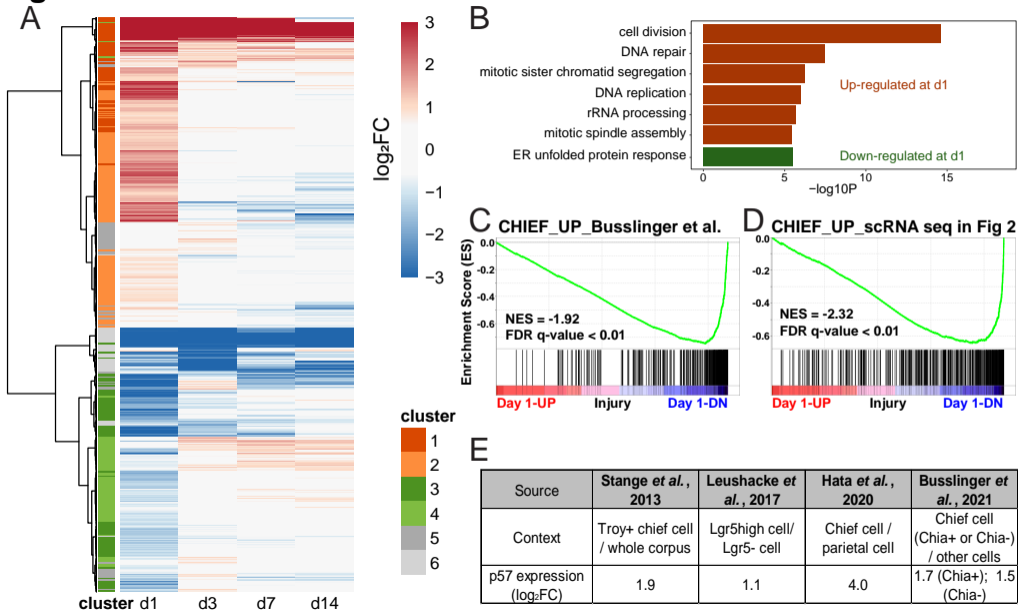


## Supplemental Information

**p57<sup>Kip2</sup> imposes the reserve stem cell**

**state of gastric chief cells**

**Ji-Hyun Lee, Somi Kim, Seungmin Han, Jimin Min, Brianna Caldwell, Aileen-Diane Bamford, Andreia Sofia Batista Rocha, JinYoung Park, Sieun Lee, Szu-Hsien Sam Wu, Heetak Lee, Juergen Fink, Sandra Pilat-Carotta, Jihoon Kim, Manon Jossierand, Réka Szep-Bakonyi, Yohan An, Young Seok Ju, Anna Philpott, Benjamin D. Simons, Daniel E. Stange, Eunyong Choi, Bon-Kyoung Koo, and Jong Kyoung Kim**

