

UHMK1 promotes gastric cancer progression through reprogramming nucleotide metabolism

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Appendix Table S1. Relationship between UHMK1 expression and clinicopathological features of GC patients (n=100)

variable	Relative UHMK1 Expression		P-value
	Low (n=44)	High (n=56)	
Age			NS
≤50	25	26	
>50	19	30	
Gender			NS
Male	24	33	
Female	20	23	
Histological differentiation			NS
Well/Moderately	28	28	
Poorly	16	28	
Tumor size			P<0.05
≤5cm	31	24	
>5cm	13	32	
Distant metastasis			P<0.05
Yes	5	18	
No	39	38	
Tumor stage			P<0.05
I-II	27	21	
III-IV	17	35	
Lymphatic invasion			P<0.05
Yes	18	35	
No	26	21	
Vascular invasion			NS
Yes	19	30	
No	25	26	
<i>H.pylori</i> infection			P<0.05
Yes	18	34	
No	26	22	

Note: GC patients were divided into UHMK1 high group and low group according to the analysis of qRT-PCR detection. NS, not significant between different groups. Differences among variables were evaluated by χ^2 or Fisher's exact χ^2 -test.

Appendix Table S2. Univariate and multivariate analysis of factors associated with survival in GC patients (n=100)

Variable	Univariate analysis		multivariate analysis	
	HR (95% CI)	P-value	HR (95% CI)	P-value
Gender				
Male vs. Female	0.800(0.488-1.311)	0.375		
Age				
≤50 vs. >50	1.030(0.636-1.670)	0.903		
Histological differentiation				
Well/Moderately vs. Poorly	1.118(0.726-1.916)	0.504		
Tumor size				
≤5cm vs. >5cm	1.707(1.049-2.775)	0.031		
Distant metastasis				
Yes vs. No	2.256(1.328-3.832)	0.003	1.836(1.049-3.214)	0.033
Tumor stage				
I-II vs. III-IV	1.693(1.030-2.782)	0.038		
Lymphatic invasion				
Yes vs. No	1.625(0.991-2.666)	0.055		
Vascular invasion				
Yes vs. No	1.236(0.762-2.004)	0.391		
H.pylori infection				
Positive vs. Negative	1.808(1.104-2.961)	0.019	1.864(1.109-3.187)	0.023
UHMK1 expression				
High vs. Low	3.104(1.808-5.328)	0.001	1.977(1.085-3.603)	0.026

Appendix Table S3. UHMK1 related top 500 differentially expressed genes in GC

Top 500 genes upregulated

gene	logFC	adj. P value	gene	logFC	adj. P value	gene	logFC	adj. P value
UHMK1	2.4000218	2.044E-73	HIPK1	0.9530314	6.172E-29	TMEM184C	0.6328096	2.991E-25
NHLRC2	1.3161737	3.086E-43	ADAR	0.7407452	6.775E-29	ZNF81	1.0044275	3.148E-25
ANKRD36BP1	1.8001811	4.968E-43	KIF2A	0.9948283	8.529E-29	REL	0.9587622	3.117E-25
SFT2D2	1.2489058	9.74E-40	PTPLB	1.3651592	1.18E-28	ZNF678	1.2524419	3.103E-25
ASXL2	1.387653	6.198E-39	C9orf102	1.2811579	1.2E-28	CNOT1	0.7926673	3.139E-25
DENND1B	1.6793154	5.47E-37	AP1G1	0.8042917	2.067E-28	POLR3A	0.9392427	3.503E-25
C22orf30	0.909826	4.791E-37	TRIP12	0.7578423	9.807E-28	MPHOSPH9	1.0031505	4.225E-25
TAOK1	1.4673326	1.197E-36	CLTC	0.6839019	1.338E-27	IREB2	0.7391494	4.425E-25
MAP3K2	1.0038034	2.114E-35	RASA2	1.1907286	2.23E-27	FAM199X	0.823473	4.519E-25
SPTY2D1	0.7876738	4.669E-35	ZDHHC20	1.4325445	2.488E-27	PDS5A	0.6371682	5.834E-25
IDE	1.0851064	6.143E-35	RSPRY1	0.8739165	2.936E-27	ETV3	1.1455421	7.126E-25
STRN	1.1206	6.803E-35	TMEM48	1.2371771	3.896E-27	C9orf41	1.1300585	7.677E-25
ADAM10	1.1559253	1.217E-34	KLHDC10	0.9600864	5.29E-27	FBXL4	0.8323583	8.588E-25
MOBKL1B	0.792599	4.82E-34	EDEM1	0.9311928	6.18E-27	ANAPC1	0.9275185	1.053E-24
RC3H2	1.1281025	6.309E-34	EYA3	1.1009207	1.008E-26	PLEKHB2	0.7164953	1.06E-24
RBBP5	0.9266372	9.786E-34	RFX3	1.5337798	1.231E-26	MGAT5	1.6302772	1.174E-24
C1orf58	1.185804	5.845E-33	KIAA0317	0.7192506	1.246E-26	STAG1	0.8019166	1.185E-24
BARD1	1.3805954	1.168E-32	BIRC6	0.835761	1.396E-26	CDK12	0.8030107	1.493E-24
GTF2A1	1.2412344	1.01E-31	ATP6V1A	0.6654869	1.549E-26	GTF2H3	0.8975051	1.503E-24
IPMK	1.5119633	9.804E-32	PAFAH1B2	0.9683713	1.812E-26	RALGAPA2	1.3613737	1.641E-24
HEATR5A	0.905195	1.885E-31	ATIC	1.621867	2.302E-26	KIAA2018	0.8189621	1.977E-24
STT3B	1.0303327	3.04E-31	C9orf129	1.362427	3.014E-26	KIAA0100	0.7416497	2.549E-24
SLC30A6	0.9984082	3.817E-31	RIF1	0.8712397	3.05E-26	SLC30A1	0.9482514	2.783E-24
LRBA	0.956573	4.444E-31	BRWD3	1.2154355	4.118E-26	CLCN3	1.1122852	2.788E-24
PDZD8	1.3829544	4.487E-31	UEVLD	0.8935806	5.442E-26	GMCL1	0.8660903	2.822E-24
NCOA2	1.4314557	8.495E-31	SLC31A1	0.9505428	6.795E-26	BRIP1	1.4646701	3.637E-24
CEP97	1.2143757	1.349E-30	ATE1	1.1071539	9.171E-26	GTF2I	0.8718274	3.812E-24
CCNT1	1.3499531	2.991E-30	DDI2	1.3451586	1.419E-25	NUP98	0.6585367	4.687E-24
RAPGEF6	1.2301429	3.249E-30	NBEAL1	1.479392	1.565E-25	TNPO1	0.610642	4.672E-24
C10orf12	1.1703076	4.2E-30	SETX	0.8505129	1.543E-25	ASCC3	0.8762151	5.308E-24
ZBTB41	0.9959707	1.047E-29	TMPPE	1.152866	1.546E-25	UBR2	0.9132527	5.44E-24
ATF6	0.7109123	1.103E-29	CDC14C	1.3054607	1.763E-25	DNAJB14	0.7432964	6.805E-24
MED13	0.9099892	1.114E-29	MBNL3	1.834858	2.081E-25	VPS13B	0.8397101	8.077E-24
PUS7L	1.0692045	1.128E-29	XRN1	0.9438384	2.055E-25	HEATR5B	0.6652618	8.154E-24
CEP350	0.8931274	1.108E-29	LATS1	0.9592099	2.23E-25	LNPEP	1.3006619	9.468E-24
GTF3C4	1.0682798	1.922E-29	AVL9	0.947364	2.251E-25	LOC284441	1.1998469	1.005E-23
MAN2A1	1.2090687	2.965E-29	ELK4	0.7739442	2.568E-25	PPP1R15B	0.634379	1.197E-23
SGK196	1.7160869	3.056E-29	SPTLC2	0.8776674	2.84E-25	MCM9	0.8965165	1.787E-23
PANK3	1.0910574	3.445E-29	DHX9	0.5811611	3.023E-25	LRRC8B	0.7825015	2.275E-23
gene	logFC	adj. P	gene	logFC	adj. P	ALMS1	0.8679354	2.425E-23
						RSC1A1	0.9401114	2.745E-23
						FRK	1.5865505	2.89E-23

ZNF619	0.8370897	4.548E-23	ZNF770	0.6898259	5.313E-21	SPATA13	1.1457412	1.561E-19
SMG1	0.8485956	4.975E-23	POLR2B	0.5730563	5.413E-21	GNPTAB	0.6653454	1.93E-19
IGF2R	0.9424684	7.058E-23	CAPRIN1	0.5712546	7.172E-21	EPT1	0.8654129	1.943E-19
GAN	1.2622266	9.419E-23	SBNO1	0.7239773	7.235E-21	KIAA1715	0.5901042	1.975E-19
MAPK8	0.8389523	9.847E-23	RLIM	0.6980406	7.267E-21	PRKAR2A	0.8598004	2.126E-19
PTPRJ	1.1381485	9.801E-23	INO80D	0.6883839	7.707E-21	GART	1.2140752	2.204E-19
TOR1AIP2	1.0065199	1.02E-22	SCYL2	0.7090304	8.799E-21	INTS2	0.7073429	2.731E-19
URB2	0.8638302	1.055E-22	LMBRD2	1.0419302	8.857E-21	TRIP11	0.6441355	3.061E-19
DDX3X	0.6251061	1.112E-22	MTOR	0.7111882	1.01E-20	NUFIP2	0.558453	3.216E-19
SMG7	0.5671699	1.188E-22	COPB1	0.5697791	1.017E-20	RBL1	1.0082697	3.336E-19
USP24	0.6771454	1.315E-22	RBM15	0.6756147	1.033E-20	ASH1L	0.7331325	3.63E-19
DHX8	0.6240093	1.379E-22	UHRF1BP1	0.7365303	1.067E-20	ACTR8	0.5041095	3.859E-19
MED1	0.8042572	1.43E-22	PARP4	0.8285502	1.243E-20	KLHL11	1.3033655	4.524E-19
CLOCK	0.979051	2.386E-22	AQR	0.5808321	1.355E-20	SEL1L	0.6730485	5.347E-19
PPTC7	0.9413065	2.448E-22	TGFBRAP1	0.9202566	1.392E-20	FMN1	1.681558	6.079E-19
SEC24A	0.8077737	2.594E-22	FBXW11	0.6676025	1.486E-20	UTP20	0.7414295	6.529E-19
ACAP2	0.6427453	3.142E-22	KIAA1958	1.169563	1.69E-20	SETD2	0.5961075	7.556E-19
RBM12	0.4928092	3.277E-22	PIKFYVE	0.7318107	1.792E-20	CTDSPL2	0.6252622	7.942E-19
EAF1	0.6482976	3.874E-22	CPD	1.0876931	2.154E-20	SEC16A	0.7300993	8.251E-19
VPRBP	0.6063967	3.918E-22	MMGT1	0.6625443	2.149E-20	XPO4	0.770916	8.381E-19
PPAT	1.2136772	4.893E-22	RQCD1	0.7117332	2.444E-20	DENND4A	0.805951	8.838E-19
PDP2	0.8504752	5.105E-22	KIAA0494	0.6145399	2.583E-20	ZFP106	0.687137	9.018E-19
ZNF484	0.8014699	6.429E-22	43530	0.7356534	2.594E-20	KLHL18	0.5454983	9.027E-19
SLC25A40	0.9650098	6.996E-22	EPRS	0.6533141	2.7E-20	ENTPD4	0.7501759	9.716E-19
IBTK	0.8353649	7.065E-22	ZNF460	1.1373267	2.721E-20	TET2	0.7506727	9.895E-19
CSNK1G1	0.6280766	7.076E-22	SMC5	0.7488952	2.843E-20	LIMS1	0.8113826	1.013E-18
N4BP2	1.2541466	7.281E-22	C20orf94	1.0869339	3.136E-20	DIP2B	0.68738	1.014E-18
RANBP2	0.7371729	9.986E-22	UBE3C	0.5919234	3.243E-20	DIAPH1	0.7377202	1.11E-18
ATF2	0.8213289	1.087E-21	MFSB9	0.7819983	3.89E-20	SLC39A9	0.5231427	1.131E-18
APAF1	0.7634362	1.119E-21	IQGAP1	0.6940981	3.944E-20	ERCC6	0.7324272	1.227E-18
PRDM10	0.6369584	1.182E-21	ISG20L2	0.6404436	4.12E-20	ZZZ3	0.52416	1.242E-18
RNF111	0.5963893	1.275E-21	LCOR	0.9856684	4.105E-20	PIK3R4	0.5676919	1.246E-18
DCUN1D1	0.7081318	1.402E-21	HELZ	0.6112895	5.319E-20	ADSL	1.0274341	1.337E-18
SPG11	0.6658187	1.396E-21	ZNF800	0.6399907	5.774E-20	PSME4	0.591024	1.349E-18
ZNF41	0.638438	1.444E-21	C1orf163	0.7047422	5.838E-20	ZCCHC6	0.6253278	1.645E-18
FKBP15	0.5649523	1.567E-21	CPSF2	0.5590333	7.06E-20	RLF	0.6157705	1.706E-18
ROD1	0.7489587	1.61E-21	FAM102B	0.9152397	7.427E-20	NBAS	0.7214519	2.106E-18
NEU3	0.9954672	1.75E-21	LASS6	1.0500063	7.46E-20	RABGAP1L	0.7911188	2.146E-18
GPRIN3	1.8284328	1.751E-21	ZNF699	1.4274288	8.272E-20	CTCF	0.3619852	2.14E-18
ADAT1	0.8105047	1.875E-21	AP2B1	0.6912921	8.556E-20	KIAA1109	0.8068943	2.219E-18
CAND1	0.7638659	3.626E-21	ATR	0.8055855	9.552E-20	HIPK3	1.0745277	2.327E-18
DCLRE1A	0.8145676	3.753E-21	C10orf118	0.9006365	1.071E-19	SNRNP200	0.644248	2.318E-18
SEC23IP	0.6178249	3.919E-21	KDM4A	0.5934932	1.151E-19	NPAT	0.690592	2.331E-18
DOCK7	0.7654935	4.453E-21	SEL1L3	0.9759881	1.172E-19	STARD4	1.2775374	2.353E-18
KCTD20	0.7979825	4.466E-21	PALB2	0.6549874	1.172E-19	TOPBP1	0.7195635	2.559E-18
WAPAL	0.6012358	5.265E-21	DHX15	0.5762793	1.32E-19	TBC1D5	0.6498546	3.044E-18

