

Molecular Pathogenesis of Pancreatic Ductal Adenocarcinoma: Impact of *miR-30c-5p* and *miR-30c-2-3p* Regulation on Oncogenic Genes

Takako Tanaka, Reona Okada, Yuto Hozaka, Masumi Wada, Shogo Moriya, Souichi Satake, Tetsuya Idichi, Hiroshi Kurahara, Takao Ohtsuka and Naohiko Seki

Table S1. Clinical samples' patient characteristics

No.	Age	Sex	Location	T	N	M	stage	Differentiation
Tumor 1	42	M	pancreas head	3	1	0	2B	well-moderate
Tumor 2	44	M	pancreas head	3	1	0	2B	modetrade
Tumor 3	76	M	pancreas head	3	1	0	2B	mode-poor
Tumor 4	67	M	pancreas head	3	1	0	2B	moderate
Tumor 5	78	F	pancreas head	3	0	0	2A	Papillary
Tumor 6	66	M	pancreas head	3	1	0	2B	moderate
Tumor 7	58	F	pancreas head	3	0	0	2A	moderate
Tumor 8	42	F	pancreas head	3	1	0	2B	well
Tumor 9	65	M	pancreas body	3	1	1	4	well
Tumor 10	56	F	pancreas body	3	1	0	2B	well
Tumor 11	70	M	pancreas head	3	1	0	2B	well
Tumor 12	63	F	pancreas head	3	0	0	2A	poor
Tumor 13	52	M	pancreas body	3	1	0	2B	well
Tumor 14	56	M	pancreas body	3	1	1	4	well
Tumor 15	65	M	pancreas body	2	0	0	1B	well
Tumor 16	78	F	pancreas head	3	1	0	2B	well+poor
Tumor 17	50	F	pancreas head	3	0	1	4	neuro
Tumor 18	66	F	pancreas head	3	0	0	2A	well
Tumor 19	66	F	pancreas head	3	1	0	2B	well+poor
Tumor 20	67	M	pancreas tail	0	0	0	0	no date
Tumor 21	74	M	pancreas tail	3	0	0	2A	well
Tumor 22	74	F	pancreas body	3	1	0	2B	well
Tumor 23	65	F	pancreas head	3	1	0	2B	well+poor
Tumor 24	78	M	pancreas head	3	0	0	2A	well
Tumor 25	71	F	pancreas body	3	0	0	2A	well+poor
Tumor 26	64	M	pancreas head	3	0	0	2A	moderate
Tumor 27	72	F	pancreas tail	3	1	0	2B	moderate

Features of patients in noncancerous pancreatic tissues.

No.	Age	Sex
Normal 1	65	F
Normal 2	58	F
Normal 3	77	F
Normal 4	67	M
Normal 5	42	F
Normal 6	65	F
Normal 7	60	M
Normal 8	56	F
Normal 9	67	M
Normal 10	85	F
Normal 11	66	F
Normal 12	65	F
Normal 13	76	M
Normal 14	71	F
Normal 15	64	M

Normal 16	72	F
-----------	----	---

Table S2. Putative target genes by *miR-30c-5p* and *miR-30c-2-3p* regulation in PDAC cells.

Putative target genes by <i>miR-30c-5p</i> regulation in PDAC cells.							
Entrez Gene ID	Gene Symbol	Gene name	GEO FC	GEO log2 FC	PANC-1 <i>miR-30c-5p</i> transfectant FC	PANC-1 <i>miR-30c-5p</i> transfectant log2 FC	Total binding sites
7534	YWHAZ	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	2.107888	1.075798213	−1.8025312	−0.850024	1
776	CACNA1D	calcium channel, voltage-dependent, L type, alpha 1D subunit	2.1054492	1.074128067	−1.8065524	−0.853239	1
865	CBFB	core-binding factor, beta subunit	2.2276592	1.155528538	−2.3320081	−1.221573	2
79026	AHNAK	AHNAK nucleoprotein	2.1226394	1.085859303	−2.5719824	−1.362881	1
5357	PLS1	plastin 1	2.1775904	1.122732612	−1.5772574	−0.657418	1
55450	CAMK2N1	calcium/calmodulin-dependent protein kinase II inhibitor 1	2.8895435	1.530841589	−1.7339722	−0.794081	1
285761	DCBLD1	discoidin, CUB and LCCL domain containing 1	3.3312216	1.736051328	−1.7587084	−0.813653	2
4547	MTTP	microsomal triglyceride transfer protein	2.0088177	1.006346646	−2.8433008	−1.507567	1
114907	FBXO32	F-box protein 32	3.750639	1.90713641	−1.6121457	−0.688982	3
23333	DPY19L1	dpy-19-like 1 (C. elegans)	2.8526917	1.512323838	−2.2663465	−1.180368	3
3977	LIFR	leukemia inhibitory factor receptor alpha	2.258954	1.175654893	−2.001093	−1.000788	2
4907	NT5E	5'-nucleotidase, ecto (CD73)	2.9813142	1.575948429	−3.7137697	−1.892884	2
25963	TMEM87A	transmembrane protein 87A	2.0282607	1.020243099	−1.6889185	−0.7561	1
84230	LRRC8C	leucine rich repeat containing 8 family, member C	2.0576832	1.041020883	−1.5065249	−0.591225	2
54855	FAM46C	family with sequence similarity 46, member C	2.5071456	1.326045782	−1.8364283	−0.876903	2
53616	ADAM22	ADAM metallopeptidase domain 22	2.3424919	1.228044059	−1.8035026	−0.850801	1
90	ACVR1	activin A receptor, type I	2.838798	1.505280195	−1.5178666	−0.602045	1
54492	NEURL1B	neuralized homolog 1B (Drosophila)	2.3553534	1.23594354	−1.517008	−0.601229	1
25960	GPR124	G protein-coupled receptor 124	2.2712364	1.183477876	−2.3105528	−1.208238	1
5783	PTPN13	protein tyrosine phosphatase, non-receptor type 13 (APO-1/CD95 (Fas)-associated phosphatase)	2.0204637	1.014686432	−1.8147175	−0.859745	2
2494	NR5A2	nuclear receptor subfamily 5, group A, member 2	2.9269483	1.549397263	−1.6877522	−0.755103	2
57157	PHTF2	putative homeodomain transcription factor 2	2.4678419	1.303249973	−1.7268459	−0.788139	3
10484	SEC23A	Sec23 homolog A (S. cerevisiae)	2.3764641	1.248816608	−4.183498	−2.06471	2
3680	ITGA9	integrin, alpha 9	2.3379743	1.225259071	−1.6452351	−0.718294	1
10672	GNA13	guanine nucleotide binding protein (G protein), alpha 13	2.157417	1.109305057	−1.8154717	−0.859829	4
63895	PIEZO2	piezo-type mechanosensitive ion channel component 2	2.6537354	1.408024529	−2.4506588	−1.29317	1
5738	PTGFRN	prostaglandin F2 receptor inhibitor	2.642839	1.40208854	−5.7623205	−2.52665	3
1756	DMD	dystrophin	2.4918914	1.317241195	−1.5377088	−0.620782	1

