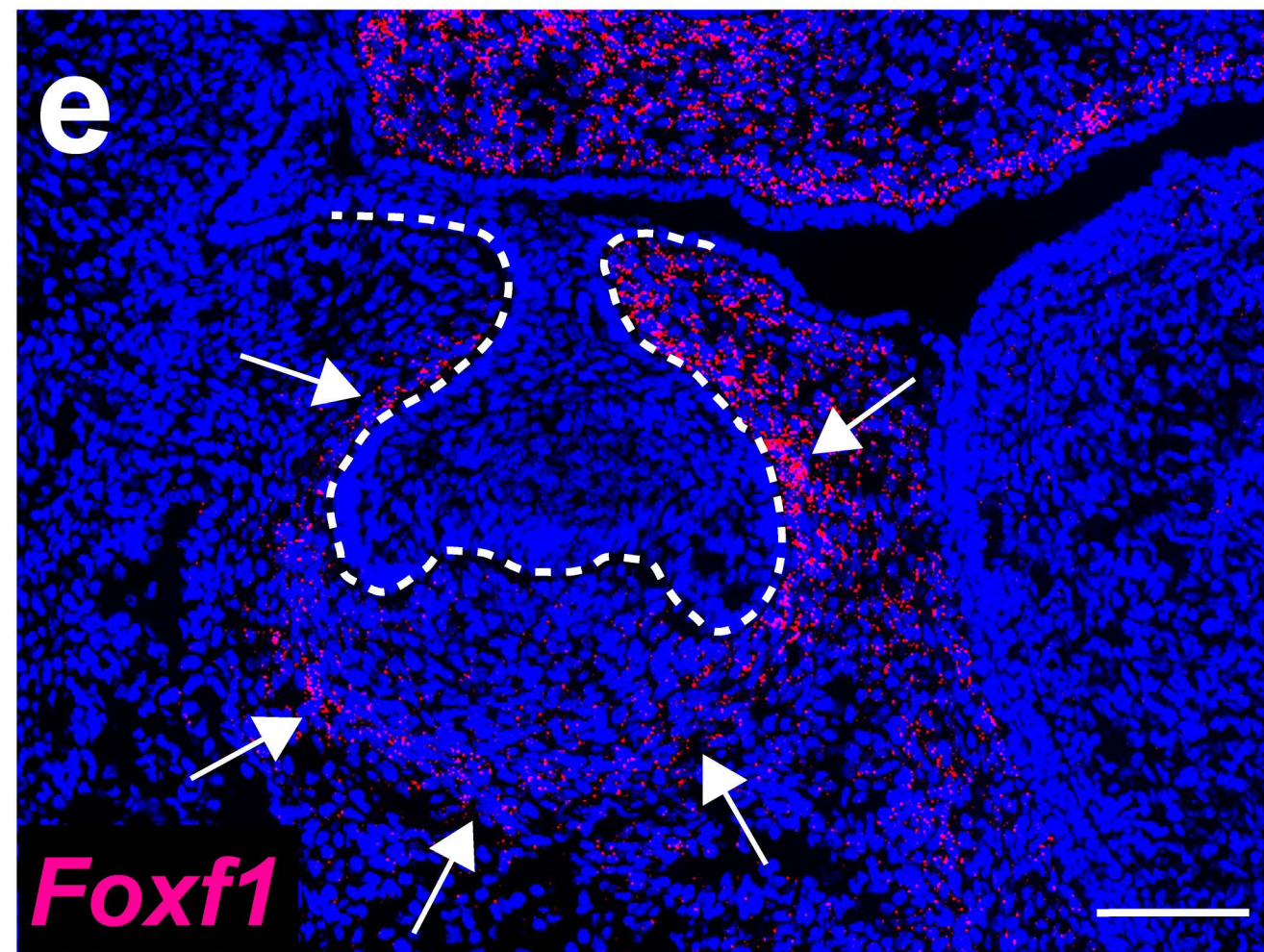
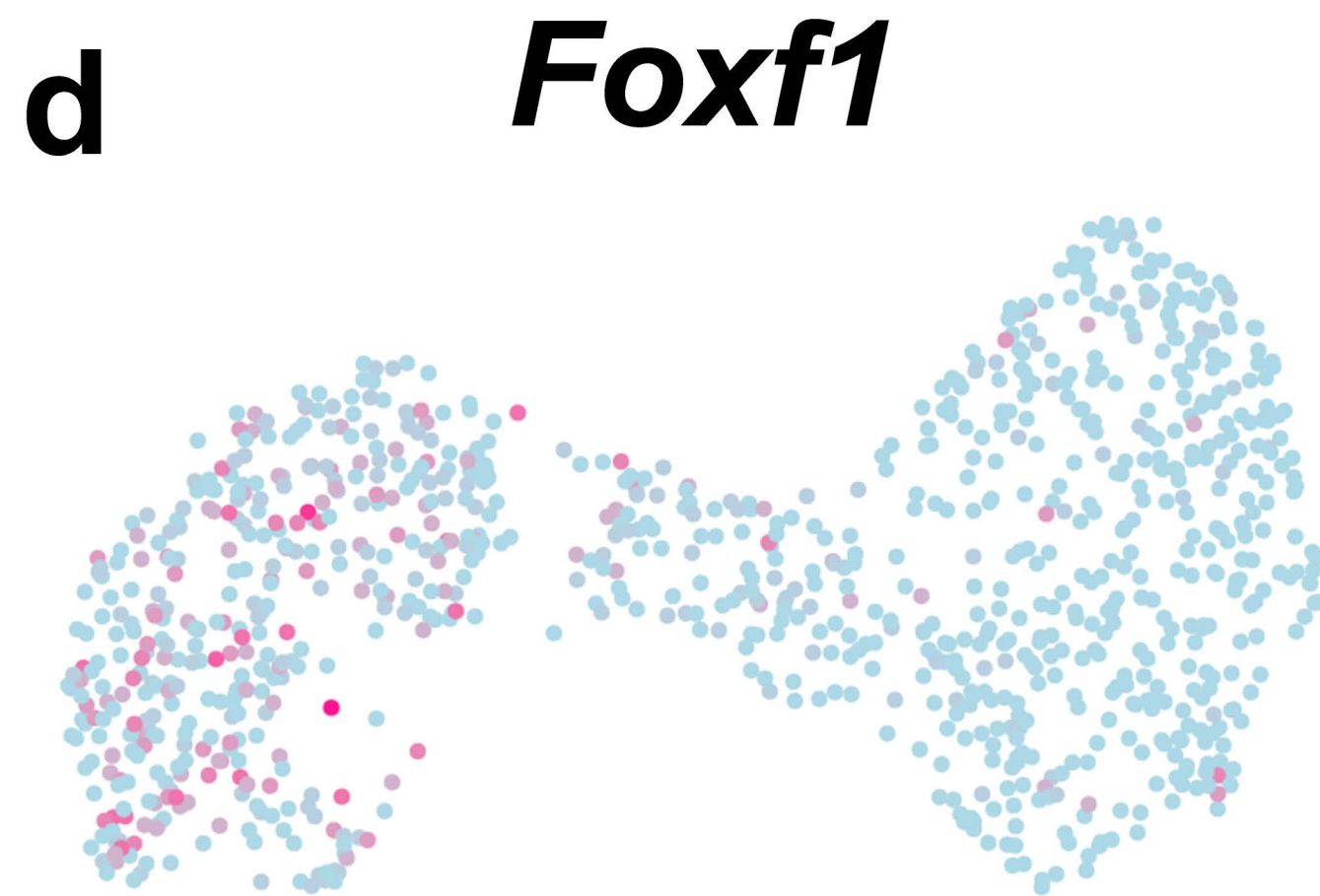


Supplementary Fig. 2 Cell populations in the mouse molar and its surrounding tissue at E14.5. a UMAP plot of cell types in the mouse molar and its surrounding tissue at E14.5. **b** Dotplot of signature genes in the cell populations shown in **a**. **c** Feature plot of markers genes shown in **b**.

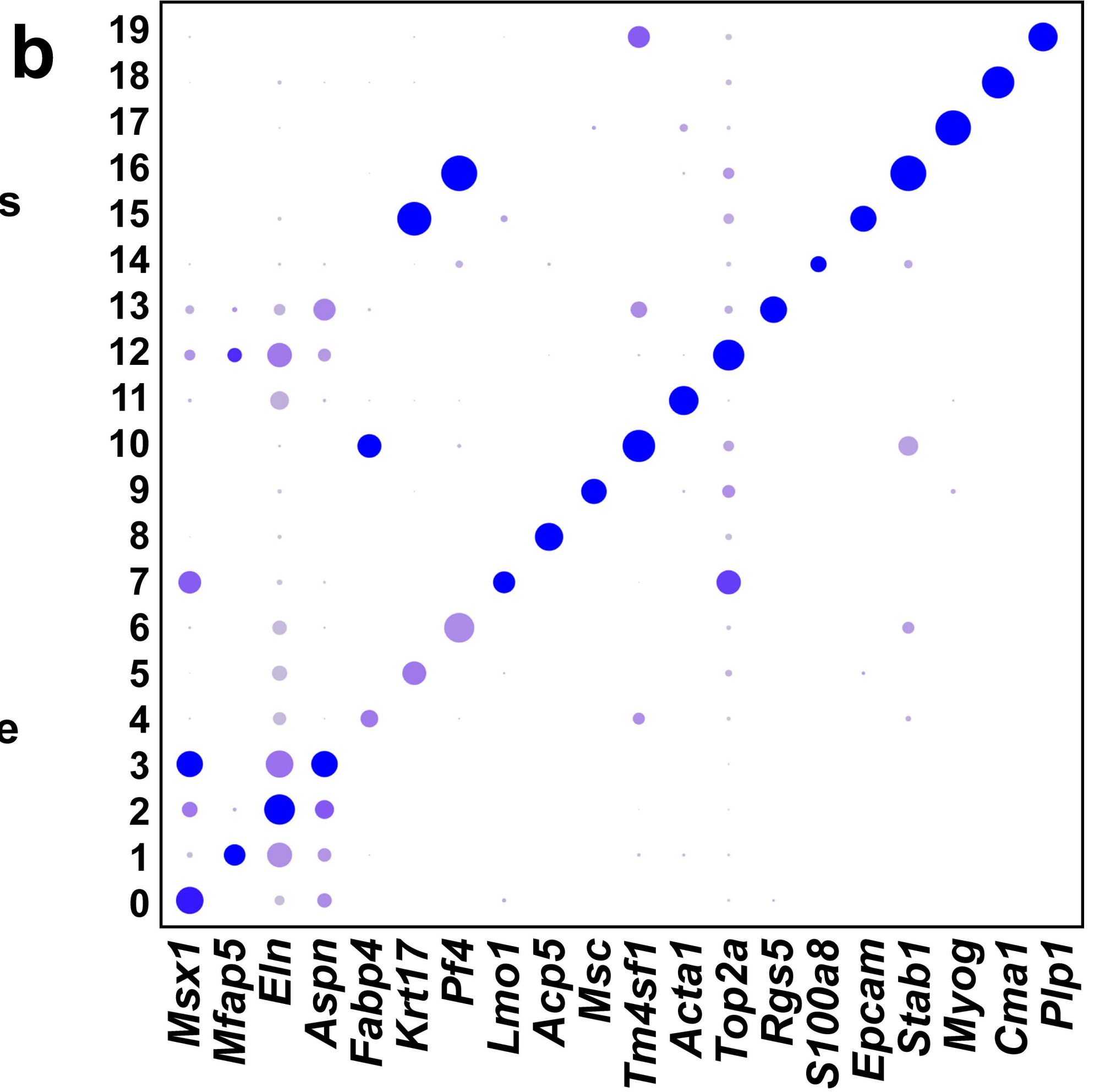
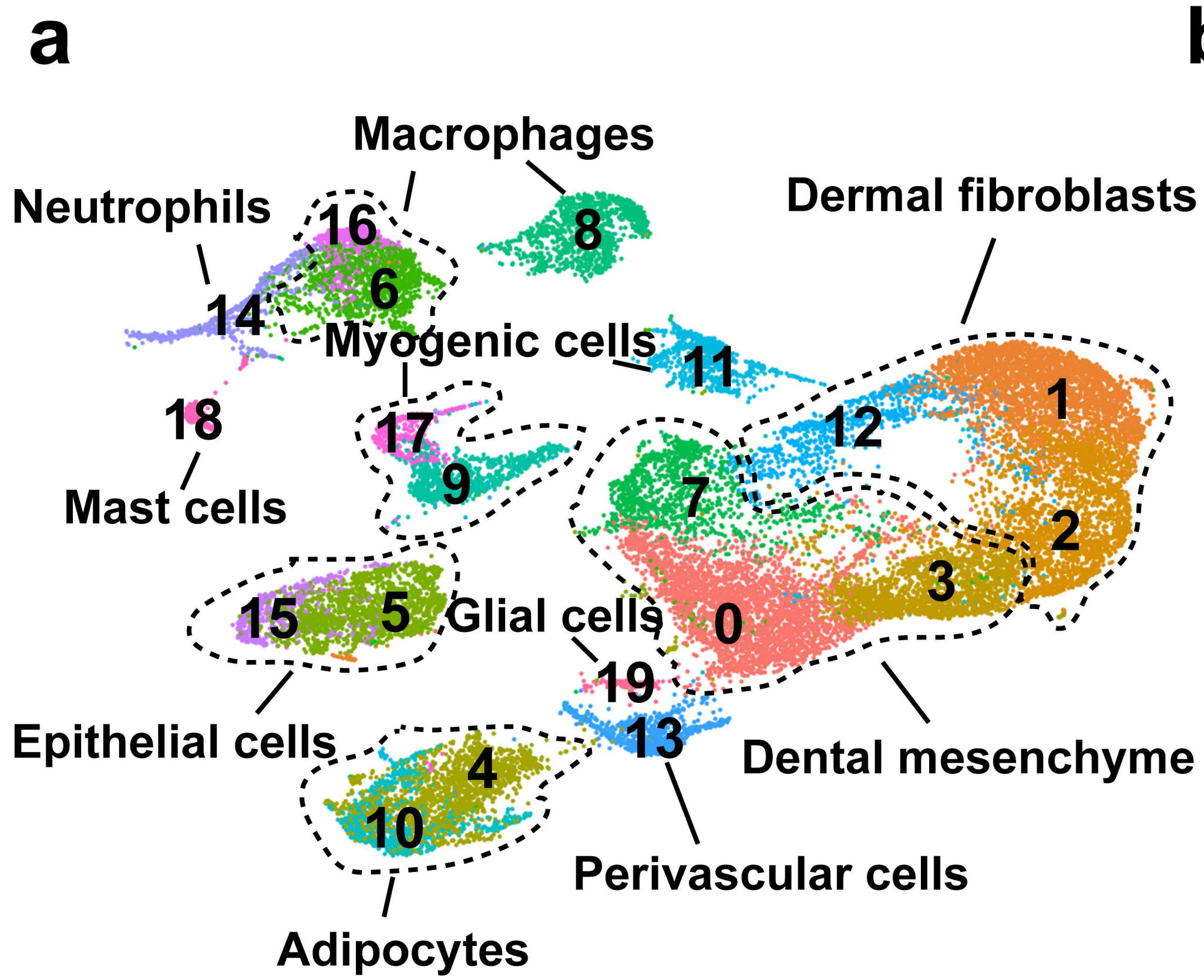
Dental papilla