KIAA0947	0.7025393	3.18E-18	FAM45B	0.7527754	1.381E-17	ASAH2B	1.963869	1.556E-16
FOXN2	0.7033758	3.241E-18	ALG10	0.8271822	1.655E-17	SPTBN1	0.8367197	1.641E-16
MTF1	0.5647801	3.323E-18	BTAF1	0.8126863	1.679E-17	PI4K2B	0.6893848	1.691E-16
ZBTB37	1.0366886	3.387E-18	IPO11	0.5742801	2.173E-17	WRN	0.7432747	1.748E-16
CHUK	0.6240544	3.396E-18	ZNF192	0.9595774	2.179E-17	LPGAT1	0.724762	1.743E-16
QTRTD1	0.5454608	3.42E-18	FAM73A	0.7638516	2.353E-17	MSI2	0.8720946	1.938E-16
MFAP3	0.5282795	3.523E-18	GSK3B	0.4784307	2.371E-17	FNDC3A	0.6829733	2.475E-16
STIL	1.1852174	3.617E-18	WDR7	0.7927071	2.381E-17	DNAJC3	0.5484379	2.571E-16
PRRC1	0.5628554	3.614E-18	BMP2K	0.8172116	2.429E-17	HECTD1	0.5508082	2.683E-16
SSH2	0.7764629	3.606E-18	SERINC5	1.3531302	2.685E-17	CHD8	0.4784602	2.759E-16
ARFGEF1	0.7806325	3.781E-18	SF3A1	0.4162869	2.694E-17	WDFY1	0.5928	2.81E-16
LARP4	0.6826046	3.96E-18	COPB2	0.5251289	2.849E-17	ANKFY1	0.5944399	3.245E-16
ABHD2	1.2646957	4.604E-18	TRPM7	0.6852402	2.921E-17	NUPL1	0.6237633	3.326E-16
MTMR4	0.6288162	4.913E-18	DNAJC13	0.580492	3.009E-17	SF3B1	0.5480818	3.354E-16
NUP155	0.9578863	5.214E-18	PIK3CB	0.6398871	3.335E-17	TFRC	1.1283161	3.357E-16
USP32	0.5558164	5.196E-18	NSUN3	0.7009751	3.448E-17	TBL1XR1	0.6497281	3.462E-16
SLC30A9	0.5344999	5.371E-18	DDX21	0.7031014	3.587E-17	CTAGE1	1.0511673	3.549E-16
KIF4B	1.2712464	5.76E-18	GPD2	0.7886559	4.284E-17	KDM3B	0.5079985	3.725E-16
PRKDC	0.8194073	5.797E-18	NSD1	0.6132135	4.375E-17	RFX7	0.7035135	3.819E-16
SEC24B	0.5217742	6.09E-18	TMEM2	0.9775282	4.362E-17	RREB1	0.6903584	4.321E-16
MPZL3	1.3730154	6.624E-18	TM9SF2	0.701501	4.439E-17	CNNM4	0.9939645	4.511E-16
AP4E1	0.6202797	6.647E-18	POLR1A	0.716721	4.601E-17	ATXN7	0.5416866	4.523E-16
REST	0.5443734	6.775E-18	G3BP2	0.5416574	4.599E-17	C2CD3	0.5611609	4.573E-16
PGM3	0.8831538	7.358E-18	CSNK2A1P	0.6906516	5.194E-17	DPP8	0.5445881	4.621E-16
ZFP91	0.4290525	7.799E-18	NIPA1	0.6997826	5.57E-17	LARS2	0.6635522	4.754E-16
FNIP2	0.8610446	7.823E-18	BTBD8	1.3538041	6.115E-17	ATP2A2	0.475559	5.104E-16
NSF	0.6647775	8.245E-18	ARFGEF2	0.7628006	6.312E-17	DYRK2	0.7156478	5.182E-16
HTT	0.6916441	8.344E-18	SMARCA5	0.5403742	6.52E-17	ERLIN1	0.6661009	5.449E-16
FKTN	0.6710692	8.316E-18	CENPI	1.3031027	6.579E-17	RNF213	0.9327672	5.49E-16
HEATR1	0.7168909	8.351E-18	TMED5	0.5684286	7.518E-17	GMCL1L	1.2875447	6.849E-16
LIMD1	0.6542044	8.661E-18	TUBGCP4	0.5802599	7.617E-17	PPP4R2	0.5958449	7.056E-16
ERMP1	1.0156618	8.807E-18	STXBP5	0.8058563	7.883E-17	ARAP2	1.0668953	7.109E-16
SFRS2IP	0.5245054	1.029E-17	TGOLN2	0.6085787	8.158E-17	GAPVD1	0.5022573	7.623E-16
NUP205	0.7207926	1.035E-17	FUBP1	0.5238287	9.709E-17	CDKL5	1.3466473	7.825E-16
UBR1	0.6980804	1.051E-17	PUM1	0.3592088	9.736E-17	NCAPD3	0.8126927	8.712E-16
MYSM1	0.9400762	1.138E-17	EIF2AK3	0.6127188	9.726E-17	SLC35A5	0.5923324	9.602E-16
UBQLN1	0.4942418	1.182E-17	SH3RF1	0.8731329	1.004E-16	NLN	0.7838389	9.902E-16
ROCK2	0.8630819	1.18E-17	IL6ST	1.4021001	1.005E-16	ARHGEF12	0.5301204	1.001E-15
SLC30A5	0.4487112	1.195E-17	BRAF	0.7710247	1.058E-16	SPPL2A	0.5833979	1.092E-15
LMTK2	1.1768241	1.197E-17	NDUFS1	0.5553454	1.067E-16	RASEF	1.7257407	1.11E-15
SHPRH	1.0533896	1.2E-17	OSBP	0.4339179	1.065E-16	PIK3CA	0.703236	1.256E-15
HUWE1	0.5896624	1.235E-17	HPS5	0.6092356	1.116E-16	CNOT6L	0.5899587	1.274E-15
RRM1	0.6869498	1.253E-17	BAG4	0.897102	1.177E-16	NAA50	0.5389056	1.274E-15
CDC27	0.5188291	1.26E-17	DR1	0.4588871	1.203E-16	DHX33	0.7574955	1.282E-15
FAT1	1.044697	1.268E-17	SLC9A7	1.5430361	1.24E-16	PDPK1	0.5616041	1.319E-15
YIPF6	0.6378656	1.349E-17	KIAA1632	0.7372292	1.488E-16	NCBP1	0.5639412	1.375E-15

INTS7	0.6083912	1.394E-15	TP53BP1	0.565024	4.97E-15	MFHAS1	0.8689751	2.116E-14
GOSR1	0.3784716	1.49E-15	SEC23B	0.6658158	5.24E-15	FGD4	0.8379665	2.126E-14
NRAS	0.618176	1.505E-15	CBL	0.6493016	5.568E-15	ARHGAP11B	1.2058354	2.129E-14
EDEM3	0.9222087	1.605E-15	SMCR8	0.6700403	5.662E-15	RBMXL1	0.4584505	2.155E-14
NUP160	0.6022887	1.624E-15	NF1	0.5652314	5.829E-15	SLC33A1	0.5573013	2.218E-14
DMXL2	0.8203279	1.719E-15	PDXDC1	0.5955602	6.162E-15	FOXJ3	0.519847	2.225E-14
MFSD6	0.7323377	1.715E-15	ZKSCAN1	0.8885373	6.259E-15	PLCXD2	0.8811793	2.306E-14
NIPAL2	1.0275282	1.787E-15	AP3B1	0.4655733	6.321E-15	57714	0.9536393	2.317E-14
CD2AP	0.8166448	1.93E-15	ATF7IP	0.6343516	6.379E-15	TTC37	0.7508069	2.367E-14
KIAA0586	0.5987422	1.926E-15	LEPROT	0.8302925	6.528E-15	EP300	0.4102693	2.366E-14
ITGA6	0.9838335	1.98E-15	SLC35A3	0.8944533	6.715E-15	NUP133	0.5134086	2.374E-14
VPS13C	0.7518527	2.08E-15	TCF20	0.6159907	7.236E-15	EMR2	1.2138997	2.478E-14
BTBD1	0.4695351	2.396E-15	SLC5A3	0.7839411	7.31E-15	QRICH1	0.3708178	2.703E-14
DGKH	1.1475872	2.415E-15	C14orf21	0.7457484	7.354E-15	ITCH	0.4749164	2.715E-14
MTMR1	0.5077666	2.419E-15	CD84	1.6914447	7.745E-15	RAB14	0.4325738	2.72E-14
RAD18	0.7306809	2.613E-15	HELB	1.0347354	7.846E-15	DDB1	0.4479016	2.718E-14
TNPO3	0.4451733	2.872E-15	PHF6	0.6609087	8.438E-15	EHF	1.5088519	2.752E-14
NFXL1	0.7104029	2.96E-15	PLEKHA7	0.8810731	8.648E-15	SUCNR1	2.0853095	2.786E-14
USP1	0.5433327	2.973E-15	ADNP2	0.6439617	9.008E-15	DCTN5	0.4582491	2.93E-14
MUT	0.5211166	3.194E-15	WDR11	0.5330979	9.338E-15	MANEA	0.7051	2.992E-14
MYST3	0.5371385	3.291E-15	LCORL	0.6590242	1.004E-14	CCDC21	0.7222294	3.155E-14
TMOD3	0.512109	3.366E-15	TTBK2	1.0777733	1.051E-14	RFWD3	0.6447155	3.166E-14
WDR76	0.8392711	3.538E-15	KIAA1804	1.0600231	1.05E-14	DICER1	0.5522122	3.221E-14
RAB27B	1.9997532	3.54E-15	SMCHD1	0.6769025	1.077E-14	PLXNC1	1.7734766	3.24E-14
PIGN	0.7479326	3.569E-15	MON1B	0.534154	1.11E-14	HMGCR	0.7873399	3.287E-14
FRYL	0.7503661	3.564E-15	MOSPD2	0.7035593	1.299E-14	ZBTB5	0.6401336	3.281E-14
TTF2	0.7179287	3.608E-15	TMF1	0.5674536	1.326E-14	APPL1	0.5169293	3.422E-14
RTTN	0.8429029	3.737E-15	C14orf118	0.5799249	1.613E-14	USP33	0.4464995	3.45E-14
CPNE3	0.6140078	3.787E-15	GAS2L3	1.1794478	1.709E-14	RHBDD1	0.5256043	3.604E-14
GNS	0.6970842	3.848E-15	INO80	0.38618	1.88E-14	ZNF148	0.4670945	3.755E-14
SAMD8	0.8835312	3.969E-15	ZBTB6	0.5760469	1.887E-14	KBTBD4	0.5738921	3.97E-14
FUT10	0.7890463	3.981E-15	PTPRG	0.9940412	1.903E-14	GPATCH8	0.4330936	4.011E-14
EXOC6	0.6229367	4.075E-15	VPS13D	0.6688274	1.938E-14	EIF2C2	0.783575	4.145E-14
PRPF8	0.5815694	4.266E-15	SMCR7L	0.4336673	1.954E-14	ZNF121	0.8322075	4.225E-14
CXorf38	0.7451763	4.39E-15	MADD	0.5379461	2.06E-14			