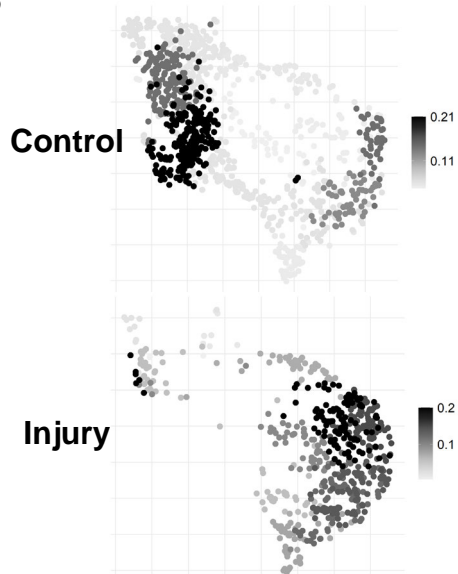
**Figure S1**

# Figure S2

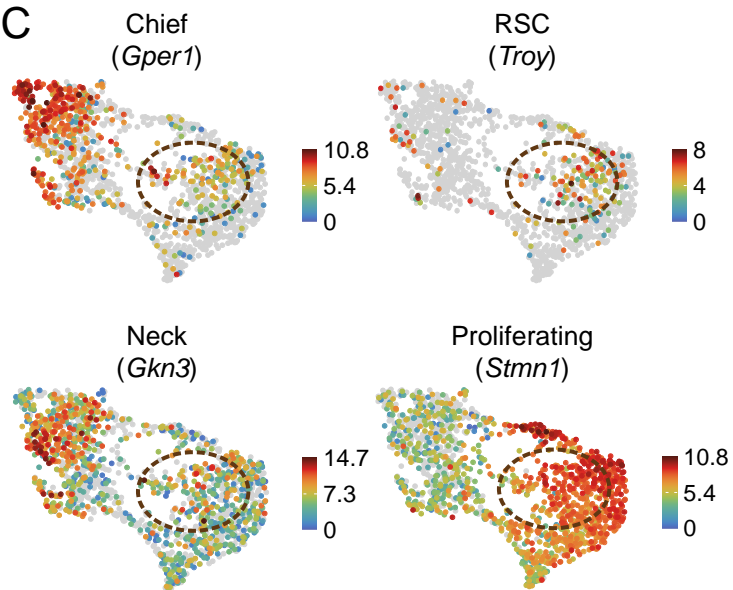
A

Cluster #	11	1	4	0	9	8	2	6	3	5	7	10	Total
	Chief	C/N-1	C/N-2	Neck	C/Pr-1	C/Pr-2	Pr-2	Pr-1	N/P	Pr/P-2	Pr/P-1	Pit	Total
Control	54	144	145	217	56	46	53	41	124	56	50	44	1030
Injury	11	31	7	2	39	54	110	81	32	76	68	42	553

