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CORRECTION

Correction to: Sulforaphane protects granulosa cells against oxidative stress via activation of NRF2-ARE pathway

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There is an error in the original publication of this paper. Figures 1-6 were shown in the wrong version, thus corrected figures provided below:

The original article has been corrected.

The online version of the original article can be found at https://doi.org/10.1007/s00441-018-2877-z

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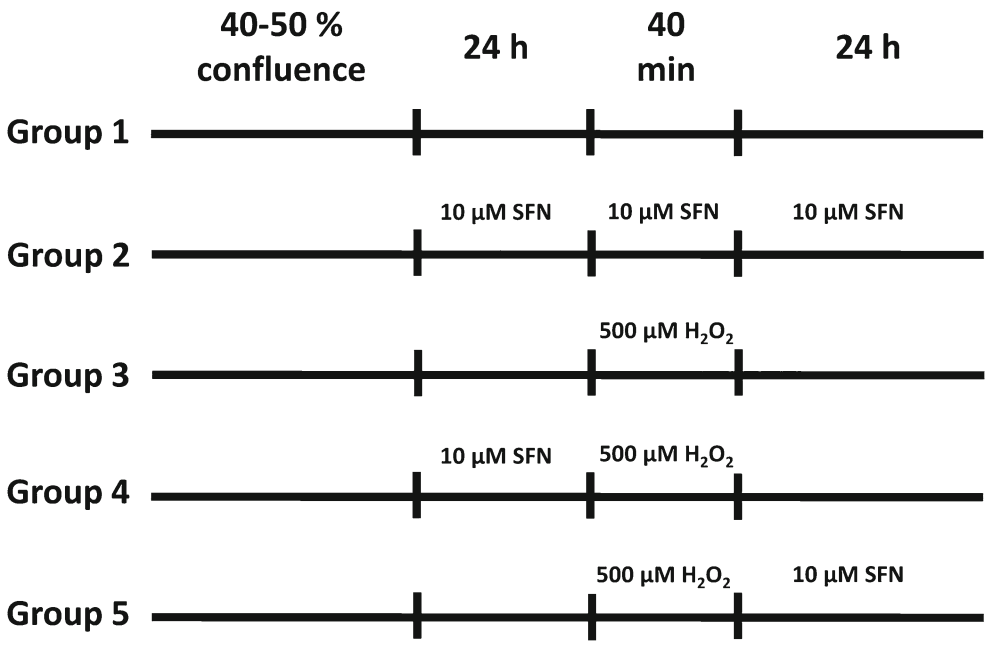

Fig. 1 Simplified experimental groups. Cells in all groups were grown to 40–50% confluence and continued different treatments under optimum culture conditions. Group 1: no treatment, cells were grown with complete medium; group 2: cells were treated with 10 μM SFN; group 3: cells were continued with complete medium up to 40–50% confluence followed by an incubation with 500 μM H_2O_2 for 40 min and continued with complete medium; group 4: cells were treated with 10 μM SFN for 24 h followed by 40-min incubation with 500 μM H_2O_2; group 5: cells were continued with complete medium followed by an incubation with 10 μM SFN + 500 μM H_2O_2 for 40 min and continued with 10 μM SFN

