

## **Supplementary Information**

### **Cigarette smoke extract disturbs mitochondria-regulated airway epithelial cell responses to pneumococci**

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## Supplemental Tables

Antibody	Company	Working concentrations	Cat-number	Clone
<b>Primary antibodies</b>				
AMPK- $\alpha$	Cell signaling Technology	1:1000	2532	-
p-AMPK $\alpha$ (Thr172)	Cell signaling Technology	1:1000	2535	40H9
$\beta$ -Actin	Cell signaling Technology	1:2000-1:5000	4970	13E5
BNIP3	Cell signaling Technology	1:1000	3769S	-
BNIP3L	Cell signaling Technology	1:1000	12396	D4R4B
COXIV	Cell signaling Technology	1:1000	4850	3E11
DRP1	Cell signaling Technology	1:1000	8570	D7C7
ERR $\alpha$	Abcam	1:1000	ab76228	EPR46Y
FUNDC1	Santa Cruz Biotechnology	1:500	sc-133597	H22
GABARAPL1	Proteintech Group	1:1000	11010-1-AP	-
GAPDH	Cell signaling Technology	1:5000-1:10000	5174	D16H11
HKII	Cell signaling Technology	1:1000	2867	C64G5
LC3B	Cell signaling Technology	1:1000	2775	-
MFN2	Santa Cruz Biotechnology	1:500	sc-515647	F-5
NLRX1	Cell signaling Technology	1:1000	13829	D4M3Z
NRF1	Abcam	1:1000	ab55744	2F9
OXPHOS subunits	MitoScience LLC	1:1000	MS604	-
PINK	Novus Biologicals	1:2000	BC100-494	-
SQSTM1 (p62)	Cell signaling Technology	1:1000	5114	-
TOMM20	Abcam	1:1000	ab186734	EPR15581-39
ULK1	Cell signaling Technology	1:1000	8054	D8H5
p-ULK1 (Ser555)	Cell signaling Technology	1:1000	5869	D1H4
VDAC1	Cell signaling Technology	1:500	4866	-
<b>Secondary antibodies</b>				
Polyclonal Goat anti-Mouse IgG HRP	Vector laboratories	1:10000	BA-9200	-
Polyclonal Goat anti-Rabbit IgG HRP	Cell signaling Technology	1:10000	7074S	-
Polyclonal Swine anti-	Dako-Agilent	1:1000-1:10000	P0399	-

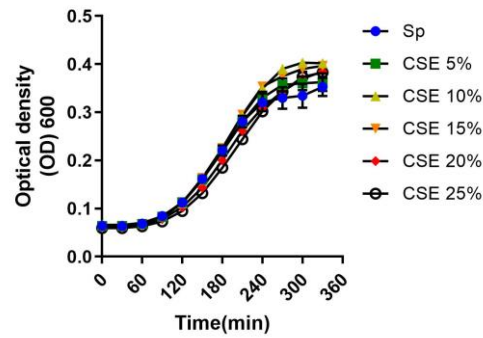
Rabbit IgG HRP				
Polyclonal Rabbit anti-Mouse IgG HRP	Dako-Agilent	1:1000-1:10000	P0161	-

**Table S1:** Antibodies used for immunoblotting. Abbreviations: AMPK $\alpha$ , AMP-activated protein kinase; p-AMPK $\alpha$ , Phosphorylated AMP-activated protein kinase;  $\beta$ -Actin, beta-Actin; BNIP3, BCL2-interacting protein 3; BNIP3L, BCL2 interacting protein 3-like; COXIV, Cytochrome c oxidase subunit IV; DRP1, Dynamin-related protein 1; ERR $\alpha$ , Estrogen-related receptor alpha; FUNDC1, Fun14 domain-containing protein 1; GABARAPL1, Gamma-aminobutyric acid receptor-associated protein-like 1; GAPDH, Glyceraldehyde-3-phosphate dehydrogenase; HKII, hexokinase II; HRP, Horseradish peroxidase; LC3B, Microtubule-associated protein 1A/1B-light chain 3B; MFN2, Mitofusion 2; NLRX1, Nucleotide-binding domain and leucine-rich repeat-containing protein X1; NRF1, Nuclear respiratory factor 1; OXPHOS, Oxidative phosphorylation antibody cocktail (containing SDHB: Succinate dehydrogenase subunit B, UQCRC2: Ubiquinol-cytochrome C reductase core protein 2, ATP5A: adenosine triphosphate 5A); PINK, Phosphatase and tensin homolog (PTEN)-induced kinase; SQSTM1, Sequestosome 1; TOMM20, Translocase of the outer mitochondrial membrane complex subunit 20; ULK1, Unc-51 like autophagy activating kinase 1; p-ULK1, Phosphorylated Unc-51 like autophagy activating kinase 1; VDAC1, Voltage-dependent anion channel 1.

