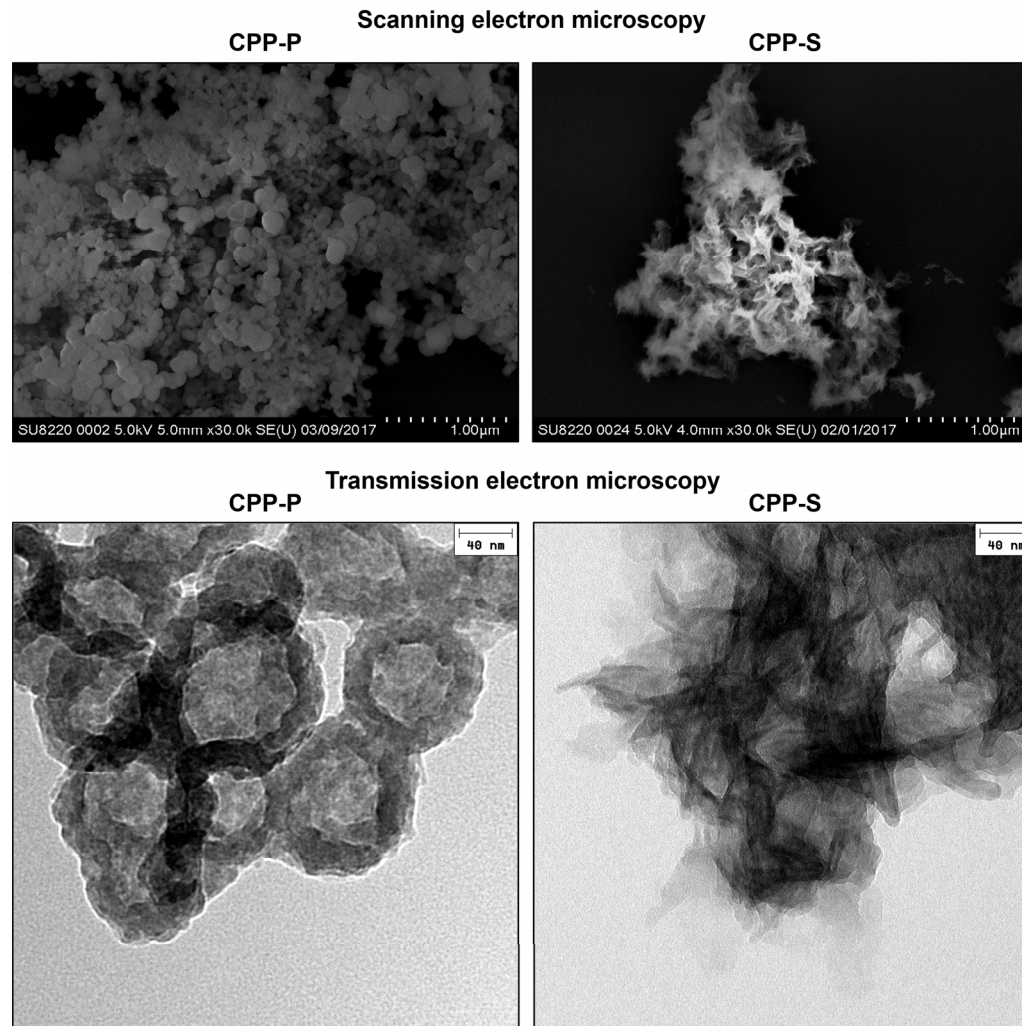
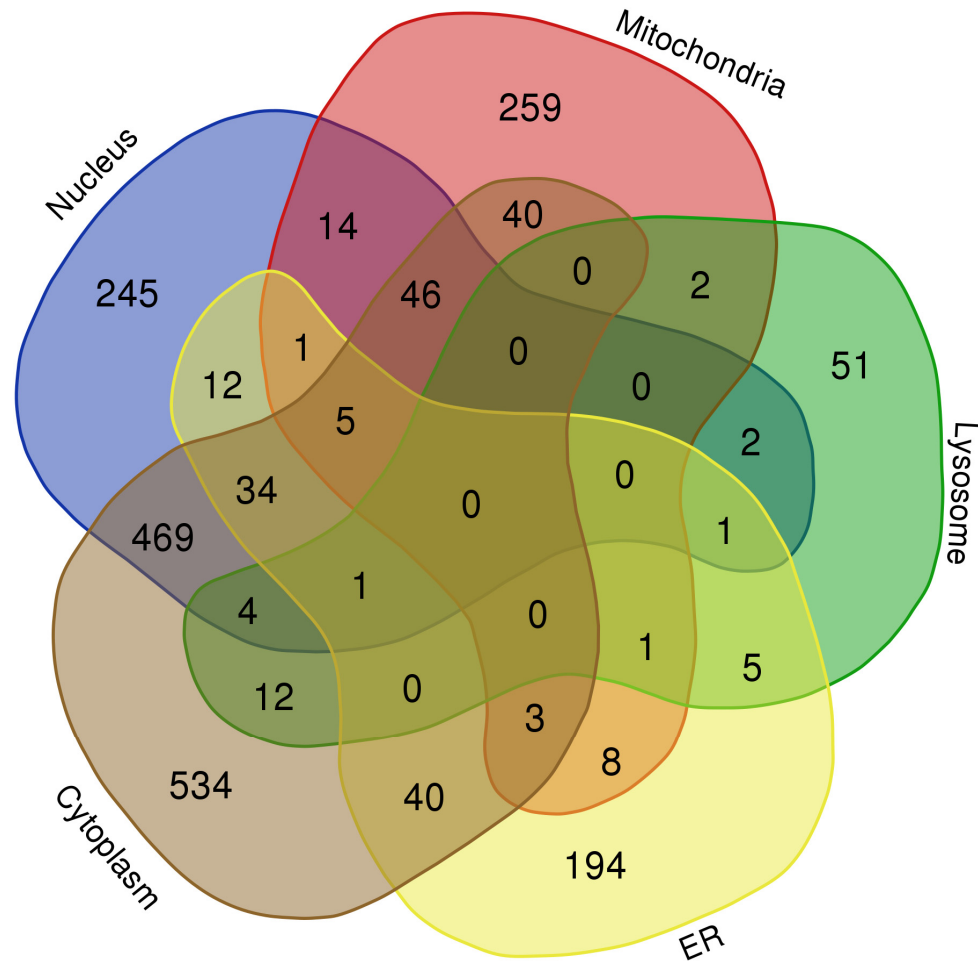


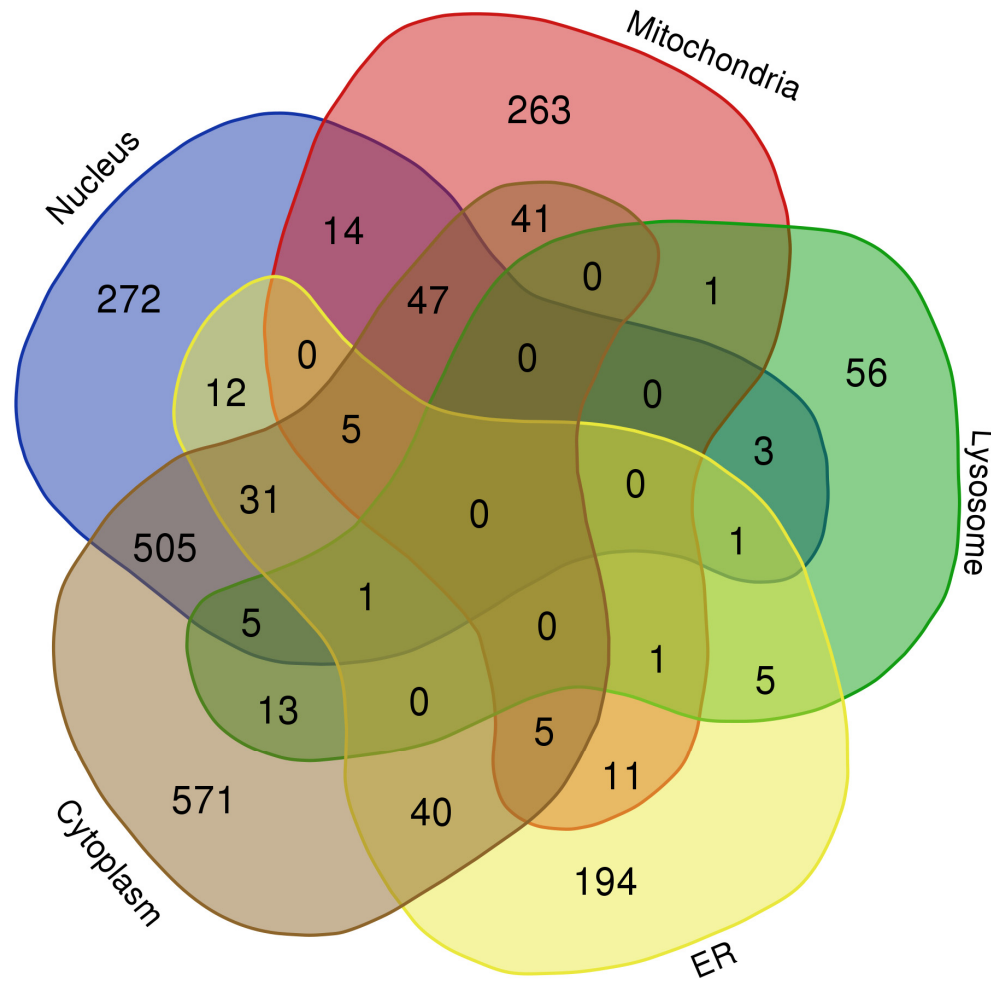
**Supplementary Figure S1.** Electron microscopy visualisation of primary calcioprotein particles (CPP-P, left) and secondary calcioprotein particles (CPP-S, right). Top: scanning electron microscopy. Bottom: transmission electron microscopy. Note the absence of mature CPPs (i.e., CPP-S) in immature CPP preparations (i.e., CPP-P).



**Supplementary Figure S2.** Venn diagram indicating an overlap of the indicated proteins between the cellular compartments (cytosol, nucleus, mitochondria, lysosomes, and endoplasmic reticulum) and organelle-specific proteins in human coronary artery endothelial cells (HCAEC) upon the bioinformatic filtration.