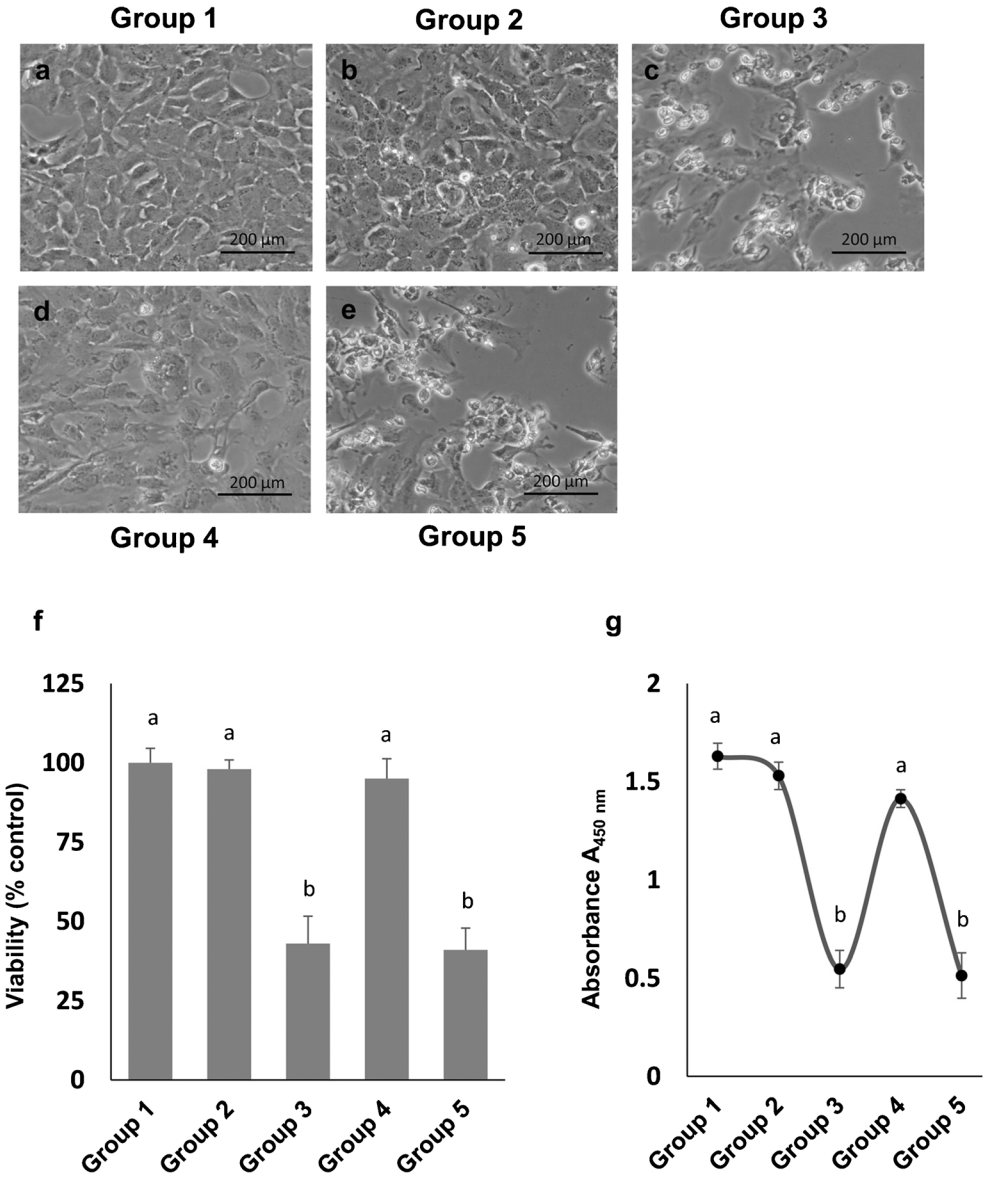

Fig. 2 Effects of different treatments on cellular morphology, viability and cytotoxicity. **a**–**e** Representative micrographs of different treatments (n = 3), scale bar 200 µm. **f** Cells were subjected to trypan blue dye exclusion test and were counted using a hemocytometer for cell viability. **g** Cytotoxicity of different treatments was determined using WST-1 kit using an ELISA reader. Data are presented as mean ± SEM (n = 3) of three independent experiments. Different superscript letters (a, b) denote a significant difference between groups, such that groups not sharing a similar letter are significantly different from each other ($p < 0.001$)

