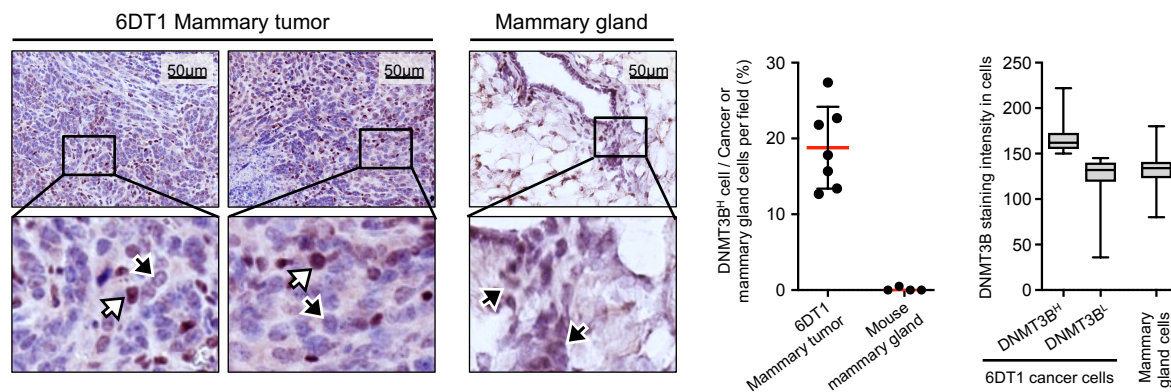
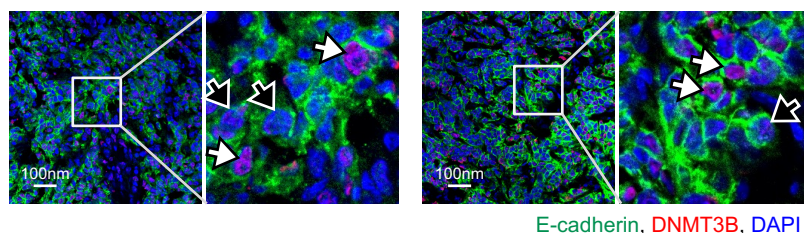
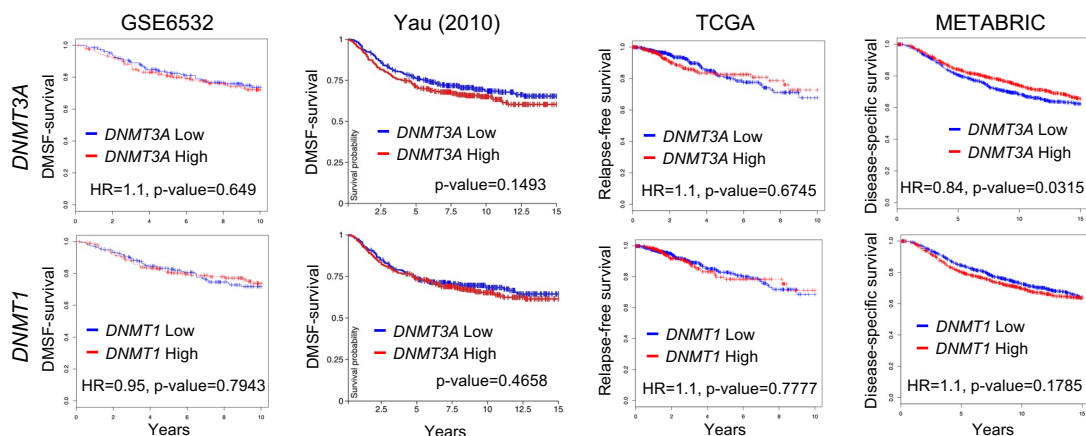
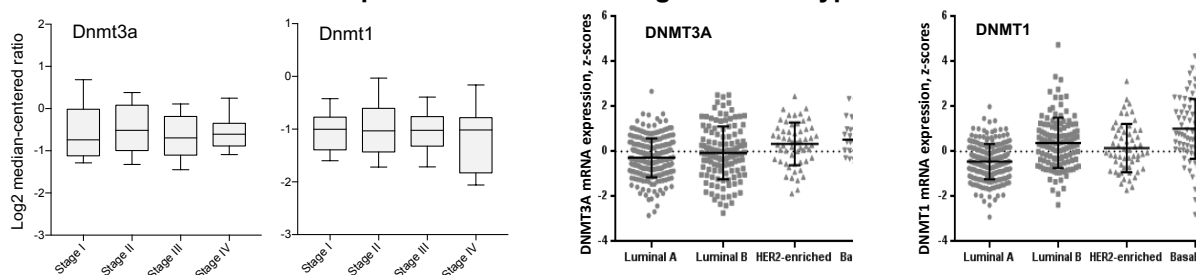
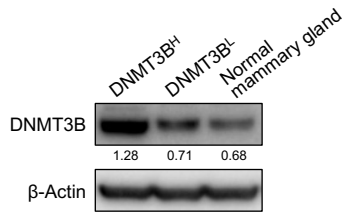
