























Actin











Α

š –

- 25

200

Number 150

0

8 -

• -









🗖 G2

🗖 S

🗖 G1

Control

si-LINC00460#1

si-LINC00460#2













HIF-1α

β-actin



MiaPaCa2



F





0-

0

























Ε









F



CFPAC





















Α



Relative expression of p53,log2(FPKM)







Β





si-NC

si-USP10#1



si-USP10#2





С

ATCC CELL PANEL PANCREATIC CANCER PANEL

Α

Pancreatic Cancer Panel (ATCC® <u>TCP-1026</u>^{III}) is composed of seven pancreatic cancer cell lines. They have genomic mutations in one or more of the following genes according to the Sanger COSMIC database: CDKN2A, FBXW7, KRAS, MAP2K4, SMAD4, and TP53. The table below provides more information for the cell lines included in this panel.

ATCC [®] No.	Name	Histology	Tumor Source	Gene	Zygosity	Gene Sequence	Sequence
HTB-80**	Capan-2	Adenocarcinoma	primary	KRAS	heterozygous	c.35G>T	p.G12V
CRL-2547**	Panc 10.05	Adenocarcinoma	primary	KRAS	heterozygous	c.35G>A	p.G12D
				TP53	heterozygous	c.764T>A	p.1255N
CRL-1918**	CFPAC-1	Ductal adenocarcinoma	metastasis, liver	KRAS	heterozygous	c.35G>T	p.G12V
				SMAD4	homozygous	c.1_1659del1659	p.0?
				TP53	homozygous	c.724T>C	p.C242R
CRL-1997	HPAF-II	Adenocarcinoma	metastasis, ascites	CDKN2A	homozygous	c.85_101del17	p.R29fs*9
				KRAS	heterozygous	c.35G>A	p.G12D
				TP53	homozygous	c.451C>T	p.P1515
RL-2172	SW 1990	Adenocarcinoma	metastasis, spleen	CDKN2A	homozygous	c.1_471del471	p.0?
				KRAS	homozygous	c.35G>A	p.G12D
RL-1687	BxPC-3	Adenocarcinoma	primary	CDKN2A	homozygous	c.1_471del471	p.0?
				MAP2K4	homozygous	c.1041_1200del160	p.7
				SMAD4	homozygous	c.1_1659del1659	p.0?
				TP53	homozygous	c.659A>G	p.Y220C
RL-1682	AsPC-1	Adenocarcinoma	metastasis, ascites	CDKN2A	homozygous	c.233_234delTC	p.L78fs*4
				FBXW7	heterozygous	c.1393C>T	p.R465C
				KRAS	homozygous	c.35G≽A	p.G12D
				MAP2K4	homozygous	c.1-?_393+?del	p.?
				TP53	homozygous	c.403delT	p.C135fs ⁴
e mutation da atalogue of Ser implied, nor as her trademarks r use in humans	ta was obtaine natic Mutation sumes any lega listed are trade c animals or dia	d from the Sanger Instit s in Cancer) database and I liability or responsibilit marks of the American Ty gnestics.	ute Catalogue Of Somatic Muta website. Br J Cancer, 91,355-358 y for any purpose for which the o pe Culture Collection unless indi	tions In Cancer web si ATCC and The Sanger lata are used. The ATC cated otherwise. ATCC	ite, <u>http://www.sanger</u> histitute provide these C trademark and trade r products are intended fi	ac.uk/cosmic Bamford et a fata in good faith, but make same, any and all ATCC catal or laboratory research only. T	l (2004) The C no warranty, o og numbers, a hey are not in

Cell line name	PANC-1
Synonyms	Panc 1: PANC 1: Panc 1: PanC1: PANC1: Panc 1.P
Accession	CVCL 0480
Resource Identification Initiative	To cite this cell line use: PANC-1 (RRID:CVCL_0480)
Comments	Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE). Part of: ENCODE project common cell types; tier 3. Part of: KuDOS 95 cell line panel. Population: Caucasian. Doubling time: 25.83 + 2.03 hours (PubMed=25394408); 21 + 1.6 hours (PubMed=21515691); 52 hours (CLS); ~42 hours (DSMZ); ~32 hours (PBCF); 15.02 hours (https://www.synapse.org/#ISynapse:syn2347014). Karyotypic information: Has lost chromosome Y. Omics: Deep exome analysis. Omics: Deep quantitative proteome analysis. Omics: Deep quantitative proteome analysis. Omics: H3K4me3 OhP-seq epigenome analysis. Omics: Protein expression by reverse-phase protein arrays. Omics: Protein expression by reverse-phase protein arrays. Omics: Transcriptome analysis. Omics: Transcriptome analysis. Omics: Transcriptome analysis.

