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## SUPPLEMENTARY

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### Manuscript Title

Spermatozoal mitochondrial dynamics markers and other functionality-related signaling molecules exert circadian-like response to repeated stress of whole organism

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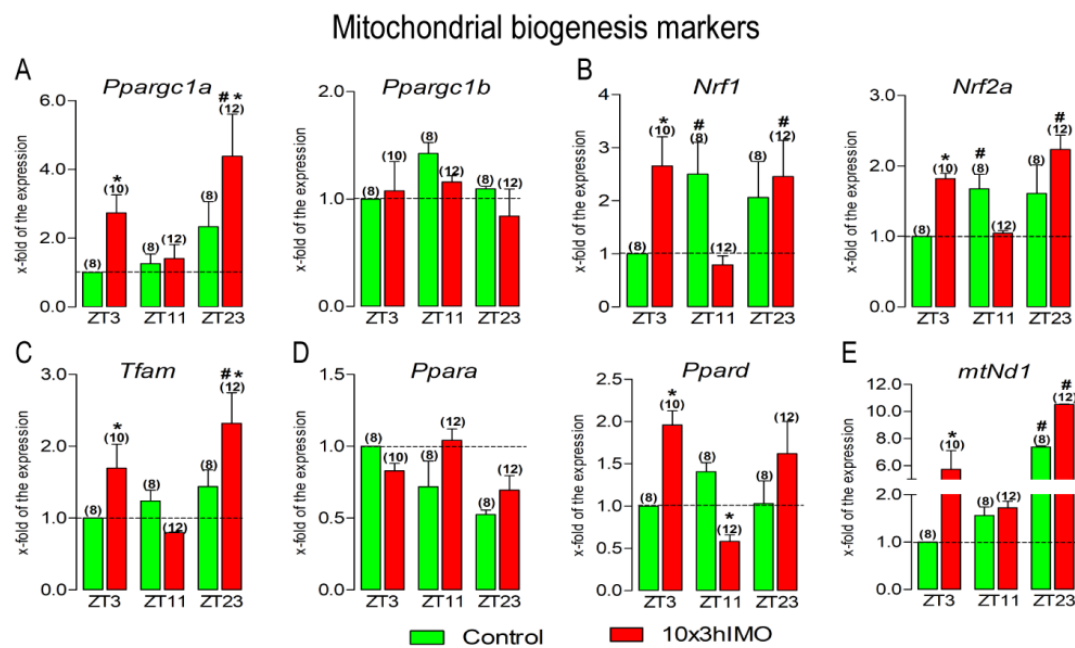
Web: <http://wwwold.dbe.pmf.uns.ac.rs/en/nauka-eng/lares>

Supplementary information file contains supplementary results and supplementary material and methods sections. Supplementary results section has presentation of the results from the main manuscript file calculated using the controls from ZT3 time point as calibrator. Material and methods section contains key resource table and tables of primers and antibodies used in the research.

## SUPPLEMENTARY RESULTS

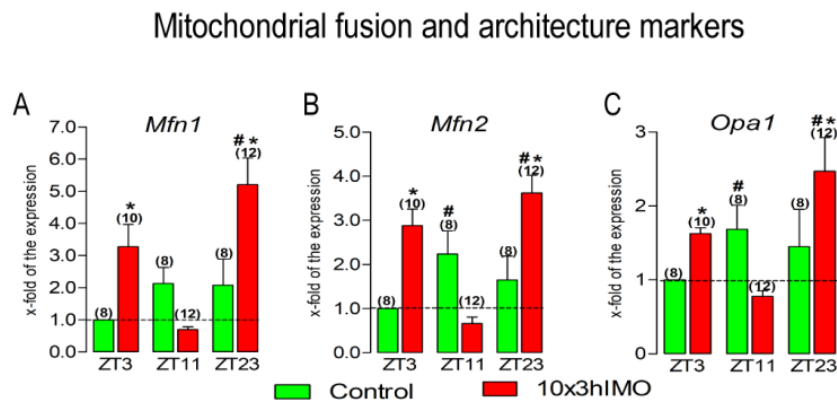
**Relative expression of transcripts of mitochondrial biogenesis and functionality markers as well as markers of signaling pathways regulating mitochondrial dynamic and spermatozoa functionality calculated using the control group of the ZT3 time point as a calibrator.**

