Effects of Moderate Global Maternal Nutrient Reduction on Fetal Baboon Renal Mitochondrial Gene Expression at 0.9 Gestation.

Susana P Pereira, M.Sc [1,2,3], Paulo J Oliveira, PhD [1,2], António J. Moreno, PhD [2], Laura A Cox, PhD [4], Peter W Nathanielsz, MD, PhD [3] and Mark J Nijland, PhD [3].

[1] CNC - Center for Neuroscience and Cell Biology, University of Coimbra, Coimbra, Portugal, 3004-517.

[2] Department of Life Sciences, School of Sciences and Technology, University of Coimbra, Coimbra, Portugal, 3004-517.

[3] Center for Pregnancy and Newborn Research, University of Texas Health Science Center at San Antonio, San Antonio, Texas, United States, 78229-3900.

[4] Department of Genetics, Texas Biomedical Research Institute, San Antonio, Texas, United States, 78245-0549.

To whom correspondence should be addressed: Paulo J. Oliveira, PhD, Center for Neuroscience and Cell Biology, Largo Marquês de Pombal, 3004-517 Coimbra – Portugal, Phone: +351 239 855760, Fax: +351 239 855789, email: pauloliv@ci.uc.pt

Table 2: mRNA abundance for mitochondrial proteins was assessed by PCR array in whole kidney samples from baboon fetuses from mothers fed *ad libitum* (controls, C) or 70% of the control diet (maternal nutrient restricted, MNR) at 0.9 gestation. Symbol denotes the gene identification, RefSeq denotes the Reference Sequence from the National Center for Biotechnology Information collection, Description gives a summary information about the gene identification and/or function, Fold difference was calculate between the groups enunciated, positive values for up regulation and negative values for a down regulation. Fold differences relevant to the mitochondrial profile of the control fetus (control female, C-F *vs* control male, C-M) were presented in the C-F *vs* C-M section, as well the comparison of transcripts expression based on maternal diet for the same gender (in the MNR-M *vs* C-M and MNR-F *vs* C-F sections), the gender dimorphism in the mitochondrial profile of the MNR fetus (in the MNR-F *vs* MNR-M section) and global diet-dependent effects in the mitochondrial expression profile (MNR *vs* C section). The transcripts presented have either 0.05<p<0.1 or p<0.05 in bold.

Symbol	**Refseq**	**Description**	**Fold difference**	**p-value**
		C-F *vs* C-M		
NDUFB8	NM_005004	NADH dehydrogenase (ubiquinone) 1 beta subcomplex	2.656	0.075
NDUFV1	NM_007103	NADH dehydrogenase (ubiquinone) flavoprotein 1	**2.302**	**0.048**
COX6A1	NM_004373	Cytochrome c oxidase subunit VIa polypeptide 1	**1.758**	**0.001**
ATP5C1	NM_005174	ATP synthase, H+ transporting, mitochondrial F1 complex	**9.543**	**0.005**
IMMP1L	NM_144981	IMP1 inner mitochondrial membrane peptidase-like	**1.397**	**0.016**
OPA1	NM_130837	Optic atrophy 1	**-1.138**	**0.024**
CPT2	NM_000098	Carnitine palmitoyltransferase 2	3.063	0.061
SLC25A17	NM_006358	Solute carrier family 25 (mitochondrial carrier), member 17	**-1.170**	**0.037**
TIMM17A	NM_006335	Translocase of inner mitochondrial membrane 17	**-1.131**	**0.016**
TIMM9	NM_012460	Translocase of inner mitochondrial membrane 9	**1.787**	**0.010**
TOMM70A	NM_014820	Translocase of outer mitochondrial membrane 70	-1.155	0.052
SOD1	NM_000454	Superoxide dismutase 1, soluble	**-1.289**	**0.034**