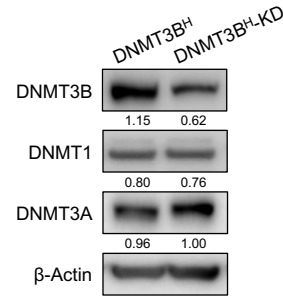
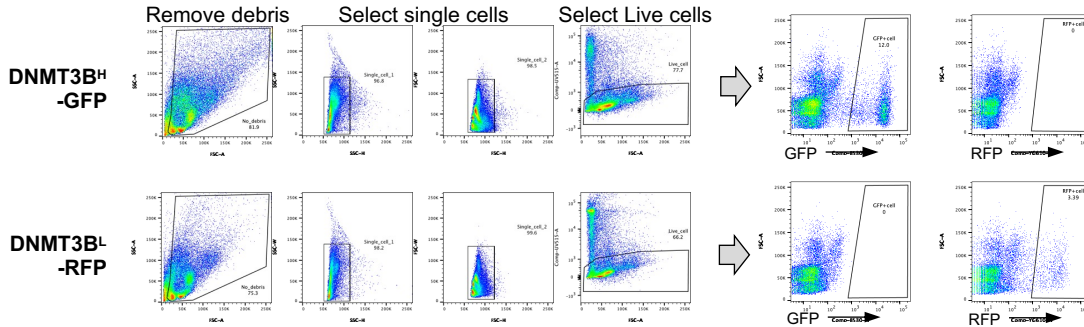
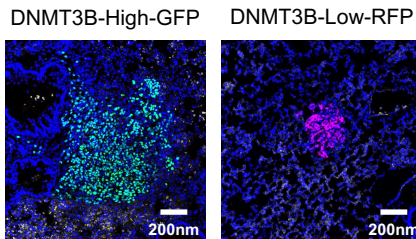
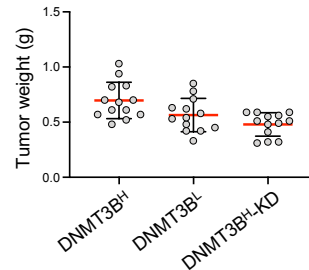
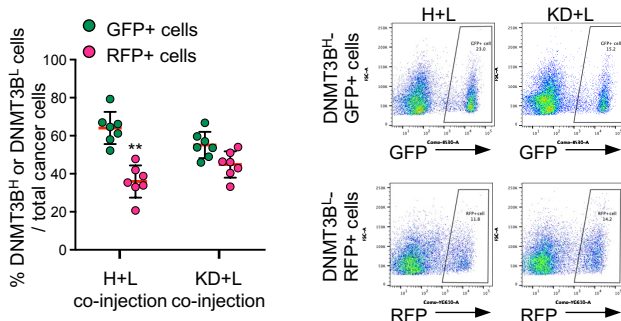