9859	CEP170	centrosomal protein 170kDa	3.615709	1.854278571	-1.8422364	-0.881458	1
9315	NREP	neuronal regeneration related protein	4.4351254	2.148974896	-2.4860835	-1.313875	1
115908	CTHRC1	collagen triple helix repeat containing 1	21.539711	4.428926988	-3.2357185	-1.694086	1
285598	ARL10	ADP-ribosylation factor-like 10	2.0289125	1.020706648	-1.6264279	-0.701707	5
860	RUNX2	runt-related transcription factor 2	7.6337624	2.932394284	-2.316619	-1.212021	4
6443	SGCB	sarcoglycan, beta (43kDa dystrophin-associated glycoprotein)	2.172902	1.119623109	-3.9752877	-1.991059	1
1734	DIO2	deiodinase, iodothyronine, type II	4.1299953	2.04614014	-2.2864702	-1.193122	1
222658	KCTD20	potassium channel tetramerization domain containing 20	2.6426406	1.401980231	-1.8270454	-0.869513	1
5396	PRRX1	paired related homeobox 1	6.295065	2.654221275	-2.6690764	-1.416341	1
154141	MBOAT1	membrane bound O-acyltransferase domain containing 1	2.0484128	1.034506479	-1.6067419	-0.684138	1
29887	SNX10	sorting nexin 10	2.3028336	1.203410167	-1.7153641	-0.778515	1
8417	STX7	syntaxin 7	2.1770043	1.122344257	-2.014982	-1.010767	4
8819	SAP30	Sin3A-associated protein, 30kDa	2.1350708	1.094283911	-3.6536663	-1.869345	2
5159	PDGFRB	platelet-derived growth factor receptor, beta polypeptide	3.4799414	1.799063012	-3.8238856	-1.8839725	1
1131	CHRM3	cholinergic receptor, muscarinic 3	2.8919995	1.532067303	-1.8628036	-0.897476	2
7431	VIM	vimentin	2.1574442	1.109323246	-3.127566	-1.64504	2
170954	PPP1R18	protein phosphatase 1, regulatory subunit 18	2.5516028	1.351403767	-1.7732465	-0.826393	3
54749	EPDR1	ependymin related 1	2.011554	1.008310468	-2.9045637	-1.538322	3
54566	EPB41L4B	erythrocyte membrane protein band 4.1 like 4B	3.2564375	1.703294538	-2.165876	-1.0574225	1
60481	ELOVL5	ELOVL fatty acid elongase 5	3.1485033	1.654666179	-1.7085098	-0.772739	1
4325	MMP16	matrix metalloproteinase 16 (membrane-inserted)	2.0137687	1.009897986	-2.4893477	-1.315768	1
8829	NRP1	neuropilin 1	2.4660127	1.30218023	-1.9796517	-0.985247	1
57482	KIAA1211	KIAA1211	3.3908448	1.761644753	-1.854175	-0.890777	1

Putative target genes by *miR-30c-2-3p* regulation in PDAC cells.

Entrez Gene ID	Gene Symbol	Gene Name	GEO FC	GEO log2 FC	PANC-1 <i>miR-30c-2-3</i> <i>p</i> transfectant FC	PANC-1 <i>miR-30c-2-3</i> <i>p</i> transfectant log2 FC	Total binding sites
23052	ENDOD1	endonuclease domain containing 1	2.2613354	1.17717499	-1.5562582	-0.638082	1
2152	F3	coagulation factor III (thromboplastin, tissue factor)	2.6254416	1.3925601	-1.6159481	-0.692381	1
29766	TMOD3	tropomodulin 3 (ubiquitous)	2.0454962	1.03245086	-2.7957864	-1.483254	2
3675	ITGA3	integrin, alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor)	2.5118082	1.32872631	-2.564058	-1.358429	2
7153	TOP2A	topoisomerase (DNA) II alpha 170kDa	2.8882535	1.53019737	-2.2842295	-1.191708	1
9208	LRRFIP1	leucine rich repeat (in FLII) interacting protein 1	2.648011	1.40490912	-2.430869	-1.281472	2
6237	RRAS	related RAS viral (r-ras) oncogene homolog	2.2145765	1.14703083	-1.8885567	-0.917284	1
9603	NFE2L3	nuclear factor, erythroid 2-like 3	2.8481824	1.51004154	-2.1272888	-1.089016	3