Top 500 genes downregulated

gene	logFC	adj. P value	gene	logFC	adj. P value	gene	logFC	adj. P value
NDUFA3	-1.414433	4.116E-32	GABARAP	-0.752319	1.772E-24	COMMD1	-0.786559	4.4E-22
COMMD6	-1.169603	2.524E-32	RPL27A	-1.004193	1.772E-24	NDUFB8	-0.714299	4.59E-22
PRR24	-1.412302	2.14E-32	FAM128B	-1.013756	2.215E-24	UBL5	-0.692747	5.172E-22
MYEOV2	-0.973756	3.249E-31	ZNF414	-0.802528	3.043E-24	HCFC1R1	-1.070875	6.113E-22
C1orf86	-1.117663	2.339E-30	FDX1L	-0.785018	3.269E-24	C17orf49	-0.788063	7.046E-22
THAP3	-1.029667	6.72E-30	ROMO1	-0.994893	3.861E-24	NDUFS5	-0.824905	7.267E-22
LIN37	-0.928874	2.648E-29	CCDC85B	-1.190244	5.085E-24	POLR2F	-0.801491	7.51E-22
BCL7C	-1.142575	4.385E-29	TBCB	-0.856676	7.123E-24	ATP6V1F	-0.792494	7.508E-22
TRAPPC1	-0.885406	4.85E-29	RP9	-1.077618	8.643E-24	DNLZ	-1.078668	7.545E-22
SCAND1	-1.119013	4.856E-29	PTMS	-1.309071	8.825E-24	MED19	-0.821285	1.274E-21
RNF181	-0.962048	6.336E-29	NDUFA11	-0.852834	8.744E-24	DNAJC17	-0.680339	1.419E-21
OST4	-1.054574	6.844E-29	BGLAP	-1.364138	1.215E-23	ZNF688	-0.881192	1.642E-21
NDUFA13	-0.851127	2.319E-28	TOMM7	-1.030072	1.345E-23	C14orf156	-0.992456	1.962E-21
SNORD17	-2.246153	4.148E-28	C19orf56	-0.635234	1.56E-23	RPL23A	-0.926483	1.95E-21
NDUFB7	-0.98414	1.267E-27	C19orf70	-0.881741	1.756E-23	SIVA1	-0.775418	2.492E-21
NDUFS8	-1.099276	1.63E-27	RPL28	-1.127002	2.195E-23	USE1	-0.809046	2.469E-21
CCS	-0.743418	4.409E-27	PPP1R14A	-2.223525	3.105E-23	C16orf13	-0.91468	4.119E-21
ATOX1	-0.957082	4.742E-27	COX17	-0.903163	3.162E-23	LOC440957	-0.991133	4.246E-21
RNASEK	-0.898542	1.596E-26	ATP5G2	-0.832715	3.192E-23	MPV17	-0.786415	4.541E-21
NCRNA00116	-1.231589	1.866E-26	C1orf123	-0.762674	3.396E-23	RHEB	-0.689893	4.838E-21
C17orf61	-1.20831	2.201E-26	ZNF580	-0.994109	3.611E-23	COX7A1	-1.616037	5.114E-21
RNASEH2C	-0.87625	2.601E-26	MOB2	-0.791889	3.893E-23	CEBPD	-1.164032	5.07E-21
PFN1	-0.798378	3.546E-26	NDUFB4	-0.753773	5.152E-23	RPL36	-1.018865	5.541E-21
GPS2	-0.801709	4.11E-26	RPS19BP1	-0.74725	5.077E-23	C11orf10	-0.752305	5.739E-21
RPL38	-1.115006	4.081E-26	EGFL8	-1.554236	6.959E-23	SRP14	-0.613222	6.418E-21
MRPL53	-0.94508	4.014E-26	ZNF358	-1.179073	8.254E-23	SERF2	-0.779767	6.752E-21
LSMD1	-1.051584	5.243E-26	RPP21	-0.945756	8.401E-23	SYCE1L	-2.014839	7.324E-21
RPS20	-1.041563	9.318E-26	PABPN1	-0.908371	9.005E-23	RANGRF	-0.833802	8.702E-21
RPLP1	-0.984141	1.098E-25	NENF	-0.970517	9.124E-23	TMEM160	-0.964229	8.967E-21
POLR21	-0.99393	1.228E-25	RPL37A	-0.925633	9.963E-23	NDUFC1	-0.892117	1.141E-20
FKBP2	-1.05687	1.389E-25	MRPS24	-0.792415	9.994E-23	RPPH1	-2.897785	1.616E-20
UQCR11	-0.89816	1.493E-25	FAM127A	-1.515525	1.058E-22	RAB11B	-0.692336	1.768E-20
ARL2	-0.882599	2.58E-25	DYNLL1	-0.657184	1.08E-22	GNG5	-0.692623	1.863E-20
UBXN1	-0.742044	3.047E-25	PFDN5	-0.76346	1.361E-22	POLR2J	-0.830453	1.897E-20
DYNLRB1	-0.939946	3.008E-25	C19orf53	-0.864573	1.419E-22	TMEM91	-1.148542	2.555E-20
TRMT112	-0.8587	3.885E-25	MSRB2	-1.062832	1.626E-22	RPL13	-0.950603	3.725E-20
GADD45GIP1	-0.913076	3.804E-25	RP9P	-1.114472	1.764E-22	TMEM93	-0.780741	3.709E-20
C19orf43	-0.86435	3.876E-25	SNRNP35	-0.669842	1.85E-22	EXOSC1	-0.674379	3.77E-20
RPL39	-1.672971	5.166E-25	BANF1	-0.90343	2.371E-22	RAMP2	-1.322499	4.274E-20
HIGD2A	-0.990014	6.703E-25	JOSD2	-1.004764	2.551E-22	FBXL15	-0.846775	4.526E-20
EDF1	-0.804574	9.263E-25	RPLP2	-0.973239	3.107E-22	C17orf81	-0.743932	4.579E-20
gene	logFC	adj. P value	gene	logFC	adj. P value	ZMAT5	-0.831134	4.653E-20
						RNU11	-2.229883	5.095E-20
						FAM176B	-1.211004	5.272E-20

FAM89B	-0.777965	5.362E-20	PSENEB	-0.892469	2.543E-18	MRPL20	-0.641387	2.023E-17
RPL6	-0.77861	5.762E-20	PHPT1	-0.851268	2.534E-18	DNAJC30	-0.647872	2.426E-17
KRTCAP2	-0.87906	8.051E-20	SNHG6	-1.096873	2.726E-18	PIN4	-0.888316	2.665E-17
LENG1	-0.759304	8.75E-20	MYL6	-0.845673	2.789E-18	MAP1LC3A	-1.262023	2.798E-17
DRAP1	-0.791341	9.234E-20	VPS28	-0.684005	3.062E-18	FAM195B	-1.019315	3.382E-17
C17orf79	-0.737216	9.337E-20	PFDN1	-0.510817	3.519E-18	CCDC23	-0.67924	3.413E-17
POLR2L	-0.832756	1.129E-19	CCDC12	-0.639681	3.686E-18	HES4	-1.384766	3.562E-17
MRP63	-0.776775	1.315E-19	C7orf50	-0.855397	4.079E-18	C12orf45	-0.78986	3.708E-17
ATP5I	-0.956589	1.426E-19	PPDPF	-1.028508	4.134E-18	FUNDC2	-0.636171	3.767E-17
SURF2	-0.895854	1.676E-19	C11orf67	-0.970226	4.64E-18	TIMM17B	-0.807045	3.831E-17
RPS15	-0.951586	1.682E-19	NAT14	-1.329364	5.056E-18	LOC145474	-1.323478	4.019E-17
TRAPPC2L	-0.761643	1.695E-19	C14orf2	-0.829147	5.188E-18	FLOT1	-0.671906	4.116E-17
ARL6IP4	-0.682211	1.921E-19	C11orf48	-0.751759	5.648E-18	ARF5	-0.608224	4.331E-17
LIN7B	-1.073737	2.212E-19	COX5B	-0.851842	5.658E-18	YPEL3	-0.99815	4.993E-17
NDUFAF3	-0.748428	2.42E-19	NME4	-1.191308	5.832E-18	IFI27L2	-1.104019	5.109E-17
MIF	-1.138297	2.696E-19	SNHG9	-1.513581	5.806E-18	MRPL52	-0.794087	5.495E-17
SPAG7	-0.618895	3.33E-19	AURKAIP1	-0.797953	5.914E-18	IFITM3	-1.046754	5.706E-17
EEF1D	-0.710027	3.391E-19	DGUOK	-0.652192	5.998E-18	C4orf48	-1.605594	6.215E-17
MRPL55	-0.74886	4.002E-19	NDUFA7	-0.772961	6.197E-18	C9orf142	-0.775945	6.528E-17
BLOC1S1	-0.776171	4.529E-19	MRPL27	-0.678722	6.193E-18	LOC654342	-1.264024	6.504E-17
LOC144571	-1.462063	5.472E-19	SELM	-1.577535	6.369E-18	CCDC101	-0.707926	6.499E-17
USMG5	-0.888461	5.581E-19	BAD	-0.723296	6.608E-18	RPS27A	-0.934031	6.513E-17
COX6B1	-0.872457	6.59E-19	PRKCDBP	-1.43764	6.594E-18	PSMG4	-0.767491	7.326E-17
SCARNA7	-2.197709	6.734E-19	SSNA1	-0.722509	7.623E-18	C9orf16	-1.009605	7.598E-17
RAB13	-0.938429	6.739E-19	FAM104B	-0.776379	7.878E-18	PGLS	-0.769961	7.614E-17
CCDC107	-0.937649	7.295E-19	RPS17	-0.831958	7.985E-18	SIRT3	-0.57053	8.084E-17
RPS26P11	-1.152752	7.946E-19	UQCRQ	-0.838478	7.951E-18	C19orf24	-0.779721	9.137E-17
SCARNA10	-1.711372	8.234E-19	SHARPIN	-0.691696	8.048E-18	VEGFB	-0.832113	9.257E-17
HTRA2	-0.674267	8.252E-19	THAP7	-0.70119	8.037E-18	AP2S1	-0.646591	9.394E-17
TAF10	-0.852721	8.264E-19	TCEA2	-1.39769	8.455E-18	CBY1	-0.718276	9.987E-17
SNRPF	-0.983921	9.49E-19	EIF5B	-0.832157	8.568E-18	TMEM39B	-0.569177	1.043E-16
NDUFB1	-0.804295	1.005E-18	RPL35	-0.941425	8.648E-18	WDR74	-0.691271	1.136E-16
C22orf40	-0.74093	1.019E-18	ZCRB1	-0.784194	8.837E-18	FIS1	-0.621754	1.342E-16
PSMB6	-0.618886	1.077E-18	RBMX2	-0.786451	9.023E-18	RPL30	-0.758052	1.416E-16
UBA52	-0.709927	1.183E-18	COX16	-0.679068	9.413E-18	NDUFB11	-0.742179	1.429E-16
C7orf59	-0.808875	1.331E-18	TBCA	-0.692105	1.062E-17	RING1	-0.641494	1.442E-16
ATP5J	-0.767271	1.338E-18	TRAPPC5	-0.72133	1.314E-17	HIST1H4J	-1.092409	1.451E-16
ATP5J2	-0.967403	1.555E-18	ZNF428	-0.941003	1.337E-17	C7orf55	-0.82983	1.448E-16
RPL11	-0.78421	1.596E-18	C22orf32	-0.708853	1.388E-17	ZBTB8OS	-0.712261	1.464E-16
ZNF593	-0.967191	1.676E-18	MAF1	-0.594882	1.413E-17	RPAIN	-0.646587	1.464E-16
RPL35A	-0.754671	1.692E-18	HSPB1	-1.491353	1.415E-17	RPL32	-0.77974	1.532E-16
LOC388789	-0.760701	1.815E-18	C14orf153	-0.543988	1.45E-17	TIMM16	-0.812472	1.54E-16
SEC61B	-0.697671	1.872E-18	TIAF1	-1.051419	1.668E-17	CUEDC2	-0.619987	1.536E-16
CCDC72	-0.791294	1.918E-18	ALKBH7	-0.879721	1.663E-17	MYL6B	-1.024188	1.597E-16
RPS9	-0.718728	2.362E-18	PPP1R14B	-0.913239	1.983E-17	C2orf28	-0.55817	1.721E-16
C19orf60	-0.703724	2.479E-18	NOP10	-0.713299	1.996E-17	RNF7	-0.580706	1.895E-16