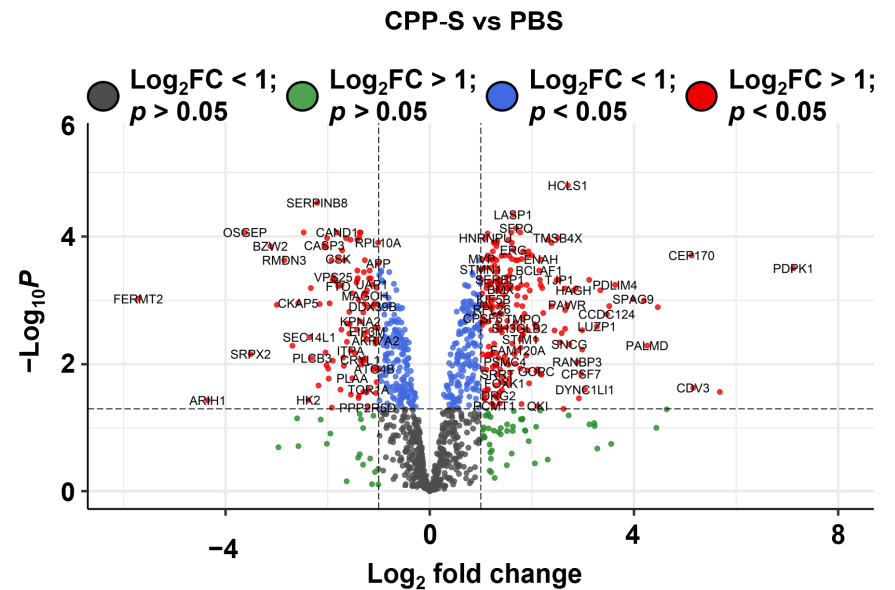
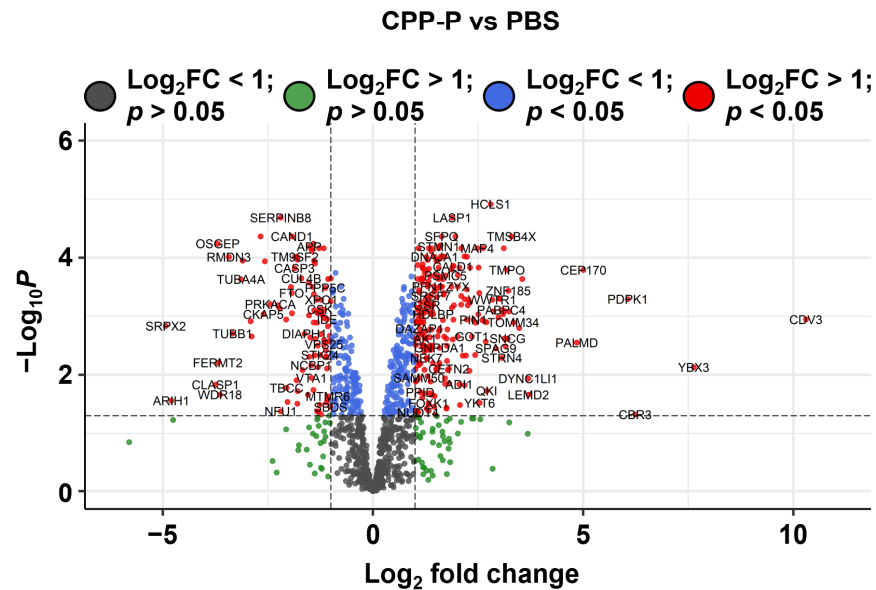


**Supplementary Figure S3.** Venn diagram indicating an overlap of the indicated proteins between the cellular compartments (cytosol, nucleus, mitochondria, lysosomes, and endoplasmic reticulum) and organelle-specific proteins in human internal thoracic artery endothelial cells (HITAEC) upon the bioinformatic filtration.



**Supplementary Figure S4.** Bioinformatic analysis of cytosolic proteins in CPP-P- and CPP-S-treated human coronary artery endothelial cells (HCAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Cytosol

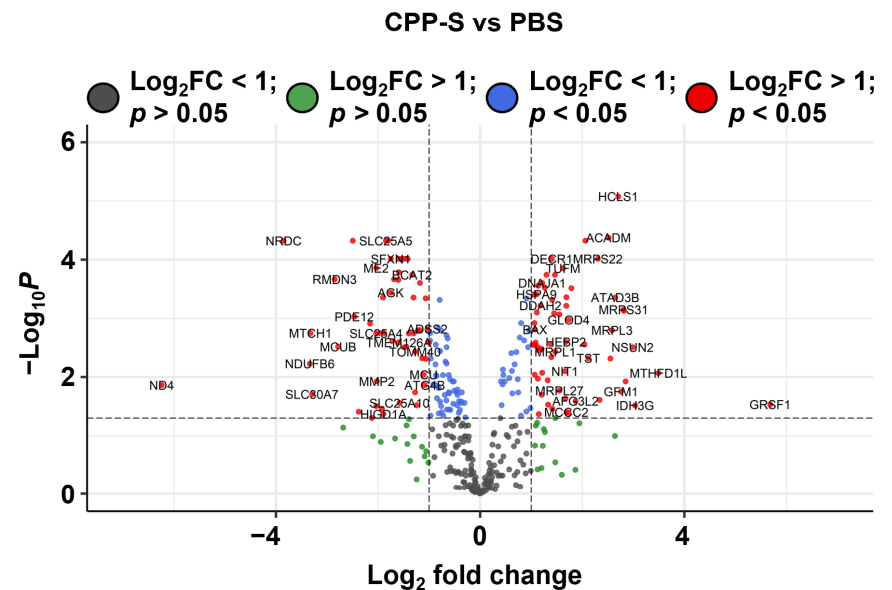
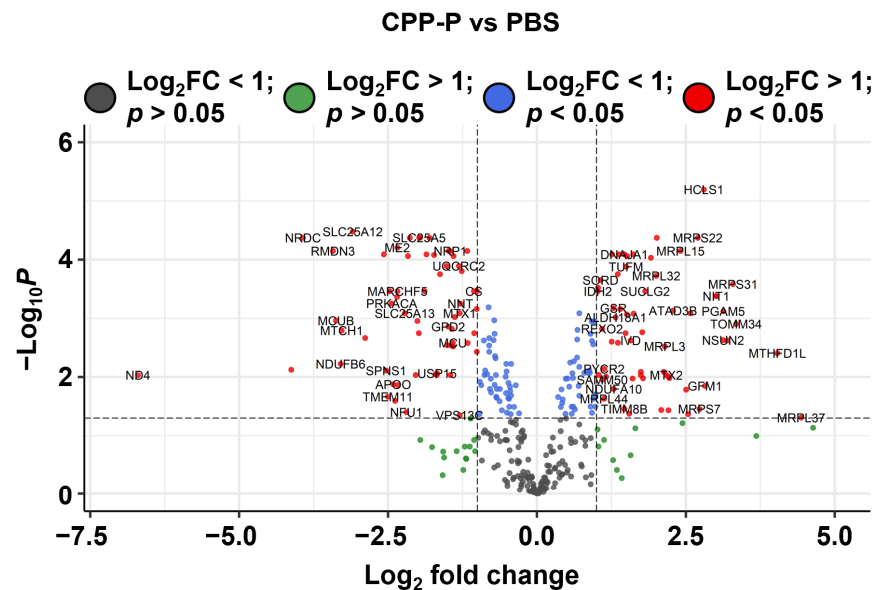






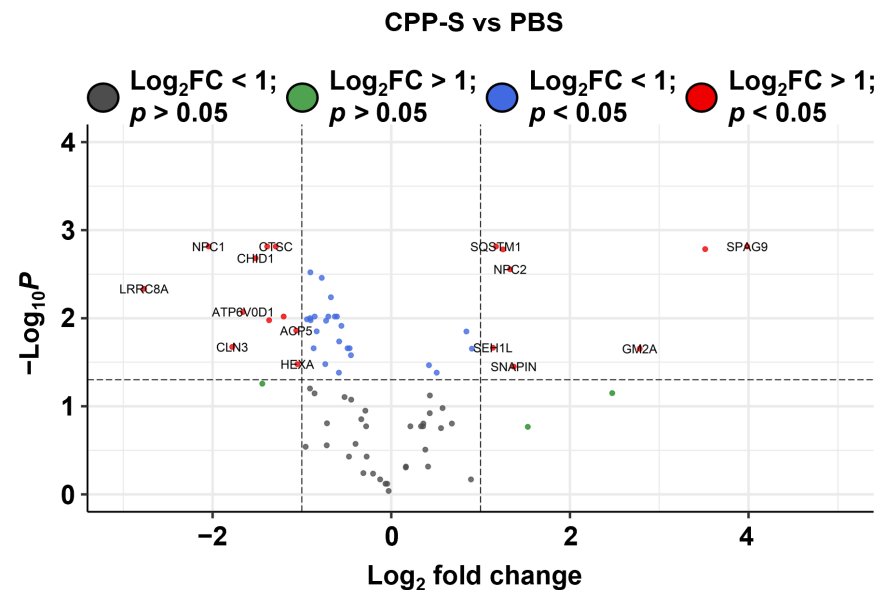
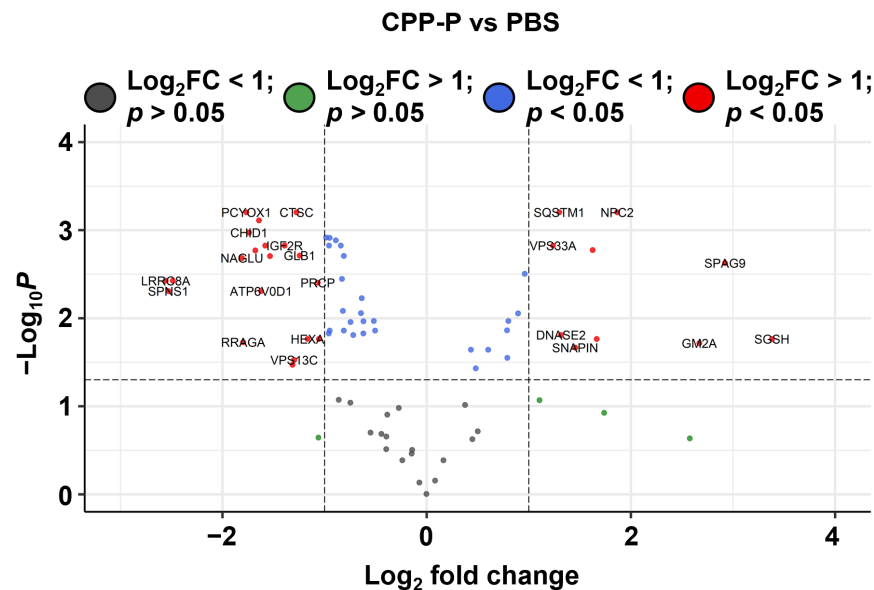
**Supplementary Figure S6.** Bioinformatic analysis of mitochondrial proteins in CPP-P- and CPP-S-treated human coronary artery endothelial cells (HCAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Mitochondria