Calculation of relative gene expression, using the control group of the ZT3 time point as a calibrator, showed the changes of control and 10x3hIMO groups of each time point compared to the control group of the ZT3 time point. Transcriptional changes of mitochondrial dynamics and functionality markers in spermatozoa of repeatedly stressed adult rats are the most prominent at the ZT3 and ZT23 time points, compared to the ZT3-Controls. All of the followed mitochondrial biogenesis markers (except *Ppargc1b* and *Ppara*) and markers of mitochondrial fusion and architecture are significantly increased in spermatozoa from ZT3 and ZT23 10x3hIMO group compared to ZT3-Control group. In addition, *Drp1*, *Pink1*, *Prkn* and *Cox4i2* also increased, while *Ucp3* decreased, indicating significant transcriptional changes of mitochondrial autophagy and function at the ZT3 and ZT23 time point (Supplementary Figure S1, S2, S3, S4, S5). Also, transcription of the signaling molecules of cAMP and MAPK pathways (regulating mitochondrial dynamics and functionality as well as spermatozoa number and functionality) is the most significantly changed in the spermatozoa of repeatedly stressed adult rats at ZT3 and ZT23 time points, compared to the controls of the ZT3 time point (Supplementary Figure S6, S7).

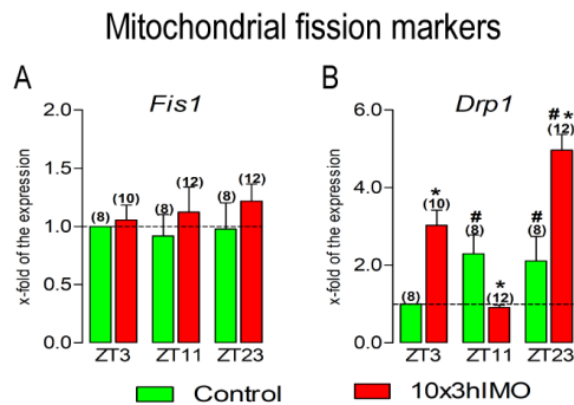


**Supplementary Figure S1.** Different transcriptional profiles of mitochondrial biogenesis markers in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point.

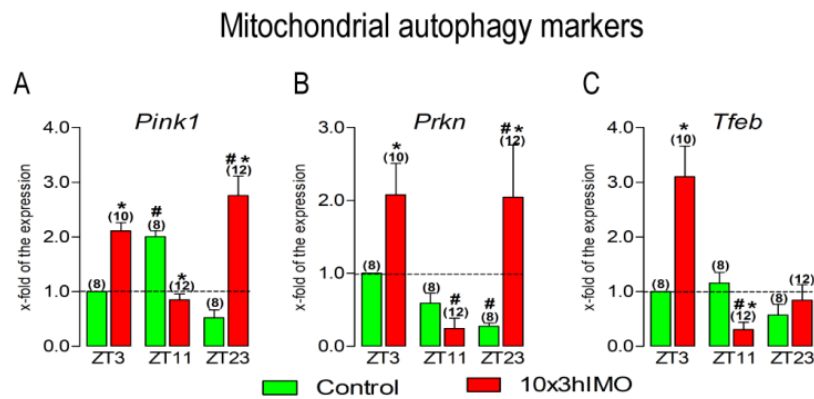
Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA and protein isolation and further analysis of the transcriptional profile of mitochondrial biogenesis markers. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.



