Figure S1. Regulation of subtype marker genes in classical and basal-like cell lines. (A) mRNA expression was determined by qPCR and calculated in relation to the housekeeper gene *TBP* (n=3). (B) ChIP analysis of H3K27ac and IgG (antibody control) for the *EPCAM*, *ELF3* and *VIM* promoter. ChIP-qPCR data were normalized as % of input (n=2-4). All data are presented as mean; P-values were calculated by two-tailed, unpaired Student's t or non-parametric Mann-Whitney test. *P<0.05, ***P<0.001, ****P<0.0001. TBP, TATA box binding protein; ChIP, chromatin immunoprecipitation; q, quantitative; EPCAM, epithelial cell adhesion molecule; ELF3, E74 like ETS transcription factor 3; VIM, vimentin; KLF5, KLF transcription factor 5.

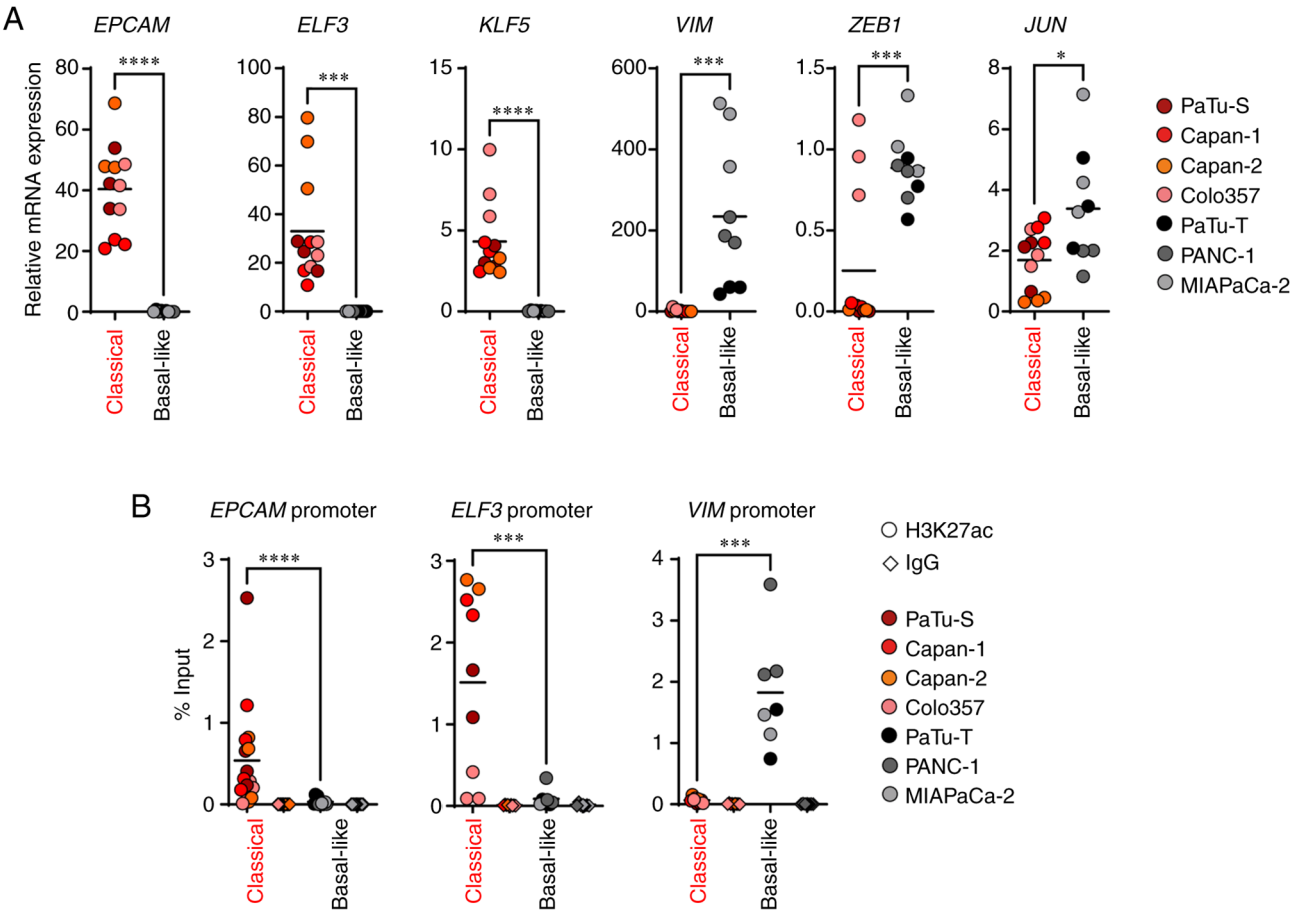

Figure S2. Epigenetic drug response and cytotoxicity. Drug response curves for A485- and SAHA-treated cell lines were generated 72 h after treatment by MTT cell viability assay. Data are presented as mean (n=6-7). SAHA, Suberoylanilide hydroxamic acid.