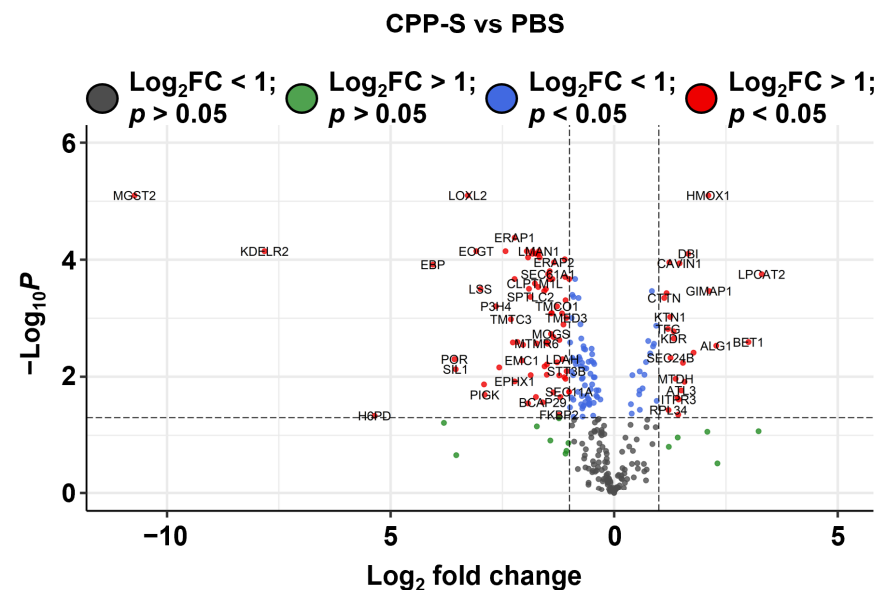
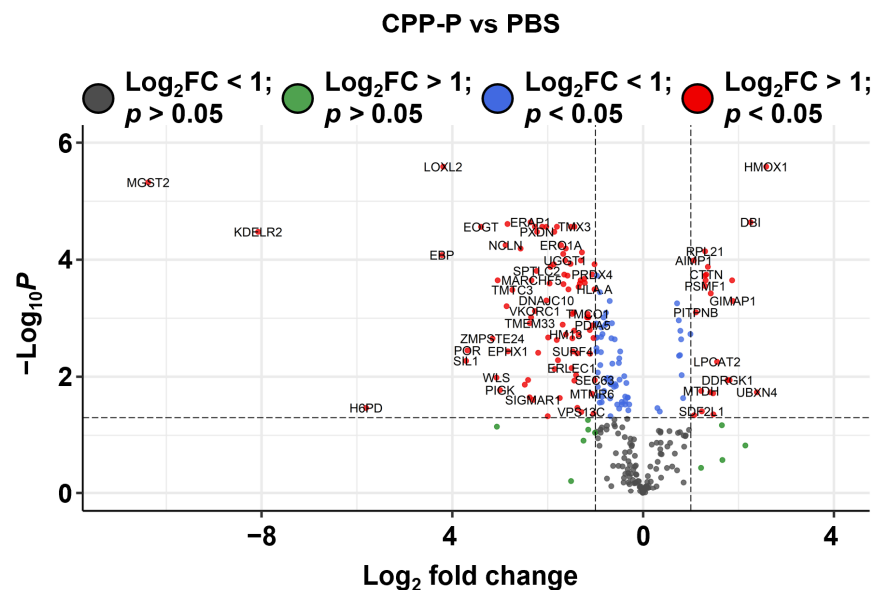
**Supplementary Figure S7.** Bioinformatic analysis of lysosomal proteins in CPP-P- and CPP-S-treated human coronary artery endothelial cells (HCAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Lysosomes

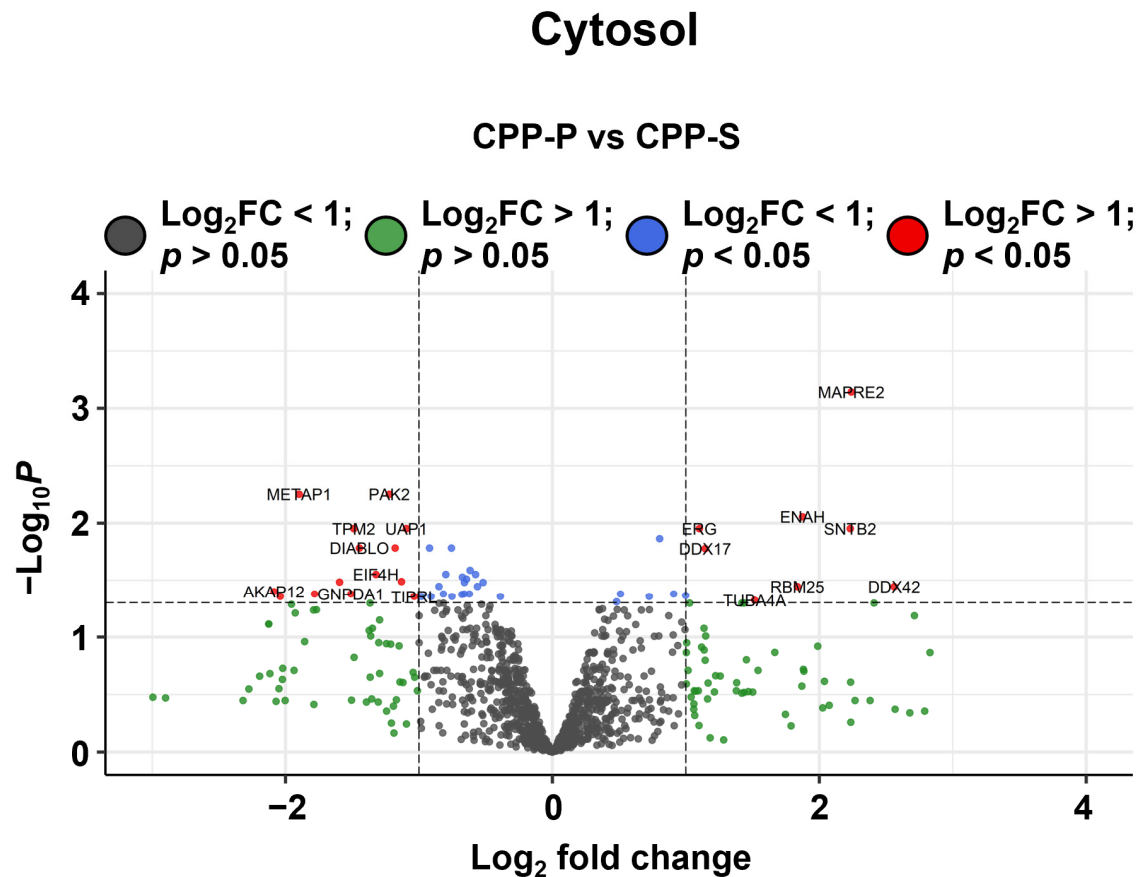


**Supplementary Figure S8.** Bioinformatic analysis of endoplasmic reticulum proteins in CPP-P- and CPP-S-treated human coronary artery endothelial cells (HCAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