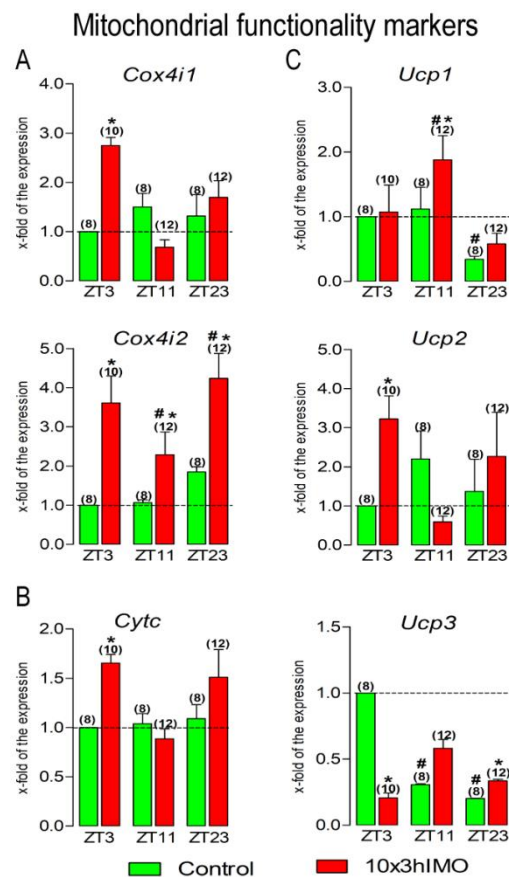
**Supplementary Figure S2.** Different transcriptional profiles of mitochondrial fusion and architecture markers in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point. Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA isolation and further analysis of the transcriptional profile of markers of mitochondrial fusion and architecture. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.



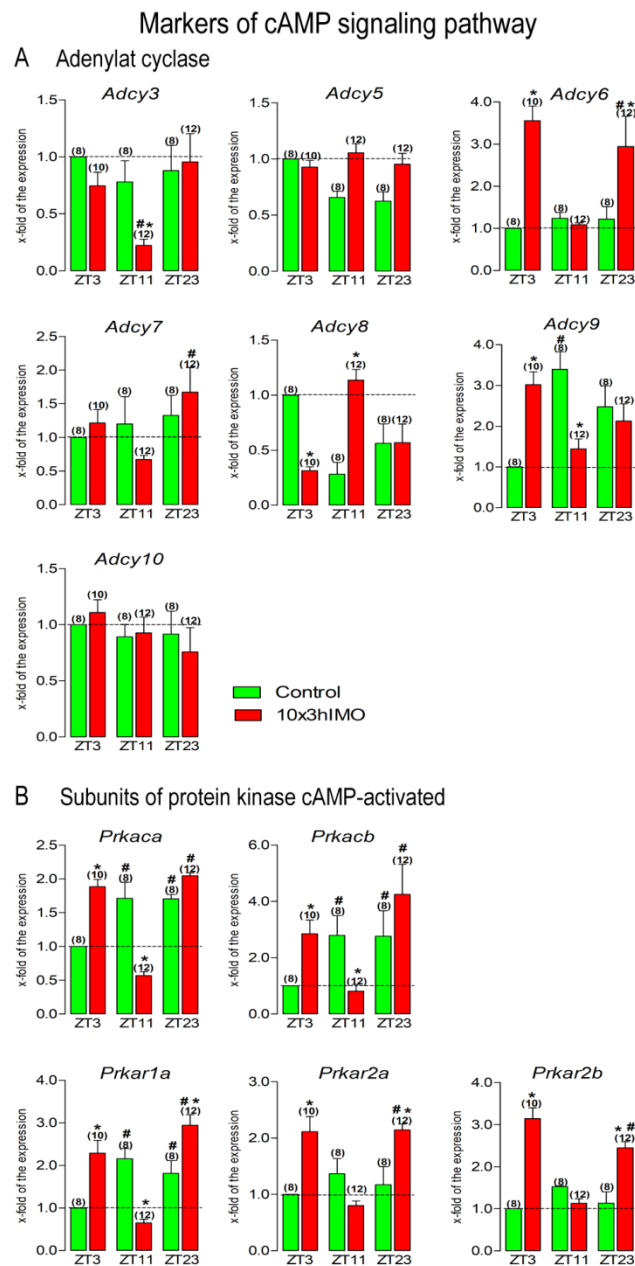
**Supplementary Figure S3.** Different transcriptional profiles of mitochondrial fission markers in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point. Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA isolation and further analysis of the transcriptional profile of markers of mitochondrial fission. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.



