Supplemental Data

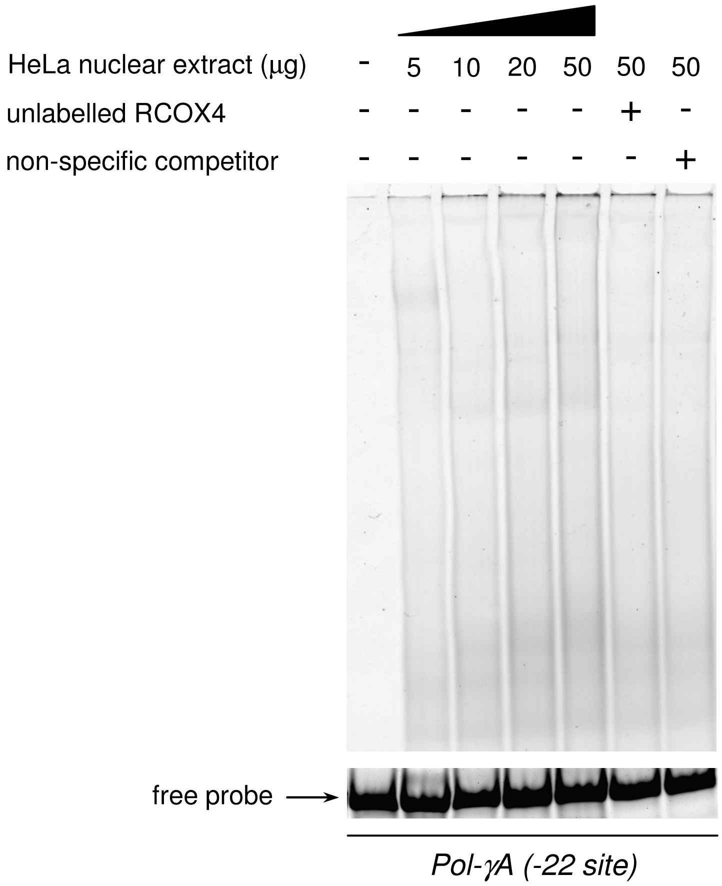
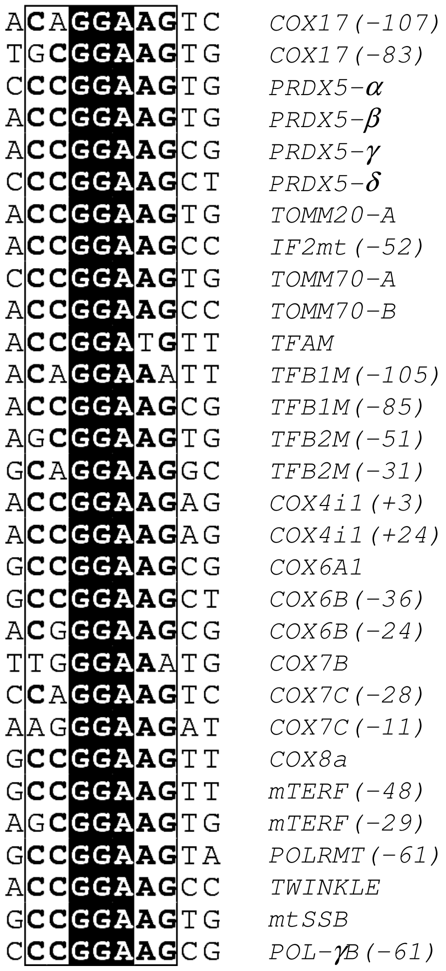


FIGURE S1. NRF-2 does not bind *in vitro* the predicted -22 site in Pol-γA gene promoter. NRF-2 binding was evaluated by EMSA using increasing amounts (from 5 μg to 50 μg) of Heparin-Sepharose purified HeLa nuclear extract and a radiolabelled double-stranded oligonucleotide probe containing the NRF-2 predicted -22 site. The unlabelled specific (RCOX4) and non-specific competitor oligonucleotides (100-fold molar excess) are indicated above each lane. The figure shows that no binding to the probe occurred in the presence of increasing amounts of protein extract.

Table S1

Dataset of functional NRF-2 binding sites that were aligned to obtain the NRF-2 consensus.