11098	PRSS23	protease, serine, 23	2.7526407	1.46081631	-1.9241873	-0.944249	1
3556	IL1RAP	interleukin 1 receptor accessory protein	2.0077293	1.00556477	-1.7964197	-0.825645	1
129642	MBOAT2	membrane bound O-acyltransferase domain containing 2	2.9205017	1.54621622	-3.6262991	-1.858498	2
27042	DIEXF	digestive organ expansion factor homolog (zebrafish)	2.1144078	1.08025365	-1.6244218	-0.699926	5
130340	AP1S3	adaptor-related protein complex 1, sigma 3 subunit	2.0921135	1.06496112	-4.180721	-2.04955067	3
6307	MSMO1	methylsterol monooxygenase 1	2.137287	1.09578065	-3.8763406	-1.954695	3
8553	BHLHE40	basic helix-loop-helix family, member e40	3.2192662	1.68673188	-1.5556555	-0.637523	1
23603	CORO1C	coronin, actin binding protein, 1C	2.9602175	1.56570318	-2.8987157	-1.535414	1
6241	RRM2	ribonucleotide reductase M2	2.2445	1.1663941	-2.0015752	-1.001136	1
64108	RTP4	receptor (chemosensory) transporter protein 4	2.265131	1.17959449	-5.888388	-2.557873	1
29108	PYCARD	PYD and CARD domain containing	2.0466015	1.03323022	-2.5309663	-1.339688	1
131566	DCBLD2	discoidin, CUB and LCCL domain containing 2	3.1744227	1.66649425	-2.2274199	-1.155374	2
84441	MAML2	mastermind-like 2 (Drosophila)	2.519923	1.33337965	-1.8320524	-0.873461	2
7414	VCL	vinculin	2.0701628	1.04974423	-1.788988	-0.839144	3
22925	PLA2R1	phospholipase A2 receptor 1, 180kDa	2.3120809	1.20919188	-1.9828366	-0.987566	1
22822	PHLDA1	pleckstrin homology-like domain, family A, member 1	3.0949705	1.62992566	-2.4945047	-1.318753	1
55107	ANO1	anoctamin 1, calcium activated chloride channel	7.8534274	2.97332241	-3.279582	-1.713512	1
50515	CHST11	carbohydrate (chondroitin 4) sulfotransferase 11	2.9458146	1.55866663	-1.8003976	-0.848316	1
684	BST2	bone marrow stromal cell antigen 2	2.957019	1.56414351	-2.9614215	-1.564264	1
1942	EFNA1	ephrin-A1	2.0360727	1.02578908	-1.870977	-0.903792	2
4015	LOX	lysyl oxidase	8.548389	3.09565256	-1.5591584	-0.640768	2
10379	IRF9	interferon regulatory factor 9	2.1249146	1.08740486	-1.5612102	-0.642665	1
355	FAS	Fas cell surface death receptor	2.9723217	1.57159027	-2.8188543	-1.495109	1
29	ABR	active BCR-related	2.08959	1.0632199	-2.49846555	-1.3182065	1
284723	SLC25A34	solute carrier family 25, member 34	2.1012342	1.07123697	-2.2505753	-1.170294	2
57198	ATP8B2	ATPase, aminophospholipid transporter, class I, type 8B, member 2	2.2136514	1.14642805	-3.3745415	-1.754692	1
25878	MXRA5	matrix-remodelling associated 5	5.2305136	2.38695262	-4.461383	-2.157491	1
3656	IRAK2	interleukin-1 receptor-associated kinase 2	2.2026823	1.13926143	-3.5588243	-1.831401	1
203068	TUBB	tubulin, beta class I	2.081564	1.05766792	-1.74200455	-0.7978345	1
91404	SESTD1	SEC14 and spectrin domains 1	2.61934	1.38920334	-1.713972	-0.777344	1
2053	EPHX2	epoxide hydrolase 2, cytoplasmic	2.686746	1.42585994	-1.5061291	-0.590846	1
2069	EREG	epiregulin	2.4593692	1.29828833	-3.0630414	-1.614965	1
56937	PMEPA1	prostate transmembrane protein, androgen induced 1	4.4851875	2.1651683	-1.6591595	-0.7277565	1
9770	RASSF2	Ras association (RalGDS/AF-6) domain family member 2	2.853415	1.51268959	-2.571092	-1.362381	2
5339	PLEC	plectin	2.1774795	1.12265914	-2.614268	-1.386407	3
558	AXL	AXL receptor tyrosine kinase	2.9549663	1.56314168	-2.58509	-1.370215	3
57713	SFMBT2	Scm-like with four mbt domains 2	2.4176946	1.27363202	-2.0261168	-1.018717	4

2000	<i>ELF4</i>	E74-like factor 4 (ets domain transcription factor)	2.6211767	1.39021461	-1.7536374	-0.810351	2
11213	<i>IRAK3</i>	interleukin-1 receptor-associated kinase 3	3.9714346	1.98966025	-2.6676056	-1.415546	1
162073	<i>ITPR1PL2</i>	inositol 1,4,5-trisphosphate receptor interacting protein-like 2	2.0831883	1.05879325	-1.7624962	-0.81762	4
57125	<i>PLXDC1</i>	plexin domain containing 1	3.7879417	1.92141413	-1.5919814	-0.6693795	1
10135	<i>NAMPT</i>	nicotinamide phosphoribosyltransferase	2.0969985	1.06832583	-1.5757401	-0.65603	1
5912	<i>RAP2B</i>	RAP2B, member of RAS oncogene family	2.7403688	1.45437006	-4.9478607	-2.306805	2
3777	<i>KCNK3</i>	potassium channel, subfamily K, member 3	2.4246292	1.27776413	-2.9468246	-1.559161	4
9123	<i>SLC16A3</i>	solute carrier family 16 (monocarboxylate transporter), member 3	6.238611	2.64122485	-1.5706434	-0.651356	2
57619	<i>SHROOM3</i>	shroom family member 3	2.1864073	1.12856218	-1.93803985	-0.948166	4
23043	<i>TNIK</i>	TRAF2 and NCK interacting kinase	2.1772404	1.12250071	-2.91195425	-1.485177	2
1296	<i>COL8A2</i>	collagen, type VIII, alpha 2	3.9824197	1.99364527	-3.2619098	-1.6652685	2
59339	<i>PLEKHA2</i>	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 2	2.0061517	1.0044307	-2.3900883	-1.257064	1
710	<i>SERPING1</i>	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1	2.8698225	1.52096151	-2.8072548	-1.48916	4
4939	<i>OAS2</i>	2'-5'-oligoadenylate synthetase 2, 69/71kDa	2.6352875	1.39796036	-2.34519413	-1.16816167	2
85415	<i>RHPN2</i>	rhophilin, Rho GTPase binding protein 2	2.1334422	1.09318303	-1.80605875	-0.8398745	2
368	<i>ABCC6</i>	ATP-binding cassette, sub-family C (CFTR/MRP), member 6	2.0255477	1.01831206	-5.51934563	-2.20208975	1
55083	<i>KIF26B</i>	kinesin family member 26B	7.422415	2.89188867	-1.8272907	-0.869706	2
340024	<i>SLC6A19</i>	solute carrier family 6 (neutral amino acid transporter), member 19	2.0228834	1.01641316	-1.5889257	-0.668052	1
3718	<i>JAK3</i>	Janus kinase 3	2.0072212	1.00519961	-12.895146	-3.688756	3
7220	<i>TRPC1</i>	transient receptor potential cation channel, subfamily C, member 1	2.8364346	1.5040786	-3.6420674	-1.864758	1
4175	<i>MCM6</i>	minichromosome maintenance complex component 6	2.0213459	1.01531622	-2.1289797	-1.090162	1
219285	<i>SAMD9L</i>	sterile alpha motif domain containing 9-like	2.292748	1.19707779	-1.6227703	-0.698459	1
1999	<i>ELF3</i>	E74-like factor 3 (ets domain transcription factor, epithelial-specific)	2.274228	1.1853769	-2.3688393	-1.24418	1
10846	<i>PDE10A</i>	phosphodiesterase 10A	2.24667	1.16778823	-1.66160585	-0.729165	1
3092	<i>HIP1</i>	huntingtin interacting protein 1	3.1944785	1.67558043	-8.986034	-3.167685	3
1122	<i>CHML</i>	choroideremia-like (Rab escort protein 2)	2.3433568	1.22857664	-6.369226	-2.671118	2
80005	<i>DOCK5</i>	dedicator of cytokinesis 5	2.30235	1.20310717	-1.5297543	-0.6133	2
9388	<i>LIPG</i>	lipase, endothelial	2.760285	1.46481723	-4.932008	-2.302175	3
6581	<i>SLC22A3</i>	solute carrier family 22 (organic cation transporter), member 3	2.1399078	1.09754864	-1.6263621	-0.701649	3
26112	<i>CCDC69</i>	coiled-coil domain containing 69	2.4701278	1.30458569	-1.514434	-0.598779	1
9902	<i>MRC2</i>	mannose receptor, C type 2	2.612301	1.38532114	-2.5926282	-1.374415	1
9456	<i>HOMER1</i>	homer homolog 1 (Drosophila)	2.461455	1.29951136	-1.6948876	-0.76119	1
51278	<i>IER5</i>	immediate early response 5	2.0735698	1.05211661	-2.4117854	-1.270102	5