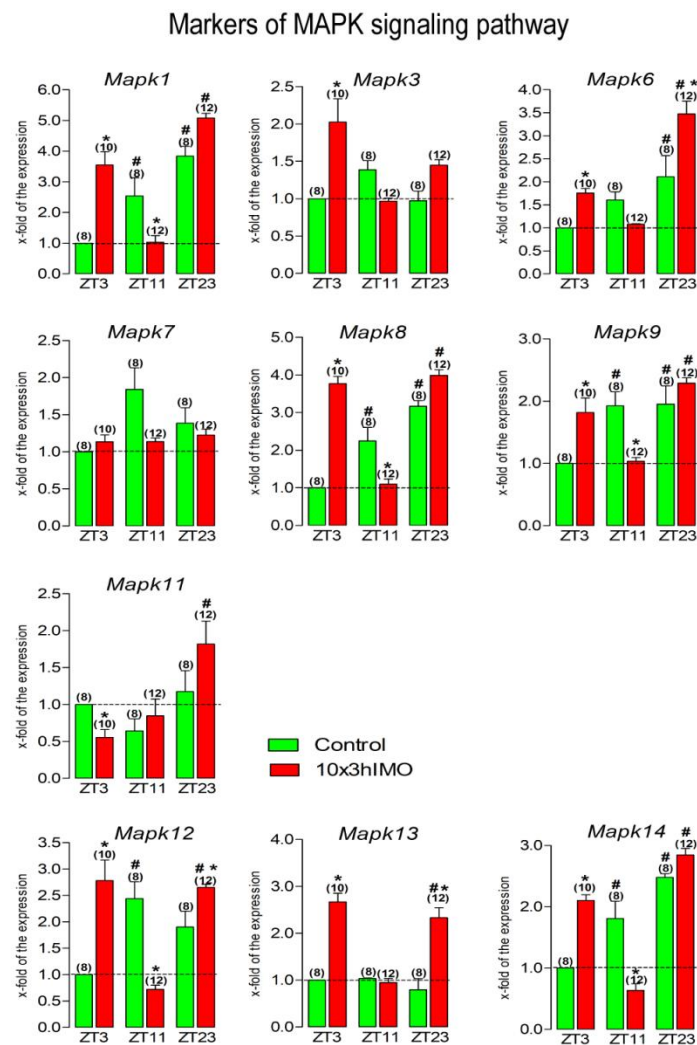
**Supplementary Figure S4.** Different transcriptional profiles of mitochondrial autophagy markers in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point. Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA isolation and further analysis of the transcriptional profile of markers of mitochondrial autophagy. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.



**Supplementary Figure S5.** Different transcriptional profiles of mitochondrial functionality markers in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point. Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA isolation and further analysis of the transcriptional profile of markers of mitochondrial functionality. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.



**Supplementary Figure S6.** Different transcriptional profiles of markers of cAMP signaling regulating mitochondrial dynamics and functionality as well as spermatozoa number and functionality in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point. Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA isolation and further analysis of the transcriptional profile of markers of cAMP signaling pathway. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.



**Supplementary Figure S7.** Different transcriptional profiles of markers of MAPK signaling regulating mitochondrial dynamics and functionality as well as spermatozoa number and functionality in spermatozoa of repeatedly stressed adult rats at different time points normalized to the control group of the ZT3 time point. Spermatozoa isolated from undisturbed and repeatedly stressed rats were used for RNA isolation and further analysis of the transcriptional profile of markers of MAPK signaling pathway. Data bars are mean  $\pm$  SEM values of two independent *in vivo* experiments. Statistical significance was set at level  $p < 0.05$ : \* vs. control group of the same time point, # vs. control group of the ZT3 time point.

