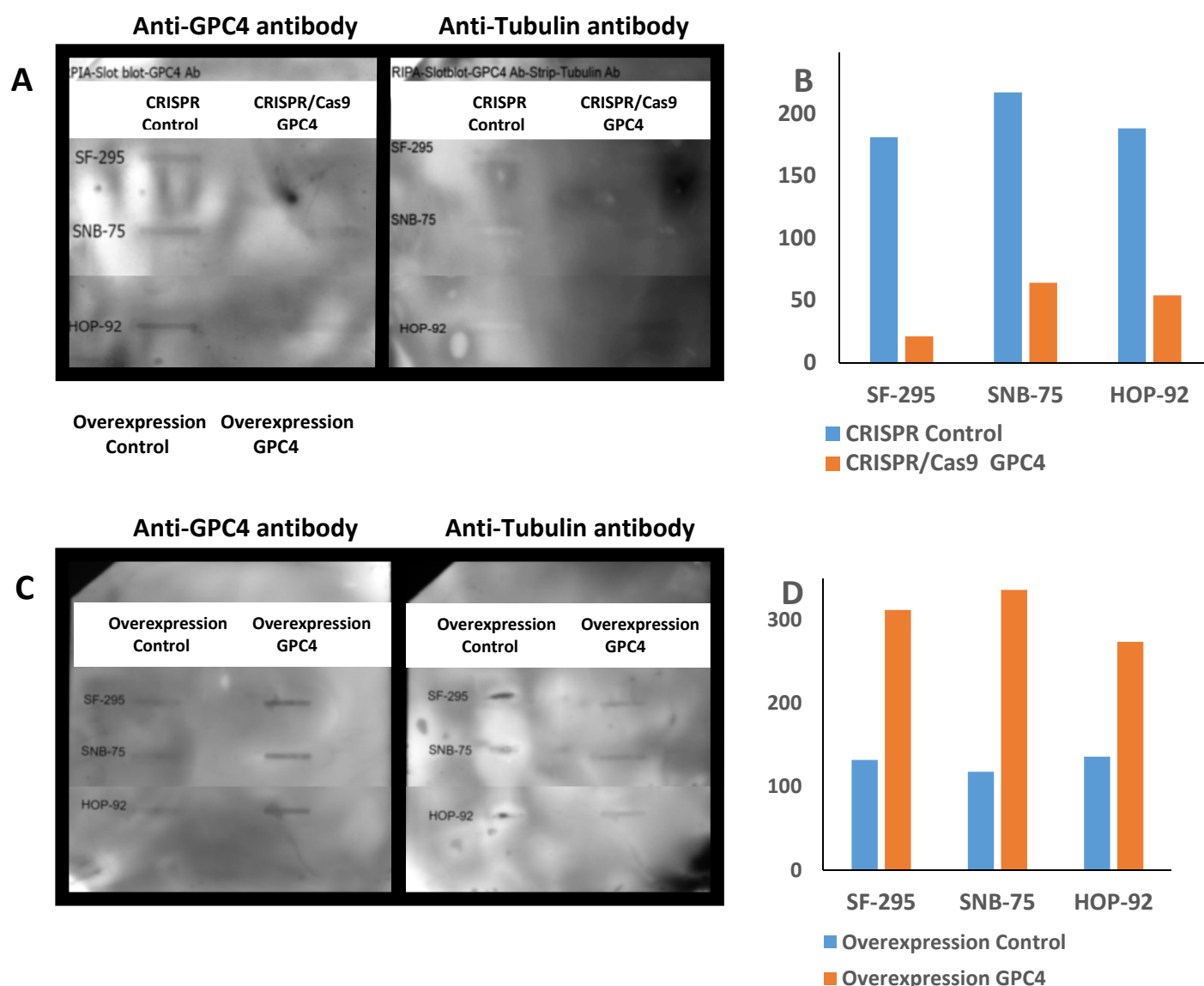


Supplementary Table S1: List of TCGA study abbreviations

Study Abbreviation	Study Name
ACC	Adrenocortical carcinoma
BLCA	Bladder Urothelial Carcinoma
BRCA	Breast invasive carcinoma
CESC	Cervical squamous cell carcinoma and endocervical adenocarcinoma
CHOL	Cholangiocarcinoma
COAD	Colon adenocarcinoma
DLBC	Lymphoid Neoplasm Diffuse Large B-cell Lymphoma
ESCA	Esophageal carcinoma
GBM	Glioblastoma multiforme
HNSC	Head and Neck squamous cell carcinoma
KICH	Kidney Chromophobe
KIRC	Kidney renal clear cell carcinoma
KIRP	Kidney renal papillary cell carcinoma
LAML	Acute Myeloid Leukemia
LGG	Brain Lower Grade Glioma
LIHC	Liver hepatocellular carcinoma
LUAD	Lung adenocarcinoma
LUSC	Lung squamous cell carcinoma
MESO	Mesothelioma
OV	Ovarian serous cystadenocarcinoma
PAAD	Pancreatic adenocarcinoma
PCPG	Pheochromocytoma and Paraganglioma
PRAD	Prostate adenocarcinoma
READ	Rectum adenocarcinoma
SARC	Sarcoma
SKCM	Skin Cutaneous Melanoma
STAD	Stomach adenocarcinoma
TGCT	Testicular Germ Cell Tumors
THCA	Thyroid carcinoma
THYM	Thymoma
UCEC	Uterine Corpus Endometrial Carcinoma
UCS	Uterine Carcinosarcoma
UVM	Uveal Melanoma

Supplementary Table S2: List of genes with divergent gene expression profiles between TCGA-LUAD and TCGA-GBM subjects

	Term	Overlap	P.value	Adjusted P.val	Old.Adjus	Odds.Rat	Combined Genes	database
1	Hypoxia	2/200	0.007218	0.021654	0	18.17172	89.60771	CA12-STC MSigDB Hallmark 2020
2	Estrogen Response Early	2/200	0.007218	0.021654	0	18.17172	89.60771	CA12-PTG MSigDB Hallmark 2020
3	Estrogen Response Late	2/200	0.007218	0.021654	0	18.17172	89.60771	ITGA5-DK1 MSigDB Hallmark 2020
4	Epithelial Mesenchymal Transition	2/200	0.007218	0.021654	0	18.17172	89.60771	ITGA5-DK1 MSigDB Hallmark 2020
5	Fibronectin Matrix Formation R-HSA-156977	1/6	0.003894	0.046096	0	333.0333	1847.767	ITGA5 Reactome 2022
6	Signaling By LRP5 Mutants R-HSA-5339717	1/6	0.005189	0.046096	0	237.8571	1251.416	ITGA5 Reactome 2022
7	POLR1 (CTCF), SOX2, NANOG Repress Genes Related To Differentiation R-HSA-2892345	1/9	0.005856	0.046096	0	208.1146	1070.484	DK1 Reactome 2022
8	Signaling By Activated Point Mutants Of FGFR3 R-HSA-1839122	1/18	0.007129	0.046096	0	166.475	822.9949	FGF5 Reactome 2022
10	FGFR3 Mutant Receptor Activation R-HSA-2033514	1/12	0.007774	0.046096	0	151.3333	735.0173	FGF5 Reactome 2022
11	Reversible Hydration Of Carbon Dioxide R-HSA-1475029	1/12	0.007774	0.046096	0	151.3333	735.0173	ITGA5 Reactome 2022