10100	TSPAN2	tetraspanin 2	2.6602573	1.41156579	-2.5570564	-1.354484	3
3976	LIF	leukemia inhibitory factor	2.2362914	1.16110819	-2.25570925	-1.1157615	2
2687	GGT5	gamma-glutamyltransferase 5	2.1869118	1.12889504	-3.0339217	-1.601184	1
4148	MATN3	matrilin 3	4.523766	2.17752431	-2.1714654	-1.118669	1
5069	PAPPA	pregnancy-associated plasma protein A, pappalysin 1	3.3934433	1.76274991	-1.6303263	-0.705161	2
344558	SH3RF3	SH3 domain containing ring finger 3	2.101751	1.07159176	-2.0393922	-1.028139	2
5476	CTSA	cathepsin A	2.1106308	1.07767424	-3.55539295	-1.820275	1
84168	ANTXR1	anthrax toxin receptor 1	7.4770546	2.90247007	-2.7002661	-1.433102	1
9830	TRIM14	tripartite motif containing 14	2.3578706	1.23748455	-2.26918445	-1.124839	2
875	CBS	cystathionine-beta-synthase	4.0390577	2.01401876	-2.9737785	-1.572297	7
1794	DOCK2	dedicator of cytokinesis 2	2.2617252	1.17742365	-1.5354911	-0.6187	1
5272	SERPINB9	serpin peptidase inhibitor, clade B (ovalbumin), member 9	3.1824975	1.67015938	-2.953741	-1.562543	3
4065	LY75	lymphocyte antigen 75	3.5984533	1.84737694	-3.0177822	-1.593489	1
871	SERPINH1	serpin peptidase inhibitor, clade H (heat shock protein 47), member 1, (collagen binding protein 1)	4.0745363	2.02663588	-2.719987	-1.4436	2
4638	MYLK	myosin light chain kinase	2.6462674	1.40395885	-2.41026485	-1.2675595	2
8324	FZD7	frizzled family receptor 7	3.0004196	1.58516427	-1.7274305	-0.788628	2
9644	SH3PXD2A	SH3 and PX domains 2A	3.098084	1.63137626	-2.3469895	-1.230165	1
10052	GJC1	gap junction protein, gamma 1, 45kDa	2.4474685	1.29129029	-1.7094983	-0.773573	1
10687	PNMA2	paraneoplastic Ma antigen 2	4.17114	2.06044174	-6.3219113	-2.660361	3
7162	TPBG	trophoblast glycoprotein	3.1523435	1.65642475	-1.7106761	-0.774567	2
56648	EIF5A2	eukaryotic translation initiation factor 5A2	2.7315953	1.44974376	-3.0672145	-1.616929	4
83742	MARVELD1	MARVEL domain containing 1	2.2957945	1.19899351	-2.5303726	-1.33935	1
130271	PLEKHH2	pleckstrin homology domain containing, family H (with MyTH4 domain) member 2	2.3987784	1.26229989	-1.818772	-0.862965	2
659	BMPR2	bone morphogenetic protein receptor, type II (serine/threonine kinase)	2.4564056	1.2965488	-1.6440841	-0.717284	1
2274	FHL2	four and a half LIM domains 2	3.8398573	1.9410527	-1.65125545	-0.7195805	2
56243	KIAA1217	KIAA1217	2.6544228	1.40839818	-2.2281299	-1.155833	1
2151	F2RL2	coagulation factor II (thrombin) receptor-like 2	5.936649	2.56964882	-7.8835106	-2.978838	4
4053	LTBP2	latent transforming growth factor beta binding protein 2	3.249144	1.70005968	-2.5622756	-1.357426	2
1690	COCH	cochlin	3.8746495	1.95406581	-3.2093477	-1.68228	1
4093	SMAD9	SMAD family member 9	2.2520816	1.1712591	-2.51712345	-1.3037185	2
55243	KIRREL	kin of IRRE like (Drosophila)	3.0286162	1.59865876	-2.18751375	-1.12549	2
284611	FAM102B	family with sequence similarity 102, member B	2.593979	1.3751668	-5.2071325	-2.375539	2
57722	IGDCC4	immunoglobulin superfamily, DCC subclass, member 4	2.6780534	1.42118473	-2.9324749	-1.552119	3
718	C3	complement component 3	4.95801	2.30976118	-1.8616517	-0.896583	6
22797	TFEC	transcription factor EC	3.1502035	1.65544503	-2.4804018	-1.310574	1