## SUPPLEMENTARY MATERIAL AND METHODS

**Supplementary Table S1.** Key resources table.

Resource or reagent	Source	Identifier
<b>Experimental model and biological samples</b>		
Wistar rat	LaRES and ChronAge Laboratories (DBE, Faculty of Sciences, University of Novi Sad, Serbia)	<a href="http://wwwold.dbc.pmf.uns.ac.rs/en/nauka-eng/lares">http://wwwold.dbc.pmf.uns.ac.rs/en/nauka-eng/lares</a>
Primary culture of spermatozoa	Three months-old male rats	NA
Serum	Three months-old male rats	NA
<b>Commercial Reagents/Assays</b>		
Anti-testosterone serum №250 for Radioimmunoassay (T+DHT)	NA	NA
Corticosterone EIA Kit	Cayman Chemical, USA	<a href="https://www.caymanchem.com">https://www.caymanchem.com</a>
GenElute™ Mammalian Total RNA Miniprep Kit	Sigma Aldrich, Germany	<a href="https://www.sigmaaldrich.com">https://www.sigmaaldrich.com</a>
DNase I (RNase-free) treatment	New England Biolabs, USA	<a href="https://international.neb.com">https://international.neb.com</a>
High Capacity Kit for cDNA	Applied Biosystems/Thermo Fisher Scientific, USA	<a href="https://www.thermofisher.com">https://www.thermofisher.com</a>
Power SYBR® Green PCR Master Mix	Applied Biosystems/Thermo Fisher Scientific, USA	<a href="https://www.thermofisher.com">https://www.thermofisher.com</a>
<b>Primers</b>		
Supplementary Tables S2 to S8	This paper	<a href="http://www.ncbi.nlm.nih.gov/sites/entrez">www.ncbi.nlm.nih.gov/sites/entrez</a>
<b>Antibodies</b>		
Rabbit polyclonal anti-PGC-1 (H-300) antibody	Santa Cruz Biotechnology Inc.	Cat # sc-13067
Rabbit polyclonal anti-NRF2 (C-20)	Santa Cruz Biotechnology Inc.	Cat # sc-722

antibody		
Mouse monoclonal anti-PKA[C]	BD Transduction Laboratories	Cat # 610980
Rabbit polyclonal anti-p38MAPK antibody	Cell Signaling Technology	Cat # 9212
<b>Software</b>		
GraphPad Prism 5 Software	GraphPad Prism	<a href="https://www.graphpad.com/scientific-software/prism">https://www.graphpad.com/scientific-software/prism</a>

**Supplementary Table S2.** Primers sequences used for the real-time PCR analysis of molecular markers of mitochondrial biogenesis.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT11	ZT23
<i>Ppargc1a</i>	NM_031347	F: 5'-AGCCGTAGGCCCAGGTATGACA-3' R: 5'-TGCTTGGCCCTTTCAGACTCCC-3'	22 bp 22 bp	107 bp	30.32	31.06	31.47
<i>Ppargc1b</i>	NM_176075	F: 5'-ACCTCCGGTGTTCGGAGCATG-3' R: 5'-GTGGAAGGAGGGCTCATTGCGT-3'	22 bp 22 bp	81 bp	28.64	28.63	29.07
<i>Tfam</i>	NM_031326	F: 5'-TATAGTCGTCGGCCGAGGGAT-3' R: 5'-AAGGCTGACAGGCGAGGGTATG-3'	22 bp 22 bp	125 bp	28.32	28.62	28.46
<i>Nrf1</i>	NM_001100708	F: 5'-GACCATCCAGACGACGCAAGCA-3' R: 5'-ATGGGCGGCAGCTTCACTGTT-3'	22 bp 21 bp	136 bp	28.31	27.86	30.28
<i>Nrf2a</i>	NM_001108841	F: 5'-AGCGGAACTGAACCGCTTGGT-3' R: 5'-GTGACTGGCTGAGCAATCCCGT-3'	21 bp 22 bp	84 bp	28.02	27.55	28.27
<i>Ppara</i>	NM_013196	F: 5'-GTCCTGGAAGTGAAGCGACGCT-3' R: 5'-TTACGCCCAAATGCACCACGC-3'	22 bp 21 bp	110 bp	28.36	28.86	27.77
<i>Ppard</i>	NM_013141	F: 5'-ACGGTAAAGGCGGTCCATCTGC-3' R: 5'-TCCTCCTGTGGCTGTTCATGAC-3'	22 bp 23 bp	109 bp	26.63	26.29	27.62
<i>mtNd1</i>		F: 5' GCGTGGGAGGAGCATCAGGG 3' R: 5' GCGAATGGTCTCGGCGT A 3'	20 bp 20 bp	271 bp	18.44	18.73	20.00
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	21.42	21.25	21.23

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from the NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.



