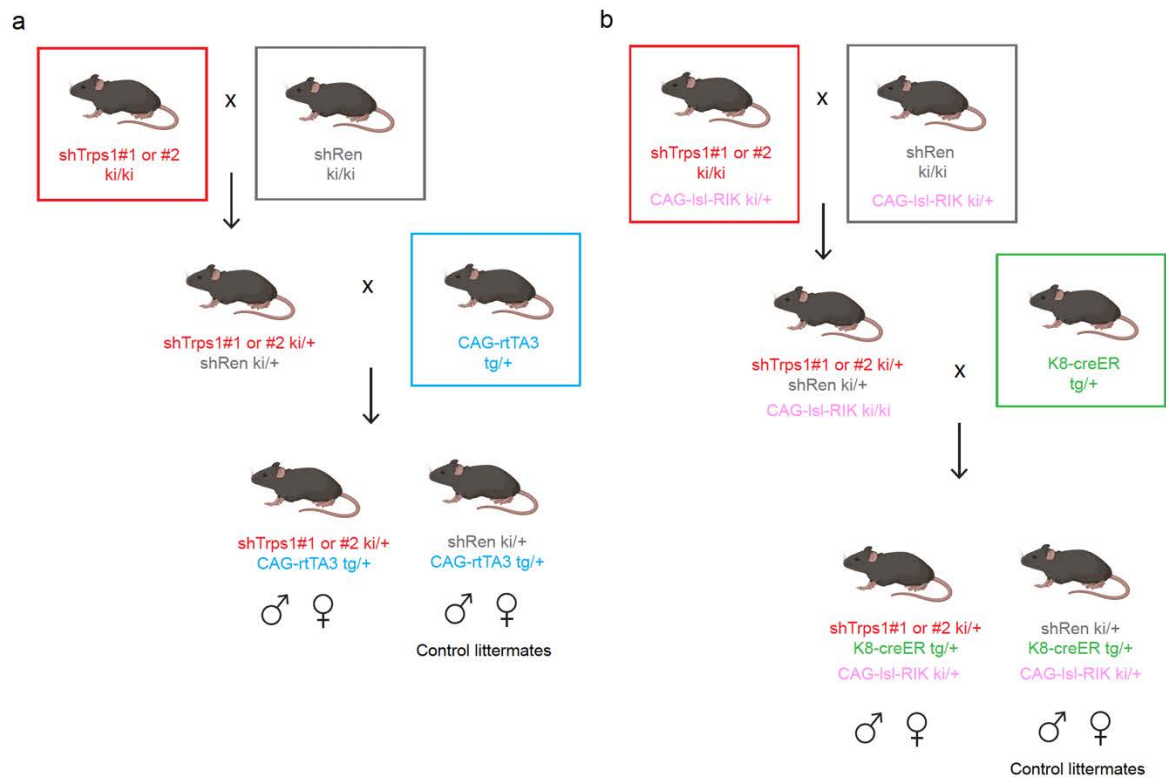
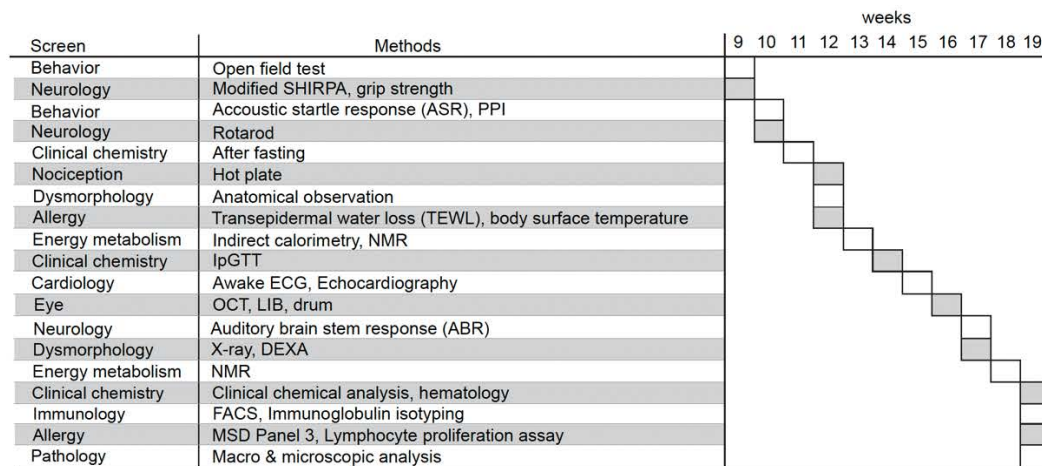