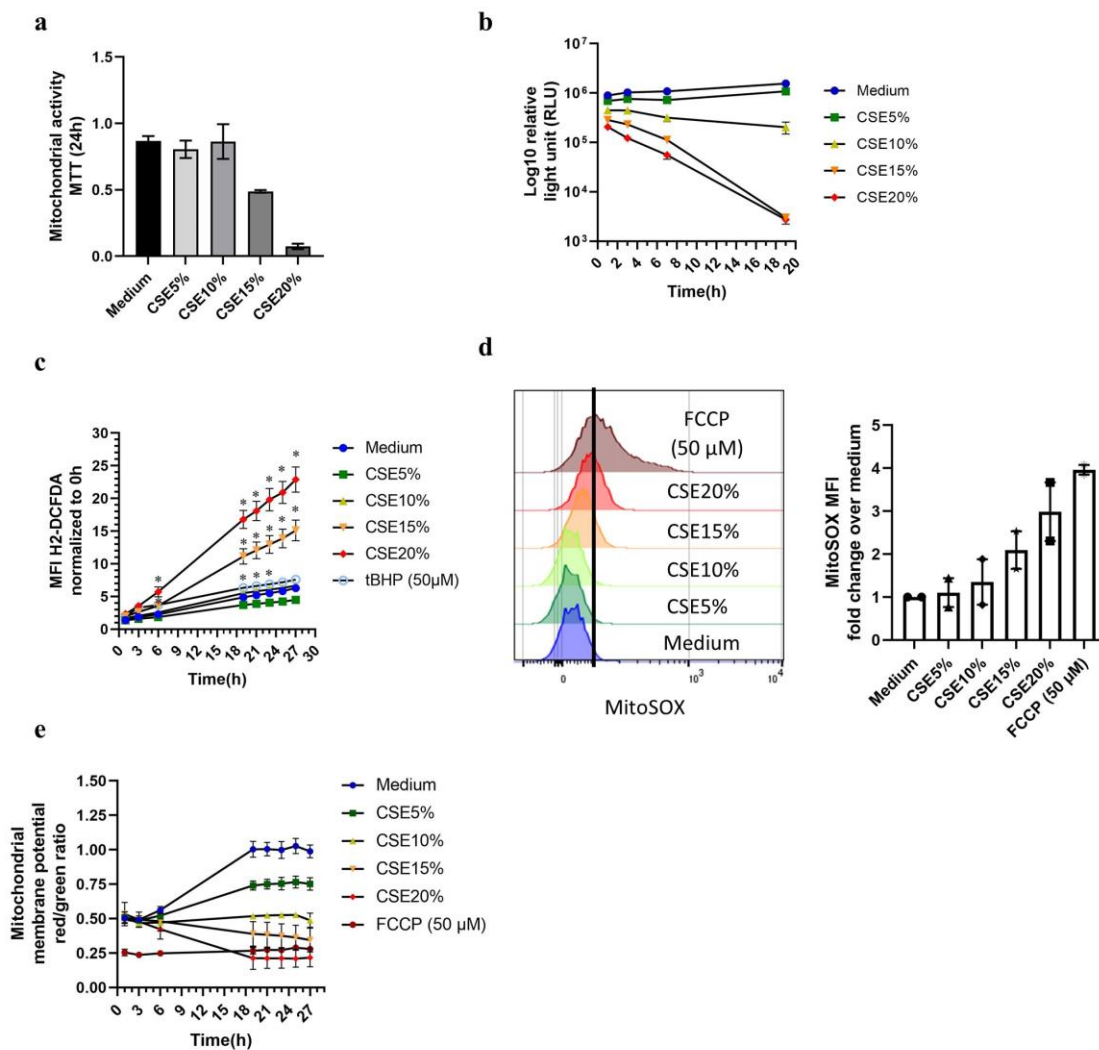
Antibody	Company	Working concentration	Cat-number	Clone
<b>Primary antibodies</b>				
DRP1	Santa Cruz Biotechnology	1:50	sc-271583	C-5
p-DRP1 (Ser616)	Cell signaling	1:300	3455	-
TOMM20 (F-10)	Santa Cruz Biotechnology	1:50	sc-17764	-
ZO-1	Cell signaling	1:400	13663	D6L1E
E-cadherin	Cell signaling	1:200	3195	24E10
ERR $\alpha$	Abcam	1:100	EPR46Y	ab76228
<b>Secondary antibody</b>				
Anti-rabbit IgG Fab2 Alexa fluor (R) 488	Cell signaling	1:1000	4412S	-
Anti-rabbit IgG Fab2 Alexa fluor (R) 647	Cell signaling	1:1000	4410S	-
Alexa fluor 647 Donkey Anti-Rabbit IgG	Biolegend	1:1000	406414	Poly4064

**Table S2:** Antibodies used for immunocytochemistry. Abbreviations: DRP1, Dynamin-related protein 1; p-DRP1, phosphorylated dynamin-related protein 1; ERR $\alpha$ , Estrogen-related receptor alpha; TOMM20, Translocase of the outer mitochondrial membrane complex subunit 20; ZO-1, Zonula occludens 1.

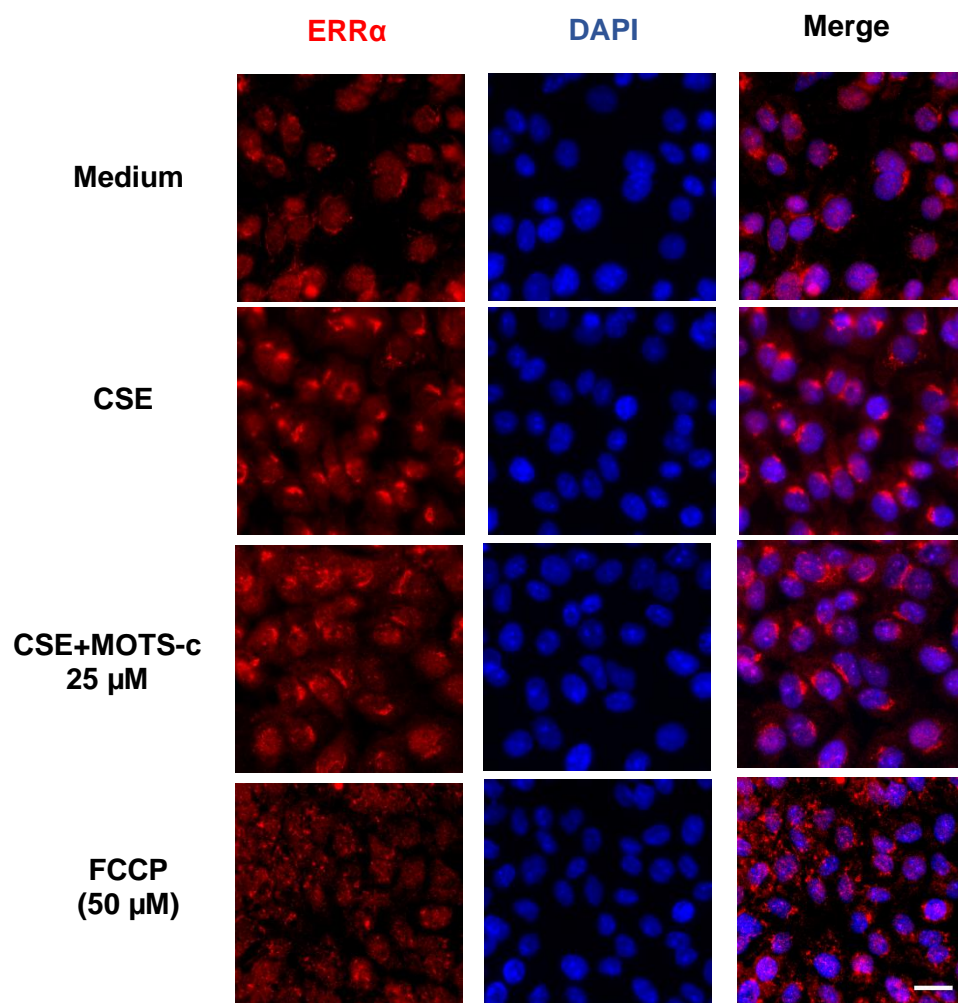
## Supplemental Figures and Figures and Legends



