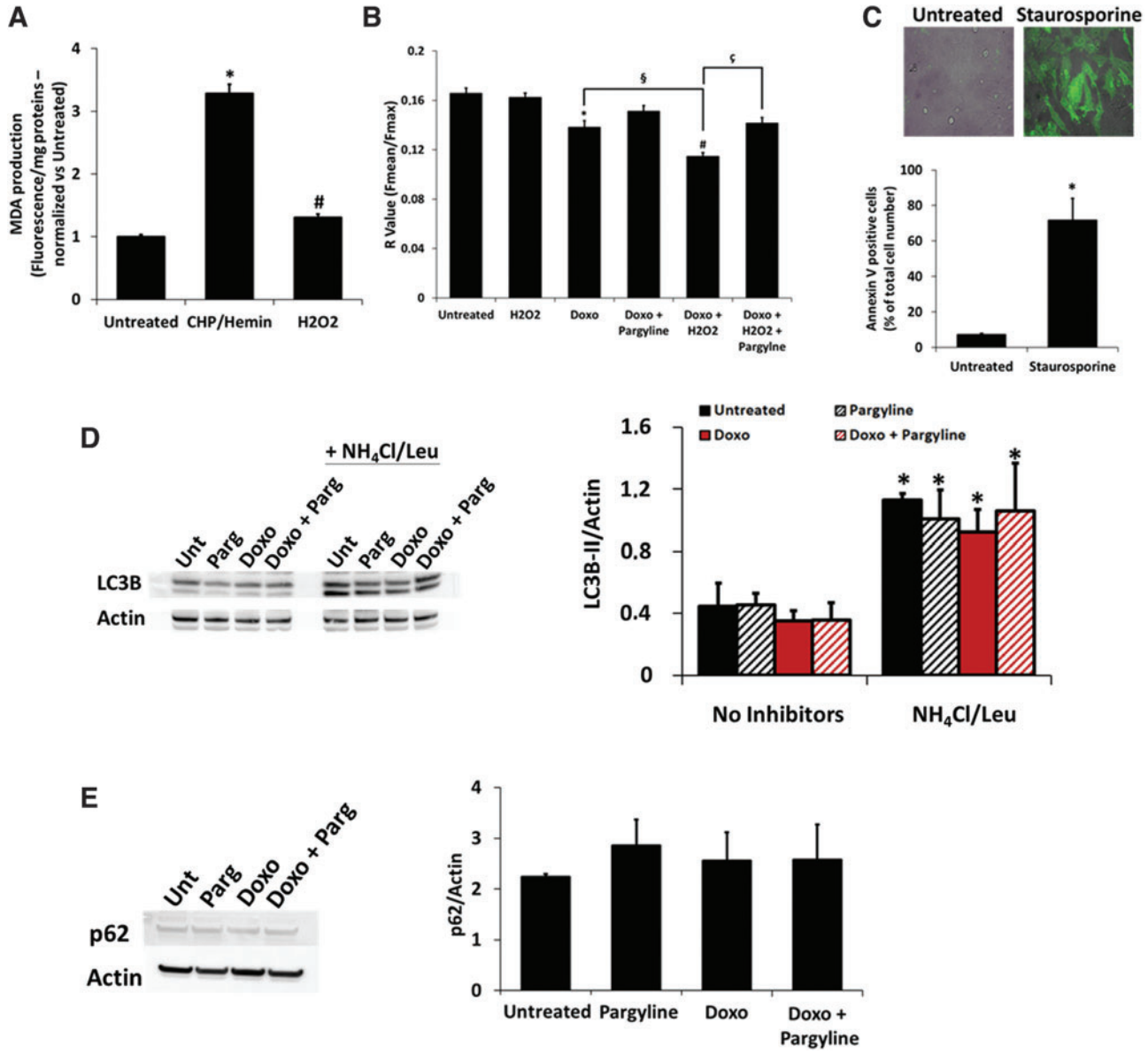

SUPPLEMENTARY FIG. S3. Effects of MAO inhibition on mitochondrial and cell function and morphology. (A) MDA formation in isolated NRVMs treated with 25 m*M* CHP and 50 μM hemin for 15 min, or with 100 μM H_2O_2 for 1 h. Raw fluorescence values were normalized to milligram proteins, and then normalized *versus* Untreated. $^{*}p < 0.001$ *versus* Untreated, $^{\#}p < 0.05$ *versus* Untreated by one-way ANOVA with *post hoc* Tukey's multiple comparison test. **(B)** Average of mitochondrial distribution representing *R* value evaluated in isolated NRVMs treated with 0.5 μM doxorubicin for 24 h, in the presence or absence of 100 μM pargyline. Cells have been further stimulated with 10 μM H_2O_2 for 1 h. $^{*}p < 0.01$, $^{\#}p < 0.001$ *versus* Untreated, $^{\S}p < 0.01$ *versus* Doxo, $^{\varsigma}p < 0.01$ *versus* Doxo+H_2O_2 by one-way ANOVA with *post hoc* Tukey's multiple comparison test. Where data were not normally distributed, the Kruskal–Wallis test has been applied. **(C)** Apoptosis evaluated by Annexin-V-Fluos staining in isolated NRVMs treated with 2 μM staurosporine for 1 h. Histogram displays the percentage of Annexin V-positive cells normalized to the total number of cells identified by bright-field images. $^{*}p < 0.001$ *versus* Untreated by the Kruskal–Wallis test. **(D)** LC3B-II abundance in isolated NRVMs treated with 0.5 μM doxorubicin for 24 h, in the presence or absence of 100 μM pargyline. Cells have been also incubated with inhibitors of lysosomal degradation for 4 h (i.e., 20 m*M* NH_4Cl, 100 μM Leupeptin). $^{*}p < 0.05$ *versus* No inhibitors by one-way ANOVA with *post hoc* Tukey's multiple comparison test. **(E)** p62 expression levels in isolated NRVMs treated with 0.5 μM doxorubicin for 24 h, in the presence or absence of 100 μM pargyline. For the evaluation of the *R* parameter, $\sim$30 cells were analyzed per condition in each experiment. For the evaluation of apoptosis, $\sim$100 cells were analyzed per condition in each experiment. All the experiments were performed three times using three different animal preparations. Western blot analyses were performed six times using six different animal preparations. Data are expressed as mean $\pm$ SEM. Integral blots are shown in Supplementary Figure S2. CHP, cumene hydroperoxide; MDA, malondialdehyde.