C17orf89	-0.84827	1.923E-16	ATP5D	-0.819548	9.666E-16	MXD3	-0.794233	3.829E-15
PKIG	-1.1102	2.069E-16	SHFM1	-0.867796	9.763E-16	IDH3G	-0.624943	4.095E-15
RBX1	-0.625432	2.234E-16	ANAPC11	-0.665109	9.82E-16	RWDD1	-0.653031	4.149E-15
RFXANK	-0.609738	2.574E-16	FKBP8	-0.658969	9.817E-16	FAM167B	-0.963932	4.311E-15
FKBP1A	-0.591948	2.569E-16	ZRSR2	-0.846899	9.842E-16	RPL10	-0.752435	4.329E-15
MRPL36	-0.760654	2.702E-16	INO80B	-0.766773	9.82E-16	CCDC92	-0.788836	4.319E-15
C11orf83	-0.780296	2.713E-16	ISCU	-0.555345	1.061E-15	C2orf79	-0.738635	4.648E-15
COMMD4	-0.570305	2.74E-16	ZNHIT1	-0.753117	1.059E-15	COX4I2	-1.113457	5.953E-15
TMEM88	-1.343852	2.833E-16	NT5C	-0.658068	1.077E-15	RPL29	-0.773823	6.124E-15
HRAS	-0.737422	2.876E-16	RNF5	-0.700717	1.082E-15	FAM158A	-0.754978	6.36E-15
COX8A	-0.716904	2.883E-16	SYF2	-0.596019	1.128E-15	ATP5E	-0.84745	6.815E-15
QTRT1	-0.733962	2.964E-16	NDUFA2	-0.629068	1.136E-15	CAMTA1	-0.626591	7.396E-15
SEPW1	-0.858235	3.037E-16	C12orf10	-0.575236	1.147E-15	MDP1	-0.584877	7.453E-15
MEA1	-0.683313	3.032E-16	RPL22	-0.69284	1.195E-15	PLSCR3	-0.698492	7.495E-15
TMSB10	-0.868311	3.037E-16	VAMP2	-0.815282	1.221E-15	NDUFS6	-0.75222	7.919E-15
RPL37	-0.933652	3.2E-16	SNF8	-0.541773	1.287E-15	CUTA	-0.607016	7.909E-15
DPM3	-0.916558	3.257E-16	CYHR1	-0.606948	1.373E-15	NDUFAF2	-0.724219	8.051E-15
GLI4	-0.939354	3.318E-16	CHCHD10	-1.123286	1.374E-15	NFKBIL1	-0.64686	8.051E-15
RPL34	-0.908903	3.488E-16	PFND4	-0.907571	1.402E-15	C20orf199	-0.935137	9.11E-15
CCDC28B	-0.945944	3.554E-16	C8orf59	-0.713087	1.412E-15	MRPS21	-0.859019	9.293E-15
NDUFA12	-0.664809	3.771E-16	TMEM150A	-0.698442	1.447E-15	THYN1	-0.596764	9.478E-15
C11orf31	-0.614543	3.928E-16	LOC729156	-1.61588	1.669E-15	C6orf125	-0.685872	9.879E-15
LYRM4	-0.684922	3.937E-16	UQCR10	-0.724527	1.677E-15	UXT	-0.754921	9.911E-15
MED11	-0.600241	4.228E-16	NAGK	-0.580029	1.981E-15	U2AF1	-0.615337	1.009E-14
COX7C	-0.742216	4.285E-16	C6orf1	-0.825928	1.997E-15	DPM2	-0.663074	1.019E-14
SAT2	-0.744773	4.297E-16	SDR39U1	-0.615213	1.996E-15	C22orf27	-0.835652	1.044E-14
LGALS1	-1.273643	4.421E-16	CCDC56	-0.738521	2.024E-15	NDUFS7	-0.712019	1.045E-14
ASAP1IT1	-1.041728	4.818E-16	MRPL23	-0.741654	2.048E-15	DULLARD	-0.432913	1.044E-14
DPY30	-0.678468	4.975E-16	ZSWIM7	-0.594453	2.092E-15	CCDC73	-1.065436	1.043E-14
NDUFC2	-0.765671	5.184E-16	COX6A1	-0.746175	2.1E-15	RPL36AL	-0.658446	1.056E-14
STX8	-0.661453	5.184E-16	MPV17L2	-0.596356	2.144E-15	DGCR6L	-0.691716	1.091E-14
CDC34	-0.664344	5.289E-16	TSSC4	-0.579488	2.289E-15	FAM100A	-0.641049	1.122E-14
TCEB2	-0.749664	5.509E-16	RPL41	-0.806207	2.304E-15	DBNDD2	-0.660338	1.143E-14
FAM128A	-0.828607	5.803E-16	MRPL54	-0.659311	2.442E-15	C15orf63	-0.825187	1.219E-14
THAP8	-0.833802	5.813E-16	RABAC1	-0.772145	2.549E-15	RPS29	-0.802615	1.246E-14
EMD	-0.618501	5.888E-16	LOC152217	-0.643605	2.939E-15	SCNM1	-0.628272	1.262E-14
IGFBP6	-1.459351	6.49E-16	NEDD8	-0.549593	3.045E-15	TOMM6	-0.685926	1.27E-14
RPS27	-1.419436	6.839E-16	RRAS	-1.071455	3.111E-15	ELOF1	-0.623908	1.295E-14
PCGF1	-0.600092	7.962E-16	RPL15	-0.575899	3.135E-15	ZNF524	-0.750375	1.31E-14
CD99	-0.943332	8.064E-16	SOX18	-1.090731	3.273E-15	RPL23AP32	-1.147108	1.329E-14
GTF2H5	-0.721092	8.263E-16	LDLRAD2	-0.993612	3.363E-15	SNAPC2	-0.699848	1.414E-14
MTCP1NB	-0.735131	8.557E-16	FAM127B	-1.243311	3.359E-15	H2AFJ	-1.020479	1.482E-14
TRMT61A	-0.775953	8.606E-16	AIP	-0.61032	3.448E-15	C9orf119	-0.700287	1.727E-14
CWC15	-0.584699	8.779E-16	PTOV1	-0.646399	3.676E-15	RPL18	-0.740778	1.862E-14
CCDC130	-0.52035	9.172E-16	DNAJC4	-0.71586	3.727E-15	MRPL28	-0.621387	1.87E-14
C11orf51	-0.663918	9.332E-16	LSM7	-0.741708	3.728E-15	EGFL7	-1.152405	2.024E-14

NPF	-1.064734	2.131E-14	ERCC1	-0.553163	6.02E-14	TXN2	-0.534702	1.816E-13
LAGE3	-0.695465	2.234E-14	PSMC1	-0.564404	6.138E-14	C1orf151	-0.63608	1.832E-13
WASH3P	-0.732059	2.356E-14	ITGB1BP1	-0.455395	6.4E-14	ZNF771	-0.707026	1.874E-13
NDUFB2	-0.58904	2.444E-14	TMEM219	-0.513316	6.721E-14	ABHD14A	-0.752424	1.979E-13
ROBLD3	-0.549072	2.629E-14	NRM	-0.719984	6.998E-14	SERF1A	-0.594961	2.017E-13
SRM	-0.702669	2.83E-14	COMMD9	-0.508253	7.079E-14	PIN1	-0.545694	2.037E-13
C14orf179	-0.512776	2.839E-14	ATPIF1	-0.663781	7.465E-14	HINT2	-0.668783	2.116E-13
SNORA48	-1.321843	2.878E-14	NXT1	-0.582922	7.522E-14	PDLIM4	-1.346097	2.262E-13
PLAC9	-1.661964	2.9E-14	LSM10	-0.497724	7.943E-14	PPIG	-0.644372	2.273E-13
MRPL21	-0.741719	2.926E-14	ROM1	-0.873534	7.948E-14	MRPL51	-0.576805	2.501E-13
C11orf74	-0.885492	2.967E-14	LOC643719	-1.210979	8.388E-14	ALKBH6	-0.619697	2.589E-13
MLF2	-0.545584	3.019E-14	MRPL34	-0.616203	8.411E-14	C3orf54	-1.000266	2.646E-13
GUK1	-0.580087	3.033E-14	NDUFS3	-0.515897	8.424E-14	FAM108A1	-0.637581	2.854E-13
RPL31	-0.70642	3.112E-14	RPL27	-0.724016	9.571E-14	TRAPPC3	-0.43205	2.853E-13
INO80E	-0.601484	3.271E-14	COX4I1	-0.622704	9.598E-14	FHL3	-0.899738	2.852E-13
RBPMS	-1.214257	3.31E-14	C1orf35	-0.675394	9.963E-14	C6orf226	-0.796287	2.885E-13
TMEM223	-0.638362	3.338E-14	PIIB	-0.627025	1.011E-13	OAZ1	-0.553429	3.189E-13
HSP90AB4P	-1.276955	3.502E-14	GPX4	-0.784608	1.106E-13	JMJD8	-0.519245	3.205E-13
SYNC	-2.00827	3.59E-14	RPS24	-0.702638	1.145E-13	SSU72	-0.44392	3.23E-13
TCEAL4	-0.946945	3.609E-14	CHCHD5	-0.685735	1.201E-13	C12orf57	-0.85973	3.414E-13
SSSCA1	-0.625936	3.944E-14	NACA	-0.599941	1.224E-13	TRPT1	-0.550327	3.423E-13
NUDT14	-0.840483	4.208E-14	GLRX5	-0.601693	1.302E-13	CHST12	-0.668951	3.462E-13
POLE4	-0.777476	4.273E-14	RAB2B	-0.504261	1.306E-13	DNAJC8	-0.432602	3.577E-13
RPL23	-0.68619	4.558E-14	TUBG2	-0.875626	1.314E-13	CHMP4B	-0.539881	3.923E-13
MRPL41	-0.778575	4.575E-14	SAP18	-0.502209	1.422E-13	NPIPL3	-1.062661	3.95E-13
NDUFB10	-0.585965	4.616E-14	COX7B	-0.744506	1.497E-13	RAB24	-0.579167	4.143E-13
LOC729991	-0.420698	4.643E-14	SNX22	-0.715059	1.583E-13	BUD31	-0.644205	4.223E-13
TIMM8B	-0.677043	4.635E-14	NME3	-0.736895	1.585E-13	C19orf73	-0.845633	4.331E-13
CAPZB	-0.476114	5.069E-14	MANBAL	-0.545264	1.6E-13	PTBP2	-0.845962	4.53E-13
SNRPB2	-0.807863	5.083E-14	SF3A2	-0.713732	1.599E-13	DOHH	-0.709744	5.082E-13
APRT	-0.767069	5.106E-14	SF3B5	-0.540597	1.601E-13	METAP2	-0.488338	5.139E-13
PEF1	-0.406459	5.383E-14	AES	-0.607337	1.604E-13	C19orf20	-0.836004	5.329E-13
DEXI	-0.547532	5.906E-14	SNRPD2	-0.607043	1.679E-13			

Appendix Table S4. The metabolic profiling of SGC7901 cells treated with NC (negative control) or sh-*UHMK1*, or reintroduce ATF4 while knocking down *UHMK1*.