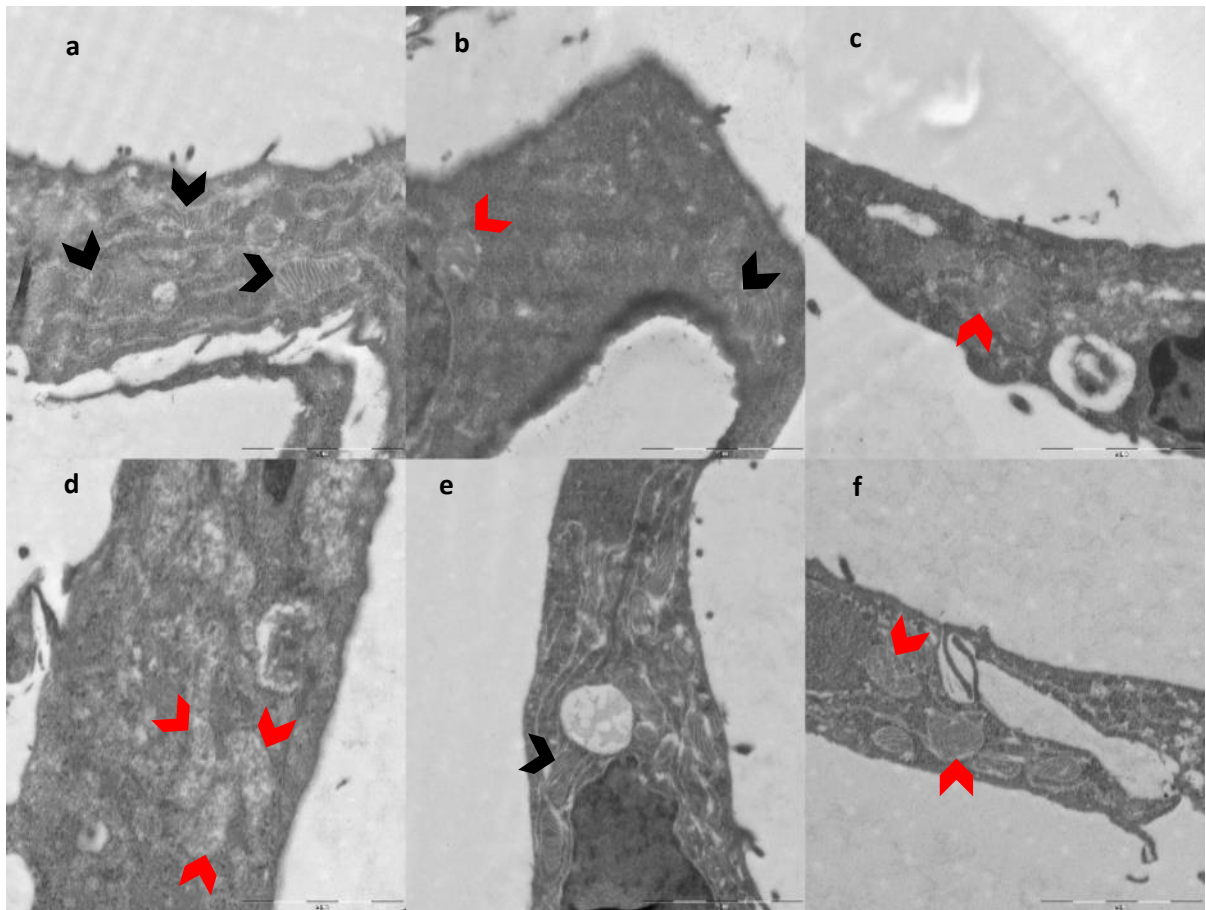
**Figure S1:** Growth curve of *Streptococcus pneumoniae* upon CSE exposure. *Sp* growth curve in presence and absence of different concentrations of cigarette smoke extract (CSE) (5-25%) for 5 h. Data were represented as mean  $\pm$  SEM of triplicate samples for each condition.



**Figure S2:** Optimization of CSE-induced mitochondrial dysfunction model. 16HBE cells were incubated with medium control or various concentrations of cigarette smoke extract (CSE) (5, 10, 15 and 20%) for 24 h. **a)** Proliferation of the treated 16HBE cells was quantified using 3-(4,5-dimethylthiazole-2-yl) 2,5-diphenyl-2H-tetrazolium bromide (MTT) test. The data is presented as mean of triplicates ( $\pm$  SEM) and representative of one out of two independent experiments with similar outcomes. **b)** Real-Time Glo MT assay for time-point measurement of cell proliferation until time 19 h. The data is representative of one out of two independent experiments with similar outcome in triplicates. **c)** Total reactive oxygen species (ROS) levels analyzed with dichlorodihydrofluorescein diacetate (H2-DCFDA) test presented as mean fluorescent intensity (MFI) of triplicates ( $\pm$  SEM) normalized to measurement at assay start (0 h). Tert-butyl hydroperoxide (tBHP) 50  $\mu$ M was used as positive regulator of ROS. Statistically significant difference was calculated with multiple t-test compared to the medium control (\* $p < 0.05$ ). The data is representative of one out of three independent experiments with similar outcome and in triplicates. **d)** Half offset histogram was used to display shift in the MitoSOX fluorescent signal detected by FACS and analyzed by FlowJo, indicative of changes in mitochondrial ROS levels (left panel) and fold change of MFI MitoSOX upon CSE and carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP; positive regulator of mitochondrial ROS). MitoSOX MFI fold change was calculated for each condition compared to the medium. The MFI is representative of two independent experiments. **e)** Mitochondrial membrane potential was measured using JC-1 test by dividing J-aggregate (red signal) by monomer (green signal) and normalized to the ratio in the corresponding condition at 0 h. The data is representative of one experiment out of two independent experiments with triplicate samples.