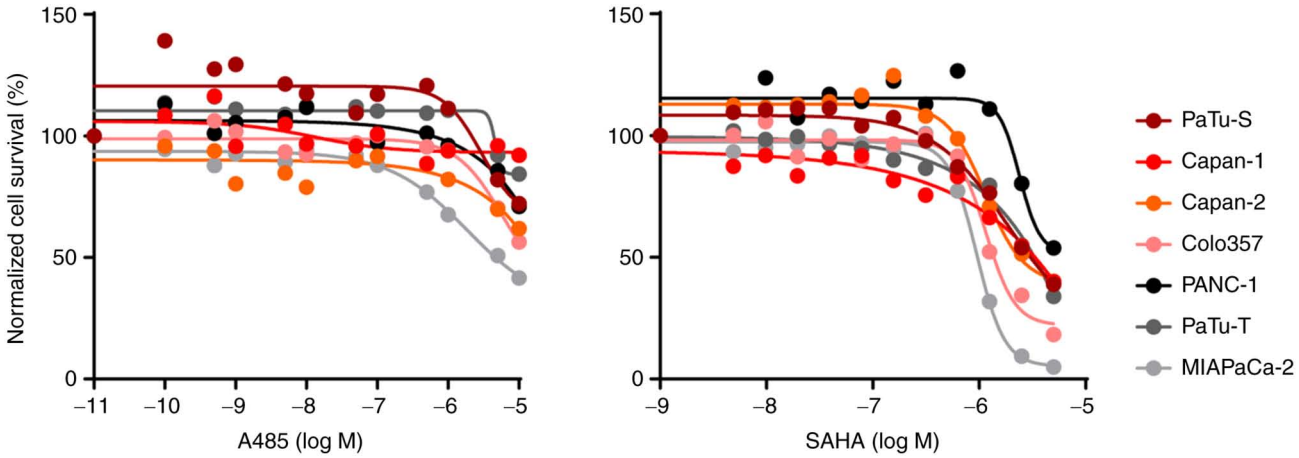

Figure S3. Influence of epigenetic drug treatment on gemcitabine sensitivity. (A) mRNA expression of *SLC29A1* was determined by qPCR in relation to the housekeeper gene *TBP* (n=3). (B) ChIP analysis of H3K27ac and IgG (antibody control) for the *SLC29A1* promoter. ChIP-qPCR data are normalized as % of input (n=3). (C) mRNA expression of *SLC29A1* in control-, 1 μM A485- and 0.5 μM SAHA-treated cell lines after 24 h was determined by qPCR and calculated in relation to the housekeeper gene *TBP* (n=2). (D) Survival of cells treated with 1 μM A485 and 0.5 μM SAHA for 96 h followed by 72 h gemcitabine treatment was measured by MTT assay (n=3). All data are presented as mean. P-values were calculated by two-tailed, unpaired Student's t or non-parametric Mann-Whitney test or one-way ANOVA with Fisher's LSD post hoc test. *SLC29A1*, solute carrier family 29 member 1; q, quantitative; TBP, TATA box binding protein; ChIP, chromatin immunoprecipitation; SAHA, Suberoylanilide hydroxamic acid.

