# The human Obg protein GTPBP10 is involved in mitoribosomal biogenesis

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#### SUPPLEMENTARY DATA

#### Table S1: Interactome of GTPBP10

Related to Table 1.

#### Figure S1: Sequence alignment of Gtpbp10-WT and *Gtpbp10<sup>64K65R</sup>* mutant

Genomic DNA (gDNA) or RNA were isolated from wild type and *Gtpbp10<sup>64K65R</sup>* mutant HEK293T cell lines. PCR amplicons from the respective gDNA or generated cDNA covering the guide RNA region were sequenced and analyzed using Geneious.

#### Figure S2: Expression titration of GTPBP10<sup>FLAG</sup>

HEK293T cells expressing GTPBP10FLAG were induced with different concentration of tetracycline as indicated. Protein extracts were analyzed by immunoblotting. Relative expression level of GTPBP10 was compared to endogenous GTPBP10 of HEK293T WT cells.

#### Figure S3: Co-immunoprecipitation of uL1m

Isolated mitochondria from HEK293T WT and *Gtpbp*<sup>64R65K</sup> cells were lysed and subjected to coimmunoprecipitation using uL1m antibodies and control IgGs. Protein complexes were eluted via pHshift and analyzed by western blotting. Total, 5%; Eluate, 100%.

#### Table S1: Interactome of GTPBP10

Related to Table 1.

Protein	Gene	Maiority protein IDs	mean	p-value
	names	·····	ratio	P
GTPBP10	GTPBP10	A4D1E9 C9 JEQ8 C9 J8R7 C9 JNI1	5 677	0.000129
SMCR7I	SMCR7I	10B8E8	4 681	0.000155
bl 20m	MRPI 20	O9BYC9	4 525	0.000259
ml 44	MRPI 44		4.020	0.000266
111244 ul 15m			4.435	0.000200
mL 52	MDDI 52		4.440	0.000303
hl 01m		Q772W0:D4DXI4:A0A024DEC7:FEU7//9	4.407	0.000207
DL21111		Q722W9,B4DX14,A0A024R5G7,F5H7V6	4.427	0.000293
DL2/m	MRPL27		4.425	0.000274
ML65	MRPS30		4.421	0.000328
mL49	MRPL49	A0A024R578;Q13405;H0YDP7;E9PNF1;Q59GE9	4.415	0.000286
mL63	MRP63;	A0A024RDM4;Q9BQC6	4.408	0.000313
	MRPL57			
uL13m	MRPL13	Q9BYD1;E5RJI7	4.400	0.000305
mL42	MRPL42	S4R360;J3KPP0;A0A024RBG3;S4R2Z7;Q9Y6G3	4.393	0.000335
mL50	MRPL50	Q8N5N7	4.385	0.000324
MTERF4	MTERF4	Q7Z6M4;B4DFP7;C9JNJ7;B4DKD5;H7C316	4.377	0.000310
uL4m	MRPL4	A0A024R7C5;Q9BYD3;K7ES61;X6RAY8;K7ELQ0	4.372	0.000323
mL43	MRPL43	H0Y6Y8;B1AL05;Q8N983;H0YBU8	4.372	0.000300
uL30m	MRPL30	Q8TCC3	4.371	0.000341
uL18m	MRPL18	A8K9D2:Q9H0U6	4.369	0.000301
ml 38	MRPI 38	Q96DV4	4 334	0.000325
ul 14m	MRPI 14	A0A024RD78-06P1L8	4 330	0.000336
		096EH3	4 295	0.000377
ml 45	MPDI 45		4.284	0.000400
ul 11m		00V3P7:053C10	4.204	0.000408
uLIIII bl.29m			4.200	0.000408
	MDDL 54		4.200	0.000429
mL51	MRPL51		4.228	0.000416
mL00	MRPS18A		4.224	0.000439
bL19m	MRPL19	A8K5D5;P49406;B4DIG4;S4R3W9	4.197	0.000453
bL17m	MRPL17	Q9NRX2;E9PKV2	4.157	0.000491
bL35m	MRPL35	Q9NZE8;D3YTC1	4.151	0.000512
uL3m	MRPL3	H0Y9G6;E7ETU7;P09001;B4DKM0;B4DW56;D6RC14;E9PF0	4.131	0.000546
		6		
uL2m	MRPL2	Q5T653;A0A024RD44	4.122	0.000526
uL29m	MRPL47	Q9HD33	4.106	0.000613
DDX28	DDX28	Q9NUL7	4.104	0.000548
mL41	MRPL41	Q8IXM3	4.102	0.000602
uL24m	MRPL24	Q96A35;X6RJ73	4.101	0.000573
mL39	MRPL39	Q9NYK5;C9JG87	4.066	0.000609
uL23m	MRPL23	A0A024RCB2;Q16540;B2R9J4;A6NJD9;A8MVT4;A8MYK1;H	4.052	0.000632
		7C2P7		
uL16m	MRPL16	Q9NX20;E9PI14	4.040	0.000663
uL1m	MRPL1	A0PJ79;Q9BYD6;H0Y8N7	3.991	0.000790
bL12m	MRPL12:	P52815:Q96Q74	3.980	0.000821
	MRPL7/			
	L12			
mL54	MRPL54	Q6P161	3.944	0.000808
uL22m	MRPL22	E7ESL0:J3KQY1:Q9NWU5	3.929	0.000845
ml 53	MRPI 53	Q96FL3	3 910	0.000885
ml 64	GADD45		3 888	0.000978
111201	GIP1		0.000	0.000010
bl 32m	MRPL 32		3 877	0.001055
ml 62	ICT1	J3KS15:014197	3 868	0.001742
hl 34m	MPDI 24		3 851	0.001102
	NSUNA		3.001	0.001102
ml 27	MDDI 27		2.001	0.001023
hL 20m		Q9DLE 1,34K309	3.0//	0.001508
	IVIKPL33		3.507	0.002385
TRUB2		AUAU24K886;U95900	3.361	0.003298
YARS2	YARS2	Q9Y2Z4;H0YHS6	3.325	0.003652
bL9m	MRPL9	Q9BYD2;Q5SZR1	3.244	0.004687
uL10m	MRPL10	B4DEH0;Q7Z7H8	3.238	0.005836
NGRN	NGRN	Q9NPE2	3.186	0.005129
RNMTL1	RNMTL1	Q9HC36;I3L443	3.132	0.005932
GTPBP7	MTG1	A8K900;U3KQ69;E9PI62;Q9BT17;B4DF93;B3KWF9;E7EVK2	3.130	0.005905
PTCD1	PTCD1;	Q3ZB84;A4D273;G3V325;B4DJ38;O75127;B3KMD7;Q3SYP6	3.103	0.006355