**Supplementary Table S3.** Primers sequences used for the real-time PCR analysis of molecular markers of mitochondrial fusion and architecture.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT11	ZT23
<i>Mfn1</i>	NM_138976.1	F: 5'-CCTTGTACATCGATTCTGGGTTC-3' R: 5'-CCTGGGCTGCATTATCTGGTG-3'	24 bp 21 bp	143 bp	29.33	29.49	31.27
<i>Mfn2</i>	NM_130894.4	F: 5'-TCAAGCGCCAGTTTGTGGAG-3' R: 5'-CACAGATGAGCAAATGTCCCAGA-3'	20 bp 23 bp	118 bp	27.50	27.42	29.87
<i>Opa1</i>	NM_133585.3	F: 5'-AAAAGCCCTTCCCAGTTCAGA-3' R: 5'-TACCCGCAGTGAAGAAATCCTT-3'	21 bp 22 bp	101 bp	26.37	26.55	27.07
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	21.42	21.25	21.23

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.

**Supplementary Table S4.** Primers sequences used for the real-time PCR analysis of molecular markers of mitochondrial fission.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT11	ZT23
<i>Fis1</i>	NM_001105919.1	F: 5'-ACGCCTGCCGTTACTTCTTC-3' R: 5'-GCAACCCTGCAATCCTTCAC-3'	20 bp 20 bp	108 bp	29.29	29.57	28.47
<i>Drp1</i>	NM_053655.3	F: 5'-AGGTGCCCCGTGACAAATGA-3' R: 5'-CACAGGCATCAGCAAAGTCG-3'	20 bp 20 bp	94 bp	30.05	29.92	32.32
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	23.16	21.31	20.83

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.

**Supplementary Table S5.** Primers sequences used for the real-time PCR analysis of molecular markers of mitochondrial autophagy.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT11	ZT23
<i>Pink1</i>	NM_001106694.1	F: 5'-CAAGCAAGTGTCTGACCCAC-3' R: 5'-GCTTCATACACAGCGGCATT-3'	20 bp 20 bp	111 bp	26.18	25.25	27.67
<i>Prkn</i>	NM_020093.1	F: 5'-CTTCCAGCTCAAGGAAGTGG-3' R: 5'-CAGAGGCATTGTTCGTGA-3'	20 bp 20 bp	182 bp	32.70	33.43	34.79
<i>Tfeb</i>	NM_001025707.1	F: 5'-CGACAACATTATGCGCCTGG-3' R: 5'-CTGTACACGTTTCAGGTGGCT-3'	20 bp 20 bp	102 bp	29.53	29.70	30.38
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	21.45	21.61	21.51

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.

**Supplementary Table S6.** Primers sequences used for the real-time PCR analysis of molecular markers of mitochondrial functionality.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT3	ZT3
<i>Cox4i1</i>	NM_017202	F: 5'-CGCTGAGATGAACAAGGGCACC-3' R: 5'-TCCCAGATCAGCACAAGCGCA-3'	22 bp 21 bp	93 bp	22.55	22.48	24.20
<i>Cox4i2</i>	NM_053472	F: 5'-CACAGCCCAGGAAGTGTGCTA-3' R: 5'-TGTGCAGTAAGGTCATCCGGC-3'	22 bp 22 bp	105 bp	31.34	32.60	32.20
<i>Cytc</i>	NM_012839	F: 5'-GCAAGCATAAGACTGGACCAAA-3' R: 5'-TTGTTGGCATCTGTGTAAGAGAATC-3'	22 bp 25 bp	88 bp	23.62	23.85	23.87
<i>Ucp1</i>	NM_012682	F: 5'-TCAGCTCTTGTCGCCGGTTT-3' R: 5'-TGCACAGCTGGGTACACTTGGG-3'	21 bp 22 bp	114 bp	29.77	30.06	29.85
<i>Ucp2</i>	NM_019354	F: 5'-ACGACCTCCCTTGCCACTTCAC-3' R: 5'-GGTACTGGCCCAAGGCAGAGTT-3'	22 bp 22 bp	117 bp	23.06	22.54	24.87
<i>Ucp3</i>	NM_013167	F: 5'-TGCTCAACCCACGGATGTGGT-3' R: 5'-CCTGGCGATGGTCTGTAGGCA-3'	21 bp 22 bp	112 bp	28.97	29.80	29.71
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	21.42	21.25	21.23

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from the NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.

