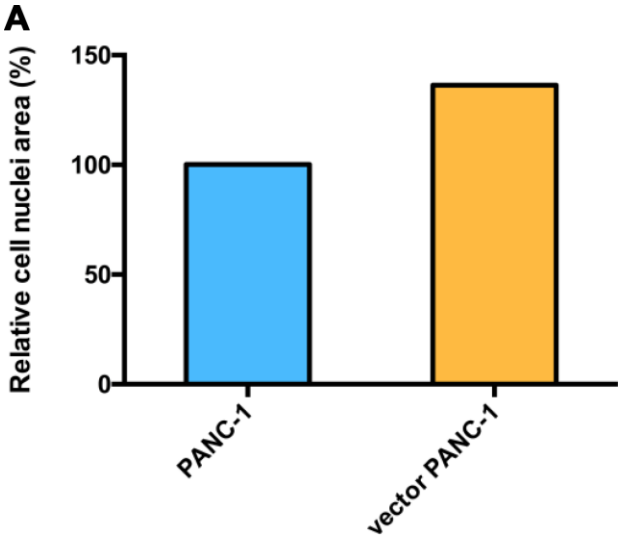
## SUPPLEMENTARY FIGURES




**Supplementary Figure 1. (related to Figure 1). Quantification of the cell nuclei size.** (**A**) The cell nuclei size was quantified with Image J software.

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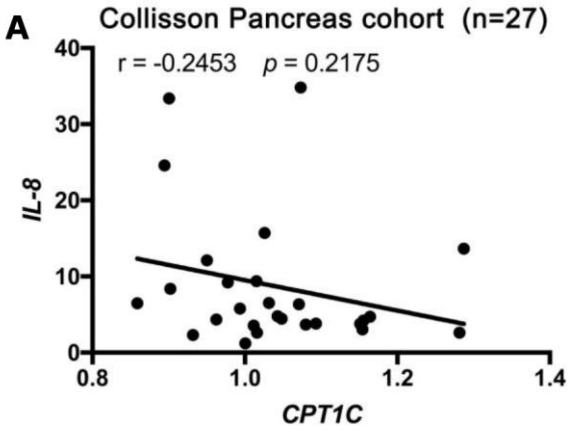
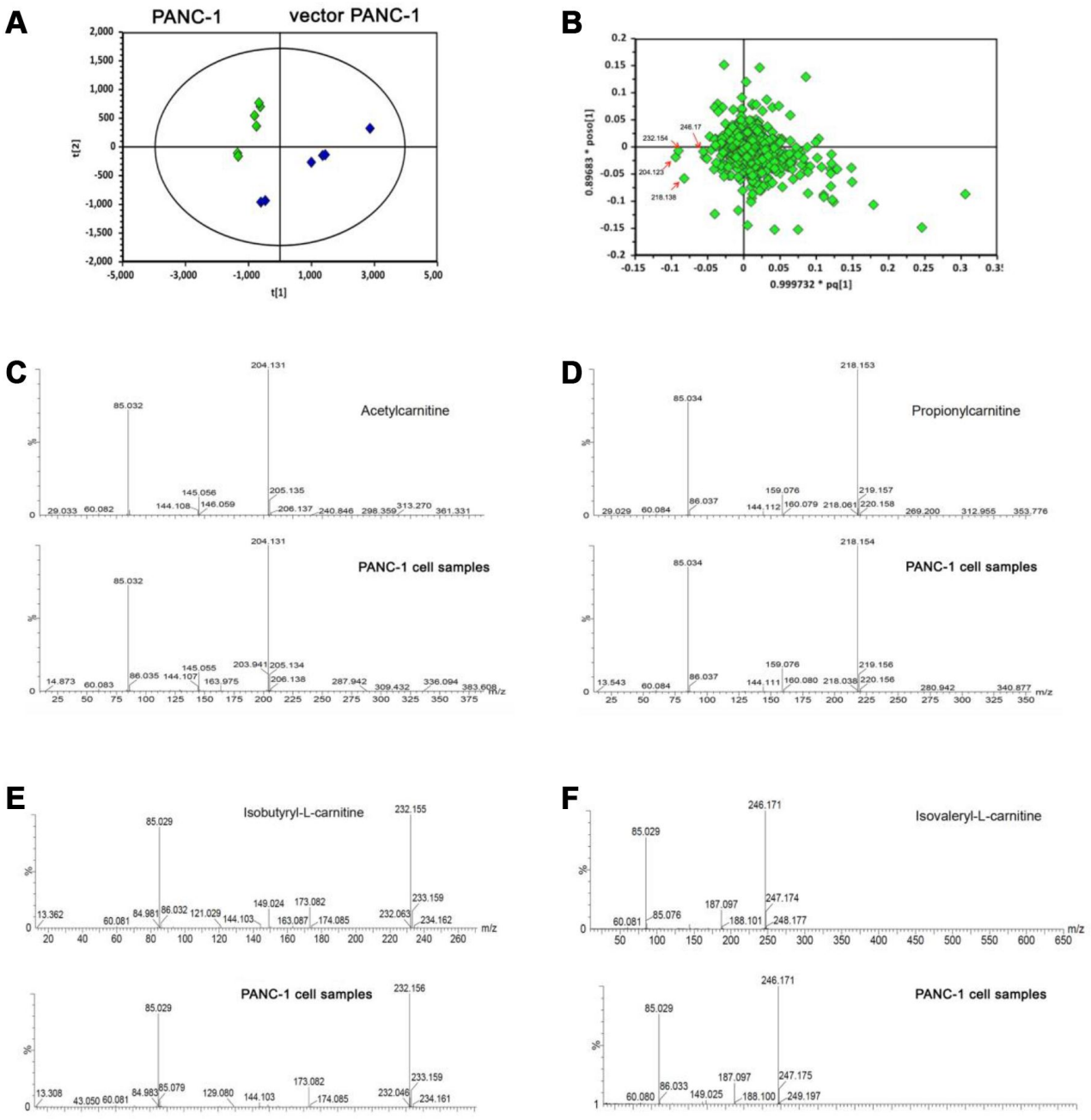
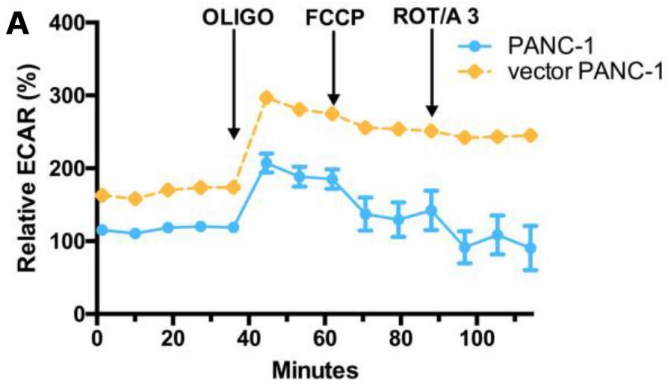