6533	<i>SLC6A6</i>	solute carrier family 6 (neurotransmitter transporter), member 6	6.4249697	2.68368965	-4.171237	-2.060475	3
5740	<i>PTGIS</i>	prostaglandin I2 (prostacyclin) synthase	4.4972715	2.16904998	-5.5244417	-2.465829	4
7070	<i>THY1</i>	Thy-1 cell surface antigen	5.038337	2.33294762	-1.9090989	-0.932892	1
867	<i>CBL</i>	Cbl proto-oncogene, E3 ubiquitin protein ligase	2.0819829	1.05795822	-1.7303138	-0.791034	2
84662	<i>GLIS2</i>	GLIS family zinc finger 2	3.0599735	1.61351916	-2.0631127	-1.044823	3
51303	<i>FKBP11</i>	FK506 binding protein 11, 19 kDa	2.5678456	1.36055846	-2.53125675	-1.3380525	1
6480	<i>ST6GAL1</i>	ST6 beta-galactosamide alpha-2,6-sialyltransferase 1	2.023059	1.01653839	-5.692959	-2.509179	1
2266	<i>FGG</i>	fibrinogen gamma chain	3.3034732	1.72398364	-3.9274867	-1.973606	2
285203	<i>EOGT</i>	EGF domain-specific O-linked N-acetylglucosamine (GlcNAc) transferase	2.3285272	1.21941773	-1.7727354	-0.825977	2
1728	<i>NQO1</i>	NAD(P)H dehydrogenase, quinone 1	4.5524726	2.18665033	-1.7585198	-0.814362	1
3613	<i>IMPA2</i>	inositol(myo)-1(or 4)-monophosphatase 2	2.8482149	1.510058	-3.329885	-1.7180095	3
4330	<i>MN1</i>	meningioma (disrupted in balanced translocation) 1	3.5127406	1.81259704	-1.570467	-0.651194	1
1959	<i>EGR2</i>	early growth response 2	3.8833003	1.95728328	-2.5051596	-1.324903	1
686	<i>BTB</i>	biotinidase	2.1993654	1.13708731	-2.089345	-1.063051	11
11037	<i>STON1</i>	stonin 1	3.027899	1.59831708	-2.28250615	-1.1797175	1
60681	<i>FKBP10</i>	FK506 binding protein 10, 65 kDa	2.018864	1.01354373	-3.4984043	-1.806697	1
79627	<i>OGFRL1</i>	opioid growth factor receptor-like 1	2.0309052	1.0221229	-2.8983648	-1.535239	1
493869	<i>GPX8</i>	glutathione peroxidase 8 (putative)	4.398069	2.13687024	-1.5208063	-0.604836	3
89796	<i>NAV1</i>	neuron navigator 1	2.4964359	1.31986986	-4.78107215	-2.2445055	4
144165	<i>PRICKLE1</i>	prickle homolog 1 (Drosophila)	3.1929393	1.67488513	-3.0424352	-1.605227	1
4811	<i>NID1</i>	nidogen 1	3.1419613	1.65166541	-7.9136095	-2.984336	2
57616	<i>TSHZ3</i>	teashirt zinc finger homeobox 3	2.1751404	1.12110853	-4.710902	-2.236003	1
57333	<i>RCN3</i>	reticulocalbin 3, EF-hand calcium binding domain	2.312374	1.20937476	-1.633107	-0.707619	1
5010	<i>CLDN11</i>	claudin 11	5.816361	2.54011681	-2.4935548	-1.318204	2
3667	<i>IRS1</i>	insulin receptor substrate 1	2.6697042	1.4166799	-1.9530267	-0.965712	2
84706	<i>GPT2</i>	glutamic pyruvate transaminase (alanine aminotransferase) 2	2.363553	1.24095722	-4.603926	-2.202865	3
3212	<i>HOXB2</i>	homeobox B2	3.2313602	1.69214158	-2.760372	-1.464863	1
10855	<i>HPSE</i>	heparanase	2.1441035	1.10037455	-1.6127669	-0.689538	1
3111	<i>HLA-DOA</i>	major histocompatibility complex, class II, DO alpha	2.0180554	1.01296578	-2.9175372	-1.544751	1
3487	<i>IGFBP4</i>	insulin-like growth factor binding protein 4	3.1715395	1.66518331	-1.9788606	-0.98467	3
23301	<i>EHBP1</i>	EH domain binding protein 1	2.1654549	1.11467013	-1.6429753	-0.710911	1
285590	<i>SH3PXD2B</i>	SH3 and PX domains 2B	2.481224	1.31105198	-5.5057864	-2.460949	1
388610	<i>TRNP1</i>	TMF1-regulated nuclear protein 1	2.1865497	1.12865614	-1.9689997	-0.977463	2
8477	<i>GPR65</i>	G protein-coupled receptor 65	2.574515	1.36430068	-1.9066031	-0.931005	2
65108	<i>MARCKSL1</i>	MARCKS-like 1	2.511199	1.32837636	-3.3468802	-1.742817	3
91663	<i>MYADM</i>	myeloid-associated differentiation marker	2.2757297	1.18632921	-1.5950052	-0.673561	2

