Table W1. List of the 41 Genes Analyzed in the RNAi Screen.

Gene Symbol	Relative Viability (siRNA Sequence 1)	Relative Viability (siRNA Sequence 2)	Relative Viability (siRNA Sequence 3)	Mean Viability Relative to Control	Significance Criteria
SIRT2	0.60	0.64	0.76	**0.67**	*
GJA1	0.77	0.65	0.59	**0.67**	*
GRIA3	0.71	0.57	0.88	**0.72**	*
PVRL3	0.68	0.57	0.97	**0.74**	*
CXCL12	0.45	0.95	0.42	**0.61**	*
FMOD	0.88	1.46	1.25	**1.20**	*
ARNTL	1.47	1.65	1.13	**1.42**	*
S100A10	0.80	0.43	0.89	**0.71**	
LLT1	0.56	0.76	0.86	**0.73**	
TFDP1	0.84	0.45	1.07	**0.78**	
PDLIM1	0.87	0.78	0.72	**0.79**	
SEMA3A	0.61	0.81	1.06	**0.83**	
MMP3	0.82	0.90	0.82	**0.85**	
ANK1	1.16	0.78	0.65	**0.86**	
ETV4	1.01	0.66	0.93	**0.87**	
HMGN1	1.11	0.85	0.65	**0.87**	
ITGA5	0.55	0.97	1.09	**0.87**	
COL4A1	0.73	0.88	1.09	**0.90**	
SERPINA3	0.87	1.02	0.82	**0.90**	
SLIT2	0.91	0.81	1.01	**0.91**	
CDH2	1.10	0.69	1.01	**0.93**	
CHI3L2	0.82	0.94	1.08	**0.94**	
EFNA2	0.76	1.16	0.94	**0.95**	
NRAS	1.17	0.67	1.01	**0.95**	
CDH18	0.67	0.98	1.26	**0.97**	
TM4SF1	0.66	0.98	1.30	**0.98**	
ITGA6	0.82	1.26	0.86	**0.98**	
COL3A1	0.68	0.86	1.42	**0.99**	
RPS27	1.17	0.79	1.03	**1.00**	
SAA1	0.95	1.20	0.87	**1.00**	
CD34	1.12	1.22	0.75	**1.03**	
MYBL1	1.41	0.67	1.02	**1.03**	
DCK	1.13	1.13	0.84	**1.03**	
LUM	0.77	1.05	1.28	**1.03**	
GSTZ1	0.95	1.13	1.10	**1.06**	
DAB2	0.69	0.95	1.65	**1.10**	
LGALS9	0.96	1.20	1.14	**1.10**	
IL1A	1.01	1.08	1.22	**1.10**	
EPHA1	0.69	1.21	1.44	**1.11**	
ALCAM	1.31	0.99	1.07	**1.12**	
PTN	1.04	1.46	1.18	**1.23**	

Cell viability relative to the mean viability of 11 nonsilencing control sequences, as determined by CellTiter-Glo assays, is shown as mean and separately for silencing sequences 1 to 3. The genes used for the screen were previously identified as regulated by CUX1 in a microarray approach [10]. Changes in cell viability greater than 25% after knock-down of a particular gene in two of three silencing sequences were considered as significant, and these are marked with an asterisk.

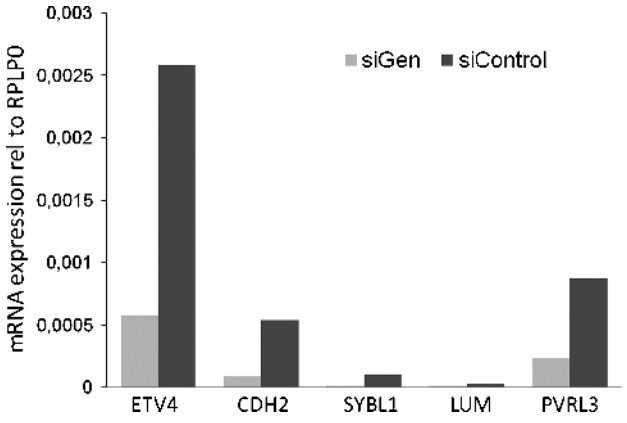

Figure W1. Knock-down efficiency of five randomly selected genes from the RNAi library as assessed by quantitative RT-PCR in HT1080 cells, normalized to *RPLP0* expression as the housekeeping gene. Results are expressed as mean ± SEM and are representative of three independent experiments.

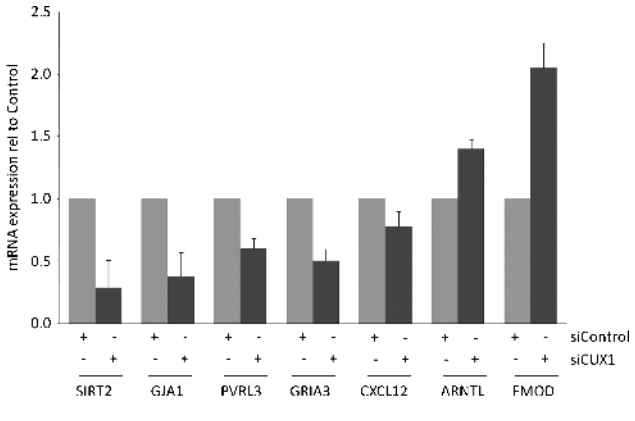

Figure W2. mRNA expression, as quantified by quantitative RT-PCR, of the seven screen hits in PANC1 cells transiently transfected with siRNA against CUX1 (siCUX) or nonsilencing control siRNA. Results are shown as mean ± SEM normalized to *RPLP0* expression as the housekeeping gene. Results are representative of three independent experiments.

