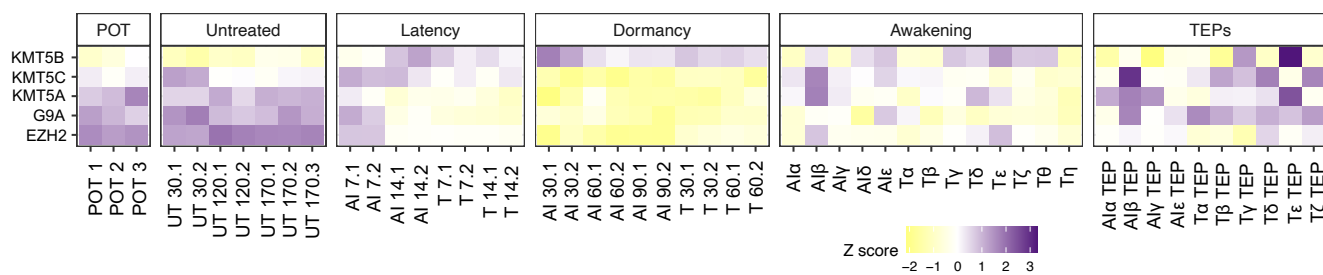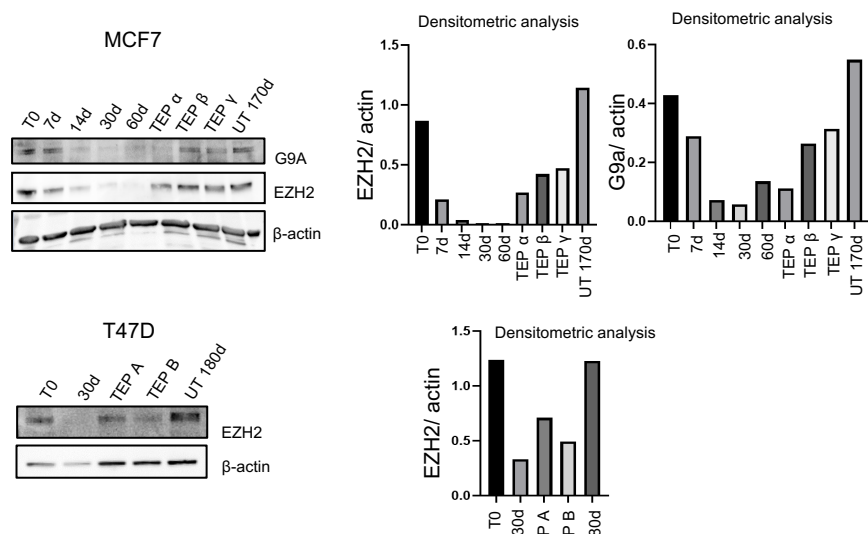# Supplementary Figure S28. Expression of the epigenetic dormancy signature genes

a Bulk RNA-seq

b

MCF7

Densitometric analysis

Densitometric analysis

T47D

Densitometric analysis

c Spatial transcriptomics (CK+ segment)

G9a

d TRADITIOM LSC (MCF7 –E2)

