

## Supplementary data to:

### Original article:

## SIMULTANEOUS MICRORNA-612 RESTORATION AND 5-FU TREATMENT INHIBIT THE GROWTH AND MIGRATION OF HUMAN PANC-1 PANCREATIC CANCER CELLS

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**Supplementary Table 1:** Raw data showing investigated genes' expression after transfection of PANC-1 cells with the miR-612 or their corresponding control group. The relative expression of each gene was analyzed by comparative threshold cycle (Ct). Ct value was normalized using the formula  $\Delta Ct = Ct$  (investigated genes) -  $Ct$  (SNORD and GAPDH). Then formula  $\Delta\Delta Ct = \Delta Ct$  (treated) -  $\Delta Ct$  (control) was used. Finally, the formula  $2^{-\Delta\Delta Ct}$  was used for estimating relative expression of each gene.

Group	CT values SNORD				CT values miR-612				Fold induction				
	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>PANC1</b>													
<b>Dose 60</b>	25.87	25.75	26.2	25.94	29.83	29.42	29.42	29.42	156.498	164.2785	147.0334	155.9366	7.051464
<b>Dose 80</b>	25.53	25.52	25.81	25.62	28.09	27.81	27.81	27.81	413.0006	427.565	415.8732	418.8129	6.298781
<b>Dose 100</b>	26.29	26.28	25.83	26.13333	28.91	28.7	28.7	28.7	396.1766	390.7224	385.3432	390.7474	4.422752
<b>Control</b>	25.7	25.89	25.71	25.76667	36.95	36.92	36.92	36.92	1	1	1	1	0
CT values SNORD				CT values miR-612				Fold induction					
<b>PANC1</b>	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>24h</b>	23.31	23.78	23.01	23.36667	26.04	26.26	26.03	26.11	367.0925	380.038	352.1387	366.4231	11.39969
<b>48h</b>	26.22	26.38	26.43	26.34333	28.74	28.68	29.16	28.86	424.6116	430.539	430.539	428.5632	2.794183
<b>72h</b>	27.18	27.31	27.04	27.17667	31.44	31.43	31.45	31.44	127.1158	121.9377	134.3637	127.8057	5.096325
<b>Control</b>	25.7	25.87	25.71	25.76	36.95	36.92	37.19	37.02	1	1	1	1	0
CT values GAPDH				CT values BAX				Fold induction					
<b>PANC1</b>	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>5FU</b>	19.95	19.82	20.13	19.96667	26.3	26.1	26.32	26.24	2.42839	2.297397	2.114036	2.279941	0.128927
<b>miR</b>	20.51	20.89	21.07	20.82333	27.82	28.2	27.98	28	1.248331	1.125058	1.283426	1.218938	0.067912
<b>miR+5FU</b>	20.23	20.46	20.88	20.52333	26.24	26.24	26.42	26.3	3.07375	3.24901	3.317278	3.213346	0.102568
<b>Control</b>	21.67	22.03	21.88	21.86	29.3	29.51	29.15	29.32	1	1	1	1	0
CT values GAPDH				CT values CAS3				Fold induction					
<b>PANC1</b>	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>5FU</b>	19.95	19.82	20.13	19.96667	32.27	31.45	31.62	31.78	30.06473	35.0174	33.59093	32.89102	2.081609
<b>miR</b>	20.51	20.89	21.07	20.82333	35.91	35.48	35.7	35.69667	3.555371	4.500234	3.810552	3.955386	0.399102
<b>miR+5FU</b>	20.23	20.46	20.88	20.52333	30.9	30.54	30.82	30.75333	94.35323	102.5369	98.36001	98.41673	3.341228
<b>Control</b>	21.67	22.03	21.88	21.86	38.9	38.79	38.44	38.71	1	1	1	1	0

**Supplementary Table 1 (cont.):** Raw data showing investigated genes' expression after transfection of PANC-1 cells with the miR-612 or their corresponding control group. The relative expression of each gene was analyzed by comparative threshold cycle (Ct). Ct value was normalized using the formula  $\Delta Ct = Ct$  (investigated genes) - Ct (SNORD and GAPDH). Then formula  $\Delta\Delta Ct = \Delta Ct$  (treated) -  $\Delta Ct$  (control) was used. Finally, the formula  $2^{-\Delta\Delta Ct}$  was used for estimating relative expression of each gene.

Group	CT values GAPDH				CT values BCL2				Fold induction				
	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>PANC1</b>	19.95	19.82	20.13	19.96667	34.45	32.31	32.96	33.24	0.051119	0.086569	0.115824	0.084504	0.026456
<b>5FU</b>	20.51	20.89	21.07	20.82333	30.9	30.32	31.14	30.78667	0.882703	0.721965	0.784584	0.796417	0.066152
<b>miR</b>	20.23	20.46	20.88	20.52333	36.22	38.54	40.3	38.35333	0.018199	0.001797	0.001202	0.007066	0.007876
<b>Control</b>	21.67	22.03	21.88	21.86	31.88	30.99	31.6	31.49	1	1	1	1	0
CT values GAPDH				CT values MMP9				Fold induction					
<b>PANC1</b>	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>5FU</b>	19.95	19.82	20.13	19.96667	39.36	39.46	39.05	39.29	0.285191	0.351111	0.438303	0.358202	0.062708
<b>miR</b>	20.51	20.89	21.07	20.82333	39.21	40.33	39.68	39.74	0.466516	0.403321	0.543367	0.471068	0.057264
<b>miR+5FU</b>	20.23	20.46	20.88	20.52333	41.77	42.03	43.34	42.38	0.065154	0.092142	0.037681	0.064992	0.022234
<b>Control</b>	21.67	22.03	21.88	21.86	39.27	40.16	39.61	39.68	1	1	1	1	0
CT values GAPDH				CT values PD-L1				Fold induction					
<b>PANC1</b>	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>5FU</b>	19.95	19.82	20.13	19.96667	33.34	33.12	33.77	33.41	0.895025	0.742262	0.707107	0.781465	0.081572
<b>miR</b>	20.51	20.89	21.07	20.82333	34.73	34.54	35.34	34.87	0.503478	0.582367	0.456916	0.514253	0.051779
<b>miR+5FU</b>	20.23	20.46	20.88	20.52333	35.75	34.84	35.84	35.47667	0.204476	0.351111	0.283221	0.279603	0.059918
<b>Control</b>	21.67	22.03	21.88	21.86	34.9	34.9	35.02	34.94	1	1	1	1	0
CT values SNORD				CT values miR612				Ratio					
	R1	R2	R3	mean	R1	R2	R3	mean	R1	R2	R3	mean	SD
<b>PANC1</b>	26.4	26.89	26.21	26.5	33.36	33.71	32.91	33.3267	0.00803	0.008851	0.009618	0.00881	0.000649
<b>Mia pacá2</b>	24.56	24.81	25.02	24.79667	29.06	29.52	29.98	29.52	0.044	0.038	0.032	0.038	0.004899

**Supplementary Table 2:** Raw data of MTT assay analysis showing the capacity of cell proliferation of the miR-612-transfected cells and 5-FU treated groups in comparison with the control group

8000 cell/well	OD1	OD2	OD3
<b>control</b>	100.000	92.730	94.880
<b>Just shocked</b>	88.005	83.350	94.850
<b>5-FU IC25</b>	83.76402	70.7947	68.2225
<b>5-FU IC50</b>	60.2231	51.0365	56.0702
<b>miR-612</b>	81.1896	86.8844	80.5948
<b>miR-612+IC25</b>	43.83715	47.78157	44.96831
<b>miR-612+IC50</b>	15.92394	11.53584	25.56330