	Derived from sampling site: Pancreas.
Sequence variations	 Gene deletion; HGNC; 1787; CDKN2A; Zygosity=Homozygous (PubMed=11787853; PubMed=15367885). Mutation; HGNC; 6407; KRAS; Simple; p.Gly12Asp (c.35G>A); ClinVar=VCV000012582; Zygosity=Heterozygous (PubMed=7809022; PubMed=7961102; PubMed=8026879; PubMed=11115575; PubMed=11787853; PubMed=15367885; PubMed=21607521; DepMap). Mutation; HGNC; 11998; 1P53; Simple; p.Arg273His (c.818G>A); ClinVar=VCV000012366; Zygosity=Homozygous (PubMed=1630814; PubMed=1764370; PubMed=7961102; PubMed=8026879; PubMed=11115575; PubMed=11115575; PubMed=11787853; PubMed=11787853; PubMed=11787853; PubMed=15367885; PubMed=15367885; PubMed=15367885; PubMed=15367885; PubMed=15367885; PubMed=15367885; PubMed=21607521; DepMap).

Cell line name	CFPAC-1					
Synonyms	CFPac-1; CF PAC-1; CF-PAC1; CF-Pac1; CF Pac1; CFPAC1; CFPAC1; CFPAC					
Accession	CVCL_1119					
Resource Identification Initiative	To cite this cell line use: CFPAC-1 (RRID:CVCL_1119)					
Comments	Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE). Part of: CUSNIC cell lines project. Part of: KUDOS 95 cell line panel. Part of: KUDOS 95 cell lines Project. Part of: KURAS program mutant KRAS cell line panel. Doubling time: 30 hours (at 17th passage), 32 hours (at 74th passage) (PubMed=1692630); 45 hours (PubMed=25984343). Microsatelitie instability: Stable (MSS) (Sanger). Omics: Array-based CGH. Omics: Deep proteome analysis. Omics: Deep proteome analysis. Omics: Deep RNAseg analysis. Omics: Matabolome analysis. Omics: Proteome analys					
Sequence variations	 Gene deletion; HGNC; 6770; SMAD4; Zygosity=Homozygous (PubMed=10408907; PubMed=11169959; PubMed=11787853; PubMed=15367885; PubMed=18380791). Mutation; HGNC; 1884; CFTR; Simple; p.Phe508del (c.1521_1523delCTT); ClinVar=VCV000007105; Zygosity=Homozygous (PubMed=15463957; ATCC). Mutation; HGNC; 6407; KRAS; Simple; p.Gly12Val (c.35G>T); ClinVar=VCV000012583; Zygosity=Heterozygous (PubMed=11169959; PubMed=11787853; PubMed=15367885; Cosmic-CLP). Mutation; HGNC; 11998; TP53 Simple; p.Cys242Arg (c.724T>C); ClinVar=VCV000449512; Zygosity=Homozygous (PubMed=11169959; PubMed=11787853; PubMed=15367885; Cosmic-CLP). 					

_				
Cell line name	MIA PaCa-2			
Synonyms	MIA-PaCa-2; MIA-PACA-2; MIA-Pa-Ca-2; MIA Paca2; MIA PaCa2; MIAPACa-2; MIAPACA-2; MiaPaca2; MIAPaCa2; MIAPaCa2; MIAPACA2; Mia PACA 2; MIAPaCa-2; PaCa2			
Accession	CVCL_0428			
Resource Identification Initiative	To cite this cell line use: MIA PaCa-2 (RRID:CVCL_0428)			
Comments	Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE). Part of: KuDOS 95 cell line panel. Part of: KUDAS program wutant KRAS cell line panel. Papt of: ND Anderson Cell Lines Project. Part of: NI RAS program wutant KRAS cell line panel. Population: Caucasian. Doubling time: 26 hours (PubMed=25984343); 25.7 +- 4.3 hours (PubMed=27087801); 40 hours, 18 hours, in serum-free medium (PubMed=23386380); ~40 hours (ATCC); ~30-40 hours (DSMZ). Microsatellite instability: Stable (MSS) (Sanger). Omics: Deep proteome analysis. Omics: Deep proteome analysis. Omics: Deep proteome analysis. Omics: Deep quantitative proteome analysis. Omics: Protein expression by reverse-phase protein arrays. Omics: Protein expression by reverse-phase protein arrays. Omics: SNP array analysis. Omics: SNP array analysis. Omics: SNP array analysis. Omics: SNP array analysis. Omics: MRNA library screening. Omics: SNP array analysis. Caution: Additional TPS3 mutation in c.818G>A indicated incorrectly in PubMed=1630814. Misspelling: HubMed=1570730. Derived from sampling site: Pancreas.			
Sequence variations	 Gene deletion; HGNC; 1787; CDKN2A; Zygosity=Homozygous (PubMed=11787853). Mutation; HGNC; 6407; KRAS; Simple; p.Gly12Cys (c.34G>T); ClinVar=VCV000012578; Zygosity=Homozygous (PubMed=7961102; PubMed=8026879; PubMed=11115575; PubMed=11169959; PubMed=11787853; PubMed=12068308; PubMed=21607521; Cosmic-CLP; DepMap). Mutation; HGNC; 11998; TP53; Simple; p.Arg248Trp (c.742C>T); ClinVar=VCV000012347; Zygosity=Homozygous (PubMed=1630814; PubMed=1764370; PubMed=7961102; PubMed=8026879; PubMed=11115575; PubMed=11115575; PubMed=11169959; PubMed=1169959; PubMed=1169959;			