4499	<i>MT1M</i>	metallothionein 1M	2.7478464	1.45830136	−2.3982008	−1.261952	1
83879	<i>CDCA7</i>	cell division cycle associated 7	2.4945168	1.31876039	−3.52452985	−1.733681	1
5481	<i>PPID</i>	peptidylprolyl isomerase D	2.1669471	1.11566393	−1.7721004	−0.82546	1
8459	<i>TPST2</i>	tyrosylprotein sulfotransferase 2	3.4068055	1.76841958	−1.973812	−0.980985	1
2043	<i>EPHA4</i>	EPH receptor A4	2.785011	1.47768303	−3.0478623	−1.607798	1
84056	<i>KATNAL1</i>	katanin p60 subunit A-like 1	2.2414992	1.16446398	−1.9797919	−0.985349	3
54796	<i>BNC2</i>	basonuclin 2	4.100778	2.03589764	−5.485393	−2.455595	2
9075	<i>CLDN2</i>	claudin 2	2.3763666	1.24875742	−1.5970572	−0.675416	1
10962	<i>MLLT11</i>	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11	2.389446	1.25667616	−4.943322	−2.305481	1
5552	<i>SRGN</i>	serglycin	2.812706	1.49195876	−2.3373752	−1.224889	1
972	<i>CD74</i>	CD74 molecule, major histocompatibility complex, class II invariant chain	2.9994717	1.58470842	−1.5113016	−0.595792	1
50807	<i>ASAP1</i>	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1	2.6920624	1.42871185	−1.5026035	−0.587464	1
2869	<i>GRK5</i>	G protein-coupled receptor kinase 5	2.0465665	1.03320555	−2.7596712	−1.464496	2
10365	<i>KLF2</i>	Kruppel-like factor 2 (lung)	2.0431898	1.03082323	−2.627674	−1.393786	3
11317	<i>RBPJL</i>	recombination signal binding protein for immunoglobulin kappa J region-like	5.1099987	2.35332292	−1.981117	−0.986314	1
495	<i>ATP4A</i>	ATPase, H+/K+ exchanging, alpha polypeptide	2.9357285	1.55371855	−1.87758	−0.908874	1

Table S3. The expression levels of protein

Gene	Antibody	Antibody staining			
		High	Medium	Low	Not detected
<i>YWHAZ</i>	CAB005065	12/12	–	–	–
<i>CBFB</i>	HPA038852	–	3/12	6/12	3/12
<i>F3</i>	CAB009438	4/12	6/12	2/12	–
<i>TMOD3</i>	HPA001849	9/10	1/10	–	–
<i>NFE2L3</i>	HPA055889	–	–	–	11/11
<i>ENDOD1</i>	HPA008932	2/11	5/11	3/11	1/11
<i>ITGA3</i>	HPA008572	7/11	3/11	–	1/11
<i>RRAS</i>	CAB10160	–	2/9	4/9	3/9
<i>PRSS23</i>	HPA030591	–	–	1/11	10/11
<i>TOP2A</i>	HPA006458	5/11	6/11	–	–

<i>BHLHE40</i>	HPA028922	2/11	4/11	1/11	4/11
<i>CHST11</i>	HPA052828	–	2/8	1/8	5/8
<i>IL1RAP</i>	HPA035293	–	4/12	2/12	6/12
<i>DIEXF</i>	HPA026640	4/11	5/11	1/11	1/11
<i>CORO1C</i>	HPA041737	3/12	9/12	–	–
<i>RTP4</i>	HPA064887	–	8/9	–	1/9
<i>AP1S3</i>	HPA066782	–	–	–	8/8
<i>LRRFIP1</i>	HPA006979	5/10	5/10	–	–

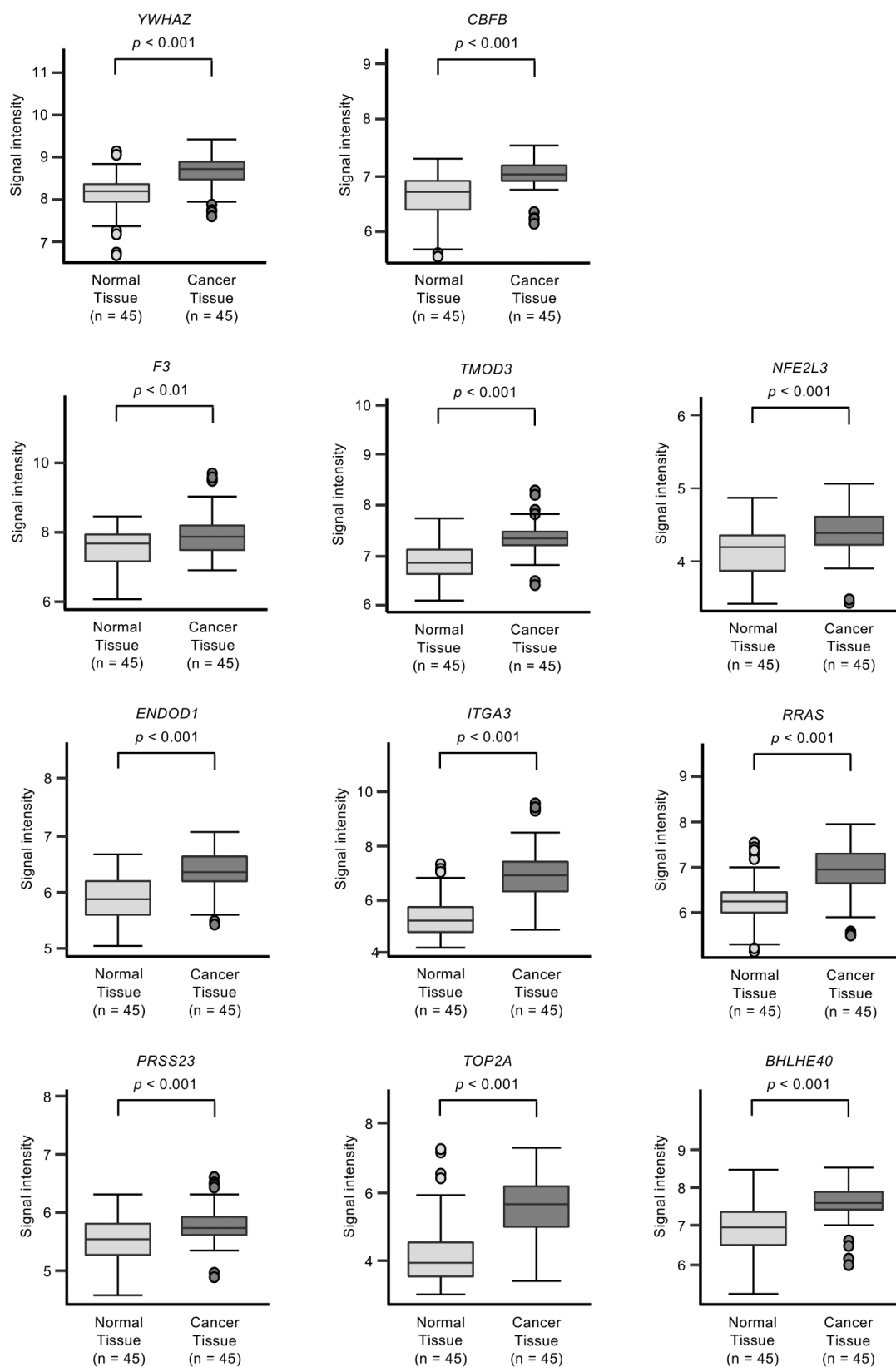
Table S4. Gene Ontology classification.

