

Supplementary Table S1. Biomarkers found modulated after DOX administration for the two time-points selected. The assessment (morphometric/serum/cardiac tissue) and the biological/molecular pathway of each biomarker is indicated. No changing (=), upregulation (↑) and downregulation (↓) is indicated for each time-point considering the modulation found for DOX compared to CTRL group. The predisposition to increased (⊕) or decreased (⊖) values in DOX compared to CTRL group is also indicated.

Assessment	Biological pathway	Biomarker	first time-point (one week)	second time-point (five months)
Morphometric	biometric	<i>whole-body weight</i>	=	↓
Morphometric	biometric	<i>heart weight</i>	=	↓
Morphometric	biometric	<i>tibial length</i>	=	↓
Morphometric	biometric	<i>heart weigh-to-whole-body weight</i>	=	=
Morphometric	biometric	<i>heart weigh-to-tibial length</i>	=	=
Serum	systemic whole-body metabolism	<i>glucose</i>	=	=
Serum	system inflammation	<i>total protein</i>	=	=
Serum	system inflammation	<i>albumin</i>	⊖	=
Serum	system inflammation	<i>CRP</i>	=	⊖
Serum	system inflammation	<i>DNP</i>	=	=
Serum	system inflammation	<i>nitrotyrosine</i>	=	=
Serum	cardiac inflammation	<i>CK-MB</i>	=	=
Cardiac tissue	energetic metabolism	<i>GLUT4</i>	⊖	=
Cardiac tissue	energetic metabolism	<i>PFKM</i>	=	=

Cardiac tissue	energetic metabolism	<i>ETF-QO</i>	↑	=
Cardiac tissue	energetic metabolism	<i>ATPB</i>	↑	=
Cardiac tissue	energetic metabolism	<i>SIRT3</i>	=	=
Cardiac tissue	energetic metabolism	<i>PPARα</i>	=	=
Cardiac tissue	energetic metabolism	<i>PPARγ</i>	=	=
Cardiac tissue	energetic metabolism	<i>GSK-3β</i>	=	=
Cardiac tissue	energetic metabolism	<i>AMPK</i>	↓	=
Cardiac tissue	energetic metabolism	<i>pAMPK</i>	=	=
Cardiac tissue	energetic metabolism	<i>pAMPK-to-AMPK</i>	=	=
Cardiac tissue	redox/oxidative stress status	<i>DNP</i>	=	=
Cardiac tissue	redox/oxidative stress status	<i>nitrotyrosine</i>	=	=
Cardiac tissue	redox/oxidative stress status	<i>MnSOD</i>	=	↓
Cardiac tissue	mitochondrial density	<i>CS activity</i>	↑	↓
Cardiac tissue	mitochondrial biogenesis	<i>PGC-1α</i>	=	=
Cardiac tissue	mitochondrial biogenesis	<i>Tfam</i>	=	=
Cardiac tissue	mitochondrial fusion	<i>Mfn1</i>	↓	=
Cardiac tissue	autophagy	<i>Beclin1</i>	=	↓
Cardiac tissue	autophagy	<i>ATG5</i>	=	↓
Cardiac tissue	autophagy	<i>LC3B</i>	=	↓

Cardiac tissue	mitophagy	<i>Parkin</i>	=	=
Cardiac tissue	mitophagy/apoptosis	<i>BNIP3</i>	↑	=
Cardiac tissue	apoptosis	<i>BAX</i>	↑	=
Cardiac tissue	apoptosis	<i>BCL2</i>	=	=
Cardiac tissue	apoptosis	<i>BAX-to-BCL2</i>	↑	=
Cardiac tissue	autophagy/protein folding	<i>HSP27</i>	=	↑
Cardiac tissue	autophagy/protein folding	<i>HSP70</i>	=	=
Cardiac tissue	regeneration	<i>SCFR</i>	=	=
Cardiac tissue	regeneration	<i>C/EBPβ</i>	=	=
Cardiac tissue	regeneration	<i>CITED4</i>	=	=