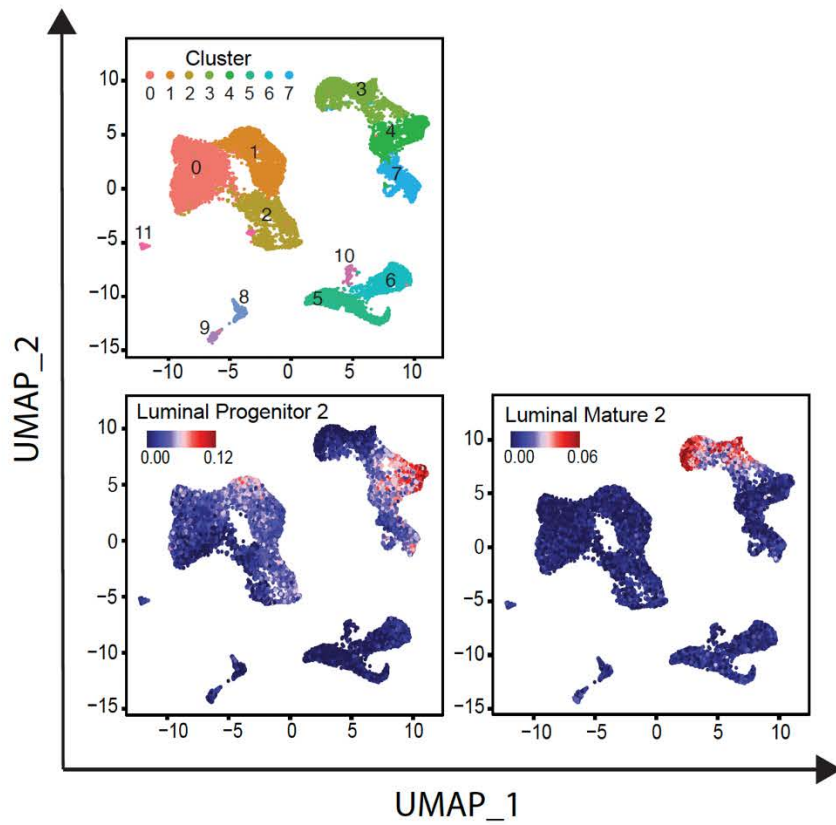
Additional Figure 1: Breeding Schemes

(a) generation of animals ubiquitously expressing shTrps1: homozygous shTrps1 (ki/ki) are crossed with homozygous shRen (ki/ki) to obtain progeny carrying both shTrps1 (ki/+) and shRen (ki/+) alleles. These animals are then crossed with CAG-rtTA3 heterologous (tg/+) animals to obtain shTrps1 ki/+, CAG-rtTA3 tg/+ experimental animals and shRen ki/+ CAG-rtTA3 tg/+ control littermates.

(b) generation of animals expressing shTrps1 specifically in the luminal compartment: animals homozygous for shTrps1 (ki/ki) and carrying a CAG-lsl-RIK allele (ki/+) are crossed with animals homozygous for shRen (ki/ki) and carrying a CAG-lsl-RIK allele (ki/+) to obtain progeny carrying both shTrps1 (ki/+) and shRen (ki/+) alleles and homozygous for CAG-lsl-RIK (ki/ki). These animals are then crossed with K8-CreER (tg/+) animals to obtain shTrps1 ki/+, CAG-lsl-RIK ki/+, K8-CreER tg/+ experimental animals and shRen ki/+, CAG-lsl-RIK ki/+, K8-CreER tg/+ control animals.