Term	Annotation	hyp_pval	Genes
protein binding,cytoplasm,nucleus,DNA binding,negative regulation of transcription by RNA polymerase II, regulation of transcription by RNA polymerase II,regulation of transcription, DNA-templated, RNA polymerase II cis-regulatory region sequence-specific DNA binding, DNA-binding transcription repressor activity, RNA polymerase II-specific	GO:0005515,GO:0005737,GO:0005634,GO:0003677,GO:0000122,GO:0006357,GO:0006355,GO:0000978,GO:0001227	1.35E-06	<i>NFE2L3,LRRFIP1,BHLHE40</i>
protein binding,cytoplasm,protein homodimerization activity,nucleus,DNA binding	GO:0005515,GO:0005737,GO:0042803,GO:0005634,GO:0003677	6.20E-06	<i>LRRFIP1,BHLHE40,TOP2A</i>
protein binding,nucleus,DNA binding,negative regulation of transcription by RNA polymerase II, regulation of transcription by RNA polymerase II	GO:0005515,GO:0005634,GO:0003677,GO:0000122,GO:0006357	6.19E-05	<i>NFE2L3,LRRFIP1,CBFB,BHLHE40</i>
extracellular exosome,protein binding,focal adhesion	GO:0070062,GO:0005515,GO:0005925	0.0002313 24	<i>YWHAZ,RRAS,ITGA3</i>
positive regulation of NF-kappaB transcription factor activity	GO:0051092	0.0001972 63	<i>LRRFIP1,IL1RAP,RIP4</i>
protein binding,cytoplasm,nucleus,DNA binding	GO:0005515,GO:0005737,GO:0005634,GO:0003677	0.0003517 21	<i>NFE2L3,LRRFIP1,BHLHE40,TOP2A</i>
protein binding,protein domain specific binding	GO:0005515,GO:0019904	0.0007610 23	<i>BHLHE40,YWHAZ,ITGA3</i>
Cytokine-mediated signaling pathway	GO:0019221	0.0010900 9	<i>YWHAZ,IL1RAP,F3</i>

protein binding,protein heterodimerization activity	GO:0005515,GO:0046982	0.0010264 9	<i>BHLHE40, TOP2A, ITGA3</i>
protein binding,nucleus,DNA binding	GO:0005515,GO:0005634,GO:0003677	0.0045147 2	<i>NFE2L3, LRRFIP1, CBFβ, BHLHE40, TOP2A</i>
membrane,hydrolase activity	GO:0016020,GO:0016787	0.0100205	<i>ENDOD1, RRAS, IL1RAP</i>
extracellular region,membrane	GO:0005576,GO:0016020	0.0152731	<i>ENDOD1, IL1RAP, F3</i>

Table S5. Reagents used in this study.

TaqMan Primers And Probes	Assay ID	Company	
<i>hsa-miR-30c-5p</i>	000419	Applied Biosystems, Waltham, MA, USA	
<i>hsa-miR-30c-2-3p</i>	002110	Applied Biosystems, Waltham, MA, USA	
<i>RNU48</i>	001006	Applied Biosystems, Waltham, MA, USA	
<i>TOP2A</i>	Hs01032137	Applied Biosystems, Waltham, MA, USA	
<i>GUSB</i>	Hs99999908_m1	Applied Biosystems, Waltham, MA, USA	
Pre-miR miRNA Presursors	Assay ID	Concentration	
<i>hsa-miR-30c-5p</i>	PM11060	10 nM	Applied Biosystems, Waltham, MA, USA
<i>hsa-miR-30c-2-3p</i>	PM12646	10 nM	Applied Biosystems, Waltham, MA, USA
negative control miRNA #1	AM17010	10 nM	Applied Biosystems, Waltham, MA, USA
Stealth RNAi siRNA	Assay ID	Concentration	
<i>siTOP2A</i>	HSS110896 HSS186387	10 nM	Invitrogen, Waltham, MA, USA
Antibody	Catalog Number	Dilution	
Anti- <i>TOP2A</i>	12286	WB 1:1000	Cell Signaling Technology, Danvers, MA, USA
		IHC 1:400	
GAPDH	SAF6698	WB 1:2000	Wako, Osaka, Japan
Ki-67	M7240	IHC 1:100	Dako, Denmark, Denmark
HMGB2	ab124670	IHC 1:250	abcam, Cambridge, UK
SP1	9389	IHC 1:2000	Cell Signaling Technology, Danvers, MA, USA



