

Supplementary Materials

Supplementary Methods. Expanded description of methods not included in the main manuscript text due to space limitations.

Supplementary Table 1. Proteins associated with FLAG-MTDH were identified by MS.

Supplementary Table 2. mRNAs pull-down by MTDH antibody from Hec50 cells without BEZ 235 treatment were identified by RNA-IP and micro-array.

Supplementary Table 3. BEZ 235 decreases specific mRNAs pulled-down by MTDH antibody identified by RNA-IP and micro-array.

Supplementary Table 4. BEZ 235 increases specific mRNAs pulled-down by MTDH antibody identified by RNA-IP and micro-array.

Supplementary Table 5. Novel mRNAs pulled-down by MTDH antibody were identified by RNA-IP and micro-array from Hec50 cells treated with 100nM BEZ 235.

Supplementary Figure 1. Sub-cellular distribution of MTDH was detected by immuno-staining in endometrial cancer cell lines AN3CA, ECC1, Hec1A, and RL95, and ovarian cancer cell lines PA-1 and SKOV3.

Supplementary Figure 2. Sub-cellular localization of MTDH was detected by different MTDH antibodies.

Supplementary Figure 3. Mutation of kinase phosphorylation sites in MTDH did not alter MTDH sub-cellular distribution.

Supplementary Figure 4. Substitution of kinase phosphorylation sites to alanine in MTDH did not disrupt MTDH association with cytoplasmic proteins SND1 and RPL4.

Supplementary Figure 5. Heat shock did not alter protein expression of MTDH.

Supplementary Figure 6. MTDH is homologous to leucyl- tRNA synthetase. BLAST was used to identify regions of MTDH that possessed homology with other proteins.

Supplementary Figure 7. Putative RNA binding sites were identified in MTDH by three bioinformatics analysis on-line service.

Supplementary Figure 8. Effect of exogenous expression of MTDH on nuclear accumulation of Rad51 in MTDH depleted cells.

Supplementary Materials

Immunostaining—Sub-cellular distribution of endogenous and exogenous MTDH and exogenous MTDH fragments in Hec50 cells was detected by microscopy and electron-microscope using a rabbit antibody against MTDH (a.a. 315-461, Sigma) or FLAG antibody (Sigma). For confocal imaging, nuclei were stained with DAPI (Vector Laboratories). For co-localization studies, cells were co-stained with primary antibodies against MTDH (rabbit) and RPL4 (mouse, Sigma) followed by Alexa Fluor 546-conjugated anti-rabbit and Alexa Fluor 488-conjugated anti-mouse secondary antibodies, then visualized by confocal microscopy.

Establishment of FLAG-MTDH stable cell lines—First, shRNA binding sites (1) were mutated by site-directed mutagenesis without altering the amino acid sequence of MTDH. FLAG-MTDH stable Hec50 cell lines were generated, and then MTDH shRNA was stably expressed as previously described (1) to deplete endogenous MTDH.

MTDH protein co-immunoprecipitation assays—Cell lysates from Hec50-FLAG-MTDH (with mutated shRNA binding site) transfected with MTDH shRNA or parental Hec50 cells were subjected to immunoprecipitation (IP) using agarose conjugated with anti-FLAG antibody (anti-FLAG agarose, Sigma). IPs were eluted using 3xFLAG peptide and separated by SDS-PAGE. The gel was stained with Coomassie blue and five stained bands, which were present only in Hec50-FLAG MTDH IPs but not in Hec50 IPs, were cut and subjected to liquid chromatography tandem mass spectrometry (LC-MS/MS) analysis after in-gel trypsin digestion. For validation, lysates were IPd with control IgG or MTDH antibody, then blotted with anti-RPL4, SND1, or NPM1 (Sigma). The reciprocal was performed using anti-SND1, anti-RPL4, and anti-NPM1 antibodies for IP followed by immunoblotting with anti-FLAG. Where indicated, lysates were treated with benzonase nuclease (50 U/ml, EMD) prior to and during immunoprecipitation (IP).

Reference for Supplementary Materials

1. Meng, X., Brachova, P., Yang, S., Xiong, Z., Zhang, Y., Thiel, K. W., and Leslie, K. K. (2011) *PLoS One* **6**, e20920

Supplementary Table 1. Proteins associated with FLAG-MTDH were identified by MS.