Ε

С

Cell line name	Capan-2				
Synonyms	CaPan-2; CAPAN-2; Capan 2; CAPAN 2; Capan2; CAPAN2				
Accession	CVCL_0026				
Resource Identification Initiative	To cite this cell line use: Capan-2 (RRID:CVCL_0026)				
Comments	Part of: Cancer Dependency Map project (DepMap) (includes Cancer Cell Line Encyclopedia - CCLE). Part of: COSMIC cell lines project. Part of: NCI RAS program mutant KRAS cell line panel. From: Memorial Stoan Kettering Cancer Center; New York; USA. Registration: Memorial Stoan Kettering Cancer Center Office of Technology Development; SK2000-049. Population: Caucasian. Doubling time: 96 hours (PubMed=3019537); 45-60 hours (CLS); ~50-70 hours (DSMZ). Microsatellite instability: Stable (MSS) (Sanger). Omics: Array-based CGH. Omics: Deep partite or to the stability: Stable (MSS) (Sanger). Omics: Deep partite or to the stability: Stable (MSS) (Sanger). Omics: Deep quantitative proteome analysis. Omics: Deep RNAseq analysis. Omics: Proteome analysis. Omics: Proteome analysis by 2D-DE/MS. Omics: Transcriptome analysis. Omics: Transcriptome analysis. Omics: Transcriptome analysis. Omics: Transcriptome analysis. Omics: Transcriptome analysis. Caution: TP53 mutation indicated incorrectly as being at c.818G>A in PubMed=1630814. Misspelling: CANPAN-2; In Cosmic 2434087.				
Sequence variations	 Mutation; HGNC; 1787; CDKN2A; Simple; p.Thr18_Ala19dup (c.52_57dupACGGCC); ClinVar=VCV000579466; Zygosity=Homozygous (PubMed=7972006; DepMap). Mutation; HGNC; 6407; KRAS; Simple; p.Gly12Val (c.35G>T); ClinVar=VCV000012583; Zygosity=Heterozygous (PubMed=7961102; PubMed=8026879; PubMed=8426738; PubMed=11169959; PubMed=15367885; Cosmie CLP; DepMap). Mutation; HGNC; 11998; TP53; Simple; p.Thr125Thr (c.375G>T); ClinVar=VCV000237948; Zygosity=Homozygous; Note=Impairs TP53 splicing dramatically (PubMed=7961102; PubMed=8026879; PubMed=802680079; PubMed=8026879; PubMed=8026879; PubMed=8026879; PubMed=				

Figure. S1 Knocking down LINC00460 promotes cell apoptosis. A The cell apoptosis rate of PANC1 while knocking down LINC00460. **B** The cell apoptosis rate of CFPAC while knocking down LINC00460. **C** The cell apoptosis rate of MiaPaCa2 while overexpressing LINC00460. **D** The protein level of BAX, Caspase3 and Caspase8 while knocking down LINC00460 in PANC1 and CFPAC or overexpressing LINC00460 in MiaPaCa2. ***P<0.001

Figure S2 A The cell numbers of G1, S and G2 phase while knocking down LINC00460 or not in PANC1. **B** The cell numbers of G1, S and G2 phase while knocking down LINC00460 or not in CFPAC. **C** The protein level of CDK4 and CDK6 while knocking down LINC00460 in PANC1 and CFPA or overexpressing LINC00460 in MiaPaCa2. **D** The protein level of Ki-67, N-cad and E-cad while knocking down LINC00460 in PANC1 and CFPAC or overexpressing LINC00460 in MiaPaCa2. *P<0.05; **P<0.01; ***P<0.001