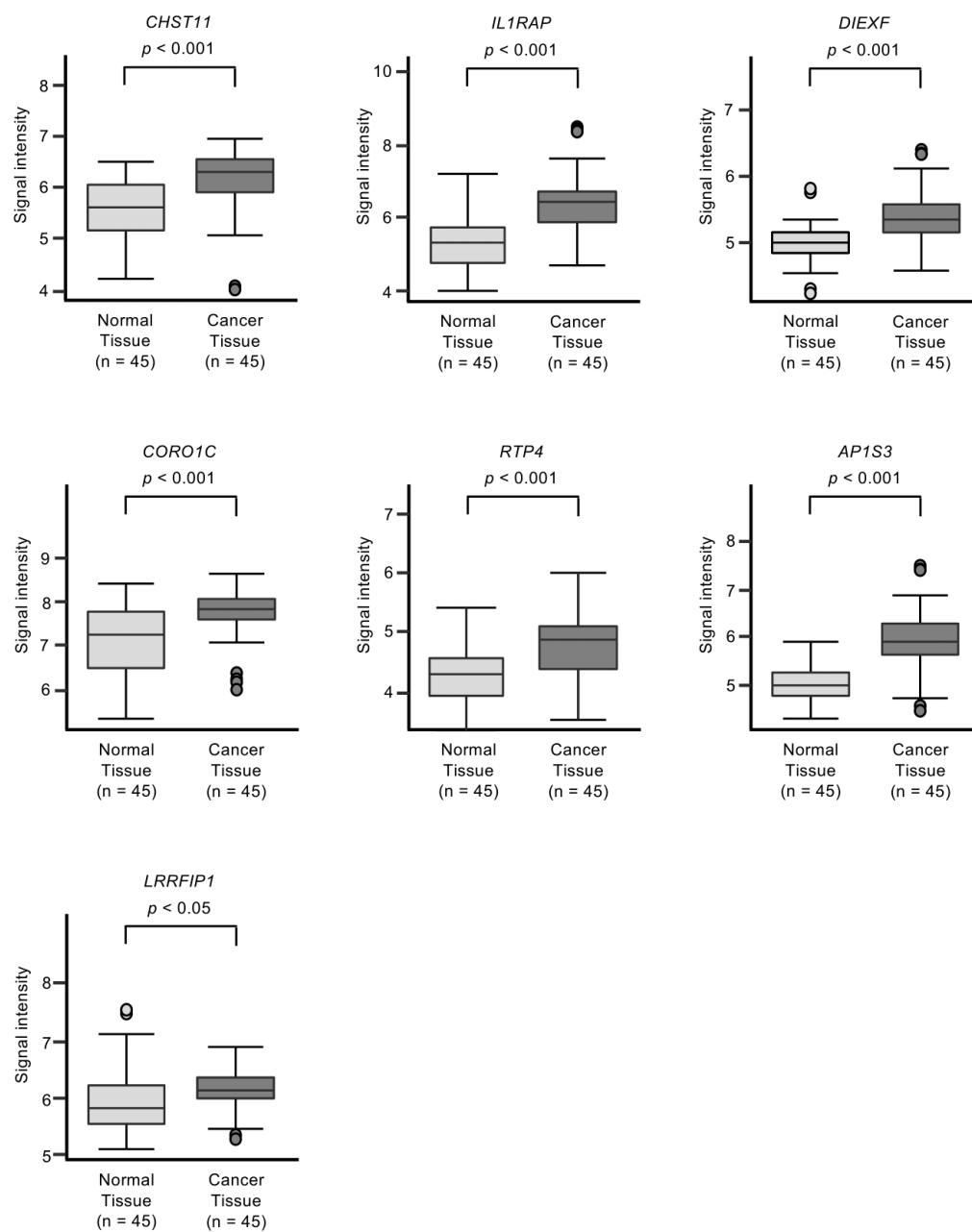


Figure S1. Expression levels of 18 target genes using GSE28735.

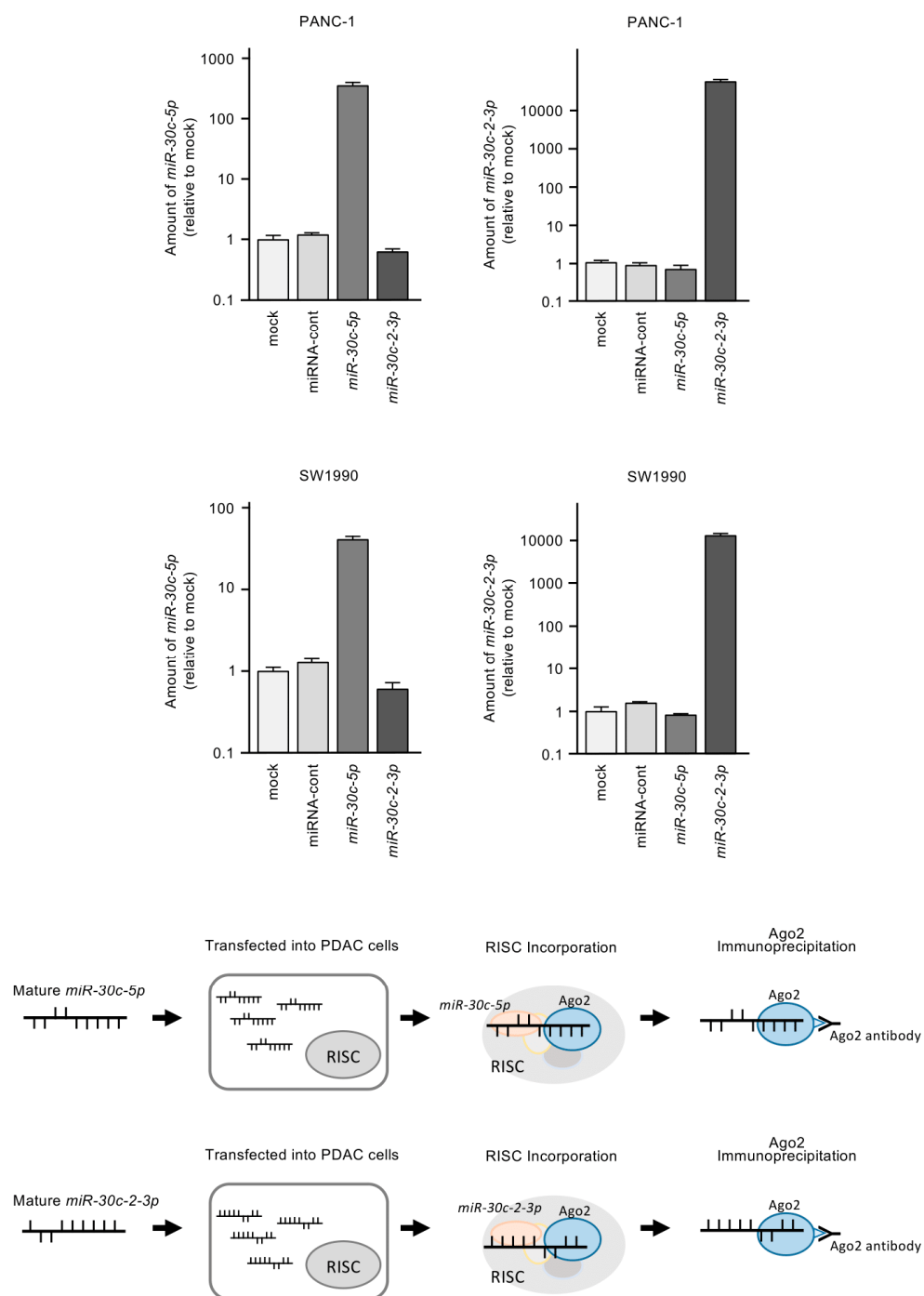


Figure S2. Incorporation of *miR-30c-5p* and *miR-30c-2-3p* into the RISC in PDAC cells.