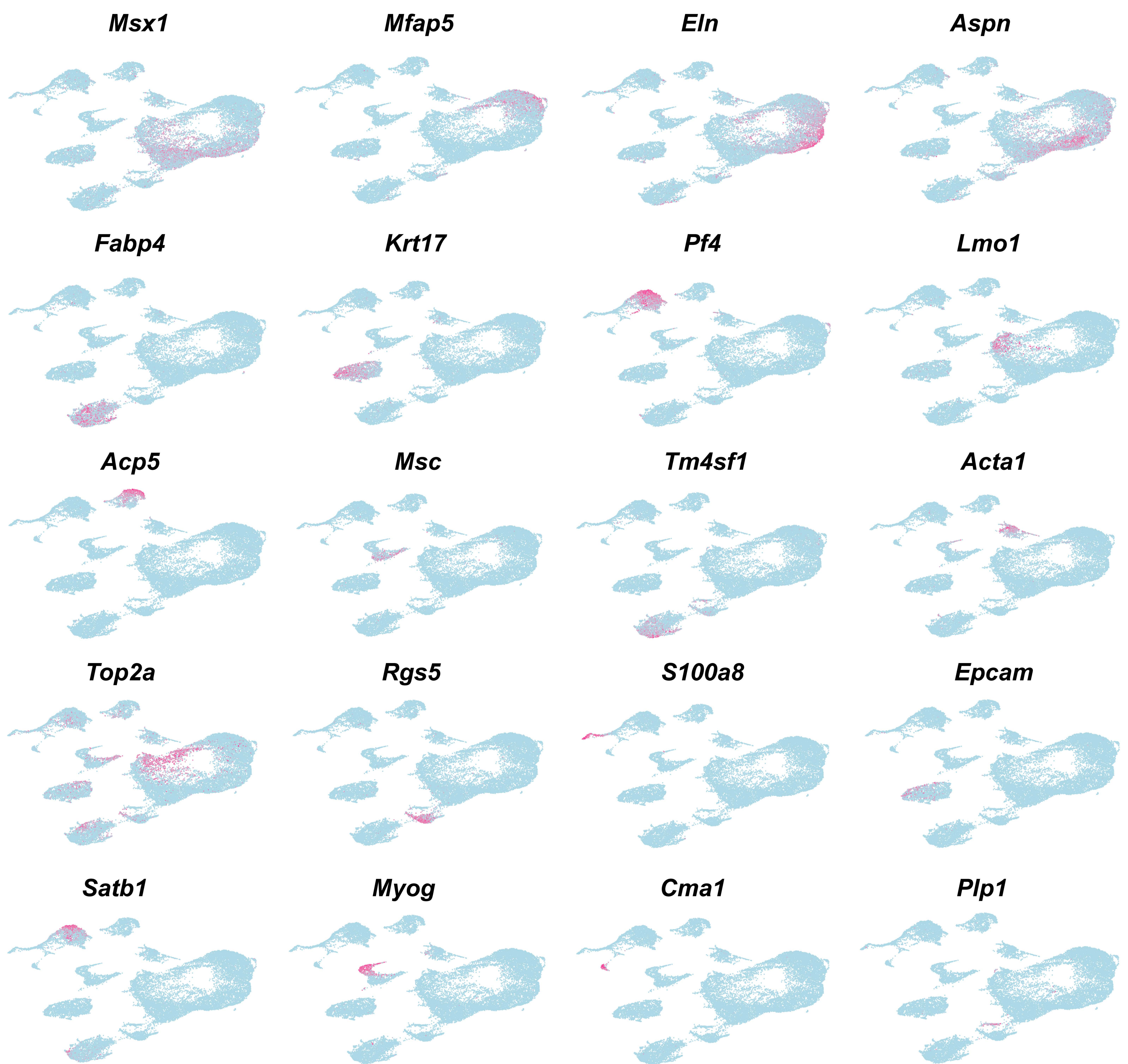
Dental follicle



Supplementary Fig. 3 Cellular domain of the dental mesenchyme at E14.5. **a, b** Feature plot and RNAscope staining of *Fgf3* in the dental papilla (n=3). **c** Cellular domain of the dental papilla in the mouse molar at E14.5. **d, e** Feature plot and RNAscope staining of *Foxf1* in the dental follicle (n=3). **f** Cellular domain of the dental follicle in the mouse molar at E14.5. White dotted lines outline the dental epithelial cells in the mouse molar. White arrows point to the positive signals. Scale bars, 100 μ m.