A DNMT3B expression in 6DT1 tumors and normal mammary glands**B DNMT3B expression in E-cadherin positive 4T1 cancer cells in tumors****C DNMT3A and DNMT1 expression and patient survival****D DNMT3A and DNMT1 expression and tumor stages and subtypes**

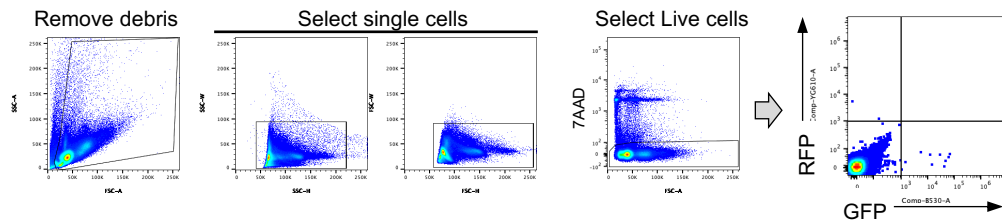
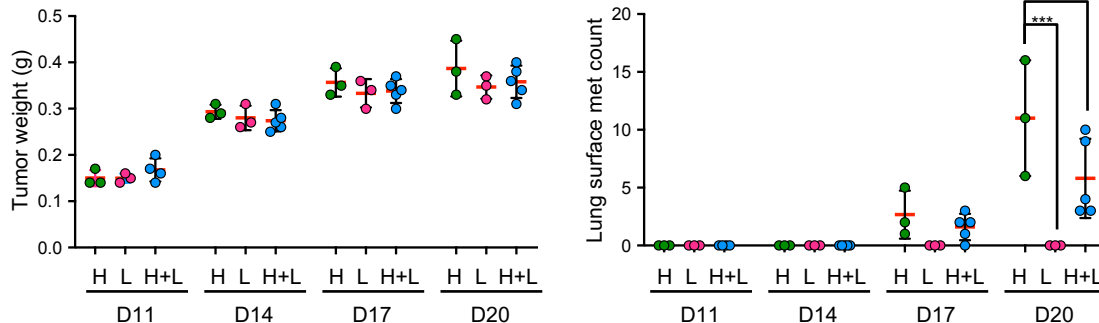
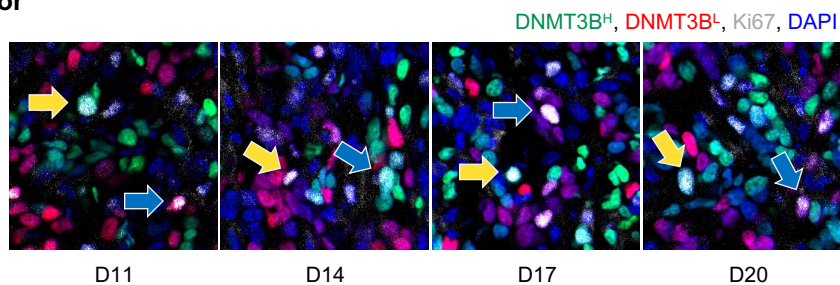
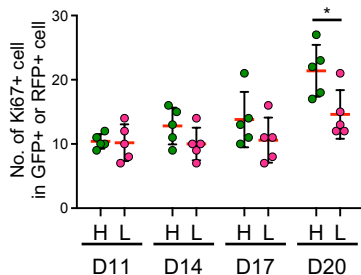
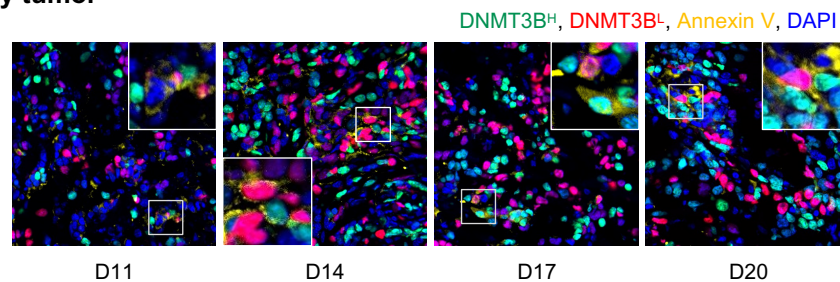
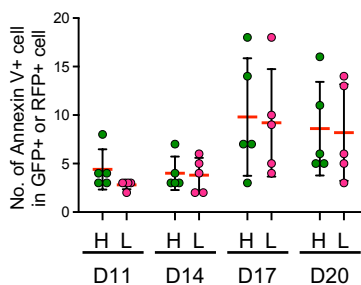
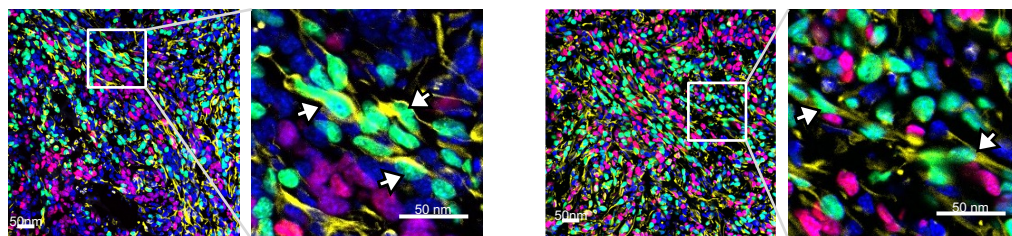
Supplementary Figure 1. A. DNMT3B IHC of 6DT1 mammary tumors and normal mammary glands from BALB/c mice. Percentage of DNMT3B^H cells in cancer and mammary glands cells. Average DNMT3B intensity of DNMT3B^H and DNMT3B^L 6DT1 cancer cells and mammary gland cells on the right panels. Shown are representative images of DNMT3B^H (white arrow) and DNMT3B^L cells (black arrows). **B.** E-cadherin (green) and DNMT3B (red) IF of 4T1 mammary tumors. **C.** Kaplan-Meier plots for correlation DNMT3A (upper panel) or DNMT1 (lower panel) to patient survival in human breast cancer datasets. **D.** DNMT3A and DNMT1 expression levels in breast tumors at different stages (left 2 panels) and with different subtypes (right 2 panels).