12	FGFR3c Ligand Binding And Activation R-HSA-190373	1/12	0.007774	0.046096	0	151.3333	735.0173	FGF5 Reactome 2022
13	FGFR2c Ligand Binding And Activation R-HSA-190375	1/13	0.00842	0.046096	0	138.7153	662.6705	FGF5 Reactome 2022
14	FGFR3 Ligand Binding And Activation R-HSA-190239	1/13	0.00842	0.046096	0	138.7153	662.6705	FGF5 Reactome 2022
15	FGFR1 Modulation Of FGFR3 Signaling R-HSA-5658623	1/13	0.00842	0.046096	0	138.7153	662.6705	FGF5 Reactome 2022
16	Phospholipase C-mediated Cascade, FGFR3 R-HSA-5654227	1/13	0.00842	0.046096	0	138.7153	662.6705	FGF5 Reactome 2022
17	Synthesis Of Prostaglandins [PG] And Thromboxanes [TX] R-HSA-2162123	1/15	0.007079	0.046096	0	118.8869	551.0048	PTGES Reactome 2022
18	Signaling By Activin R-HSA-1502540	1/15	0.007079	0.046096	0	118.8869	551.0048	FST Reactome 2022
19	Negative Regulation Of TGF-dependent Signaling By WNT Ligand Antagonists R-HSA-3772470	1/15	0.007079	0.046096	0	118.8869	551.0048	DK1 Reactome 2022
20	Phospholipase C-mediated Cascade, FGFR3 R-HSA-5654239	1/16	0.010353	0.046096	0	110.9556	507.1178	FGF5 Reactome 2022
21	FGFR3 Ligand Binding And Activation R-HSA-190242	1/16	0.010353	0.046096	0	110.9556	507.1178	FGF5 Reactome 2022
22	Formation Of Senescence-Associated Heterochromatin Foci (SAHF) R-HSA-2559584	1/17	0.010997	0.046096	0	104.0156	469.1243	HMG2 Reactome 2022
23	Activated Point Mutants Of FGFR2 R-HSA-2033519	1/17	0.010997	0.046096	0	104.0156	469.1243	FGF5 Reactome 2022
24	SHC-mediated cascade FGFR3 R-HSA-5654704	1/17	0.010997	0.046096	0	104.0156	469.1243	FGF5 Reactome 2022
25	PI-3K cascade FGFR3 R-HSA-5654710	1/19	0.01164	0.046096	0	97.89216	435.9406	FGF5 Reactome 2022
26	Phospholipase C-mediated Cascade, FGFR2 R-HSA-5654221	1/18	0.01164	0.046096	0	97.89216	435.9406	FGF5 Reactome 2022
27	FRS-mediated FGFR3 Signaling R-HSA-5654706	1/19	0.012283	0.046096	0	92.44907	406.7303	FGF5 Reactome 2022
28	SHC-mediated cascade FGFR3 R-HSA-5654688	1/20	0.012926	0.046096	0	87.7895	380.8382	FGF5 Reactome 2022
29	Signal Transduction By L1 R-HSA-445144	1/20	0.012926	0.046096	0	87.7895	380.8382	ITGA5 Reactome 2022
30	FGFR3 Ligand Binding And Activation R-HSA-190241	1/20	0.012926	0.046096	0	87.7895	380.8382	FGF5 Reactome 2022
31	PI-3K cascade FGFR1 R-HSA-5654689	1/20	0.013568	0.046096	0	83.15983	357.7439	FGF5 Reactome 2022
32	Signaling By FGFR3c In Ductal R-HSA-5654533	1/21	0.013568	0.046096	0	83.15983	357.7439	FGF5 Reactome 2022
33	FRS-mediated FGFR1 Signaling R-HSA-5654532	1/22	0.01421	0.046096	0	79.23016	337.0294	FGF5 Reactome 2022