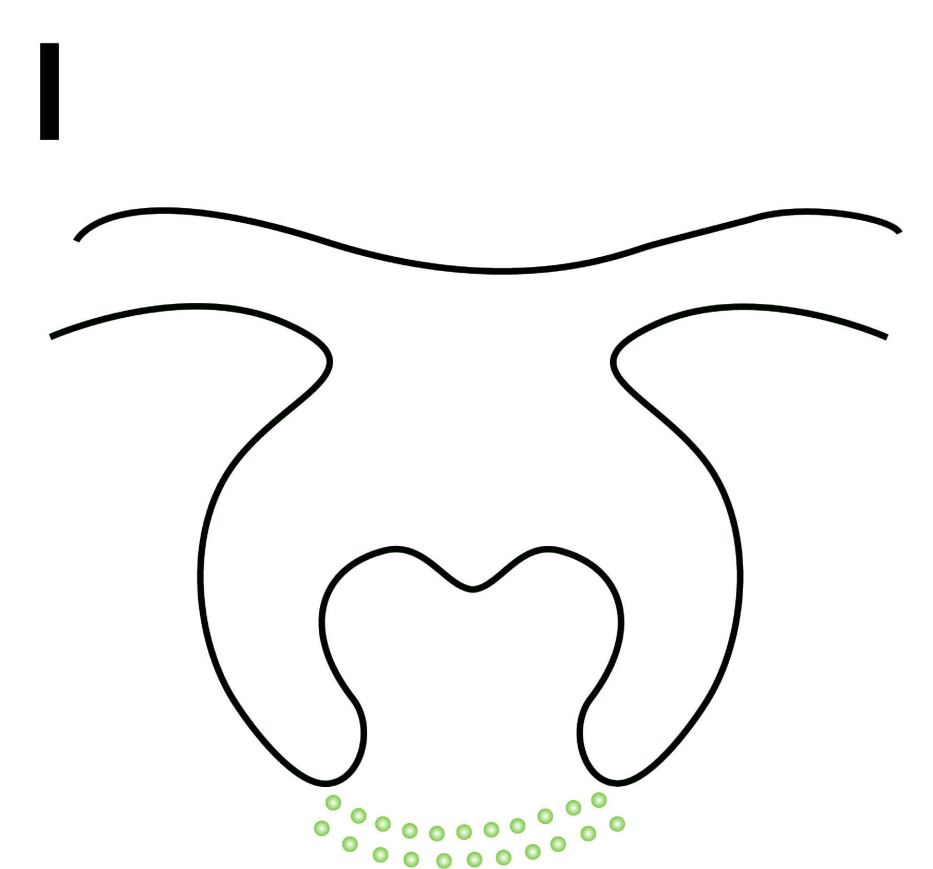
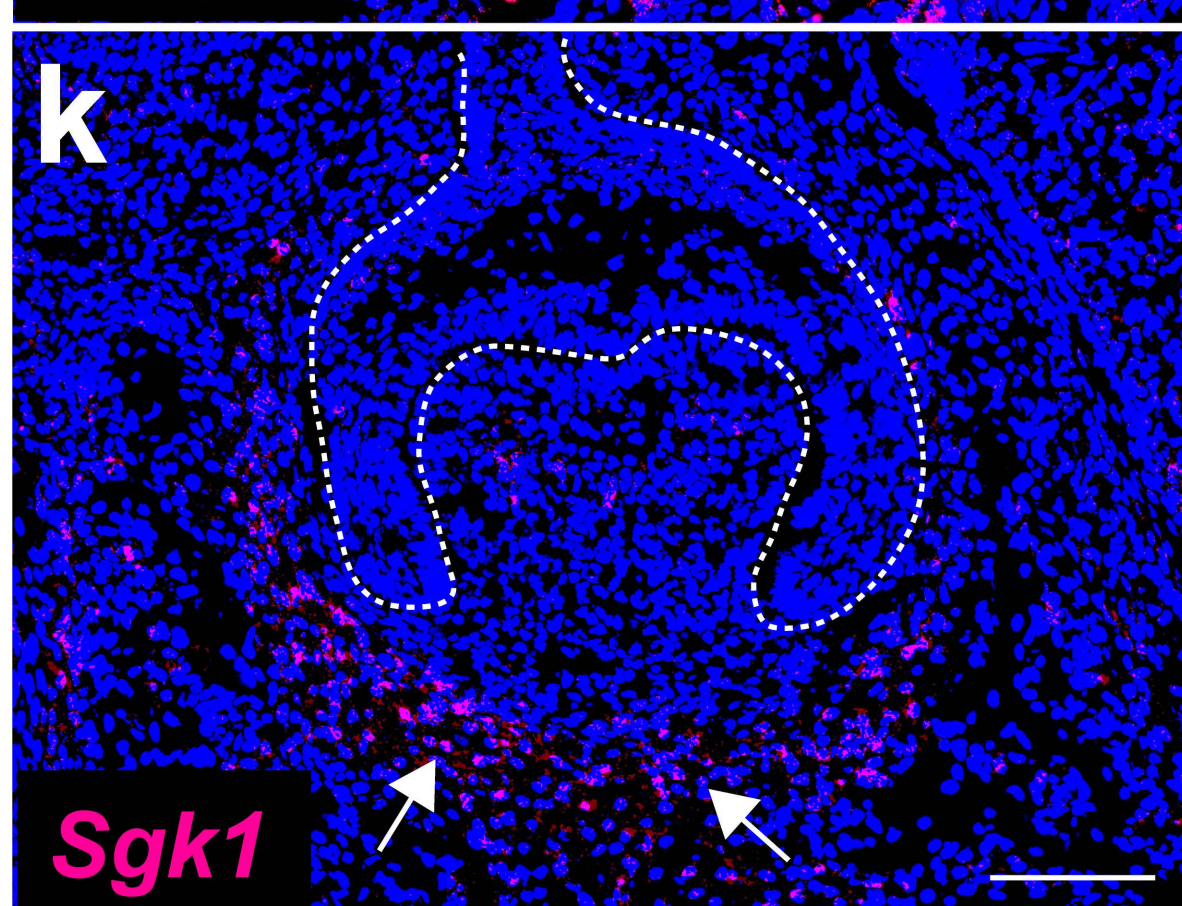
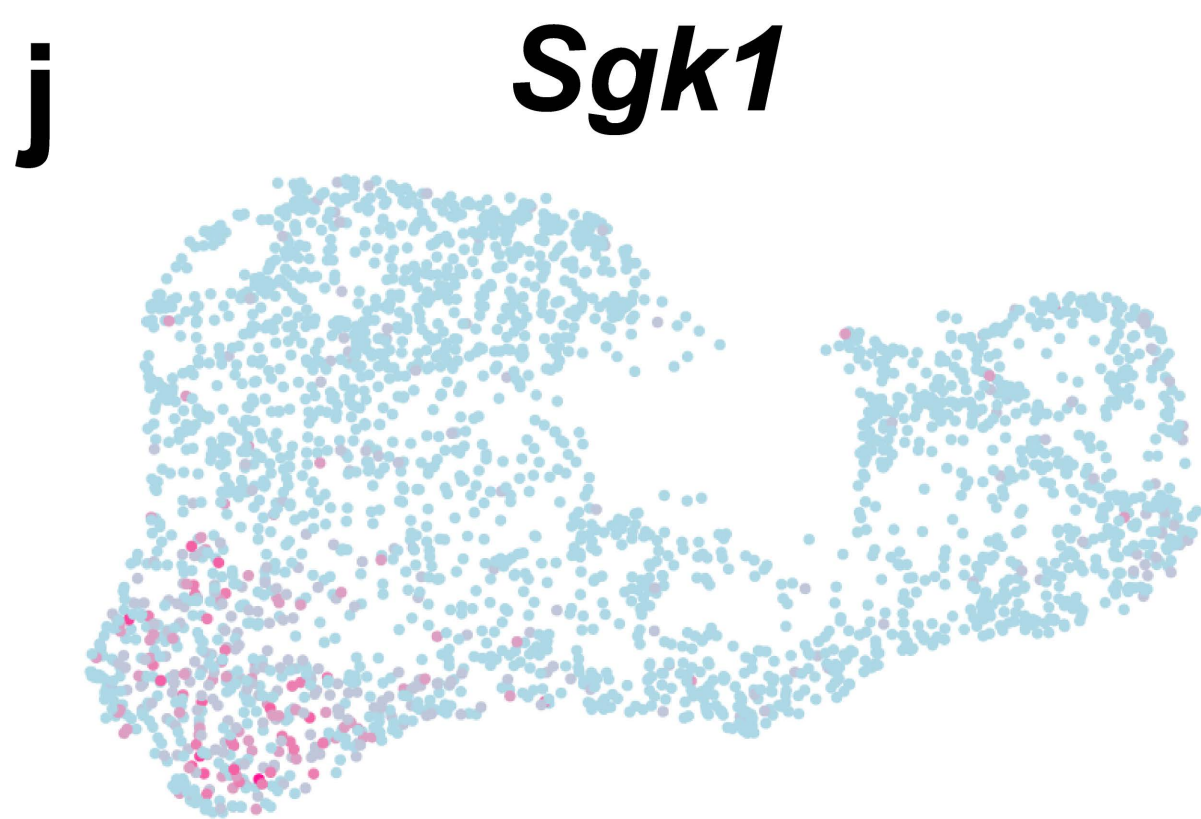
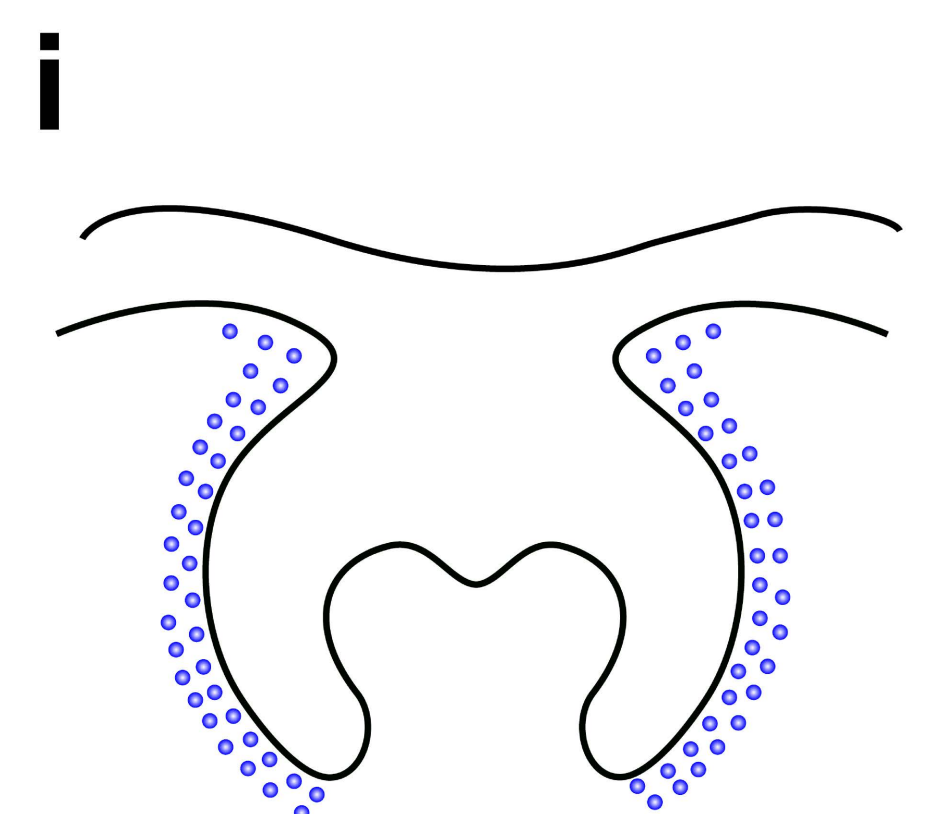
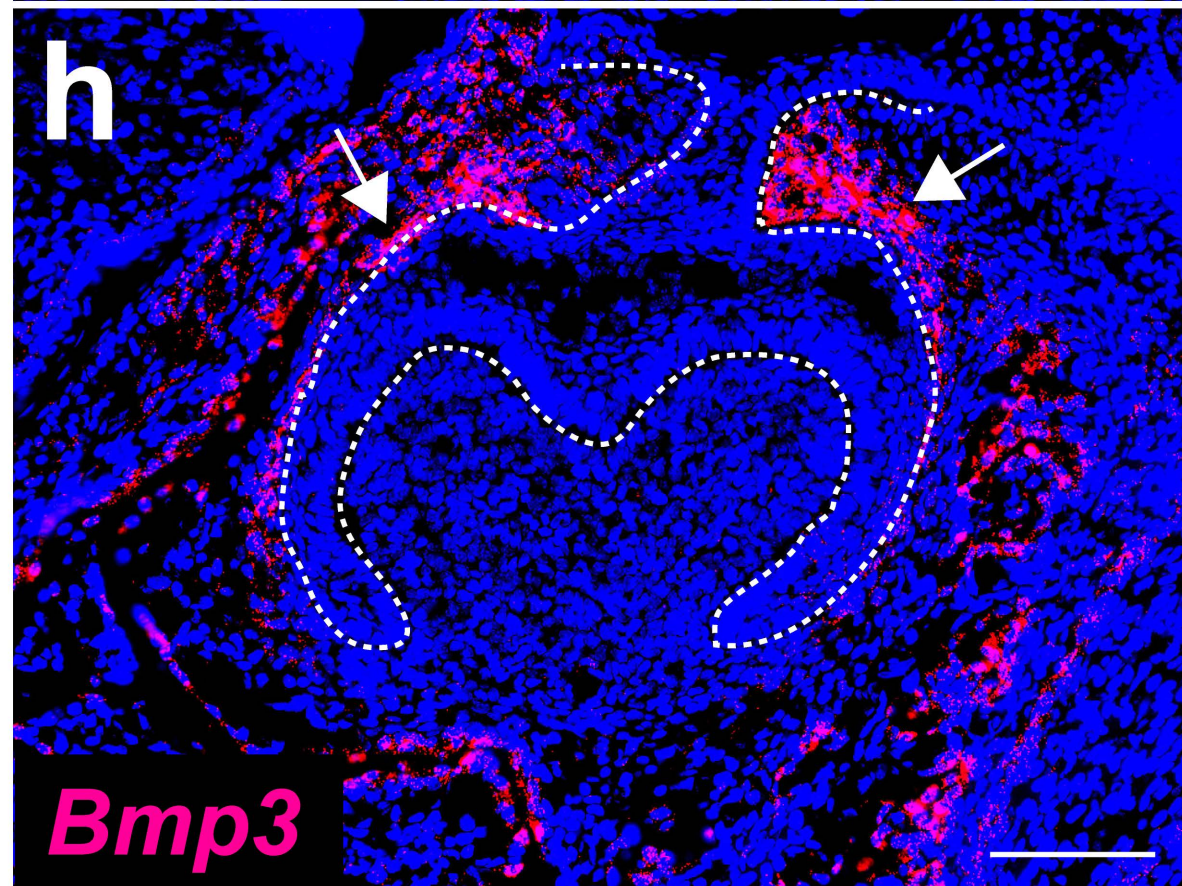
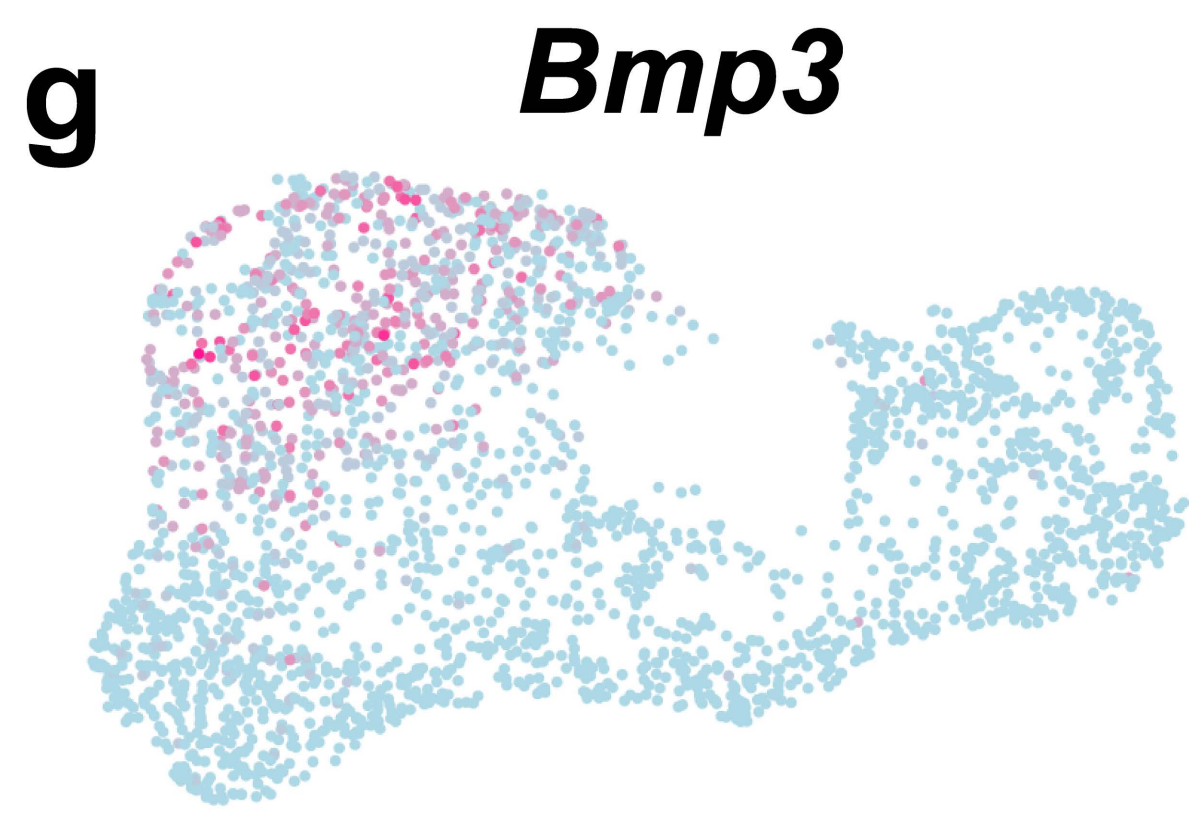
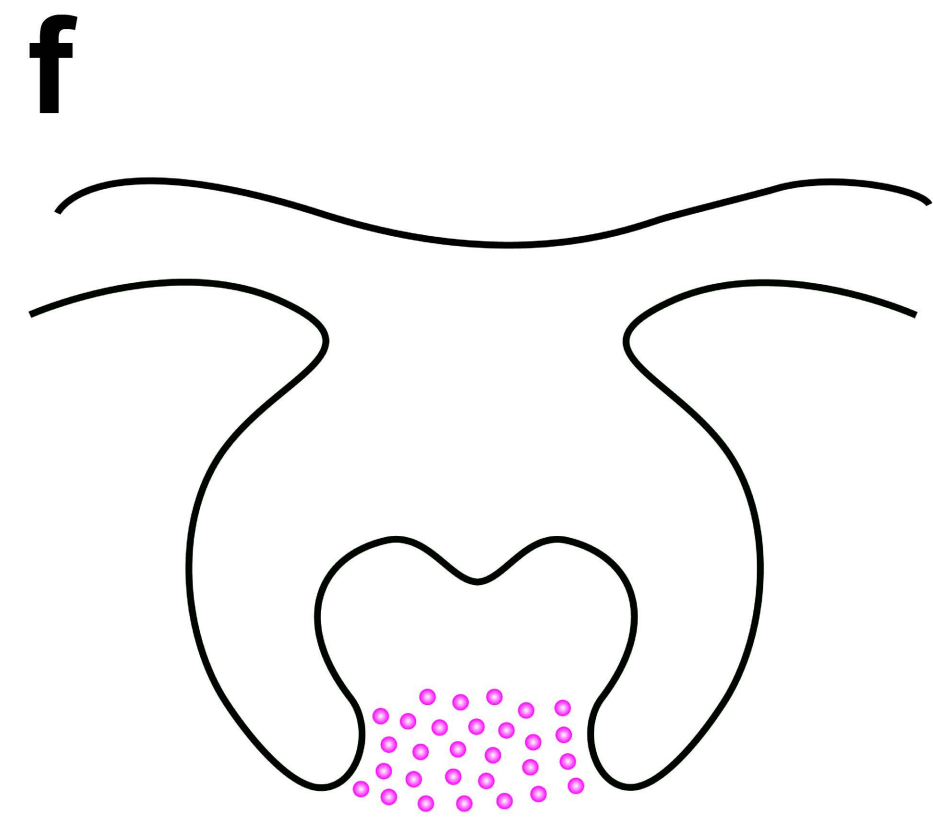
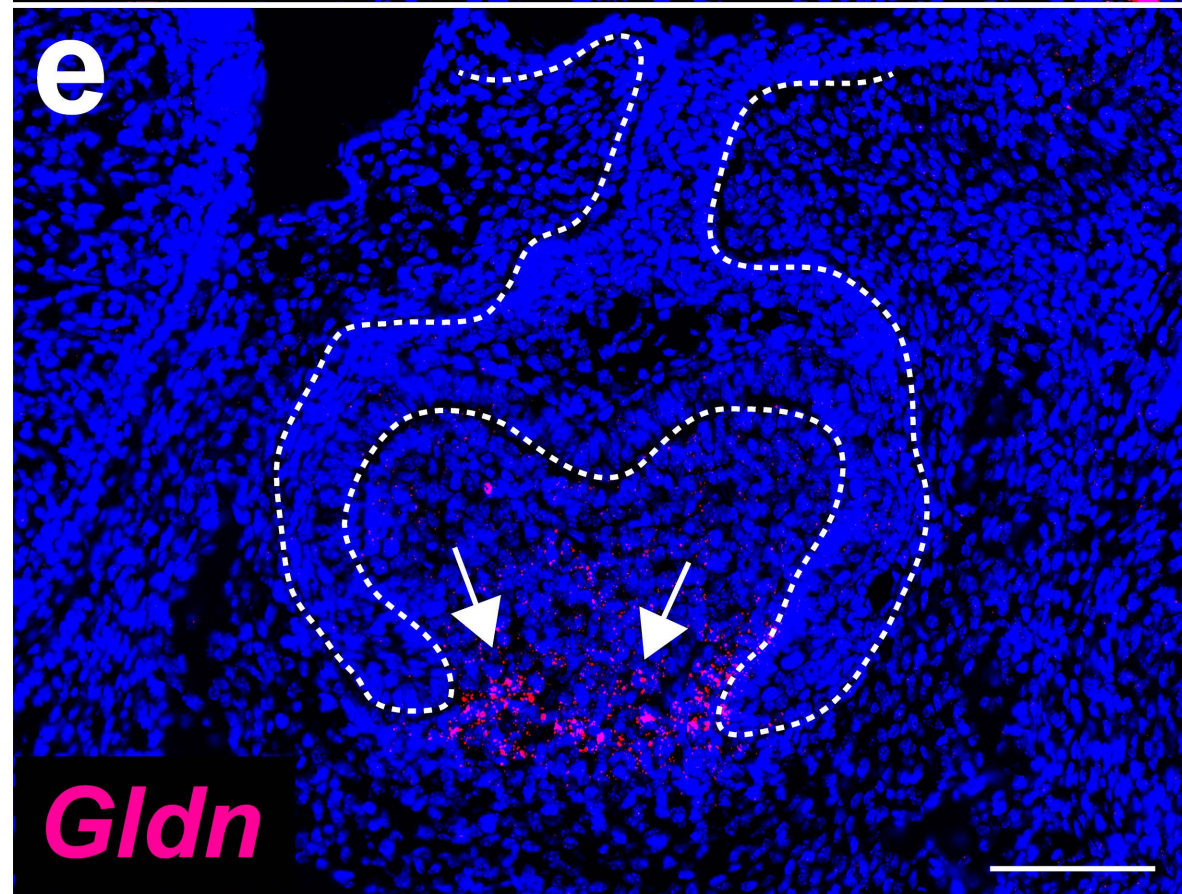
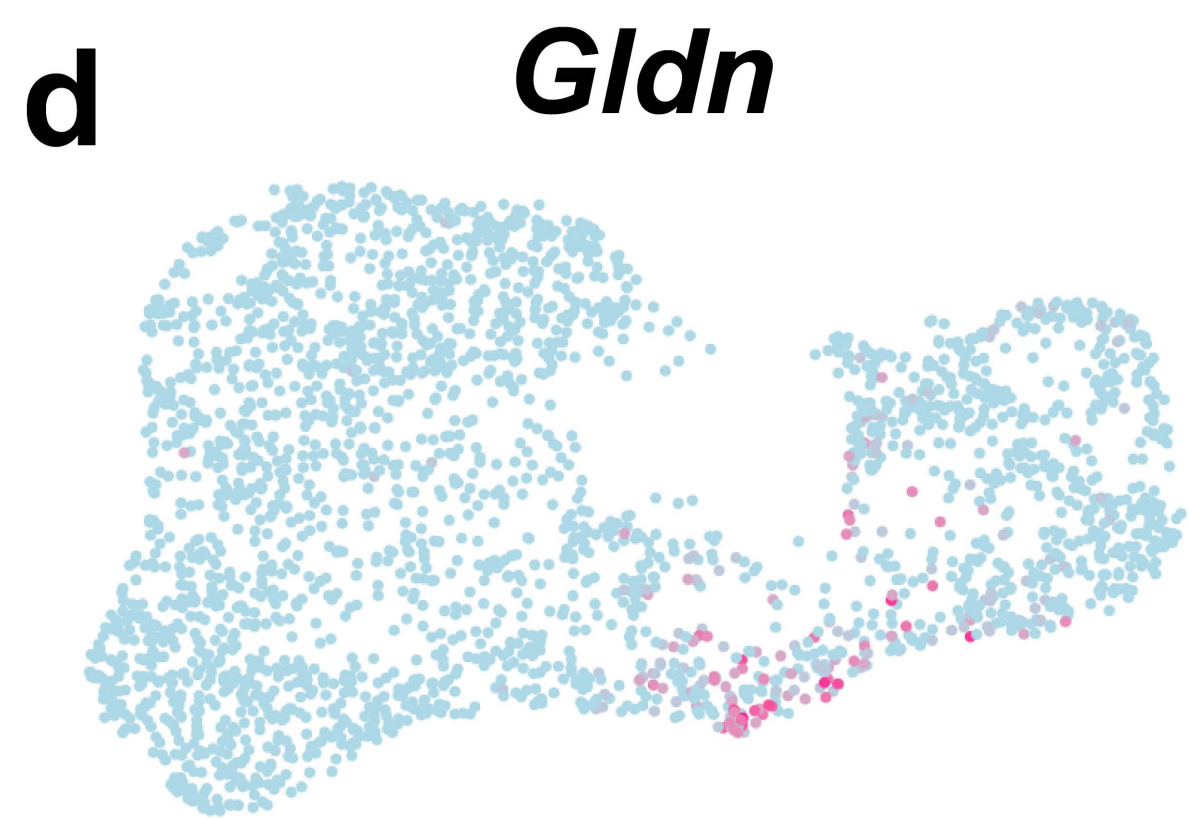
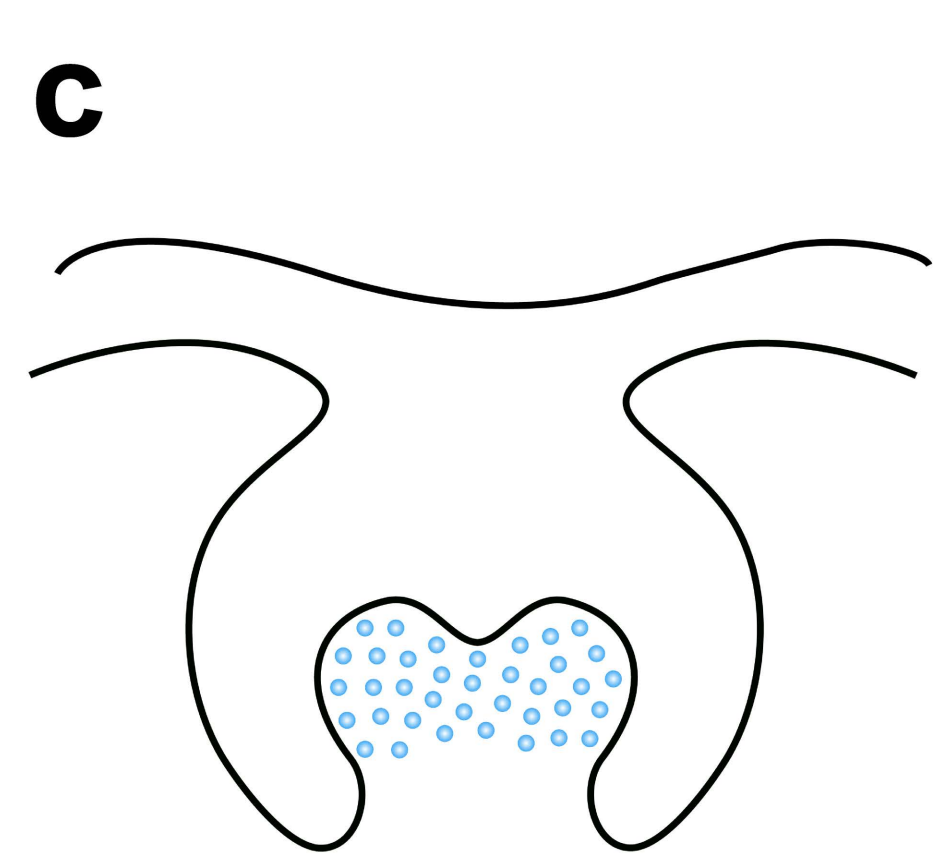
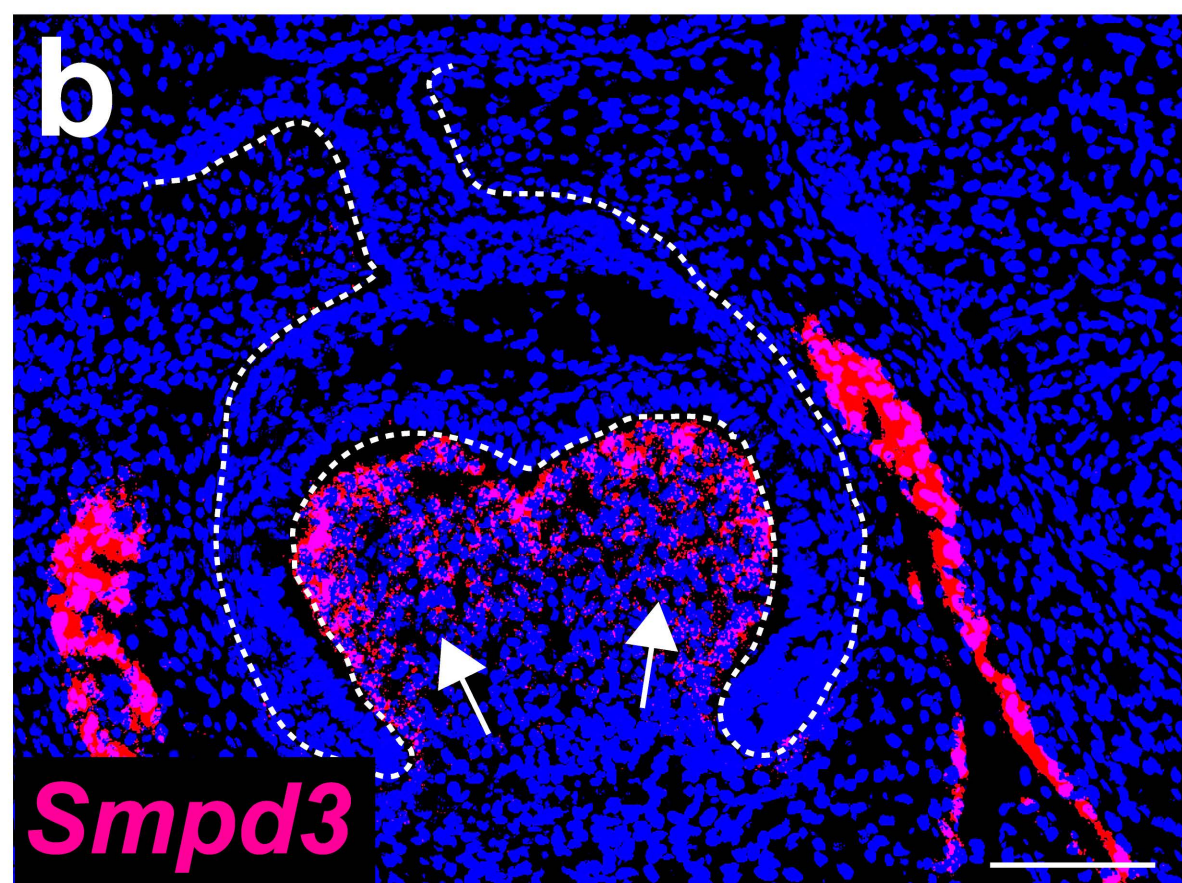
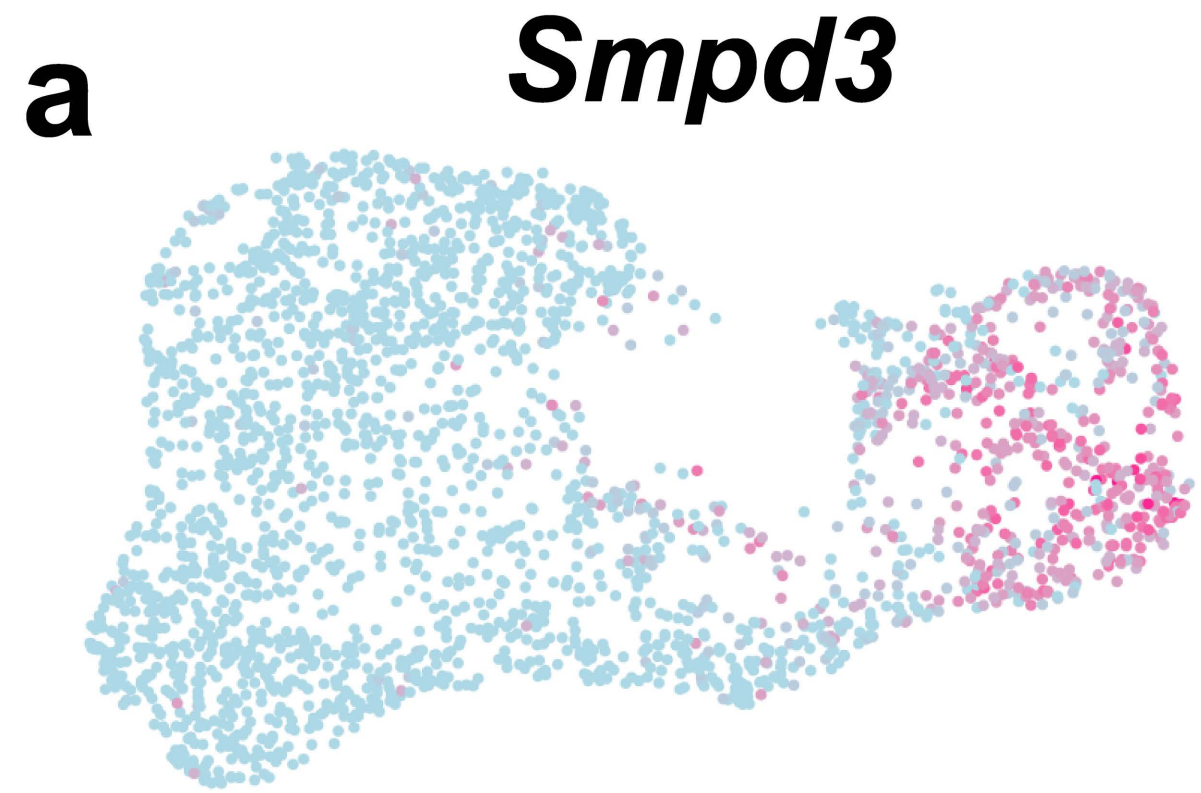


