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Supplemental Material

Evaluation of Early Biomarkers of Atherosclerosis Associated with Polychlorinated Biphenyl Exposure: An *in Vitro* and *in Vivo* Study

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Table of Contents

Figure S1. Functional analyses of genes targeted by differentially expressed miRNAs. High-throughput sequencing analysis of differentially expressed miRNAs after 5 µM PCB29-pQ treatment of HUVECs for 24 h (n = 3). Target gene of differentially expressed genes were screened and functional analyses performed. Gene ontology has three ontologies: molecular function, cellular component, and biological process. The exact data are presented in Excel Table S3.

Figure S2. KEGG pathway analyses of genes targeted by differentially expressed miRNAs. High-throughput sequencing analysis of differentially expressed miRNAs in HUVECs with 5 µM PCB29-pQ treatment for 24 h (n = 3). KEGG pathway enrichment in miRNA, the rich factor represents the degree of enrichment. The node size shows the number of selected genes, and the color scale represents -log (P value). The exact data are presented in Excel Table S4.

Figure S3. The expression of *HDAC7-AS1, MIR-7-5p* and Ago2 in HUVECs exposed to PCB29-pQ. RT-qPCR was performed to validate (**a**) lncRNAs and (**b**) miRNAs identified as differentially expressed by RNA sequencing assay. *β-Actin* was used as housekeeping genes for lncRNAs quantification and *U6* was used as housekeeping genes for miRNAs quantification, respectively. RP5-1057120.4 (termed as *HDAC7-AS1*) and *MIR-7-5p* were selected as target lncRNA and miRNA for further investigation (indicated with red boxes). Data are presented as mean ± SD (n = 3). (c) Anti-Ago2 RNA binding protein immunoprecipitation assay was used to pull down endogenous RNAs associated with Ago2; IgG served as the control. Ago2 in proteins from Ago2-RIP assay was measured by western blotting. Data are presented as mean ± SD (n = 3). P values were determined by two-way ANOVA, followed by Tukey's *post hoc* test. Data are graphed relative respective vehicle controls. The exact mean and SD value are presented in Table S20.

Figure S4. The expression of *HDAC7* level in HUVECs transfected with *HDAC7-AS1* siRNA or pEZ-M61-*HDAC7-AS1*. (**a**) Predicted relationship between ENST00000080059 (*HDAC7*) and ENST00000599515 (*HDAC7-AS1*) *via* RNAplex (http://www.tbi.univie.ac.at/RNA/RNAplex.1.html) (**b**) After transfection with NC siRNA or *HDAC7-AS1* siRNA (25, 50, or 100 nM) for 48 h, the silencing efficiency of *HDAC7-AS1* siRNA in HUVECs was determined by RT-qPCR. Data are presented as mean ± SD (n = 3). (**c**) After transfection with 2.5 μg pEZ-M61-NC or pEZ-M61-*HDAC7-AS1* (2.5, 5, or 7.5 μg) for 6 h, HUVECs were treated with 5 μM PCB29-pQ. *HDAC7-AS1* level was determined by RT-qPCR. Data are presented as mean ± SD (n = 3). *HDAC7* expression of PCB29-pQ-exposed cells or control after (**d**) transfection with 25 nM NC siRNA or 25 nM *HDAC7-AS1* siRNA for 24 h or (**e**) transfection with 2.5 μg pEZ-M61-NC or 2.5 μg pEZ-M61-*HDAC7-AS1* for 6 h. Data are presented as mean ± SD (n = 3). The housekeeping gene *β-actin* was used for quantification, and the primer information is shown Table S3. P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. For b and c, expression is shown relative to NC siRNA control and pEZ-M61-NC controls, respectively. The exact mean and SD values are presented in Table S21.

Figure S5. The localization of LncRNA *HDAC7-AS1* in HUVECs. HUVECs were treated with 5 μM PCB29-pQ for 24 h. (n = 3). Fluorescent *in situ* hybridization (FISH) assay was used to investigate the localization of *HDAC7-AS1* in in the cells. *HDAC7-AS1* was stained red using an RNA probe, and the nucleus was stained blue with DAPI. Scale bar = 10 μm.

Figure S6. Volcano plots analyzing differential expression with mRNA sequencing (mRNA-Seq) in the control group and PCB29-pQ group. The abscissa represents the logarithmic values of two different groups, and the ordinate represents mRNAs differences (fold change≥2 and P value$<$0.05) between two groups. Red dots indicated PCB29-pQ group is higher relative to control group). Green dots indicated lower expression in PCB29-pQ group than control group (judgment standard is P value <0.05, and the difference multiple is more than 2). Black dots indicted no difference between two groups.