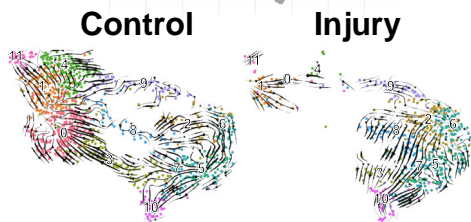
B



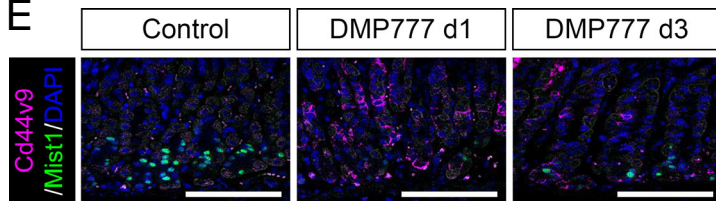
C



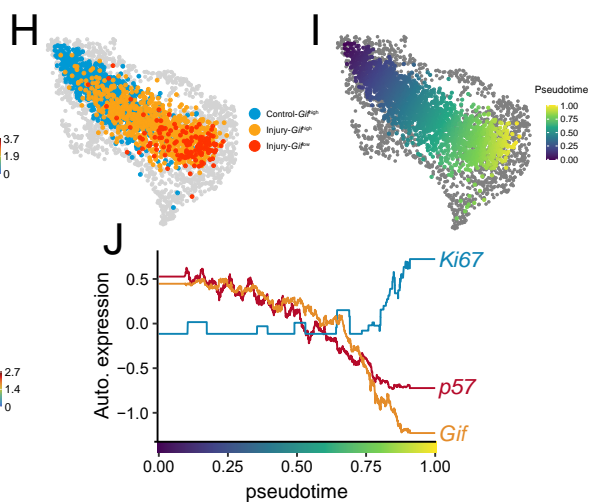
