# Supplementary information

Experimental mitochondria-targeted DNA methylation identifies GpC methylation, not CpG methylation, as potential regulator of mitochondrial gene expression.

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**Supplementary Figure 1.** Methylated DNA immunoprecipitation (MeDIP) of three mtDNA regions. (a) Cancerous (C33A, HCT116) and normal (OSE-C2, CiGenCs, immortalized human hepatocytes (IHH)) cell lines were exposed to high (H, 25 mM) versus low (L, 5 mM) glucose for 4 days. Thereafter, their mtDNA methylation level was determined in three mtDNA regions (D-loop, mtCYTB, mtCOX2). (b) The mtDNA methylation level of HCT116 cells stably expressing mitochondria-targeted M.SssI (MLS-M.SssI) or empty vector (MLS-NoED) was determined in three mtDNA regions (D-loop, mtCYTB, mtCOX2) and a (c) hypomethylated nuclear DNA region (GAPDH, N=2) using a MeDIP approach.

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Supplementary Figure 2. Gene expression relative to  $\beta$ -actin. The effect of our mitochondria-targeting construct (MLS-NoED) on mitochondrial gene expression was determined compared to wild-type (wt) HCT116 and C33A cells. Note that the MLS-NoED expressing cells were processed in a different set of experiments (M.SssI experiments) compared to the wt cells (M.CviPI experiments). Only those genes showing an effect on mitochondrial gene expression in Figure 5 and those taken along in both M.SssI and M.CviPI experiments, were compared in our analysis.

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**Supplementary Figure 3.** Mitochondrial DNA copy number and gene expression. (**a**, **b**) As a positive control for mtDNA depletion, HeLa cells were treated for 2 days with 0.25  $\mu$ M EtBr. The effect on mtDNA copy number (**a**) and mtDNA gene expression of four mitochondrial genes (*mtND1*, *mtND6*, *mtCOX1* and *mtCYTB*) (**b**) was determined (N=1). (**c**) Validation of decrease in mtDNA copy number in HCT116 cells expressing a mitochondria-targeted M.SssI (MLS-M.SssI) using an independent primer pair (mtCOX1 region).

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Supplementary Figure 4. Standard curves for all primers used in q(RT)-PCR.

# Supplementary Table 1

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Locus (position	# of Cs	Cell line	Unconverted Cs	Unconverted Cs
in mtDNA)			at CpG sites	at non-CpG sites
D-loop	H: 99	C33A	H: 6/109 (5.5%)	H: 8/1615 (0.5%)
H: 357–621 bp	(95x non-CpG,		H: 0/108 (0%)	H: 0/2565 (0%)
	4x CpG)		H: 6/86 (8.8%)	
			L: 0/76 (0%)	L: 6/1598 (0.4%)
L: 357–608 bp	L: 98	HCT116	H: 1/40 (2.5%)	H: 1/950 (0.1%)
	(94x non-CpG,			
	4x CpG)			
		HeLa	H: 0/28 (0%)	H: 3/376 (0.8%)
			L: 0/24 (0%)	L: 2/564 (0.4%)
		SKOV3	H: 1/36 (2.8%)	H: 1/846 (0.1%)
mtCOX2	L: 81	C33A	1/204 (0.5%)	1/768 (0.1%)
L: 7909–8165 bp	(64x non-CpG,			
	17x CpG)			
		HCT116	0/119 (0%)	2/448 (0.4%)
			0/323 (0%)	6/704 (0.9%)
		HeLa	1/85 (1.2%)	2/256 (0.8%)

**Supplementary Table 1.** Overview of CpG and non-CpG methylation in the mtDNA in several cancer cell lines (analyzed by bisulfite sequencing). Each row represents an independent bisulfite sequencing batch. H, heavy strand; L, light strand.

# Supplementary Table 2

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Category	Gene/Transcript	C33A (2 <sup>-ΔCt</sup> )	HCT116 (2 <sup>-ΔCt</sup> )	Difference (HCT116/C33A)
mtDNA	mtND1 (H)	4.889	6.028	1.2x
<b>OXPHOS</b> genes	mtND6 (L)	2.511	4.260	1.7x
	mtCOX2 (H)	3.162	3.434	1.1x
	mtCYTB (H)	2.144	2.878	1.3x
mtDNA rRNA	12S rRNA	13.486	47.229	3.5x
genes	16S rRNA	25.865	40.303	1.6x
Nuclear-	PGC1a	0.0011	0.0034	3.1x
encoded	NRF1	0.012	0.021	1.8x
mtDNA	TFAM	0.040	0.064	1.6x
biogenesis				
genes	TFAM/mtDNA	0.0000232	0.0000347	1.5x
DNA	7S DNA primer	0.83	0.70	0.8x
replication				
	mtDNA copy number	1722	1840	1.1x

**Supplementary Table 2.** Overview of the differences between C33A and HCT116 cells regarding mtDNA transcription and replication.  $2^{-\Delta Ct}$ , relative expression to  $\beta$ -actin (genes), to mtDNA (7S DNA), or to nDNA (mtDNA copy number).