Human mtRF1 terminates COX1 translation and its ablation induces mitochondrial ribosome-associated quality control

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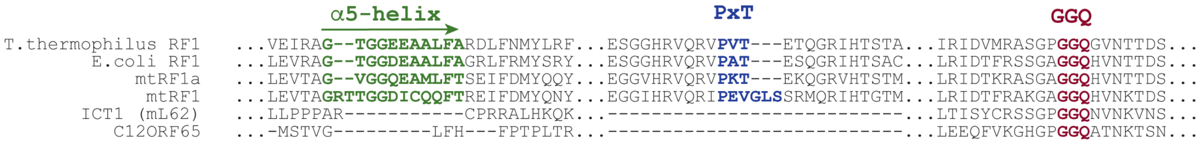
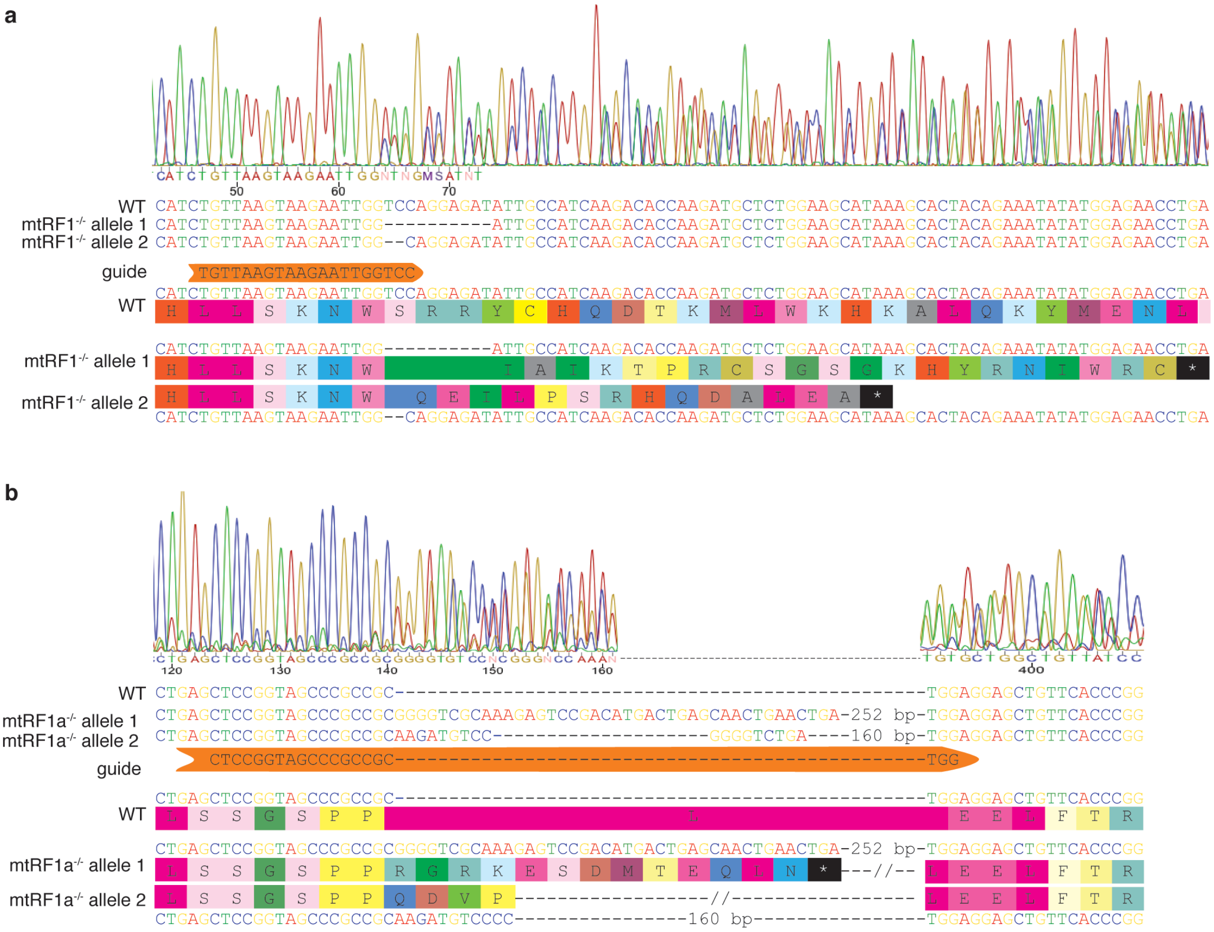
Supplementary information