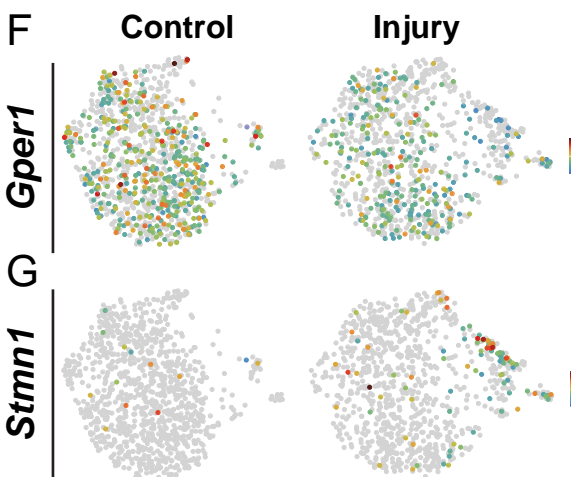
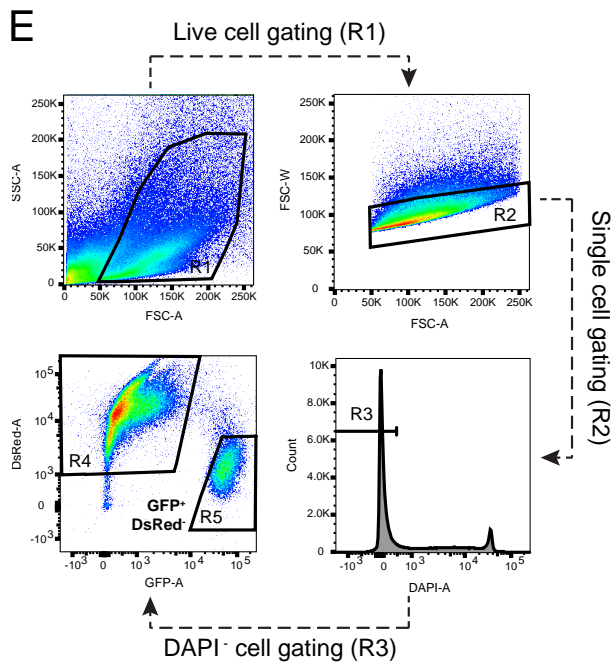
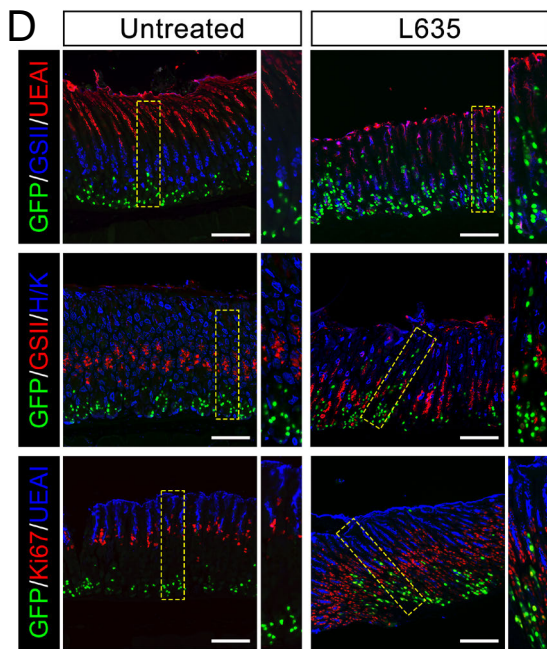
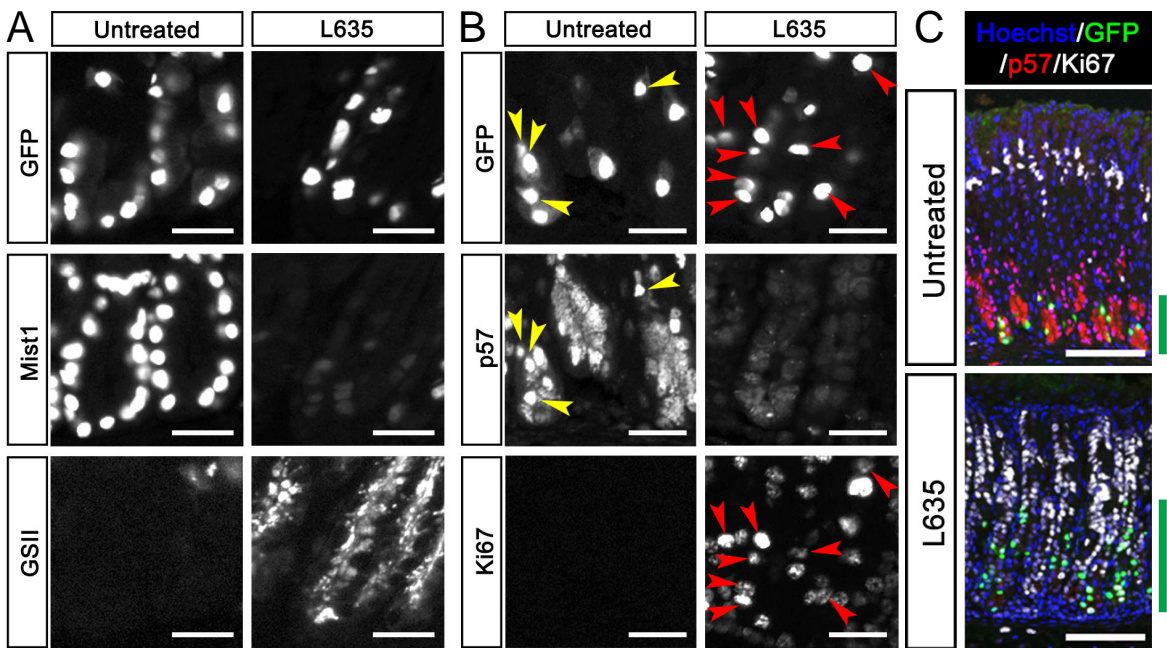
D