T0.1 T0.2 AI 1mo.1 AI 1mo.2 AI 2mo.1 AI 2mo.2 AI aw1 AI aw2 AI aw3 AI aw4

EHMT2

EZH2

KMT5A

KMT5B

KMT5C

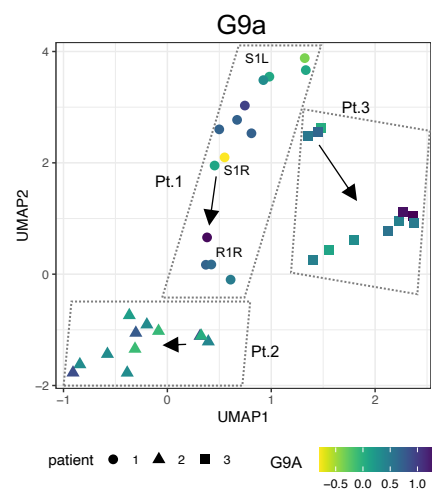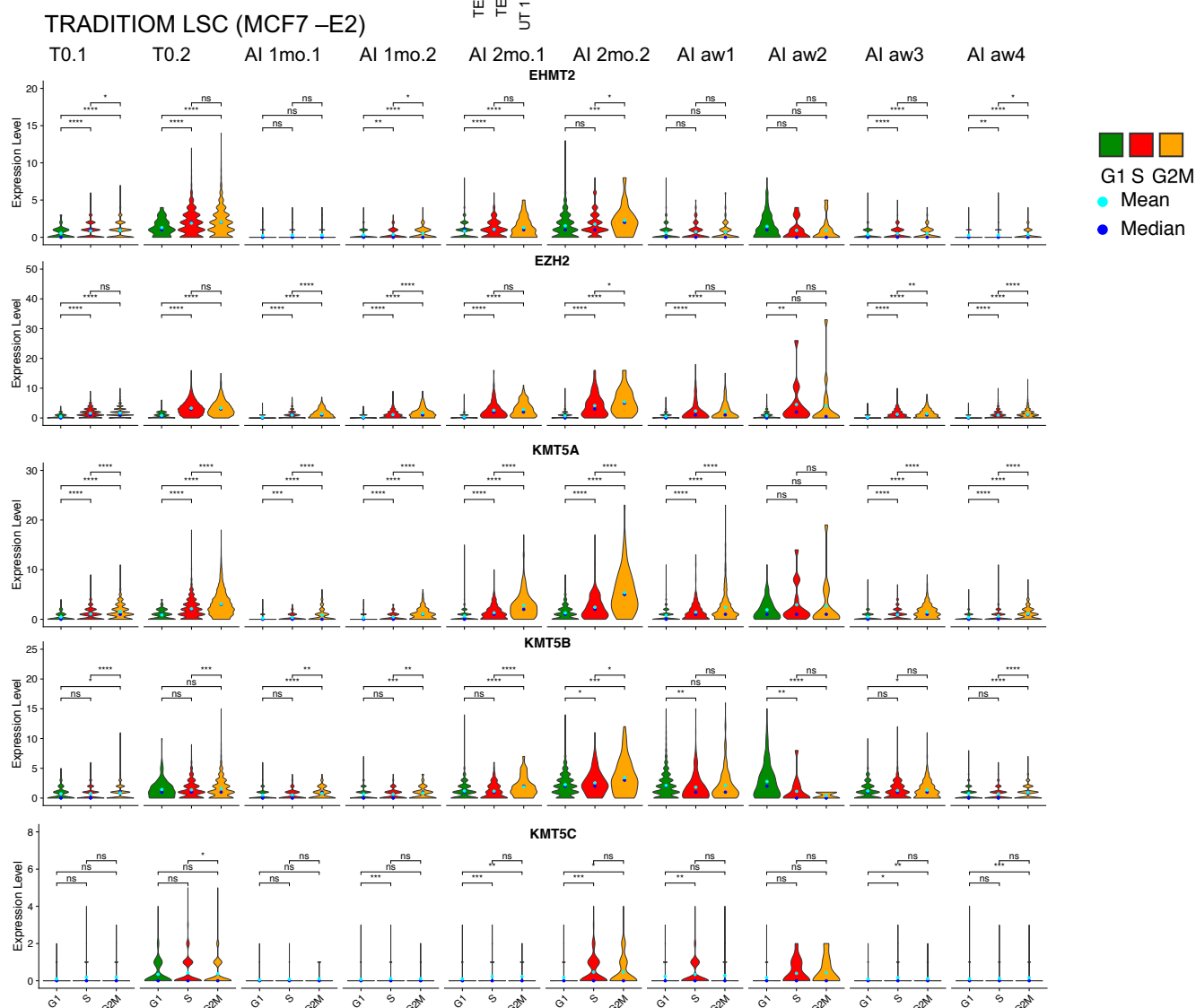**Supplementary Figure S28. Expression of the epigenetic dormancy signature genes. a)** Heatmap depicting RNA expression levels of *KMT5A/B/C*, *G9A* and *EZH2* from bulk RNA-seq in TRADITIOM MCF7 dataset. **b)** Protein expression levels of G9A (for MCF7) and EZH2 (for MCF7 and T47D) are shown with Western blotting for TRADITIOM samples from POT (pre-treatment) to TEPs (late progression). Densitometric analyses of the bands (normalized to beta-actin) are shown as bar plots. **c)** UMAP projection of spatial transcriptomic data for G9A expression from patients 1-3 are shown for CK+ segment. **d)** Violin plots depicting scRNA-seq expression levels of *EZH2*, *G9A (EHMT2)*, *KMT5A/B/C* in cells at different cell cycle stages (G1, S and G2M) for TRADITIOM LSC (live single cell) MCF7 –E2 (AI) arm from T0, early dormancy (1 month, 1mo), late dormancy (2 months, 2mo) to awakenings.