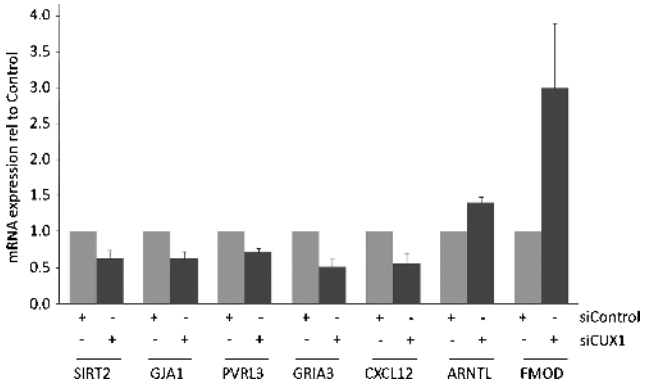

Figure W3. mRNA expression, as quantified by quantitative RT-PCR, of seven screen hits in PaTu-8988t cells transiently transfected with siRNA against CUX1 (siCUX) or nonsilencing control siRNA. Results are shown as mean ± SEM normalized to *RPLP0* expression as the housekeeping gene. Results are representative of three independent experiments.

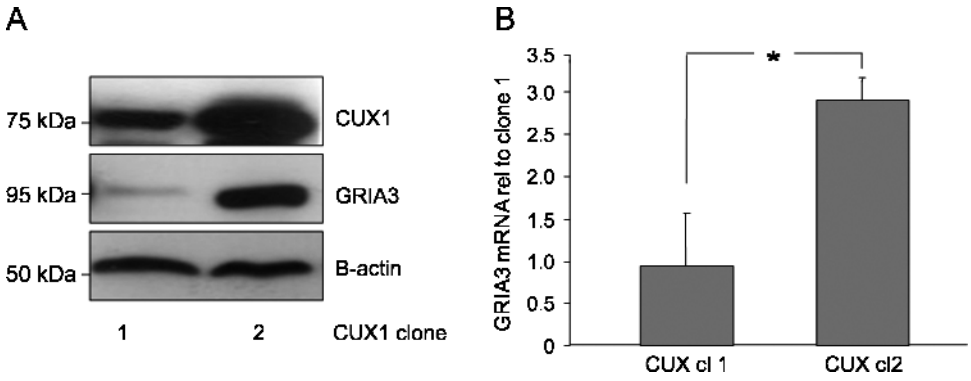

Figure W4. (A) Stable overexpression of CUX1 increases GRIA3 protein. PANC1 cells were stably transfected with the transcriptionally active CUX1 expression plasmid. GRIA3 protein levels were analyzed in two different clones with different CUX1 expression levels by Western blot using specific antibodies; *β-actin* was determined as the housekeeping gene. (B) Stable overexpression of CUX1 increases GRIA3 mRNA. PANC1 clones 1 and 2 stably expressing two different levels of the transcriptionally active CUX1 expression plasmid (shown in panel A) were analyzed for GRIA3 mRNA by quantitative RT-PCR, normalized to *RPLP0* expression as the housekeeping gene, and expressed relative to clone 1. *$P < .05$ compared with clone 1. Results are expressed as mean ± SEM and are representative of three independent experiments.

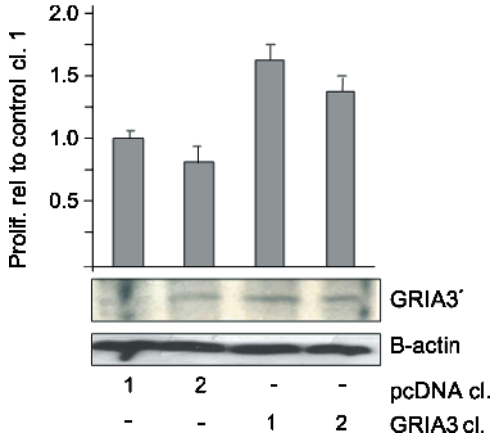

Figure W5. PANC1 cells stably expressing GRIA3 or control plasmid (two clones each) were assessed for differences in proliferation by using BrdU proliferation assays 24 hours after seeding. Results were normalized to control clone 1; these are shown as mean ± SEM and are representative of three independent experiments. GRIA3 expression level and *β-actin* as the housekeeping gene, as determined by Western blot, are shown below.

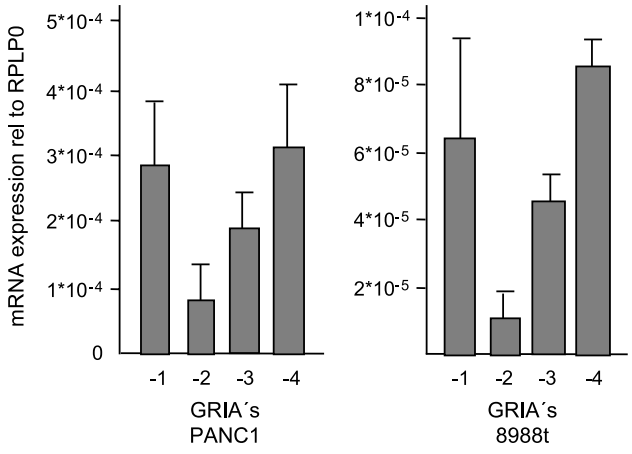

Figure W6. Expression of hGRIA1-4 in PANC1 and PaTu-8988t cells, as assessed by quantitative RT-PCR normalized to *RPLP0* expression as the housekeeping gene. Results are expressed as mean ± SEM and are representative of three independent experiments.