34	SHC-mediated cascade FGFR3 R-HSA-5654699	1/22	0.01421	0.046096	0	79.23016	337.0294	FGF5 Reactome 2022
35	PI-3K cascade FGFR2 R-HSA-5654695	1/23	0.014894	0.046096	0	75.64	318.3547	FGF5 Reactome 2022
36	FRS-mediated FGFR2 Signaling R-HSA-5654700	1/24	0.015493	0.046096	0	72.33333	301.4412	FGF5 Reactome 2022
37	Downstream Signaling Of Activated FGFR3 R-HSA-5654708	1/24	0.015493	0.046096	0	72.33333	301.4412	FGF5 Reactome 2022
38	Signal Transduction R-HSA-455262	1/46	0.015317	0.046096	0	4.502958	18.50209	FGF5-FOSI Reactome 2022
39	Endomembran Cell Differentiation (GO:0035987)	2/31	0.000179	0.19946	0	125.1285	1079.321	HMG2JTG GO Biological Process 2023
40	Endomembran Formation (GO:0001706)	2/35	0.000229	0.19946	0	109.3934	924.3629	HMG2JTG GO Biological Process 2023
41	Negative Regulation Of Binding (GO:0051100)	3/18	0.001382	0.036266	0	6.30809	283.6409	HMG2JTG GO Biological Process 2023
42	Positive Regulation Of Macromolecule Metabolic Process (GO:0010604)	3/364	0.001493	0.036266	0	16.3097	106.1258	FGF5-HMG GO Biological Process 2023
43	Negative Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling (GO:0032947)	2/111	0.002288	0.036266	0	33.15763	201.6045	FST-DK1 GO Biological Process 2023
44	Positive Regulation Of Angiogenesis (GO:0045766)	1/19	0.002346	0.036266	0	87.7895	380.8382	FGF5 Reactome 2022
45	Positive Regulation Of Wnt Signaling Pathway, Planar Cell Polarity Pathway (GO:2000096)	1/5	0.003246	0.036266	0	416.3125	2385.602	DK1 GO Biological Process 2023
46	Cell Junction Disassembly (GO:005146)	1/5	0.003246	0.036266	0	416.3125	2385.602	DK1 GO Biological Process 2023
47	Regulation Of Metabolic Anion Transport (GO:0040470)	1/5	0.003246	0.036266	0	416.3125	2385.602	STC1 GO Biological Process 2023
48	Positive Regulation Of Tau-Protein Kinase Activity (GO:1902949)	1/5	0.003246	0.036266	0	416.3125	2385.602	DK1 GO Biological Process 2023
49	Negative Regulation Of Cardiac Muscle Cell Differentiation (GO:2000726)	1/5	0.003246	0.036266	0	416.3125	2385.602	DK1 GO Biological Process 2023
50	Positive Regulation Of Gene Expression (GO:0046028)	3/480	0.003322	0.036266	0	71.7205	FGF5-HMG GO Biological Process 2023	
51	Negative Regulation Of Apoptotic Process (GO:0043066)	3/482	0.003322	0.036266	0	12.21795	69.72839	HMG2JTG GO Biological Process 2023
52	Positive Regulation Of Cell Population Proliferation (GO:0008284)	3/483	0.003322	0.036266	0	12.19188	69.5082	FGF5-FOSI GO Biological Process 2023
