

**Supplementary Data 1. Differentially expressed genes across bulk RNAseq samples.**

Bulk RNA-seq data were analyzed with DESeq2 ( $p_{adj} < 0.05$ ;  $|\log_2 \text{fold-change}| > 1.5$ ). Default settings were used for statistical analysis (Wald test).

**Supplementary Data 2. scRNAseq PDGFRA<sup>+</sup> population markers.**

scRNA-seq data from PDGFRA<sup>+</sup> cells were analyzed using Seurat FindMarkers tool with default settings (Wilcoxon rank sum test, logfc threshold 0.25).

**Supplementary Data 3. scRNAseq of foveolar cells population isolated from WT and *Fgf7* KO mice.**

scRNA-seq data from PDGFRA<sup>+</sup> cells were analyzed using Seurat FindMarkers tool with default settings (Wilcoxon rank sum test, logfc threshold 0.25).

**Supplementary Movie 1.** 3D video rendering of murine corpus blood vessels (CD31 in red).

**Supplementary Movie 2.** 3D video rendering of murine antral blood vessels (CD31 in red).

**Supplementary Movie 3.** 3D video rendering of murine corpus muscle fibers (SMA1 in yellow).

**Supplementary Movie 4.** 3D video rendering of murine antral muscle fibers (SMA1 in yellow).

**Supplementary Movie 5.** 3D video rendering of *Pdgfra*<sup>Cre(ER-T2);Rosa26<sup>mT/mG</sup> mouse (stained green after tamoxifen treatment) corpus to show the morphology of *Pdgfra*<sup>Hi</sup> cells enveloping each gland and additional *Pdgfra*<sup>Lo</sup> cells lying in the space beneath glands.</sup>

**Supplementary Movie 6.** 3D video rendering of *Pdgfra*<sup>Cre(ER-T2);Rosa26<sup>mT/mG</sup> mouse (stained green after tamoxifen treatment) antrum to show the morphology of *Pdgfra*<sup>Hi</sup> cells enveloping each gland and additional *Pdgfra*<sup>Lo</sup> cells lying in the space beneath glands.</sup>