Supplementary Figures



```
T.thermophilus RF1   ...VEIRAG--TGGEEAALFARDLFNMYLRF...ESGGHRVQRVPVT---ETQGRIHTSTA...IRIDVMRASGPGGQGVNTTDS...
        E.coli RF1   ...LEVRAG--TGGDEAALFAGRLFRMYSRY...ESGGHRVQRVPAT---ESQGRIHTSAC...LRIDTFRSSGAGGQHVNTTDS...
           mtRF1a    ...LEVTAG--VGGQEAMLFTSEIFDMYQQY...EGGVHRVQRVPKT---EKQGRVHTSTM...LRIDTKRASGAGGQHVNTTDS...
            mtRF1    ...LEVTAGRTTGGDICQQFTREIFDMYQNY...EGGIHRVQRIPEVGLSSRMQRIHTGTM...LRIDTFRAKGAGGQHVNKTDS...
       ICT1 (mL62)   ...LLPPPAR-----------CPRRALHKQK...---------------------------...LTISYCRSSGPGGQNVNKVNS...
         C12ORF65    ...-MSTVG---------LFH---FPTPLTR...---------------------------...LEEQFVKGHGPGGQATNKTSN...
```

Supplementary Fig. S1. Sequence alignment of mitochondrial and bacterial release factors. Extended alignment as shown in Fig. 1a is provided with the decoding motifs labeled in green and blue and the GGQ motif in red.



Supplementary Fig. S2. Genomic sequences of *mtRF1*$^{-/-}$ and *mtRF1a*$^{-/-}$. Genomic DNA was isolated from the respective knockout cell lines, respective target region was PCR amplified and products were analyzed using TOPO cloning and subsequent sequencing. Chromatograms and respective DNA sequences of allele 1 and 2 with corresponding amino acid sequences are provided.

a COX1 termination codons

Homo sapiens
5‵...CCACCCUACCACACAUUCGAAGAACCCGUAUACAUAAAAUC**UAGA**CAAAAAAGGAAGGAAUCGAA...3‵
... P P Y H T F E E P V Y M K S *

Pan troglodytes
5‵...CCACCCUACCACACAUUCGAAGAACCCGUAUACAUAAAAUC**UAGA**CAAAAAAGGAAGGAAUCGAA...3‵
... P P Y H T F E E P V Y M K S *

Mus musculus
5‵...CCAUAUCACACAUUCGAGGAACCAACCUAUGUAAAAGUAAAA**UAA**GAAAGGAAGGAAUCGAACCC...3‵
... P Y H T F E E P T Y V K V K *

Rattus norvegicus
5‵...CCCUACCACACAUUCGAAGAACCUUCCUAUGUAAAAGUUAAA**UAA**GAAAGGAAGGAUUCGAACCC...3‵
... P Y H T F E E P S Y V K V K *

Bos taurus
5‵...CCAUAUCACACAUUUGAAGAACCCACCUAUGUUAACCUAAAA**UAA**GAAAGGAAGGAAUCGAACCC...3‵
... P Y H T F E E P T Y V N L K *

Sus scrofa
5‵...CCCUAUCACACAUUUGAAGAACCAACAUAUAUCAACCUAAAA**UAA**GCAUAAGAAAGGAAGGAAUC...3‵
... P Y H T F E E P T Y I N L K *

b ND6 termination codons

Homo sapiens
5‵...UUUGUUGGUGUAUAUAUUGUAAUUGAGAUUGCUCGGGGGAA**UAGG**UUAUGUGAUUAGGAGUAGGG...3‵
... F V G V Y I V I E I A R G N *

Pan troglodytes
5‵...UUUGUUGGUGUAUACAUUGUGAUUGAGAUUGCUCGGGGGAA**UAGG**UUAUGUGAUUAGGAGUAAGG...3‵
... F V G V Y I V I E I A R G N *

Mus musculus
5‵...UUGUUUGCGGGUAUUUUUAUUAUUAUCGAGAUUACUCGAGAU**UAA**UUGAGUAUAAGAUAAUAAUU...3‵
... L F A G I F I I I E I T R D *

Rattus norvegicus
5‵...UUGUUUGCGGGGAUUUUUAUUAUUAUUGAAAUCACUCGGGAU**UAA**GUGUGUGUAAGAUAAAAAUU...3‵
... L F A G I F I I I E I T R D *

Bos taurus
5‵...UUAAUUGGUGUUGUGGUUAUUAUAGAAAUUACUCGUGGAAAU**UAA**AUAAGAUUAUGCUGAUAAGG...3‵
... L I G V V V I M E I T R G N *