SOD2	NM_000636	Superoxide dismutase 2, mitochondrial	1.679	0.076
BID	NM_001196	BH3 interacting domain death agonist	**5.864**	**0.030**
SFN	NM_006142	Stratifin	**1.863**	**0.050**
C-M *vs* MNR-M				
NDUFA1	NM_004541	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1.	**-1.755**	**0.044**
NDUFA2	NM_002488	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2.	-1.540	0.078
NDUFA4	NM_002489	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4.	**-5.377**	**0.045**
NDUFA8	NM_014222	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8.	-1.192	0.086
NDUFA10	NM_004544	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10.	-1.756	0.052
NDUFAB1	NM_005003	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1.	-1.510	0.098
NDUFC1	NM_002494	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1.	-1.502	0.097
NDUFS3	NM_004551	NADH dehydrogenase (ubiquinone) Fe-S protein 3.	-1.269	0.080
NDUFS5	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5.	-1.250	0.051
NDUFV3	NM_021075	NADH dehydrogenase (ubiquinone) flavoprotein 3.	-1.290	0.080
SDHB	NM_003000	Succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	**-1.240**	**0.006**
COX6A1	NM_004373	Cytochrome c oxidase subunit VIa polypeptide 1	**1.741**	**0.000**
OXA1L	NM_005015	Oxidase (cytochrome c) assembly 1-like	**-1.484**	**0.042**
ATP5B	NM_001686	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	-1.602	0.059
ATP5J	NM_001685	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6	-1.406	0.085
ATP6V1C2	NM_144583	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C2	**-2.032**	**0.027**
OPA1	NM_130837	Optic atrophy 1	-1.152	0.087
FIS1	NM_016068	Fission 1 (mitochondrial outer membrane)	-1.185	0.080
SLC25A13	NM_014251	Solute carrier family 25, member 13	-1.271	0.099
SLC25A16	NM_152707	Solute carrier family 25 (mitochondrial carrier), member 16	-1.185	0.072
SLC25A17	NM_006358	Solute carrier family 25 (mitochondrial carrier), member 17	-1.112	0.073
TIMM23	NM_006327	Translocase of inner mitochondrial membrane 23	**-1.152**	**0.042**
TIMM9	NM_012460	Translocase of inner mitochondrial membrane 9	**1.886**	**0.014**
SOD1	NM_000454	Superoxide dismutase 1, soluble	**-1.375**	**0.009**
AIFM2	NM_032797	Apoptosis-inducing factor, mitochondrion-associated, 2	-1.222	0.072
SFN	NM_006142	Stratifin	**1.385**	**0.021**
C-F *vs* MNR-F				