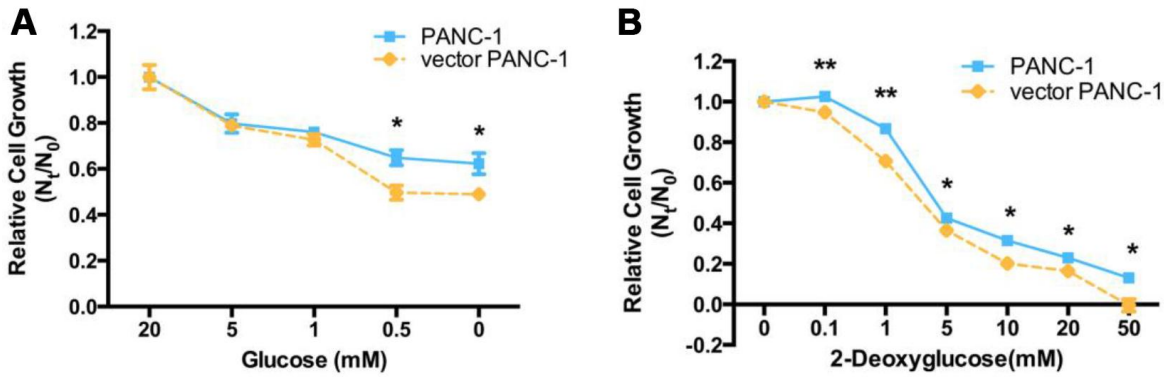

**Supplementary Figure 2. (related to Figure 1). Correlation of key SASP factor, IL-8 with CPT1C expression in pancreatic cancer patients.** (**A**) *IL-8* negatively correlates with *CPT1C* mRNA expression in pancreatic cancer patients.



