**Supplemental figures**

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**Supplemental Figure 1: *SLFN5*, *SLFN12*, *SLFN13*, and *SLFN14* expression patterns and their association with survival outcomes in PC patients.**

Analysis of *SLFN5*, *SLFN12*, *SLFN13*, and *SLFN14* mRNA expression levels in tumors (n = 179, red box) and normal tissues (n = 171, gray box) from the TCGA and GTEx databases using GEPIA. Dots represent individual sample data. \**p* < 0.05.An overall survival rate analysis of PC patients using the TCGA database was conducted. Each dot represents the expression level of *SLFN5*, *SLFN12*, *SLFN13*, and *SLFN14* in one sample. The overall survival rate of PC patients was analyzed according to the expression levels of *SLFN5*, *SLFN12*, *SLFN13*, and *SLFN14* using the Kaplan-Meier method and log rank test.

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**Supplemental Figure 2: *SLFN11*-knockdown PC cells induce cell apoptosis and polyploidy population.**

(A) Western blot analysis of total cell lysates harvested 48 hours after transfection of control, *SLFN11* siRNA\_1, *SLFN11* siRNA\_2, and *SLFN11* siRNA\_3 into Panc10.05 cells. Western blotting was performed to assess the protein expression levels of SLFN11 and β-actin.

(B) CCK-8 assays were conducted to assess the proliferation of control and *SLFN11*-knockdown PC cells over 0–72 hours. Curves were constructed from biological triplicates, with values expressed as means ± SEMs.

(C) Panc10.05 cells were transfected with control or *SLFN11* siRNA and subjected to FACS analysis at 72 hours. The FACS plots and data are representative of at least two independent experiments.

(D) Percentages of cells in sub-G1 (apoptosis, red), G0/G1 (blue), G2/M (orange), S (green), and polyploidy (purple) phases.

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**Supplemental Figure 3: Quantification of western blot results from thymidine double block-synchronized cells.**

Western blot analysis was performed on thymidine double block-synchronized cells to assess the expression levels of SLFN11, CDC6, and cyclin A. The protein bands were quantified using ImageJ software (version 1.50i), and the relative expression levels were normalized to β-actin. The bar graphs represent the quantified data, showing the relative protein expression levels of SLFN11, CDC6, and cyclin A in synchronized cells.

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**Supplemental Figure 4: *SLFN11* expression was correlated with cisplatin and olaparib drug sensitivity.**

(A) Correlation analysis between gemcitabine sensitivity (GDSC database) and *SLFN11* mRNA expression (CCLE database) across various tissues. *r* = 0.29, *p* = 1.3 × 10⁻13.

(B) Correlation analysis between gemcitabine sensitivity (NCI-60 database) and *SLFN11* mRNA expression (NCI-60 database) in various PC cell lines. Pearson coefficient correlation *r* = 0.69, *p* = 7.8 × 10⁻10.

(C) Western blot analysis of total cell lysates harvested after WT and *SLFN11*-KO transfection into PANC-1 and Panc10.05 cells, followed by selection with puromycin. Western blotting was performed to assess the protein expression levels of SLFN11 and β-actin.

(D) WT and *SLFN11*-KO Panc10.05 cells were visualized by immunofluorescence staining for GFP (SLFN11, green) and DNA (blue).

(E) Correlation analysis between cisplatin drug sensitivity (GDSC database) and *SLFN11* mRNA expression (CCLE database) across various tissues. Pearson coefficient correlation *r* = 0.34, *p* = 6.7 × 10⁻17.

(F) Correlation analysis between olaparib drug sensitivity (GDSC database) and *SLFN11* mRNA expression (CCLE database) across various tissues. Pearson coefficient correlation *r* = 0.26, *p* = 1.8 × 10⁻10.

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**Supplemental Figure 5. *IC50* values of Gemcitabine, Cisplatin, Olaparib, Ceralasertib, and Adavosertib in PC cells.**

*IC50* values of gemcitabine, cisplatin, olaparib, ceralasertib, and adavosertib in PC cells obtained from the CellMiner Cross-Database.