Sus scrofa
5‵...CUUAUUGGAGUUGUUGUUAUUAUAGAGAUUACUCGUGGUAAU**UAA**AUAGUGUUAUGCUGAUUAUA...3‵
... L I G V V V I M E I T R G N *

Supplementary Fig. S3. Comparison of COX1 (a) and ND6 (b) termination codons in different species. Only the 3’ end for COX1 and ND6 mRNA including the UTRs are presented with the corresponding amino acid sequence. Termination codons are marked in bold.

```
mtRF1 M.musculus        -MSHHLCIWLFRNP-FLRACPQRHVFLSCQQFRQISLDTRPWNFRQKKTHVLYQLLNKSW  58
mtRF1 R.norvegicus      -MSFHLCVWLFRNLSSLSACSQRHVFLYGQQFRQINLDPRLWNFRQNKTHVLYRLLNKSW  59
mtRF1 H.sapiens         -MNRHLCVWLFRHPSL-NGYLQCHIQLHSHQFRQIHLDTRLQVFRQNRNCILH-LLSKNW  57
mtRF1 B.taurus          MNRRHLFAWLFRHLSL-NGHLQCHVHRHSHQLTQIPLDTRLWVFRRNRNHTVHRLLNKNC  59
mtRF1a M.musculus       -----------------------------------------------------------M  1
mtRF1a R.norvegicus     -----------------------------------------------------------M  1
mtRF1a H.sapiens        -----------------------------------------------------------M  1
mtRF1a B.taurus         -----------------------------------------------------------M  1


mtRF1 M.musculus        SRGCCHQGTRKLWKHKALQKYMEDLNKEYQTLDQCLQGISENEGDRR------------A  106
mtRF1 R.norvegicus      SRGYC-QGTRKLWKHKALQKYMEGLNDEYQSLDQCLQDISEDEGDRR------------A  106
mtRF1 H.sapiens         SRRYCHQDTKMLWKHKALQKYMENLSKEYQTLEQCLQHIPVNEENRR------------S  105
mtRF1 B.taurus          SRRYCHQDTSMLWKHKALQKYMEDLNKEYQTLDHCLHHISASEGDRR------------S  107
mtRF1a M.musculus       RSGFLS-GARRLWARR-------AFSRTPPPSEELL----ARGGPLRAFLERRVGSEAGG  49
mtRF1a R.norvegicus     RSGFLR-SARRLWARR-------AISRMPPPSEELL----ARGGPLRAFLERRVGSEAGG  49
mtRF1a H.sapiens        RSRVLWGAARWLWPRRAVGPARRPLSSGSPPLEELF----TRGGPLRTFLERQAGSEAH-  56
mtRF1a B.taurus         RPRLVWNVFRGFWARRGVVPACRHLSCSNLPLEELF----ARGGALRTFLERQVGAEAQ-  56
                                   :* ::        :.      :. :          *

mtRF1 M.musculus        LHRRHAQLAPLAAVYQEIQEAEQAIEELESLCKSLNKQDEKQLQELVSEERQIIDQKIHR  166
mtRF1 R.norvegicus      SHRRHAELAPLVAVYQEIQEAEQAIEELESMCKSLNKQDEKQLQELVSEERQIIDQKIHR  166
mtRF1 H.sapiens         LNRRHAELAPLAAIYQEIQETEQAIEELESMCKSLNKQDEKQLQELALEERQTIDQKINM  165
mtRF1 B.taurus          LTRRHAELAPLAVIYKEIQEAEQAIEELESMCKSLNKQDEKQLQELALEERQTIAQKINM  167
mtRF1a M.musculus       LDAGYPQ---LAAAARLLSEKERELRDTESLLH----DENEDLKKLAESEIALCQKQITE  102
mtRF1a R.norvegicus     LDAGSPQ---LAAAARLLNEKERELRDTESLLH----DENEDLKKLAESEIALCQKEIAE  102
mtRF1a H.sapiens        LKVRRPE---LLAVIKLLNEKERELRETEHLLH----DENEDLRKLAENEITLCQKEITQ  109
mtRF1a B.taurus         FQVRRPE---LVAVAKLLSDKEQELQETQHLLH----DENEDLRKLAENEITSCEKEIAQ  109