Identified MTDH associated Proteins	Accession Number	band 1 Hi	band 2 hit	band3 hit	band4 hit	band5 hit	Total hit
EBNA-2 co-activator variant	Q59FF0_HUMAN	90	304	9	0	0	403
Nucleophosmin (Nucleolar phosphoprotein B23, numatrin)	D3DQL6_HUMAN	0	0	0	121	2	123
Ribosomal protein L4 variant	Q59GY2_HUMAN (+1)	0	0	70	7	0	77
60S ribosomal protein L6	Q8N5Z7_HUMAN (+3)	0	0	0	23	43	66
Protein LYRIC, MTDH, AEG-1	LYRIC_HUMAN	4	0	14	19	12	49
Serum albumin	ALBU_BOVIN (+1)	11	10	9	11	5	46
Elongation factor 1-alpha 1	EF1A1_HUMAN (+7)	0	0	24	7	5	36
cDNA FLJ10452 fis, clone NT2RP1000966, highly similar to NUCLEOL	B3KM80_HUMAN (+3)	0	0	20	4	4	28
Ig gamma-1 chain C region,	IGH1M_MOUSE (+2)	3	3	5	6	11	28
Annexin A2	ANXA2_HUMAN	0	0	0	0	26	26
Putative uncharacterized protein DBN1	A8MV58_HUMAN (+1)	0	19	2	0	0	21
GIG35	Q53YD7_HUMAN	0	0	21	0	0	21
Ribosome production factor 2 homolog	RPF2_HUMAN	0	0	0	0	21	21
rRNA 2'-O-methyltransferase fibrillarin	FBRL_HUMAN (+1)	0	0	0	0	19	19
AP-2 complex subunit alpha-1	AP2A1_HUMAN	0	18	0	0	0	18
cDNA FLJ54371, highly similar to Serum albumin	B4DPP6_HUMAN	2	3	3	12	2	22
Ribosomal protein L5	A2RUM7_HUMAN (+2)	0	0	0	0	17	17
Eukaryotic translation initiation factor 2 subunit 2	IF2B_HUMAN (+1)	0	0	16	0	0	16
Mc5 VLCL (Fragment)	AON7J3_9MURI	0	0	3	5	7	15
Tubulin beta-7 chain	B7ZAF0_HUMAN (+5)	0	0	15	0	0	15
Eukaryotic translation initiation factor 2 subunit 1	IF2A_HUMAN (+1)	0	0	0	14	0	14
Phosphoribosyl pyrophosphate synthase-associated protein 1 1	KPRA_HUMAN	0	0	0	14	0	14
cDNA FLJ7549, highly similar to Homo sapiens ribosomal protein,	A8K4Z4_HUMAN (+1)	0	0	0	5	8	13
Nuclease-sensitive element-binding protein 1	YBOX1_HUMAN	0	0	13	0	0	13
Heterogeneous nuclear ribonucleoprotein A3, isoform CRA_a	B4DD86_HUMAN (+4)	0	0	0	12	0	12
cDNA, FLJ93570, highly similar to Homo sapiens phosphoribosyl py	B2R7R5_HUMAN (+1)	0	0	0	19	0	19
RNA binding protein, autoantigenic (HnRNP-associated with lethal	Q5QPL9_HUMAN	0	0	0	11	0	11
Putative uncharacterized protein NOP2	A8MQ38_HUMAN (+2)	0	11	0	0	0	11
cDNA FLJ78244, highly similar to Homo sapiens eukaryotic translati	A8K7F6_HUMAN (+2)	0	0	10	0	0	10
52 kDa Ro protein	RO52_HUMAN	0	0	10	0	0	10
Major allergen beta-lactoglobulin	B5B0D4_BOVIN	10	0	0	0	0	10
cDNA FLJ78733, highly similar to Homo sapiens adaptor-related pro	A8K0G3_HUMAN (+4)	0	9	0	0	0	9
Aminoacyl tRNA synthetase complex-interacting multifunctional p	AIMP2_HUMAN (+1)	0	0	0	8	0	8
cDNA FLJ58286, highly similar to Actin, cytoplasmic 2	B4DVQ0_HUMAN (+7)	0	0	2	0	6	8
Alpha S1 casein	B5B3R8_BOVIN (+1)	8	0	0	0	0	8
CDW7/WDR12	Q53T99_HUMAN (+1)	0	0	7	0	0	7
Heterogeneous nuclear ribonucleoprotein A1	Q0VACO_HUMAN	0	0	0	0	7	7
cDNA FLJ78587	A8JZY9_HUMAN (+15)	0	0	6	0	0	6
cDNA FLJ51625, highly similar to Ubiquinol-cytochrome-c reductas	B4DUL5_HUMAN (+1)	0	0	6	0	0	6
cDNA FLJ60713, highly similar to Homo sapiens heterogeneous nuc	B4DMY3_HUMAN (+3)	0	0	0	6	0	6
Serine/threonine-protein phosphatase	B3KXM2_HUMAN (+4)	0	0	0	5	0	5
Heat shock 70 kDa protein 4	B4DH02_HUMAN (+1)	0	5	0	0	0	5
Major vault protein (may act as scaffolds for proteins involved in si	B4DXN0_HUMAN (+1)	0	5	0	0	0	5
Transcriptional activator protein Pur-beta	PURB_HUMAN	0	0	0	5	0	5
cDNA FLJ39996 fis, clone STOMA2002166, highly similar to Splicing	B3KUJ0_HUMAN (+4)	0	0	5	0	0	5
If kappa light chain (Fragment)	A2NHM3_MOUSE (+3)	0	0	0	6	6	12
Heterogeneous nuclear ribonucleoprotein F	B4DKS8_HUMAN (+3)	0	0	4	0	0	4
Butyrophilin subfamily 1 member A1	BT1A1_HUMAN (+2)	4	0	0	0	0	4
Heterogeneous nuclear ribonucleoprotein A0	ROA0_HUMAN	0	0	0	0	4	4
39S ribosomal protein L44, mitochondrial	RM44_HUMAN	0	0	0	0	4	4
Ribosomal protein L14,	A8K7N0_HUMAN	0	0	0	2	2	4
Sperm-associated antigen 10 (Protein HP47).	P783Z8_HUMAN	4	0	0	0	0	4
Putative uncharacterized protein HNRNPA2B1	B8ZZ37_HUMAN (+1)	0	0	0	0	3	3
cDNA FLJ77432, highly similar to Homo sapiens poly(rC) binding pr	A8K7X6_HUMAN (+7)	0	0	0	3	0	3
CDW11/WDR57	A0MNP2_HUMAN (+3)	0	0	0	2	0	2
cDNA FLJ44920 fis, clone BRAMY3011501, highly similar to Heteroge	B3KX72_HUMAN (+5)	2	0	0	0	0	2
Putative uncharacterized protein RCC1	C9J3R0_HUMAN (+8)	0	0	2	0	0	2
Leucine rich repeat containing 59, isoform CRA_	D3DTX8_HUMAN (+1)	0	0	0	0	2	2
Alpha-enolase	ENOA_HUMAN	0	0	2	0	0	2
Translocase of inner mitochondrial membrane 50 homolog	Q0VAB1_HUMAN	0	0	0	2	0	2
Splicing factor, arginine/serine-rich 5 variant (Fragment)	Q59EK7_HUMAN (+1)	0	0	0	2	0	2
Topoisomerase (DNA)	B9EG90_HUMAN (+1)	0	2	0	0	0	2
Elongation factor Tu, mitochondrial	EFTU_HUMAN	0	0	0	2	0	2
Staphylococcal nuclease domain-containing protein 1	SND1_HUMAN	57	0	0	0	0	57
cDNA, FLJ94025, highly similar to Homo sapiens tripartite motif-co	B2R8R5_HUMAN	0	2	0	0	0	2

