

Figure S1. Effect of miR-769-5p inhibition on cell motility. (A and B) miR-769-5p inhibition influenced neither (A) migration in DU145 nor (B) invasion in PC-3. Values are expressed as the mean \pm standard deviation (n=3). miR, microRNA; Neg, negative control.

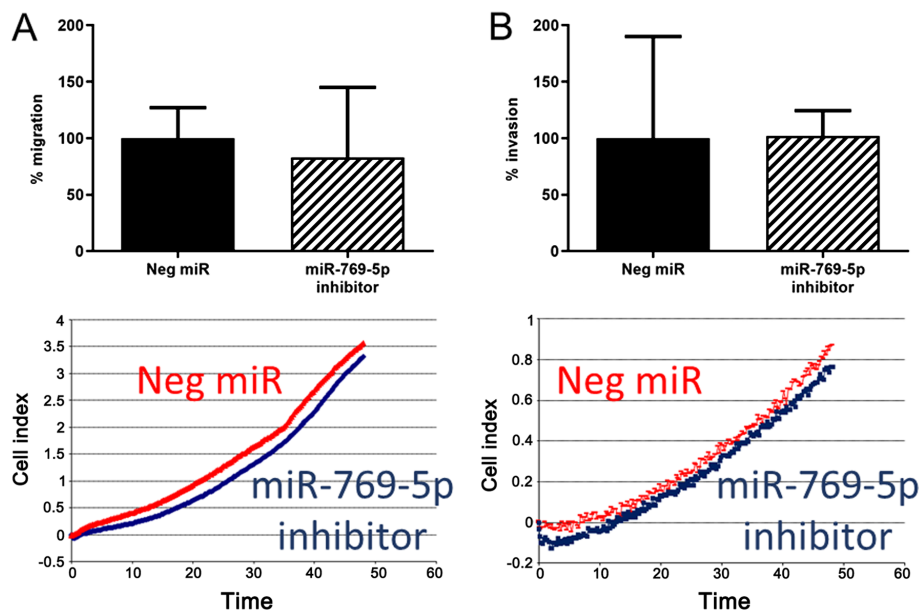


Table SI. Luciferase reporter constructs.