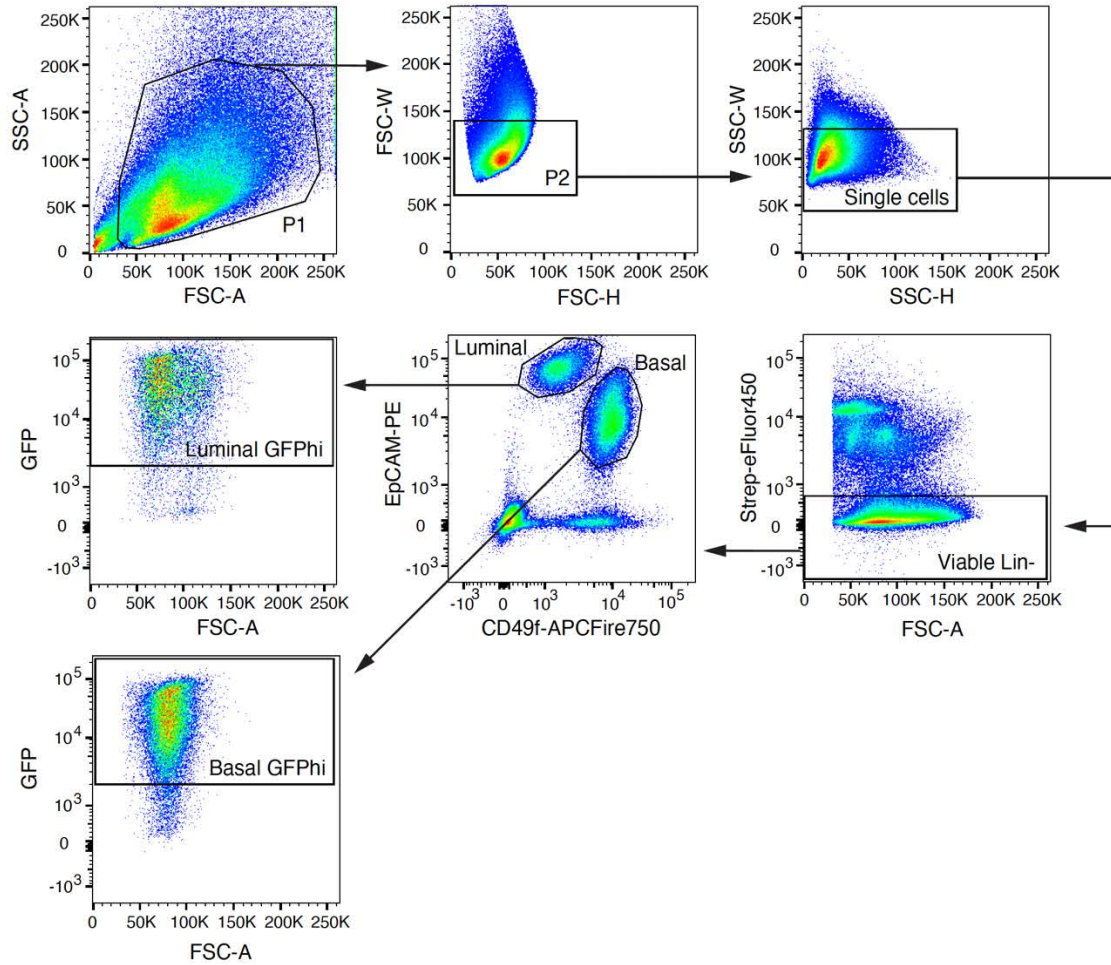


Additional Figure 2: Mouse Phenotypic analysis timeline

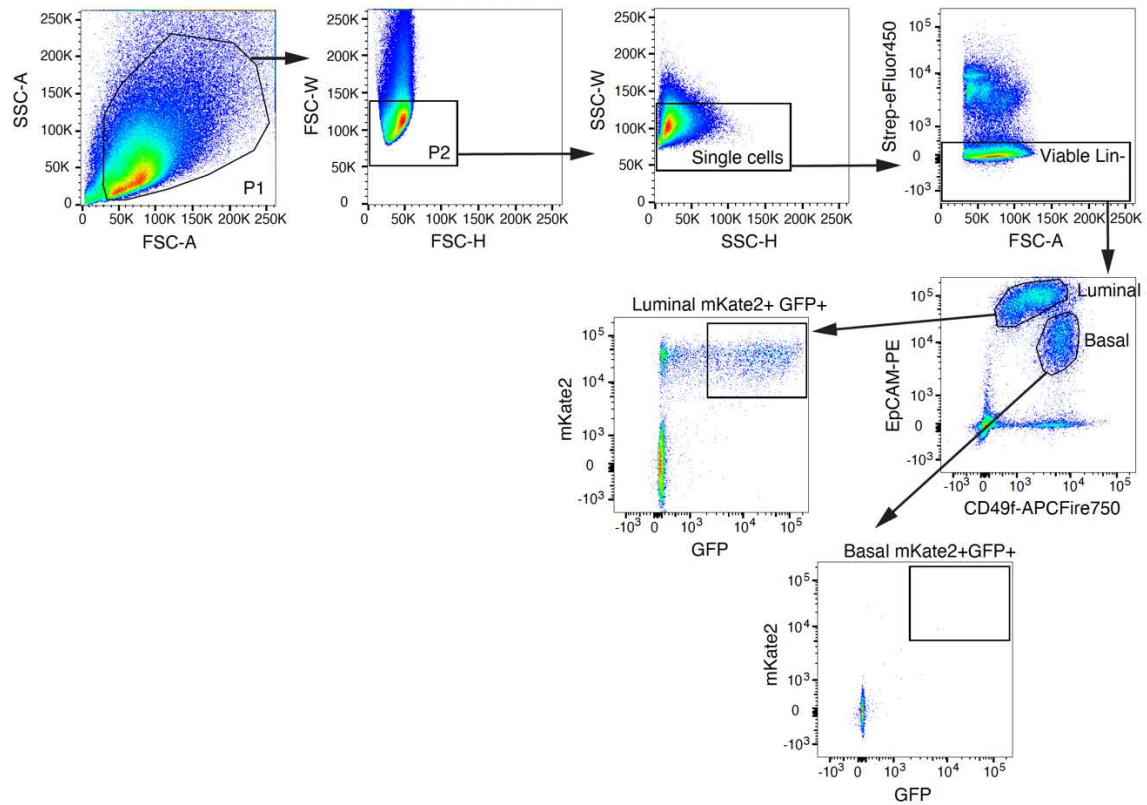


Additional Figure 3:

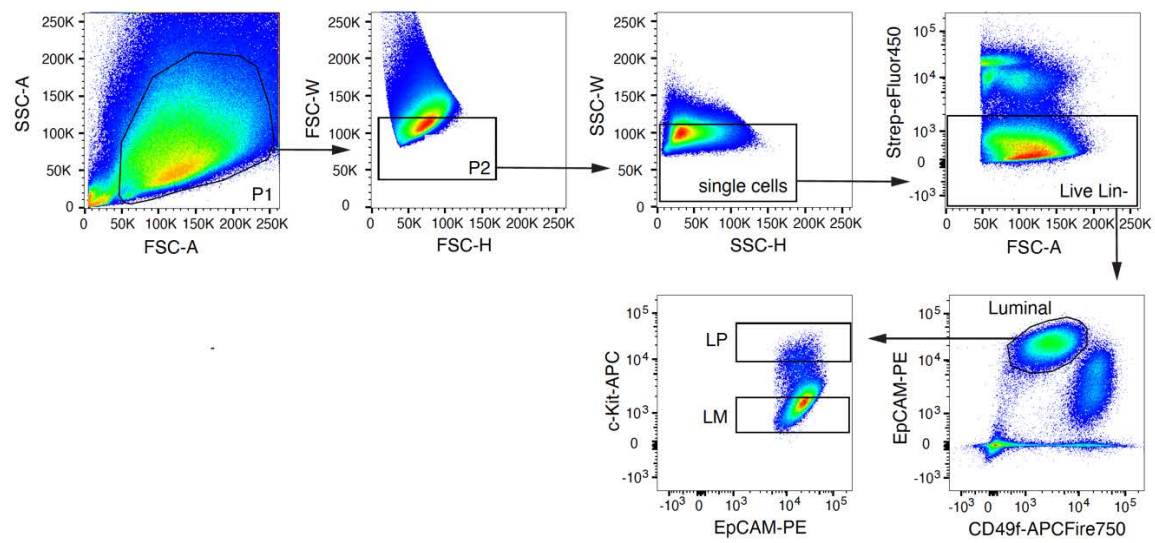
UMAP dimensionality reduction plots of the CITE-Seq data from shTrps1 and shRen mammary gland cells combined (see Figure 3) showing the gene set activity based on AUCs of a luminal progenitor and a luminal mature gene set published by Lim et al. (2010).