                              :   * .  : :.: *: :.: : : :     ::::*::*. .*     ::*

mtRF1 M.musculus        LYSELLERLVPKEKYDWSDVILEVTSGRTTGGDICQQFTREIFDMYQNYSYYKHWKFELL  226
mtRF1 R.norvegicus      LYSELLEHLVPKEKCDRSNVILEVTSGRTTGGDICQQFTREIFDMYQNYSYYKHWRFELL  226
mtRF1 H.sapiens         LYNELFQSLVPKEKYDKNDVILEVTAGRTTGGDICQQFTREIFDMYQNYSCYKHWQFELL  225
mtRF1 B.taurus          LYSELFQSLLPKEKYDKNDVILEVTSGRTTGGDICQQFTREIFDMYQNYSSYKHWRFELL  227
mtRF1a M.musculus       LKHQIISLLVPSEEMDGSDLILEVTAG--VGGQEAMLFTSEMFDMYQQYAAFKRWHFETL  160
mtRF1a R.norvegicus     LKHRIISLLVPSEDMDGSDLILEVTAG--VGGQEAMLFTSEMFDMYQQYAAFKRWHFETL  160
mtRF1a H.sapiens        LKHQIILLLVPSEETDENDLILEVTAG--VGGQEAMLFTSEIFDMYQQYAAFKRWHFETL  167
mtRF1a B.taurus         LKHQIILLLVPSEETDKNDLILEVTAG--VGGQEAMLFTSEIFDMYQQYAAFKRWHFETL  167
                        *  .::  *:*.*. * .::*****:*  .**: .  ** *:*****:*: :*:*:** *

mtRF1 M.musculus        NYTPADYGGLHHAAARISGDSVYKHLKYEGGIHRVQRIPEVGLSSRMQRIHTGTMSVIVL  286
mtRF1 R.norvegicus      NYTPADYGGLHHAAARISGDSVYKHLKYEGGIHRVQRIPEVGLSSRMQRIHTGTMSVIVL  286
mtRF1 H.sapiens         NYTPADYGGLHHAAARISGDGVYKHLKYEGGIHRVQRIPEVGLSSRMQRIHTGTMSVIVL  285
mtRF1 B.taurus          NYTPADYGGLHHAAARISGDNVYKHLKYEGGIHRVQRIPEVGLSSRMQRIHTGTMSVIVL  287
mtRF1a M.musculus       EYFPSELGGLRHASASVGGPEAYRHMKFEGGVHRVQRVPKTE---KQGRIHTSTMTVAIL  217
mtRF1a R.norvegicus     EYFPSELGGLRHASASIGGPEAYRHMKFEGGVHRVQRVPKTE---RQGRIHTSTMTVAIL  217
mtRF1a H.sapiens        EYFPSELGGLRHASASIGGSEAYRHMKFEGGVHRVQRVPKTE---KQGRVHTSTMTVAIL  224
mtRF1a B.taurus         EYFPSEIGGLRHASASIGGSEAYKHMKFEGGVHRVQRVPKTE---KQGRIHTSTMTVAIL  224
                        :* *:: ***:**:* :.*  .*:*:*:***:*****:*:.    :  *:**.**:* :*

mtRF1 M.musculus        PQPDEVDVKVDPKDLRVDTFRARGAGGQHVNTTDSAVRLVHIPTGLVVECQQERSQLKNK  346
mtRF1 R.norvegicus      PQPDEVDVKVDPRDLRVDTFRARGAGGQHVNTTDSAVRLVHIPTGLVVECQQERSQLKNK  346
mtRF1 H.sapiens         PQPDEVDVKLDPKDLRIDTFRAKGAGGQHVNKTDSAVRLVHIPTGLVVECQQERSQIKNK  345
mtRF1 B.taurus          PHPDEVDVKVDPKDLRIDTFRAKGAGGQHVNTTDSAVRLVHIPTGLVVECQQERSQIKNK  347
mtRF1a M.musculus       PQPTEIKLVINPKDLRIDTKRASGAGGQHVNTTDSAVRIVHLPTGIISECQQERSQLKNR  277
mtRF1a R.norvegicus     PQPTEIKLVINPKDLRIDTKRASGAGGQHVNTTDSAVRIVHLPTGIISECQQERSQLKNR  277
mtRF1a H.sapiens        PQPTEINLVINPKDLRIDTKRASGAGGQHVNTTDSAVRIVHLPTGVVSECQQERSQLKNK  284
mtRF1a B.taurus         PQPTEINLVINPKDLRIDTKRASGAGGQHVNTTDSAVRIVHLPTGIVSECQQERSQLKNK  284
                        *:* *:.: ::*:***:** ** ********.******:**:***:: ********:**:

mtRF1 M.musculus        EIALRVLRARLYQQIIEKDRCQQQNARKLQVGTRAQSERIRTYNFTQDRVTDHRIAYEVR  406
mtRF1 R.norvegicus      EIALRVLRARLYQQIIEKDKCQQQNARKLQVGTRAQSERIRTYNFTQDRVTDHRIAYEVR  406
mtRF1 H.sapiens         EIAFRVLRARLYQQIIEKDKRQQQSARKLQVGTRAQSERIRTYNFTQDRVSDHRIAYEVR  405
mtRF1 B.taurus          EIALRVLRARLYQQIIEKDKCQQRSARKLQVGTRAQSERIRTYNFTQDRVTDHRIAYEVR  407
mtRF1a M.musculus       ELAMKKLRARLYSMHLEEETAKRYNARKIQVGTKGRSEKIRTYNFPQNRVTDHRINKSLH  337
mtRF1a R.norvegicus     ELAMKKLRARLYSMRLEEETAKRYSARKIQVGTKGRSEKIRTYNFPQNRVTDHRINKSLH  337
mtRF1a H.sapiens        ELAMTKLRAKLYSMHLEEEINKRQNARKIQIGSKGRSEKIRTYNFPQNRVTDHRINKTLH  344
mtRF1a B.taurus         EMAMKKLRAKLYSLQLEEETSKRYNARKIQIGTKGRSEKIRTYNFPQNRVTDHRINKSLH  344
                        *:*:  ***:**.  :*::  :: .***:*:*::.:**:****** *:**:****   ::

mtRF1 M.musculus        DIKEFLRGEKCLDQLIERLLQSADEEAISEFLDESLQSVK   446
mtRF1 R.norvegicus      DIKEFLRGEKCLDQLIERLLQSADEEAIAEFLDESLQSVK   446
mtRF1 H.sapiens         DIKEFLCGGKGLDQLIQRLLQSADEEAIAELLDEHLKSAK   445
mtRF1 B.taurus          NIKEFLCGEKCLDQLIQRLLQSADEEAITEFLDENLKSVK   447
mtRF1a M.musculus       DLESFMQGDCLLDDMIQSLKDCSDYEALVEMISRRD----   373
mtRF1a R.norvegicus     DLESFMQGDCLLDDLIQSLKDYSDYESLVEMISRKD----   373
mtRF1a H.sapiens        DLETFMQGDYLLDELVQSLKEYADYESLVEIISQKV----   380
mtRF1a B.taurus         DLETFMQGEYLLDELVQSLKDYANYESLVEIIAKEV----   380
                        ::: *: *   **:::: * : :: *:: *:: .
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Supplementary Fig. S4. CLUSTAL multiple sequence alignment of mtRF1 and mtRF1a.

Supplementary Table S1. Key reagents

REAGENT or RESOURCE	SOURCE	IDENTIFIER
Antibodies		
Rabbit polyclonal anti-uS15m	ProteinTech	Cat# 17006-1-AP
Rabbit polyclonal anti-uL23m		PRAB1716
Mouse monoclonal anti-FLAG	Sigma Prestige	Cat# F1804
Rabbit polyclonal anti-TIM23		PRAB1527
Rabbit polyclonal anti-TIM70		PRAB3280
Mouse monoclonal anti-Calnexin	ProteinTech	Cat#66903-1-Ig
Rabbit polyclonal anti-ND1		PRAB5021
Rabbit polyclonal anti-ND2	ProteinTech	Cat# 19704-1-AP
Rabbit polyclonal anti-NDUFB8		PRA3765
Mouse monoclonal anti-SDHA	Invitrogen	Cat#459200
Rabbit polyclonal anti-CYTB		PRAB5131
Rabbit polyclonal anti-RIESKE		PRAB1512
Rabbit polyclonal anti-COX1		PRAB5121
Mouse monoclonal anti-COX2	Abcam	Cat# ab110258
Rabbit polyclonal anti-COX4l		PRAB1522
Rabbit polyclonal anti-ATP5B		PRAB4826
Rabbit polyclonal anti-ATP6		PRAB5159
Rabbit polyclonal anti-C12orf62		PRAB 4845
Rabbit polyclonal anti-MITRAC12		PRAB3761
Rabbit polyclonal anti-MITRAC15		PRAB4814
Rabbit polyclonal anti-mtRF1		RRDAB5461
Rabbit polyclonal anti-mtRF1a	ProteinTech	Cat# 16694-1-AP
