

**Supplementary Table S1.** Baseline demographic and clinical characteristics of individuals with pancreatic ductal adenocarcinoma in this study

	Cohort 1 (Guangzhou)		Cohort 2 (Beijing)		Pooled sample	
	Alive (N=36)	Deceased (N=122)	Alive (N=17)	Deceased (N=56)	Alive (N=53)	Deceased (N=178)
Age, mean (SD <sup>a</sup> )	59.8 (11.7)	61.1 (11.4)	59.1 (8.6)	63.1 (11.2)	59.6 (10.8)	61.7 (11.3)
Sex, N (%)						
Male	23 (63.9)	68 (55.7)	10 (58.8)	35 (62.5)	33 (62.3)	103 (57.9)
Female	13 (36.1)	54 (44.3)	7 (41.2)	21 (37.5)	20 (37.7)	75 (42.1)
Differentiation, N (%)						
Well	7 (19.4)	13 (10.7)	4 (23.5)	6 (10.7)	11 (20.8)	19 (10.7)
Moderate	22 (61.1)	81 (66.4)	10 (58.8)	31 (55.4)	32 (60.4)	112 (62.9)
Poor	7 (19.4)	28 (23.0)	3 (17.6)	19 (33.9)	10 (18.9)	47 (26.4)
Lymph node metastasis, N (%)						
Positive	14 (38.9)	66 (54.1)	10 (58.8)	27 (48.2)	24 (45.3)	93 (52.2)
Negative	22 (61.1)	56 (45.9)	7 (41.2)	29 (51.8)	29 (54.7)	85 (47.8)
Vascular invasion, N (%)						
Yes	10 (27.8)	39 (32.0)	6 (35.3)	27 (48.2)	16 (30.2)	66 (37.1)
No	26 (72.2)	83 (68.0)	11 (64.7)	29 (51.8)	37 (69.8)	112 (62.9)
Neural invasion, N (%)						
Yes	23 (63.9)	74 (60.7)	4 (23.5)	10 (17.9)	27 (50.9)	84 (47.2)
No	13 (36.1)	48 (39.3)	13 (76.5)	46 (82.1)	26 (49.1)	94 (52.8)
TNM stage <sup>b</sup> , N (%)						
I	1 (2.8)	7 (5.7)	4 (23.5)	9 (16.1)	5 (9.4)	16 (9.0)
II	29 (80.6)	99 (81.1)	11 (64.7)	27 (48.2)	40 (75.5)	126 (70.8)
III	0 (0.0)	4 (3.3)	2 (11.8)	10 (17.9)	2 (3.8)	14 (7.9)
IV	6 (16.7)	12 (9.8)	0 (0.0)	10 (17.9)	6 (11.3)	22 (12.4)

<sup>a</sup>SD, standard deviation.<sup>b</sup>Tumor TNM staging were reviewed by at least 3 pathologists and defined according to the American Joint Committee on Cancer (AJCC) 8th edition.

**Supplementary Table S2.** Sequences of siRNAs and gRNAs in this study

Sequences of siRNA	
siControl	5'-UUCUCCGAACGUGUCACGUTT-3'
siFER1L4	5'-GGGUCAACCUCAUUUCUAUTT-3'
siRP11-356M20.1	5'-GCAAAGAGCGAUCCUCUAATT-3'
siAC073150.6	5'-CCAGGAUCACCCAGUCUUUTT-3'
siDUXAP9	5'-CCAGGAAUUGUGAGAUAATT-3'
siPSMC1P2	5'-GCAAUCUGCACAGAAGCUATT-3'
siCELP	5'-CCAUCAACAAGGGCAACAATT-3'
siEGFEM1P	5'-GCUCUGCAUCAACUAUUUATT-3'
siAC093724.2	5'-CCAGGUGAACCACACAGUATT-3'
siMXRA5Y	5'-GCUGCAGAUGGGUAGAAUATT-3'
siWTAPP1-1	5'-GCACAUGCCUCACAGAAUUTT-3'
siWTAPP1-2	5'-GCAAGAACGCUGACCUCAATT-3'
siWTAP-1	5'-CACAGAUCUUAACUCUAAUTT-3'
siWTAP-2	5'-GACCCAGCGAUAACUUGUTT-3'
siMETTL3-1	5'-GGAGAUCCUAGAGCUAUUATT-3'
siMETTL3-2	5'-GCACAUCCUACUCUUGUAATT-3'
siCNBP-1	5'-CCAGACAUUUGUUAUCGCUTT-3'
siCNBP-2	5'-GAGGAUGCCUGCUAUAACUTT-3'
siEIF3B-1	5'-GGAAGCAGAUGGAAUCGAUTT-3'
siEIF3B-2	5'-GCACCUACCUGGCUACCUUTT-3'
Sequences of sgRNA	
WTAPP1-gRNA1	GCTGGCGGTGGGTGACCACGGCCGCATCTGGGAGGCGACT
WTAPP1-gRNA2	GCTGCCGTGAGGAAAGCCAGCCTCAAGGGGACTGAATAAG