Supplementary Table 2. mRNAs pulled-down by MTDH antibody from Hec50 cells without BEZ 235 treatment were identified by RNA-IP and micro-array.

Gene Symbol	Ratio(MTDH vs. IgG)
CD109	7.00752
EML1	6.92845
PDCD11	6.76481
ABCA12	6.53697
ELN	6.48163
ATRN	6.43971
NPC1	6.41534
NUP210	6.08822
TACR2	5.95146
PCCB	5.91637
RGS13	5.71245
EML1	5.65916
PCDH7	5.64802
GLG1	5.63337
FASN	5.62332
ANKRD13D	5.50822
KDM6A	5.44271
OGT	5.43334
FANCI	5.34351
BCS1L	5.29098
NEO1	5.22842
CCL20	5.11139
SIAE	5.08112
EPT1	5.02396
OSMR	5.00977

Supplementary Table 3. Association of MTDH with select mRNAs is decreased with BEZ 235 (shown are mRNAs pulled-down by MTDH antibody from BEZ-treated cells).

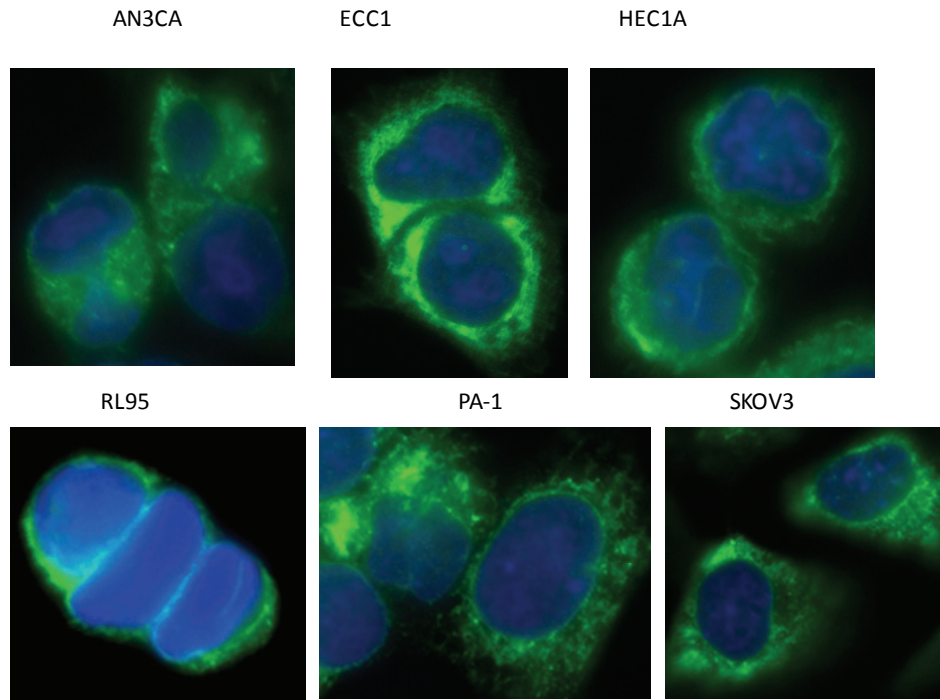
Gene Symbol	MTDH IP (BEZ235/CON)				
		E2F8	-5.60501	BUB1	-2.89757
		EPT1	-5.60175	RNF168	-2.88119
		GNB4	-5.59059	MRE11A	-2.87161
WHSC1L1	-10.7984	GORASP1	-5.58087	HDAC8	-2.86757
TFRC	-8.85908	UBE2E1	-5.57845	RASA2	-2.86034
PTPRD	-8.5142	GATS	-5.55212	RAD18	-2.85759
PCDH15	-8.30018	C12orf43	-5.54671	KLHL13	-2.78522
LMNB1	-8.23591	DEPDC1	-5.54234	APAF1	-2.76614
VPS13A	-8.19292	SLC4A7	-5.47148	DDX21	-2.75191
POLQ	-8.15895	POLQ	-5.35422	FANCD2	-2.69716
TACR2	-7.67065	PLCE1	-5.33904	FNDC3A	-2.68101
SLCO1B3	-7.57798	LIMCH1	-5.32107	AURKA	-2.67645
MMP16	-7.52976	AEBP2	-5.30501	PPP2R1B	-2.67156
MAP3K2	-7.31467	C2CD3	-5.305	FBXW2	-2.66226
SESN3	-7.27753	KIF14	-5.23366	CHD1	-2.65239
ARNTL	-7.24666	HEATR5A	-5.21911	MDM2	-2.64047
SLC7A11	-7.16277	FAM72A	-5.21888	CENPL	-2.62219
VPS45	-7.02886	FER	-5.21436	RAPGEF5	-2.6148
EPT1	-6.79868	BCS1L	-5.18244	SOX6	-2.61104
ASNS	-6.7549	UNKL	-5.18063	TOR1AIP2	-2.5847
CENPK	-6.5074	EGF	-5.17439	GPR111	-2.57092
ISG20L2	-6.48759	GBE1	-5.15837	RAD54B	-2.56937
GCNT2	-6.36049	MAGOHB	-5.13412	WWP1	-2.56054
ZNF271	-6.35852	ZNF431	-5.13284	WDR7	-2.53623
DDX6	-6.35387	ASNS	-5.1291	PPP2R1B	-2.53387
GPD1L	-6.21163	SESN3	-5.11394		
CALML4	-6.07633	GAN	-5.093		
GGH	-6.00909	FBN2	-5.06198		
RAB8B	-6.00786	OR1L4	-5.0556		
CA5B	-6.00749	VAV3	-5.04449		
KLKB1	-5.95345	PLCE1	-5.02442		
ARNTL	-5.92487	CDC7	-5.0231		
IQCG	-5.87833	DDIT4	-4.11335		
RWDD3	-5.86385	FANCC	-3.57742		
SGK2	-5.83207	PPP2R1B	-3.15464		
EXOSC8	-5.7774	FANCA	-3.13919		
ULBP1	-5.73818	MAP2K6	-3.04818		
PACRGL	-5.73031	PPP2R1B	-2.99997		
ERVWE1	-5.71374	DDX21	-2.98607		
NEIL3	-5.68865	PTPRD	-2.94372		
MRS2	-5.65951	DDX60	-2.92042		
RAVER1	-5.6528				
STAG1	-5.62965				

Supplementary Table 4. Association of MTDH with select mRNAs is increased with BEZ 235 (shown are mRNAs pulled-down by MTDH antibody from BEZ-treated cells).