	NC	NC	NC	sh <i>UHMK1</i> -#1	sh <i>UHMK1</i> -#1	sh <i>UHMK1</i> -#1	sh <i>UHMK1</i> -#1 + ov-ATF4	sh <i>UHMK1</i> -# 1+ ov-ATF4	sh <i>UHMK1</i> -# 1+ ov-ATF4
PRPP	1159.84	1485.46	1185.6	621.45	554.58	489.85	2156.8	1920.36	1745.81
IMP	3125.65	3358.74	3096.1	1568.91	2130.21	1423.8	2984.56	2781.59	3005.84
inosine	1984.6	2156.8	2251.41	1152.36	1589.45	1741.23	2236.51	1956.58	2064.25
hypoxanthine	6123.21	5684.98	5894.78	4123.85	4592.36	4325.15	5623.89	5541.56	5398.66
xanthine	5124.3	4769.99	5023.65	3369.89	3001.58	3695.89	4858.12	4456.84	4560.98
xanthosine	4489.5	4005.65	4213.51	3126.55	2810.56	2798.56	3985.65	3884.52	4001.56
AMP	9077.55	9470.67	8671.08	6797.73	6469.05	7250.52	8395.74	8683.68	9037.74
adenine	4156.8	4002.51	3852.13	2213.04	2841.23	2456.12	4415.65	4123.06	4215.98
adenosine	2184.2	2356.14	2258.45	1568.94	1452.13	1389.54	2005.64	2152.32	2265.84
GMP	1457.28	1628.44	1577.81	576.16	493.115	672.945	1342.73	1392.06	1528.115
guanine	3365.8	3120.56	3285.56	3036.51	2856.21	2301.75	3085.69	3451.21	3285.69
guanosine	2214.5	2105.65	2385.78	1125.36	1256.74	1002.36	1986.85	2007.45	2130.54
PHP	5678.91	5786.35	5468.21	4123.15	3641.25	3896.32	4989.56	5436.99	5145.98
P-ser serine	3456.28 11856.23	3366.85 10258.96	3789.56 9856.89	2926.66 12003.64	3211.41 9911.56	3369.56 10423.85	3562.31 11884.21	3489.21 10236.85	3341.22 10089.5
G1P	4156.89	3987.66	4312.3	4412.36	4122.58	4215.69	3906.88	4268.51	4107.25
G6P	6897.56	7542.3	7166.8	7166.23	6945.31	6823.77	7025.68	7356.75	7245.89
F6P	3156.8	3066.5	3323.55	2986.58	3268.52	3125.78	3341.55	3120.56	3004.89
F1,6P	4156.3	4065.7	4321.88	4082.65	4120.36	4256.13	4320.14	3965.87	4128.98
DHAP	2189.74	2068.99	2341.54	2256.4	2013.8	1985.66	2235.4	2356.14	2100.56
2,3BPG	1153.69	995.5	1289.58	1187.66	895.69	1123.58	1389.56	1203.5	1005.46
3PG	5612.3	5513.46	5823.45	6041.23	6120.8	5841.9	6123.89	5741.23	6089.12
2PG	2891.5	3001.2	2744.8	3211.56	2987.45	3004.25	2689.74	2985.46	2741.68
PEP	4015.6	3897.41	4152.36	3685.45	3845.21	4001.23	4123.5	4006.89	3964.58
Pyruvate	11569.23	10054.85	13895.41	13426.57	9687.98	11568.42	12568.98	15462.3	13456.21
6-phosphogluconate	1023.56	956.23	1156.21	982.56	1200.3	1009.85	1156.41	1023.86	1006.24
Ribulose 5P	732.89	885.6	945.21	912.3	745.6	812.3	689.5	758.9	845.9
Ribose 5P	1556.89	1325.89	1645.23	1289.99	1489.56	1541.23	1326.56	1203.65	1185.21
Sedoheptulose 7P	1385.96	1200.56	1156.41	1523.45	1320.5	1286.59	1198.9	1250.4	1352.3
erythrose 4P	986.56	756.8	854.1	659.8	885.69	741.56	841.25	947.65	723.4
xylulose 5P	2156.36	2310.23	1956.24	1856.99	2355.61	2005.85	2251.23	2185.69	1952.31
N-carbamoyl-L-asp artate	1082.13	1236.33	1158.47	761.64	652.79	719.55			
UMP	1952.28	1898.53	2031.42	1471.15	1399.16	1342.95			

Appendix Table S5. Peptides identified by MS of UHMK1 interacting proteins

NCOA3	PEPSc ore	qvalue	ABL1	PEPSc ore	qvalue
K.MSQCTSSTIPSSSQEK.D	6.989	0	K.EIKHPNLVQLLGVCTR.E	6.384	0
R.NVTVTQTPSSGDWGLPN SK.A	6.801	0	R.QVTVAPASGLPHKEEAG K.G	6.251	0
R.AVSLDSPVSVGSSPPVK. N	6.345	0	R.DISNGALAFPLDTADPA K.S	6.08	0
K.TPHDILEDINASPEMR.Q	6.208	0	R.LKPAPPPPAASAGK.A	6.06	0
R.FFSLNDGQSWSQK.R	6.132	0	K.HKLGQGQYGEVYEGVW K.K	5.925	0
K.ESSVEGAENQRGPESK. G	5.973	0	K.LGGGQYGEVYEGVWKK .Y	5.446	0
M.SGLGENLDPLASDSR.K	5.93	0	L.MTGDTYTAHAGAK.F	5.403	0
K.LPCDTPGQGLTCSGEK.R	5.908	0	R.HGGPHCNVFEHEALQR .P	5.399	0
R.HGFVSTHFLQR.E	5.534	0	R.LMTGDTYTAHAGAK.F	5.249	0
R.AYGLADPSTTGQMSG R.Y	5.406	0	K.HSWYHGPVSR.N	4.901	0
K.RKLPCDTPGQGLTCSGE K.R	5.393	0	K.ERGPPEGGLNEDER.L	4.864	0
K.LLQLLTCSSDDR.G	4.837	0	R.PVASDFEPQGLSEAAAR.W	4.819	0
K.LDNSPNMNITQPSK.V	4.783	0	R.INTASDGKLYVSSESR.F	4.682	0
K.LLQNGNSPAEVAK.I	4.536	0	K.ATSLVDAVNSDAAK.P	4.585	0
K.STVNGVSWTNETQR.Q	4.332	0	R.SCSASCVPHGAKDTEWR .S	4.312	0
M.SGLGENLDPLASDSR. R	4.179	0	L.YDFVASGDNTLSITKGE K.L	4.208	0
R.ALGIPELVNQGQALEPK. Q	3.932	0	K.KPVLPAATPK.P	4.079	0
R.KLPCDTPGQGLTCSGEK R.R	3.712	0	K.HPNLVQLLGVCTR.E	3.919	0
K.QDAFQGEAAVMMDQ K.A	3.604	0	W.CEAQTKNGQGW.V	3.771	0
R.FSLADGTIVTAQTK.S	3.417	0	K.NLYTFCVSYVDSIQQMR. N	3.721	0
R.ILHKLLQNGNSPAEVAK. I	3.277	0	R.GAVSTLLQAPLPTK.T	3.55	0
K.DSLGPLLQALDGFLFV VNR.D	3.121	0	E.ALQRPVASDFEPQGLSE AAR.W	3.494	0
K.LFRNPVTNDR.H	3.085	0	R.LATGEEEGGSSSK.R	3.424	0
A.GRMEPMNSNSM.G	3.072	0	K.FPIKWTAPESLAYNK.F	3.325	0

R.NPVTNDR.H	3.022	0	K.NGQGWVPSNYITPVNSL EK.H	3.295	0
R.KLPCDTPGQGLTCSGEEK. R	2.861	0	R.NAAEYLLSSGINGSFLVR .E	3.214	0
R.HDLSGKVVNIDTNSLR.S	2.734	0	K.AGSGAPGGTSK.G	3.139	0
G.SPKIASHQF.S	2.732	0	K.KNEEAADDEVFK.D	3.135	0
K.QQVFQGTNSLGLK.S	2.719	0	R.EAINKLENNLR.E	3.113	0
R.NSSFSQQQFAH.Q	2.628	0	K.TLKEDTMEVEEFLK.E	3.015	0
K.ELQPQVEGVDNK.M	2.555	0	K.LGGGQYGEVYEGVWK. K	2.962	0
R.TFPSNPESFITR.H	2.544	0	K.DIMESSPGSSPPNLTpk.P	2.852	0
K.DTSSITSCGDGNVVK.Q	2.529	0	K.SSTLTSSR.L	2.829	0
R.DGNIVFVSENVVTQYLQY K.Q	2.514	0	R.DTTDVPEMPHsk.G	2.813	0
R.SRELLSHHFR.Q	2.5	0	R.QFDSSTFGGHK.S	2.663	0
R.YLLDRDDPSDALSK.E	2.39	0	K.LRVLGYNHNGEWCEAQ TK.N	2.61	0.001
G.MPMGPDQKY.C	2.336	0	K.RNKPTVYGVSPNYDK.W	2.521	0.001
R.FFSLNDGQSWSQKR.H	2.327	0.002	M.TGDTYTAHAGAK.F	2.442	0.001
H.TLLSNTDATGLEEIDR.A	2.323	0.002	P.ASGLPHKEEAGK.G	2.428	0.001
K.ADVSSTGQGVIDK.D	2.322	0.002	R.VLGYNHNGEWCEAQTK. N	2.328	0.001
K.TISNDDDVQK.A	2.315	0.002	R.KERGPPEGGLNEDER.L	2.327	0.001
R.GHSSLTNSPLDSSCK.E	2.312	0.002	H.KLGGGQYGEVYEGVWK .K	2.27	0.001
K.TPHDILEDINASPEMRQR .Y	2.191	0.002	R.NKPTVYGVSPNYDK.W	2.263	0.002
R.VSSPPNAMMSSR.M	2.116	0.002	R.LATGEEEGGSSSKR.F	2.207	0.002
R.QRYETMQCFALSQPR.A	2.075	0.002	K.GQGESDPLDHEPAVSPL LPR.K	2.158	0.002
H.SPMASSGNTGNHSF.S	2.069	0.002	K.PSNGAGVPNGALR.E	2.14	0.002
K.RHYQEAYLNGHAETPV YR.F	2.037	0.002	S.SVKEISDIVQR.]	2.017	0.002
R.YETMQCFALSQPR.A	2.016	0.002	R.GPPEGGLNEDER.L	2.011	0.002
R.NSLDDLVGPPSNLEGQS DER.A	2.016	0.002	R.RPSLPALHFIK.G	1.968	0.002
N.YGMGQQPDPAFGR.V	2.007	0.002	C.WQWNPSDRPSF.A	1.919	0.002
K.QEDLVNTSVYNILHEED RK.D	2.007	0.004	K.TLKEDTMEVEEFLKEAA VMK.E	1.887	0.002
P.HDILEDINASPEMR.Q	2.005	0.004	R.QVTVAPASGLPHK.E	1.839	0.002
V.SNQDSKSPLGFYCDQNP VES.S	1.997	0.004	R.MERPEGCPEKVYELMR. A	1.763	0.002
K.ESSVEGAENQR.G	1.982	0.004	K.EDTMEVEEFLK.E	1.715	0.006

K.VVNIDTNSLR.S	1.956	0.004	K.GSALGTPAAAEPVTPTS K.A	1.693	0.006
R.LQGQQFLNQSR.Q	1.954	0.004	R.EPPFYIITEFMTYGNLLD YLR.E	1.651	0.006
K.ITAEATGK.D	1.944	0.004	R.SCSASCVPHGAK.D	1.64	0.006
K.QEDLVNTSVYNILHEED R.K	1.936	0.004	K.ATSLVDAVNSDAAKPSQ PGEGLK.K	1.523	
R.SSMRPGFEDIIR.R	1.887	0.004			
A.ISEGVGTSLSTLSSPGP K.L	1.851	0.004			
K.TPHDILEDINASPEM.R	1.844	0.004			
R.AMMEEGEDLQSCMICV AR.R	1.832	0.004			
R.HYQEAYLNGHAETPVY R.F	1.812	0.004			
R.MMDSQENYGSSMGGPN R.N	1.799	0.004			
V.NQQQALEPKQDAFQQQ EA.A	1.773	0.004			
K.SPLGFYCDQNPVSSMC QSNSR.D	1.764	0.004			

SRSF1	PEPSc ore	qvalue	TMSB4X	PEPSc ore	qvalue
R.GGPPFAFVEFEDPR.D	7.6	0	T.QEKNPLPSKETLE	7.112	0
D.PRDAEDAVYGR.D	6.136	0	M.SDKPDMAEIEKFDK.S	6.957	0
R.SGRGTGRGGGGGGGGGAP RGRY.G	5.997	0	K.PDMAEIEKFDKSK.L	6.258	0
R.GGPPFAFVEFEDPRDAEDA VYGR.D	5.708	0	K.PDMAEIEKFDK.S	5.736	0
K.FRSHEGETAYIRVK.V	5.395	0	K.NPLPSKETIEQEK.Q	5.521	0
M.SGGGVIRGPAGNDCR.I	5.222	0	P.SKETIEQEKQAGES.]	5.389	0
R.SHEGETAYIRVK.V	4.793	0	D.KPDMAEIEKFDKSKLK KTET.Q	5.186	0
S.HEGETAYIR.V	4.678	0	M.SDKPDMAEIEKFDKS.K	5.186	0
K.DHMREAGDVCYADVYR.D	4.592	0	E.KNPLPSKETIEQEK.Q	4.532	0
L.KDHMREAGDVCY.A	4.511	0	D.MAEIEKFDKSKLKK.T	4.457	0
A.EDAVYGRDGYDYDGYR.L	4.486	0	D.KPDMAEIEKFDK.S	4.437	0
N.RVVVSGLPPSGSWQDLK.D	4.35	0	D.KPDMAEIEKFDKSK.L	4.426	0
R.TKDIEDVFYKY.G	4.295	0	D.KPDMAEIEKFDKSKLK KTETQEK.N.P	4.424	0
R.TKDIEDVFYKYGAIR.D	4.148	0	D.KPDMAEIEKFDKSKLK KTETQ.E	3.963	0