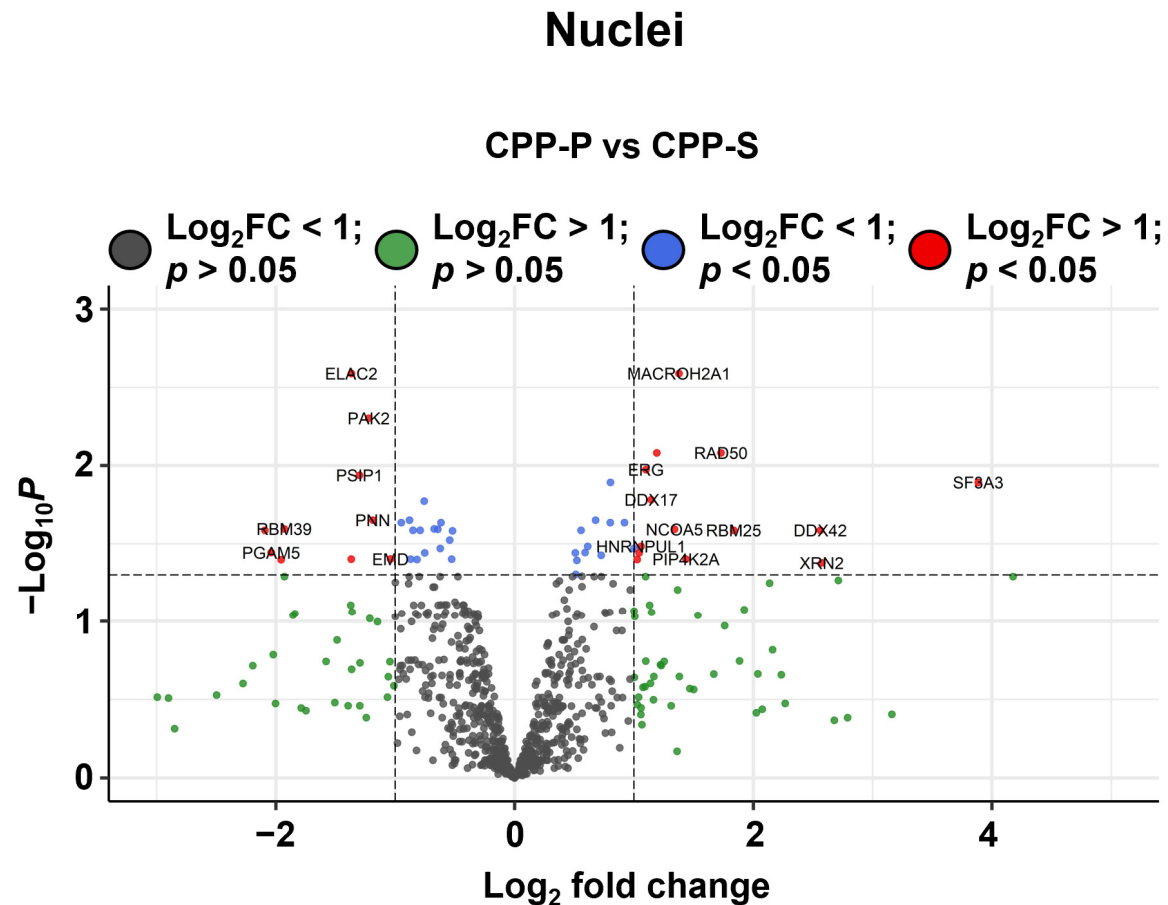
## Endoplasmic reticulum



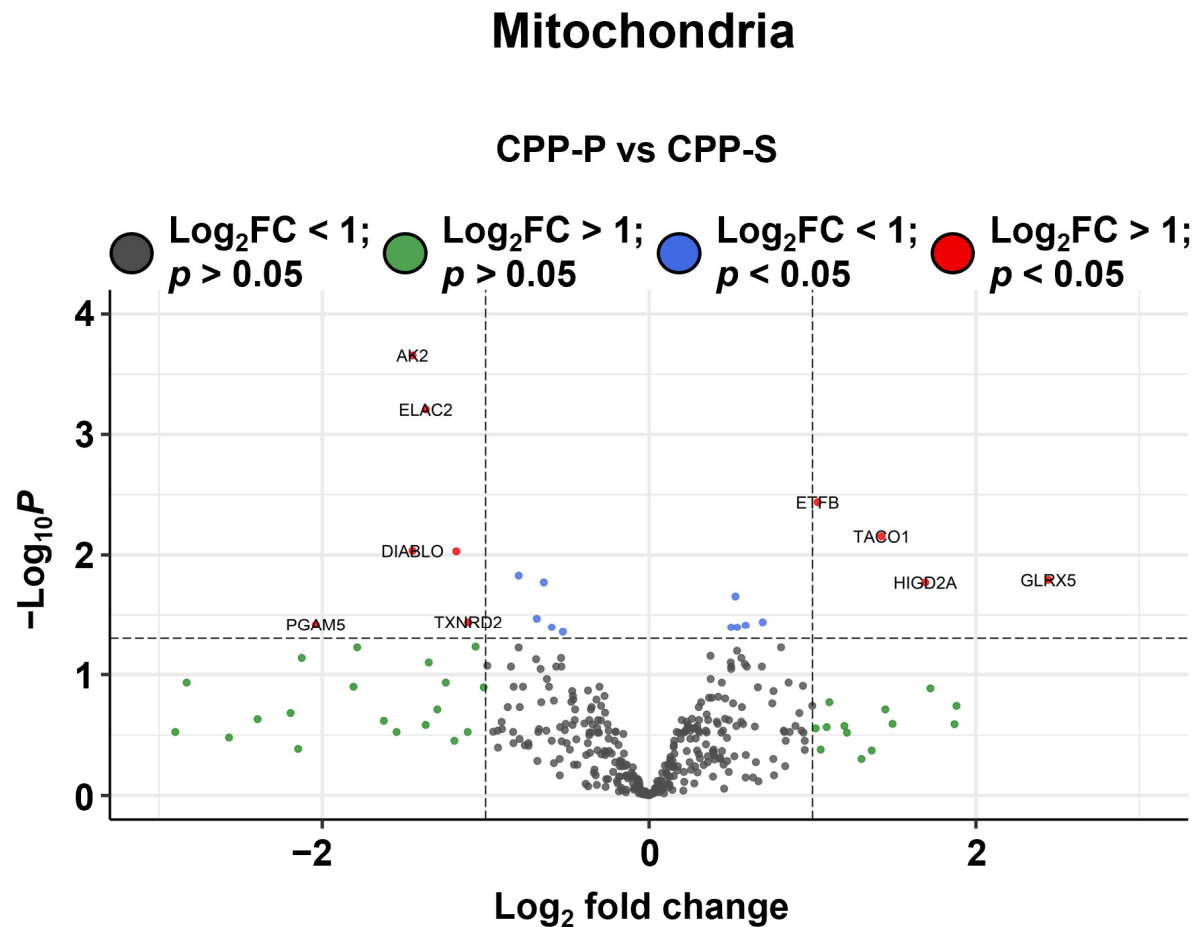
**Supplementary Figure S9.** Bioinformatic analysis of cytosolic proteins in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.



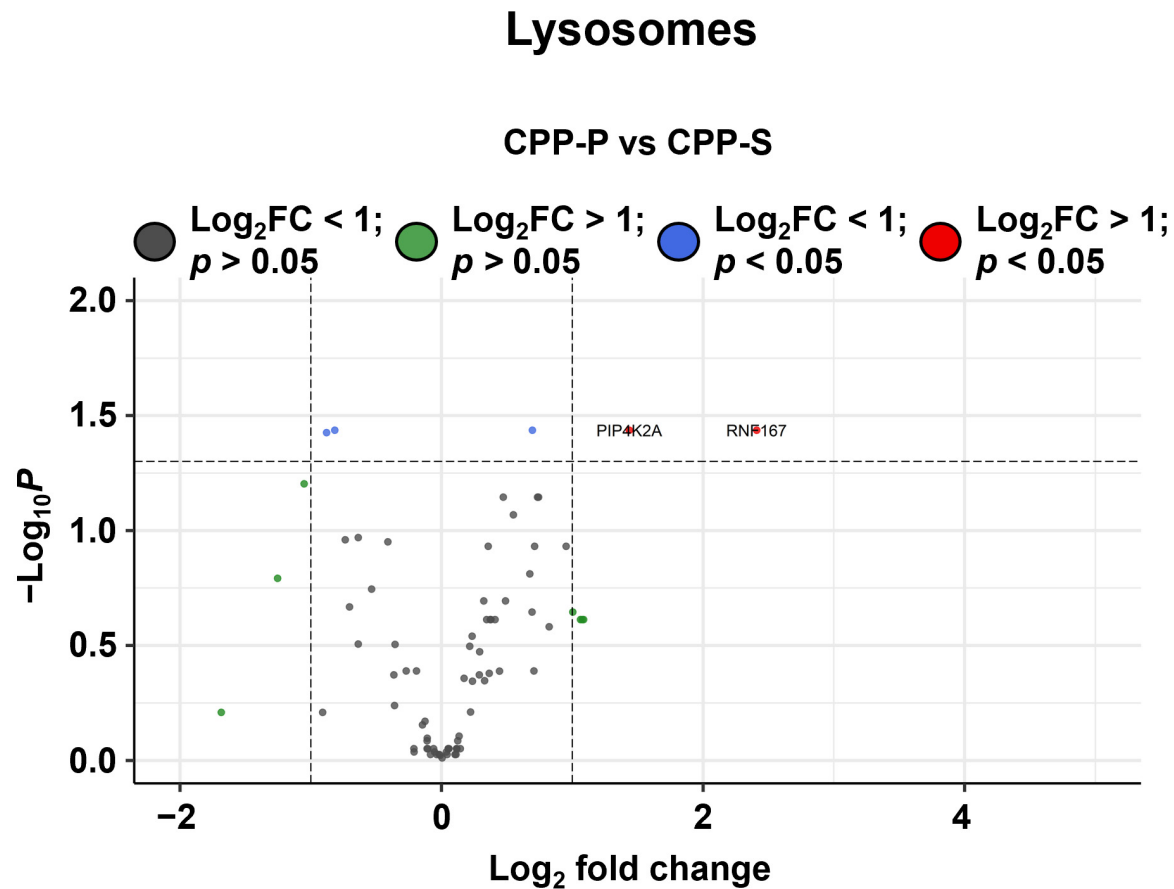
**Supplementary Figure S10.** Bioinformatic analysis of nuclear proteins in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.



**Supplementary Figure S11.** Bioinformatic analysis of mitochondrial proteins in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change < 1 and FDR-corrected  $p$  value > 0.05, green points depict the proteins with  $\log_2$  fold change > 1 and FDR-corrected  $p$  value > 0.05, blue points depict the proteins with  $\log_2$  fold change < 1 and FDR-corrected  $p$  value < 0.05, and red points depict the proteins with  $\log_2$  fold change > 1 and FDR-corrected  $p$  value < 0.05 (termed as differentially expressed proteins) in each of the indicated organelles.

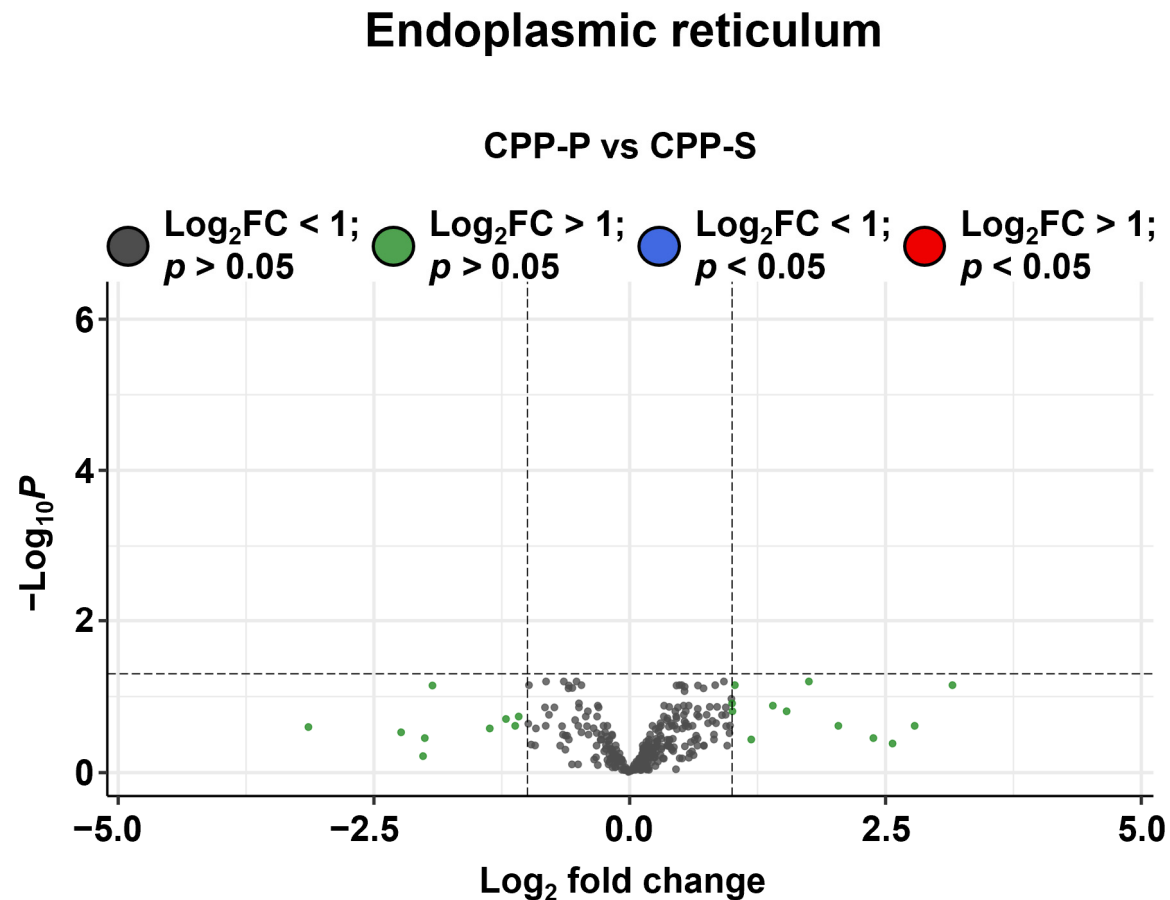


**Supplementary Figure S12.** Bioinformatic analysis of lysosomal proteins in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.