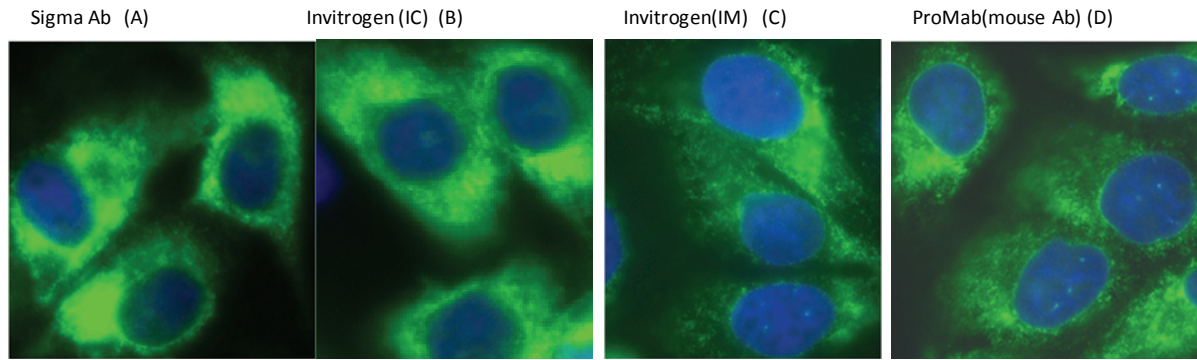
Gene Symbol	Ratio (mRNA MTDH IP BEZ/ mRNA MTDH IP control)		
		EGR1	5.83219
		KIAA1009	5.82788
KCNQ5	12.3383	PLEKHO2	5.79759
RSPO3	11.8322	CPT2	5.77706
SLC38A4	10.929	PRICKLE4	5.70704
TBC1D2B	9.37971	SQSTM1	5.70667
CENPJ	9.23572	WNK2	5.56743
MNT	8.61378	SPEF2	5.49133
MRPL39	7.97101	MAP3K12	5.45006
CCT4	7.9652	SPRED2	5.4444
SLC22A18AS	7.76626	CLMN	5.43711
GRID1	7.72989	ANKRD26P1	5.4345
IRS2	7.15201	HP1BP3	5.33552
CD22	7.14514	ABCC3	5.18356
NEB	7.10863	CTGF	5.17795
OBSCN	7.08271	PHF16	5.16807
ZXDC	6.84005	WDR78	5.1489
OR8G5	6.70385	SYNE1	5.1485
ZNF559	6.5299	CTGF	5.14518
TUBB3	6.35006	PSIP1	5.13023
SYNE1	6.34444	COL4A4	5.12833
IPO9	6.27475	CARD8	5.12567
ESAM	6.14151	EGR1	5.11289
FAM184A	6.12357	ICA1L	5.10882
AGAP3	6.01132	IL2RB	5.10508
WDFY2	5.98711	DMTF1	5.08483
DSP	5.90057	DNAH5	5.01425

Supplementary Table 5. mRNAs that associate with MTDH in response to BEZ235.

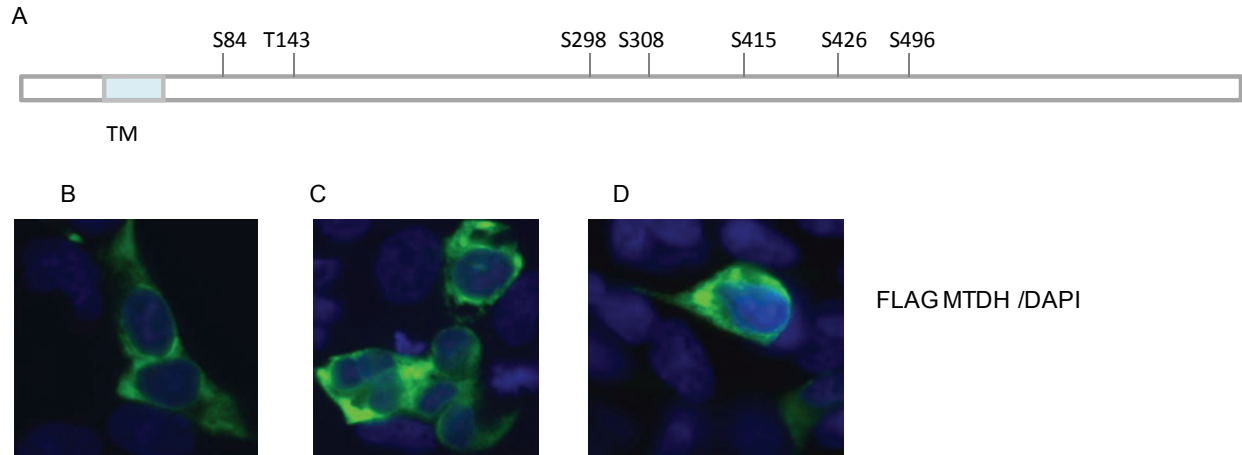
Gene Symbol	MTDH IP BEZ/ control				
CCT4	17.6824	FN1	7.6011	THBS1	6.10022
METTL3	13.1633	DOPEY2	7.44994	PKN1	6.06818
ADCK2	13.1461	LOXL4	7.25585	AXL	6.02808
STXBP1	12.5594	PLD2	7.24358	MRC2	6.00122
CYFIP2	12.3147	SYNE1	7.12225	PLXNA3	5.9912
OBSCN	12.3114	HSPG2	7.11081	CRIM1	5.97827
CUL7	12.243	ITPR3	7.07262	TENC1	5.90554
AGAP3	12.161	CAPN2	7.06472	CTSB	5.88552
MMP2	11.7531	FLNC	7.06392	FCGRT	5.88257
