

## Supplement Figure S1

	PL45	Panc0203	Panc1
Cell type Disease	Epithelial/Adherent ductal adenocarcinoma	Epithelial/Adherent Adenocarcinoma	Epithelial/Adherent Pancreatic carcinoma of ductal origin.
Character	derived in 1992 primary tumor the pancreas of a man poorly differentiated pancreatic adenocarcinoma of ductal origin.	derived in 1995 primary tumor the head-of-the- pancreas of a female pancreatic adenocarcinoma.  cytokeratins 7 and 18+	derived in 1975 [Int. J. Cancer., 15, 741-747, 1975(PMID: <a href="#">1140870</a> )]. Primary tumor the head-of-the-pancreas of a male Pancreatic epitheloid carcinoma. Hypertriploid

## Genetics

PL45					
Gene	Chr	Type	CDS Position	Codons	Amino Acids
KDR	4	snv	1416	caA/caT	Q472H
FGFR1	8	deletion	495-497del	gaTGAc/gac	D166del
KRAS	12	snv	35	gGt/gAt	G12D
TP53	17	snv	764	aTc/aAc	I255N
TP53	17	snv	215	cCc/cGc	P72R

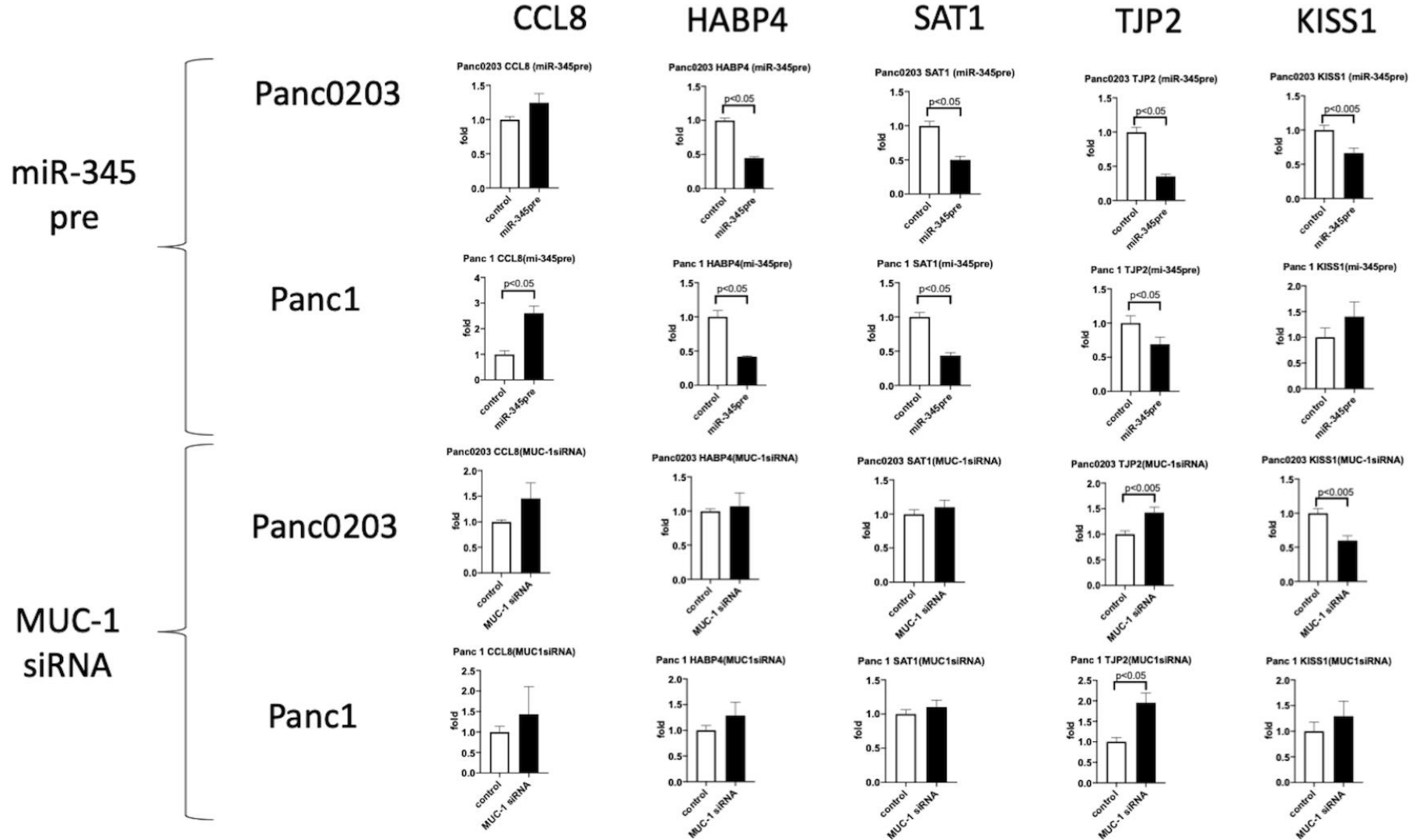
Panc0203					
Gene	Chr	Type	CDS Position	Codons	Amino Acids
KDR	4	snv	1416	caA/caT	Q472H
FGFR1	8	deletion	495-497del	gaTGAc/gac	D166del
KRAS	12	snv	35	gGt/gAt	G12D
TP53	17	snv	743	cGg/cAg	R248Q
TP53	17	snv	215	cCc/cGc	P72R
SMAD4	18	snv	403	Cga/Tga	R135*