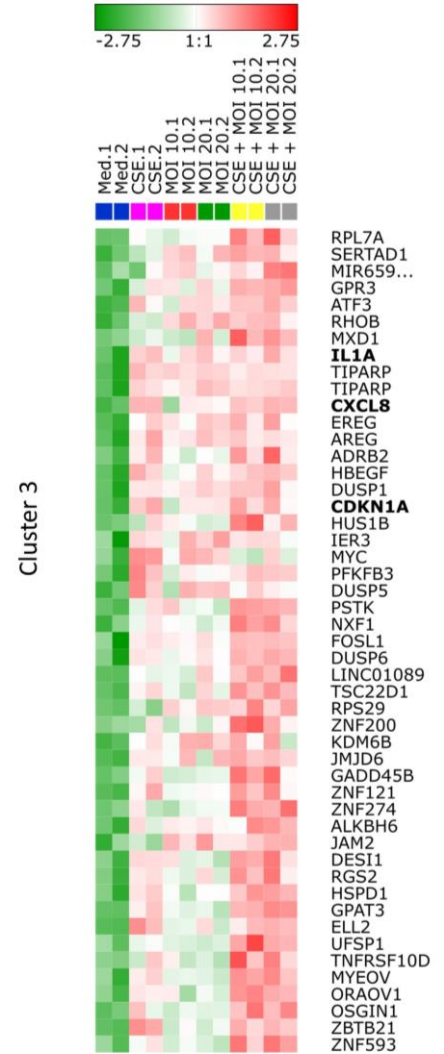
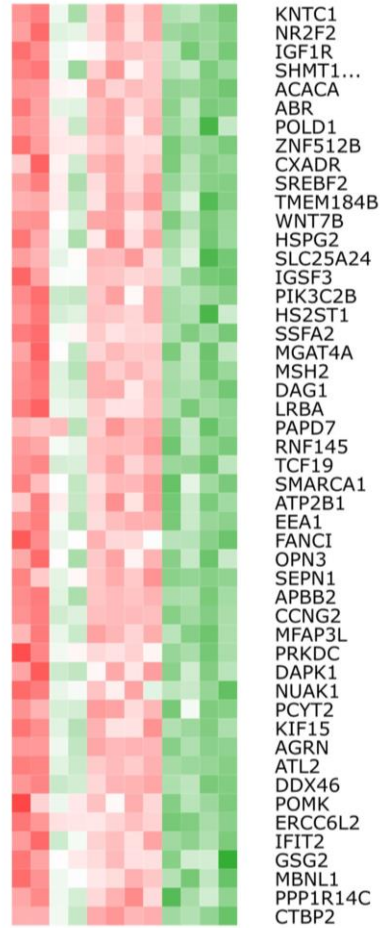
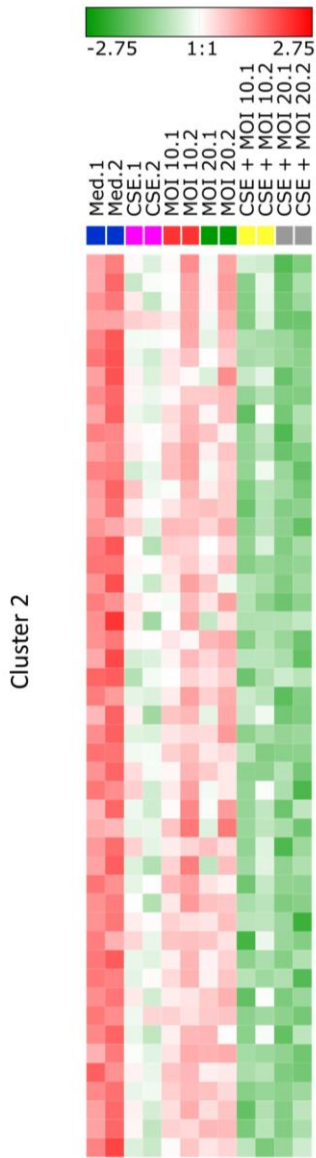


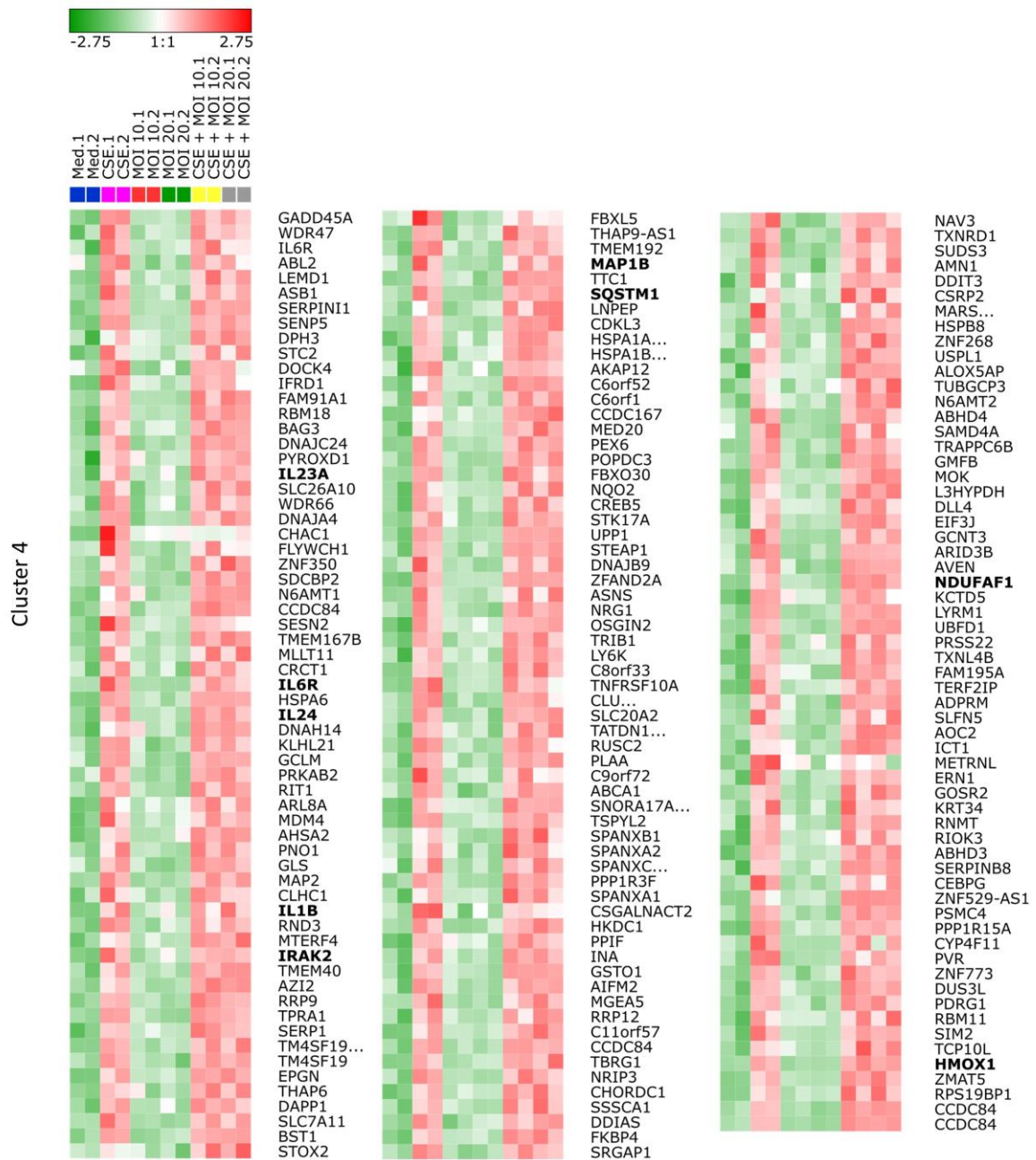
**Figure S3:** Immunostaining for estrogen related receptor  $\alpha$  (ERR $\alpha$ ). The 16HBE cells were stimulated with medium control, cigarette smoke extract (CSE) for 28 h, CSE 24 h followed by mitochondrial ORF of the 12S rRNA type-c (MOTS-c) 25  $\mu$ M for 4 h or with carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP) 50  $\mu$ M. Immunofluorescence staining was performed using an antibody against ERR $\alpha$  (red) and 4',6-diamidino-2-phenylindole (DAPI) (blue) for nuclei staining. The scale bar is equivalent to 20  $\mu$ m.