Gene	Sequence
ARHGAP10 WT	CTCCTGGCCTCAGAGCCCCTGCTGACCCTGGCACCCAGGGACC TGCTGGGGGCAGAGAGCTGTCTTCCTCCTCCGAGGCTCTGGG CTGCACCCACAGGTACCTCCACACTTGGGAGTTACCATCATCA CAGTCAGCCCTGGGGGTGGGGGGTGGTGGGCAGGGATGGGAC GCACCACACAGA AACTGTGATTGTGGATCAGGAGGGGAATGTCA GGATTCGCAAAATGGACTTTTCATTTGTCAAGTATTGGGACTTG TGATTTTTAATTATCCAGCATATAGAATGAGAGGGAGGGCAGC CTTCTGCCACCTGTGTGCGCTCCACTGGCAGTCACGCCACCAGA GCCACCCTGGCTCCCTCTCCTCCCTGAGCACCTGCTGCTGCGAT TTAAAGGGAACTGTACTACTCGCAGTGATAGGTTTGCAGAGT GTGTGCTTGGCTGTGGCAGCCTAGCTTGGAGAAGCTGCTGTTG GTGCAAGGGAGAT(GGTCTC)AAGTCAGAGGGAAGCAGAGACG CGCGTCTCAAGCCTGCCCTTCCTAGACGGCCACCTGCAGGACC CCACACTACTGCACTGGCAGCGTGCCTGGCGTATTTGTAAC AGGCTTCTCGGTGCTCCTCACCCGTGTGCTGTTTTCCAAACACC ACCTTTTTGCCTCA(AGGTCTC)TGTAATGAAATAAACTGTAAT TTAATAAAAAAAAAAAAAAAAAAAAA
ARHGAP10 MUT1	CTCCTGGCCTCAGAGCCCCTGCTGACCCTGGCACCCAGGGACC TGCTGGGGGCAGAGAGCTGTCTTCCTCCTCCGAGGCTCTGGG CTGCACCCACAGGTACCTCCACACTTGGGAGTTACCATCATCA CAGTCAGCCCTGGGGGTGGGGGGTGGTGGGCAGGGATGGGAC GCACCACACAGA AACTGTGATTGTGGATCAGGAGGGGAATGTCA GGATTCGCAAAATGGACTTTTCATTTGTCAAGTATTGGGACTTG TGATTTTTAATTATCCAGCATATAGAATGAGAGGGAGGGCAGC CTTCTGCCACCTGTGTGCGCTCCACTGGCAGTCACGCCACCAGA GCCACCCTGGCTCCCTCTCCTCCCTGAGCACCTGCTGCTGCGAT TTAAAGGGAACTGTACTACTCGCAGTGATAGGTTTGCAGAGT GTGTGCTTGGCTGTGGCAGCCTAGCTTGGAGAAGCTGCTGTTG GTGCAAGGGAGAT(AAAGGG)AAGTCAGAGGGAAGCAGAGACG CGCGTCTCAAGCCTGCCCTTCCTAGACGGCCACCTGCAGGACC CCACACTACTGCACTGGCAGCGTGCCTGGCGTATTTGTAAC AGGCTTCTCGGTGCTCCTCACCCGTGTGCTGTTTTCCAAACACC ACCTTTTTGCCTCA(AGGTCTC)TGTAATGAAATAAACTGTAAT TTAATAAAAAAAAAAAAAAAAAAAAA
ARHGAP10 MUT2	CTCCTGGCCTCAGAGCCCCTGCTGACCCTGGCACCCAGGGACC TGCTGGGGGCAGAGAGCTGTCTTCCTCCTCCGAGGCTCTGGG CTGCACCCACAGGTACCTCCACACTTGGGAGTTACCATCATCA CAGTCAGCCCTGGGGGTGGGGGGTGGTGGGCAGGGATGGGAC GCACCACACAGA AACTGTGATTGTGGATCAGGAGGGGAATGTCA GGATTCGCAAAATGGACTTTTCATTTGTCAAGTATTGGGACTTG TGATTTTTAATTATCCAGCATATAGAATGAGAGGGAGGGCAGC CTTCTGCCACCTGTGTGCGCTCCACTGGCAGTCACGCCACCAGA GCCACCCTGGCTCCCTCTCCTCCCTGAGCACCTGCTGCTGCGAT TTAAAGGGAACTGTACTACTCGCAGTGATAGGTTTGCAGAGT GTGTGCTTGGCTGTGGCAGCCTAGCTTGGAGAAGCTGCTGTTG GTGCAAGGGAGAT(GGTCTC)AAGTCAGAGGGAAGCAGAGACG CGCGTCTCAAGCCTGCCCTTCCTAGACGGCCACCTGCAGGACC CCACACTACTGCACTGGCAGCGTGCCTGGCGTATTTGTAAC AGGCTTCTCGGTGCTCCTCACCCGTGTGCTGTTTTCCAAACACC ACCTTTTTGCCTCA(CCCAAA)TGTAATGAAATAAACTGTAAT TTAATAAAAAAAAAAAAAAAAAAAAA

Table SI. Continued.

Gene	Sequence
ARHGAP10 MUT1+2	CTCCTGGCCTCAGAGCCCCTGCTGACCCTGGCACCCAGGGACC TGCCTGGGGGCAGAGAGCTGTCTTCCTCCTCCGAGGCTCTGGG CTGCACCCACAGGTACCTCCACACTTGGGAGTTACCATCATCA CAGTCAGCCCTGGGGGTGGGGGGTGGTGGGCAGGGATGGGAC GCACCACACAGAACTGTGATTGTGGATCAGGAGGGGAATGTCA GGATTCGCAAAATGGACTTTTCATTTGTCAAGTATTGGGACTTG TGATTTTTAATTATCCAGCATATAGAATGAGAGGGAGGGCAGC CTTCTGCCACCTGTGTCGCCTCCACTGGCAGTCACGCCACCAGA GCCACCCTGGCTCCCTCTCCTCCCTGAGCACCTGCTGCTGCGAT TTAAAGGGAACTGTACTACTCGCAGTGATAGGTTTGCAGAGT GTGTGCTTGGCTGTGGCAGCCTAGCTTGGAGAAGCTGCTGTTG GTGCAAGGGAGAT(AAAGGG)AAGTCAGAGGGAAGCAGAGACG CGCGTCTCAAGCCTGCCCTTCCTAGACGGCCACCTGCAGGACC CCACACTCACTGCACTGGCAGCGTGCCTGGCGTATTTGTAAC AGGCTTCTCGGTGCTCCTCACCCGTGTGCTGTTTTCCAAACACC ACCTTTTTGCCTCA(CCCAAAA)TGTAATGAAATAAACTGTAAT TACTAAAAAAAAAAAAAAAAAAAA

Bracketed areas represent the complementary binding sequence for miR-769-5p as well as the mutated bases in the mutant forms. Mut, mutant; WT, wild-type.