	ATP5J2- PTCD1			
FASTKD2	KIAA0971; FASTKD2	A0A024R419;Q9NYY8;B3KMB8	3.039	0.007697
WBSCR16	WBSCR16	Q96I51;B2RXG5	2.978	0.008737
SUPV3L1	SUPV3L1	Q8IYB8;B7Z611	2.955	0.009437
MTERF3	MTERF3/ MTERFD1	Q96E29;E5RIK9;E5RIY4	2.895	0.012104
mL46	MRPL46	Q9H2W6	2.876	0.011337
mL48	MRPL48	Q96GC5;F5H702;F5H8D0	2.862	0.011761
bL31m	MRPL55	A0A024R3R0;Q7Z7F7	2.854	0.012008
mL40	MRPL40	Q9NQ50	2.800	0.014138
TRMT61B	TRMT61B	Q9BVS5;F8WDR2	2.641	0.021453
RPUSD4	RPUSD4	A0A024R3K2;Q96CM3;B4DUN4	2.563	0.029822
mtHSP70	HEL-S- 124m; HSPA9	B7Z4V2;V9HW84;P38646;Q8N1C8;B7Z4T3;B7Z1V7	2.561	0.025818
RPL22L1	RPL22L1	C9JYQ9;H0Y8C2;Q6P5R6	2.559	0.026083
PNPT1	PNPT1	Q8TCS8	2.352	0.045804
PMPCA	PMPCA	Q10713;B4DRK5	2.344	0.046558



**Figure S1: Sequence alignment of** *Gtpbp10-WT* and *Gtpbp10*<sup>64K65R</sup> **CRISPR mutant** Genomic DNA (gDNA) or RNA were isolated from wild-type and *Gtpbp10*<sup>64K65R</sup> mutant cell lines. PCR amplicons from respective genomic DNA or generated cDNA covering the guide RNA region were sequenced and analysed using Geneious.

# WT GTPBP10<sup>FLAG</sup> 0 0 0.1 1 5 10 25 50100 Tet [ng/ ml] - GTPBP10<sup>FLAG</sup> - COX2 - SDHA

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