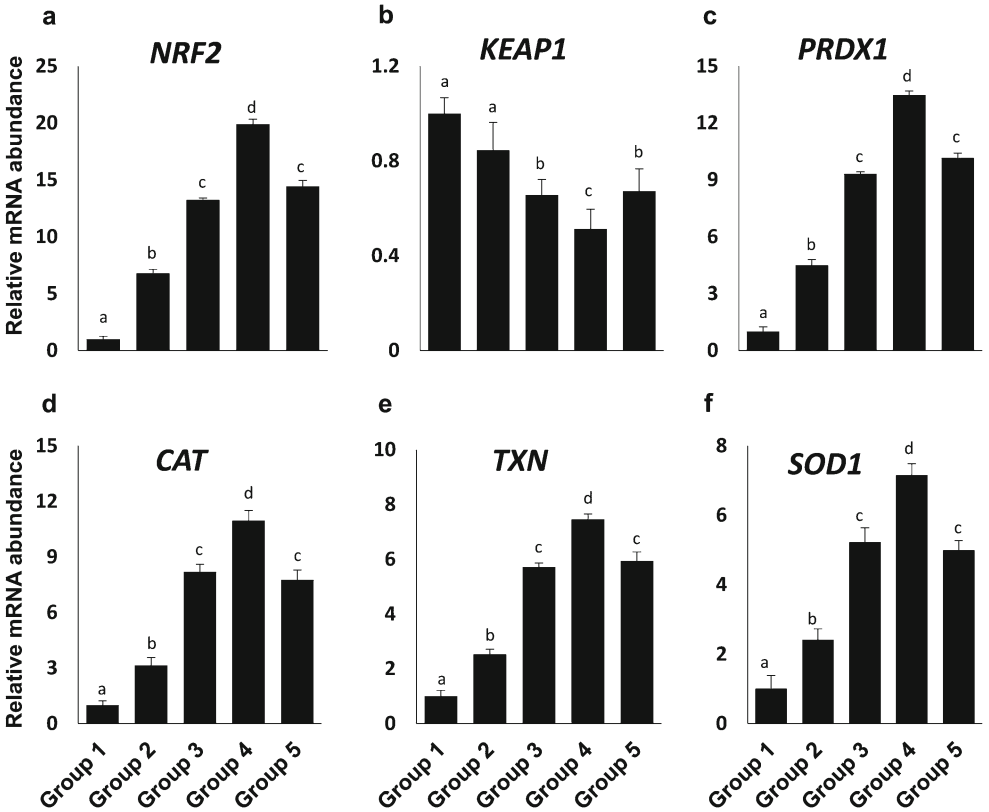

Fig. 3 (**a**–**f**) Expression of *NRF2*, *KEAP1* and candidate genes downstream to NRF2 activation. Expression of genes was quantified using qRT-PCR and relative abundance was analyzed using comparative CT ($2^{\Delta\Delta CT}$) method. Data are presented as mean ± SD of three biological replicates. Different superscript letters (*a*, *b*, *c*, *d*) denote a significant difference between groups ($p < 0.05$) as determined by Student's *t* test