NXF4	11.5469	TBCD	6.96941	MEGF11	5.86673
RYR1	11.4929	IL17RA	6.94854	CLDN2	5.86656
ESAM	10.9454	FLJ10357	6.94183	RAB24	5.85921
FLNA	10.824	STEAP3	6.91527	ANPEP	5.83928
TINAGL1	10.5983	NPR1	6.86481	EPHB1	5.83916
OBSCN	10.584	PLAT	6.77802	ABTB1	5.83009
CD22	10.4167	PPFIA2	6.7256	SDK1	5.81669
C11orf2	10.1924	SEZ6L2	6.7106	TENC1	5.80064
KCNH1	9.27805	NFKB2	6.61153	HSPG2	5.7657
EPHX2	9.21181	RNF123	6.61094	COL13A1	5.7642
VIM	9.06607	HERC5	6.60355	SPTBN5	5.74575
LRP1	9.05996	CCNDBP1	6.58892	LRIG3	5.73658
C11orf2	9.02773	RIN1	6.5688	MYL5	5.73581
COL6A1	8.93019	EPHX2	6.55253	FAM194B	5.73267
ITGB5	8.90311	ACTN1	6.51458	SH2B2	5.7166
CRIM1	8.47412	CYP27A1	6.49935	CDC14B	5.7102
ABCC3	8.42694	DUSP5	6.49217	ANPEP	5.69929
GPR124	8.37152	TEP1	6.48857	THBS1	5.69559
TRPC4AP	8.22144	GRID1	6.47752	MRC2	5.69533
RIN1	8.19444	MLPH	6.43776	MCM6	5.69252
HSPG2	8.1707	TTC15	6.41007	CLCN7	5.66976
MLL4	7.9759	GHDC	6.39285	PLEC	5.65909
SSH3	7.96339	MYH9	6.36282	RNF213	5.63485
LAMA5	7.91698	ARRDC1	6.35115	WDR81	5.63224
CTGF	7.88025	THSD4	6.35014	IKBKB	5.61907
STEAP3	7.77414	TBCD	6.2677	JAG1	5.61028
DOCK2	7.73778	RIPK1	6.24573	STK25	5.60992
LDLRAD2	7.7347	LRP5	6.21532	BCAS3	5.60442
ERCC2	7.70418	SGSM2	6.20579	CUL9	5.59638
EGFR	7.67947	ALOX5	6.19131	NOTCH3	5.58937
HACE1	7.63202	PWP2	6.18062	CYP4V2	5.57733
		ECE1	6.17497	HSPG2	5.56929
		PTHLH	6.16107	TCIRG1	5.5547
				ARNT2	5.54149