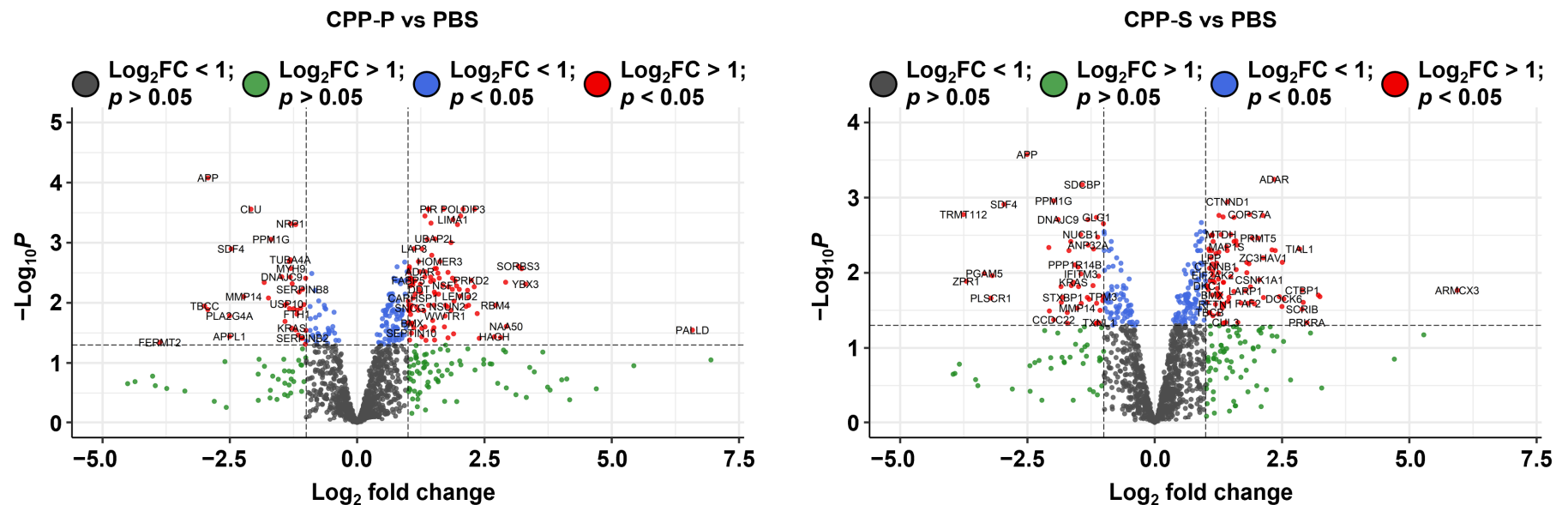


**Supplementary Figure S13.** Bioinformatic analysis of endoplasmic reticulum proteins in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.



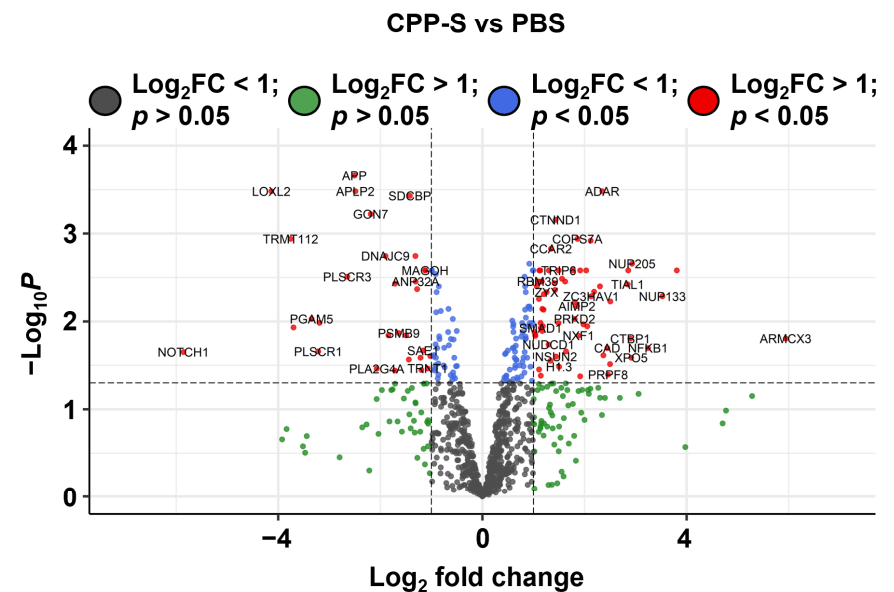
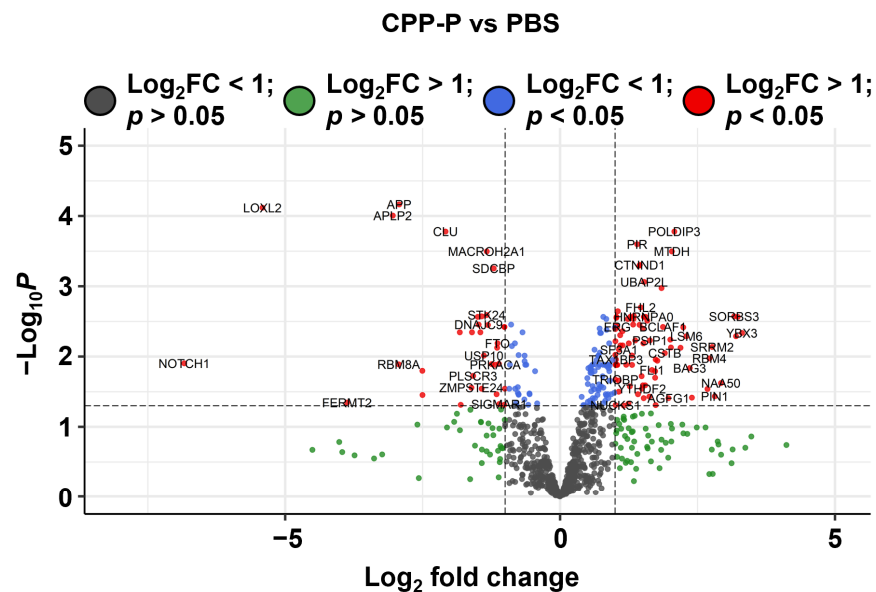
**Supplementary Figure S14.** Bioinformatic analysis of cytosolic proteins in CPP-P- and CPP-S-treated human internal thoracic artery endothelial cells (HITAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Cytosol



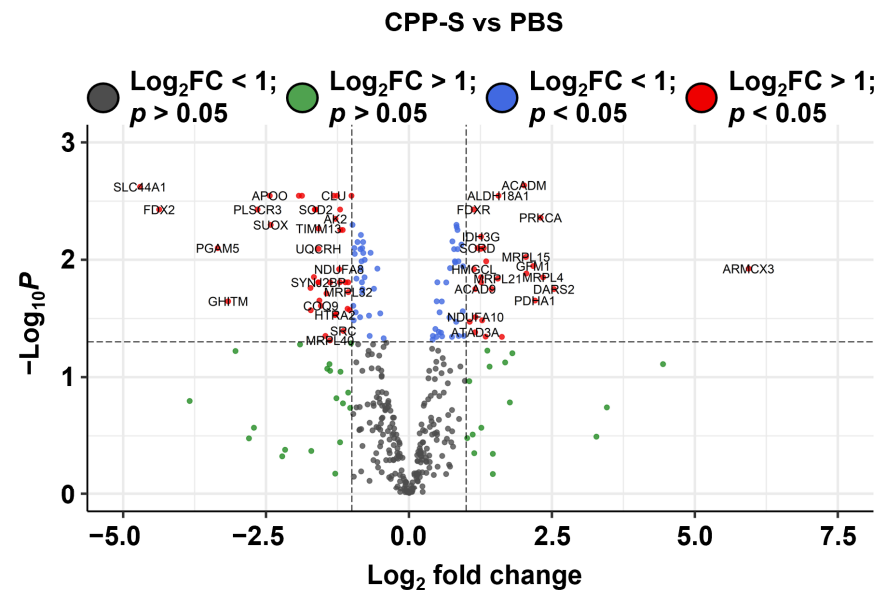
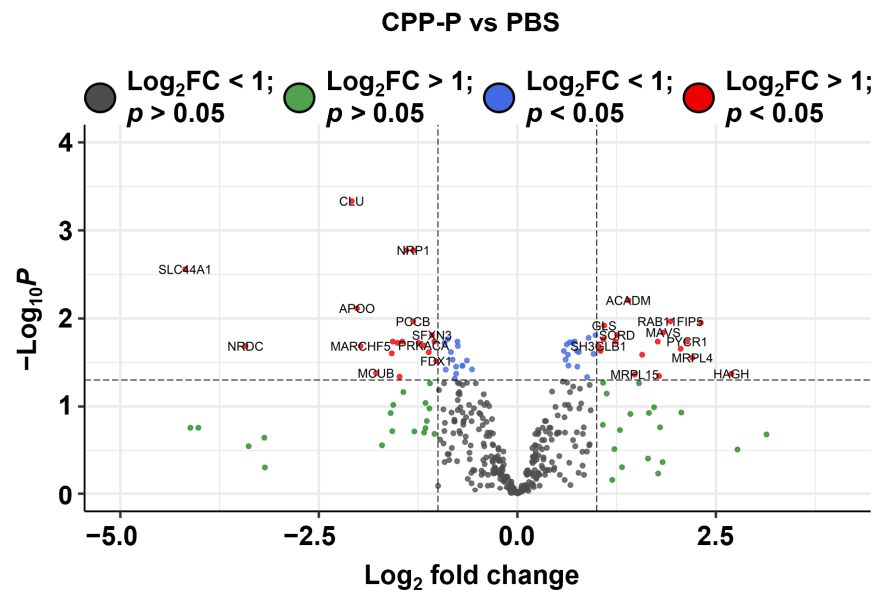
**Supplementary Figure S15.** Bioinformatic analysis of nuclear proteins in CPP-P- and CPP-S-treated human internal thoracic artery endothelial cells (HITAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Nuclei



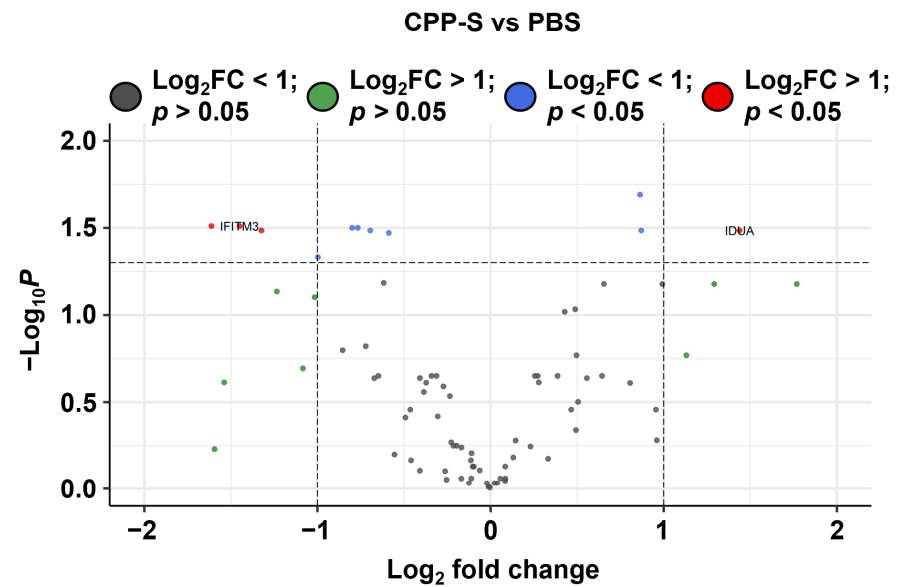
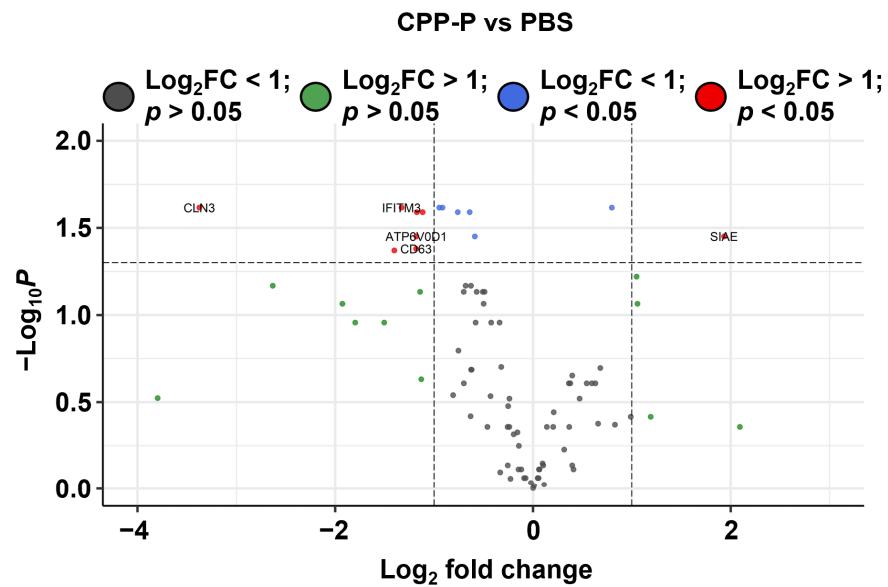
**Supplementary Figure S16.** Bioinformatic analysis of mitochondrial proteins in CPP-P- and CPP-S-treated human internal thoracic artery endothelial cells (HITAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Mitochondria