NDUFA11	NM_175614	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11	-1.443	0.098
NDUFB9	NM_005005	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	-1.438	0.072
NDUFB10	NM_004548	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-1.391	0.082
NDUFS5	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5	**-1.193**	**0.042**
NDUFV3	NM_021075	NADH dehydrogenase (ubiquinone) flavoprotein 3	**-1.949**	**0.040**
SDHA	NM_004168	Succinate dehydrogenase complex, subunit A, flavoprotein	-1.356	0.087
UQCRC2	NM_003366	Ubiquinol-cytochrome c reductase core protein II	-1.393	0.088
COX6A2	NM_005205	Cytochrome c oxidase subunit VIa polypeptide 2	**-1.206**	**0.049**
COX6C	NM_004374	Cytochrome c oxidase subunit VIc	-1.686	0.075
COX7B	NM_001866	Cytochrome c oxidase subunit VIIb	**-1.304**	**0.050**
ATP4B	NM_000705	ATPase, H+/K+ exchanging, beta polypeptide	-1.761	0.071
ATP5H	NM_006356	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit d	-1.249	0.069
ATP5J	NM_001685	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6	**-1.440**	**0.047**
ATP12A	NM_001676	ATPase, H+/K+ transporting, nongastric, alpha polypeptide	**-1.162**	**0.036**
CPT1B	NM_004377	Carnitine palmitoyltransferase 1B (muscle)	-1.633	0.091
MFN2	NM_014874	Mitofusin 2	**-1.374**	**0.008**
DNM1L	NM_005690	Dynamin 1-like	-1.220	0.097
GRPEL1	NM_025196	GrpE-like 1, mitochondrial	**-1.102**	**0.021**
SLC25A3	NM_002635	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 3	-1.945	0.083
SLC25A12	NM_003705	Solute carrier family 25 (mitochondrial carrier), member 12	-1.618	0.068
SLC25A15	NM_014252	Solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	**1.777**	**0.036**
SLC25A16	NM_152707	Solute carrier family 25 (mitochondrial carrier), member 16	**-1.331**	**0.047**
SLC25A17	NM_006358	Solute carrier family 25 (mitochondrial carrier), member 17	**-1.183**	**0.033**
SLC25A31	NM_031291	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	**-2.481**	**0.016**
AIFM2	NM_032797	Apoptosis-inducing factor, mitochondrion-associated, 2	-1.456	0.070
BBC3	NM_014417	BCL2 binding component 3	**-3.749**	**0.001**
BID	NM_001196	BH3 interacting domain death agonist	**-6.046**	**0.029**
CDKN2A	NM_000077	Cyclin-dependent kinase inhibitor 2A	**2.701**	**0.024**
STARD3	NM_006804	StAR-related lipid transfer (START) domain containing 3	**-1.147**	**0.023**
LHPP	NM_022126	Phospholysine phosphohistidine inorganic pyrophosphate phosphatase	-1.291	0.081

		MNR-F *vs* MNR-M		
NDUFA8	NM_014222	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	-1.188	0.067
NDUFB9	NM_005005	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	**-1.193**	**0.043**
NDUFC1	NM_002494	NADH dehydrogenase (ubiquinone) 1	**-1.091**	**0.033**
NDUFS4	NM_002495	NADH dehydrogenase (ubiquinone) Fe-S protein 4	-1.182	0.056
NDUFS5	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5	-1.120	0.062
SDHA	NM_004168	Succinate dehydrogenase complex, subunit A, flavoprotein	-1.226	0.071
UQCRH	NM_006004	Ubiquinol-cytochrome c reductase hinge protein	**-1.218**	**0.034**
UQCRQ	NM_014402	Ubiquinol-cytochrome c reductase, complex III subunit VII	-1.453	0.233
COX4I1	NM_001861	Cytochrome c oxidase subunit IV isoform 1	**-1.151**	**0.004**
COX4I2	NM_032609	Cytochrome c oxidase subunit IV isoform 2	**-1.293**	**0.038**
COX6A2	NM_005205	Cytochrome c oxidase subunit VIa polypeptide 2	**1.718**	**0.004**
COX6B2	NM_144613	Cytochrome c oxidase subunit VIb polypeptide 2	**1.750**	**0.026**
COX7B	NM_001866	Cytochrome c oxidase subunit VIIb	-1.121	0.093
ATP5C1	NM_005174	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	**5.818**	**0.002**
ATP5F1	NM_001688	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit B1	1.235	0.090
ATP5O	NM_001697	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-1.171	0.059
MFN2	NM_014874	Mitofusin 2	-1.302	0.053
DNM1L	NM_005690	Dynamin 1-like	**-1.306**	**0.039**
CPT1B	NM_004377	Carnitine palmitoyltransferase 1B	-1.494	0.075
MSTO1	NM_018116	Misato homolog 1	**-1.330**	**0.021**
MIPEP	NM_005932	Mitochondrial intermediate peptidase	-1.380	0.062
RHOT1	NM_018307	Ras homolog gene family, member T1	-1.301	0.092
SLC25A17	NM_006358	Solute carrier family 25 (mitochondrial carrier), member 17	**-1.244**	**0.007**
SLC25A4	NM_001151	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 4	**-1.216**	**0.012**
LRPPRC	NM_133259	Leucine-rich PPR-motif containing	-1.141	0.070
SOD1	NM_000454	Superoxide dismutase 1, soluble	1.132	0.099
BBC3	NM_014417	BCL2 binding component 3	**-2.537**	**0.030**
SH3GLB1	NM_016009	SH3-domain GRB2-like endophilin B1	-1.131	0.060
		MNR *vs* C		
NDUFA1	NM_004541	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 1	**-1.540**	**0.014**
NDUFA2	NM_002488	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2	**-1.455**	**0.014**