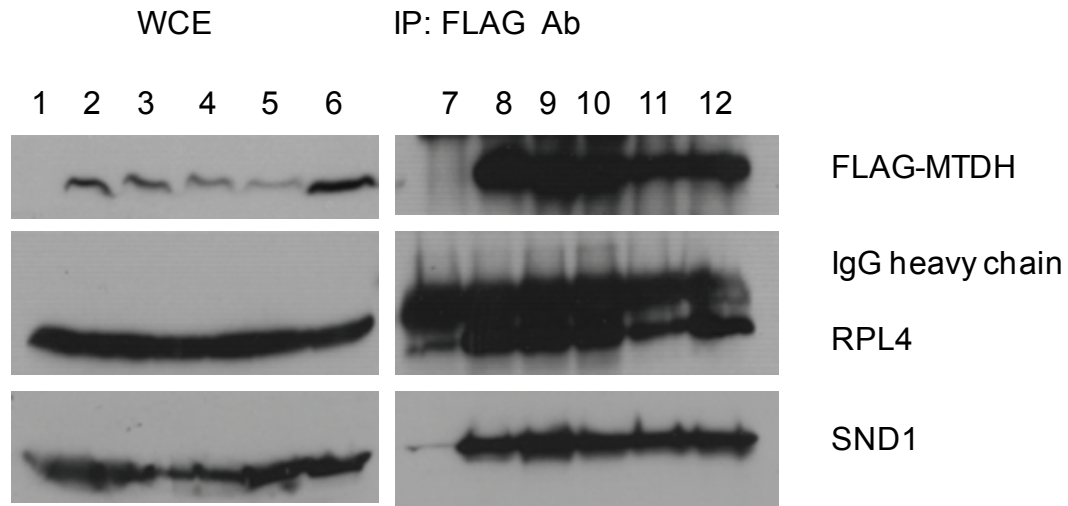
Supplementary Figure 1. Sub-cellular distribution of MTDH was detected by immuno-staining in endometrial cancer cell lines AN3CA, ECC1, Hec1A, and RL95 and ovarian cancer cell lines PA-1 and SKOV3.



