

Table SI. Mutation frequency and mutation types of UTP4 across various cancers.

Cancer study	Alteration frequency	Alteration type	Alteration count
Uterine corpus endometrial carcinoma	0.945179584	homdel	5
Uterine corpus endometrial carcinoma	0.189035917	amp	1
Uterine corpus endometrial carcinoma	4.347826087	mutated	23
Bladder urothelial carcinoma	0.243309002	multiple	1
Bladder urothelial carcinoma	0.729927007	homdel	3
Bladder urothelial carcinoma	1.946472019	amp	8
Bladder urothelial carcinoma	0.97323601	mutated	4
Esophageal adenocarcinoma	0.549450549	homdel	1
Esophageal adenocarcinoma	1.648351648	amp	3
Esophageal adenocarcinoma	1.648351648	mutated	3
Prostate adenocarcinoma	2.631578947	homdel	13
Prostate adenocarcinoma	0.4048583	amp	2
Cholangiocarcinoma	2.777777778	amp	1
Colorectal adenocarcinoma	2.693602694	mutated	16
Ovarian serous cystadenocarcinoma	2.226027397	homdel	13
Ovarian serous cystadenocarcinoma	0.342465753	amp	2
Skin cutaneous melanoma	0.225225225	amp	1
Skin cutaneous melanoma	2.027027027	mutated	9
Breast invasive carcinoma	1.383763838	homdel	15
Breast invasive carcinoma	0.184501845	amp	2
Breast invasive carcinoma	0.553505535	mutated	6
Diffuse large B-cell lymphoma	2.083333333	homdel	1
Stomach adenocarcinoma	0.681818182	homdel	3
Stomach adenocarcinoma	0.227272727	amp	1
Stomach adenocarcinoma	0.909090909	mutated	4
Lung squamous cell carcinoma	0.205338809	homdel	1
Lung squamous cell carcinoma	0.410677618	amp	2
Lung squamous cell carcinoma	0.821355236	mutated	4
Mesothelioma	1.149425287	mutated	1
Pheochromocytoma and paraganglioma	1.123595506	amp	2
Adrenocortical carcinoma	1.098901099	amp	1

Cervical squamous cell carcinoma	0.336700337	homdel	1
Cervical squamous cell carcinoma	0.673400673	mutated	2
Thymoma	0.81300813	mutated	1
Kidney renal papillary cell carcinoma	0.35335689	amp	1
Kidney renal papillary cell carcinoma	0.35335689	mutated	1
Lung adenocarcinoma	0.176678445	homdel	1
Lung adenocarcinoma	0.176678445	amp	1
Lung adenocarcinoma	0.35335689	mutated	2
Testicular germ cell tumors	0.67114094	mutated	1
Thyroid carcinoma	0.2	homdel	1
Thyroid carcinoma	0.4	mutated	2
Head and neck squamous cell carcinoma	0.191204589	multiple	1
Head and neck squamous cell carcinoma	0.382409178	homdel	2
Pancreatic adenocarcinoma	0.543478261	mutated	1
Acute myeloid leukemia	0.5	homdel	1
Sarcoma	0.392156863	amp	1
Brain lower grade glioma	0.389105058	mutated	2
Kidney renal clear cell carcinoma	0.195694716	mutated	1
Glioblastoma multiforme	0.168918919	mutated	1

Table SII. The top 100 genes co-expressed with UTP4 in pan-cancer.