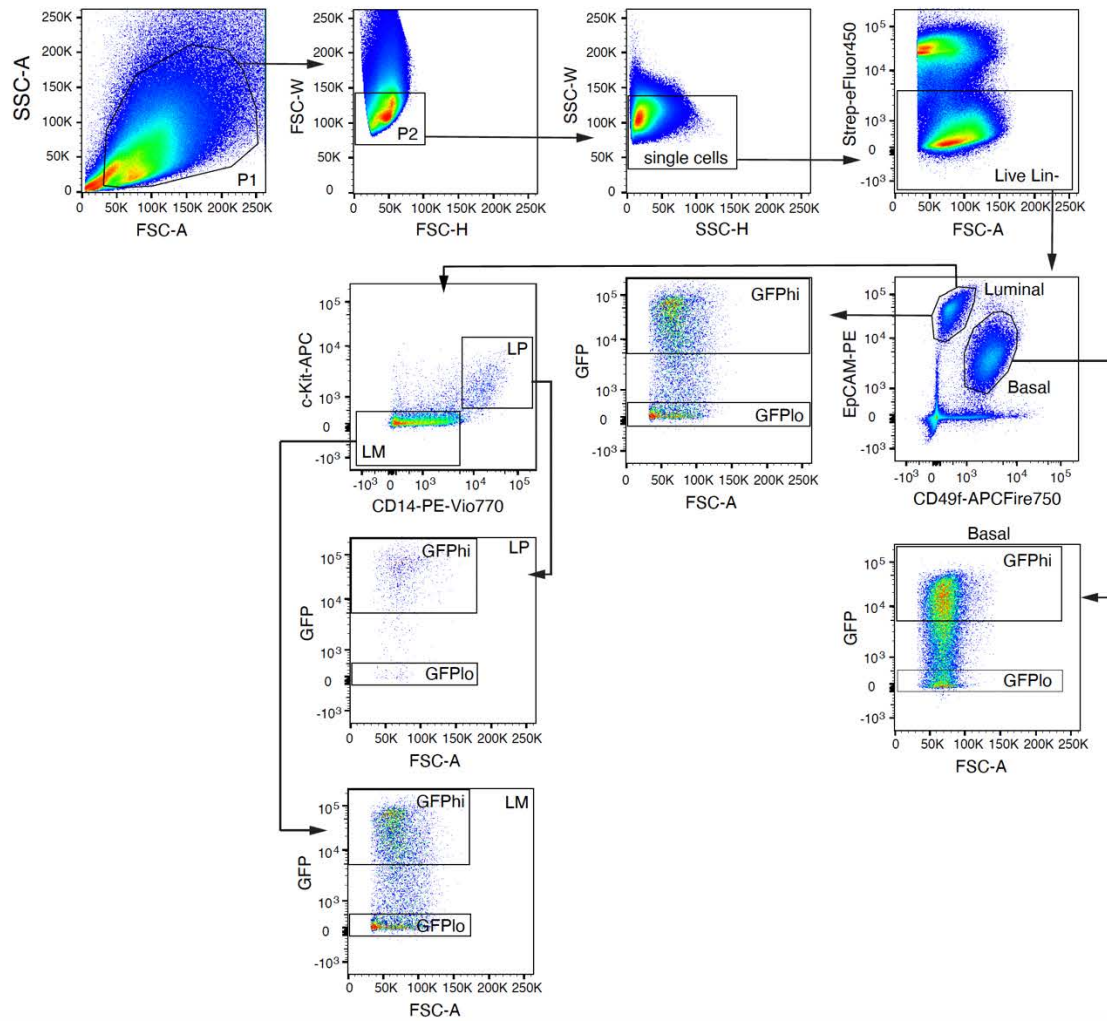
Additional Figure 4: sorting strategy used in Figure 2c to isolate basal and luminal cells expressing shTrps1 (GFPhi) from ubiquitous shTrps1 model mice.