V.SGLPPSGSWQDLKDHMR.E	4.019	0	M.SDKPDMAEIEKFD.K	3.856	0
M.SGGGVIRGPAGNDCRI.Y	3.987	0	L.PSKETIEQEKQAGES.]	3.843	0
R.DAEDAVYGRDGYDYDGY R.L	3.894	0	M.SDKPDMAEIEKFDKSK L.K.K	3.552	0
R.IYVGNLPPDIR.T	3.876	0	K.KTETQEKNPLPSKETIE QEK.Q	3.091	0
R.RGGPPFAFVEFEDPRDAED AVYG.R	3.5	0	M.SDKPDMAEIEKFDKSK LKK.T	3.019	0
R.GGPPFAFVEFEDPRD.A	3.419	0	D.MAEIEKFDKSKLKKTE. T	2.878	0
R.EAGDVCYADVYRDGTGV VEF.V	3.33	0	P.SKETIEQEK.Q	2.824	0
R.RSEN RVVVSGLPPSGSWQD LKDHMR.E	3.18	0	K.TETQEKNPLPSKETIEQ EK.Q	2.822	0
G.PPFAFVEFEDPRDAEDAVY GR.D	3.016	0	T.ETQEKNPLPSKETIEQE K.Q	2.798	0
R.GGPPFAFVEFEDPRDAEDA VY.G	2.958	0	S.KETIEQEKQAGES.]	2.632	0
R.RGGPPFAFVEFEDPRD.A	2.953	0	D.MAEIEKFDKSKL.K	2.426	0
F.RSHEGETAYIR.V	2.909	0	M.SDKPDMAEIEKFDKSK LKKT.E	2.392	0.002
R.EAGDVCYADVYRDGTGV VEFVR.K	2.828	0	K.TETQEKNPLPSKETIEQ EKQA.G	2.294	0.002
R.EAGDVCYADVYR.D	2.457	0.002	K.NPLPSKETIEQEKQ.A	2.185	0.002
F.AFVEFEDPRDAEDAVY.G	2.455	0.002	M.SDKPDMAEIEKFDKSK LKKTETQE.K	2.156	0.002
T.KDIEDVFIK.Y	2.412	0.002	D.KPDMAEIEKFDKSKL KTE.T	2.022	0.002
R.GGPPFAFVEFEDPRDAED.A	2.201	0.002	A.EIEKFDKSKLKKTE.T	1.937	0.002
F.AFVEFEDPRDAEDAVYGR. D	2.199	0.002	E.TQEKNPLPSKETIEQEK. Q	1.966	0.002
A.GDVCYADVYR.D	2.174	0.002	E.TQEKNPLPSKETIEQEK Q.A	1.944	0.002
R.RSEN RVVVSGLPPSGSWQD LK.D	2.135	0.002	D.KPDMAEIEKFDKSKL. K	1.796	0.002
E.AGDVCYADVYRDGTGVVE FVR.K	2.135	0.002	M.SDKPDMAEIEK.F	1.775	0.002
R.SHEGETAYIR.V	2.113	0.002	M.SDKPDMAEIEKF.D	1.767	0.002
K.YGAIRDIDLKNR.R	2.108	0.002	N.PLPSKETIEQEK.Q	1.703	0.002
N.RVVVSGLPPSGSW.Q	2.088	0.002	P.LPSKETIEQEK.Q	1.607	0.002
R.RGGPPFAFVEFEDPR.D	2.086	0.002	D.KPDMAEIEKFDKSKL K.T	1.599	0.006
N.RVVVSGLPPSGSWQDL.K	2.055	0.002	M.SDKPDMAEIEKFDKSK	1.504	0.006

			LKKTET.Q		
R.DGTGVVEFVRK.E	2.041	0.002	K.TETQEKNPLPSK.E	1.384	0.006
L.PPSGSWQDLKDHMR.E	1.634	0.004	M.SDKPDMAEIEKFDKSK LKKTETQ.E	1.376	0.006
E.DMTYAVRKLD.N	1.619	0.004	M.SDKPDMAEIEKFDKSK L.K	1.374	0.006
Y.VGNLPPDIRTKDIEDVIFY.K	1.6	0.004	T.QEKNPLPSKETIEQEKQ AGES.]	1.279	0.008
I.RGPAGNNDCCR.I	1.593	0.004	[.MSDKPDMAEIEKFDKSK .L	1.27	0.008
R.GGGGGGGGAPRGR.Y	1.576	0.004	D.MAEIEKFDKSKLKKTE T.Q	1.267	0.008
P.PSGSWQDLKDHMR.E	1.553	0.004	K.KTETQEKNPLPSKETI.E	1.254	0.008
Y.AVRKLDNTKF.R	1.525	0.004	T.QEKNPLPSKETIEQEK.Q	1.204	0.008
F.VEFEDPRDAEDAVYGR.D	1.486	0.004	K.LKKTETQEKNPLPSKET IEQEK.Q	1.133	0.008
I.YVGNLPPDIR.T	1.485	0.004			
R.GPAGNNDCCR.I	1.443	0.004			
R.DGYDYDGYR.L	1.404	0.004			
G.SWQDLKDHMR.E	1.396	0.006			
A.DVYRDGTGVVEFV.R	1.391	0.006			
R.RGGPPFAFVEFEDPRDAED AVY.G	1.385	0.006			

HUWE1	PEPSc ore	qvalue	FBXO6	PEPSc ore	qvalue
R.SAATSGAGSTTSGVVSGS LGSR.E	7.202	0	R.NQASSEAQPGQK.H	7.26	0
R.AGSSTPGDAPPAVAEVQ GR.S	6.876	0	K.HGQEEAAQSPYRA.V	7.141	0
R.RQQAATSESSQSEASV R	6.707	0	K.HGQEEAAQSPYR.A	7.113	0
R.RQQAATSESSQSEASV R.R	6.581	0	K.DWDQPVADWK.I	7.102	0
R.SSDPLGDTASNLGSAVD ELMR.H	6.49	0	R.ADCGCTYQLK.V	6.815	0
R.LGSSGLGSASSIQA AVR.Q	6.215	0	R.NQASSEAQPGQKHGQE EAAQSPYR.A	6.803	0
R.SSDPLGDTASNLGSAVD ELMR.H	5.74	0	R.DTQYWAGWYGPR.V	6.757	0
R.LLGPAAADILQLSSSLPL QSR.G	5.161	0	D.LIDLMTLWK.R	6.73	0
R.SHHAASSTTAPT PAAR.S	4.72	0	K.HGQEEAAQSPYRAVVQ	6.677	0

			IF.]		
R.HADHSSLTLGSGSSTR. L	4.702	0	I.LLELFTHVPAR.Q	6.217	0
R.AQC)ETLSPDGLPEEQPQ TTK.L	4.617	0	K.VESLPGAHGTFDPDK. V	6.163	0
R.DLSMSEEDQMMR.A	4.202	0	R.VTNSSIVVSPK.M	6.096	0
R.LLVGNDDVHIAR.S	3.924	0	K.MTRNQASSEAQPGQK. H	5.888	0
K.VSDGGSSTDFK.M	3.777	0	T.RNQASSEAQPGQKHGQ EEAAQSPYRA.V	5.853	0
K.KTPTEAPADCR.A	3.744	0	R.YILFQHGGGR.D	5.847	0
R.SDGSGESAQPPEDSSPPA SSESSSTR.D	3.692	0	K.SQLVDLVAEGYWEELL DTFRPDIVVK.D	4.006	0
K.VPLQGFAALEGMNGIQK .F	3.579	0	R.DLIDLMTLWK.R	3.937	0
K.TPTEAPADCR.A	3.563	0	R.NPCEEDMFAWQIDFN GGDR.W	3.92	0
R.GLQSFVQCQPFER.L	3.503	0	K.AALDSINELPENILLELF THVPAR.Q	2.774	0
R.GSGTASDDEFENLR.I	3.461	0	K.DWDQPVADWKIFYFLR .S	2.629	0.001
R.DLSMSEEDQMMR.A	3.404	0	R.EGFITK.D	2.2	0.001
R.IKGPNAVQLVK.T	3.266	0	K.HGQEEAAQSPY.R	2.176	0.001
R.IVNQPSSLFGSK.S	3.175	0	D.WDQPVADWK.I	1.459	0.001
R.QQQAATSESSQSEASVR R.E	3.106	0	K.AALDSINELPENILLELF. T	1.442	0.001
K.YLQSNNSNWR.W	3.013	0	K.YFVTSYEMCLK.S	1.431	0.001
R.NPDIFTEVANCCIR.I	2.997	0	H.GTFDPDKVKK.Y	1.42	0.001
K.VLLSPDYLPAMR.R	2.886	0	R.EGFITKDWDQPVADWK .I	1.411	0.004
R.ELQLPSMSMLTSK.T	2.616	0	N.SSIVVSPKMTR.N	1.397	0.004
K.ADGTATAPPPR.S	2.614	0	K.RKCLREGF.I	1.396	0.004
K.SILTLSHEPK.V	2.531	0	K.IFYFLRSLHRNLL.R	1.389	0.004
R.HIIEDPCTLR.H	2.496	0	K.RKCLREGFITKDWD.Q	0.974	0.004
R.EMFNPMYALFR.T	2.112	0.001	K.IFYFLRSLHRN.L	0.891	0.004
L.VGNDDVHIAR.S	1.85	0.001	K.VESLPGAHGTFDPDK.K	0.869	0.004
R.NLCYHAQTR.H	1.755	0.001	K.IFYFLRSLHRNLLRNP. A	0.864	0.004
K.YICQKPSIQK.A	1.66	0.001	R.NLLRNPCAEDMFAWQ I.D	0.841	0.008
L.SGNRGVQYTR.L	1.65	0.001	K.VKKYFVTSYE.M	0.757	0.008
R.EMFNPMYALFR.T	1.621	0.001	K.MTRNQASSEA.Q	0.738	0.008
R.LSGNRGVQYTR.L	1.511	0.001	R.LVCSLWRD.L	0.586	0.008

R.DLSMSEEDQMMR.A	1.466	0.001	K.RKCLREGFIT.K	0.581	0.008
R.VLGPAACRNPDI FTEVAN CCIR.I	1.438	0.001	R.NLLRNPCA EEDM.F	0.577	0.008
K.VFPSHFTQQR.T	1.322	0.004	R.SLHRNLL.R	0.538	0.008
R.WCSYSASNNSTIDSAWK. S	1.316	0.004	K.KYFVTSYEMCLKSQ.L	0.516	0.01
R.AIAMSLGQDIPMDQR.A	1.313	0.004	K.VQLASADYFVLAS.F	0.496	0.01
K.TQHNGMNNIIR.L	1.235	0.004	R.GVRYILFQHGG.R	0.494	0.01
K.GLSWQPPPYTPTPR.F	1.226	0.004	K.KYFVTSYEMC.L	0.489	0.01