c

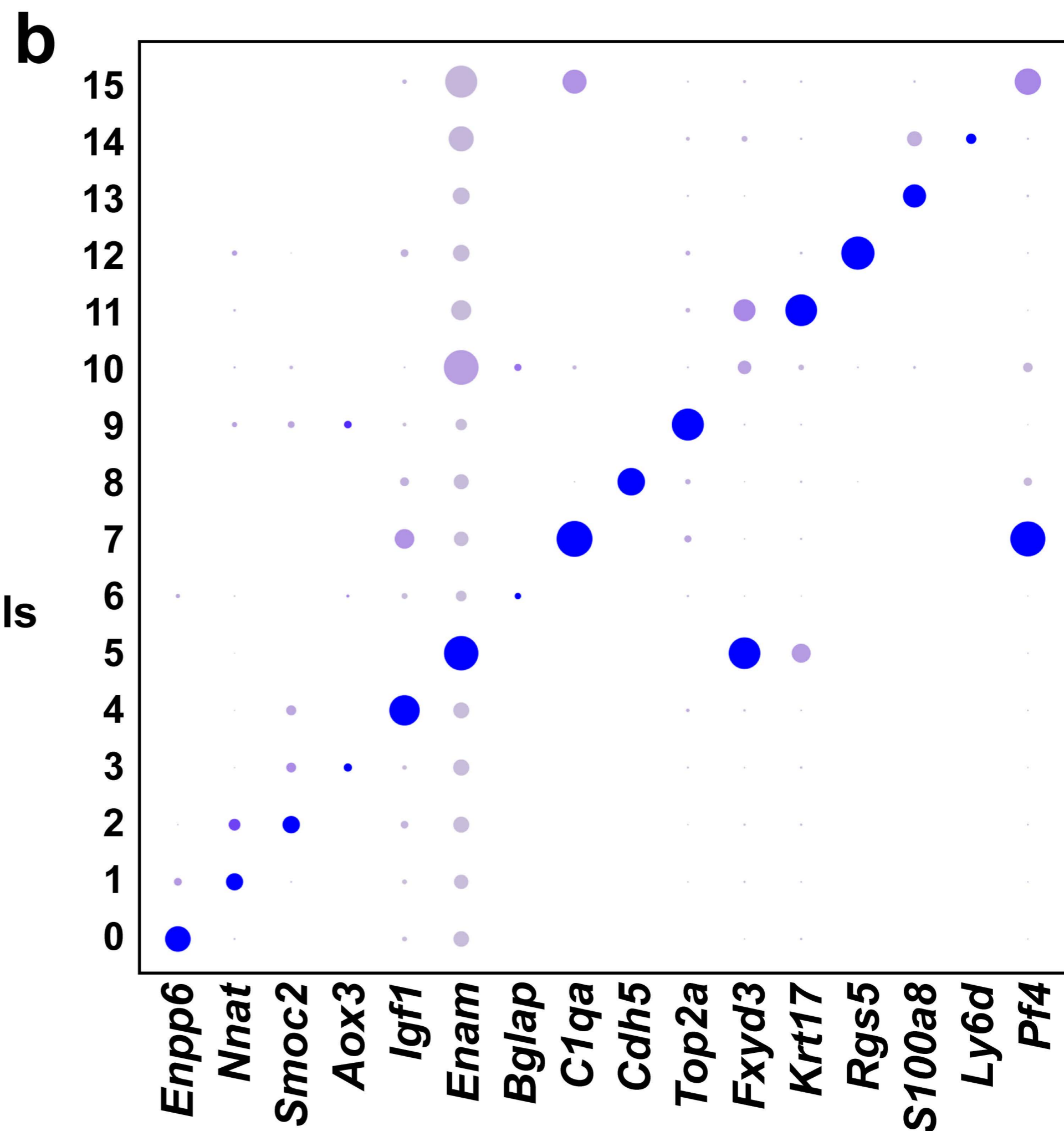
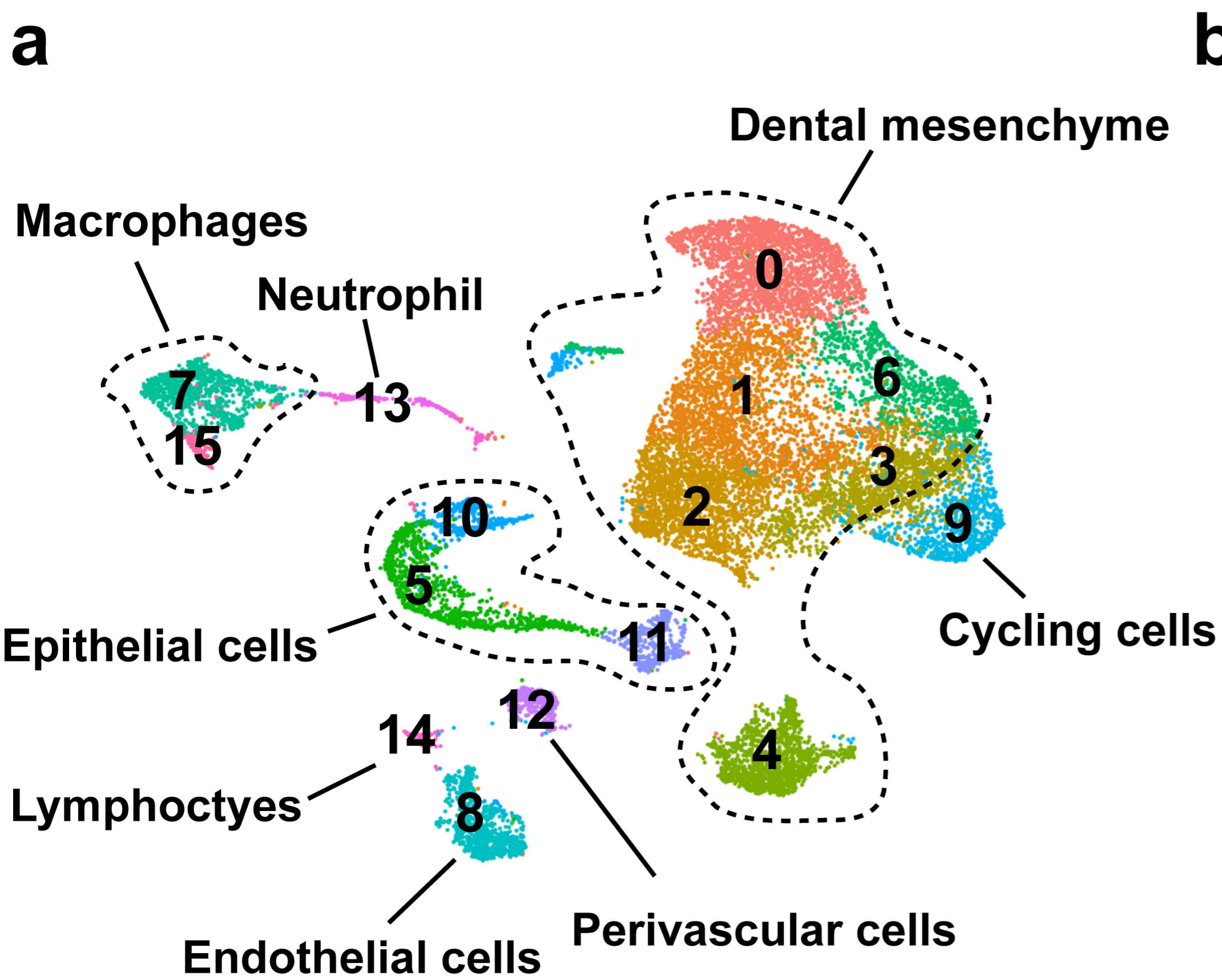