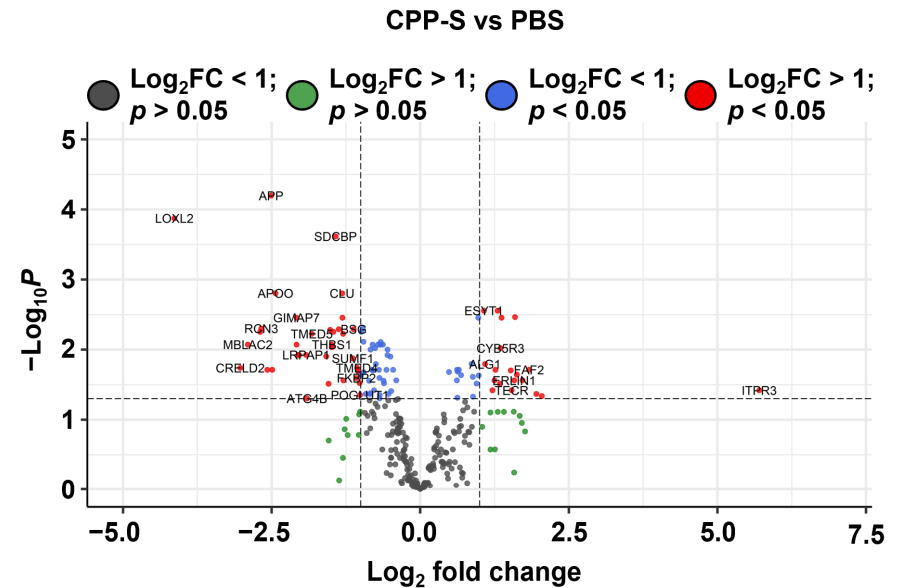
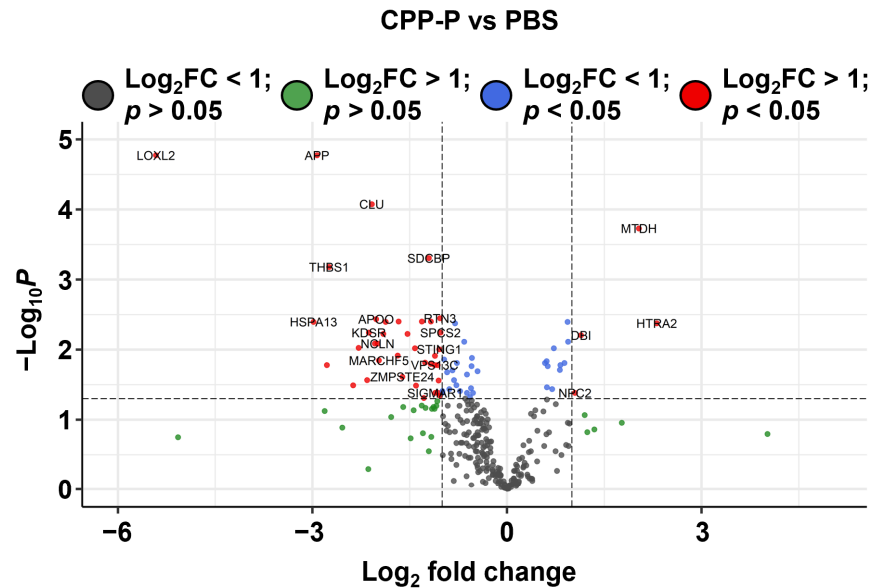
**Supplementary Figure S17.** Bioinformatic analysis of lysosomal proteins in CPP-P- and CPP-S-treated human internal thoracic artery endothelial cells (HITAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Lysosomes

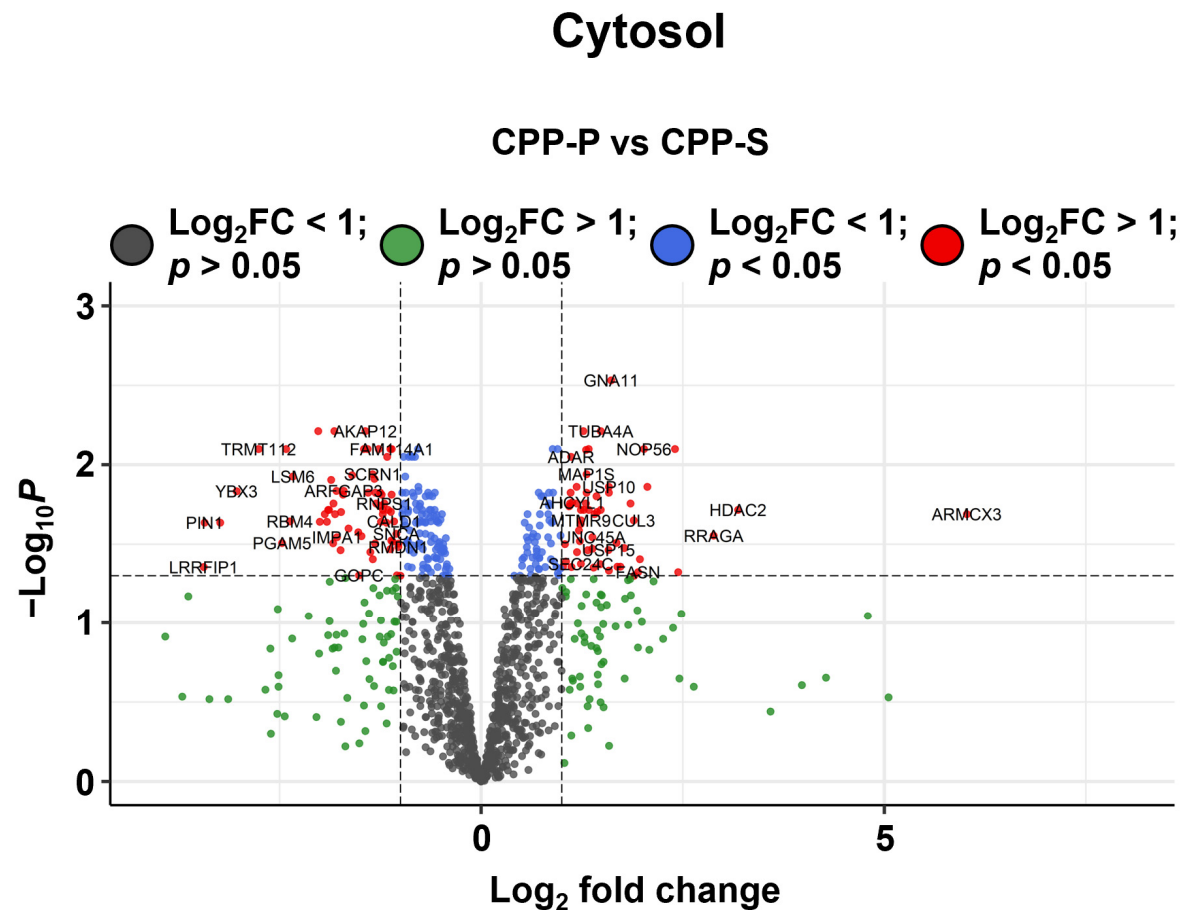


**Supplementary Figure S18.** Bioinformatic analysis of endoplasmic reticulum proteins in CPP-P- and CPP-S-treated human internal thoracic artery endothelial cells (HITAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

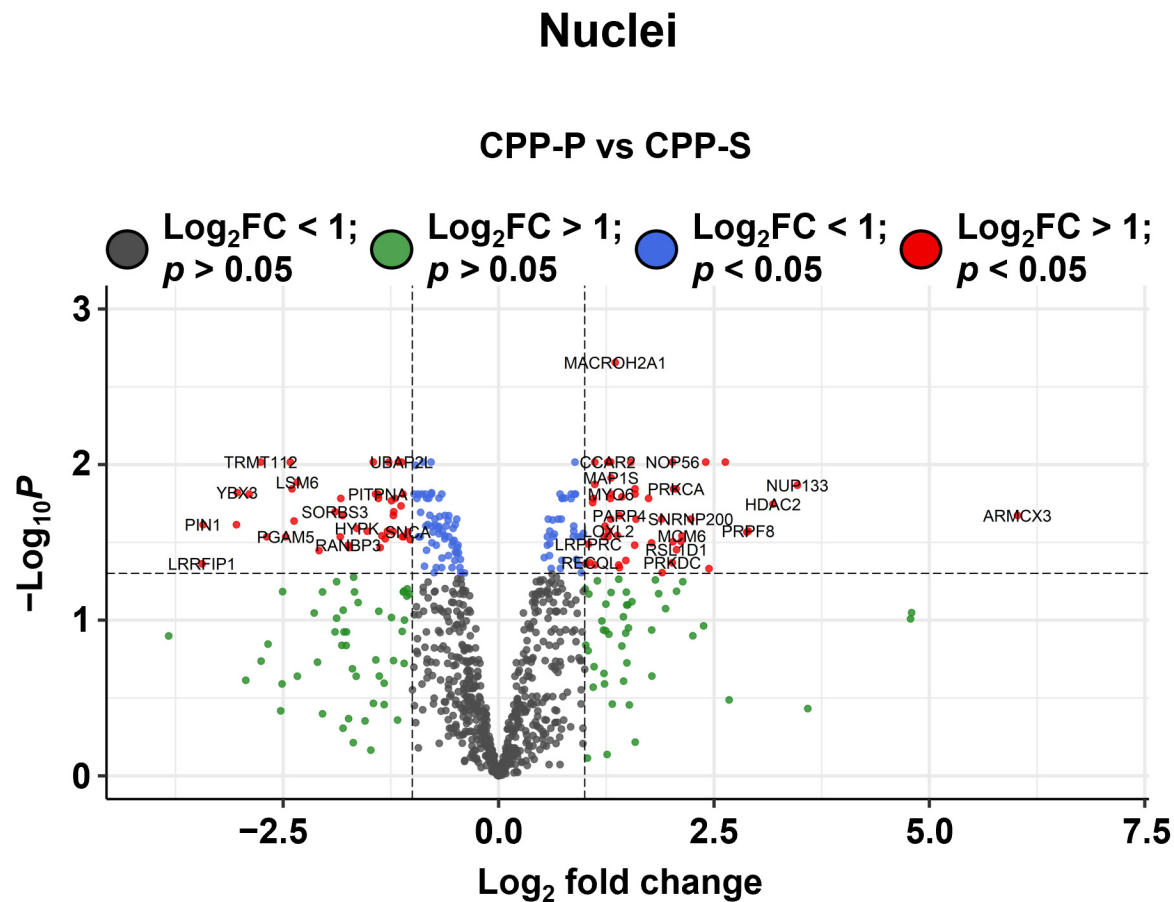
## Endoplasmic reticulum



**Supplementary Figure S19.** Bioinformatic analysis of cytosolic proteins in CPP-P-treated human internal thoracic artery endothelial cells (HITAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