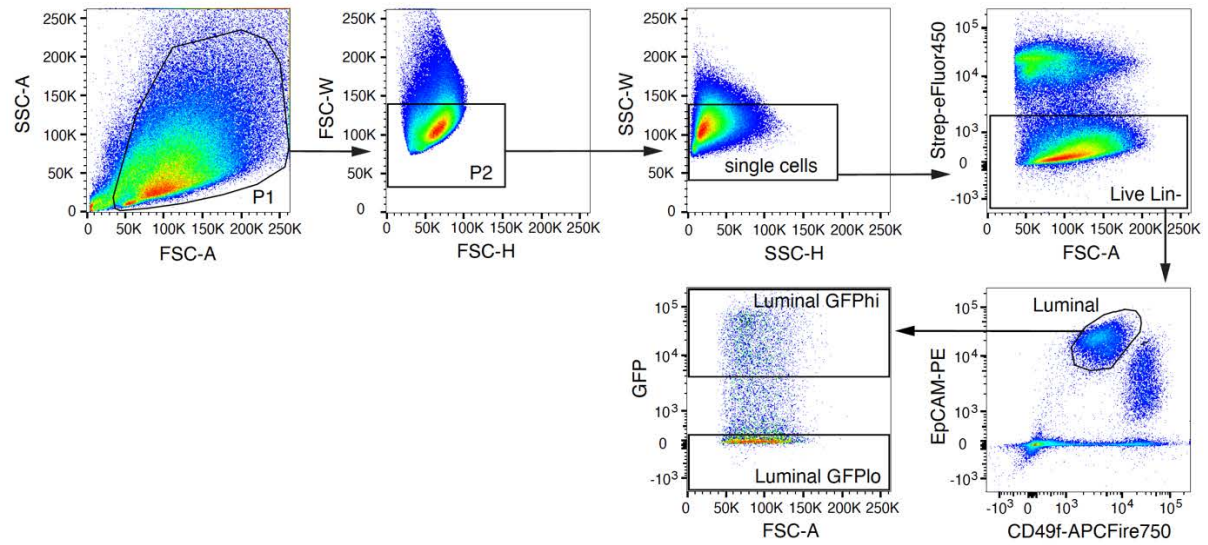
Additional Figure 5: sorting strategy used in Figure 2I to isolate mammary basal and luminal cells expressing shTrps1 (mKate2+ GFP+) from luminal-specific shTrps1 model mice.



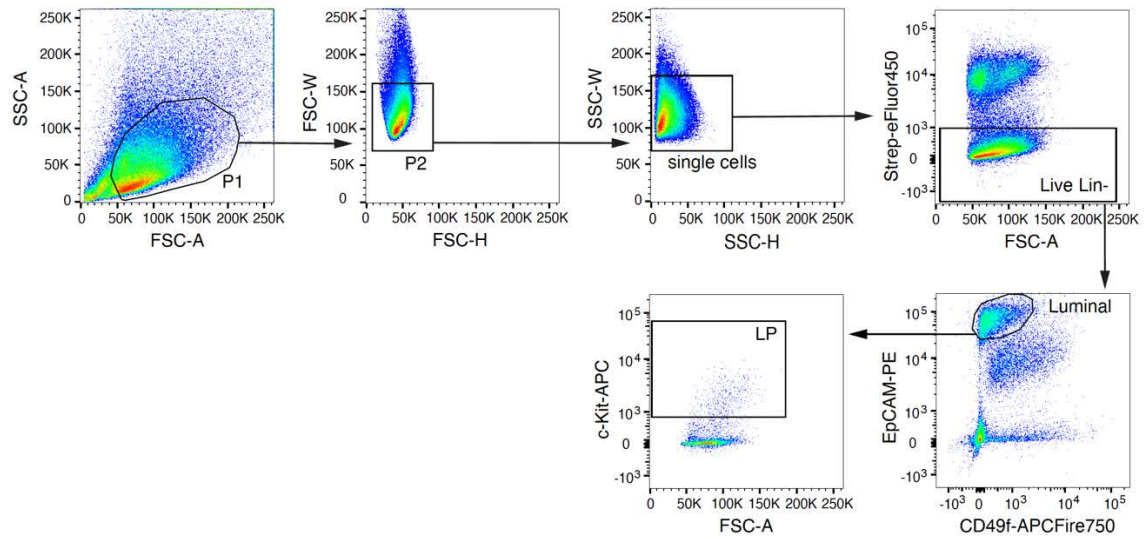
Additional Figure 6: sorting strategy used in Figure 3 to isolate mammary progenitor and mature luminal cells from wild type mice.