53	Positive Regulation Of Protein Kinase Activity (GO:0040862)	3/485	0.003322	0.036266	0	12.19188	69.5082	FGF5-FOSI GO Biological Process 2023
54	Negative Regulation Of Double-Strand Break Repair Via Nonhomologous End Joining (GO:2001032)	1/6	0.003894	0.036266	0	333.0333	1847.767	HMG2 Reactome 2022
55	Negative Regulation Of Cardiac Differentiation (GO:1906208)	1/6	0.003894	0.036266	0	333.0333	1847.767	DK1 Reactome 2022
56	Positive Regulation Of Calcium Ion Import (GO:0006439)	1/8	0.005189	0.036266	0	237.8571	1251.416	FGF5 Reactome 2022
57	Regulation Of DNA-templated Transcription Initiation (GO:2000142)	1/8	0.005189	0.036266	0	237.8571	1251.416	DK1 Reactome 2022
58	CD40 Signaling Pathway (GO:0023035)	1/8	0.005189	0.036266	0	237.8571	1251.416	DK1 Reactome 2022
59	Synapse Pruning (GO:000868)	1/8	0.005189	0.036266	0	237.8571	1251.416	DK1 Reactome 2022
60	Regulation Of Wnt Signaling Pathway, Planar Cell Polarity Pathway (GO:2000096)	1/8	0.005189	0.036266	0	237.8571	1251.416	DK1 Reactome 2022
61	Mesodermal Cell Differentiation (GO:0048438)	1/8	0.005189	0.036266	0	237.8571	1251.416	HMG2 Reactome 2022
62	Wound Healing, Spreading Of Epidermal Cells (GO:0035313)	1/9	0.005836	0.036266	0	208.1146	1070.484	STC1 Reactome 2022
63	Regulation Of Actin Filament-Based Movement (GO:1903115)	1/9	0.005836	0.036266	0	208.1146	1070.484	STC1 Reactome 2022
64	Regulation Of Tau Protein Kinase Activity (GO:1902947)	1/9	0.005836	0.036266	0	208.1146	1070.484	DK1 Reactome 2022
65	Regulation Of Cardiac Muscle Cell Differentiation (GO:2000725)	1/9	0.005836	0.036266	0	208.1146	1070.484	DK1 Reactome 2022
66	Positive Regulation Of Vascular Endothelial Growth Factor Receptor Signaling Pathway (GO:0036086)	1/9	0.005836	0.036266	0	208.1146	1070.484	ITGA5 Reactome 2022
67	Negative Regulation Of Activin Receptor Signaling Pathway (GO:0032926)	1/10	0.006462	0.037598	0	184.9815	932.0997	FST Reactome 2022
68	Positive Regulation Of Non-Canonical Wnt Signaling Pathway (GO:2000552)	1/10	0.006462	0.037598	0	184.9815	932.0997	DK1 Reactome 2022
69	Epithelial Cell Morphogenesis (GO:0030382)	1/12	0.007774	0.038778	0	151.3333	735.0173	STC1 Reactome 2022
70	Negative Regulation By Host Of Viral Transcription (GO:0043922)	1/12	0.007774	0.038778	0	151.3333	735.0173	HMG2 Reactome 2022
71	Prostanoid Biosynthetic Process (GO:006454)	1/14	0.009064	0.038778	0	128.0385	602.2149	HMG2 Reactome 2022
72	Negative Regulation Of Single Stranded Viral RNA Replication Via Double Stranded DNA Intermediate (GO:0032947)	1/14	0.009064	0.038778	0	128.0385	602.2149	HMG2 Reactome 2022