Figure S7. Target genes TGF-β2 and PPME1 protein levels in HUVECs exposed to PCB29-pQ with *MIR-7-5p* inhibitor or *TGF-β2/PPME1* siRNA. After co-transfection with 100 nM NC inhibitor or *MIR-7-5p* inhibitor and NC siRNA or *TGF-β2/PPME1* siRNA (25 nM) for 24 h, HUVECs were treated with 5 μM PCB29-pQ for 24 h. (n = 3). Protein levels of (**a**) PPME1 and (**b**) TGF-β2 were detected by western blotting (upper panel). The relative protein expression levels (lower panel) were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). β-Actin was used as an internal loading control. Data are graphed relative to the expression in cells exposed to the NC inhibitor and NC siRNA together. The exact mean and SD values are presented in Table S22.

Figure S8. Luciferase analysis of the activity of *MIR-7-5p* bind to *TGF-β2*, *PPME1*, and *HDAC7-AS1* in HUVECs transfected with NC mimic or *MIR-7-5p* mimic. (**a**) HUVECs were transfected with NC mimic or *MIR-7-5p* mimic for 48 h, together with NC-3'UTR, *TGF-β2* (WT)-3'UTR, or *TGF-β2* (MUT)-3'UTR. (**b**) HUVECs were transfected with 50 nM NC mimic or 50 nM *MIR-7-5p* mimic for 48 h, together with NC-3'UTR, *PPME1* (WT)-3'UTR, or *PPME1* (MUT)-3'UTR. (**c**) HUVECs were transfected with 50 nM NC mimic or 50 nM *MIR-7-5p* mimic for 48 h, together with Luc-NC, Luc-*HDAC7-AS1*-WT, or Luc-*HDAC7-AS1*-MUT. For all panels, Gaussia luciferase activity was analyzed, corresponding to *TGF-β2*, *PPME1*, and *HDAC7-AS1* transcription. Data are presented as mean ± SD (n = 3). P values were determined by two-way ANOVA, followed by Tukey's *post hoc* test. Data are graphed relative to the NC-mimic treated, NC-3'UTR controls. The exact mean and SD values are presented in Table S23.

Figure S9. The tube forming ability in HUVECs exposed to PCB29-pQ and transfected with a MIR-7-5p inhibitor. (Left panel) After transfection with 100 nM NC inhibitor or 100 nM *MIR-7-5p* inhibitor for 48 h, followed by exposure to 5 μM PCB29-pQ for 24 h, cells were plated on Matrigel to conduct tube formation assay. Scale bar = 200 μm. (Right panel) Quantification of tube formation through measurement of branch point number with ImageJ software. Data were presented as mean ± SD (n = 3). P values were determined by two-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S24.

Figure S10. Apoptosis and proliferation rates in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* mimic or pEZ-M61-*HDAC7-AS1*. (**a**) Cell apoptosis was assessed by Annexin V-FITC/PI double staining with a flow cytometer. (n = 3). (**b**) Cell proliferation was measured by BrdU/PI double staining with a flow cytometer. (n = 3).

Figure S11. *HDAC7-AS1*, *MIR-7-5p*, *TGF-β2*, *PPME1* mRNA levels, TGF-β2 and PPME1 protein levels, and apoptosis or proliferation rates in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor or *HDAC7-AS1* siRNA. After co-transfection with 100 nM NC inhibitor or 100 nM *MIR-7-5p* inhibitor and NC siRNA or *HDAC7-AS1* siRNA (25 nM) for 24 h, HUVECs were treated with 5 μM PCB29-pQ for 24 h. RNAs expression of (**a**) *MIR-7-5p,* (**b**) *HDAC7-AS1*, (**c**) *TGF-β2* and (**d**) *PPME1* were detected by RT-qPCR. *β-actin* was used as a housekeeping gene, except U6 was used for *MIR-7-5p* quantification. The primer information is shown in Table S3-4. (**e**) Protein levels of TGF-β2 and PPME1 were detected by western blotting. β-Actin was used as an internal loading control. (**f**) TGF-β2, (**g**) PPME1 protein expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). (**h**) Cell viability was measured by CCK-8 kit. Data were presented as mean ± SD (n = 3). (**i**) Cell apoptosis was performed by Annexin V-FITC/PI assay with a flow cytometer. (**j**) Cell proliferation was performed by BrdU/PI staining. P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. Data are graphed relative to the cells exposed to NC inhibitor, NC siRNA, and vehicle control. The exact mean and SD values are presented in Table S25.

