

Supplementary Table S1: Primer sequences

Gene	Primer orientation	Sequence (5'→3')
PIP5K1C	Forward	CGAATCGGATGACACGATGGG
	Reverse	AAGCGCTCGGCATAGAAGC
GAPDH	Forward	AAGGTCGGAGTCAACGGATTT
	Reverse	ACCAGAGTTAAAAGCAGCCCTG
U6	Forward	CTCGCTTCGGCAGCACA
	Reverse	AACGCTTCACGAATTTGCGT

Supplementary Table S2: Top 20 downregulated genes in miR-4649-5p mimic transfected SUM159 cells determined by RNA-seq. The genes were ranked according to log2 fold change.

Ensembl Gene ID	Gene Name	Log2 fold change	Adjusted p-value
ENSG00000130590	<i>SAMD10</i>	-0,996	0.0002234
ENSG00000171992	<i>SYNPO</i>	-0,991	0.0005251
ENSG00000240668	<i>KRT8P36</i>	-0,956	0.0405872
ENSG00000182979	<i>MTA1</i>	-0,946	3.307e-14
ENSG00000175115	<i>PACSI</i>	-0,941	0.0003574
ENSG00000175221	<i>MED16</i>	-0,920	4.311e-06
ENSG00000188735	<i>TMEM120B</i>	-0,918	5.985e-14
ENSG00000186111	<i>PIP5K1C</i>	-0,916	0.0002384
ENSG00000218175	<i>AC016739.1</i>	-0,914	0.0171539
ENSG00000266074	<i>BAHCCI</i>	-0,906	0.0039849
ENSG00000174996	<i>KLC2</i>	-0,891	1.864e-10
ENSG00000179632	<i>MAF1</i>	-0,832	3.685e-10
ENSG00000135074	<i>ADAM19</i>	-0,830	0.0311261
ENSG00000171246	<i>NPTX1</i>	-0,825	5.164e-22
ENSG00000182158	<i>CREB3L2</i>	-0,797	2.129e-13
ENSG00000126003	<i>PLAGL2</i>	-0,793	1.095e-06
ENSG00000198858	<i>R3HDM4</i>	-0,792	2.122e-10
ENSG00000130382	<i>MLLT1</i>	-0,787	0.0003162
ENSG00000100599	<i>RIN3</i>	-0,787	0.0297205
ENSG00000130734	<i>ATG4D</i>	-0,785	7.972e-07

positive regulation of transcription by RNA polymerase II	1259	28	11,43	2,45	+	1.88E-05	2.27E-02
positive regulation of DNA-templated transcription	1715	33	15,58	2,12	+	4.77E-05	3.40E-02
positive regulation of nucleic acid-templated transcription	1715	33	15,58	2,12	+	4.77E-05	3.56E-02
positive regulation of RNA biosynthetic process	1721	33	15,63	2,11	+	4.97E-05	3.39E-02
positive regulation of nitrogen compound metabolic process	3174	53	28,83	1,84	+	9.37E-06	2.10E-02
positive regulation of metabolic process	3858	61	35,04	1,74	+	7.66E-06	2.00E-02
positive regulation of biological process	6304	89	57,26	1,55	+	1.41E-06	1.11E-02
positive regulation of macromolecule metabolic process	3542	57	32,17	1,77	+	9.51E-06	1.86E-02
positive regulation of cellular biosynthetic process	2048	39	18,60	2,10	+	1.18E-05	1.86E-02
positive regulation of biosynthetic process	2087	39	18,96	2,06	+	1.49E-05	2.12E-02
positive regulation of macromolecule biosynthetic process	1943	36	17,65	2,04	+	4.35E-05	3.59E-02
regulation of signal transduction	2989	50	27,15	1,84	+	1.52E-05	1.98E-02
regulation of response to stimulus	4034	60	36,64	1,64	+	6.02E-05	3.78E-02
regulation of cell communication	3369	53	30,60	1,73	+	4.07E-05	3.55E-02
regulation of signaling	3381	54	30,71	1,76	+	2.55E-05	2.86E-02
organonitrogen compound metabolic process	5013	73	45,53	1,60	+	1.07E-05	1.86E-02

nitrogen compound	6710	87	60,94	1,43	+	8.30E-05	4.82E-02
metabolic process							