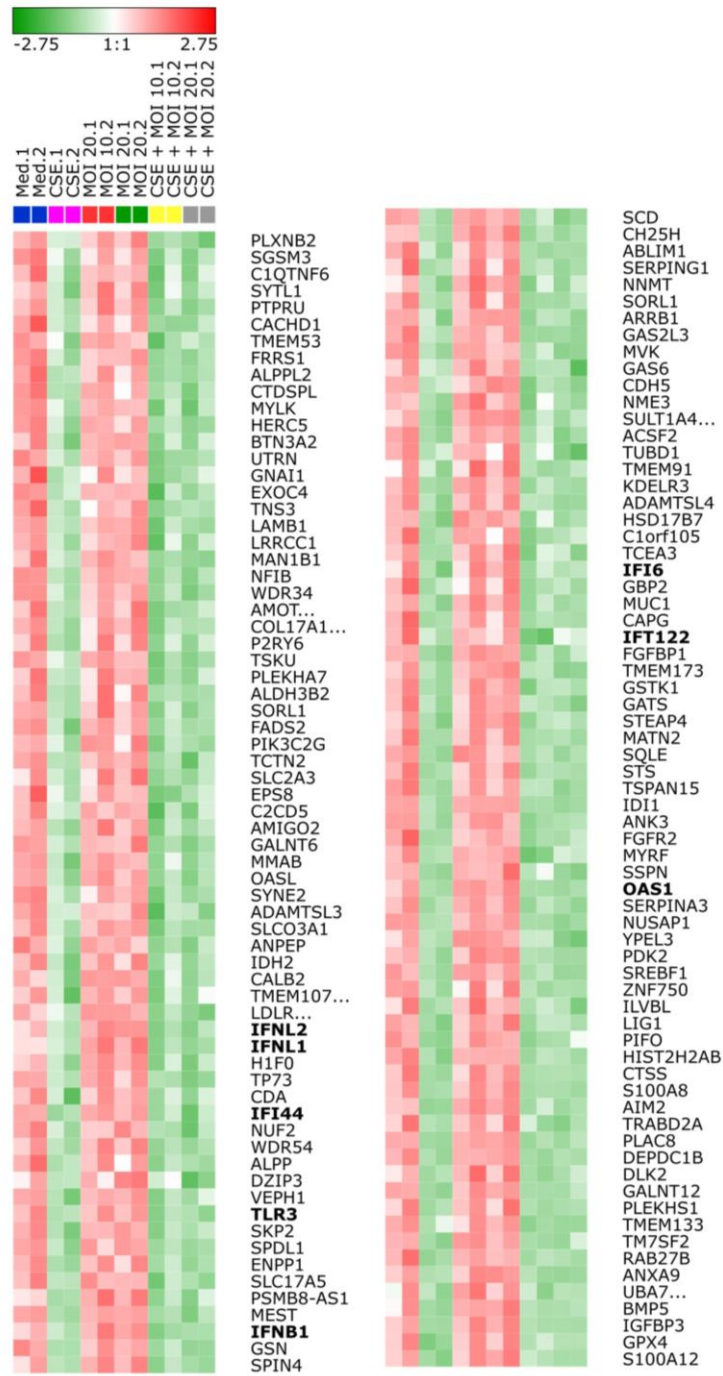
**Figure S4:** Ultrastructure of 16HBE cells upon CSE stimulation and *Streptococcus pneumoniae*. Mitochondrial morphological changes were analyzed under transmission electron microscope (TEM). Dark arrows indicating normal mitochondrial morphology, whereas red arrows showing loss of crista and swollen mitochondria. Representative images of 16HBE cells incubated with **a)** medium for 28 h, **b)** cigarette smoke extract (CSE) for 28 h, **c)** *Streptococcus pneumoniae* (*Sp*) multiplicity of infection (MOI) 10 for 4 h, **d)** CSE for 24 h followed by *Sp* MOI 10 for 4 h **e)**, CSE for 24 h followed by medium for 4 h and **f)** carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP) 50  $\mu$ M for 4 h. The scale bar is equivalent to 2  $\mu$ m.