Supplementary Fig. 4 Cell populations in the mouse molar and its surrounding tissue at E16.5. a UMAP plot of cell types in the mouse molar and its surrounding tissue at E16.5. **b** Dotplot of signature genes in the cell populations shown in **a**. **c** Feature plot of markers genes shown in **b**.

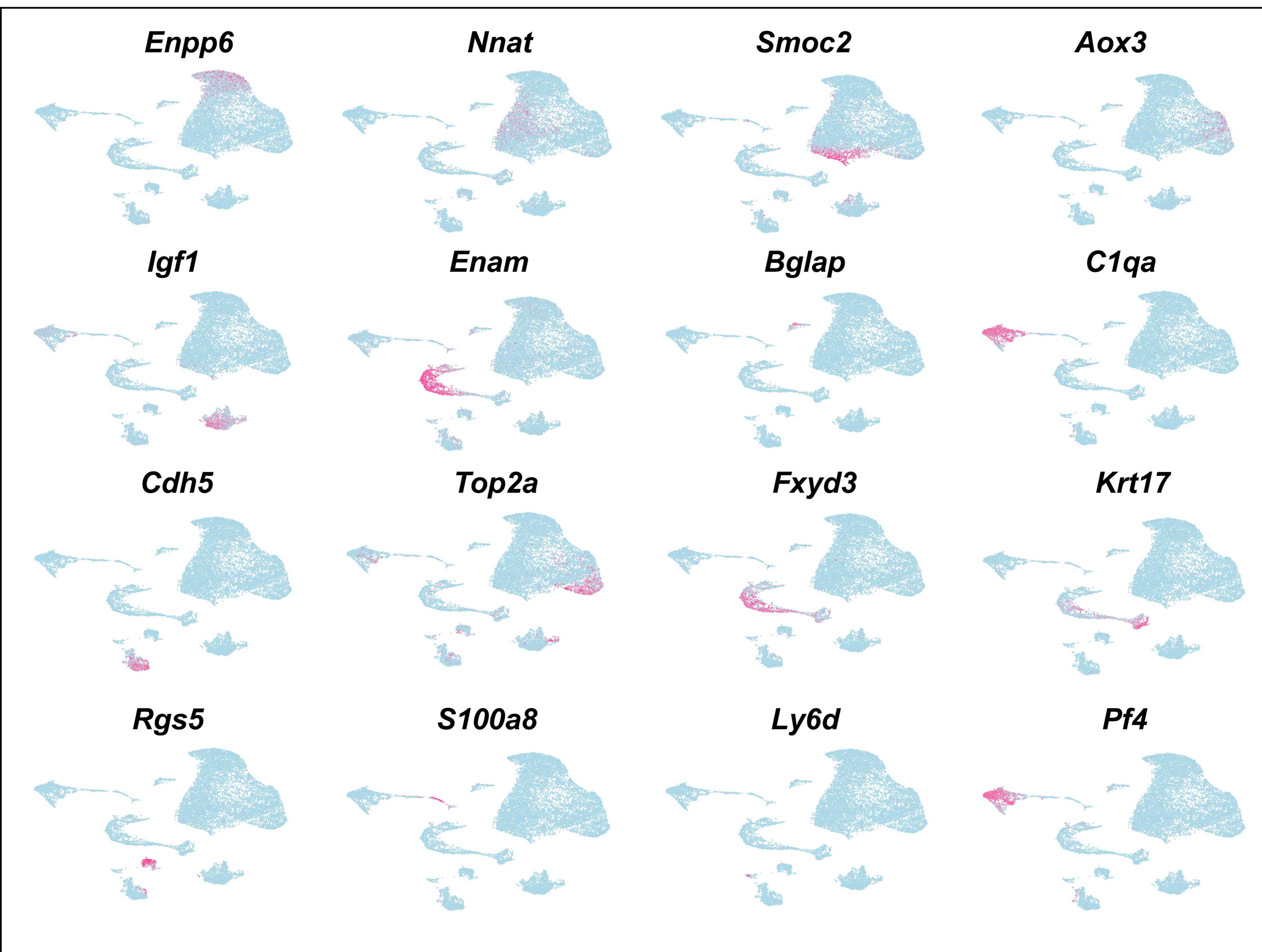
Apical papilla
Apical papilla
Lateral follicle
Lateral follicle
Apical follicle
Apical follicle



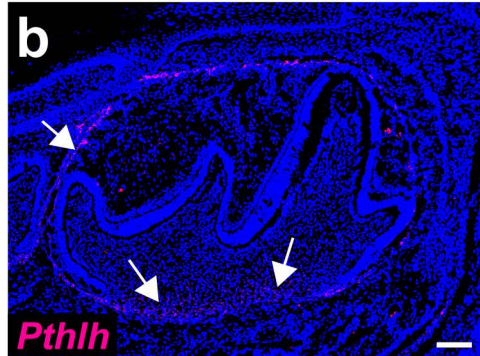
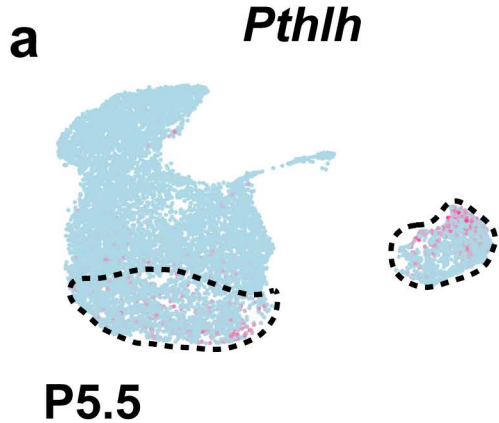
Supplementary Fig. 5 Cellular domain of the dental mesenchyme at E16.5. **a, b** Feature plot and RNAscope staining of *Smpd3* in the coronal papilla (n=3). **c** Cellular domain of the coronal papilla in the mouse molar at E16.5. **d, e** Feature plot and RNAscope staining of *Gldn* in the apical papilla of the mouse molar at E16.5 (n=3). **f** Cellular domain of the apical papilla in the mouse molar at E16.5. **g, h** Feature plot and RNAscope staining of *Bmp3* in the lateral follicle (n=3). **i** Cellular domain of the lateral follicle in the mouse molar at E16.5. **j, k** Feature plot and RNAscope staining of *Sgk1* in the apical follicle (n=3). **l** Cellular domain of the apical follicle in the mouse molar at E16.5. White dotted lines outline the dental epithelial cells in the mouse molar. White arrows point to the positive signals. Scale bars, 100µm.



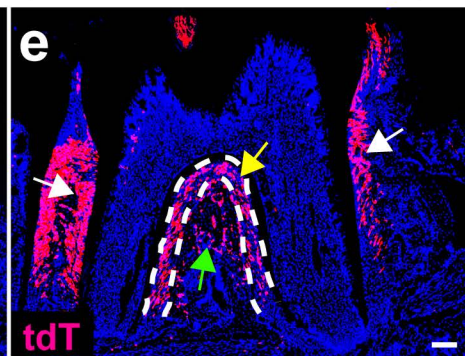
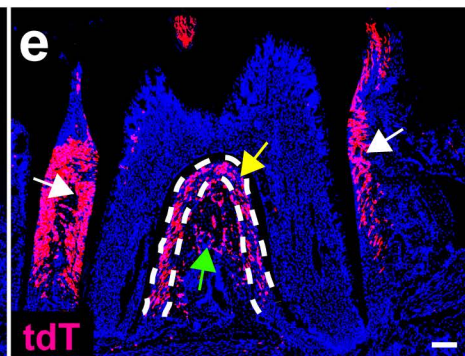
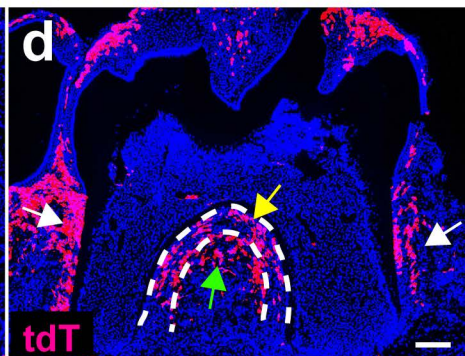
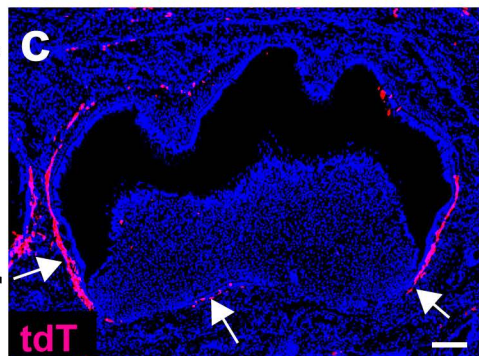
c



Supplementary Fig. 6 Cell populations in the mouse molar at P3.5. a UMAP plot of cell types in the mouse at P3.5. **b** Dotplot of signature genes in the cell populations shown in **a**. **c** Feature plot of markers genes shown in **b**.