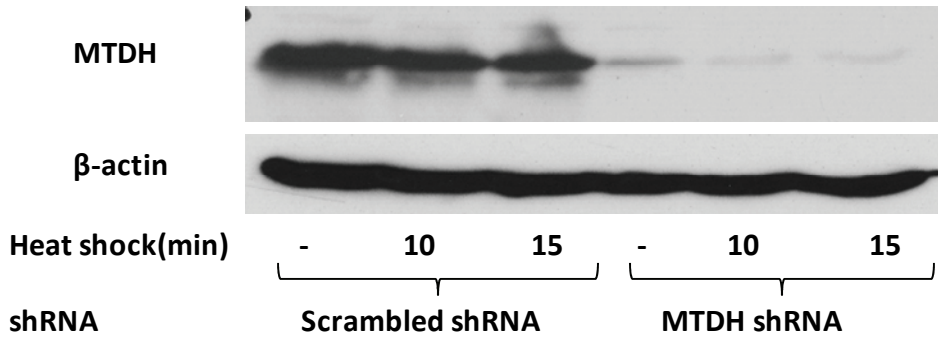
Supplementary Figure 2. Sub-cellular localization of MTDH was detected by MTDH antibodies including rabbit Abs against MTDH 315-461 from Sigma (A), MTDH internal region (B), and C-terminal region from Invitrogen (C), and mouse anti-MTDH antibody 2F11C3 from ProMab (D).



Supplementary Figure 3. Mutation of kinase phosphorylation sites in MTDH did not alter MTDH sub-cellular distribution. (A) Schematic representation of MTDH highlighting the different phosphorylation sites. Sub-cellular distribution of FLAG tagged MTDH mutated at T143A, S415A, S84A, S308A (B), MTDH mutated at S298A S496A S426A (C), or MTDH mutated at S84A T143A (D) was detected by immuno-staining with FLAG antibody. Several phospho-proteomic studies have identified MTDH phosphorylation on seven sites (S84, T143, S298, S308, S415, S426, and S496). All the seven phosphorylation sites of MTDH have been confirmed in mammalian cells. The data can be found in the following two websites and the following references: <http://www.phosphonet.ca/> ; <http://www.phosphosite.org/> ; T143: Dephoure et al. PNAS 2008, 105:10762; S298: Villén et al. PNAS 2007, 104:1488; S84, S308, S415, S426: Olsen et al. Cell 2006, 127:635; S496: Olsen et al. Sci Signal 2010, 3:ra3.



Supplementary Figure 4. Mutation of known phosphorylation sites in MTDH to alanine did not disrupt MTDH association with cytoplasmic proteins SND1 and RPL4. Left panel: Expression of FLAG-tagged MTDH, RPL4, and SND1 in whole cell protein extracts (WCE). Right panel: Immunoprecipitation with FLAG antibody M2. Lanes 1,7: control Hec50; lanes 6,12: Hec50 cells expressing wild-type FLAG-MTDH; lanes 2, 8: MTDH mutated at T143A,S415A, S84A, S308A; lanes 3, 9: MTDH mutated at S298A S496A S426A; lanes 4, 10: MTDH mutated at S84AT143A; and lanes 5, 11: MTDH mutated at S78A(5,11).



Supplementary Figure 5. Heat shock does not alter MTDH protein levels. Expression of MTDH was detected at control or 10min/15min after heat shock in scrambled shRNA and MTDH shRNA expressing cells.

GENE ID: 1443290 leuS | leucyl-tRNA synthetase

MTDH	92	AAAVPAAAPDDLALLKNLRSEEQKKKNRKKLSEKPKPNGRTVE-VAEGEAVRTPQSVTAK	150
		+VPA AP D L++L+ E + + EK + R VE + ++	
leuS	322	VMSVPAHAPFDHVALEDLKRETE-----ILEKYDIDPRIVENITYISLIKLEGYGDFP	374
MTDH	151	QPPEIDKKNEKSKKNKKKSKSDAKAVQNSSRHG	184
		E++K KS+K+K+K + K + + H G	
leuS	375	AVEEVNKLGIKSQKDKLEQATKTIYKAEYHKG	408

Supplementary Figure 6. MTDH is homologous to leucyl- tRNA synthetase. BLAST was used to identify regions of MTDH that possessed homology with other proteins.

Sequence: STEPSVILSKSDSDKSSSQVPPILQETDKSKSNTKQNSVPPSQTKSETSWESPKQIK
 Prediction: -----++-+++-----++++++-+-++++-----++-+
 Confidence: 013316461871898800173489331089999998072707899710003217719

Sequence: KKKKARRET
 Prediction: ++++++--
 Confidence: 99999911

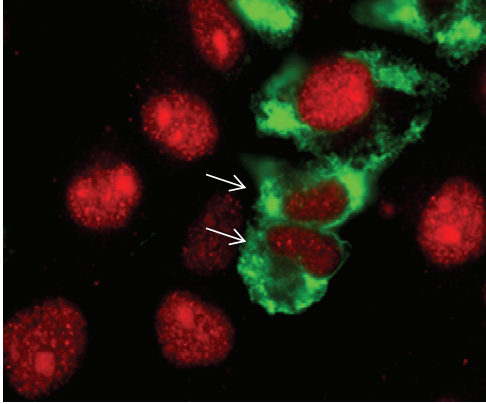
*** Prediction: binding residues are labeled with '+' and in red;
 non-binding residues labeled with '-' and in green.
 *** Confidence: from level 0 (lowest) to level 9 (highest).