Table SII. Selected candidate gene targets of miR-769-5p in DU145 and PC-3.

A, DU145

Log ₂ Fold Δ	P-value	Gene
-2.342544	3.27E-196	AGPAT1 ^a
-2.189684	6.63E-138	RUNX3 ^a
-1.992766	1.59E-143	ATP6V1C1 ^a
-1.80693	8.12E-95	B3GALT6 ^a
-1.709423	8.61E-25	GJB7
-1.605018	3.30E-64	KREMEN1 ^a
-1.551363	2.13E-58	CERCAM ^a
-1.54224	0.000967	COL5A1
-1.530549	1.52E-108	CCNDBP1 ^a
-1.508622	1.81E-59	ARHGAP10 ^a
-1.502003	9.92E-74	DDIT3 ^a
-1.486378	7.15E-154	FAM167A ^a
-1.469792	3.35E-52	SLC35D1 ^a
-1.466198	5.22E-06	HTR7 ^a
-1.463738	1.02E-22	FHL3 ^a
-1.444438	3.44E-14	CPA4 ^a
-1.443158	3.38E-108	CDH1 ^a
-1.423682	7.98E-130	PHF5A ^a
-1.420213	7.19E-53	TFAM ^a
-1.395702	5.88E-46	ZADH2 ^a
-1.377184	2.81E-56	TK2 ^a
-1.357833	4.88E-13	MX2 ^a
-1.306699	1.74E-16	COPZ2 ^a
-1.27103	7.73E-23	KCTD11 ^a
-1.250755	1.82E-16	PPM1L
-1.237424	4.93E-46	MORN4 ^a
-1.234926	2.33E-92	PRUNE ^a
-1.22553	5.46E-118	FKBP5 ^a
-1.211856	4.32E-46	MLLT6
-1.187327	5.14E-54	TBC1D13 ^a
-1.178658	2.19E-09	TMEM154
-1.17065	1.02E-57	ENC1
-1.157368	2.82E-47	FBXO21 ^a
-1.156569	3.52E-40	HEYL
-1.147648	4.58E-19	BIN3 ^a
-1.137515	1.43E-21	FBLN5 ^a
-1.078594	6.78E-28	KCTD12 ^a
-1.077083	8.73E-10	LZTS1
-1.076987	2.16E-39	GIN51 ^a
-1.070394	2.44E-10	MUC3A
-1.0661	1.08E-42	MBP ^a
-1.051708	1.04E-06	FXYD6
-1.043364	1.88E-65	PPFIBP1 ^a
-1.034609	0.000386	NKD1
-1.025286	7.22E-20	CBX7 ^a
-1.019029	8.39E-21	TTYH2
-1.005169	2.82E-59	SNX18 ^a
-1.00399	8.19E-14	C8orf46
-1.002828	1.45E-17	C11orf45 ^a
-0.993735	3.00E-57	CHST11 ^a
-0.992695	2.24E-21	PIK3C2B ^a
-0.985829	1.85E-40	NT5DC1 ^a
-0.981525	2.27E-18	SLFN5

Table SII. Continued.

