OMTN, Volume *13*

Supplemental Information

Synthetic Circular RNA Functions as a miR-21 Sponge to Suppress Gastric Carcinoma Cell Proliferation

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Entrez Symbol (updated curatedMar-17)	1h (ratio)		8h (ratio)		24h (ratio)	
	ScRNA21/ blank-Cont	ScRNA21/ nscRNA	ScRNA21/ blank-Cont	ScRNA21/ nscRNA	ScRNA21/ blank-Cont	ScRNA21/ nscRNA
GRB2	1.01	0.87	1.08	1	2.37	1.85
PPP1CC	1.18	0.85	1.26	0.95	1.86	1.61
TSNAX	0.88	1	1.43	1.39	1.17	0.88
CDC42SE2	0.87	1.06	0.73	1.17	1.7	1.79
C15orf57	1.46	1.6	1.33	1.12	0.68	1.06
TRAPPC11	1.65	1.42	1.32	1.04	0.82	0.87
SARAF	0.74	0.94	0.81	0.88	1.33	2.19
DUT	1.36	1.03	1.09	1.13	2.28	1.95
CHMP1A	1.65	1.57	0.93	0.64	1.57	1.76
DAXX	0.99	1.02	1.33	1.56	0.51	0.55
TTPAL	1.58	1.21	1.03	1.2	0.72	0.55
RPRD1B	1.02	0.88	1.29	1.17	3.2	2.63
SLX4IP	0.99	0.99	1.22	0.98	2.39	2.04
SNX5	1.71	1.18	0.81	0.76	1.85	2.25
CEBPB	0.8	0.77	1.49	1.57	1.11	1.04
STAMBPL1	1.28	1.24	1.08	1.46	1.24	0.91
PRUNE1	0.99	0.81	0.96	0.82	1.49	1.79
PHYHIPL	0.31	0.78	1.55	1.05	0.96	0.87
RYBP	0.89	0.76	1.17	1.48	0.8	0.8

Supplementary Table 1. Results of Tandem Mass Tag global proteomic analysis of scRNA21-treated NCI-N87 GC cells

Cells in table display arithmetic fold-change ratios of scRNA21-treated *vs.* nsc-treated or untreated (“blank-cont”) control cells. Ratios are displayed after 1 h, 8 h, and 24 h of scRNA treatment. All proteins in this table are putative direct binding targets of miR-21, as predicted by Ingenuity Pathway Analysis (there were 235 such target proteins among the 6,314 proteins ID’d by TMT). All HIGHLIGHTED proteins in this table increased by at least 2 SD over control at one or more treatment timepoints.