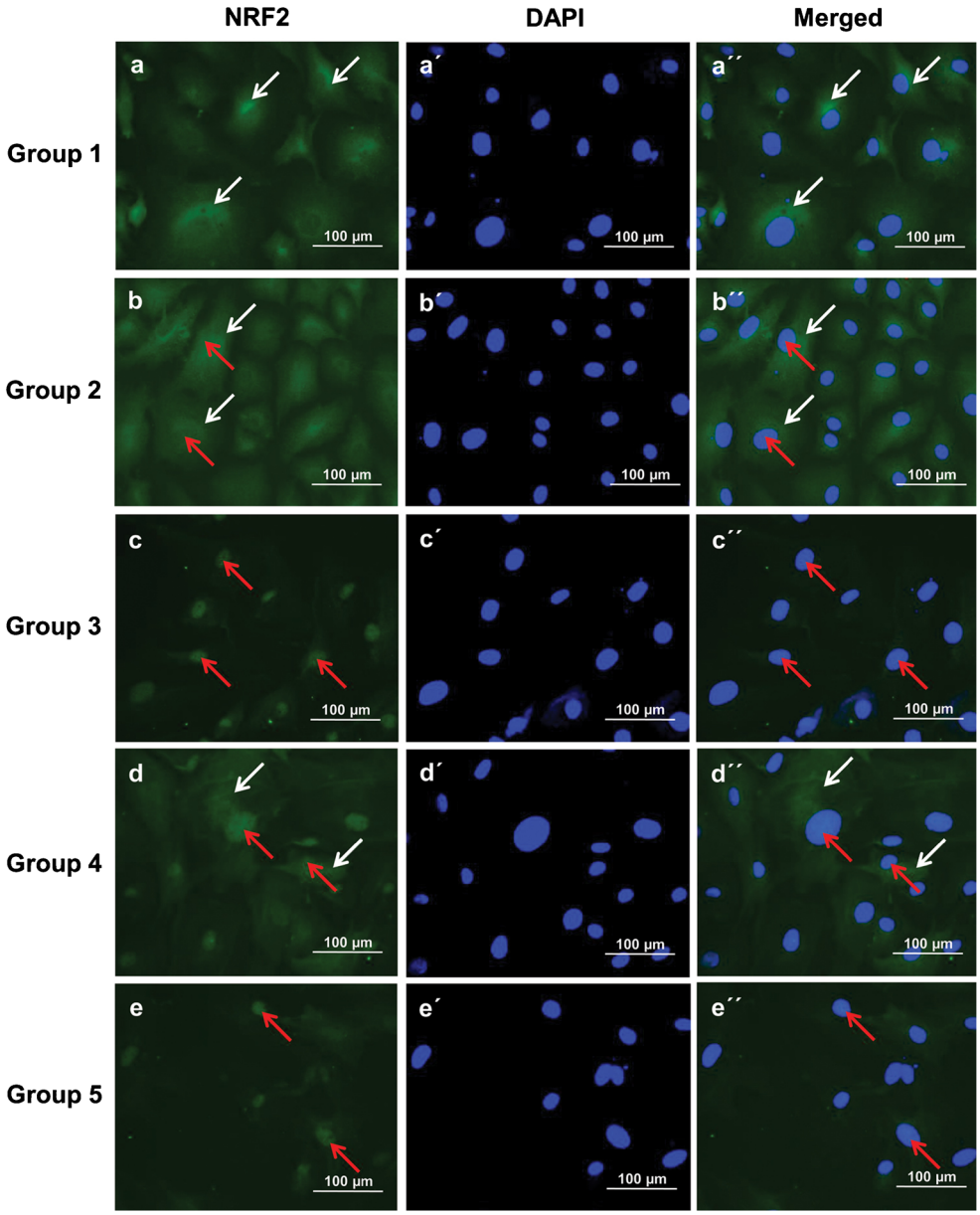

Fig. 4 Nuclear translocation of NRF2. Following different treatments, GCs were subjected to immunocytochemistry to localize NRF2 proteins. Images were acquired with a fluorescence microscope using a green fluorescence filter. Representative images showing the location of NRF2 proteins in green (**a**–**e**), while nuclear staining with DAPI (**a′**–**e′**) and merged image of NRF2 protein and DAPI (**a″**–**e″**). Scale bar 100 μm. White arrows indicate NRF2 in the cytoplasm, while red arrows represent the translocated NRF2 in the nucleus