Log ₂ Fold Δ	P-value	Gene
-0.977364	2.36E-100	GPRC5A ^a
-0.974122	4.98E-43	ZNF689 ^a
-0.97202	7.67E-29	RPS6KA5 ^a
-0.971894	8.59E-09	GATA6
-0.965423	1.94E-25	DNAJC3 ^a
-0.944995	1.05E-60	HAUS2
-0.929672	8.64E-68	BNC1 ^a
-0.924587	1.27E-23	IGFBP3
-0.913039	4.90E-12	NBL1 ^a
-0.910182	2.99E-23	KLF7
-0.905572	1.00E-28	DSC3
-0.903236	1.09E-24	PPM1F ^a
-0.898077	0.002288	UNC5B
-0.891074	3.45E-09	CREB5
-0.886961	1.84E-58	GPX8 ^a
-0.878836	3.12E-30	TAB1 ^a
-0.865673	7.26E-35	ETV6 ^a
-0.864534	1.80E-12	KIAA1919 ^a
-0.861236	1.46E-67	SS18 ^a
-0.86029	4.57E-55	CRTC3 ^a
-0.846525	4.78E-87	ALKBH5
-0.846142	3.72E-32	EIF4EBP2 ^a
-0.845809	9.82E-31	RAI14
-0.844843	9.08E-11	NMNAT2 ^a
-0.840407	7.55E-29	SYNPO ^a
-0.835484	3.05E-38	UBP1 ^a
-0.835228	2.02E-69	IGF2R
-0.834303	0.002483	RASD2
-0.827093	4.98E-14	EVI5L ^a
-0.819979	4.68E-08	DUSP18
-0.803766	7.27E-22	B3GALT5
-0.80101	0.001108	MYB
-0.797409	9.14E-13	FAM46A
-0.790737	9.91E-22	F2RL1 ^a
-0.777406	4.05E-29	JAK1 ^a
-0.774742	2.81E-38	SETD7 ^a
-0.774737	8.37E-41	SLC9A1 ^a
-0.77464	0.003047	CD302 ^a
-0.773945	0.002904	ARC
-0.764492	1.90E-48	STK35 ^a
-0.764193	1.38E-54	PDE4DIP
-0.763432	1.32E-26	NDNL2 ^a
-0.756	4.54E-16	CARD10
-0.743276	6.30E-22	CENPM ^a
-0.736671	7.97E-16	TRIOBP ^a
-0.733288	1.71E-35	RIPK1 ^a
-0.733029	3.40E-14	ARNT2
-0.723588	0.003209	RCBTB2 ^a
-0.719481	9.72E-10	EPM2A ^a
-0.712964	1.34E-07	POU6F1
-0.706676	2.74E-23	DTNB
-0.701795	7.86E-17	KBTBD11 ^a
-0.699641	1.93E-15	KIAA1324L
-0.699317	4.48E-34	TNFAIP2 ^a
-0.696702	3.36E-36	ANKRD40 ^a
-0.695581	5.87E-26	TEAD3 ^a

Table SII. Continued.

Log ₂ Fold Δ	P-value	Gene
-0.69367	2.13E-13	ATN1 ^a
-0.693621	2.46E-09	SPIRE2
-0.693166	6.35E-28	ETS1
-0.69271	8.29E-14	TMCO6 ^a
-0.689877	1.96E-14	NAPG
-0.687246	1.36E-27	TMEM50A
-0.686177	4.74E-12	DPYSL5
-0.683697	0.001653	MAP1A ^a
-0.681822	1.02E-11	ZNF280B ^a
-0.681255	1.99E-70	GRAMD1B ^a
-0.676129	7.08E-29	SLC15A4
-0.675738	0.005437	RNF165
-0.675021	5.47E-09	SHANK3 ^a
-0.672779	0.003994	S1PR2
-0.666941	4.73E-07	EBF4
-0.662044	2.95E-33	SERINC3 ^a
-0.661423	6.25E-06	RWDD2A
-0.66111	2.42E-10	GLIS3
-0.660654	7.68E-07	CPEB1 ^a
-0.655903	3.24E-14	MCC
-0.649018	4.84E-18	DLGAP4
-0.648391	1.77E-31	RGP1 ^a
-0.647487	7.26E-09	TBX3
-0.640882	1.89E-06	JAK3
-0.634232	2.46E-05	TGFBR3
-0.63357	2.43E-09	FGF2 ^a
-0.633554	7.80E-13	MARK4 ^a
-0.628986	2.01E-09	HACE1
-0.622298	4.41E-09	WDR91
-0.620449	4.39E-19	H6PD
-0.619309	4.85E-15	COL17A1
-0.6187	9.56E-22	FRMD8
-0.618534	8.33E-10	ZNF629
-0.616808	6.45E-06	PLEKHF1 ^a
-0.616196	7.14E-34	EXTL3
-0.613059	2.24E-08	ACBD4
-0.610594	4.99E-38	E2F4
-0.607982	5.01E-45	DFFA
-0.607766	2.41E-34	EIF3A ^a
-0.604683	2.25E-20	HERPUD1
-0.604153	3.05E-18	ENTPD7
-0.603126	0.003138	PLAC8
-0.601817	1.61E-21	FOXJ2
-0.600622	7.64E-19	ZHX3
-0.599866	5.29E-37	FOXK2
-0.597996	5.16E-37	MRPL49 ^a
-0.592505	7.27E-05	C1orf106
-0.589053	2.05E-28	KIAA0226 ^a
-0.588808	1.87E-06	TRAF1
-0.588782	7.71E-34	PSMB2
-0.586773	0.00044	ITGB3
-0.586417	1.25E-18	PODXL
-0.585755	3.76E-16	PLEKHA2

Table SII. Continued.