Panc1					
Gene	Chr	Type	CDS Position	Codons	Amino Acids
FGFR1	8	deletion	495-497del	gaTGAc/gac	D166del
KRAS	12	snv	35	gGt/gAt	G12D
TP53	17	snv	818	cGt/cAt	R273H
TP53	17	snv	215	cCc/cGc	P72R



Putative target of miR-345

CCL8	chemokine (C-C motif) ligand 8
HABP4	hyaluronan binding protein 4
SAT1	spermidine/spermine N1-acetyltransferase 1
TJP2	tight junction protein 2
KISS1	KiSS-1 metastasis-suppressor



**Table s1** Immunohistchemical analysis of the prostatic tissue

Antigen	Antibody clone	Dilution	Source
MUC-1	Ma695	Prediluted	Novocastra, U.K
MUC-2	Ccp58	Prediluted	Novocastra, U.K
MUC-4	8G7	1:100	SANTA CRUZ, U.S.A
MUC-5AC	CLH2	1:200	Novocastra, U.K
MUC-6	CLH5	1:200	Novocastra, U.K
EMA	E29	1:800	DAKO, Glostrup, Denmark
Cytokeratin	CAM5.2	1:10	BD, U.S.A
CK7	OV-TL12/30	1:200	Novocastra, U.K
CK20	Ks20.8	1:50	Novocastra, U.K
CK19	b170	Prediluted	Leica, German

**Table s2 Primer sequences**

primer name		sequence	
MUC-1 sense	5'	TCCAATATTAAGTTCAGGCCAGGA	3'
MUC-1 antisense	5'	CACATCACTCACGCTGACGT	3'
SAT1 sense	5'	CCGTGGATTGGCAAGTTATT	3'
SAT1 antisense	5'	TCCAACCCTCTTCACTGGAC	3'
TJP2 sense	5'	GAGACAACCCCCACTTTGAA	3'
TJP2 antisense	5'	GCTGAACTGCAAACGAATGA	3'
CCL8 sense	5'	TGCCCTCCAAGATGAAGGTT	3'
CCL8 antisense	5'	TCACAGCTTCCTTGGGACA	3'
HABP4 sense	5'	TTGATCGAGACAGACCGTTG	3'
HABP4 antisense	5'	ACTCCACATCCACCCATGTT	3'
KISS1 sense	5'	TGGCAGCTACTGCTTTTCCT	3'
KISS1 antisense	5'	CAGTAGCAGCTGGCTTCCTC	3'
Actin sense	5'	CTCTTCCAGCCTTCCTTCCT	3'
Actin antisense	5'	AGCACTGTGTTGGCGTACAG	3'