Gene symbol	Gene ID	PCC
NIP7	ENSG00000132603.13	0.66
CIAPIN1	ENSG00000005194.14	0.6
SF3B3	ENSG00000189091.12	0.59
KARS	ENSG00000065427.14	0.55
DDX19A	ENSG00000168872.15	0.55
NOB1	ENSG00000141101.12	0.55
CSNK2A2	ENSG00000070770.8	0.54
DDX28	ENSG00000182810.6	0.53
USP10	ENSG00000103194.15	0.53
E2F4	ENSG00000205250.8	0.52
PDF	ENSG00000258429.1	0.51
RFWD3	ENSG00000168411.13	0.51
ATXN1L	ENSG00000224470.7	0.51
COG8	ENSG00000213380.13	0.49
POLR2C	ENSG00000102978.12	0.49
CNOT1	ENSG00000125107.16	0.49
AP1G1	ENSG00000166747.12	0.48
EMC8	ENSG00000131148.8	0.48
TSR1	ENSG00000167721.10	0.47
NUDT21	ENSG00000167005.13	0.47
OGFOD1	ENSG00000087263.16	0.47
PWP1	ENSG00000136045.11	0.47
SLC7A6OS	ENSG00000103061.11	0.47
NUTF2	ENSG00000102898.11	0.47
DDX19B	ENSG00000157349.15	0.47
PSME3	ENSG00000131467.10	0.46
THAP11	ENSG00000168286.2	0.46
WDR43	ENSG00000163811.11	0.46
DDX18	ENSG00000088205.12	0.45
CBFB	ENSG00000067955.13	0.45

CHTF8	ENSG00000168802.12	0.45
WDR12	ENSG00000138442.9	0.45
NAE1	ENSG00000159593.14	0.45
PSMD7	ENSG00000103035.10	0.44
IST1	ENSG00000182149.20	0.44
VPS35	ENSG00000069329.15	0.44
PNO1	ENSG00000115946.7	0.43
POLR1B	ENSG00000125630.15	0.43
SLC38A7	ENSG00000103042.8	0.43
ADAT1	ENSG00000065457.10	0.43
B4GALT5	ENSG00000158470.5	0.43
DUS2	ENSG00000167264.17	0.43
RNASEH1	ENSG00000171865.9	0.42
DNAJC11	ENSG00000007923.15	0.42
IMMT	ENSG00000132305.20	0.42
PUS7	ENSG00000091127.13	0.42
DCTN5	ENSG00000166847.9	0.42
PGAM5	ENSG00000247077.6	0.42
RP11-343C2.12	ENSG00000272617.1	0.42
ATMIN	ENSG00000166454.9	0.42
PA2G4	ENSG00000170515.13	0.42
TOMM70A	ENSG00000154174.7	0.41
EIF2S1	ENSG00000134001.12	0.41
ABCF2	ENSG00000033050.7	0.41
RP5-991G20.1	ENSG00000259768.5	0.41
GPN1	ENSG00000198522.13	0.41
ANKRD11	ENSG00000167522.14	0.41
PNPT1	ENSG00000138035.14	0.41
POLR2D	ENSG00000144231.10	0.41
GART	ENSG00000159131.16	0.41
SMNDC1	ENSG00000119953.12	0.41
ZC3H18	ENSG00000158545.15	0.41

SMYD5	ENSG00000135632.11	0.41
HEATR1	ENSG00000119285.10	0.41
ENO1	ENSG00000074800.13	0.41
SERBP1	ENSG00000142864.14	0.41
DNAJA2	ENSG00000069345.11	0.4
PGAM1	ENSG00000171314.8	0.4
GATAD2A	ENSG00000167491.17	0.4
RAN	ENSG00000132341.11	0.4
NHEJ1	ENSG00000187736.12	0.4
PATL1	ENSG00000166889.13	0.4
TBRG4	ENSG00000136270.13	0.4
NOL10	ENSG00000115761.15	0.4
ACD	ENSG00000102977.13	0.4
DPH2	ENSG00000132768.13	0.4
ABCE1	ENSG00000164163.10	0.4
DHX37	ENSG00000150990.7	0.4
CSNK2A1	ENSG00000101266.16	0.4
MTIF2	ENSG00000085760.14	0.4
DDX21	ENSG00000165732.12	0.4
MTMR2	ENSG00000087053.18	0.4
DNAAF5	ENSG00000164818.15	0.4
URB2	ENSG00000135763.9	0.4
AGPS	ENSG00000018510.12	0.4
CHCHD3	ENSG00000106554.11	0.4
MIEF1	ENSG00000100335.12	0.4
MARS2	ENSG00000247626.4	0.4
COX10	ENSG00000006695.10	0.4
CMTR2	ENSG00000180917.16	0.4
CD3EAP	ENSG00000117877.10	0.4
NOC3L	ENSG00000173145.11	0.4
PKM	ENSG00000067225.17	0.4
UTP20	ENSG00000120800.4	0.39