Log ₂ Fold Δ	P-value	Gene
-2.2229312	9.96E-90	RUNX3 ^a
-2.1341568	4.15E-91	AGPAT1 ^a
-1.9698423	4.45E-17	COPZ2 ^a
-1.9627379	6.34E-93	ATP6V1C1 ^a
-1.8799076	6.04E-107	TFAM ^a
-1.8747969	5.89E-48	CERCAM ^a
-1.7819675	2.05E-108	CDH1 ^a
-1.5764824	1.98E-23	BNC1 ^a
-1.5756972	7.28E-11	FBLN5 ^a
-1.5238795	3.39E-83	CCNDBP1 ^a
-1.4993534	1.49E-57	B3GALT6 ^a
-1.4970858	1.20E-50	KREMEN1 ^a
-1.4829985	0.001257	XYLT1
-1.4773294	2.44E-24	SOD3
-1.4547267	2.58E-97	ZADH2 ^a
-1.4414072	1.85E-08	MX2 ^a
-1.4254666	5.48E-32	SLC35D1 ^a
-1.3855895	4.77E-05	SNAI3
-1.3358104	4.11E-75	PHF5A ^a
-1.3103806	4.17E-42	ARHGAP10 ^a
-1.2868673	1.83E-10	EPST11
-1.2624291	6.80E-54	CPA4 ^a
-1.1908324	6.89E-22	TK2 ^a
-1.1708553	1.84E-46	TBC1D13 ^a
-1.1613944	7.37E-35	FHL3 ^a
-1.155566	1.43E-08	FAM167A ^a
-1.1519809	2.96E-13	RPS6KA5 ^a
-1.1504799	1.37E-35	FKBP5 ^a
-1.1482078	3.94E-19	BIN3 ^a
-1.1203454	6.76E-20	CBX7 ^a
-1.1092956	2.95E-53	FST
-1.106174	6.02E-05	HTR7 ^a
-1.1003833	4.34E-37	ANKRD40 ^a
-1.0950242	1.28E-39	MBP ^a
-1.0767989	2.25E-16	TRIOBP ^a
-1.0703336	1.87E-18	PIK3C2B ^a
-1.0293373	8.43E-10	EPM2A ^a
-1.0125463	2.94E-24	MORN4 ^a
-1.0109874	1.00E-10	CENPM ^a
-0.9835786	2.82E-18	PPFIBP1 ^a
-0.977487	0.003824	IFFO1
-0.9664992	6.68E-52	PRUNE ^a
-0.9642812	3.17E-28	CRTC3 ^a
-0.9583287	9.67E-43	FBXO21 ^a
-0.9420463	2.76E-31	GINS1 ^a
-0.9378461	1.34E-09	KCNMB4
-0.9341459	8.60E-08	NBL1 ^a
-0.9336706	2.31E-16	S100A2
-0.9132788	2.06E-16	C1QTNF1
-0.911177	3.18E-51	TNFAIP2 ^a
-0.9045839	5.77E-19	KCTD11 ^a

Table SII. Continued.