**Supplementary Table S3.** Primers used for quantitative real time-PCR and other assays in this study

<b>Gene</b>	<b>Forward primer (5'→3')</b>	<b>Reverse primer (5'→3')</b>
<i>WTAPP1</i>	TTCTCAGTGCAAGGTGGTGA	CGAGCTCCTGTTTATTGCACC
<i>WTAP</i>	CTTCCCTTACTGAGCTTGCTG	TGGGAAGAGGTTCTTCGTTGG
<i>CNBP</i>	ACTGCGACCATGCAGATGAG	CAGAAAAAGGAGGGGCGACA
<i>XIST</i>	CCTACCGCTTTGGCAGAGAA	AGCCCTAAGCCGAGTTATGC
<i>METTL3</i>	AGATGGGGTAGAAAGCCTCCT	TGGTCAGCATAGGTTACAAGAGT
<i>GAPDH</i>	TTGGCCAGGGGTGCTAAG	AGCCAAAAGGGTCATCATCTC
<i>U6</i>	CTCGCTTCGGCAGCACA	AACGCTTCACGAATTTGCGT
<i>β-Actin</i>	CAGGGCGTGATGGTGGGCATG	GTAGAAGGTGTGGTGCCAGATT
<b>Primers used for MeRIP-qPCR and CLIP-qPCR</b>		
WTAPP1-Forward	CAAACGGATGGCAGGAGATG	
WTAPP1-Reverse	GAGGTTGAGGTCAGCGTTCT	
<b>Primers used for in vitro transcription</b>		
WTAPP1-Sense-Forward	TAATACGACTCACTATAATCTGTAAAATGGGGTGGAT	
WTAPP1-Sense-Reverse	GAAGTGGAGGCTGATGATCTTTATT	
WTAPP1-Antisense-Forward	TAATACGACTCACTATAGAAGTGGAGGCTGATGATCT	
WTAPP1-Antisense -Reverse	ATCTGTAAAATGGGGTGGATATAAC	

**Supplementary Table S4.** Sequences of probes used in this study

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**Probe used for WTAPP1 RNA Northern blot**

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CATACTCACTCACACTCACCAGTCTGCGACCATGTAGACAAGCCAGTGAGCCTCATGTGCACA  
GCTGTGGGATGTGGGAGGAAACCAAGTACCCAGAGAAAATCCACAAAGACACAGGGAGAA  
CCTGAAAACCTCCACACAGACCATGGCCCTGACCGGAAATGGATTTTTTTCTCTTCGACGTCAT  
AACTAATCCATGTTATTTGAAGACCTGCTCTTTAGAGTTTCTAAGTCACTATGCTCAAGGGTAA  
GAGCAATGCATAGTCCATTTTCCATTTTACTGGAATTTATGTTCAATTCATGATTTAAAGTCTCC  
AGGTTTTCAATTTCTCCGAACTGTCCAAAGACATTGTGTGCCTTAGGACCTGTTTCTCCCTCTAT  
TTTCTTCAAACAGAAACATTTCTCAAGTATCCACATGTTCCCAAAGAGGAATTCTTCAGAGGT  
GGCCGCTTCTTTGGGATAGTGCAAGTCTACCAGGCTTCTGAAGCAAAGCGGATGGGGAGGG  
AAAGAACTGAAGTGCAAGGTTTATTGGTAAGTTTACATTAACCATTAGGAGCTGGGGAGTAT  
AAAAATGCGGCTTTTTTCTTTCTCTCAAAAAGTCTGAGTGTTGGTGTAGAAACGAGTCCTT  
GGCTGTCCCCCAGTGACTTTCTAGTAGTGGGACTGTCAGGGAAGCCTTGACTGAGAATATG  
ACTGGAGAGTTTACCTACCAGGCGTAAACTTCCAGGCACTCTGTTTCAATTTGGGCTTGTCCC  
GTTTGTCTTCAGTCAGGGCCAGATCACCTTTTCAATTTTAGGAAAACAGGTTGATGGCTCGGTC  
TACCATTGTTGATCGGGCCACGCTGGGCCACAGATTTGCTGGAGGTACTAAATTCGGGTAGG  
ACGCCTCGCATCTCCTGCCTTTGTCTGCTAGTCGCATCGCAAGGACGTTTGCCTCCGCGCAGA  
CTCTTGCTGCTTTTGTCTTAGTTTTCACTGAGGTTGAGGTCAGCGTTCTTGCCTCCAAAGCTTG  
CGCATGTGTTTCATATTGTTTCCATTTTAGAA TTCATTCATCTCCTGCCATCCGTT

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**Probe used for ChIRP assay**