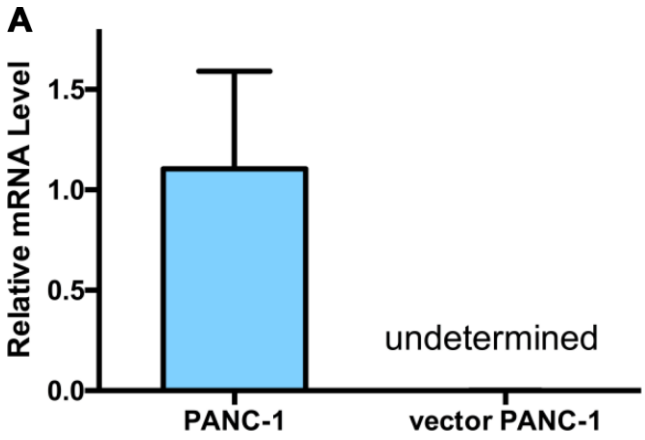

**Supplementary Figure 3. (related to Figure 2). Metabolomics profiles reveal significantly decreased acylcarnitines in senescent vector PANC-1 cells.** (**A**) PCA score plots of HILIC-ESI$^-$-MS metabolomics profiles obtained from HILIC-ESI$^-$-MS, n = 6/group. (**B**) S-plot of OPLS/DA models of HILIC-ESI$^+$-MS data. (**C**–**F**) Validation of cell metabolite biomarkers by LC-MS/MS analysis. Corresponding MS/MS spectra of authentic chemicals (up) and cell samples (bottom) are shown.



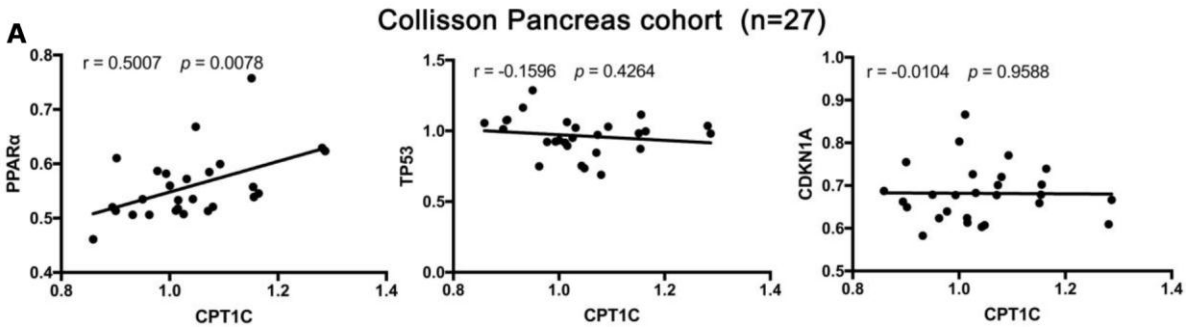

**Supplementary Figure 4. (related to Figure 3). Vector PANC-1 cells exhibited higher glycolytic function.** (**A**) Glycolytic function in the forms of ECARs (mpH.min$^{-1}$) in senescent vector PANC-1 cells. Data are presented as the mean ± S.E.M, n = 3.




**Supplementary Figure 5. (related to Figure 5). Cell sensitivity to metabolic stress.** Cell sensitivity to metabolic stress from (**A**) glucose withdrawal and (**B**) glycolytic inhibition in senescent vector PANC-1 cells at the indicated concentrations is shown. Data are presented as the mean ± S.E.M, n = 5 (*$p < 0.05$, **$p < 0.01$).




**Supplementary Figure 6. Reduced *CDKN1A* (*P16*) mRNA in the senescent vector PANC-1 cells.** (**A**) Quantitative RT-PCR analysis for *P16* was performed in the senescent vector PANC-1 cells.




**Supplementary Figure 7. (related to Figure 6). Correlation of crucial signaling components of cellular senescence with CPT1C expression in pancreatic cancer patients.** (**A**) Correlation analysis between *PPARα*, *TP53*, and *CDKN1A* with *CPT1C* mRNA expression in pancreatic cancer patients (data from the Collisson Pancreas cohort, n = 27).