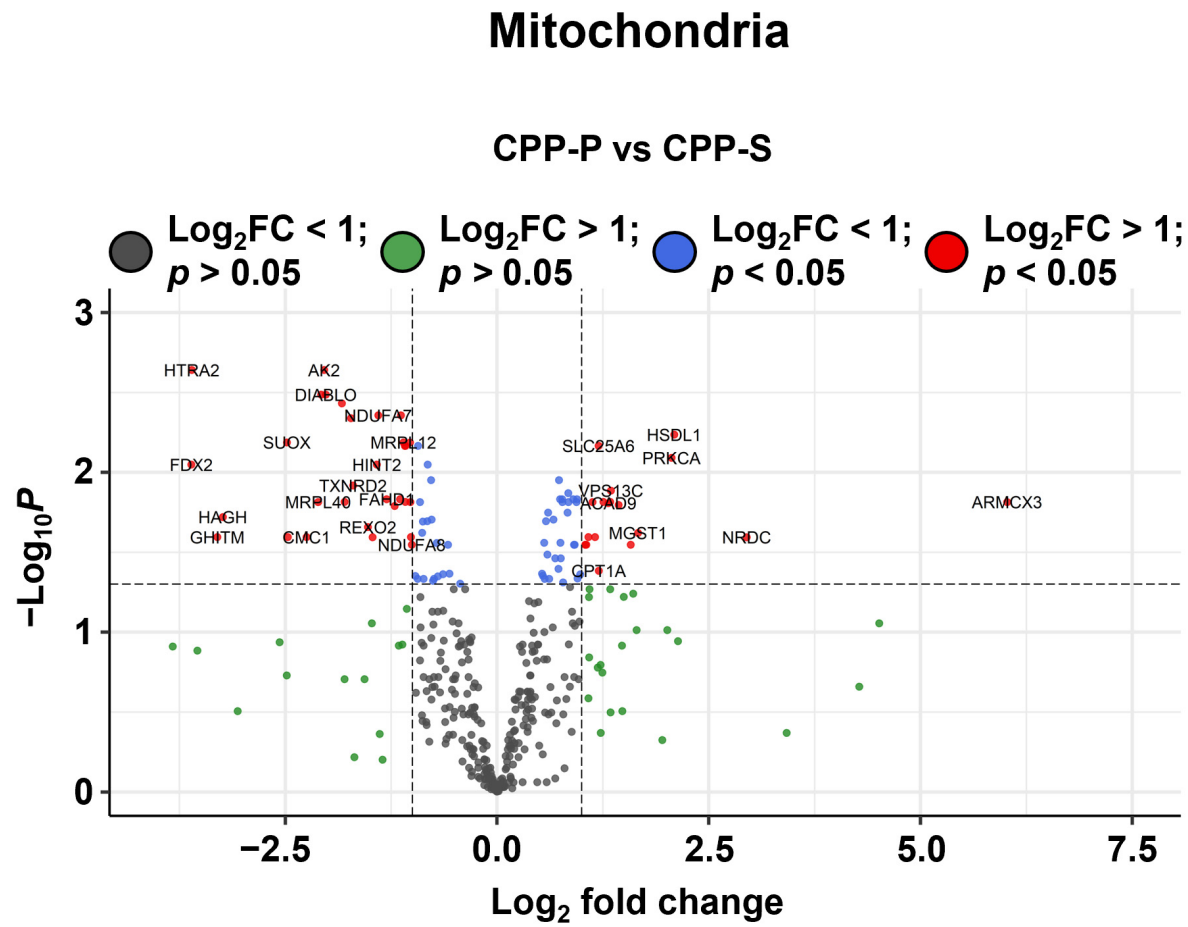


**Supplementary Figure S20.** Bioinformatic analysis of nuclear proteins in CPP-P-treated human internal thoracic artery endothelial cells (HITAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.





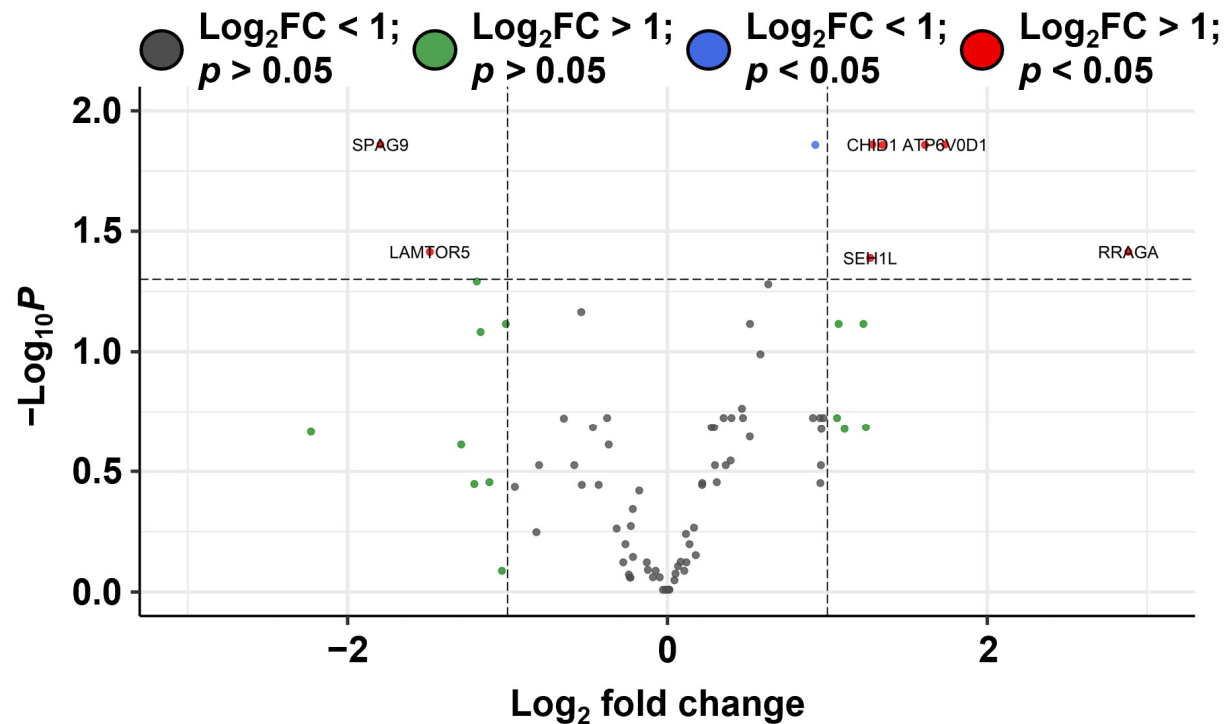
**Supplementary Figure S21.** Bioinformatic analysis of mitochondrial proteins in CPP-P-treated human internal thoracic artery endothelial cells (HITAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.



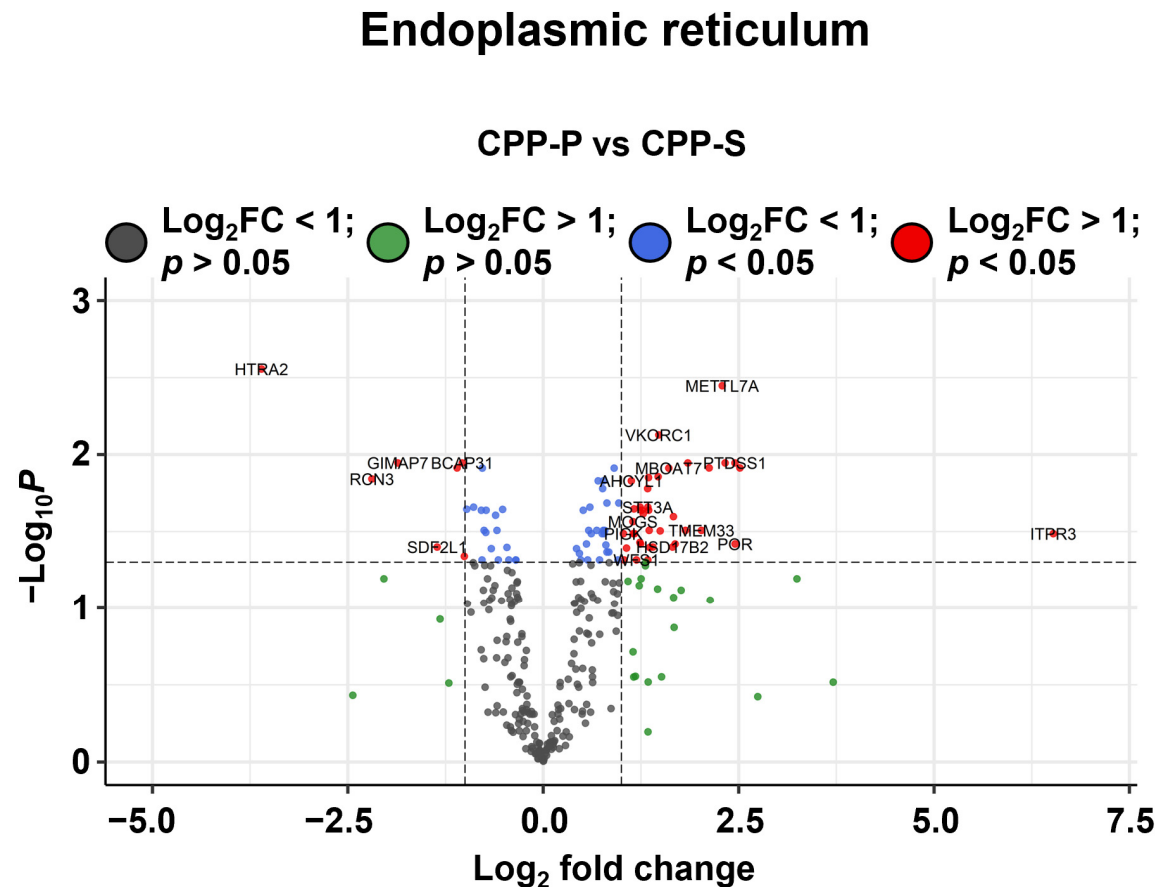
**Supplementary Figure S22.** Bioinformatic analysis of lysosomal proteins in CPP-P-treated human internal thoracic artery endothelial cells (HITAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