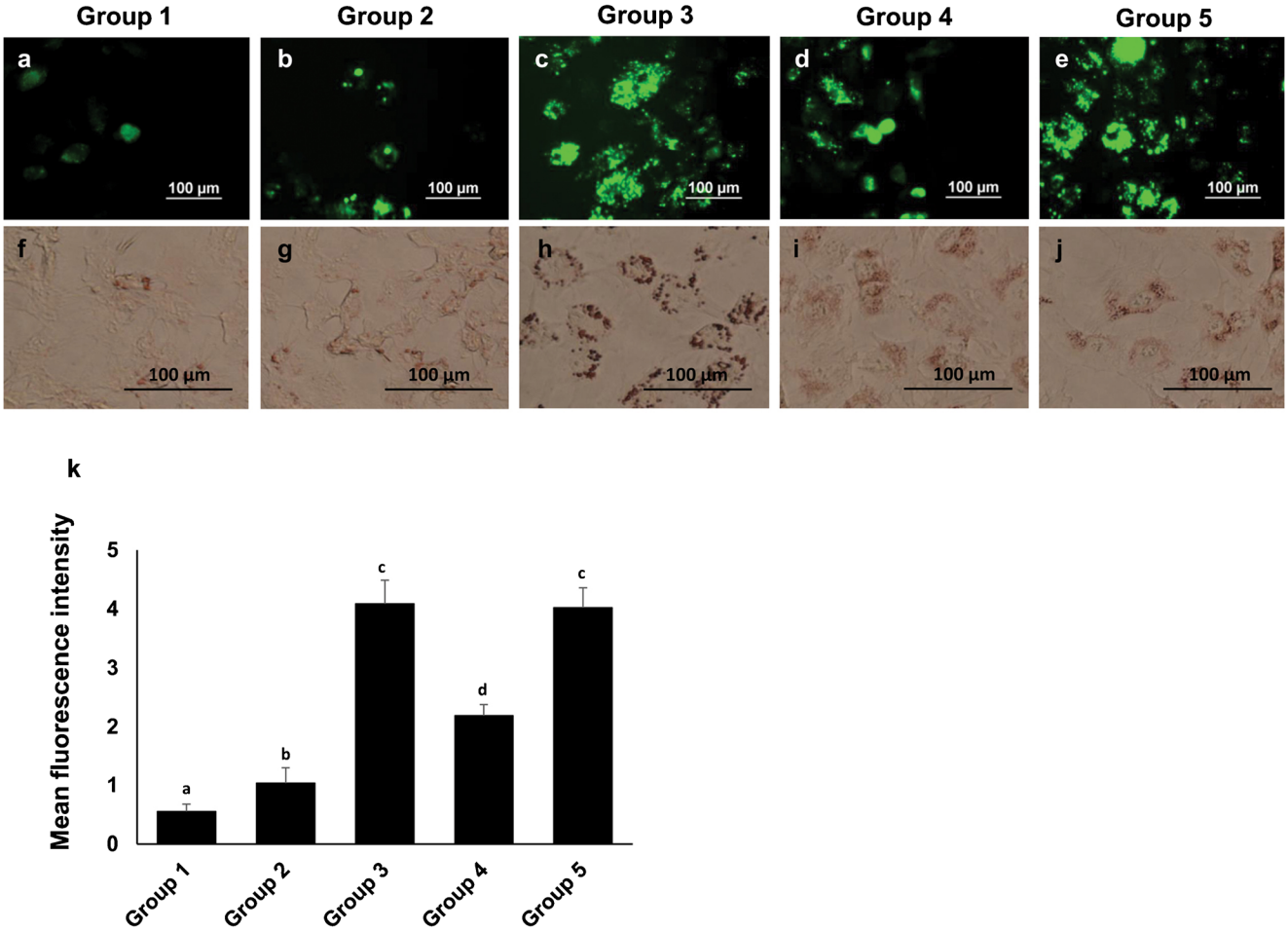

Fig. 5 ROS and lipid droplet accumulation in GCs after different treatments according to Fig. 1. GCs were (**a**–**e**) washed and loaded with H2DCFDA (15 μM for 20 min) and visualized under a fluorescent microscope, scale bar 100 μm. **f**–**j** Following treatments, GCs were loaded with Oil Red O stain working solution (for 40 min), washed several times and visualized with an inverted microscope ($n = 3$). Scale bar 100 μm. k Mean fluorescence intensity was quantified by ImageJ software from five nonoverlapping fields per well; experiments were performed in triplicate, $^{***}p < 0.001$. Data are presented as mean ± SD