73	Regulation Of Cell Fate Specification (GO:0042659)	1/14	0.009064	0.038778	0	128.0385	602.2149	HMG2 Reactome 2022
74	Negative Regulation Of Multicellular Organismal Process (GO:0051241)	1/13	0.009217	0.038778	0	110.0239	517.0317	STC1-DK1 Reactome 2022
75	Regulation Of Activin Receptor Signaling Pathway (GO:0032925)	1/15	0.009709	0.038778	0	118.8869	551.0048	FST Reactome 2022
76	Positive Regulation Of Sprouting Angiogenesis (GO:1903672)	1/15	0.009709	0.038778	0	118.8869	551.0048	ITGA5 Reactome 2022
77	Prostanoid Metabolic Process (GO:006452)	1/16	0.010353	0.038778	0	110.9556	507.1178	FGF5 Reactome 2022
78	Negative Regulation Of RNA Biosynthetic Process (GO:190679)	1/16	0.010353	0.038778	0	110.9556	507.1178	ITGA5 Reactome 2022
79	Positive Regulation Of Stem Cell Proliferation (GO:2000648)	1/16	0.010353	0.038778	0	110.9556	507.1178	HMG2 Reactome 2022
80	Regulation Of Stem Cell Proliferation (GO:0020591)	1/16	0.010353	0.038778	0	110.9556	507.1178	HMG2 Reactome 2022
81	Negative Regulation Of Anion (GO:2000811)	1/16	0.010353	0.038778	0	110.9556	507.1178	ITGA5 Reactome 2022
82	Prostanoid Biosynthetic Process (GO:0001516)	1/17	0.010997	0.038778	0	104.0156	469.1243	PTGES Reactome 2022
83	Negative Regulation Of Striated Muscle Cell Differentiation (GO:0051514)	1/17	0.010997	0.038778	0	104.0156	469.1243	DK1 Reactome 2022
84	Mesenchyme Development (GO:0006485)	1/17	0.010997	0.038778	0	104.0156	469.1243	HMG2 Reactome 2022
85	Regulation Of Single Stranded Viral RNA Replication Via Double Stranded DNA Intermediate (GO:0032947)	1/17	0.010997	0.038778	0	104.0156	469.1243	HMG2 Reactome 2022
86	Negative Regulation Of Calcium Ion Transport (GO:0051026)	1/17	0.010997	0.038778	0	104.0156	469.1243	STC1 Reactome 2022
87	Negative Regulation Of Cellular Senescence (GO:2000773)	1/17	0.010997	0.038778	0	104.0156	469.1243	HMG2 Reactome 2022
88	Negative Regulation Of Monatomic Ion Transport (GO:0043271)	1/18	0.01164	0.038778	0	97.89216	435.9406	STC1 Reactome 2022
89	Negative Regulation Of Transcription By RNA Polymerase I (GO:0001022)	1/18	0.01164	0.038778	0	97.89216	435.9406	STC1 Reactome 2022
90	Regulation Of Cellular Response To Growth Factor Stimulus (GO:0000287)	1/19	0.012283	0.038778	0	92.44907	406.7303	FST Reactome 2022
91	Regulation Of Acute Inflammatory Response (GO:0002073)	1/19	0.012283	0.038778	0	92.44907	406.7303	PTGES Reactome 2022
92	Negative Regulation Of Peptidyl Serine Phosphatase (GO:0033137)	1/20	0.012926	0.038778	0	87.7895	380.8382	HMG2 Reactome 2022