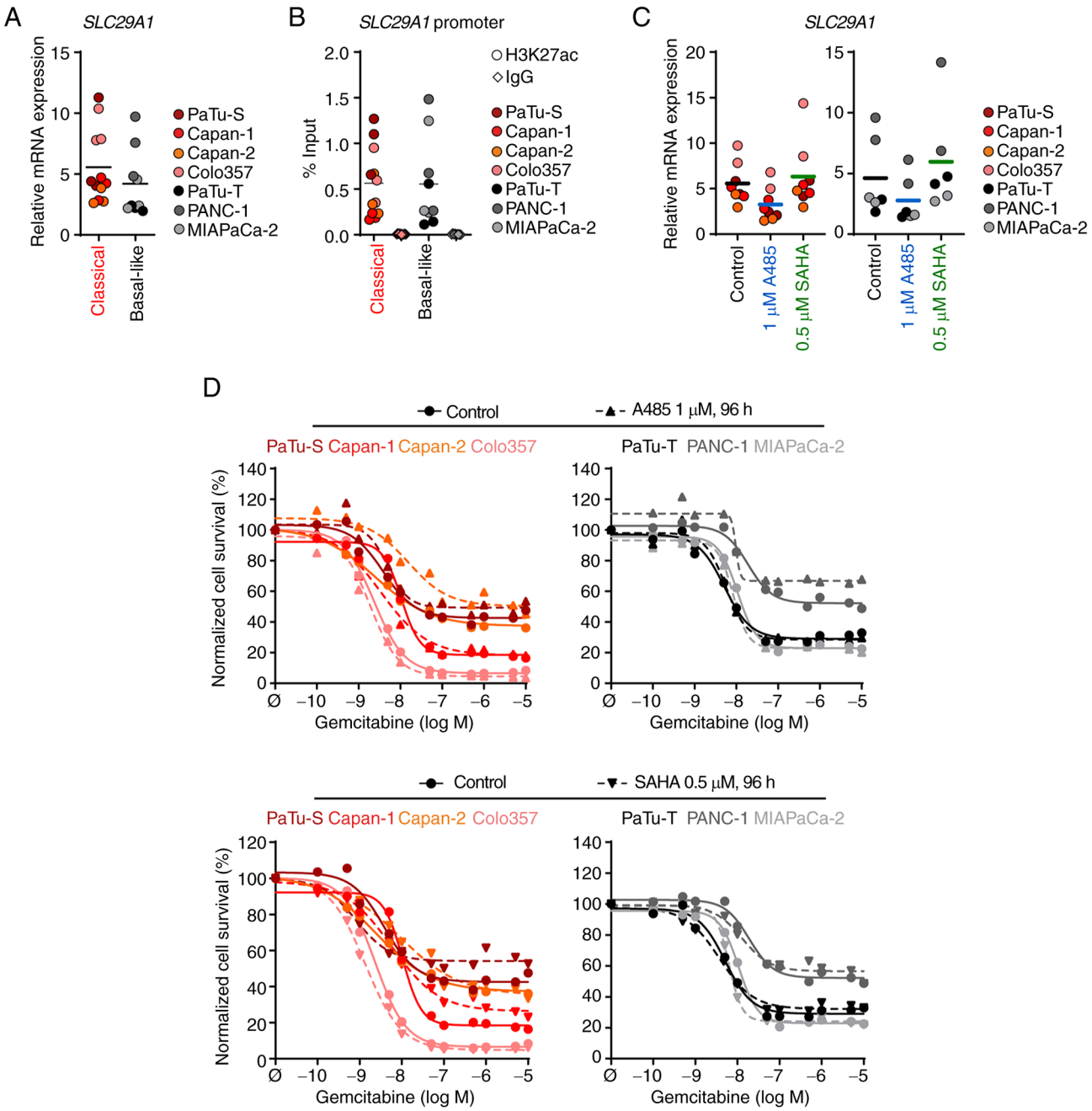

Figure S4. Effects of long-term epigenetic drug treatment on classical and basal-like cell lines. Cell lines were treated with 1 μM A485 or 0.5 or 0.05 μM (MIAPaCa-2) SAHA between 4-30 weeks before use. (A) Proliferation of cells was measured by MTT assay (n=3). (B) Representative images (magnification, x50) of cell migration assay. Yellow lines indicate inflicted cell wound area. All data are presented as mean ± SEM. SAHA, Suberoylanilide hydroxamic acid; LT, long-term treatment.

