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Suppl. Fig. 1. Representative *gel electrophoresis of qPCR products*.

Suppl. Fig. 2. Lipid peroxidation and pro-inflammatory markers, as assessed using untargeted metabolomic analyses. Values are expressed as mean \pm SEM (n = 5) of the fold change over non-ischemic retinas (broken lines). $^{\$}P < 0.01$; $^{\$\$}P < 0.001$; $^{\$\$\$}P < 0.0001$ against non-ischemic controls; $^{*}P < 0.01$; $^{**}P < 0.001$; $^{**}P < 0.0001$ against untreated ischemic retinas, ANOVA.

Suppl. Fig. 3. Arginine-citrulline-ornithine nitric oxide-related metabolism and secondary messenger metabolites (including cyclic AMP, inositol triphosphate, PIP2 and PIP3), as assessed using untargeted metabolomic analyses. Values are expressed as mean \pm SEM (n = 5) of the fold change over non-ischemic retinas (broken lines). $^{\$}P < 0.01$; $^{\$\$\$}P < 0.0001$ against non-ischemic controls; $^{*}P < 0.01$; $^{**}P < 0.001$; $^{**}P < 0.0001$ against untreated ischemic retinas, ANOVA.

Suppl. Fig. 4. Krebs cycle metabolites, as assessed using untargeted metabolomic analyses. Values are expressed as mean \pm SEM (n = 5) of the fold change over non-ischemic retinas (broken lines). $^{\$}P < 0.01$; $^{\$\$\$}P < 0.0001$ against non-ischemic controls; $^{\$}P < 0.01$; $^{\$**}P < 0.001$ against untreated ischemic retinas, ANOVA.

Suppl. Fig. 5. Purine metabolism, as assessed using untargeted metabolomic analyses. Values are expressed as mean \pm SEM (n = 5) of the fold change over non-ischemic retinas (broken lines). $^{\$}P < 0.01$; $^{\$\$\$}P < 0.0001$ against non-ischemic controls; $^{*}P < 0.01$; $^{***}P < 0.0001$ against untreated ischemic retinas, ANOVA.