**Correlation of gene expression and promoter methylation
for DNMT3B target genes**

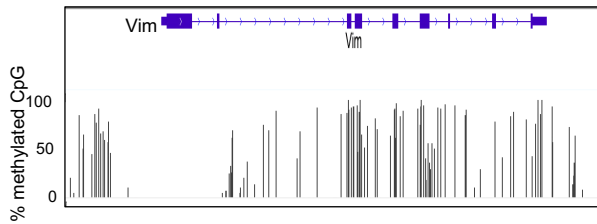
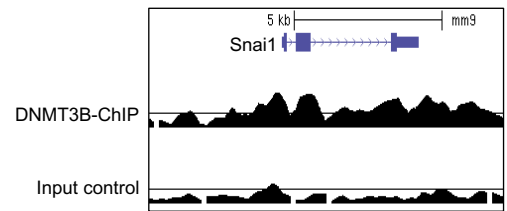
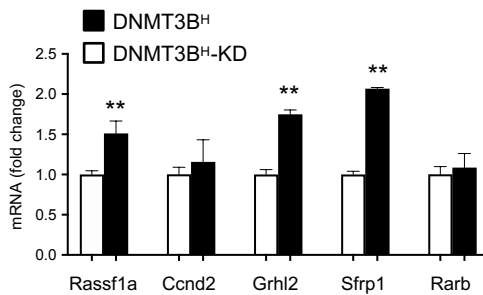
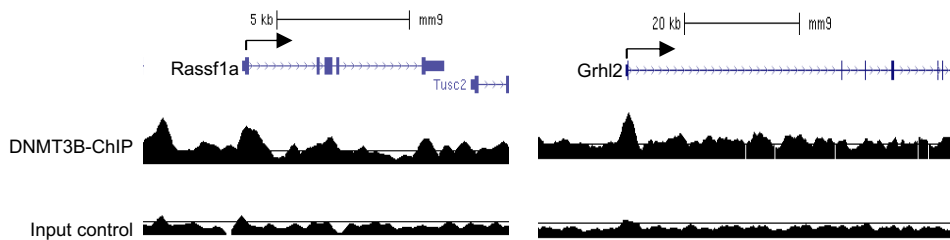
Gene	Spearman r
<i>PTPN7</i>	-0.785
<i>INPP5D</i>	-0.599
<i>CLDN4</i>	-0.327
<i>TCF7</i>	-0.31
<i>SFRP1</i>	-0.278
<i>PMEPA1</i>	-0.273
<i>INPP5J</i>	-0.26
<i>NF1</i>	-0.239
<i>CLDN9</i>	-0.229
<i>SOX9</i>	-0.226
<i>CLDN3</i>	-0.118
<i>DUSP4</i>	-0.083
<i>FZD1</i>	-0.03
<i>CDH11</i>	-0.021
<i>LFNG</i>	0.009
<i>TNFAIP3</i>	0.035
<i>SERPINE1</i>	0.058
<i>CLDN5</i>	0.092
<i>WNT7A</i>	0.169