## Lysosomes

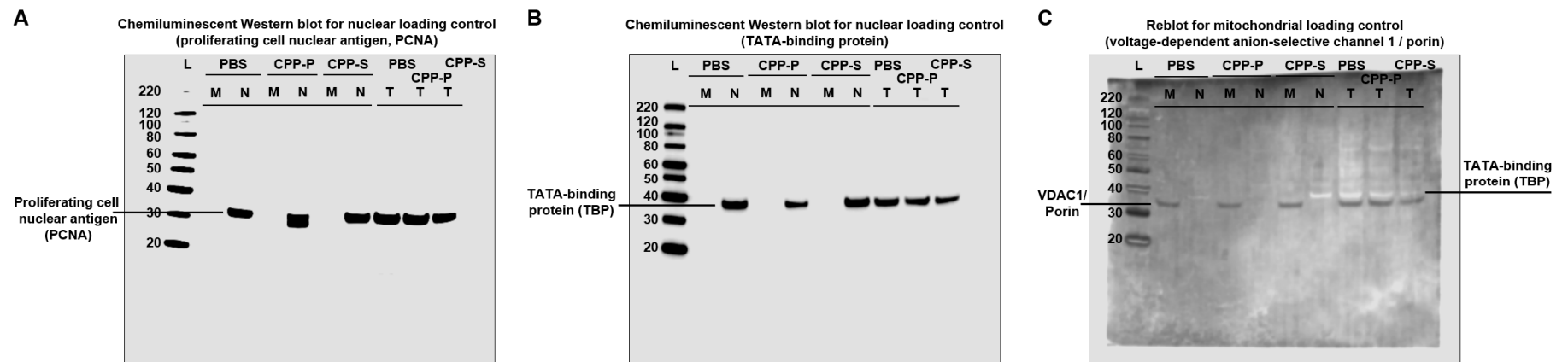
### CPP-P vs CPP-S



**Supplementary Figure S23.** Bioinformatic analysis of endoplasmic reticulum proteins in CPP-P-treated human internal thoracic artery endothelial cells (HITAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

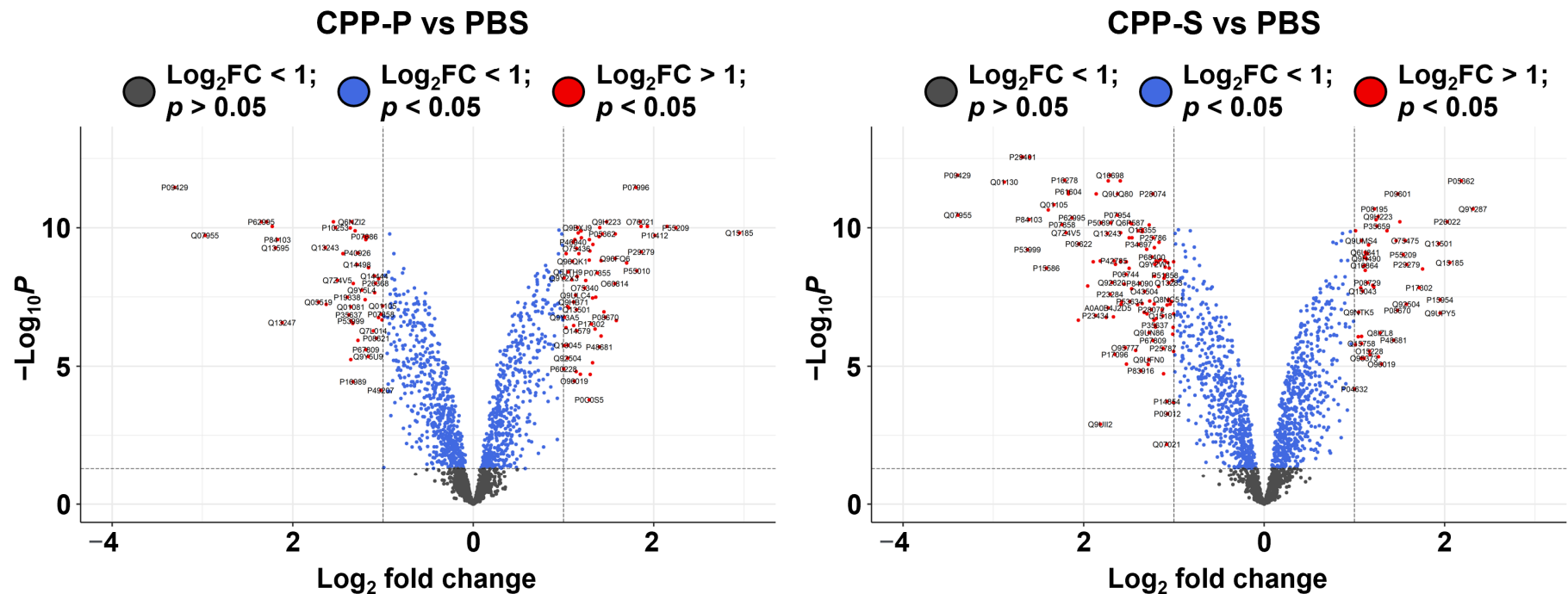


**Supplementary Figure S24.** Western blotting for nuclear and mitochondrial markers indicating successful fractionation of mitochondrial and nuclear fractions. **A.** Western blotting for nuclear loading control (proliferating cell nuclear antigen, PCNA). **B.** Western blotting for another nuclear loading control (TATA-binding protein, TBP). **C.** Reblot of the blot from B for mitochondrial loading control (voltage-dependent anion-selective channel 1 (VDAC1) / porin). Note the remaining bands for TATA-binding protein above the bands for VDAC1/porin after the reblot. MagicMark XP Western Protein Standard was used as a marker of molecular weight. L: ladder, M: mitochondria lysate, N: nuclear lysate, T – total (i.e., non-fractionated) protein used as a positive control. Shown are uncropped blots.



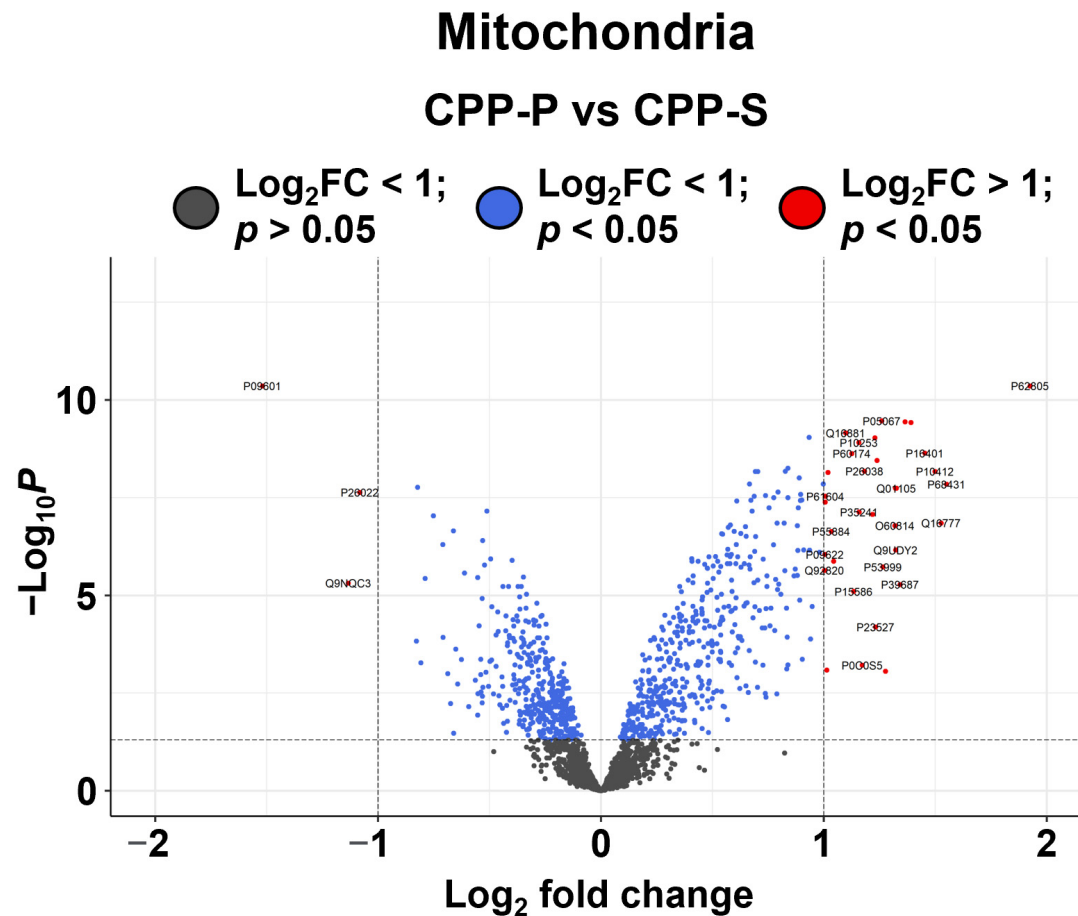
**Supplementary Figure S25.** Bioinformatic analysis of mitochondrial lysate in CPP-P- and CPP-S-treated human coronary artery endothelial cells (HCAEC) as compared to control (PBS-treated) cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change < 1 and FDR-corrected  $p$  value > 0.05, green points depict the proteins with  $\log_2$  fold change > 1 and FDR-corrected  $p$  value > 0.05, blue points depict the proteins with  $\log_2$  fold change < 1 and FDR-corrected  $p$  value < 0.05, and red points depict the proteins with  $\log_2$  fold change > 1 and FDR-corrected  $p$  value < 0.05 (termed as differentially expressed proteins) in each of the indicated organelles.

## Mitochondria





**Supplementary Figure S27.** Bioinformatic analysis of mitochondrial lysate in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.



**Supplementary Figure S28.** Bioinformatic analysis of nuclear lysate in CPP-P-treated human coronary artery endothelial cells (HCAEC) as compared to CPP-S-treated cells, presented as volcano plots. Gray points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $> 0.05$ , green points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $> 0.05$ , blue points depict the proteins with  $\log_2$  fold change  $< 1$  and FDR-corrected  $p$  value  $< 0.05$ , and red points depict the proteins with  $\log_2$  fold change  $> 1$  and FDR-corrected  $p$  value  $< 0.05$  (termed as differentially expressed proteins) in each of the indicated organelles.