Rabbit polyclonal anti-mL62/ICT1	ProteinTech	Cat# 10403-1-AP
Rabbit polyclonal anti-C12ORF65	ProteinTech	Cat# 24646-1-AP
Rabbit polyclonal anti-MTRES1	Sigma	Cat# HPA049535
Chemicals		
L-[^{35}S]methionine	Hartmann Analytic	Cat# SCM-01
Adenosine 5'-triphosphate, [γ-^{32}P]	Hartmann-Analytic	Cat# SRP-501
Emetine dihydrochloride hydrate	Sigma-Aldrich	Cat# 219282
Lipofectamine 3000	Invitrogen	Cat# L3000-015
GeneJuice	Novagen	Cat# 70967-3
Alt-R® CRISPR-Cas9 tracrRNA, ATTO™ 550	Integrated DNA technologies	Cat# 1075927
Alt-R® S.p. Cas9 Nuclease V3	Integrated DNA technologies	Cat# 1081058
TRIzol® Reagent	Ambion	Cat# 15596018
Critical Commercial Assays		
Rapid DNA Ligation Kit	ThermoFisher Scientific	Cat# K1423
T4 Polynucletide Kinase (T4 PNK)	ThermoFisher Scientific	Cat# EK0031
KOD Hot Start DNA Polymerase	Merck	Cat# 71086-3
Wizard® Plus SV Minipreps DNA Purification System	Promega	Cat# A1460
Wizard® SV Gel and PCR Clean-Up System	Promega	Cat# A9282
QuikChange Lightning Site-Directed Mutagenesis Kit	Agilent Technologies	Cat# 210519-5

TOPO TA Cloning® Kit	ThermoFisher Scientific	Cat# 45-0030
OneShot®TOP10 Chemically Competent Cells	ThermoFisher Scientific	Cat# C404004
Complex I Enzyme Activity Assay Kit (Colorimetric)	abcam	Cat# ab109721
Seahorse FluxPaks	Agilent Technologies	Cat# 102416-100
MitoSOX™ Red Mitochondrial Superoxide Indicator	ThermoFisher Scientific	Cat# M36008
Experimental Models: Cell Lines		
HEK293-Flp-In T-Rex	ThermoFisher Scientific	R78007
HEK293-Flp-In T-Rex-*mtRF1*$^{-/-}$	This study	N/A
HEK293-Flp-In T-Rex-*mtRF1a*$^{-/-}$	This study	N/A
HEK293-Flp-In T-Rex-mtRF1$^{\text{FLAG-GGQ}}$	This study	N/A
HEK293-Flp-In T-Rex-mtRF1$^{\text{FLAG-AAQ}}$	This study	N/A
HEK293-Flp-In T-Rex-mtRF1a$^{\text{FLAG-GGQ}}$	This study	N/A
HEK293-Flp-In T-Rex-mtRF1a$^{\text{FLAG-AAQ}}$	This study	N/A
Oligonucleotides		
Guide RNA: targeting the Exon 2 of mtRF1: 5’-TGTTAAGTAAGAATTGGTCC-3’	This study; IDT	N/A
Guide RNA: targeting the Exon 1 of mtRF1a: 5’-CTCCGGTAGCCCGCCGCTGG-3’	This study; IDT	N/A
siRNA C12orf65 Oligo: GCAAAGGAAACCCUGGAAA	This study; Eurogentec	N/A
Primer: Generation of the FLAG-tagged version of mtRF1 Forward: 5'-CTCTCCAAGCTTCCACCATGAATCGTCACCTGTGTGTTTGGC-3'	This study; Microsynth	N/A
Primer: Generation of the FLAG-tagged version of mtRF1 Reverse: 5'-CTTTCTCTCGAGCTACTTATCGTCGTCATCCTTGTAATCTTTTGCTGATTTAAGGTGTTCATCC-3'	This study; Microsynth	N/A
Primer: Generation of the FLAG-tagged mutant (GGQ→AAQ) version of mtRF1: Forward: 5’-GATACATTTCGAGCCAAAGGAGCAGCAGCGCAGCATGTTAATAAAAC-3’	This study; Microsynth	N/A
