Supplementary Materials: Reactive Oxygen Species Differentially Modulate the Metabolic and Transcriptomic Response of Endothelial Cells

Niklas Müller^{1,2}, Timothy Warwick^{1,2}, Kurt Noack^{1,2}, Pedro F. Malacarne^{1,2}, Arthur J.L. Cooper³, Norbert Weissmann⁴, Katrin Schröder^{1,2}, Ralf P. Brandes^{1,2} and Flávia Rezende^{1,2,*}

- ¹ Institute for Cardiovascular Physiology, Goethe University, Theodor-Stern Kai 7, 60590 Frankfurt, Germany; nmueller@vrc.uni-frankfurt.de (K.M.); warwick@vrc.unifrankfurt.de (W.T.); kunoack@students.uni-mainz.de (K.N.); malacarne@vrc.unifrankfurt.de (P.F.M.);
- schroeder@vrc.uni-frankfurt.de (K.S.); brandes@vrc.uni-frankfurt.de (R.P.B.)
 ² German Center of Cardiovascular Research (DZHK), Partner Site Rhein Main, 60590 Frankfurt, Germany
- ³ Department of Biochemistry and Molecular Biology, New York Medical College, 15 Dana Road,
- Valhalla, NY 10595, USA; arthur_cooper@nymc.edu
- ⁴ Excellence Cluster Cardio-Pulmonary Institute (CPI), University of Giessen and Marburg Lung Center (UGMLC), Member of the German Center for Lung Research (DZL), Justus-Liebig-University,
- Giessen, 35390 Germany; norbert.weissmann@innere.med.uni-giessen.de
- * Correspondence: rezende@vrc.uni-frankfurt.de; Tel.: +49-69-6301-85321; Fax: +49-69-6301-7668



Supplementary Figure S1: H₂O₂ **production by HUVEC-DAO.** H₂O₂ (n=3) assessed by chemiluminescence with luminol (100 μ M)/ HRP (1 U/mL) after exposure to D- or L-alanine with or without pre-incubation (10 min) with the DAO inhibitor 4HF (1 μ mol/L) (n=3).



Supplementary Figure S2: Changes in glycolysis and nucleotide metabolism in HUVEC in response to different oxidative stimuli. (A): Heat maps of glucose metabolism. (B): Changes in ATP, AMP, GTP and GMP after exposure to 300 μ M H₂O₂. (C): Fates of glucose and S-lactoylglutathione pathway.



Supplementary Figure S3: High degree of dissimilarity between effects of different ROS exposures to HUVEC. Time course changes in metabolomics and transcriptomics of HUVEC in response to different oxidative stimuli.



Supplementary Figure S4: Differentially expressed genes in HUVEC in response to different ROS. (A): Heatmap of DEGs. (B): Transcription factor analysis performed with ENCODE and CheA for the genes commonly regulated by 300 μ M H₂O₂, 3 mM D-Ala and 5 μ M menadione.



Supplementary Figure S5: DAO-derived H₂**O**₂ **results in a dose-dependent oxidation of peroxiredoxins in HEK-DAO.** (**A**): Representative redox western blot for Prx1, Prx2, Prx3, Prx4 and Prx-SO₃ after exposure to different concentration of D- or L-Ala. (**B**): Quantification of redox western blotting by densitometry (n=3).

Α

	3 mM D-Ala/CTL							
	3′	10′	30′	90′	270′	900′		
1	1	9	14	1	6	3		
\downarrow	1	0		2	2	2		
Total	2	9	14	3	8	5		

	10 μM H2O2/CTL					300 μM H2O2/CTL						
	3′	10′	30′	90′	270′	900′	3′	10′	30′	90′	270'	900′
↑	0	4	1	4	2	3	23	39	44	56	23	60
\downarrow	1	0	1	0	56	1	16	24	31	30	10	2
Total	1	4	2	4	58	4	39	63	75	86	33	62

	5 μM Menadione/CTL							
	3′	10′	30′	90′	270′	900′		
↑	1	6	3	16	18	4		
\downarrow	5	5	3	3	19	13		
Total	6	11	6	19	37	17		

Supplementary Table S1: Summary of altered metabolites.