NDUFS1	ENSG00000023228.13	0.39
PMS2	ENSG00000122512.14	0.39
CORO1C	ENSG00000110880.10	0.39
SYNCRIP	ENSG00000135316.17	0.39
CCT5	ENSG00000150753.11	0.39
CIAO1	ENSG00000144021.2	0.39

Table SIII. UTP4 Knockout Detection: qPCR Raw Data.

	GAPDH	GAPDH	GAPDH	mean	UTP	UTP	UTP	mean
(sgRNA#2)								
A-sgNT	20.071	20.132	19.846	20.016	23.562	23.598	23.687	23.616
					3.545	3.582	3.671	
					-0.054	-0.018	0.072	
RE					1.038	1.012	0.952	
A-sgUTP4	20.125	19.895	19.933	19.985	24.770	24.811	24.802	24.795
					4.786	4.827	4.818	
					1.186	1.227	1.219	
					1.186	1.227	1.219	
RE					0.439	0.427	0.430	
M-sgNT	19.725	19.950	19.680	19.785	23.709	23.751	23.750	23.736
					3.923	3.966	3.964	
					-0.028	0.014	0.013	
RE					1.019	0.990	0.991	
M-sgUTP4	19.858	19.805	19.794	19.819	25.206	25.226	25.079	25.171
					5.387	5.407	5.260	
					1.436	1.456	1.309	
					1.436	1.456	1.309	
RE					0.370	0.364	0.404	
(sgRNA#1)								
A-sgNT	20.154	20.088	20.012	20.085	23.645	23.712	23.588	23.648
					3.560	3.628	3.503	
					-0.028	0.039	-0.085	
RE					1.019	0.973	1.062	
A-sgUTP4	20.088	20.123	20.054	20.088	24.453	24.463	24.443	24.453
					4.365	4.375	4.355	
					0.801	0.811	0.791	
RE					0.574	0.571	0.578	

M-sgNT	19.892	19.946	19.835	19.891	23.535	23.612	23.499	23.549
					3.644	3.721	3.608	
					0.012	0.090	-0.023	
RE					0.992	0.939	1.016	
M-sgUTP4	19.877	19.912	19.899	19.896	24.393	24.403	24.383	24.393
					4.497	4.507	4.487	
					0.839	0.849	0.829	
RE					0.559	0.555	0.562	
								(sgRNA#3)
A-sgNT	20.11235	20.18765	20.05432	20.11811	23.64512	23.72346	23.58765	23.65208
					3.527016	3.605349	3.469547	
					0.013	0.091	-0.044	
RE					0.991	0.939	1.031	
A-sgUTP4	20.04568	20.11235	19.97891	20.04565	24.37903	24.38903	24.36903	24.37903
					4.333386	4.343386	4.323386	
					0.706278	0.716278	0.696278	
RE					0.613	0.61	0.617	
M-sgNT	19.92346	19.98765	19.84568	19.91893	23.45679	23.53457	23.47891	23.49009
					3.53786	3.615638	3.559983	
					-0.003	0.075	0.019	
RE					1.002	0.949	0.987	
M-sgUTP4	19.88765	19.92346	19.81235	19.87449	24.32101	24.33101	24.31101	24.32101
					4.446527	4.456527	4.436527	
					0.757662	0.767662	0.747662	
RE					0.591	0.587	0.596	