Primer: Generation of the FLAG-tagged mutant (GGQ→AAQ) version of mtRF1 Reverse: 5’-CACTATCAGTTTTATTAACATGCTGCGCTGCTGCTCCTTTGGCTC-3’	This study; Microsynth	N/A
Primer: Generation of the FLAG-tagged version of mtRF1a Forward: 5’-CTCTCCAAGCTTCCACCATGCGGTCCCGGGTTCTGTGGG-3’	This study; Microsynth	N/A
Primer: Generation of the FLAG-tagged version of mtRF1a Reverse: 5’-CTTTCTGATATCCTACTTATCGTCGTCATCCTTGTAATCAACTTTTTGGGAAATAATTTCTACTAAAGATTC-3’	This study; Microsynth	N/A

Primer: Generation of the FLAG-tagged mutant (GGQ→AAQ) version of mtRF1a Forward: 5’-GACACTAAGCGAGCCAGTGGAGCTGCGGCGCAGCATGTAAATAC-3’	This study; Microsynth	N/A
Primer: Generation of the FLAG-tagged mutant GGQ→AAQ) version of mtRF1a Reverse: 5’-CACTGTCCGTGGTATTTACATGCTGCGCCGCAGCTCCACTGGCTC-3’	This study; Microsynth	N/A
Probe: targeting MTRNR1 (12S rRNA) 5’-TCGATTACAGAACAGGCTCCTCTAG-3’	[1]	N/A
Probe for northern blot: targeting MTRNR2 (16S rRNA)5’-GTTTGGCTAAGGTTGTCTGGTAGTA-3’	[1]	N/A
Probe for northern blot: targeting MTCO1 5’- GTCAGTTGCCAAAGCCTCCGATTATG-3’	[1]	N/A
Probe for northern blot: targeting MTCO2 5’-GACGTCCGGGAATTGCATCTGTTTT-3’	[1]	N/A
Probe for northern blot: targeting MTCYTB 5’-CGTGTGAGGGTGGGACTGTCTACTG-3’	This study; Microsynth	N/A
Probe for northern blot: targeting 18S-rRNA 5’-TTTACTTCCTCTAGATAGTCAAGTTCGACC-3’	[2]	N/A
Recombinant DNA		
pOG44 Flp-Recombinase Expression Vector	ThermoFisher Scientific	Cat# V600520
pcDNA5/FRT/TO	ThermoFisher Scientific	Cat# V6520-20
Software and Algorithms		
ImageJ	[3]	https://imagej.nih.gov/ij/

Supplementary Table S2. nCounter tube sequences for NanoString analyses (provided by IDT)

Mito_JCM__008.1:591_T001	CTTCATCAGGGTTTGCTGAAGATGGCGGTATATAGGCTGAGCAAGAGGTGCCTCAAGACCTAAGCGACAGCGTGACCTTGTTTCA
Mito_JCM__009.1:481_T002	CTTTCTTAATTGGTGGCTGCTTTTAGGCCTACTATGGGTGTTAAATTTTTCATCCTCTTCTTTTCTTGGTGTTGAGAAGATGCTC
HSMT_ND1.1:461_T003	GTTCTTGTGTTGTGATAAGGGTGGAGAGGTTAAAGGAGCCACTTATTAGTCACAATTCTGCGGGTTAGCAGGAAGGTTAGGGAAC
HSMT_ND2.1:444_T004	CCTGCTATGATGGATAAGATTGAGAGAGTGAGGAGAAGGCTTACGTTTAGCTGTTGAGATTATTGAGCTTCATCATGACCAGAAG
HSMT_COX1.1:873_T005	GCGGAGGTGAAATATGCTCGTGTGTCTACGTCTATTCCTACTGTAAATATCAAAGACGCCTATCTTCCAGTTTGATCGGGAAACT
HSMT_COX2.1:216_T006	TCGTCTGTTATGTAAAGGATGCGTAGGGATGGGAGGGCGATGAGGACTAGCGAACCTAACTCCTCGCTACATTCCTATTGTTTTC
HSMT_ATP8.1:82_T007	TATTTTTATGGGCTTTGGTGAGGGAGGTAGGTGGTAGTTTGTGTTTAATACCAATTTGGTTTTACTCCCCTCGATTATGCGGAGT
HSMT_ATP6.1:331_T008	GTGGGCTAGGGCATTTTTAATCTTAGAGCGAAAGCCTATAATCACTGTGCCTTTCGGGTTATATCTATCATTTACTTGACACCCT
HSMT_COX3.1:539_T009	ATGTTGAGCCGTAGATGCCGTCGGAAATGGTGAAGGGAGACTCGAAGTACCAACAGCCACTTTTTTTCCAAATTTTGCAAGAGCC