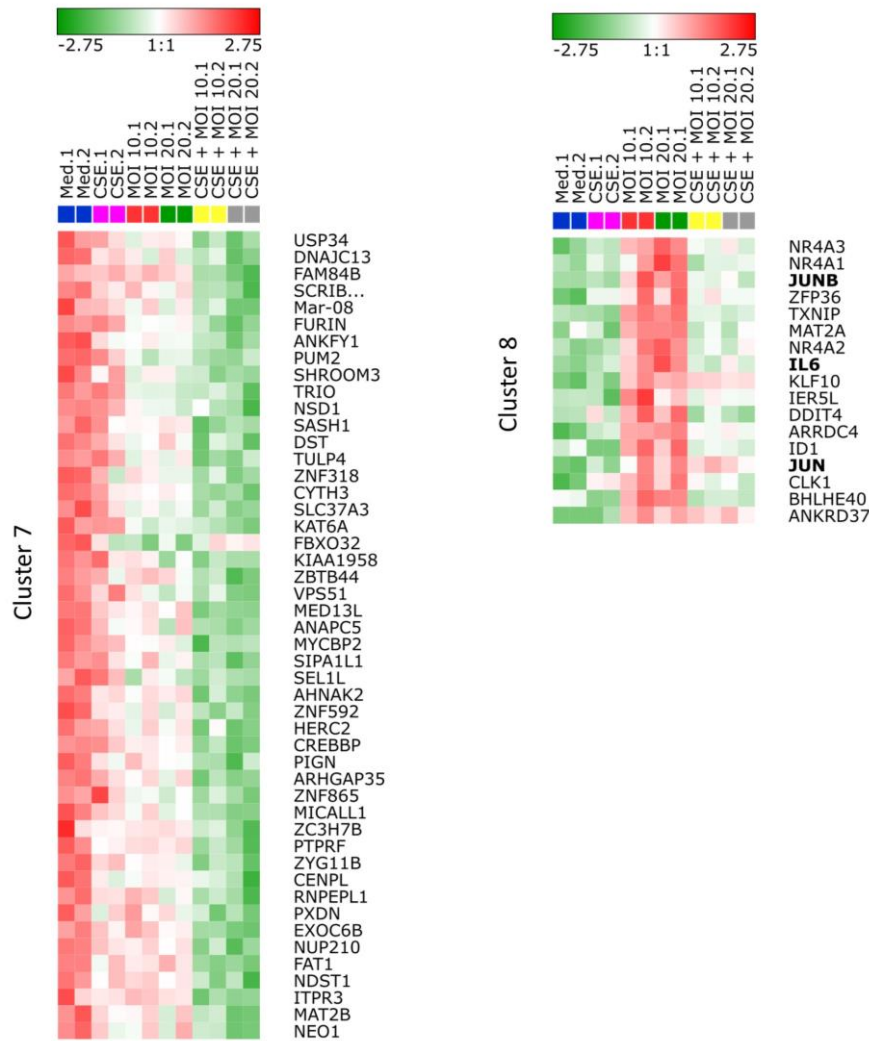




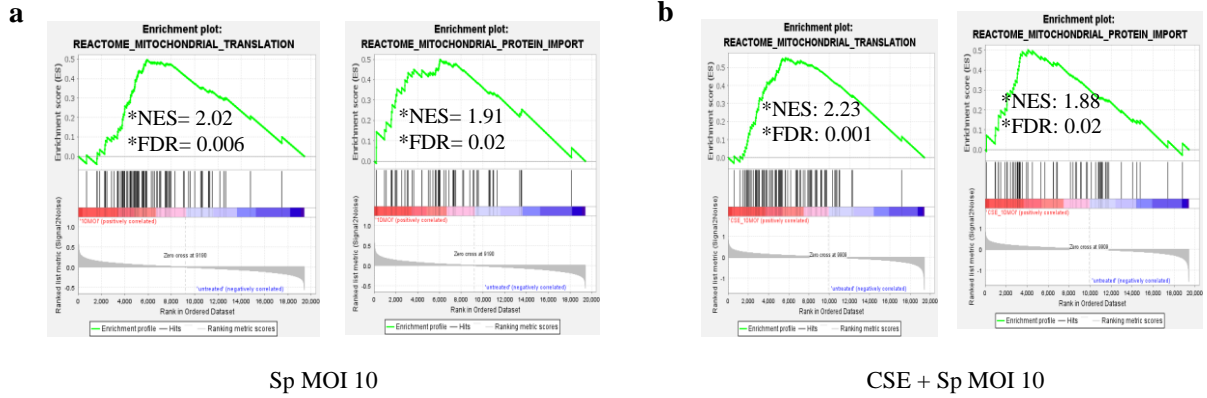
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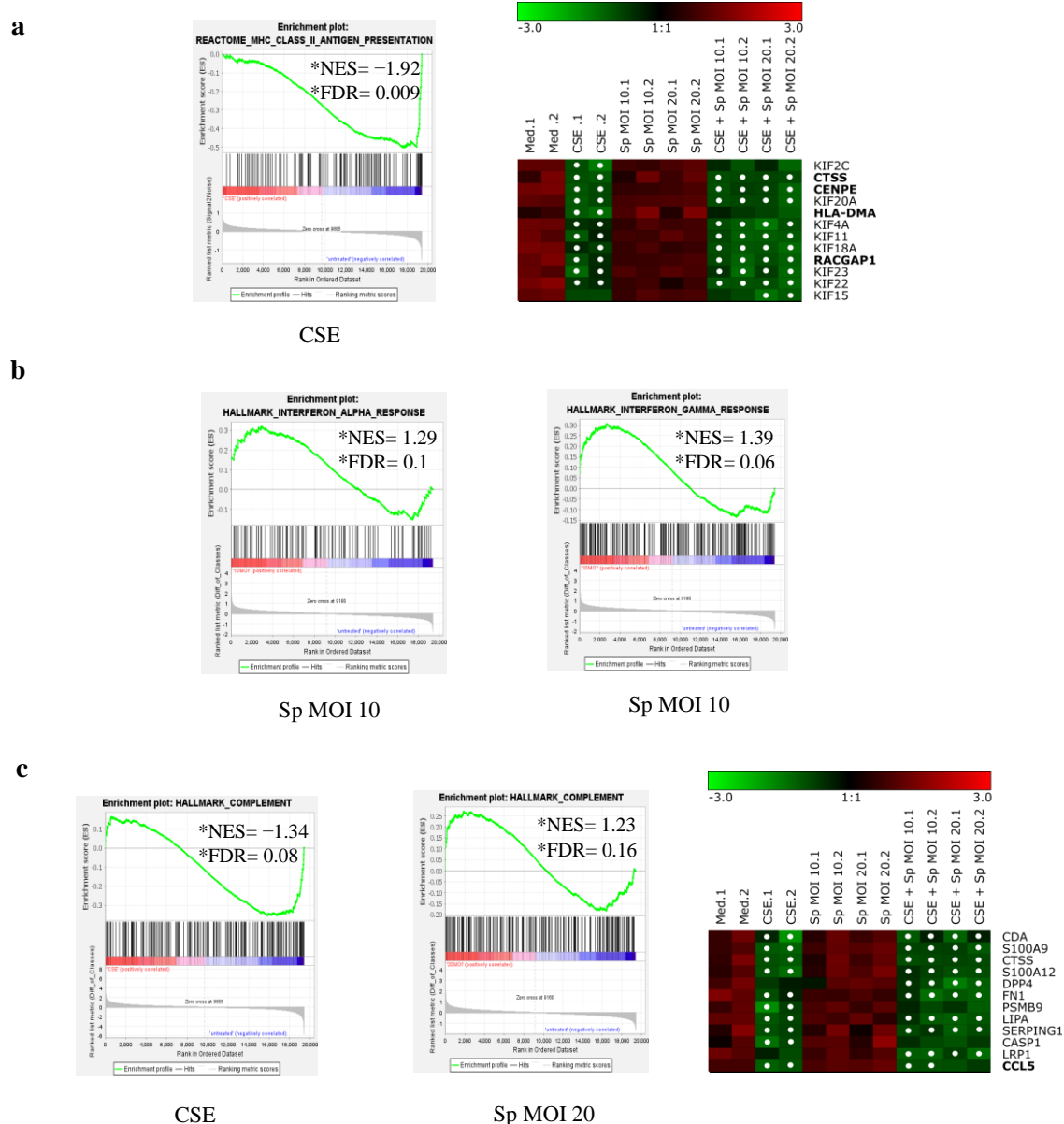