NRF-2 site	Sequence	Position	Reference
COX17(-107)	ACAGGAAGTC	-107	Takahashi Y. et al. (2002) *Biochim. Biophys. Acta*, 1574, 359-364
COX17(-83)	TGCGGAAGTG	-83	" " " "
PRDX5-α	CCCGGAAGTG	-513	Kropotov A. et al. (2007) *FEBS J.*, 274, 5804-5814
PRDX5-β	ACCGGAAGTG	-468	" " " "
PRDX5-γ	ACCGGAAGCG	-383	" " " "
PRDX5-δ	CCCGGAAGCT	-40	" " " "
TOMM20-A	ACCGGAAGTG	-23	Blesa J.R. et al (2007) *Gene*, 391, 198-208
IF2mt(-52)	ACCGGAAGCC	-52	Hayashi R. et al. (2007) *Mitochondrion*, 7, 195-203
TOMM70-A	CCCGGAAGTG	-70	Blesa J.R. et al (2006) *Biochem. Cell Biol.*, 84, 813-822
TOMM70-B	ACCGGAAGCC	-154	" " " "
TFAM	ACCGGATGTT	-7	Virbasius J.V. et al. (1994) *Proc. Natl. Acad. Sci. USA*, 91, 1309-1313
TFB1M(-105)	ACAGGAAATT	-105	Gleyzer N. et al. (2005) *Mol. Cell. Biol.*, 25, 1354-1366
TFB1M(-85)	ACCGGAAGCG	-85	" " " "
TFB2M(-51)	AGCGGAAGTG	-51	" " " "
TFB2M(-31)	GCAGGAAGGC	-31	" " " "
COX4i1(+3)	ACCGGAAGAG	+3	Ongwijitwat S. et al. (2005) *Gene*, 360, 65-77
COX4i1(+24)	ACCGGAAGAG	+24	" " "
COX6A1	GCCGGAAGCG	+27	" " "
COX6B(-36)	GCCGGAAGCT	-36	" " "
COX6B2(-24)	ACGGGAAGCG	-24	" " "
COX7B	TTGGGAAATG	-116	" " "
COX7C(-28)	CCAGGAAGTC	-28	" " "
COX7C(-11)	AAGGGAAGAT	-11	" " "
COX8a	GCCGGAAGTT	-72	" " "
mTERF(-48)	GCCGGAAGTT	-48	*this paper*
mTERF(-29)	AGCGGAAGTG	-29	*this paper*
POLRMT(-61)	GCCGGAAGTA	-61	*this paper*
TWINKLE	ACCGGAAGCC	-45	*this paper*
mtSSB	GCCGGAAGTG	-11	*this paper*
POL-γB(-61)	CCCGGAAGCG	-61	*this paper*



ACAGGAAGTC	*COX17(-107)*
TGCGGAAGTG	*COX17(-83)*
CCCGGAAGTG	*PRDX5-α*
ACCGGAAGTG	*PRDX5-β*
ACCGGAAGCG	*PRDX5-γ*
CCCGGAAGCT	*PRDX5-δ*
ACCGGAAGTG	*TOMM20-A*
ACCGGAAGCC	*IF2mt(-52)*
CCCGGAAGTG	*TOMM70-A*
ACCGGAAGCC	*TOMM70-B*
ACCGGATGTT	*TFAM*
ACAGGAAATT	*TFB1M(-105)*
ACCGGAAGCG	*TFB1M(-85)*
AGCGGAAGTG	*TFB2M(-51)*
GCAGGAAGGC	*TFB2M(-31)*
ACCGGAAGAG	*COX4i1(+3)*
ACCGGAAGAG	*COX4i1(+24)*
GCCGGAAGCG	*COX6A1*
GCCGGAAGCT	*COX6B(-36)*
ACGGGAAGCG	*COX6B(-24)*
TTGGGAAATG	*COX7B*
CCAGGAAGTC	*COX7C(-28)*
AAGGGAAGAT	*COX7C(-11)*
GCCGGAAGTT	*COX8a*
GCCGGAAGTT	*mTERF(-48)*
AGCGGAAGTG	*mTERF(-29)*
GCCGGAAGTA	*POLRMT(-61)*
ACCGGAAGCC	*TWINKLE*
GCCGGAAGTG	*mtSSB*
CCCGGAAGCG	*POL-γB(-61)*

FIGURE S2. Multiple alignment of functional NRF-2 binding sites from mitochondrial protein gene promoters. The box defines the block of conserved residues; nucleotides identical in all sequences have a black background, nucleotides well conserved are indicated by black bold letters and the remainder are in regular black. Sequence names are reported to the right.

Table S2

Prediction of transcription factor binding sites (TFBSs) in the promoter of proteins involved in DNA replication and/or repair and associated with mitochondria. The analysis was performed by using MAPPER search engine.

Gene symbol	**GenBank accession**	**Protein name**	**Positions of predicted TFBSs (scoring ≥ 2.5)**			
			NRF-1	***NRF-2***	***Sp1***	***CAAT-box***
APEX1	NM_001641	Apurinic-apyrimidinic endonuclease 1	-	-	-141	-58
DNA2	NM_001080449	DNA2-like helicase	-118 -62 -45	-	-108	-
FEN1	NM_004111	Flap endonuclease 1	-	-86	-262	-
LIG3	NM_002311	DNA ligase III	-32	-	-166 -70	-
MPG	NM_001015052	N-methylpurine DNA glycosylase	-296 -54	-68	-287 -271 -239 -123 -43	-
MUTYH	NM_001048171	A/G-specific adenine DNA glycosylase	-	-	-	-
NEIL1	NM_024608	Endonuclease VIII-like 1	-	-	-121	-
NEIL2	NM_145043	Endonuclease VIII-like 2	-158	-	-213 -118 -105 -26	-
NTHL1	NM_002528	Endonuclease III-like protein 1	-	-127 -110	-264 -176	-
NUDT1	NM_002452	7,8-dihydro-8-oxoguanine triphosphatase	-91	-25	-383 -367 -265 -232 -151 -118	-60
OGG1	NM_002542	8-oxoguanine DNA glycosylase / AP lyase	-105	-	-319 -87	-70 -44
PIF1	NM_025049	PIF1 DNA helicase homolog	-	-	-196	-371 -339
RNASEH1	NM_002936	Ribonuclease H1	-	-	-301 -279 -32	-
TOP1MT	NM_052963	Mitochondrial DNA topoisomerase I	-	-	-219 -84 -65 -46 -36 -23	-
UNG1	NM_003362	Uracil-DNA glycosylase	-94 -38	-	-140 -130 -104 -66	-