**Supplementary Table S7.** Primers sequences used for the real-time PCR analysis of cAMP signaling elements.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT3	ZT3
<i>Adcy3</i>	NM_130779	F: 5'-GCATCGAAACCTACCTCATCA-3' R: 5'-TGGGCTCCTTGGTCTCA ATAA-3'	21 bp 21 bp	141 bp	31.87	32.16	32.45
<i>Adcy5</i>	NM_022600	F: 5'-AACCAGGTGAACGCATGTCA-3' R: 5'-CTCTGGGAAGTTGCAGTTGGA-3'	20 bp 21 bp	105 bp	30.09	30.37	30.56
<i>Adcy6</i>	NM_012821	F: 5'-CTGCCTCAGCCTGCTTATGTG-3' R: 5'-GGAGTCCTGGCGGAAGCT-3'	21 bp 18 bp	99 bp	28.40	27.96	27.68
<i>Adcy7</i>	NM_053396	F: 5'-TTCCGTGCGTGTAACCCGCT-3' R: 5'-GCCTTCTGCCTCCGTCGTT-3'	20 bp 20 bp	123 bp	27.54	26.72	26.92
<i>Adcy8</i>	NM_017142	F: 5'-ATTGCCTCAGTGGTACTA-3' R: 5'-CAAACCTCTCTCGGGCT-3'	19 bp 17 bp	113 bp	29.21	30.71	29.01
<i>Adcy9</i>	NM_001106 980	F: 5'-TCACCAAGCTGTACGCCCGG-3' R: 5'-GGGCTGTCAACACGTCCCGA-3'	20 bp 20 bp	124 bp	30.41	29.40	29.17
<i>Adcy10</i>	NM_021684	F: 5'-CCAGGCATCGTGACCTGCGA-3' R: 5'-ACTGGTCCGGGATCCGCAAC-3'	20 bp 20 bp	113 bp	30.83	30.81	30.59
<i>Prkaca</i>	NM_001100 922.1	F: 5'-TCAGTGAGCCCCACGCCCGTT-3' R: 5'-TCTCGGGCTTCAGGTCCCGG-3'	21 bp 20 bp	99 bp	27.51	26.71	27.29
<i>Prkacb</i>	NM_001077 645	F: 5'-GGGTCATGGGGAACACGGCG-3' R: 5'-CCAGCATTACTCGGGGAGGGT-3'	20 bp 22 bp	124 bp	28.76	27.46	27.73
<i>Prkar1a</i>	NM_013181	F: 5'-TGTGCTGCAGCGTCGGTCAG-3' R: 5'-AGTGGCAGCCCCGAGGACGAT-3'	20 bp 20 bp	112 bp	25.94	24.74	24.63
<i>Prkar2a</i>	NM_019264	F: 5'-GCCCCACCTCGTCGACTTCG-3' R: 5'-TCCTGCGCGTGAAAGGTCGT-3'	20 bp 20 bp	108 bp	27.71	27.25	27.72
<i>Prkar2b</i>	NM_001030 020	F: 5'-CCCATGCGCTCCGATTCCGA-3' R: 5'-GCACATACCGAGGCACGCCT-3'	20 bp 20 bp	107 bp	31.51	29.87	31.13
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	21.85	21.57	21.03

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.