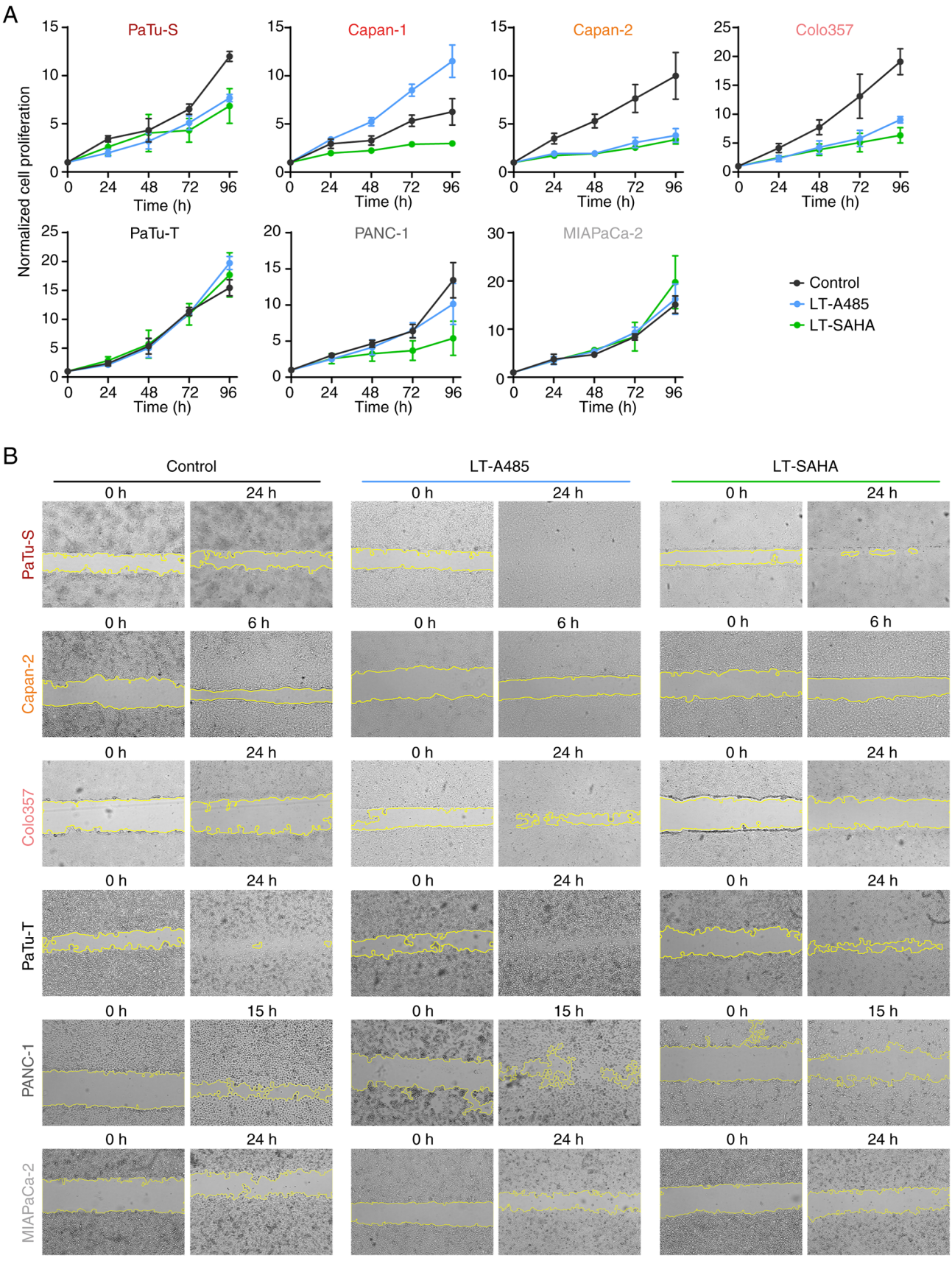

Figure S5. Gemcitabine response of classical and basal-like PDAC cell lines after long-term epigenetic drug treatment. Cell lines were treated with 1 μM A485 or 0.5 or 0.05 μM (MIAPaCa-2) SAHA between 4-30 weeks before use. Cell survival was measured by MTT assay (n=3). All data are presented as mean ± SEM. SAHA, Suberoylanilide hydroxamic acid; LT, long-term.