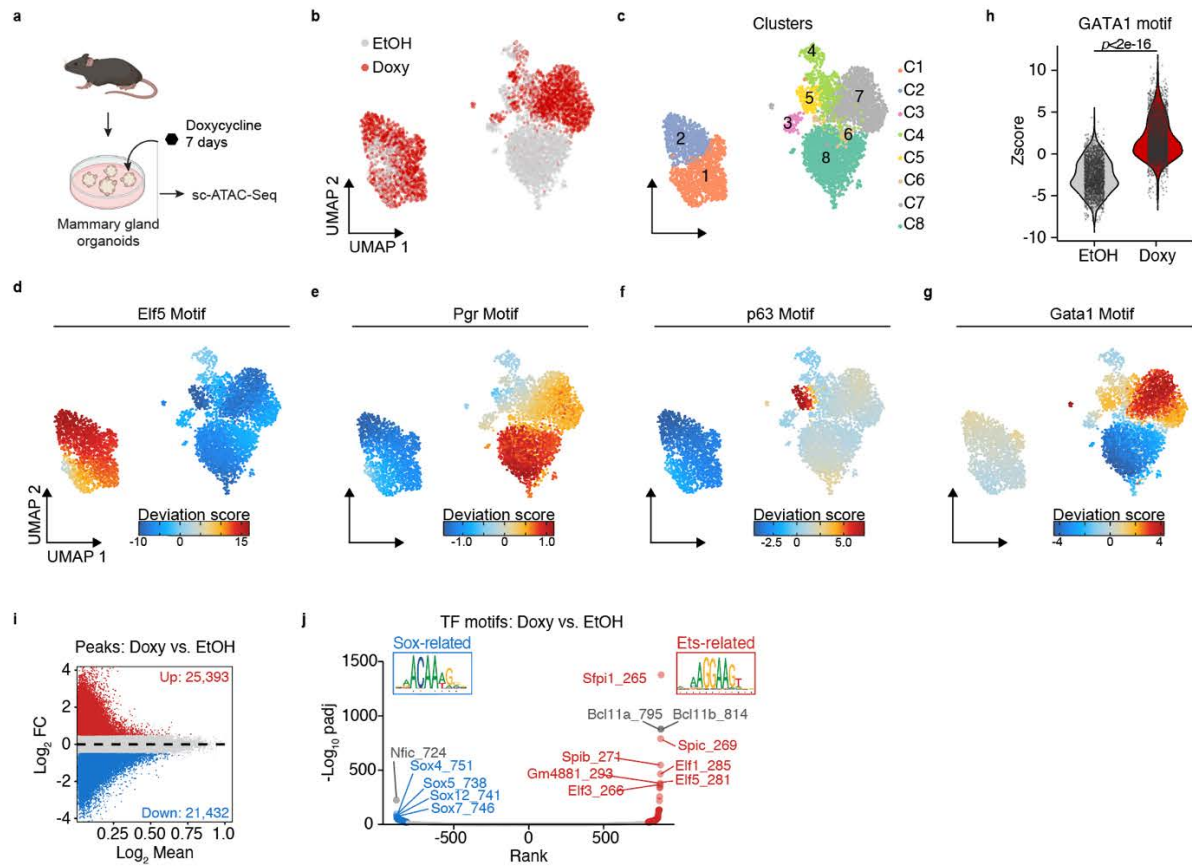
Additional Figure 7: gating strategy used in Figure 4a to analyze the proportion of GFPi and GFPlo cells in the different mammary epithelial subpopulations: Basal, Luminal, Luminal mature (LM) and Luminal progenitor (LP).



Additional Figure 8: sorting strategy used in Figure 4d-e to isolate mammary luminal cells expressing high shTrps1 (GFPhi) or expressing low of no shTrps1 (GFPlo) for a colony forming assay.