PICK1	PEPSc ore	qvalue	KCTD1	PEPSc ore	qvalue
K.PMLTDLNTYLNK.A	7.313	0	M.SRPLITRSPASPLNNQG IPTPAQLTK.S	7.112	0
R.AFGDVFSVIGVR.E	6.511	0	K.SNAPVHIDVGGHMYT SSLATLTKYPESR.I	6.986	0
K.TIKPMLTDLNTYLNK.A	6.424	0	R.FSRPCECLVVR.V	6.876	0
K.QGMSLDIVLKK.V	6.387	0	R.FPLNGYCHLNSVQVLE R.L	5.966	0
R.GAAGPLDK.G	6.291	0	K.SNAPVHIDVGGHMYT SSLATLTK.Y	5.551	0
R.AFYELSQTHR.A	6.117	0	K.LLIPDDFK.D	5.436	0
K.KYLDVKFEYL.S	5.645	0	K.SNAPVHIDVGGH.M	5.336	0
R.EPQPAASEAFVK.F	4.993	0	R.LFDGTEPIVLDLTK.Q	4.989	0
L.KVKEMDDEEY.S	4.639	0	K.SLIEEVFPEIGDVMCNS VNAGWNHDSTHVIR.F	4.765	0
K.HVQDIVFQLQR.L	4.513	0	R.GFEIVGSCGGGVDSSQ FSEYVLR.R.E	4.569	0
K.YYNDCYAVLR.D	4.456	0	R.SPASPLNNQGIPTPAQL TK.S	4.502	0
R.LVENMSSGTADALGLSR .A	3.995	0	R.IGRLFDGTEPIVLDLTK. Q	4.231	0
R.AILCNDGLVK.R	3.823	0	K.LLIPDDFKDYTLLEYE AK.Y	4.212	0
R.DADVPIEVDLAHTTLA YGLNQEEFTDGE EEEEEED TAAGEPSR.D	3.646	0	K.YPESRIGRLFDGTEPIV LDLTK.Q	3.963	0
K.VKEMDDEEYSCIALGEP LYR.V	3.631	0	P.ASPLNNQGIPTPAQLTK .S	3.861	0
R.VSTGNYEYR.L	3.584	0	Y.TSSLATLTK.Y	3.711	0
K.FEYLSYCLK.V	3.556	0	K.QHYFIDRDGQMFR.Y	3.658	0
R.DADVPIEVDLAHTTLA Y.G	3.499	0	K.YFQLQPMLLEMER.W	3.541	0

K.EMDDEEYSCIALGEPLY R.V	3.456	0	K.YFQLQPMLLEMERWK. Q	2.963	0
V.STGNYEYR.L	3.446	0	H.MYTSSLATLTK.Y	2.876	0
D.GEEEEEEEDTAAGEPSR. D	3.321	0	R.GFEIVGSCGGGVDSSQ FSEYVLR.R	2.569	0
K.QGMSLDIVLK.K	3.295	0	Q.RGFEIVGSCGGGVDSS QFSEYVLR.R	2.459	0
C.LYIVQVFDNTPAALDGT VAAGDEITGVNGR.S	3.187	0	R.PLITRSPASPLNN.Q	1.019	0.001
R.LVSTMSKYNDYAVL R.D	3.108	0	R.SPASPLNNQGIPTPAQL T.K	1.016	0.001
R.AFGDVFSVIGVREPQPA ASEAFVK.F	20887	0	K.YPESRIGRL.F	0.994	0.001
K.HRLVENMSSGTADALG LSR.A	2.789	0	R.IGRLFDGTEPIV.L	0.988	0.001
L.YIVQVFDNTPAALDGT AAGDEITGVNGRSIKGKTK VEVAKMIQEVKG.E	2.715	0	K.QHYFIDRDG.Q	0.985	0.001
K.MELLDQK.H	2.633	0	R.DGQMFYILNFLRTS.K	0.872	0.002
K.HVQDIVFQLQRLVSTMS K.Y	2.546	0	R.YILNFLRTSKL.L	0.87	0.002
D.GTVAAGDEITGVNGR.S	2.419	0	R.TSKLLIPDDF.K	0.863	0.002
E.YSCIALGEPLYRVSTGNY E.Y	2.356	0.001	K.DYTLLEYEA.K	0.848	0.002
R.GAAGPLDKGGSWCDS.]	1.618	0.001	R.WKQDRETGRFS.R	0.769	0.006
R.DADVPIEVDLAH.T	1.608	0.001	K.QDRETGRFS.R	0.733	0.006
P.AASEAFVK.F	1.594	0.001	R.ETGRFSRPEC.L	0.689	0.006
K.FADAHR.S	1.571	0.001	R.PCECLVVRVAPDLGE. R	0.665	0.006
R.LILRCR.Q	1.507	0.002	R.VAPDLGERITLSGD.K	0.587	0.006
K.LGIPTVPGKVTLQK.D	1.131	0.002	R.ITLSGDKSLIEEV.F	0.546	0.006
K.HRLVENMSSGTADALG LSRAILCNDGLVK.R	1.082	0.002	R.LQQRGFEIVGSC.G	0.455	0.006
K.FADAHRSIEK.F	1.051	0.002	R.RELRRTPRVP.S	0.454	0.006
R.LTIKKYLDVKFEY.L	0.468	0.008			
K.KYLDVKFEYLSYCL.K	0.464	0.008			

PRMT7	PEPSc ore	qvalue	ELAVL1	PEPSc ore	qvalue
R.SPCGDCEGFDVHIMDDMI K.R	6.62	0	T.NYEEAAMAIASLNGYR. L	6.957	0
K.RPELLTNEDLQGR.K	6.515	0	R.TMTQKDVEDMFSR.F	6.899	0
K.RPELLTNEDLQGRK.V	6.359	0	D.IGRTNLIVNYLPQNMTQ	6.781	0

			DE.L		
N.ILVTELFDTTELIGEGALPS YEHAHR.H	6.352	0	M.SNGYEDHMAEDCRGDI GR.T	6.653	0
R.AQVVLSWWDIEMDPEGK. I	6.32	0	K.RSEAEAAITSFNGHKPP GSSEPITVK.F	6.542	0
R.SSYADMLHDKDR.N	6.291	0	K.FAANPNQKNVALLSQ LYHSPAR.R	6.503	0
R.ANPTTGSVEWLEEDEHYD YHQEIAR.S	6.256	0	K.CKGFVMTNYEEAA MAIASLNGYR.L	6.231	0
K.QVSSAACHSR.R	5.638	0	R.TNLIVNYLPQNMTQDEL R.S	5.264	0
R.HLVEENCEAVPHR.A	5.605	0	F.VTMTNYEEAAMAIASL NGYR.L	5.258	0
R.EAEPHPLWEYPCR.S	5.501	0	S.LGYGFVNYVTAK.D	5.224	0
F.WAHSPEEMQWR.D	5.386	0	K.VSYARPSSEVIKDANLY ISGLPR.T	5.073	0
R.FGEINDQDR.TDR.Y	5.36	0	H.SLGYGFVNYVTAKDAE R.A	4.912	0
K.VINKHSTEVTVGPEGDMPC R.A	4.454	0	M.SNGYEDHMAEDCR.G	4.756	0
K.CTMAPFWAHSPEEMQW R.D	4.375	0	K.NVALLSQLYHSPAR.R	4.654	0
R.QMRPVCDCQAHLLWNR R.F	4.341	0	L.IVNYLPQNMTQDEL.R.S	4.61	0
R.TVSYAVEFHPDTGDIIMEF R.H	4.274	0	R.PSSEVIKDANLYISGLPR. T	4.543	0
K.HSTEVTVGPEGDMPCR.A	4.271	0	K.DAERAINLNLRLQSK .T	4.537	0
R.SSYADMLHDK.D	4.269	0	R.GDIGRTNLIVNYLPQNM TQDEL.R.S	3.839	0
R.FGEINDQDR.T	4.267	0	K.NVALLSQLYHSPA.R	3.785	0
R.TAVDQHLGPGAM.V	4.246	0	R.SLFSSIGEVESAKLIR.D	3.718	0
R.SPCGDCEGFDVH.I	3.632	0	F.SSIGEVESAKL.I	3.703	0
K.ANHLEDKINIEK.R	3.575	0	R.VLVDQTTGLSR.G	3.643	0
R.TDRYVQALR.T	3.524	0	V.NYLPQNMTQDEL.R.S	2.771	0
Y.DYHQEIARSSYA.D	3.496	0	R.DKVAGHSLGYGFVNY. V	2.765	0
F.TVESSAASHK.L	3.456	0	N.LIVNYLPQNMTQDEL.R. S	2.75	0
R.FGEINDQDR.TDRYVQALR .T	3.346	0	I.VNYLPQNMTQDEL.R.S	2.713	0
K.ANHLEDK.I	3.314	0	M.FGPFGAVTNVK.V	1.856	0.001
R.RFEPLTSGR.A	2.865	0	K.RSEAEAAITSFNGH.K	1.854	0.001

Y.AVEFHPDTGDIIMEFR.H	2.858	0	N.YLPQNMTQDELR.S	1.843	0.001
R.ATVYAQLVESGR.M	2.841	0	S.LFSSIGEVESAK.L	1.821	0.001
R.IRSPCGDCEGFDVHIMDD MIK.R	2.797	0	R.FSPMGVDHMSGLSGVN VPGNASSGW.C	1.809	0.001
R.SPCGDCEGFDVHIMDDMI KR.A	2.788	0	V.ALLSQLYHSPAR.R	1.801	0.001
R.SSYADMLHDKDRNVK.Y	2.788	0	R.SEAEAAITSFNGHKPPGS SEPITVK.F	1.785	0.001
R.HLVEENCEAVPHRATVY AQLVESGR.M	1.875	0			
H.HLGVEQVFTVESSAASHK .L	1.858	0			

CDKN1B	PEPSc ore	qvalue	ROCK1	PEPSc ore	qvalue
K.TDPSDSQTGLAEQCAGIR K.R	6.589	0	R.TSSNADKSLQESLQK.T	7.123	0
K.VPAQESQDVSGSR.P	6.431	0	R.GLLEEQYFELTQESK.K	6.986	0
R.NLFGPVDHEELTR.D	6.112	0	R.YLSSANPNDNRTSSNA DK.S	6.762	0
R.ANRTEENVSDGSPNAGSV EQTPK.K	6.039	0	R.GHDSEMIGDLQAR.I	6.486	0
K.WNFDFQNHKPLEGK.Y	5.987	0	K.VSQNSQLANEKLSQLQ K.Q	6.354	0
R.TEENVSDGSPNAGSVEQT PK.K	5.876	0	R.YLSSANPNDNR.T	6.216	0
P.AQESQDVSGSRPAAPLIGA PANSEDTHLVDPK.T	5.561	0	K.AFVGNQLPVGFTYYYS NR.R	5.963	0
K.RANRTEENVSDGSPNAGS VEQTPK.K	5.134	0	K.LLDLSDSTSVASFPSAD ETDGNLPESR.I	5.569	0
K.RPATDDSSTQNK.R	4.985	0	R.DMLLLACSQDEQKK. W	5.123	0
K.HCRDMEEASQRK.W	4.17	0	M.STGDSFETRFEK.M	4.962	0
R.KRPATDDSSTQNK.R.A	4.15	0	R.DRGHDSEMIGDLQAR.I	4.853	0
K.VPAQESQDVSGSRPAAPLI GAPANSEDTHLVDPK.T	4.115	0	R.NLESTVSQIEKEK.M	4.561	0
K.WNFDFQNHKPLEGKYEW QEVEK.G	4.088	0	K.AAFEKNINTER.T	3.983	0
R.TEENVSDGSPNAGSVEQT PKKPLR.R	4.067	0	R.IEGWLSVPNR.G	3.654	0
R.DMEEASQR.K	3.308	0	R.MKAEDYEVVK.V	3.261	0
K.WNFDFQNHK.P	3.306	0	K.ESDIEQLRAK.L	2.869	0
R.QAHPKPSACR.N	3.263	0	K.DVEMEPVQAEK.T	2.804	0

F.GPVDHEELTR.D	3.216	0	R.LTDKHQSIEEAK.S	2.747	0
K.YEWQEVEK.G	3.185	0	R.LEQEVNEHKVTK.A	2.713	0
R.PAAPLIGAPANSEDTHLVD PK.T	3.173	0	K.IMKELDEEGNQRR.N	2.316	0
R.KWNFDFQNHKPLEGKYE WQEVEK.G	3.169	0	L.TDKHQSIEEAK.S	1.681	0.001
A.NRTEENVSDGSPNAGSVE QTPK.K	3.146	0	K.MNKEGMVR.C	1.678	0.001
K.GACKVPAQESQDVSGSRP AAPLIGAPANSEDTHLVDPK .T	2.27	0	R.NGVVEEIKR.H	1.67	0.001
R.ANRTEENVSDGSPNAGSV EQTPKKPGLR.R	2.243	0	K.NLTLQLEQESNKR.L	1.662	0.001
R.VSNGSPSLERMDA.R	2.225	0.002	K.QLEEANDLLRTESDTA VR.L	1.645	0.001
R.MDARQAEHPKPSAC.R	2.211	0.002			
K.PSACRNLFPG.V	1.756	0.002			
R.DLEKHCRDMEEASQR.K	1.724	0.002			

