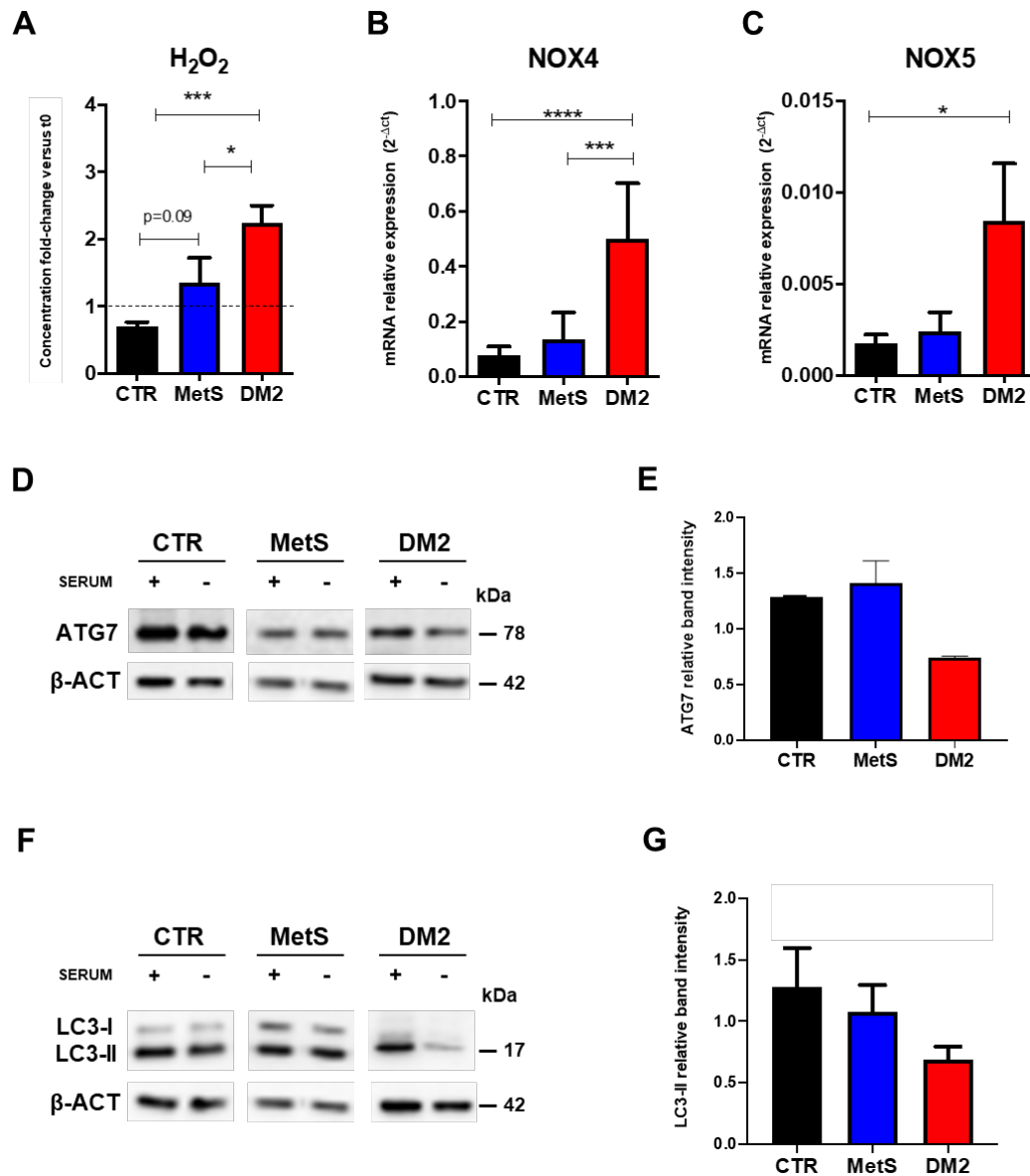


**Progressive stages of dysmetabolism are associated with impaired biological features of human cardiac stromal cells mediated by the oxidative state and autophagy**

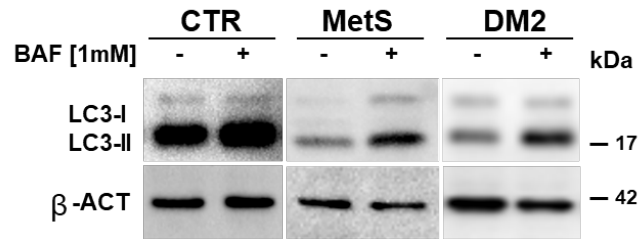
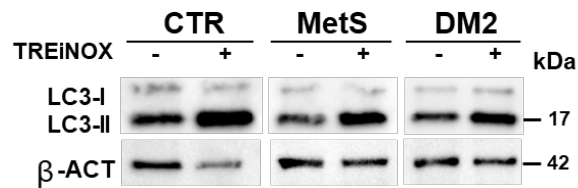
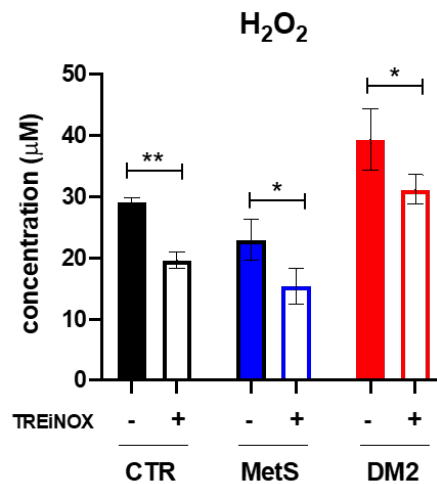
F Pagano, V Pichio, *et al.* *J Pathol* <https://doi.org/10.1002/path.5985>

**Supplementary Figures S1, S2**

**Supplementary Table S1**



**Figure S1. Oxidative state and autophagy modulation in CSCs after starvation.** (A) Quantification of H<sub>2</sub>O<sub>2</sub> concentration in conditioned media samples of CSCs from the different donor groups. Gene expression analysis by RT-qPCR of *NOX4* (B) and *NOX5* (C) in CSCs from different groups. N>=6 for each group. Representative western blot panels of ATG7 (D) LC3-II (F) protein levels in CSCs from different donor groups, and relative densitometric analysis (E-G) after 4 hours of starvation, normalized to each corresponding non-starved reference. N>=3 for each group. \* P<0.05. \*\*\* P<0.001. \*\*\*\* P<0.0001.