P21.5



TM
P3.5

Collect
P5.5

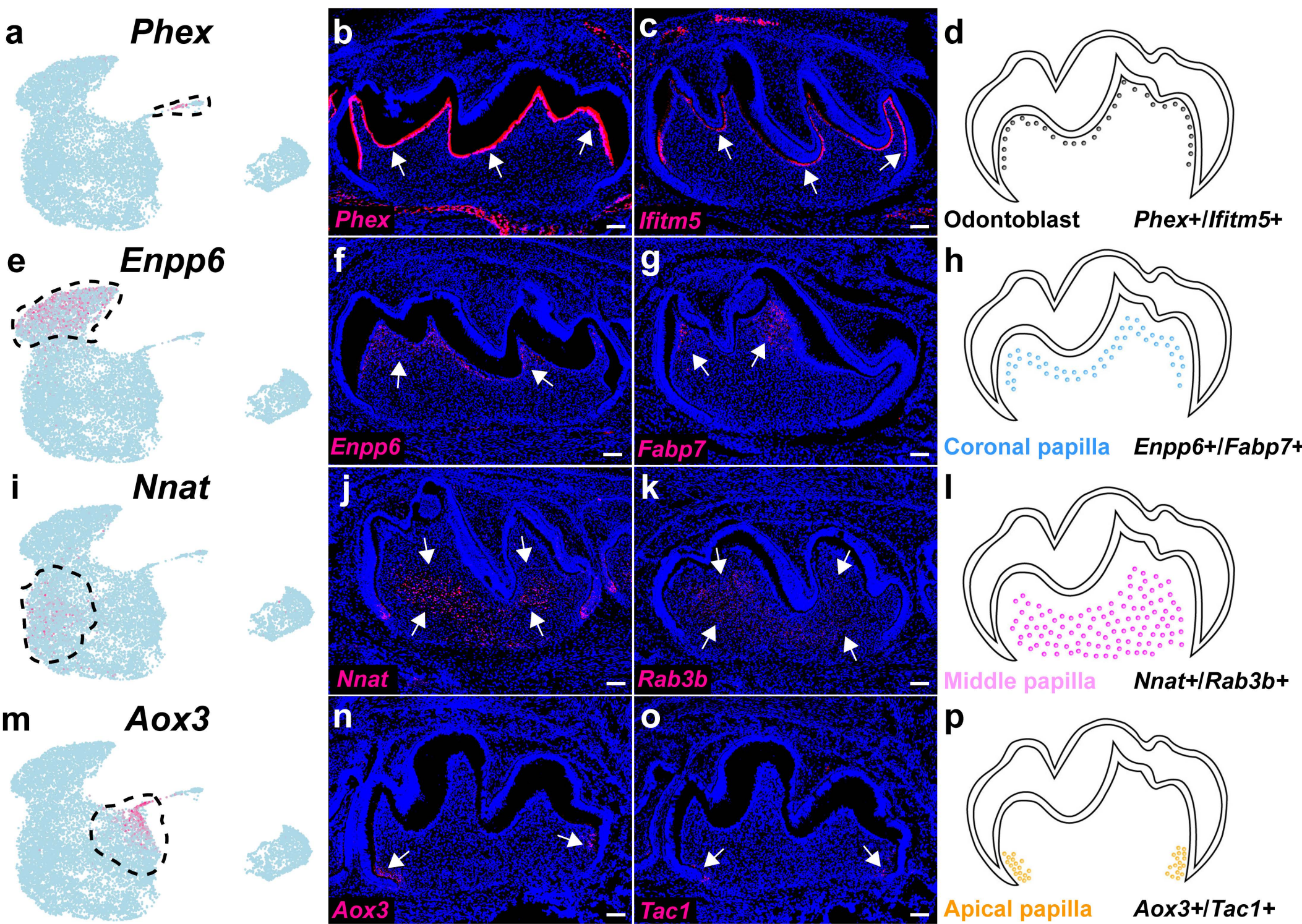
P14.5

P21.5

Pthrp-CreER^{T2};tdT

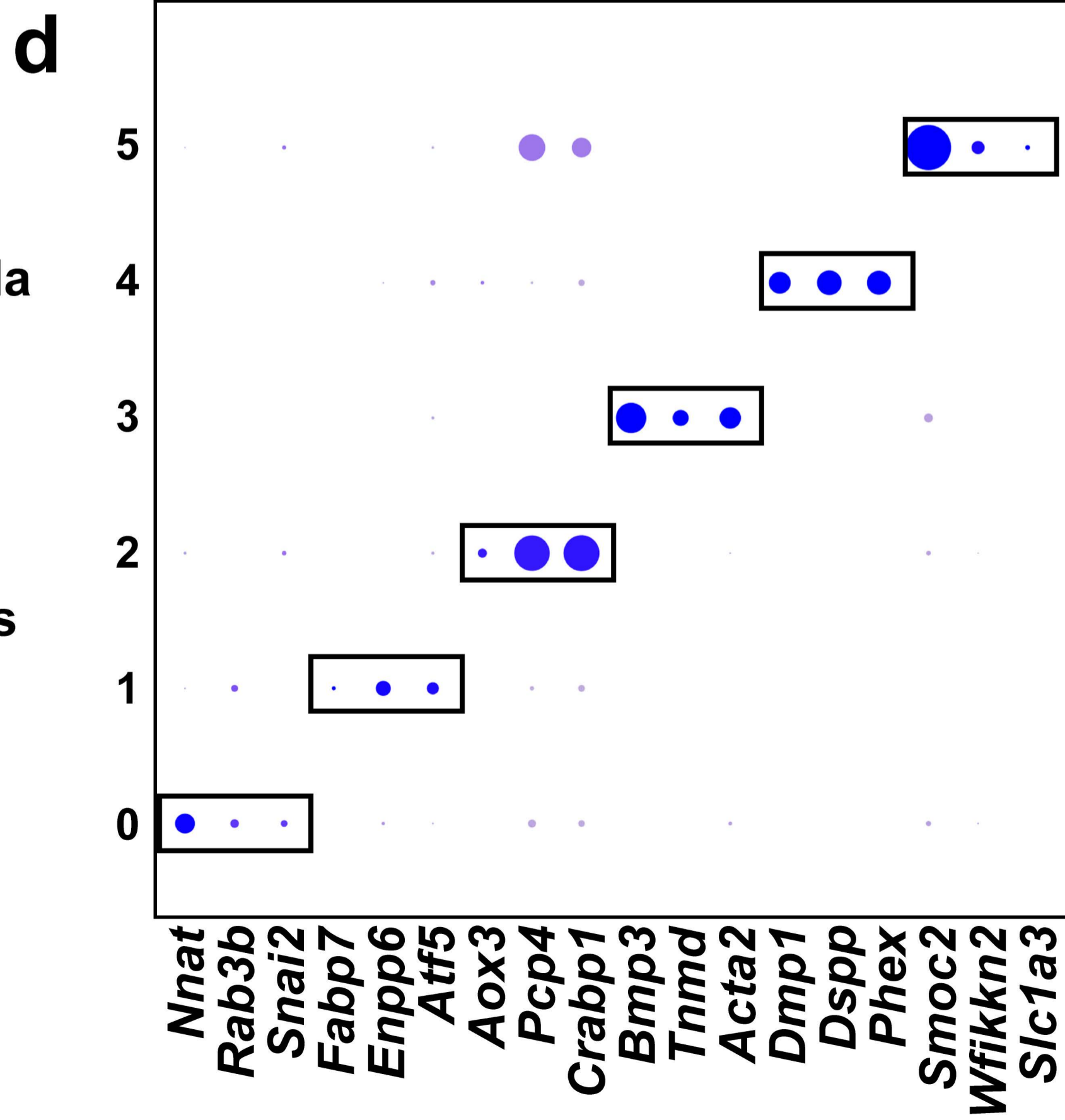
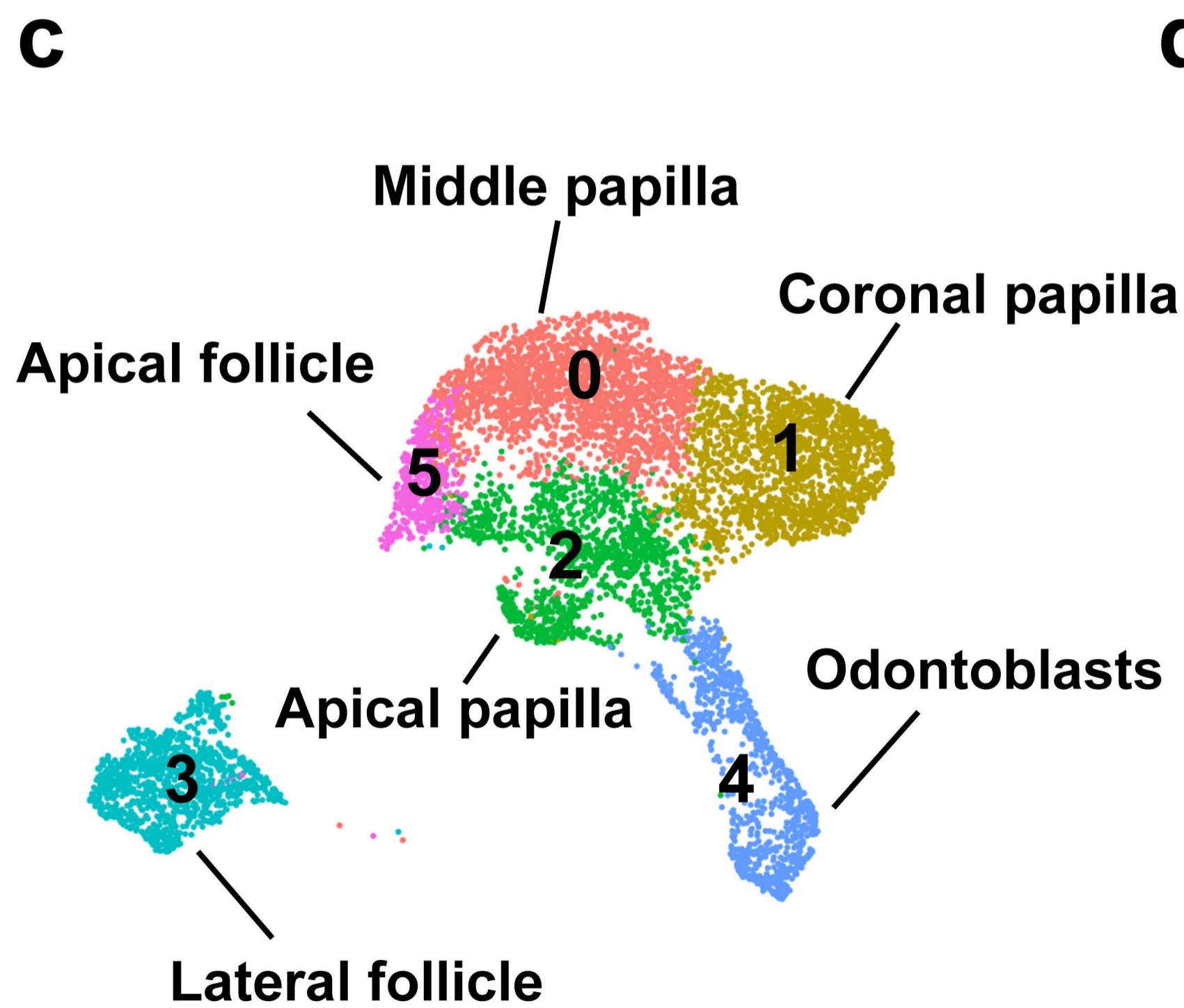
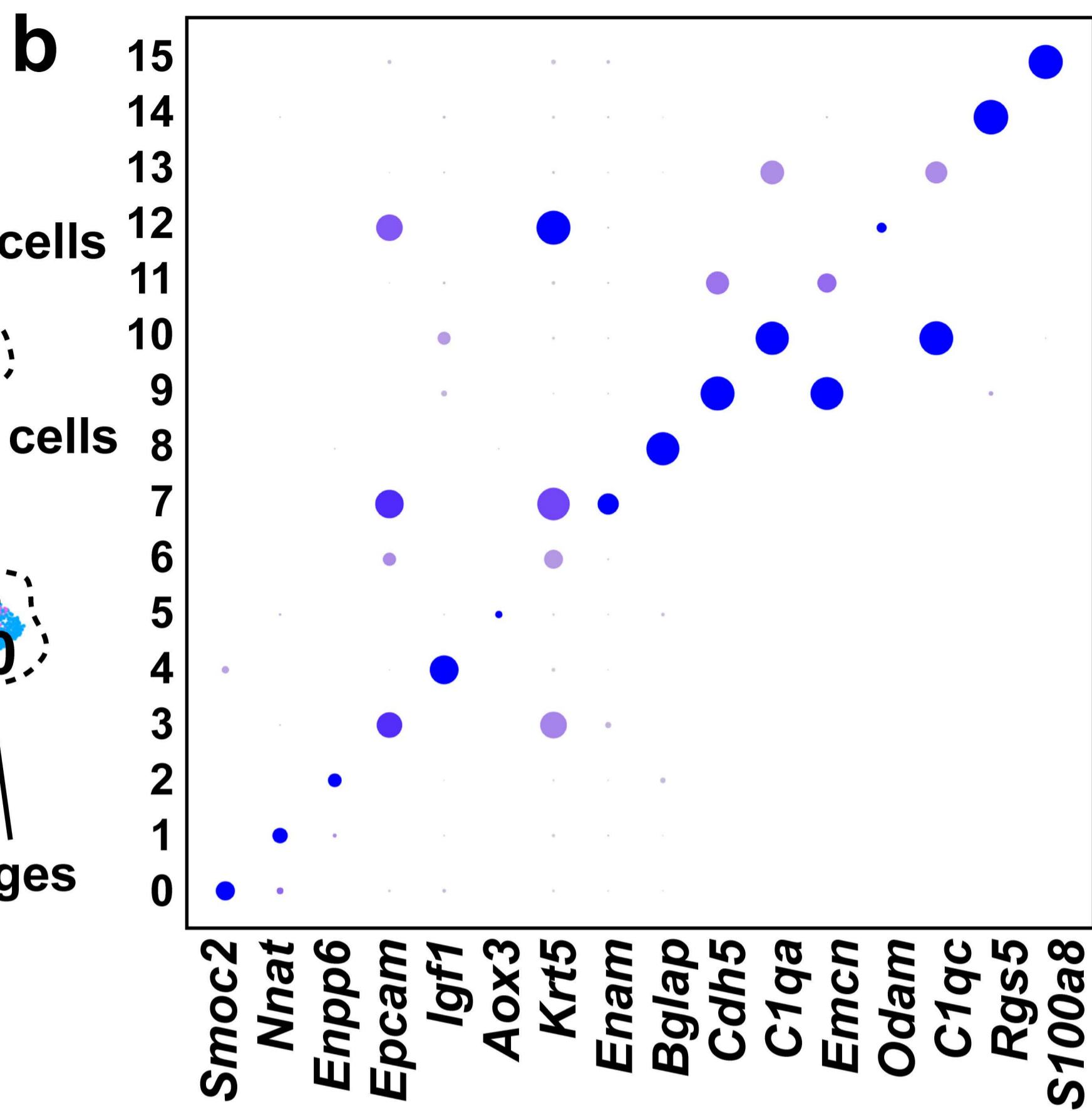
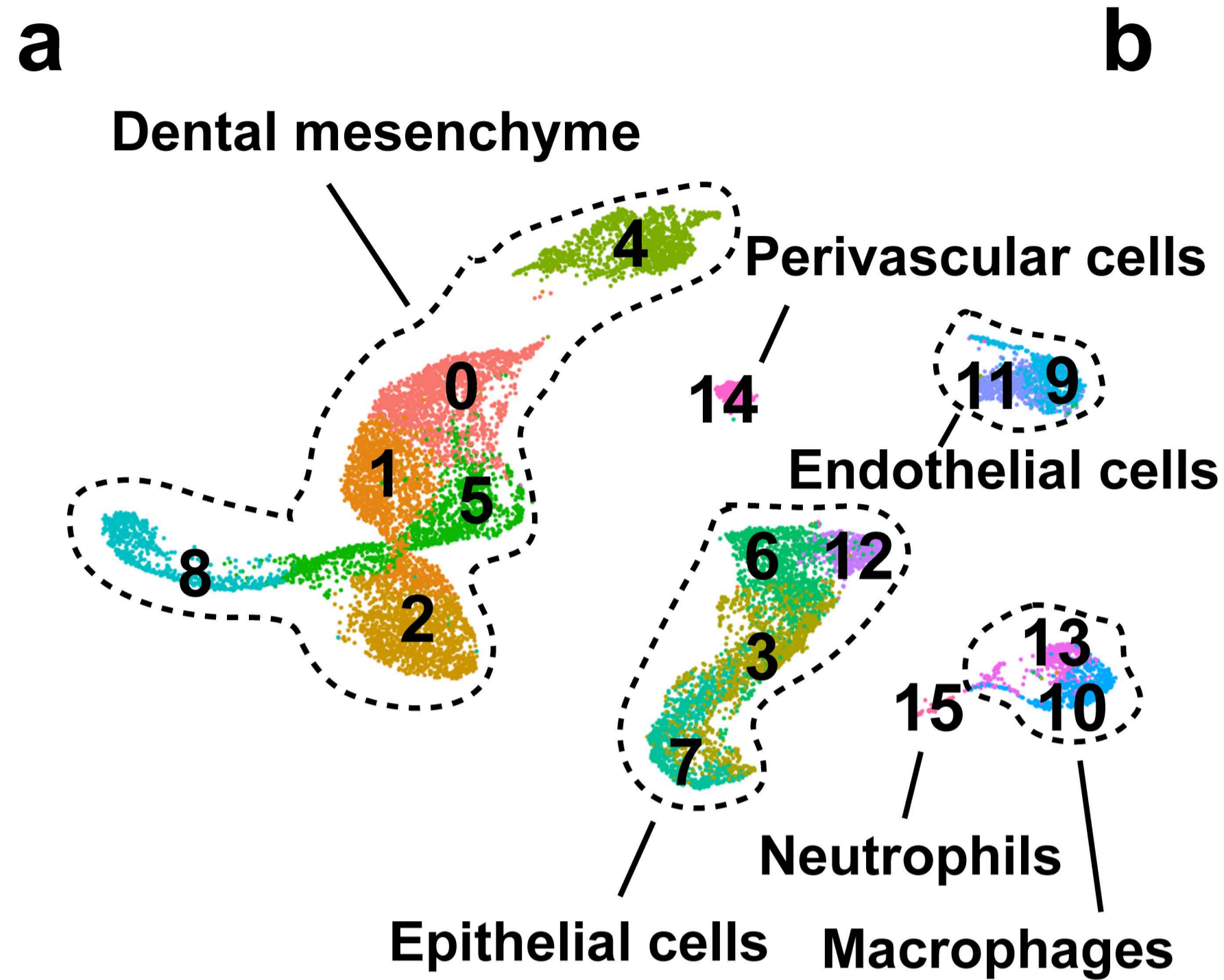


Supplementary Fig. 7 Pthrp+ cells contribute to the periodontal tissue in both root-forming and furcation regions. **a, b** Feature plot and RNAscope staining of *Pthlh* in the mouse molar at P3.5 (n=3). **c-e** Lineage tracing analysis of Pthrp+ cells in the mouse molar from P3.5 to P21.5 (n=3). Induction protocol is at the bottom of the figures. White dotted lines outline the PDL in the mouse molar. White arrows point to the positive signals. Yellow and green arrows in **d** and **e** point to the positive signals in PDL and alveolar bone in the root furcation region, respectively. Black dotted lines outline the cellular domains in the feature plots. Scale bars, 100µm.