Appendix Table S6. Identification of UHMK1-interacting proteins via MS

Swiss-Prot accession no.	Gene Symbol	Protein name	No. of unique peptides (95%)
Q9Y6Q9	NCOA3	Nuclear receptor coactivator 3	66
P00519	ABL1	Tyrosine-protein kinase ABL1	58
Q07955	SRSF1	Serine/arginine-rich splicing factor 1	55
P62328	TMSB4X	Thymosin beta-4	49
Q7Z6Z7	HUWE1	E3 ubiquitin-protein ligase HUWE1	45
Q9NRD1	FBXO6	F-box only protein 6	45
Q9NRD5	PICK1	PRKCA-binding protein	41
Q719H9	KCTD1	BTB/POZ domain-containing protein KCTD1	39
Q9NVM4	PRMT7	Protein arginine N-methyltransferase 7	35
Q15717	ELAVL1	ELAV-like protein 1	33
P46527	CDKN1B	Cyclin-dependent kinase inhibitor 1B	28
Q13464	ROCK1	Rho-associated protein kinase 1	25

Appendix Table S7. Relationship between UHMK1 or p-NCOA3 expression and clinicopathological features of GC patients (n=120)

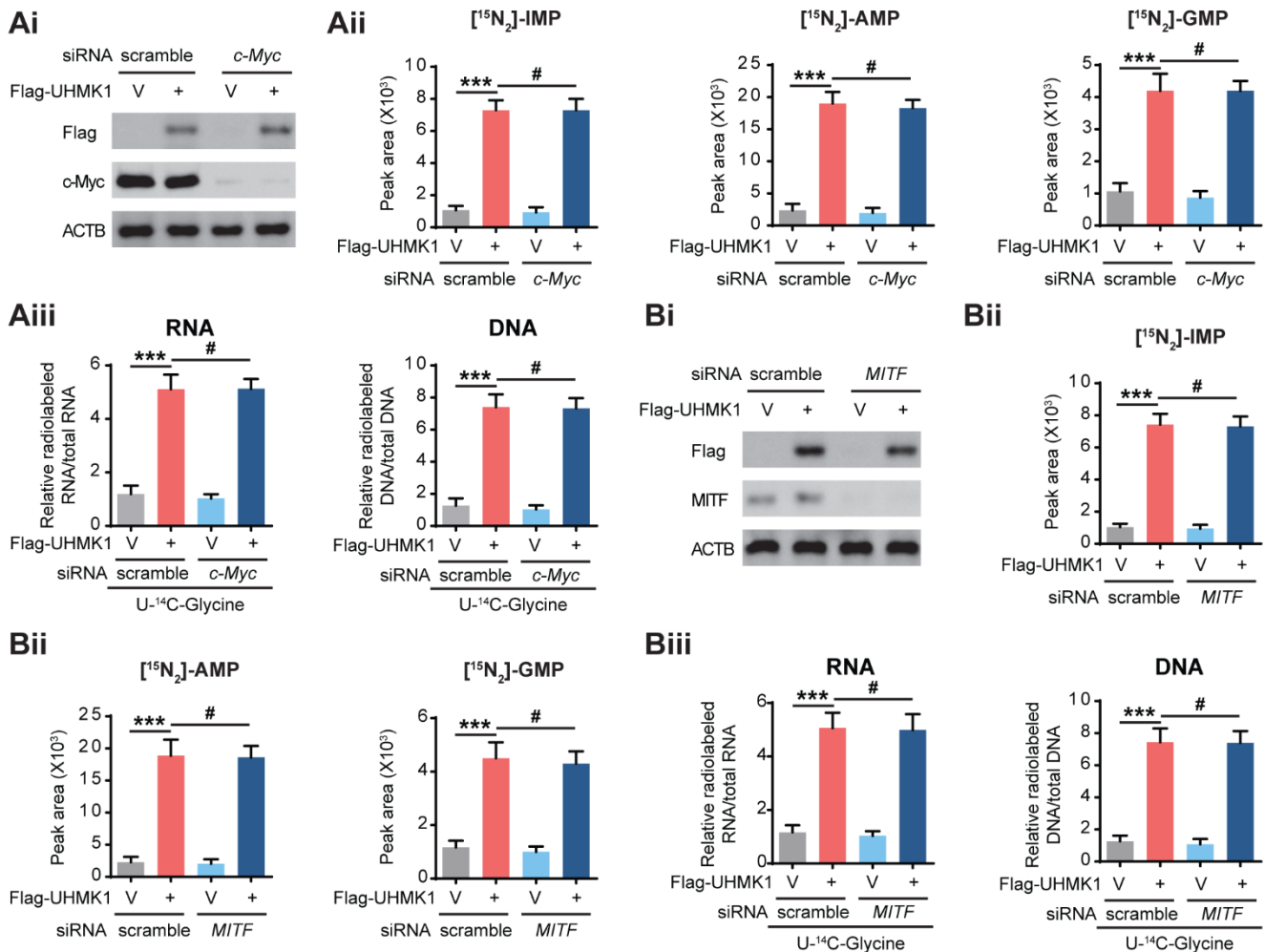
Variable	UHMK1 expression			p-NCOA3 expression		
	Low	High	P value	Low	High	P value
All cases	58	62		63	57	
Gender			NS			NS
Male	35	40		38	37	
Female	23	22		25	20	
Age			NS			NS
≤50	28	24		26	26	
>50	30	38		37	31	
Histological differentiation			NS			NS
Well/Moderately	31	34		33	32	
Poorly	27	28		30	25	
Tumor size			P<0.05			P<0.05
≤5cm	35	25		38	22	
>5cm	23	37		25	35	
Distant metastasis			P<0.05			P<0.05
Yes	8	19		6	21	
No	50	43		57	36	
Tumor stage			P<0.05			P<0.01
I-II	34	23		37	20	
III-IV	24	39		26	37	
Lymphatic invasion			P<0.05			P<0.05
Yes	20	33		22	31	
No	38	29		41	26	
Vascular invasion			NS			NS
Yes	29	28		28	29	
No	29	34		35	28	
<i>H.pylori</i> infection			P<0.05			P<0.01
Yes	25	40		26	39	
No	33	22		37	18	

Note: GC patients were divided into UHMK1 high/low or p-NCOA3 high/low groups according to the analysis of qRT-PCR detection or H-score. NS, not significant between different groups. Differences among variables were evaluated by χ^2 or Fisher's exact χ^2 -test.

Appendix Table S8. Univariate and multivariate analysis of factors associated with survival in GC patients (n=120)

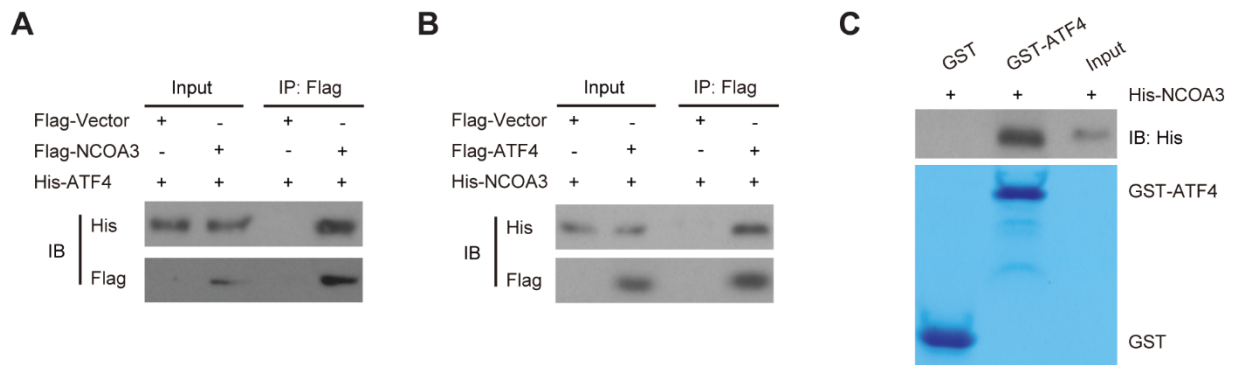
Variable	Univariate analysis		multivariate analysis	
	HR (95% CI)	P-value	HR (95% CI)	P-value
Gender				
Male vs. Female	1.108(0.700-1.754)	0.662		
Age				
≤50 vs. >50	0.999(0.626-1.596)	0.998		
Histological differentiation				
Well/Moderately vs. Poorly	0.906(0.574-1.430)	0.673		
Tumor size				
≤5cm vs. >5cm	2.202(1.271-3.216)	0.003	2.002(1.229-3.262)	0.005
Distant metastasis				
Yes vs. No	2.301(1.404-3.770)	0.001		
Tumor stage				
I-II vs. III-IV	1.765 (1.110-2.805)	0.016		
Lymphatic invasion				
Yes vs. No	1.685(1.069-2.655)	0.025		
Vascular invasion				
Yes vs. No	1.344(0.854-2.114)	0.201		
H.pylori infection				
Positive vs. Negative	2.104(1.311-3.379)	0.002	1.691(1.016-2.814)	0.043
UHMK1 expression				
High vs. Low	2.899(1.777-4.728)	<0.001	1.938(1.141-3.292)	0.014

Appendix Figure S1



Appendix Figure S1. c-Myc or MITF could not reverse UHMK1-driven increase in the purine metabolism intermediates. (Ai) Western blots confirmed UHMK1 overexpression and *c-Myc* knockdown in BGC823 cells. (Aii) Silencing *c-Myc* could not decrease the levels of metabolites as indicated in BGC823 cells overexpressing UHMK1. (Aiii) Silencing *c-Myc* could not decrease the levels of RNA and DNA with U-¹⁴C-glycine in BGC823 cells overexpressing UHMK1. (Bi) Western blots confirmed UHMK1 overexpression and *MITF* knockdown in BGC823 cells. (Bii) Silencing *MITF* could not decrease the levels of metabolites as indicated in BGC823 cells overexpressing UHMK1. (Biii) Silencing *MITF* could not decrease the levels of RNA and DNA with U-¹⁴C-glycine in BGC823 cells overexpressing UHMK1.

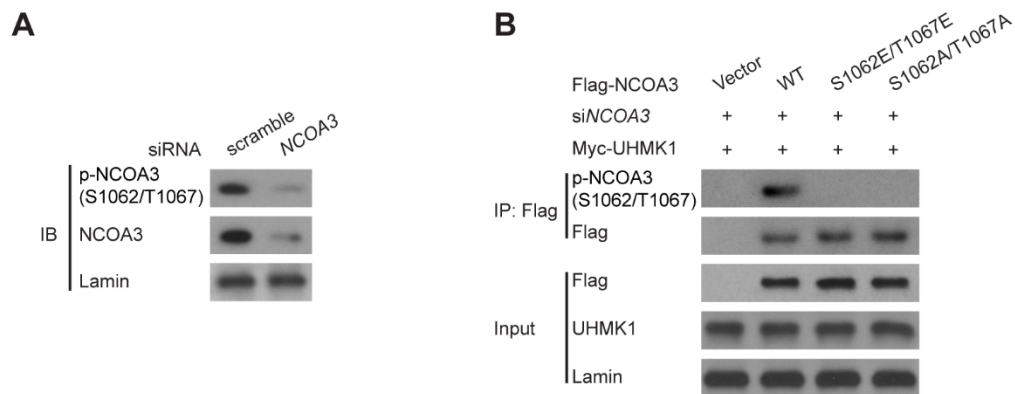
Appendix Figure S2



Appendix Figure S2. Interaction between NCOA3 and ATF4.

(A and B) Co-IP assays were performed in BGC823 cells with indicated plasmids and antibodies. (C) GST-pull down assay with indicated proteins and antibodies.

Appendix Figure S3

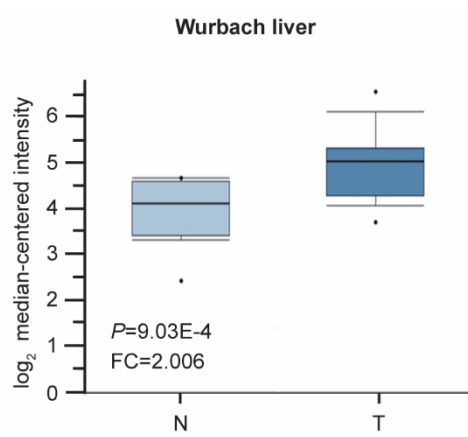


Appendix Figure S3. The validation of the phospho-S1062/T1067 NCOA3 antibody.

(A) *NCOA3* was knockdown by siRNA in SGC7091 cells. Then western blots were performed with a new phospho-S1062/T1067 NCOA3 antibody.

(B) BGC823 cells with endogenous *NCOA3* knockdown were transfected with indicated plasmids and probed with indicated antibodies.

Appendix Figure S4



Appendix Figure S4. Analysis of UHMK1 expression from liver patients in

Oncomine database.