**Supplementary Table S8.** Primers sequences used for the real-time PCR analysis of MAPK signaling elements.

Gene	Accession code	Primers	Primer length	Product length	AV Ct		
					ZT3	ZT3	ZT3
<i>Mapk1</i>	NM_053842.1	F: 5'-GTTCTGCACCGTGACCTCAAG-3' R: 5'-GCAAGGCCAAAGTCACAGATC-3'	21 bp 21 bp	80 bp	28.11	26.84	28.00
<i>Mapk3</i>	NM_017347.2	F: 5'-TCCCTCTCAAGCTGCCACAT-3' R: 5'-ACATCCAATCACCCACACACA-3'	20 bp 21 bp	60 bp	27.56	26.90	27.01
<i>Mapk6</i>	NM_031622.2	F: 5'-CATTTGAACTGGCATGTCGTTT-3' R: 5'-CCTGCACTGCATTGTTTGC-3'	22 bp 20 bp	62 bp	27.89	26.78	26.52
<i>Mapk7</i>	NM_001191547.1	F: 5'-GCCCCTTCCACTAGCCTTTT-3' R: 5'-GAACCAGGCAACCCACTAGGT-3'	20 bp 21 bp	62 bp	28.98	28.09	27.91
<i>Mapk8</i>	NM_053829.2	F: 5'-TCAACGTCTGGTATGATCCTTCA-3' R: 5'-CTGCTTGTCAGGGATCTTTGG-3'	23 bp 21 bp	62 bp	29.11	28.00	28.69
<i>Mapk9</i>	NM_017322.1 NM_001270544.1 NM_001270545.1	F: 5'-GGAAGGCTGCCGATGAAA-3' R: 5'-AGCCAGAGTCCTTCACAGACAAG-3'	18 bp 23 bp	57 bp	28.65	27.51	27.30
<i>Mapk11</i>	NM_001109532.2	F: 5'-GGGCGCTGACCTGAATAACA-3' R: 5'-GCAGCAGCTGGTAGACAAGGA-3'	20 bp 21 bp	80 bp	30.43	30.52	30.52
<i>Mapk12</i>	NM_021746.1	F: 5'-GGATGTGTTCACTCCCGATGA-3' R: 5'-CCAGGTCAGTGCCCATGAAT-3'	21 bp 20 bp	80 bp	28.99	27.46	28.60
<i>Mapk13</i>	NM_019231.2	F: 5'-CTGGTCTGTTGGCTGCATCA-3' R: 5'-TCAGCTGGTCCAGGTAGTCCTT-3'	20 bp 22 bp	80 bp	28.28	27.51	29.22
<i>Mapk14</i>	NM_031020.2	F: 5'-GCTGTCGACCTGCTGGAAAA-3' R: 5'-TAGGCATGCGCAAGAGCTT-3'	20 bp 19 bp	80 bp	27.19	26.24	26.88
<i>Gapdh</i>	NM_017008	F: 5'-TGCCAAGTATGATGACATCAAGAAG-3' R: 5'-AGCCCAGGATGCCCTTTAGT-3'	25 bp 20 bp	110 bp	21.93	21.61	21.03

Primers were designed by using software Primer Express 3.0 (Applied Biosystems) and full genes sequences from NCBI Entrez Nucleotide database ([www.ncbi.nlm.nih.gov/sites/entrez](http://www.ncbi.nlm.nih.gov/sites/entrez)). F - forward; R - reverse.

**Supplementary Table S9.** The characteristics of the antibodies.

Target	Name of antibody	Antigen sequence	Manufacturer, catalog #	Mono- or polyclonal	Dil. used
<b>PGC-1</b>	PGC-1 (H-300); sc-13067	Amino acids 1-300 mapping near the N-terminus of PGC-1 of human origin	Santa Cruz Biotechnology Inc. sc-13067 Mw (PGC-1) = 90 kDa	Rabbit polyclonal antibody	1:200
<b>NRF2</b>	NRF2 (C-20); sc-722	Peptide mapping at the C-terminus of Nrf2 of human origin	Santa Cruz Biotechnology Inc. sc-722 Mw (NRF2) = 57/100 kDa	Rabbit polyclonal antibody	1:100
<b>PKAc</b>	PKA [C]:610980	Human PKA[Ca] subunit aa. 18-347	BD Transduction Laboratories 610980 Mw (PKAc) = 40 kDa	Mouse monoclonal antibody	1:200
<b>p38MAPK</b>	p38MAPK: 9212	Detects total p38 $\alpha$ , - $\beta$ or - $\gamma$ MAPK protein	Cell Signaling Technology 9212 Mw (p38MAPK) = 43 kDa	Polyclonal Rabbit antibody	1:1000