NDUFA4	NM_002489	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4	**-2.782**	**0.008**
NDUFA5	NM_005000	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 5	**-1.926**	**0.028**
NDUFA7	NM_005001	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 7	**-1.332**	**0.043**
NDUFA8	NM_014222	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 8	**-1.251**	**0.021**
NDUFA10	NM_004544	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 10	**-1.623**	**0.009**
NDUFA11	NM_175614	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 11	**-1.420**	**0.034**
NDUFAB1	NM_005003	NADH dehydrogenase (ubiquinone) 1, alpha/beta subcomplex, 1	**-1.436**	**0.026**
NDUFB5	NM_002492	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 5	**-1.298**	**0.035**
NDUFB9	NM_005005	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 9	**-1.327**	**0.023**
NDUFB10	NM_004548	NADH dehydrogenase (ubiquinone) 1 beta subcomplex, 10	-1.325	0.055
NDUFC1	NM_002494	NADH dehydrogenase (ubiquinone) 1	**-1.415**	**0.016**
NDUFC2	NM_004549	NADH dehydrogenase (ubiquinone) 1	**-1.926**	**0.028**
NDUFS1	NM_005006	NADH dehydrogenase (ubiquinone) Fe-S protein 1	-1.277	0.062
NDUFS3	NM_004551	NADH dehydrogenase (ubiquinone) Fe-S protein 3	**-1.236**	**0.029**
NDUFS4	NM_002495	NADH dehydrogenase (ubiquinone) Fe-S protein 4	**-1.188**	**0.049**
NDUFS5	NM_004552	NADH dehydrogenase (ubiquinone) Fe-S protein 5	**-1.221**	**0.011**
NDUFS8	NM_002496	NADH dehydrogenase (ubiquinone) Fe-S protein 8	**-1.274**	**0.038**
NDUFV2	NM_021074	NADH dehydrogenase (ubiquinone) flavoprotein 2	-1.208	0.075
NDUFV3	NM_021075	NADH dehydrogenase (ubiquinone) flavoprotein 3	**-1.586**	**0.004**
SDHA	NM_004168	Succinate dehydrogenase complex, subunit A, flavoprotein	**-1.321**	**0.038**
SDHB	NM_003000	Succinate dehydrogenase complex, subunit B, iron sulfur	**-1.176**	**0.012**
UQCRC1	NM_003365	Ubiquinol-cytochrome c reductase core protein I	**-1.516**	**0.032**
UQCRC2	NM_003366	Ubiquinol-cytochrome c reductase core protein II	-1.411	0.053
UQCRFS1	NM_006003	Ubiquinol-cytochrome c reductase, Rieske iron-sulfur polypeptide 1	**-1.366**	**0.024**
CYC1	NM_001916	Cytochrome c-1	-1.307	0.101
COX4I1	NM_001861	Cytochrome c oxidase subunit IV isoform 1	**-1.281**	**0.017**
COX4I2	NM_032609	Cytochrome c oxidase subunit IV isoform 2	**-1.245**	0.082
COX5A	NM_004255	Cytochrome c oxidase subunit Va	**-1.296**	**0.037**
COX5B	NM_001862	Cytochrome c oxidase subunit Vb	**-1.254**	**0.028**
COX6A1	NM_004373	Cytochrome c oxidase subunit VIa polypeptide 1	1.306	0.078

