

Figure S1. Transduction of lentiviral Kidins220 shRNAs (sh2: GGCCTGCAAGATCCAATTATA and sh6: CGAGTATTCAAG ACTGAAGAT) in PANC1 and Mia PaCa 2 cell lines. qPCR was performed to determine the Kidins220 transcripts in the transduced cell lines (A and B). Kidins220 sh2 resulted in a reduction in the Kidins220 expression in the two cell lines which were used in the present study. Kidins220 sh6 only resulted in a reduced expression of Kidins220 in PANC1 cells. However, it had a similar effect on the expression of EGFR (C), E-cadherin and Snai1 (D) as observed in cell lines with Kidins220 knockdown using the Kidins220 sh2. **P<0.01 and ***P<0.001.

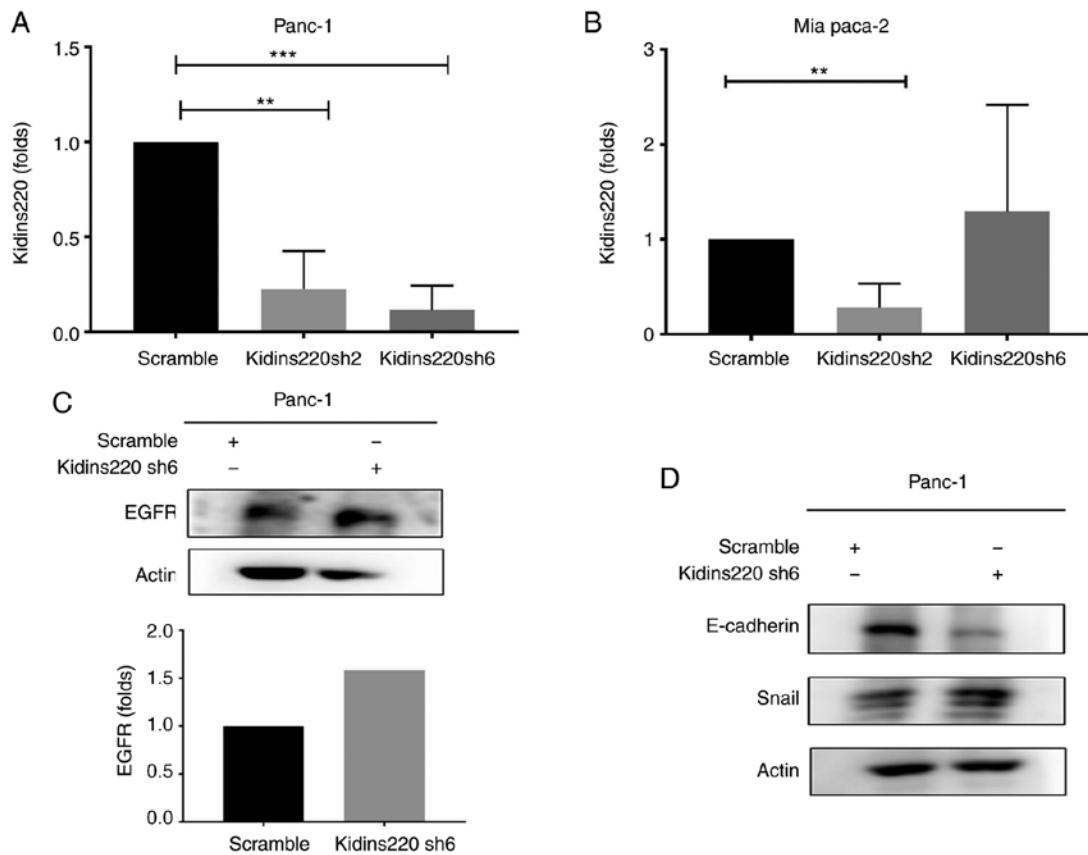


Table SI. Primer sequences.

Primer name	Primer sequence (5'-3')	Product size (bp)
<i>GAPDHF8</i>	GGCTGCTTTAACCTCTGGTA	475
<i>GAPDHR8</i>	GACTGTGGTCATGAGTCCTT	
<i>Kidins220F2</i>	AGACGTTCCATGCTCAGA CTCGAGCCACAAGAACTG	539
<i>Kidins220ZR2</i>	ACTGAACCTGACCGTACATGCCTTCTCGGTAAAGTG	136
<i>EGFRF1</i>	AGAGTCTCAAAGCCATGTTAT	
<i>EGFRZR1</i>	ACTGAACCTGACCGTACACCCTAAGCATGACTCC	120
<i>E-cadF22</i>	CAGGAGCCAGACACATTAT	
<i>E-cadR22</i>	TCTAAGGTGGTCACTTGGTC	515
<i>SnailF11</i>	CGCTCTTCCTCGTCAG	
<i>SnailR11</i>	GTTGCAGTATTGCAAGTTGA	474
<i>NF-Kb1F1</i>	CTGGCAGGTATTGACATATT	
<i>NF-kB1ZR1</i>	ACTGAACCTGACCGTACAAGCTGTTCATGTCTCCTTG	90
<i>GAPDHSGF1</i>	TGCACCACCAACTGCTTAGC	
<i>GAPDHSGR1</i>	GGCATGGACTGTGGTCATGAG	87
<i>MMP1SGF1</i>	GGGAGATCATGGGACAACTC	
<i>MMP1SGR1</i>	GGGCCTGGTTGAAAAGCAT	72

Table SII. Expression of Kidins220 in pancreatic cancer.

Variable	N	Mean ± SEM (copies/50 ng RNA)	P-value
Clinical samples			
Tumor	149	75,150±5,76,945	0.029
Normal	145	2.13 E+12±9.62 E+11	
Gentle			
Male	89	11,4106±96,478	0.32
Female	60	17,365±6,882	
Node status			
Node negative	56	1,68,646±1,53,0096	0.32
Node positive	81	13,872±5,124	
Differentiation			
High	9	1,305±1,299	
Moderate	53	12,778±5,732	0.056
Poor	10	1,767±1,226	0.8
Histology			
Adeno	61	82,114±65,598	
Ductal	6	22,796±22,739	0.39
Others	10	26,053±24,104	0.42
TNM staging			
1-2	114	20,490±6,680	0.0034
3-4	19	519±226	
Clinical outcomes			
Dead	108	99,489±7,95,413	0.28
Alive	33	13,124±73,627	
Metastasis			
Yes	10	614±338	0.2
No	139	80,512±61,835	

Table SIII. Predictive miRNAs targeting Kidins220 and its correlation with Kidins220 expression in the TCGA pancreatic cancer cohort.

Variable	miRTarBase		Correlation (n=178)
	P-value	Combined score	Spearman
miR-423-3p	0.0115	390.37	r=-0.183 P=0.0145
miR-4638-5p	0.0113	359.37	N/A
miR-223-3p	0.0150	281.14	r=-0.0971 P=0.197
miR-30a-5p	0.0367	90.21	r=-0.0318 P=0.673
miR-192-5p	0.0497	60.48	r=-0.169 P=0.0244
miR-7b-5p	0.0601	46.16	r=0.238 P=0.0014
miR-16-5p	0.0778	32.85	r=-0.285 P=0.0001

Prediction of miRNA targeting Kidins220 was performed using the miRTarbase 2017 at the Enrichr platform (<https://amp.pharm.mssm.edu/Enrichr/>) (29). Correlation between the predicted miRNAs and Kidins220 in the TCGA PAAD cohort was determined using Spearman test.