PIRaNha Prediction Result

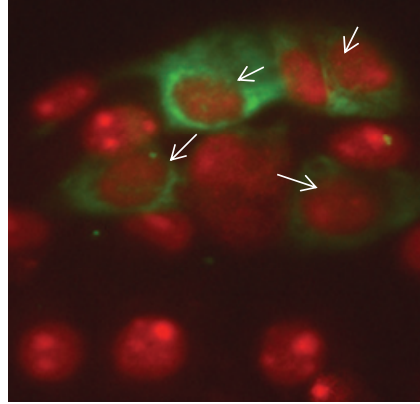
(<http://bioinformatics.sussex.ac.uk/PIRANHA/>)

0001 - 0050 : MAARSWQDEL AQAEEGSAR LREMLSVGLG FLRTELGLDL GLEPKRYPGW
 0051 - 0100 : VILVGTGALG LLLLFLLGYG WAAACAGARK KRRSPPRKRE EAAAVPAAAP
 0101 - 0150 : DDLALLKNLR SEEQKKNRK KLSEKPKPNG RTVEVAEGEA VRTPQSVTAK
 0151 - 0200 : QPPEIDKNE KS~~KKN~~KKKSK SDAKAVQNSS RHDGKEVDEG AWETKISHRE
 0201 - 0250 : KRQQRRDKV LTDSGSLDST IPGIENTITV TTEQLTTASF PVGSKKNKGD
 0251 - 0300 : SHLNVQVS NF KSGKGDSTLQ VSSGLNENLT VNGGGWNEKS VKLSSQISAG
 0301 - 0350 : EEKWSVSPA SAGKRKTEPS AWSQDTGDAN TNGKDWGRSW SDRSIFSGIG
 0351 - 0400 : STAEPVSQST TSDYQWDVSR NQPYIDDEWS GLNGLSSADP NSDWNAPAE
 0401 - 0450 : WGNWVDEERA SLLKSQEPIP DDQKVSDDDK EKGEALPTG KSKKKKKKKK
 0451 - 0500 : KQGEDNSTAQ DTEELEKEIR EDLPVNTSKT RPKQEKAFLS KTISTSDPAE
 0501 - 0550 : VLVKNSQPIK TLPPATSTEP SVILSKSDSD KSSSQVPPIL QETDKSKSNT
 0551 - 0600 : QNSVPPSQT KSETSWESPK QIKKKKARR ET

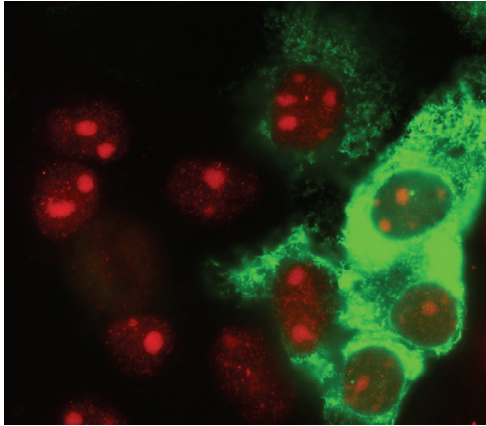
Hec50/ MTDH shRNA MTDH (1-582)



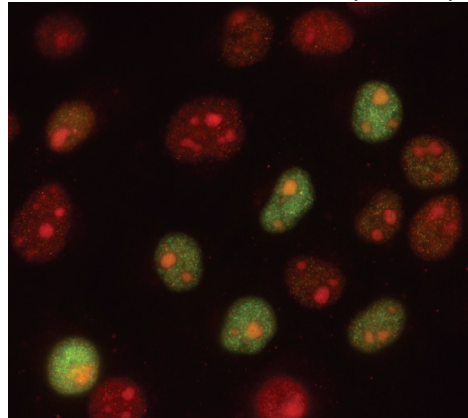
Hec50/ MTDH shRNA MTDH (1-471)



Hec50/ MTDH shRNA MTDH (1-300)



Hec50/ MTDH shRNA MTDH (471-582)



Supplementary Figure 8. Effect of exogenous expression of MTDH on nuclear accumulation of Rad51 in MTDH-depleted cells. Transient expression of exogenous full length MTDH or MTDH fragment (1-471) caused the reduction of Rad51 specific accumulation in the nuclei (marked by arrows). Transient exogenous expression of MTDH (1-300) and MTDH (471-582) did not affect Rad51 accumulation in the nuclei. MTDH: green; Rad51: red.