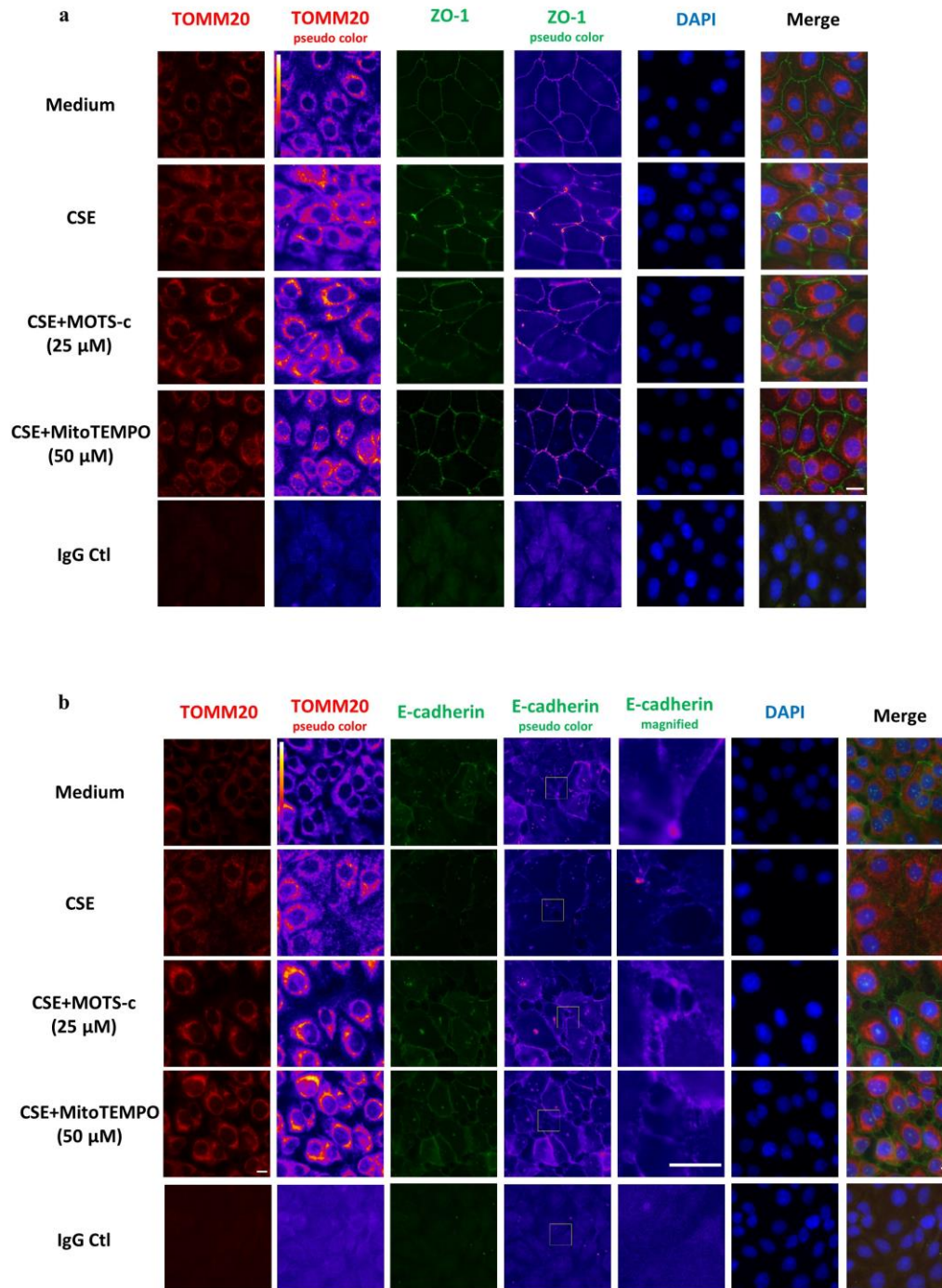
**Figure S5:** Microarray analysis of gene expression upon CSE stimulation and *Streptococcus pneumoniae* infection. 16HBE cells were stimulated with medium (Med) or cigarette smoke extract (CSE) for 28 h, CSE for 24 h followed by medium 4 h (CSE cessation), *Streptococcus pneumoniae* (*Sp*) multiplicities of infection (MOI) of 10 and 20 for 4 h, CSE for 24 h followed by *Sp* MOI 10 and 20 for 4 h. Total RNA was isolated and investigated by using human Clariom S microarray. Differentially expressed transcripts were determined by comparing each condition with medium control (fold change  $\geq 3$ -fold, false discovery rate  $< 0.05$ ).  $\log_2$  signal intensities data of the transcripts were z-score transformed and k-means clustered ( $k = 8$ ), and transcripts in resulting clusters were sorted by maximal absolute z-score (row labels: gene symbols). Data represent color-coded z-scores. Details on bold gene symbols are mentioned in the text.