Log ₂ Fold Δ	P-value	Gene
-0.9008405	1.12E-13	SETD7 ^a
-0.897514	7.50E-10	TMCO6 ^a
-0.8834371	1.53E-17	SNX18 ^a
-0.8818182	2.07E-10	LPAR5
-0.8767196	5.52E-09	RCBTB2 ^a
-0.8760609	4.98E-05	VGLL3
-0.8738295	0.000208	GPR63
-0.8614196	1.74E-23	TNFRSF11A
-0.8539737	2.18E-13	TAB1 ^a
-0.8482786	1.23E-11	PMAIP1
-0.8424874	8.56E-31	GPRC5A ^a
-0.8409095	1.61E-25	SYNPO ^a
-0.8324152	8.90E-26	CHST11 ^a
-0.8262269	7.41E-28	PPM1F ^a
-0.8193983	1.98E-24	RNF11
-0.8173272	2.55E-08	DDIT3 ^a
-0.8161782	7.91E-16	ENTPD3
-0.81611	1.17E-09	STAT1
-0.8126105	1.40E-08	MAP1A ^a
-0.8081048	0.008633	HIC1
-0.8024112	7.33E-06	PSMA2
-0.8006852	8.29E-60	ATN1 ^a
-0.7947532	1.28E-16	ZNF689 ^a
-0.7920097	1.28E-14	JAK1 ^a
-0.7909972	1.52E-08	FAM124A
-0.7889752	6.10E-17	SS18 ^a
-0.7829888	1.57E-25	UBP1 ^a
-0.7696743	2.75E-09	ID3
-0.7690493	4.98E-12	KCTD12 ^a
-0.7686072	3.21E-08	KIAA1919 ^a
-0.7664507	4.23E-22	SERINC3 ^a
-0.7648909	3.53E-05	CD302 ^a
-0.7527785	9.34E-19	F2RL1 ^a
-0.7446187	0.001865	CPEB1 ^a
-0.7437646	0.000106	FGF2 ^a
-0.742737	6.32E-08	C11orf45 ^a
-0.7335771	8.78E-47	SLC9A1 ^a
-0.7325642	1.30E-18	RGPI ^a
-0.7210472	4.51E-09	TSEN34
-0.7188159	1.12E-05	HES4
-0.7121319	2.80E-17	BLMH
-0.7095764	1.20E-15	KIAA0226 ^a
-0.7009064	1.10E-14	GRAMD1B ^a
-0.697517	4.91E-39	FKBP9
-0.6935211	8.51E-06	GXYLT2
-0.6908191	2.36E-24	TEAD3 ^a
-0.6869529	2.45E-08	KBTBD11 ^a
-0.6858715	3.19E-27	GPX8 ^a
-0.6822667	2.70E-14	NDNL2 ^a
-0.6810157	0.00039	RRAGD
-0.6789664	2.55E-08	CUL5
-0.6701761	4.30E-20	MRPL49 ^a
-0.6670205	2.96E-30	PRSS23
-0.6654154	0.001082	CASP10
-0.6644094	0.003024	UQCR11
-0.6620288	5.56E-07	DNAJC3 ^a

Table SII. Continued.

Log ₂ Fold Δ	P-value	Gene
-0.6609554	1.34E-05	KLHL3
-0.659404	3.56E-12	ZNF365
-0.654998	1.98E-24	MARK4 ^a
-0.6535302	1.28E-06	FOXA2
-0.6535199	8.64E-29	LIX1L
-0.6515205	5.49E-15	STK35 ^a
-0.6491715	1.57E-05	ZNF280B ^a
-0.6468406	4.78E-05	MAPK8IP2
-0.6414559	0.008381	LYL1
-0.641128	1.06E-11	TMX4
-0.6410306	4.42E-10	EIF4EBP2 ^a
-0.636393	9.08E-06	FTO
-0.6346604	6.14E-07	GSTO2
-0.6332617	4.44E-17	PTPRU
-0.6199476	7.59E-11	EVI5L ^a
-0.6145969	9.63E-15	NT5DC1 ^a
-0.6081245	0.000387	DGCR6L
-0.606595	2.46E-10	IER3
-0.6058245	7.08E-42	ACTN4
-0.6029642	4.22E-05	PLEKHF1 ^a
-0.6026046	0.001481	NDUFA9
-0.6017323	2.70E-09	NMNAT2 ^a
-0.6011277	1.20E-07	APOBEC3C
-0.5995144	6.79E-13	RIPK1 ^a
-0.5981072	3.63E-12	SHANK3 ^a
-0.5959862	9.61E-07	RASA4
-0.5951636	1.36E-10	ETV6 ^a
-0.5901149	3.56E-09	EIF3A ^a

The listed genes were decreased in transfected vs. normal samples in Oncomine prostate cancer cohorts. The candidate genes are shown by decreasing magnitude of fold change following miR-769-5p mimics transfection. ^aThe candidates that appeared in RNA sequencing for both DU145 and PC-3. miR, microRNA.