COX6B1	NM_001863	Cytochrome c oxidase subunit Vib polypeptide 1	-1.367	0.057
COX7B	NM_001866	Cytochrome c oxidase subunit VIIb	-1.188	0.072
COX8A	NM_004074	Cytochrome c oxidase subunit VIIIA	1.234	0.672
COX8C	NM_182971	Cytochrome c oxidase subunit VIIIC	**-1.926**	**0.028**
COX10	NM_001303	COX10 homolog, cytochrome c oxidase assembly protein	**-1.309**	0.063
OXA1L	NM_005015	Oxidase (cytochrome c) assembly 1-like	**-1.450**	**0.016**
ATP4A	NM_000704	ATPase, H+/K+ exchanging, alpha polypeptide	**-1.345**	**0.038**
ATP4B	NM_000705	ATPase, H+/K+ exchanging, beta polypeptide	**-1.926**	**0.028**
ATP5B	NM_001686	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide	**-1.421**	**0.027**
ATP5G1	NM_005175	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C1	**-2.588**	**0.023**
ATP5G3	NM_001689	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit C3	**9.231**	**0.018**
ATP5I	NM_007100	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit E	-1.194	0.063
ATP5J	NM_001685	ATP synthase, H+ transporting, mitochondrial Fo complex, subunit F6	**-1.423**	**0.003**
ATP5O	NM_001697	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	**-1.290**	**0.029**
ATP6V0A2	NM_012463	ATPase, H+ transporting, lysosomal V0 subunit a2	**-1.856**	**0.020**
ATP6V1C2	NM_144583	ATPase, H+ transporting, lysosomal, V1 subunit C2	**-1.606**	**0.028**
SLC25A13	NM_014251	Solute carrier family 25, member 13 (citrin)	-1.148	0.085
SLC25A15	NM_014252	Solute carrier family 25 (mitochondrial carrier; ornithine transporter) member 15	**1.853**	**0.014**
SLC25A16	NM_152707	Solute carrier family 25 (mitochondrial carrier), member 16	**-1.256**	**0.003**
SLC25A17	NM_006358	Solute carrier family 25 (mitochondrial carrier), member 17	-1.147	0.069
SLC25A23	NM_024103	Solute carrier family 25 (mitochondrial carrier; phosphate carrier), member 23	**-1.269**	**0.050**
SLC25A27	NM_004277	Solute carrier family 25, member 27	**10.446**	**0.029**
SLC25A31	NM_031291	Solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	**-2.199**	**0.035**
FXC1	NM_012192	Fracture callus 1 homolog	**-1.155**	**0.029**
TIMM23	NM_006327	Translocase of inner mitochondrial membrane 23	**-1.120**	**0.024**
TOMM20	NM_014765	Translocase of outer mitochondrial membrane 20	-1.159	0.062
TOMM34	NM_006809	Translocase of outer mitochondrial membrane 34	-1.339	0.082
TOMM70A	NM_014820	Translocase of outer mitochondrial membrane 70	-1.214	0.073
MIPEP	NM_005932	Mitochondrial intermediate peptidase	-1.211	0.097
OPA1	NM_130837	Optic atrophy 1	-1.096	0.072

AIFM2	NM_032797	Apoptosis-inducing factor, mitochondrion-associated, 2	**-1.334**	**0.007**
BBC3	NM_014417	BCL2 binding component 3	-1.836	0.056
CDKN2A	NM_000077	Cyclin-dependent kinase inhibitor 2A (inhibits CDK4)	1.751	0.088
SH3GLB1	NM_016009	SH3-domain GRB2-like endophilin B1	-1.125	0.082
UXT	NM_004182	Ubiquitously-expressed transcript	-1.109	0.078
PPA1	NM_021129	Pyrophosphatase (inorganic) 1	**-1.392**	**0.038**
PPA2	NM_176869	Pyrophosphatase (inorganic) 2	**-1.798**	**0.031**