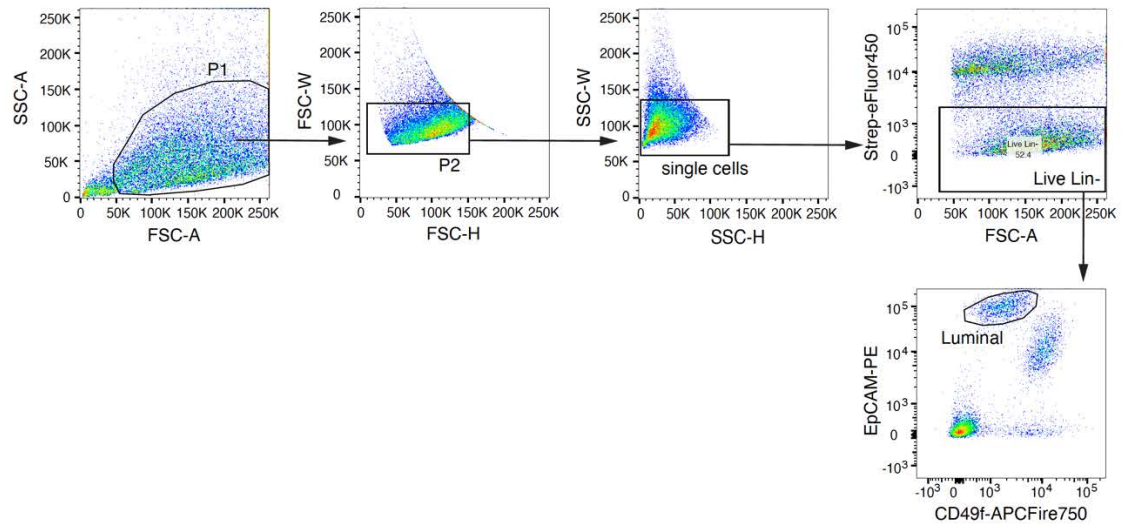


Additional Figure 9: sorting strategy used in Figure 5o-p to isolate mammary luminal progenitor cells from wild type mice for colony forming assay.

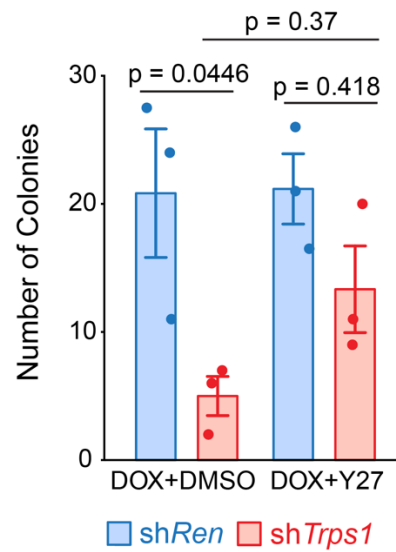


Additional Figure 10: TRPS1 prevents LP differentiation

- (a) Experimental design: organoids prepared from mammary glands isolated from wt BL6 mice were treated with doxycycline for 7 days and subjected to sc-ATAC-Seq
- (b)-(c) UMAP dimensionality reduction plots of the mammary organoid cells. (b) Cells treated with Dox or Ethanol are highlighted in red and grey respectively, (c) Graph-based clusters.
- (d)-(g) UMAP dimensionality reduction plots of the mammary organoid cells showing the motif accessibility for the indicated TF.
- (h) GATA1 motif enrichment in sc-ATAC-Seq peaks from Dox vs Ethanol-treated cells. Wilcoxon rank-sum test.
- (i) Volcano plot of the differential sc-ATAC-Seq peaks from Dox vs Ethanol-treated cells.
- (j) TF Motif enrichment in the up (red) or down (blue) regulated ATAC-Seq peaks in Dox vs Ethanol-treated cells.



Additional Figure 11: sorting strategy used in Figure 6a to isolate mammary luminal cells from wild type mice for CUT and RUN.



Additional Figure 12:

Number of colonies formed by mammary luminal progenitors sorted from shTrps1 and shRen control animals and treated *in vitro* with doxycycline (DOX) or a combination of doxycycline and the Y-27632 ROCK inhibitor (Y27).

One-way ANOVA with Tukey HSD post hoc test. Indicated *p* values are *p* adjusted.