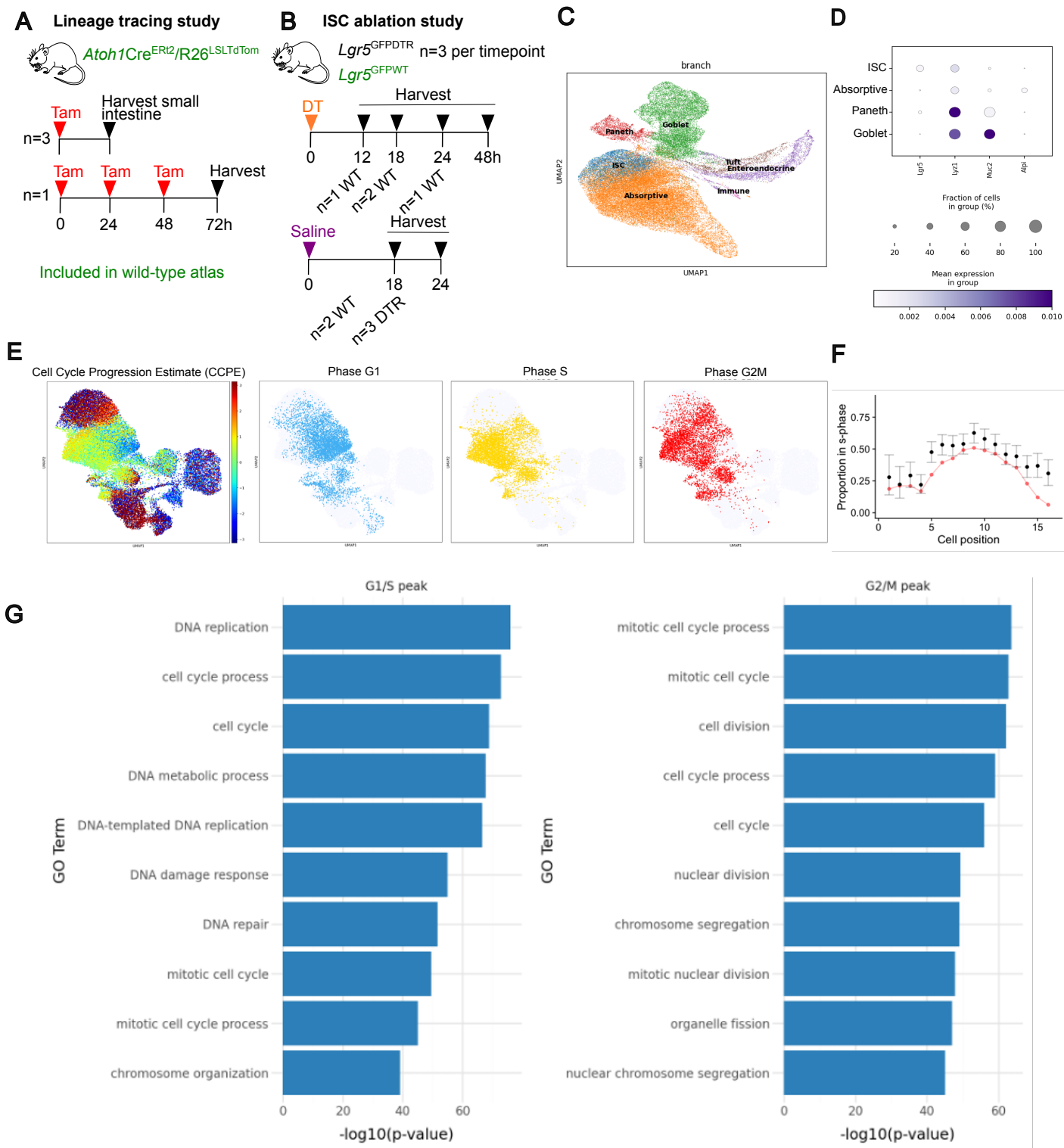




Supplementary Figure 1: Data integration through crypt villus and cell cycle axis. A) Experimental design for *Atoh1* lineage tracing experiment. Cohort, timeline of experiments and number of mice at each timepoint are indicated. Green denotes samples that were used in the wild-type atlas. B) Experimental design for Diptheria Toxin (DT) ISC ablation experiment. C) UMAP showing all cell types identified in the single cell RNA sequencing experiments. D) Dot plot validating expression of cell type markers in the relevant cell populations. E) UMAPs showing the cell cycle metric *theta* and separated cell cycle phases: G1, S and G2/M. F) Proportion of cells in S phase as estimated by CRISP (red dotted line) compared to proportion of cells in s-phase measured by BrdU incorporation quantified in tissue sections (black dots). G) Gene Set Enrichment Analysis (GSEA) for biological pathways identified in G1/S peak or G2/M peak.