**Figure S6:** Expression of genes regulating mitochondrial function in 16HBE cells upon *Streptococcus pneumoniae* infection with and without CSE pre-exposure. Gene set enrichment analysis (GSEA) for mitochondrial ribosomal translation and mitochondrial import Reactome genes upon **a)** infecting 16HBE cells with *Streptococcus pneumoniae* (*Sp*) multiplicity of infection (MOI) 10 for 4 h and **b)** incubation with cigarette smoke extract (CSE) for 24 h followed by *Sp* infection with MOI 10 for 4 h compared to the untreated medium (ranked by fold change, FDR < 0.1). The data were collected from two independent experiments.

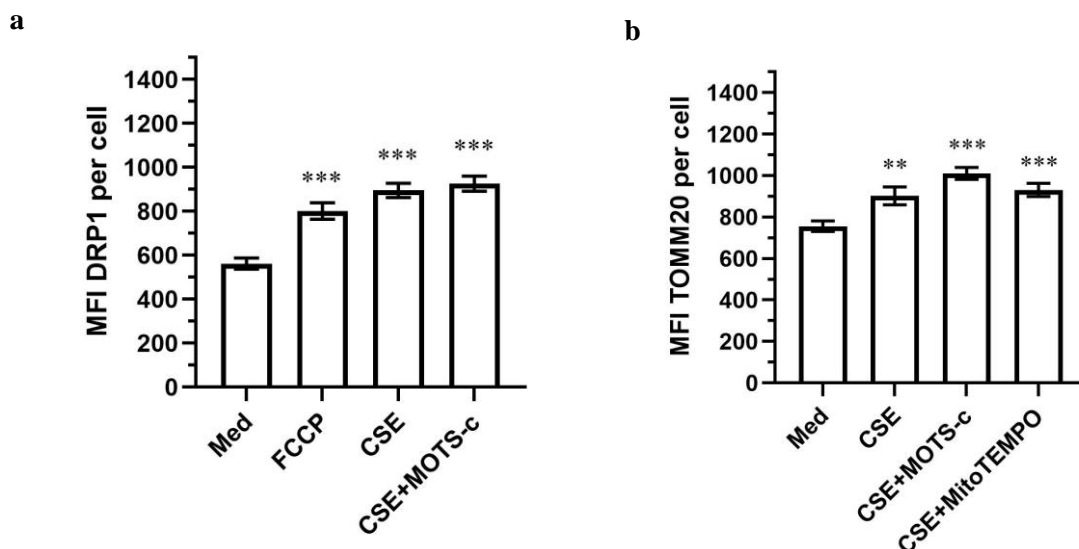


**Figure S7:** Expression of genes regulating innate immune responses upon cigarette smoke extract stimulation and *Streptococcus pneumoniae* infection. **a)** Gene set enrichment analysis (GSEA) for cell surface major histocompatibility complex II (MHCII) in Reactome gene set upon cigarette smoke extract (CSE) stimulation compared to the medium (Med) control. Normalized log<sub>2</sub> signal intensities of core-enriched genes were z-score transformed, color-coded and plotted as heatmap (row labels: gene symbols). Details on bold gene symbols are mentioned in the text. Significance of differential expression with fold change cutoff  $|FC| > 3$  in reference to Med control was calculated by ANOVA ( $p < 0.05$ ). Whitepoints in heatmap plots indicate  $|FC| > 3$  with  $p < 0.05$ . Green/black/red color bars represent z-scores. **b)** GSEA for interferon  $\alpha$  and  $\gamma$  hallmarks upon infection of 16HBE cells with multiplicity of infection (MOI) 10 of *Streptococcus pneumoniae* (Sp). **c)** GSEA for complement hallmarks upon stimulation of 16HBE cells with CSE for 28 h and Sp MOI 20 for 4 h compared to the untreated medium as well as regulated genes in this hallmark calculated by ANOVA ( $p < 0.05$ ). The data were collected from two independent experiments. \*NES: Normalized enrichment score, FDR: false discovery rate.



**Figure S8:** Airway epithelial barrier disruption induced by cigarette smoke extract is reversible with mitochondrial-targeted compounds. 16HBE cells incubated for 28 h with medium (control) or cigarette smoke extract (CSE) for 28 h, or for 24 h with CSE followed by incubation for further 4 h with either mitochondrial-targeted compounds MOTS-c (25  $\mu$ M) or MitoTEMPO (50  $\mu$ M). a) Immunofluorescence imaging of treated cells co-stained with antibodies against translocase of the outer mitochondrial membrane complex subunit 20 (TOMM20) in red, tight junction protein zonula occludens (ZO-1) in green or the nucleus with 4',6-diamidino-2-phenylindole (DAPI) for nucleus staining (blue). b) Treated cells were (co-)stained with anti-TOMM20-antibody (red) and anti-E-cadherin-antibody (green) or with

nuclear staining dye DAPI (blue). False color-coded image columns shown here to depict differences in intensities. To visualize the barrier disruption, magnified regions of interest are indicated in the fourth column and shown in column five. Merged images have been gamma corrected to visualize weak signals without losing the highlights. The scale bar is equivalent to 20  $\mu\text{m}$  (a) and 10  $\mu\text{M}$  (b).



**Figure S9:** Quantification of signal intensities of immunofluorescence staining in 16HBE cells. The cells were stained with antibodies against **a)** dynamin-related protein 1 (DRP1) and **b)** translocase of the outer mitochondrial membrane complex subunit 20 (TOMM20). Mean fluorescence intensity (MFI) was calculated for each cell in the corresponding immunofluorescence images by Fiji software. The statistically significant differences with the medium (Med) were determined by unpaired t-test and using Welch's post-hoc test (\*\*p<0.001, \*\*\*p<0.0001).