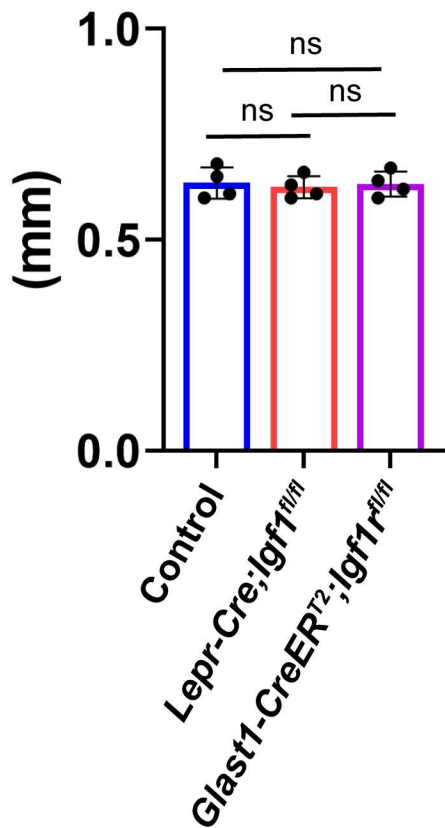
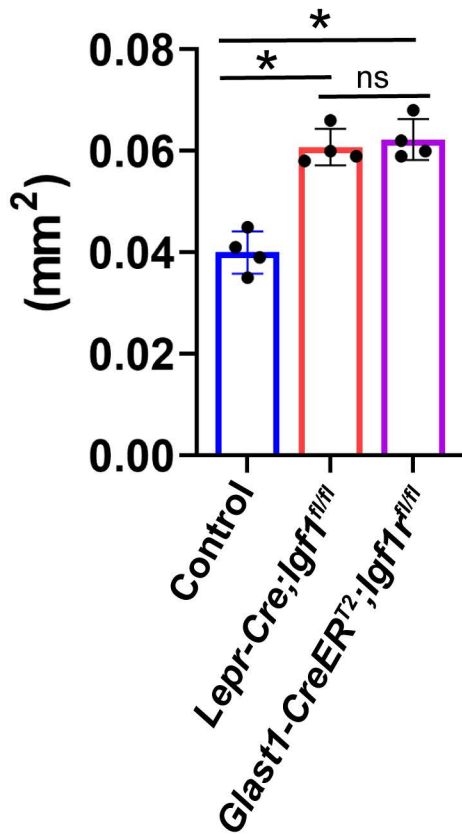
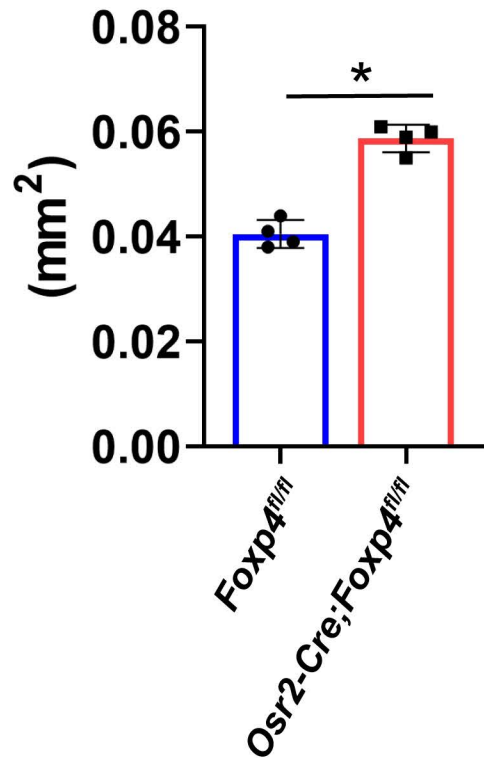
Supplementary Fig. 8 Cellular domains in the dental papilla of the mouse molar at P3.5. **a-c** Feature plot and RNAscope staining of odontoblast markers in the mouse molar at P3.5 (n=3). **d** Schematic drawing of odontoblast domain in the mouse molar at P3.5. **e-g** Feature plot and RNAscope staining of coronal papilla markers in the mouse molar at P3.5 (n=3). **h** Schematic drawing of the coronal papilla domain in the mouse molar at P3.5. **i-k** Feature plot and RNAscope staining of middle papilla markers in the mouse molar at P3.5 (n=3). **l** Schematic drawing of the middle papilla domain in the mouse molar at P3.5. **m-o** Feature plot and RNAscope staining of apical papilla markers in the mouse molar at P3.5 (n=3). **p** Schematic drawing of the apical papilla domain in the mouse molar at P3.5. Black dotted lines outline the cellular domains in the feature plots. White arrows point to the positive signals. Scale bars, 100 μ m.

P7.5



Supplementary Fig. 9 Cell populations in the mouse molar at P7.5. a UMAP plot of cell types in the mouse molar at P7.5. **b** Dotplot of signature genes of the cell populations shown in **a**. **c** UMAP plot of cell populations in the dental mesenchyme at P7.5. **d** Dotplot of signature genes of the cell populations shown in **c**.

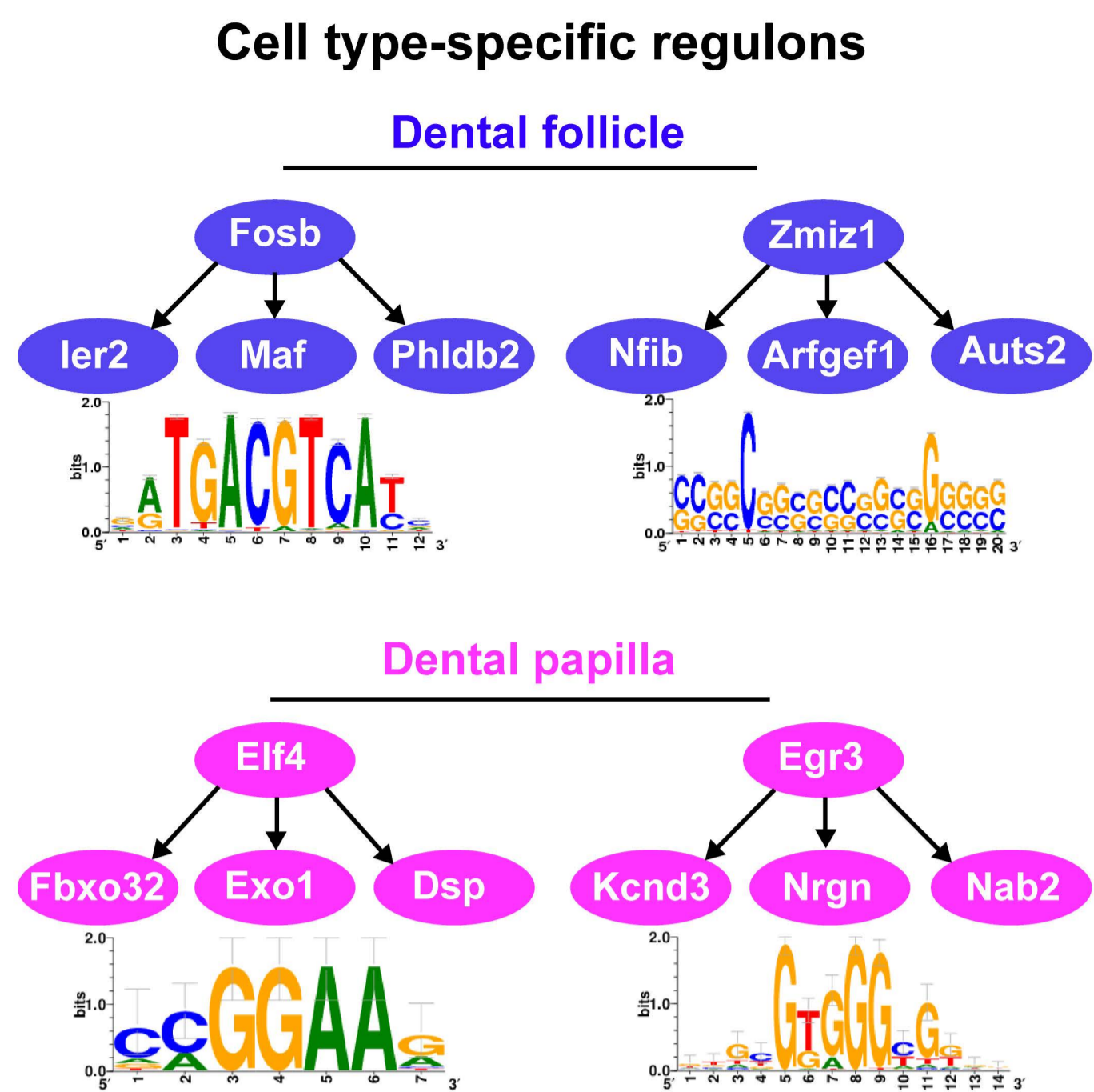
Supplementary Fig. 10 Cell-cell interactions in the dental mesenchyme of the mouse molar at P3.5. a-f Interaction between cellular domains in the dental mesenchyme in the mouse molar at P3.5. **g** Ligand-receptor interactions in the cellular domains of the dental mesenchyme at P3.5. The significant interactions between two cell groups are identified using a permutation test. The interactions with p-value < 0.05 are considered significant.

a Root length**b** PDL area**c** PDL area

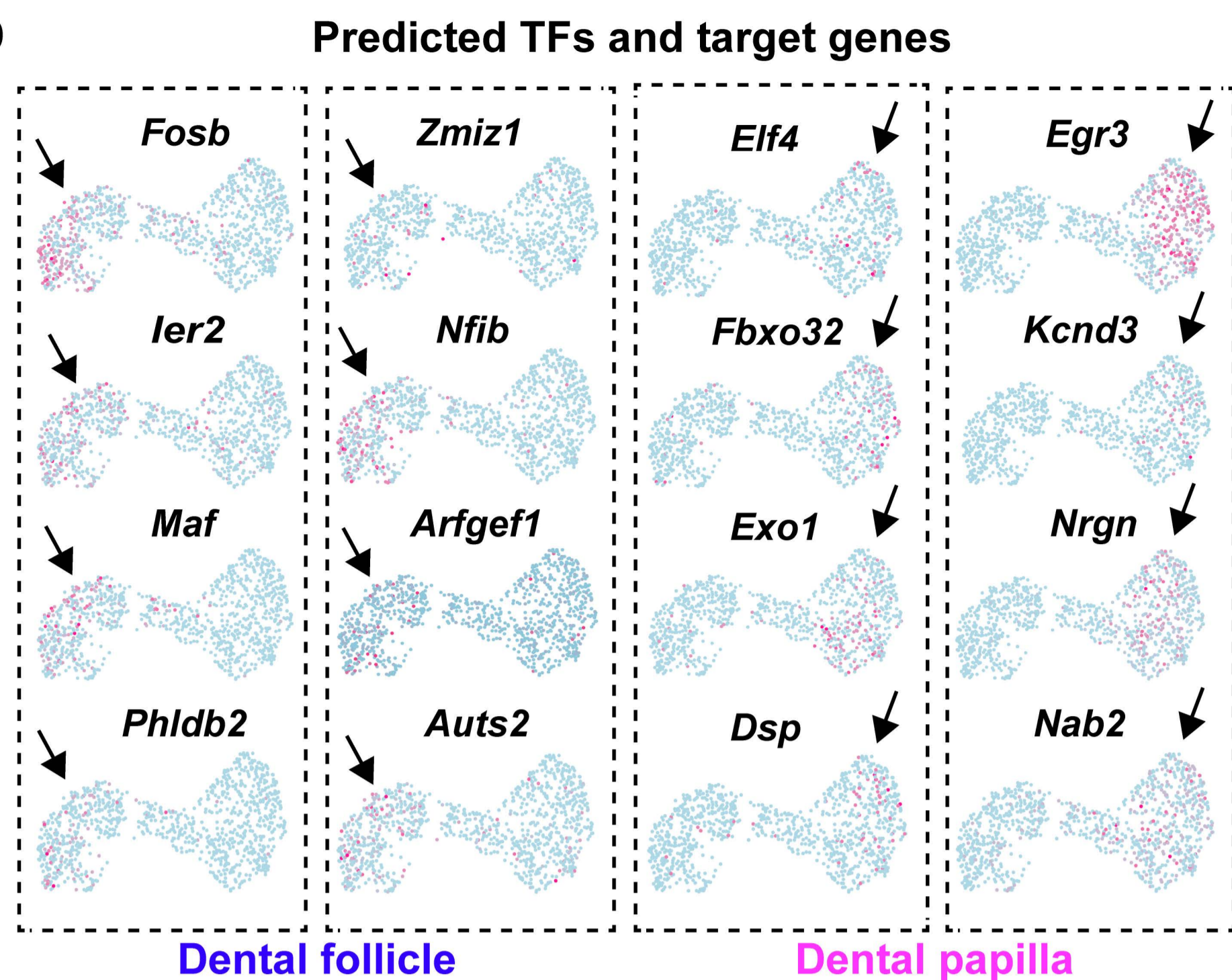
Supplementary Fig. 11 Quantitative analysis of root length and PDL area after disruption of Igf1 and Foxp4 signaling. **a,b** Quantitative analysis of root length and PDL area in control, *Lepr-Cre;Igf1^{fl/fl}* and *Slc1a3-CreER^{T2};Igf1r^{fl/fl}* molars. **c** Quantitative analysis of PDL area in in *Foxp4^{fl/fl}* and *Osr2-Cre;Foxp4^{fl/fl}* molars. Data are presented as mean values \pm SD. n=4 biologically independent samples. ns, no significant difference. p values are given for one-way ANOVA. *, p < 0.0001.