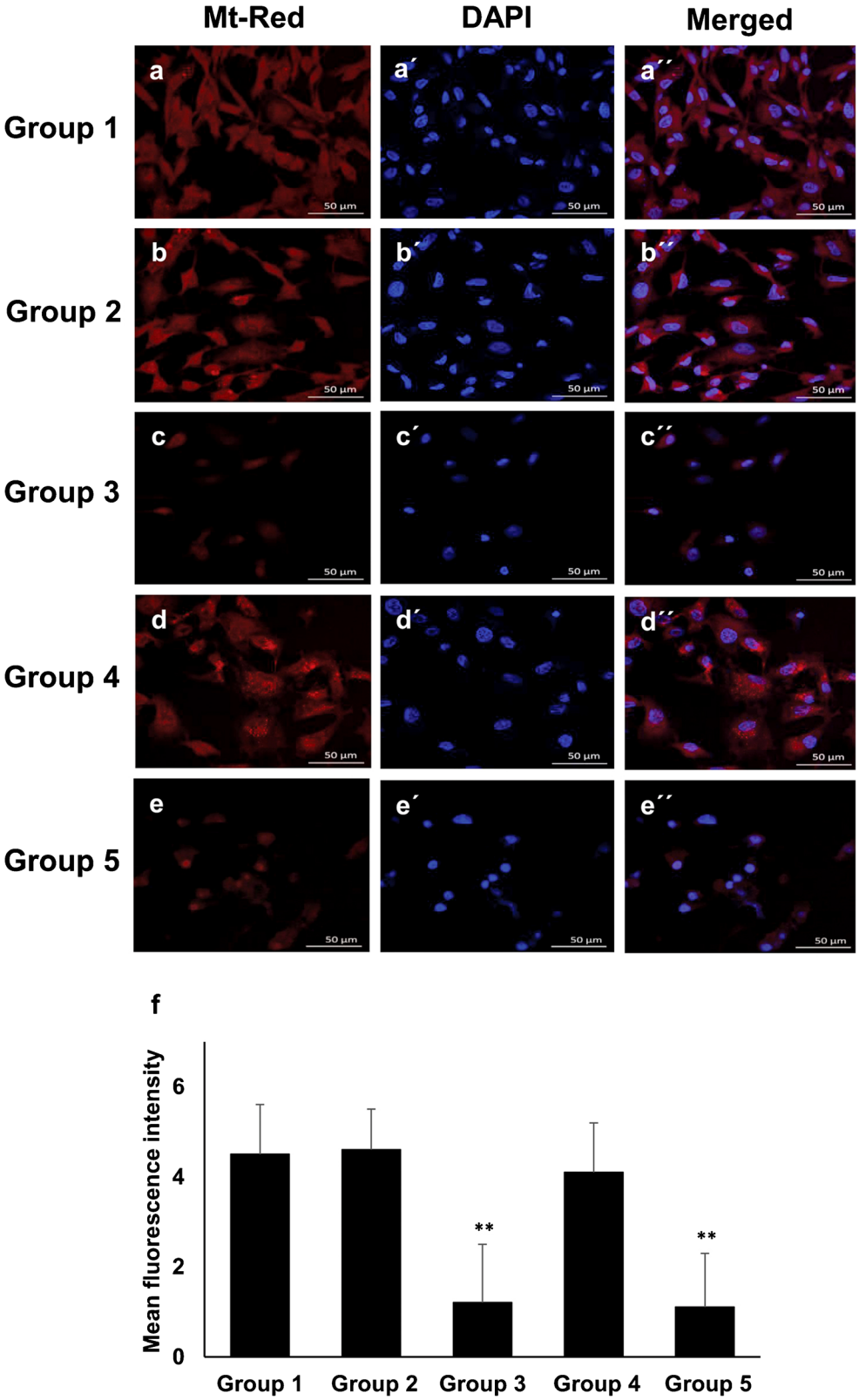

Fig. 6 Mitochondrial activity in GCs of different treatment groups. GCs were treated according to the experimental plan and 100 nM Mito Tracker red dye was added and incubated for 45 min at 37 °C. Images were acquired with a fluorescence microscope using a red filter. **a**–**e** show active mitochondria in red, while **a′**–**e′** show nuclear staining with DAPI in blue and **a″**–**e″** show merged image of active mitochondria and nucleus staining. Scale bar 50 μm, $n = 3$