93	Mesoderm Formation (GO:0001707)	1/20	0.012926	0.038778	0	87.7895	380.8382	STC1 Reactome 2022
94	Regulation Of Calcium Ion Import (GO:009279)	1/20	0.012926	0.038778	0	87.7895	380.8382	PTGES Reactome 2022
95	Sensory Perception Of Pain (GO:0039123)	1/20	0.012926	0.038778	0	87.7895	380.8382	PTGES Reactome 2022
96	Endothelial Cell Development (GO:0001885)	1/20	0.012926	0.038778	0	87.7895	380.8382	STC1 Reactome 2022
97	Regulation Of Anion (GO:2000209)	1/21	0.013568	0.040015	0	83.15983	357.7439	ITGA5 Reactome 2022
98	Regulation Of Vascular Endothelial Growth Factor Receptor Signaling Pathway (GO:0036047)	1/22	0.01421	0.04129	0	79.23016	337.0294	FGF5 Reactome 2022
99	Negative Regulation Of Ossification (GO:0030279)	1/24	0.015493	0.04192	0	72.33333	301.4412	DK1 Reactome 2022
100	Wound Healing, Spreading Of Cells (GO:0044319)	1/25	0.016133	0.04559	0	69.1597	286.0578	FGF5 Reactome 2022
101	Regulation Of Double-Strand Break Repair Via Nonhomologous End Joining (GO:2001032)	1/25	0.016133	0.04559	0	66.54	272.0119	STC1 Reactome 2022
102	Regulation Of Cardiac Muscle Cell Contraction (GO:0080044)	1/26	0.016774	0.045173	0	66.54	272.0119	STC1 Reactome 2022
103	Regulation Of Monatomic Ion Transport (GO:0043269)	1/28	0.018053	0.045173	0	61.60494	247.3091	STC1 Reactome 2022
104	Limb Development (GO:0060127)	1/28	0.018053	0.045173	0	61.60494	247.3091	DK1 Reactome 2022
105	Hematopoietic Progenitor Cell Differentiation (GO:0002244)	1/28	0.018053	0.045173	0	61.60494	247.3091	FST Reactome 2022
106	Heterotypic Cell-Cell Adhesion (GO:0044113)	1/29	0.018692	0.045173	0	59.40179	236.398	ITGA5 Reactome 2022
107	Chondrocyte Differentiation (GO:000262)	1/29						



Supplementary Figure S1: Depletion or overexpression of GPC4 demonstrated by slot blot assay. (A and B) Depletion of GPC4 expression by CRISPR/Cas9 GPC4 or (C and D) overexpression of GPC4 by GPC4 overexpression vector in SNB-75, SF-295 and HOP-92 cells. Cells were transfected with (A and B) CRISPR control or CRISPR GPC4 vector or (C and D) overexpression control or GPC4 overexpression vector. Cell extracts were blotted onto PVDF membranes and probed against an anti-GPC4 primary antibody followed by a horseradish peroxidase-conjugated anti-rabbit IgG. Loading consistencies were determined by stripping the membranes and re-probing with an anti- α -tubulin antibody. In B and D staining intensities for GPC4 were recorded by densitometry measurements using GelAnalyzer 19.1. No signal was detected when the primary antibody was omitted.