**A****B****C**

**Figure S2. Validation of autophagy activation and TREiNOX treatment in CSCs.** (A) Representative western blot panels showing LC3-II protein levels at the end of the serum starvation performed adding either DMSO or Bafilomycin A (BAF) to CTR, MetS or DM2-CSC cultures 2 hours before harvesting the cells. (B) Representative western blot panel showing LC3-II and LC3-I, with and without TREiNOX treatment, to test for boosted autophagosome formation rather than reduced lysosome activity. (C) Quantification of hydrogen peroxide release in conditioned media with or without TREiNOX treatment, in CTR, MetS or DM2-CSC cultures to check for the treatment efficacy in reducing oxidative stress. N=3 for each group. \* P<0.05. \*\* P<0.01.

**Table S1.** Sequences of the primers used for RT-qPCR.

<b>Primer name</b>	<b>Sequence</b>
<i>GATA4</i> Forward	GTTTTTCCCCTTTGATTTTGGATC
<i>GATA4</i> Reverse	AACGACGGCAACAACGATAAT
<i>ACTA2</i> Forward	ATGAAGATCCTGACTGAGCG
<i>ACTA2</i> Reverse	GCAGTGGCCATCTCATTTC
<i>THY1</i> Forward	CAGCGGAAGACCCAGT
<i>THY1</i> Reverse	CGTTAGGCTGGTCACCTTCT
<i>NKX2-5</i> Forward	GGTGGAGCTGGAGAAGACAGA
<i>NKX2-5</i> Reverse	CGCCGCTCCAGTTCATAG
<i>POU5F1</i> Forward	GATCAGCCACATCGCCCAG
<i>POU5F1</i> Reverse	TCCCCCTGAGAAAGGAGACC
<i>COL1A1</i> Forward	CACACGTCTCGGTCATGGTA
<i>COL1A1</i> Reverse	AAGAGGAAGGCCAAGTCGAG
<i>COL3A1</i> Forward	CATGCCCTACTGGTCCTCAG
<i>COL3A1</i> Reverse	ATAGCCTGCGAGTCCTCCTA
<i>MMP1</i> Forward	ACAAGTCCAAATGGGCTTG
<i>MMP1</i> Reverse	TGTCCTTGGGGTATCCGTGT
<i>NOX4</i> Forward	AACCAAGGGCCAGAGTATCA
<i>NOX4</i> Reverse	GGATAAGGCTGCAGTTGAGG
<i>NOX5</i> Forward	CATCGATGTGTGTGCACGGC
<i>NOX5</i> Reverse	ATCCGGGTCAATGGAGCCAC
<i>HPRT1</i> Forward	TCCTCCTCCTGAGCAGTCA
<i>HPRT1</i> Reverse	ACCCTTTCCAAATCCTCAGC
<i>TNNI3</i> Forward	GGACAAGGTGGATGAAGAGA
<i>TNNI3</i> Reverse	AGGGTGGGCCGCTTAAACT
<i>SNAI1</i> Forward	CTTCTCTAGGCCCTGGCTG
<i>SNAI1</i> Reverse	CATCTGAGTGGGTCTGGAGG
<i>ADRB2</i> Forward	AGGCAGCTCCAGAAGATTGA
<i>ADRB2</i> Reverse	GTCTTGAGGGCTTTGTGCTC
<i>KIT</i> Forward	GATGGATGGATGGTGGAGAC
<i>KIT</i> Reverse	GGGATTTTCTCTGCGTTCTG

<i>CDH5</i> Forward	CAACGGAACAGAAACATCCC
<i>CDH5</i> Reverse	CTGCTGCTGCCACTGCT
<i>MYH1</i> Forward	CAGAAGAAGAAGATGGATGC
<i>MYH1</i> Reverse	CGCTGGTGTCTGCTCCT
<i>SNAI2</i> Forward	TCGGACCCACACATTACCTT
<i>SNAI2</i> Reverse	GCAGTGAGGGCAAGAAAAG
<i>CTNNB1</i> Forward	AGGTCTGAGGAGCAGCTTCA
<i>CTNNB1</i> Reverse	ATTGTCCACGCTGGATTTTC
<i>KDR</i> Forward	AAAGGGTGGAGGTGACTGAG
<i>KDR</i> Reverse	CGGTAGAAGCACTTGTAGGC
<i>GJA1</i> Forward	AGGAGTTCAATCACTTGGCG
<i>GJA1</i> Reverse	GAGTTTGCCTAAGGCGCTC
<i>CDH2</i> Forward	GTGCATGAAGGACAGCCTCT
<i>CDH2</i> Reverse	AGCTTCTCACGGCATAACACC
<i>TGFBR2</i> Forward	AGAAGTCGGAATATAACACCAGC
<i>TGFBR2</i> Reverse	TCACACAGGCAGCAGGTTAG
<i>VIM</i> Forward	ACCCACTCAAAAAGGACACTTC
<i>VIM</i> Reverse	GGTCATCGTGATGCTGACAA