Supplementary materials

Supplementary material 1. a) Names, sequences and positions (in relation to the human mitochondrial DNA) of primers that were used for the determination of the sequence of the 3'-ends of selected human mitochondrial RNAs; b) The expected lengths of the final PCR products for analyzed mRNAs with and without long poly(A) tails

a)

	Examined mitochondrial RNA				
	ND3	**CYTB**	**ATP6/8**	**COXIII**	**12S rRNA**
primer for reverse transctription	*ND3-RT*	*CYTB-RT*	*ATP6/8-RT*	*COXIII-RT*	*12S-RT*
external forward primer	*ND3 LP-F*	*CYTB LP-F*	*APT6/8 LP-F*	*COXIII LP-F*	*12S LP-F*
external reverse primer	*ND3 LP-R*	*CYTB LP-R*	*APT6/8 LP-R*	*COXIII LP-R*	*12S LP-R*
nested forward primer	*ND3 SP-F*	*CYTB SP-F*	*APT6/8 SP-F*	*COXIII SP-F*	*12S SP-F*
nested reverse primer	*ND3 SP-R*	*CYTB SP-R*	*APT6/8 SP-R*	*COXIII SP-R*	*12S SP-R*

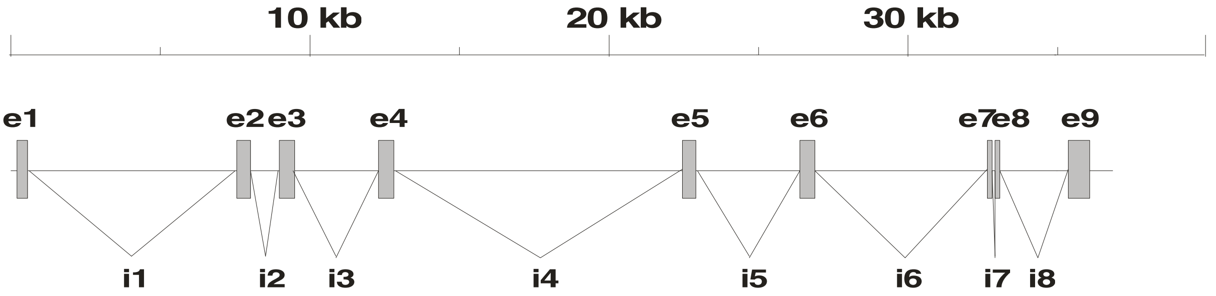
Name of the primer	**Sequence of the primer**	**Position of the primer in human mtDNA**
ND3-RT	5'-GAAGCCGCACTCGTAAGGGG-3'	10181 - 10162
ND3 LP-F	5'-CCTTTTACCCCTACCATGAG-3'	10271 - 10290
ND3 LP-R	5'-ATGTAGCCGTTGAGTTGTGG-3'	10150 - 10131
ND3 SP-F	5'-AACTAACCTGCCACTAATAG-3'	10301 - 10320
ND3 SP-R	5'-TAGTAGTAAGGCTAGGAGGG-3'	10109 - 10090
CYTB-RT	5'-GTCTGGTGAGTAGTGCATGG-3'	14920 - 14901
CYTB LP-F	5'-CAGACCTCCTCGTTCTAACC-3'	15735 - 15754
CYTB LP-R	5'-ATAGTCCTGTGGTGATTTGG-3'	14894 - 14875
CYTB SP-F	5'-AGGACAACCAGTAAGCTACC-3'	15763 - 15782
CYTB SP-R	5'-TGAGCCGAAGTTTCATCATG-3'	14851 - 14832
ATP6/8-RT	5'-GGGCAATGAATGAAGCGAAC-3'	8560 - 8541
APT6/8 LP-F	5'-CATTCAACCAATAGCCCTGG-3'	8976 - 8995
APT6/8 LP-R	5'-GTTCATTTTGGTTCTCAGGG-3'	8532 - 8513
APT6/8 SP-F	5'-CGCCTAACCGCTAACATTAC-3'	9001 - 9020
APT6/8 SP-R	5'-TTTATGGGCTTTGGTGAGGG-3'	8493 - 8474
COXIII-RT	5'-TTACATCGCGCCATCATTGG-3'	9390 - 9371
COXIII LP-F	5'-GCTTCCACGGACTTCACGTC-3'	9811 - 9830
COXIII LP-R	5'-GTGTTGGTTAGTAGGCCTAG-3'	9358 - 9339
COXIII SP-F	5'-TCACTATCTGCTTCATCCGC-3'	9850 - 9869
COXIII SP-R	5'-ATGAGGAGCGTTATGGAGTG-3'	9337 - 9318
12S-RT	5'-TGGCTGGCACGAAATTGACC-3'	896 - 877
12S LP-F	5'-GAGTGCTTAGTTGAACAGGG-3'	1445 - 1464
12S LP-R	5'-AACCCTGGGGTTAGTATAGC-3'	876 - 857
12S SP-F	5'-ACCCTCCTCAAGTATACTTC-3'	1492 - 1511
12S SP-R	5'-AATCACTGCTGTTTCCCGTG-3'	825 - 806

b)

RNA	Lenght of final PCRproduct [-poly(A)]	Lenght of final PCRproduct [+poly(A) 60 bp]
ND3	155 bp	***~215 bp***
CYTB	228 bp	***~288 bp***
ATP6/8	335 bp	***~395 bp***
COX III	271 bp	***~331 bp***
12 S	***287 bp***	-

Supplementary material 2. Genomic organization of the gene coding for the putative hmtPAP. a) Exons are depicted schematically as grey boxes and designated e1-e9. Introns are denoted i1-i9. The scale in the top illustrates the genomic region of approximately 35.5 kb, that is covered by the gene; b) ***atg*** indicates an initiation codon. Asterisk indicates the position of termination codon TGA. Two first and two last base pairs of each intron are underlined in order to emphasize that all exon/intron junctions match the criteria of GT-AG rule.

a)



b)

Number	**Exons**			**Introns**		
	length (bp)	**sequence of 5'-end**	**sequence of 3'-end**	**Length (bp)**	**sequence of 5'-end**	**sequence of 3'-end**
1	157	***atg***gcggttc	gtggagacag	7478	**GT**gatggcgc	tcgttcat**AG**
2	173	gctttgaaga	tgaaagcttt	1017	**GT**aagtattt	tttggtat**AG**
3	225	ggtctctatg	tgcagaaagt	3198	**GT**aagttttt	ggctagct**AG**
4	225	atagacgatc	cgctcacaag	10167	**GT**aagtctat	tatttttc**AG**
5	212	atctcaggaa	cgaacaatag	3806	**GT**atgaccgc	ttttttga**AG**
6	227	gattgccttg	accctagcag	6180	**GT**aagactag	tgtgttta**AG**
7	93	atgcagaaga	gaaacattag	81	**GT**aagtgtca	tttcttac**AG**
8	74	aattactact	tattcgacag	1992	**GT**aaataatg	taatctat**AG**
9	360	ggaagggagc	tactcagaca*	-	-	-