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WTAP-probe-1	CAAGCTCAGTAAGGGAAGCG
WTAP-probe-2	TCTTGAATCAGGAGAGTCGC
WTAP-probe-3	TTCGACACTTCGCCATTAAC
WTAP-probe-4	GAAGTCATTCAGTTCATCCT
WTAP-probe-5	ACAGGTTCAGAAGCTGTAGT
WTAP-probe-6	CATTCCCTGGAGAAGAAGGA
WTAP-probe-7	GTGGGAGAGTCTACACTTTC
WTAP-probe-8	ATTCTGAACGTGGCGGGAAC
WTAP-probe-9	ATTTTCTGGACAGTATCCTC
WTAP-probe-10	CCCTACACAAAATGTCCTTT
WTAP-probe-11	ATGAGTACGAATGCCCTTAC
WTAP-probe-12	ACTCCATCAATGAGTCCAAC
WTAP-probe-13	GGAGTCACAGAGCAATATGC

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**Supplementary Table S5.** Prediction of the coding potential of WTAPP1

<b>Predicted potential peptides of WTAPP1</b>					
sORF ID	Start position	End position	sORF potential peptide sequence		
Seq1	48	183	MLYAGEQISSYFTPTPLTDKACWPKSVTM PLGPDLTSCMPIFA		
Seq2	376	742	MPWSRVLSLHPGWSVVVQSWLRATSASQI QGFSCLSLLSSWDYRSQRRTDILPVFKEHHF SPNRSYSIKESLGSCETPHPRTAAAAVEESCA YWPLSSFSVQGGDLRRCVAWTLNNIIVLLP		
Seq3	1184	1397	MRLADKRQEMRGVLPEFSTSSKSVAQRGPI NNGRPSHQPVFLKMKGDLALTEDKREQAQ NEQSAWKFTPGR		
Seq4	1362	1506	MNRVPGSLRLVGKLSHILSQGFDPSTTRK SLGGQPRTRFYTNTQTF		
Seq5	1552	1630	MVNVKLTNEPCTSVLSLPIRFASEAW		
Seq6	1574	1664	MNLALQFFPSPSALLQKPGRLALSQRSGHL		
Seq7	1703	1778	MFLFEENRGRNKVLRHTMSLDSSEK		
Seq8	1827	1911	MENGLCIAALTLEHSDLETLKSRSSNNMD		
Seq9	1916	2048	MTSKRKKIHFRSGPWSVWSFQVLPVSLWIF SGYLVSSHIPQLCT		
Seq10	1957	2095	MVCVEFSGSPCVFVDFLWVLGFLPHPTAVH MRLTGLSTWSQTGECE		
Seq11	2116	2224	MMEWSPIQGWPELPGWAPATQHSELKQE VSKNLSRC		
Seq12	2227	2620	MRTFQHIGHFASKTVNFIIVVELLQNSNEIEQ VEVETDFDASSRLLSKEEWRQHSVPALSENT ARFQVTGLFCFRSDKFSTCLETLITYFFLPQKS SSLFPALQPRKHSNYFKTPGDPLVLCKHGDQ VTFQ		
Seq13	2309	2582	MRLSKLRLRQISMLPQGYSARKNGDSTRCQ LCLKTQPDSRLQGYSASDQINSPLAWKLSSPI SFFPKNPPFSLHCSLGLSTATISKHQGTL		
<b>Coding potential calculator based on sequence intrinsic features</b>					
Sequence	Fickett score	Isoelectric point	Peptide length (aa)	Coding probability	Label
WTAPP1	0.28	6.41	132	0.42	noncoding

**Supplementary Table S6. Metastasis of xenografts derived from PDAC cells**

<b>SW1990</b>					
<b>Mouse</b>	<b>Control</b>	<b>WTAPP1-OE</b>	<b>KD-Control</b>	<b>WTAPP1-KD-1</b>	<b>WTAPP1-KD-2</b>
#1	No metastasis	Lung, Liver	No metastasis	No metastasis	No metastasis
#2	No metastasis	Liver	No metastasis	No metastasis	No metastasis
#3	No metastasis	Mesentery, Liver	No metastasis	No metastasis	No metastasis
#4	No metastasis	Liver	No metastasis	No metastasis	No metastasis
#5	Liver	Liver	Lung	No metastasis	No metastasis
#6	Liver	Liver	Liver	No metastasis	No metastasis
#7	Lung	Lung, Liver	Liver	No metastasis	No metastasis
#8	Liver	Liver	Liver	No metastasis	No metastasis

  

<b>Capan-2</b>					
<b>Mouse</b>	<b>Control</b>	<b>WTAPP1-OE</b>	<b>KD-Control</b>	<b>WTAPP1-KD-1</b>	<b>WTAPP1-KD-2</b>
#1	No metastasis	No metastasis	No metastasis	No metastasis	No metastasis
#2	No metastasis	Lung, Liver	No metastasis	No metastasis	No metastasis
#3	No metastasis	Liver	No metastasis	No metastasis	No metastasis
#4	No metastasis	Liver	No metastasis	No metastasis	No metastasis
#5	Liver	Lung, Liver	No metastasis	No metastasis	No metastasis
#6	Lung	Liver	Liver	No metastasis	No metastasis
#7	Liver	Liver	Liver	No metastasis	No metastasis
#8	Liver	Liver	Liver	No metastasis	No metastasis