HSMT_ND3.1:135_T010	AAGGTAATAGCTACTAAGAAGAATTTTATGGAGAAAGGGACGCGGGCGGGCACCGTGTGGACGGCAACTCAGAGATAACGCATAT
HSMT_ND4L.1:58_T011	TATTCCTTCTAGGCATAGTAGGGAGGATATGAGGTGTGAGCGATATACTACCTGGAGTTTATGTATTGCCAACGAGTTTGTCTTT
HSMT_ND4.1:967_T012	ACTGTGAGTGCGTTCGTAGTTTGAGTTTGCTAGGCAGAATAGTAATGAGGCAGATAAGGTTGTTATTGTGGAGGATGTTACTACA

HSMT_ND5.1:1147_T013	TGCGGTTTCGATGATGTGGTCTTTGGAGTAGAAACCTGTGAGGAAAGGTACTTCCTTCCTGTGTTCCAGCTACAAACTTAGAAAC
HSMT_ND6.1:191_T014	CCTCAGGATACTCCTCAATAGCCATCGCTGTAGTATATCCAAAGACAACCCATAAAATTGGTTTTGCCTTTCAGCAATTCAACTT
HSMT_CYTB.1:946_T015	GAGGTCTGCGGCTAGGAGTCAATAAAGTGATTGGCTTAGTGGGCGAAATACTGGTCAAGACTTGCATGAGGACCCGCAAATTCCT
NR_003286.2:1640_T016	AGGGCAGGGACTTAATCAACGCAAGCTTATGACCCGCACTTACTGGGAATCTTTCGTTGGGACGCTTGAAGCGCAAGTAGAAAAC
NR_023379.1:8_T017	TGCTTAGCTTCCGAGATCAGACGAGATCGGGCGCGTTCAGGGCCAGCAGACCTGCAATATCAAAGTTATAAGCGCGT
Mito_JCM__008.1:591_ProbeB	CGAAAGCCATGACCTCCGATCACTCTACACCTTGACCTAACGTCTTTACGTGGGTACTTGCGCTTACTTTGTAGC
Mito_JCM__009.1:481_ProbeB	CGAAAGCCATGACCTCCGATCACTCTTCAGTTATATGTTTGGGATTTTTTAGGTAGTGGGTGTTGAGCTTGAACG
HSMT_ND1.1:461_ProbeB	CGAAAGCCATGACCTCCGATCACTCGATAAATCATATTATGGCCAAGGGTCATGATGGCAGGAGTAATCAGAGGT
HSMT_ND2.1:444_ProbeB	CGAAAGCCATGACCTCCGATCACTCAGTATGCTAAGATTTTGCGTAGCTGGGTTTGGTTTAATCCACCTCAACTG
HSMT_COX1.1:873_ProbeB	CGAAAGCCATGACCTCCGATCACTCCGAGTCAGCTAAATACTTTGACGCCGGTGGGGATAGCGATGATTATGGTA
HSMT_COX2.1:216_ProbeB	CGAAAGCCATGACCTCCGATCACTCAGTACCATTGGTGGCCAATTGATTTGATGGTAAGGGAGGGATCGTTGACC
HSMT_ATP8.1:82_ProbeB	CGAAAGCCATGACCTCCGATCACTCAGCGAACAGATTTTCGTTCATTTTGGTTCTCAGGGTTTGTTATAATTTTT
HSMT_ATP6.1:331_ProbeB	CGAAAGCCATGACCTCCGATCACTCATAATAACTAGTATGGGGATAAGGGGTGTAGGTGTGCCTTGTGGTAAGAA
HSMT_COX3.1:539_ProbeB	CGAAAGCCATGACCTCCGATCACTCAGTTGAGCCAATAATGACGTGAAGTCCGTGGAAGCCTGTGGCTACAAAAA
HSMT_ND3.1:135_ProbeB	CGAAAGCCATGACCTCCGATCACTCGGGCTCATGGTAGGGGTAAAAGGAGGGCAATTTCTAGATCAAATAATAAG
HSMT_ND4L.1:58_ProbeB	CGAAAGCCATGACCTCCGATCACTCGAGTGGGTGTTGAGGGTTATGAGAGTAGCTATAATGAACAGCGATAGTAT
HSMT_ND4.1:967_ProbeB	CGAAAGCCATGACCTCCGATCACTCGCTATTAGTGGGAGTAGAGTTTGAAGTCCTTGAGAGAGGATTATGATGCG
HSMT_ND5.1:1147_ProbeB	CGAAAGCCATGACCTCCGATCACTCGTAGCGATGAGAGTAATAGATAGGGCTCAGGCGTTTGTGTATGATATGTT
HSMT_ND6.1:191_ProbeB	CGAAAGCCATGACCTCCGATCACTCCGCTAACCCCACTAAAACACTCACCAAGACCTCAACCCCTGACCCCCATG
HSMT_CYTB.1:946_ProbeB	CGAAAGCCATGACCTCCGATCACTCATGGTAAAAGGGTAGCTTACTGGTTGTCCTCCGATTCAGGTTAGAATGAG
NR_003286.2:1640_ProbeB	CGAAAGCCATGACCTCCGATCACTCGCCTCACTAAACCATCCAATCGGTAGTAGCGACGGGCGGTGTGTACAA
NR_023379.1:8_ProbeB	CGAAAGCCATGACCTCCGATCACTCCGGTCTCCCATCCAAGTACTAACCAGGCCCGACCC

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