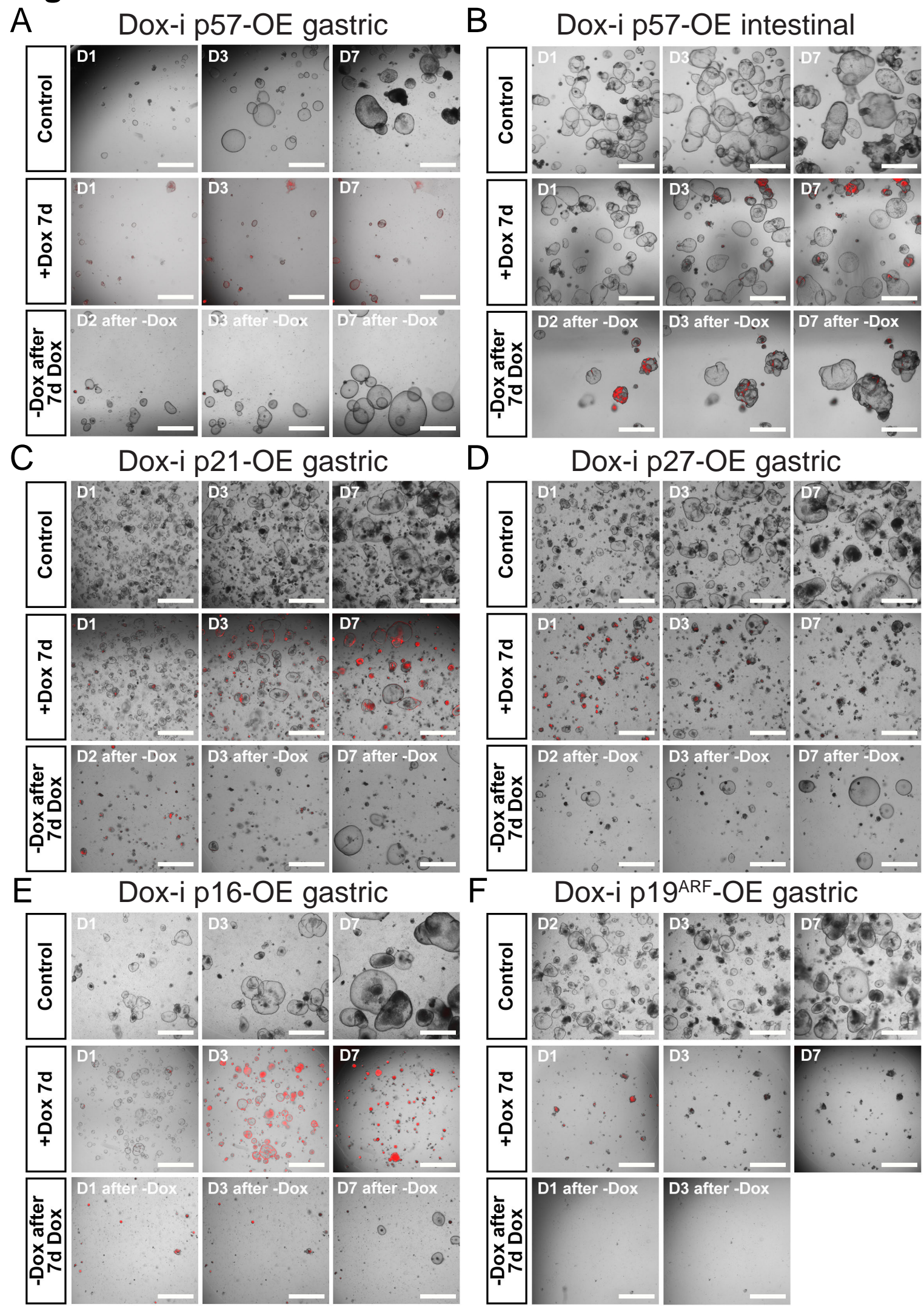
E



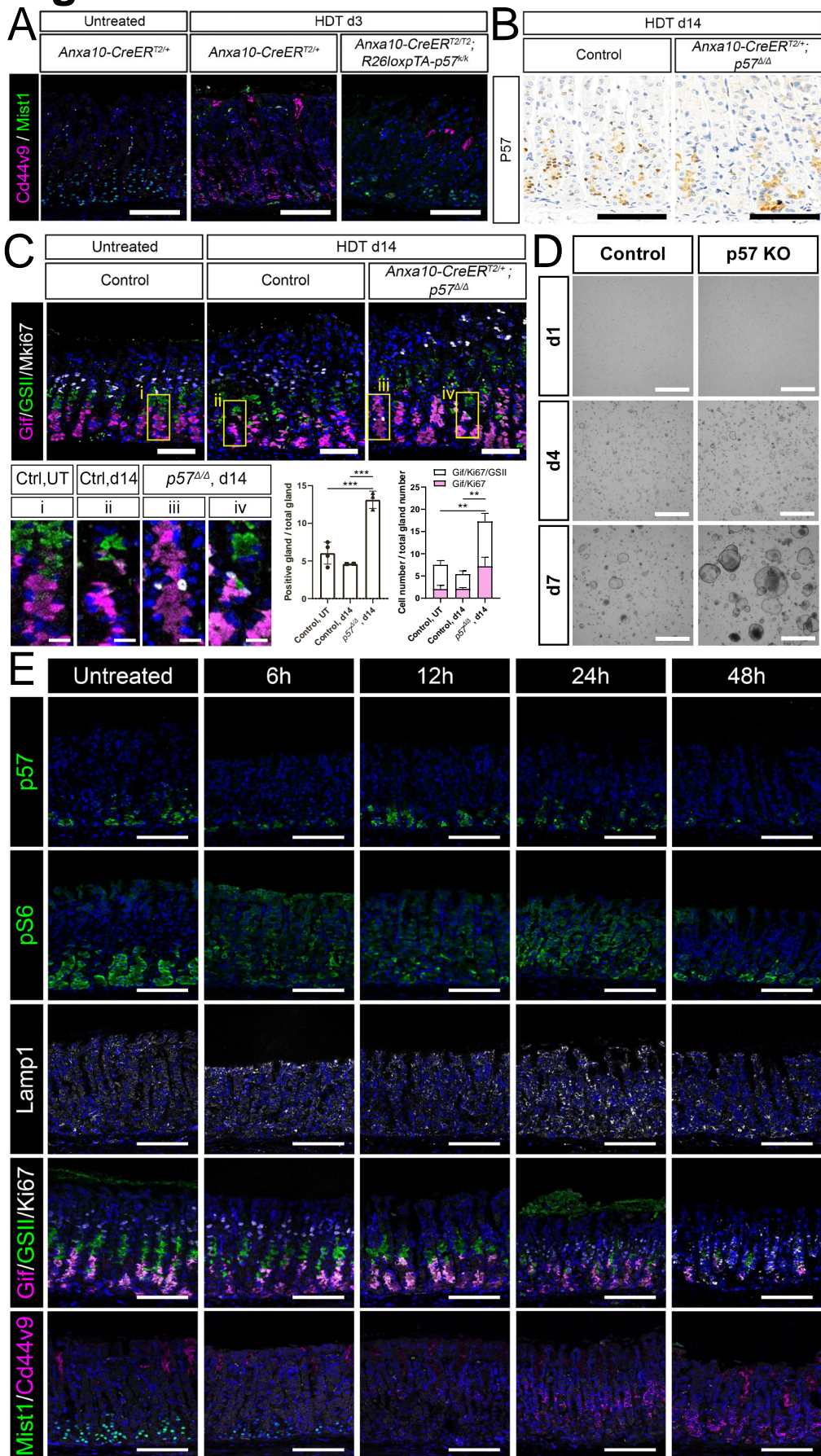
# Figure S3



# Figure S4



# Figure S5



## Supplementary figure legends

**Supplementary figure 1. Rapid transcriptome changes after injury shown in time-course bulk RNA-seq of Troy+ chief cells and enrichment of p57 expression in chief cells in homeostasis.** (A) Heatmap of 1667 DEGs clustered by 6 patterns. 2-6 mice per time point were analyzed. Cluster 1 and 2 show peak expression at 1 dpi and gradual reduction during recovery. Cluster 3 and 4 show the biggest decrease in gene expression at 1 dpi. (B) Selected GO-terms enriched in upregulated (red) or downregulated (green) genes at 1 dpi (P-value < 10<sup>-5</sup>). (C and D) GSEA of gene signatures associated with the chief cell signature from the scRNA-seq dataset from Busslinger et al., 2021 (C) and from the Pgc+ scRNA-seq dataset in Figure 2 (D). NES, Normalized Enrichment Score. (E) Enrichment of p57 expression in chief cells in homeostasis from other datasets. Related to Figure 1, Tables S1 and S2.

**Supplementary figure 2. Rapid switch of p57+ gastric chief cells to Ki67+ injury-responsive chief cells upon injury.** (A) Cell numbers of each cluster in control and injury analyzed in Pgc+ scRNA-seq. (B) The proportion of the cell number of each cluster in control and injury samples. (C) UMAP plots of further markers for chief cells (*Gper1*), RSCs (*Troy*), neck cells (*Gkn3*), and proliferating cell markers (*Stmn1*). Brown dotted circles show injury-responsive chief cells. (D) RNA velocity inferred by scVelo projected on the UMAP plots in control and injury. (E) Double labelling of markers for SPEM (Cd44v9, magenta) and chief cells (*Mist1*, green) in control, at 1 dpi, and at 3 dpi. Nuclei were counterstained with DAPI (blue). Scale bars, 100  $\mu$ m. Related to Figure 2.