E14.5

a

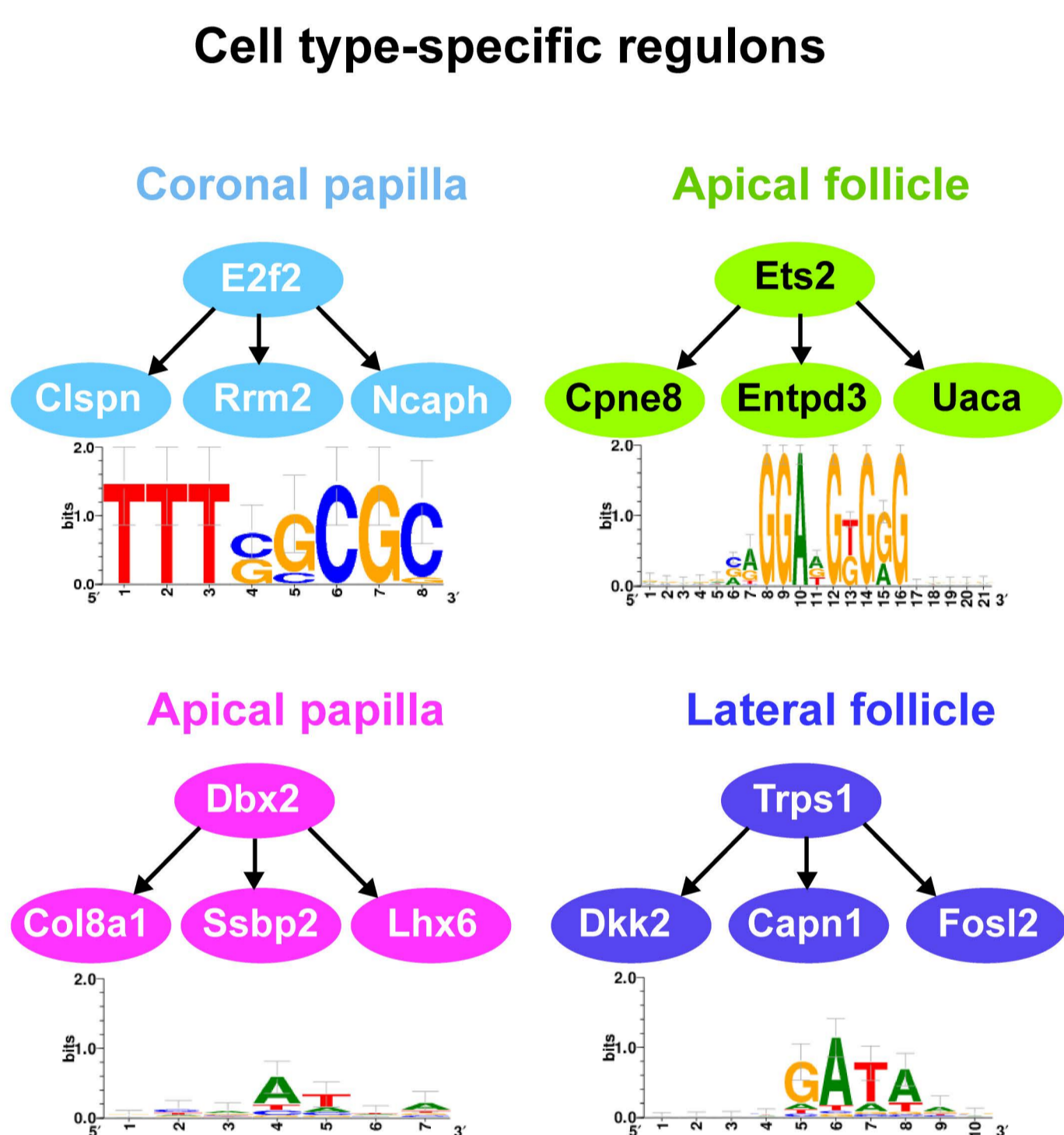


b

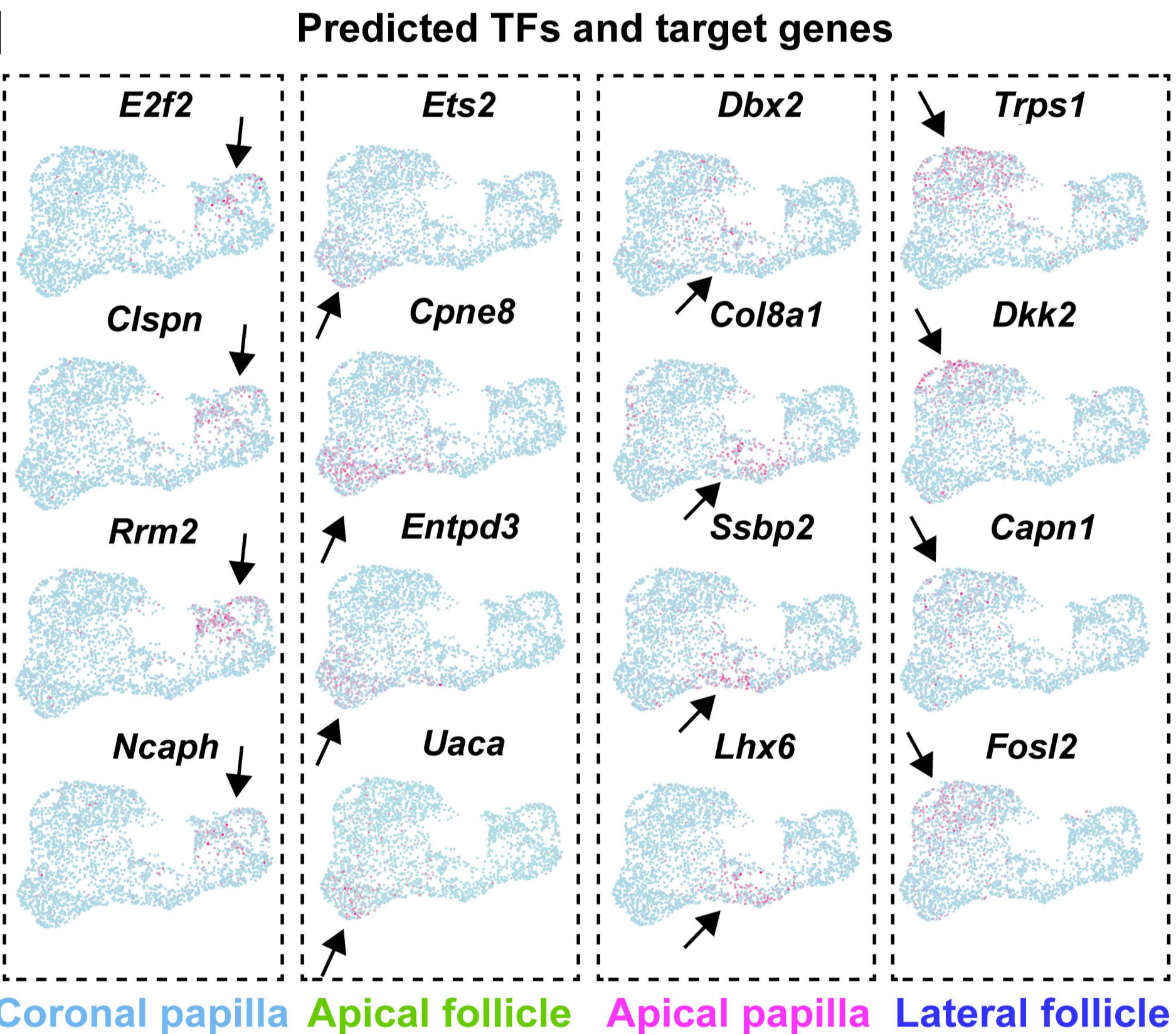


E16.5

c

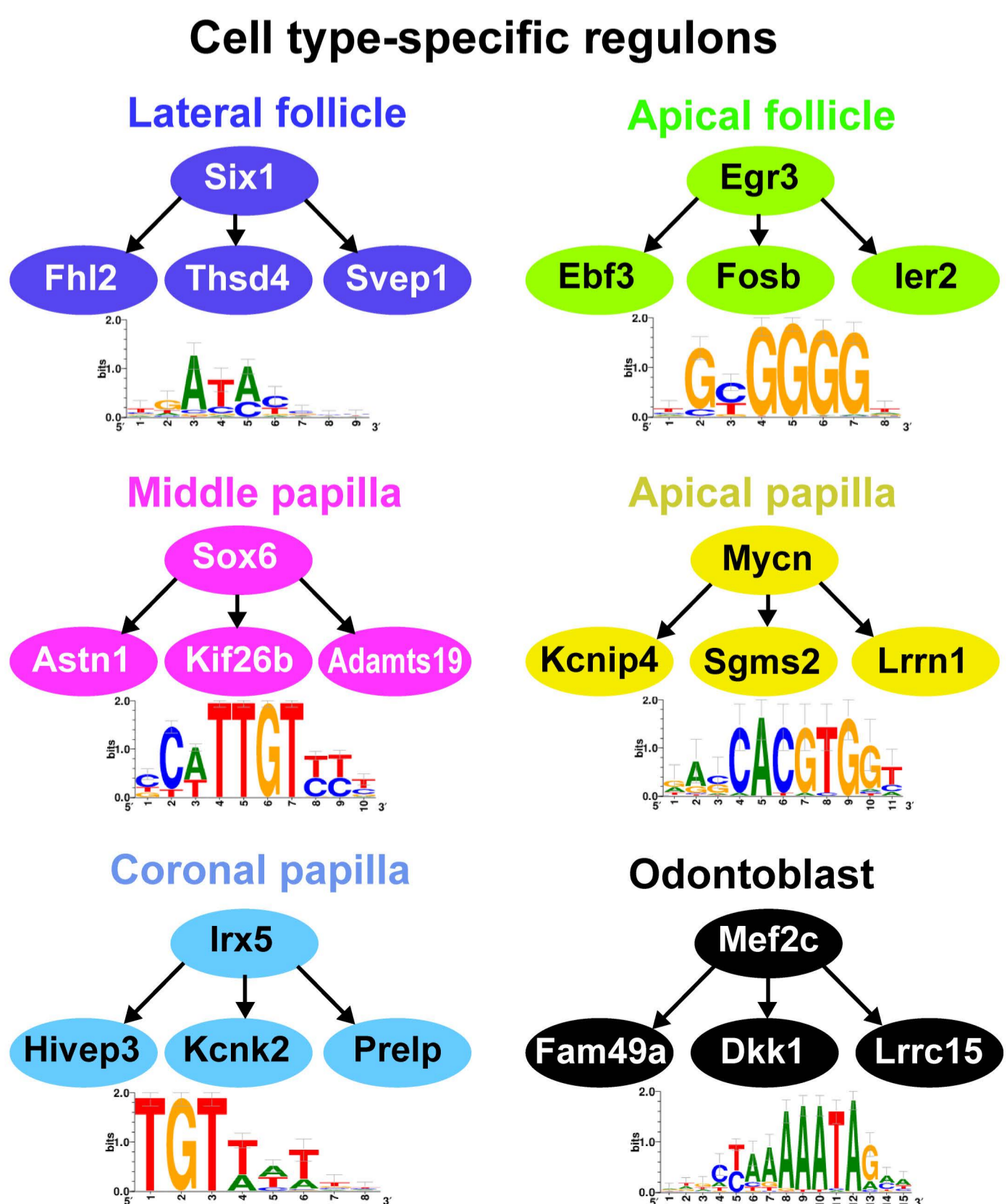


d

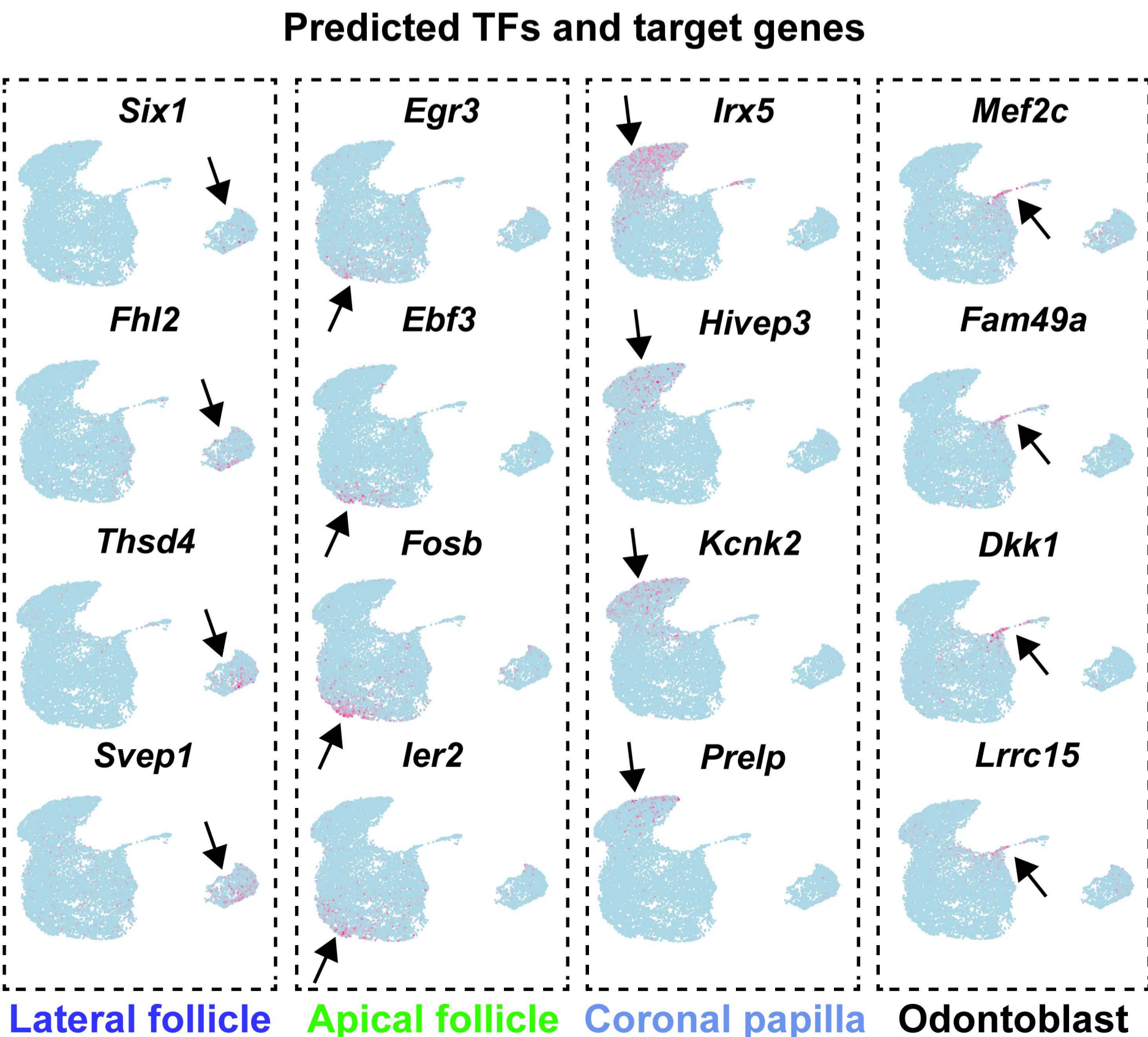


P3.5

e



f



Supplementary Fig. 12 Selected cell type-specific regulons in the dental mesenchyme. a Cell type-specific regulons highlighted in the dental mesenchyme at E14.5. **b** Feature plot of predicated TFs and corresponding target genes shown in **a**. **c** Cell type-specific regulons highlighted in the dental mesenchyme at E16.5. **d** Feature plot of predicated TFs and corresponding target genes shown in **c**. **e** Cell type-specific regulons highlighted in the dental mesenchyme at P3.5. **f** Feature plot of predicated TFs and corresponding target genes shown in **e**.