A DNMT3B in cancer cells and mammary gland**B DNMT3B, DNMT1, DNMT3A with DNMT3B-KD****C Gating strategy for DNMT3B^H and DNMT3B^L cell detection****D DNMT3B^H and DNMT3B^L lung metastases****E Tumor weights****F Clonal composition of DNMT3B^H and DNMT3B^L cells in primary tumors**

Supplementary Figure 2. A. DNMT3B Western blot for DNMT3B^H, DNMT3B^L 4T1 cells and normal mammary glands. **B.** DNMT3B, DNMT1 and DNMT3A Western blot for DNMT3B^H and DNMT3B^H-KD cells. **C.** Gating strategy to detect GFP⁺ and RFP⁺ cells in tissue samples using flow cytometry. **D.** Representative immunofluorescent images of metastatic nodules in the lungs at 4 weeks after injection of mixed DNMT3B^H-GFP and DNMT3B^L-RFP 4T1 cells. **E.** Weights of primary tumors at week 4. **F.** Flow cytometry of GFP⁺ and RFP⁺ cells in primary tumors at 4 weeks after co-injection of DNMT3B^H-GFP and DNMT3B^L-RFP (H+L) or DNMT3B^H-KD-GFP and DNMT3B^L-RFP (KD+L) 4T1 cells. Data are presented as mean ± SD. ** p < 0.01.

A Gating strategy for CTC detection**B Tumor weights and surface met counts****C Ki67+ tumor cells in primary tumor****D Annexin V+ tumor cells in primary tumor****E VIM+ DNMT3B^H cells with EMT morphology in tumors**

Supplementary Figure 3. A. Flow cytometry gating strategy to detect GFP+ and RFP+ CTCs. **B.** Tumor weights and surface metastases (met) counts in the lungs with time course experiment. **C.** Quantitated data and representative images of GFP+ (yellow arrow) and RFP+ (blue arrow) cells with Ki67 expression in primary tumors. **D.** Quantitated data and representative images of GFP+ and RFP+ cells with Annexin V expression in primary tumors. **E.** Representative images of VIM+ DNMT3B^H cells with EMT morphology, indicated by white arrows, in primary tumors. Data are presented as mean \pm SD. * $p < 0.05$, *** $p < 0.001$.

A DNA methylation levels at Vim gene locus**B DNMT3B enrichment at Snai1****C mRNA expression of methylation-sensitive genes****D DNMT3B enrichment at the promoters of Grhl2 and Rassf1a**

Supplementary Figure 4. **A.** High DNA methylation levels of CpGs in Vim gene body. **B.** DNMT3B enrichment in Snai1 gene body in comparison to input control. **C.** qPCR result showing increased mRNA expression of methylation-sensitive genes, Rassf1a, Grhl2 and Sfrp1, by DNMT3B knockdown in DNMT3B^H cells. **D.** DNMT3B enrichment in the promoter regions of Rassf1a and Grhl2 in comparison to input control. Data are presented as mean \pm SD. ** $p < 0.01$.