**Supplementary figure 3. Gif+ lineage tracing shows that Gif+ chief cells generate other cell types and acquire injury-responsive chief cell characteristics upon injury.** (A and B) Single-channel images of Figure 3C and 3D, respectively. Scale bars, 20  $\mu$ m. (C) Enlarged images of Fig 3D to show lineage tracing of Gif+ chief cells in control and injury. Green lines at the right show vertical expansion of the lineage tracing of Gif+ cells. Scale bars, 100  $\mu$ m. (D) Examples of full gland lineage tracing of Gif+ chief cells (GFP). GSII, neck cell marker; UEAI, pit cell marker; H/K, H/K-ATPase, parietal cell marker. Scale bars, 100  $\mu$ m. (E) Sorting strategy of Gif lineage cells (GFP<sup>+</sup> DsRed<sup>-</sup>) from *Gif-Cre-nTnG* mice. (F) UMAP plots of a further marker for chief cells (*Gper1*) in control (left) and injury (right). (G) UMAP plots of a further marker for proliferating cells (*Stmn1*) in control (left) and injury (right). (H) Projection of *Gif*<sup>high</sup> cells in control and *Gif*<sup>high</sup> and *Gif*<sup>low</sup> cells in injury on the UMAP plot for Pgc+ scRNA-seq. (I) Pseudotime analysis of the Gif lineage cells in the projected UMAP of Pgc+ scRNA-seq data. (J) Gene expression trajectories along the

pseudotime trajectory. The represented expression values are log<sub>2</sub>-transformed normalized read counts followed by the z transform. The pseudotime is denoted in the bar on the x axis. The expression of *Ki67* gets increased while the expression of *p57* and *Gif* gets decreased along the pseudotime trajectory. Related to Figure 3.

**Supplementary figure 4. Regrowth assay after expressing cell cycle inhibitors in gastric organoids and p57 in intestinal organoids by Dox-inducible system.** (A and B) 7d of Dox treatment and Dox withdrawal experiments in Dox-i p57-OE gastric organoids (A) and in Dox-i p57-OE intestinal organoids (B). (C and D) 7d of Dox treatment and Dox withdrawal experiments in Dox-inducible CIP/KIP family CKI expression. (C) Dox-i p21-OE gastric organoids. (D) Dox-i p27-OE gastric organoids. (E) 7d of Dox treatment and Dox withdrawal experiments in Dox-inducible expression of INK4 family of CKI, p16 in gastric organoids. (F) 7d of Dox treatment and Dox withdrawal experiments in Dox-inducible expression of p19<sup>ARF</sup> in gastric organoids. Scale bars, 1 mm. Related to Figure 4.

**Supplementary figure 5. Injury response is inhibited in p57 OE and prolonged in p57 KO *in vivo*.** (A) Double staining of markers for SPEM (Cd44v9, magenta) and chief cells (Mist1, green) in the conditions as outlined above. Scale bars, 100  $\mu$ m. (B) p57 staining in control and p57 knockout epithelium after 14 d of HDT treatment. Scale bars, 100  $\mu$ m. (C) Triple staining with markers for chief cells (Gif, magenta), neck cells (GSII, green), and proliferating cells (Ki67, white) and quantification of injury responsive chief cells. 2-4 mice per condition were analyzed. Scale bars, 100  $\mu$ m for the upper figure sets, 20  $\mu$ m for the insets. Data in the graphs are represented as mean  $\pm$  SD. \*\*P<0.01 and \*\*\*P< 0.001 calculated by one-way ANOVA. (D) Growth difference between control and p57 knockout organoids. Scale bars, 1 mm. (E) Labelling with several markers for the metabolic and molecular changes of chief cell transition upon injury. Scale bars, 100  $\mu$ m. Related to Figure 5.