Figure S3 A The sequence logo of HIF-1 α in JASPAR database. **B** The correlation analysis of USP10 and HIF-1 α using data from TCGA. **C** The correlation analysis of UBE2V1 and HIF-1 α using data from TCGA. **D** The protein level of HIF-1 α while knocking down HIF-1 α in PANC1, CFPAC and MiaPaCa2 cells. **E** The mRNA expression of HIF-1 α while knocking down HIF-1 α in PANC1, CFPAC and MiaPaCa2 cells. **F** The mRNA expression of LINC00460 while knocking down HIF-1 α in PANC1 and CFPAC cells. *P<0.05; **P<0.01; ***P<0.001

Figure S4 Knocking down LINC00460 could reverse the malignant biological behavior induced by hypoxia. PANC1 and CFPAC cells were treated with normoxia, hypoxia, a combination of si-HIF-1 α and hypoxia, a combination of si-HIF-1 α co-transfected overexpression LINC00460 and hypoxia. The results of CCK8 assays in PANC1 (A) and CFPAC (B). The representative images and results of transwell assays in PANC1 (C) and CFPAC (D). The representative images of wound healing assays and the results of wound closure rate after 24h in PANC1 (E)and CFPAC (F). *P<0.05; **P<0.01; ***P<0.001

Figure S5 A The location of U6, 18S and LINC00460 in PANC1. **B** The location of U6, 18S and LINC00460 in CFPAC. **C** Relative expression of miR-4689, miR-4649-3p and miR-6858-5p in PANC1 knocked down LINC00460. **D** Relative expression of miR-4689, miR-4649-3p and miR-6858-5p in CFPAC knocked down LINC00460 **E** Relative expression of miR-4689, miR-4649-3p and miR-6858-5p in MiaPaCa2 overexpressed LINC00460. F Relative expression of SH3TC, UBE2V1, TRIM71, TNS1, CACNA1B, UNC119B and CDKN1A after transfection of control vector, miR-4689 mimics and miR-689 inhibitor. **G** Correlation analysis of LINC00460 and UBE2V1 using data from TCGA. **H** Correlation analysis of LINC00460 and UBE2V1 using data from TCGA. **H** Correlation analysis of LINC00460 and UBE2V1 using data from TCGA.

Figure S6 A The mRNA expression of UBE2V1 when transfected si-NC and si-UBE2V1 in Capan2 cells. **B** The result of CCK8 assay in Capan2 cells. **C** The representative images and results of colony formation assay in Capan2 cells. **D** The representative images and results of transwell assays in Capan2 cells. **E** The representative images of wound healing assays and the results of wound closure rate after 24h in Capan2 cells. *P<0.05; **P<0.01; ***P<0.001

Figure S7 A The transcripts level of USP10 in 178 tumor tissues and 171 normal tissues of PAAD patients. B The expression of USP10 in 179 tumor tissues and 171 normal tissues of PAAD patients. C Correlation analysis of USP10 and p53 using data from TCGA. D Overall survival analysis of USP10 in pancreatic cancer from TCGA database. E Disease free survival analysis of USP10 in pancreatic cancer from TCGA database.

Figure S8 A The mRNA expression of USP10 while knocking down USP10 or not in PANC1 cells. **B** The mRNA expression of USP10 while knocking down USP10 or not in CFPAC cells. **C** The correlation analysis of USP10 and p53 using data from TCGA. **D** CoIP assays using USP10 and p53 antibodies to verify the combination of USP10 and p53 in PANC1. **E** CoIP assays using USP10 and p53 antibodies to verify the combination of USP10 and p53 in Capan2. *P<0.05; **P<0.01; ***P<0.001

Figure S9 A The mRNA expression of USP10 when transfected si-NC and si-UBE2V1 in Capan2 cells. **B** The mRNA expression of p53 when transfected si-NC and si-UBE2V1 in Capan2 cells. **C** The result of CCK8 assay in Capan2 cells. **D** The representative images and results of transwell assays in Capan2 cells. **E** The representative images of wound healing assays and the results of wound closure rate after 24h in Capan2 cells. *P<0.05; **P<0.01; ***P<0.001

Figure S10 A Mutation information of p53 in PANC1, CFPAC and Capan2 in ATCC website. **B** Mutation information of p53 in PANC1 in Cellosaurus website. **C** Mutation information of p53 in CFPAC in Cellosaurus website. **D** Mutation information of p53 in MiaPaCa2 in Cellosaurus website. **E** Mutation information of p53 in Capan2 in Cellosaurus website.