Figure S12. HE staining of aortic root cross-sections and TC and TG levels in *ApoE*$^{-/-}$ mice were intravenous (*i.v.*) injected with *AAV-HDAC7-AS1*. Male *ApoE*$^{-/-}$ mice were *i.v.* injected with AAV-*HDAC7-AS1 via* tail vein (4×10^{10} particles/mouse) to create an *HDAC7-AS1* overexpressed mice model. Male *ApoE*$^{-/-}$ mice that received the AAV vector were used as AAV control mice. Control and *HDAC7-AS1* overexpressed *ApoE*$^{-/-}$ mice were fed a western high-fat diet for 12 weeks and tap water ad libitum. Mice were injected with 5 mg/kg body weight of PCB29-pQ or equal volumes of corn oil by *i.p.* injection once a week for 12 continuous weeks with the first two injections during the 1st week (3 days apart). (**a**) (Left panel) HE of the aortic root (Right panel) plaque area in the aortic root was quantified by ImageJ software. Data are presented as mean ± Standard Deviation (SD). Scale bar = 200 μm. (**b**) TC level and (c) LDL-C level. Data are presented as mean ±SD (n = 5). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S26.

Figure S13. CAV1 phosphorylation and TGF-β, PPME1, and inflammatory factor levels in HUVECs exposed PCB29-pQ with *CAV1* siRNA. (**a**) HUVECs were treated with 5 μM PCB29-pQ for 1, 3, and 6 h. (upper panel) Protein levels of p-CAV1 and CAV1 were detected by western blotting. β-Actin was used as an internal loading control. The relative protein expression levels (lower panel) were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). After transfection with 25 nM NC siRNA or *CAV1* siRNA for 48 h, HUVECs were treated with 5 μM PCB29-pQ for 24 h. The siRNA information is shown in Table S6. (**b**) Protein levels of p-CAV1, CAV1, IL-1β, IL-6, and TNFα were detected by western blotting. β-Actin was used as an internal loading control. (**c-h**) p-CAV1, CAV1, IL-1β, IL-6, and TNFα were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. Data are graphed relative to the NC siRNA group. The exact mean and SD values are presented in Table S27.

Figure S14. p-CAV1 level in *ApoE*$^{-/-}$ mice that were *i.v.* injected with AAV-*HDAC7-AS1*. Male *ApoE*$^{-/-}$ mice were i.v. injected with AAV-*HDAC7-AS1 via* tail vein (4×10^{10} particles/mouse) to create an *HDAC7-AS1* overexpressed mice model. Male *ApoE*$^{-/-}$ mice that received the AAV vector were considered as AAV control mice. Control and *HDAC7-AS1* overexpressed *ApoE*$^{-/-}$ mice were fed a Western high-fat diet for 12 weeks and tap water ad *libitum*. Mice were injected with 5 mg/kg body weight of PCB29-pQ or equal volumes of corn oil by *i.p.* injection once a week for 12 continuous weeks with the first two injections during the 1st week (3 days apart). (Left panel) The presence of p-CAV1 in aortic root cross-sections was detected by double immunostaining with the use of antibodies against p-CAV1 (red), endothelial cell marker CD31 (green), and nucleus marker DAPI (blue), respectively. Scale bar = 100 μm. White arrows represent the colocalization of p-CAV1 (red) and CD31 (green). (Right panel) Co-localization of p-CAV1 and CD31 was analyzed by Pearson's correlation coefficient. Data were presented as mean ± SD (n = 3). The exact mean and SD values are presented in Table S28.

Figure S15. Gene type identification of *ApoE* and *CAV1* knockout mice. DNA from the tail of offspring mice was extracted and analyzed by PCR and agarose gel electrophoresis. (**a**) Homozygous of *ApoE*: 245 bp; Heterozygous of ApoE: 245 bp & 155 bp; WT of ApoE: 155 bp. (**b**) Homozygous of *CAV1*: 410 bp; Heterozygous of *CAV1*: 690 bp & 410 bp; WT of *CAV1*: 690 bp. The PCR primer sequences for *ApoE* and *CAV1* mice genotyping are shown in Table S2.

Figure S16. Immunohistochemistry staining of CD68 and TC and LDL-C levels in *ApoE$^{-/-}$* and *ApoE$^{-/-}$/CAV1$^{-/-}$* mice. *ApoE$^{-/-}$* mice were crossed with *CAV1$^{-/-}$* mice to generate *ApoE$^{-/-}$/CAV1$^{-/-}$* mice. *ApoE$^{-/-}$* or *ApoE$^{-/-}$/CAV1$^{-/-}$* mice were fed a Western high-fat diet for 12 weeks and tap water ad libitum. Mice were treated with 5 mg/kg body weight of PCB29-pQ or equal volumes of corn oil by *i.p.* injection. (a) (Left panel) Immunohistochemistry staining of CD68 detected macrophage infiltration located at the aortic wall. Scale bar = 200 μm. (Right panel) Quantification proportion of positive CD68 expressions area to total aortic section using was performed by ImageJ software. Data are presented as mean ± SD (n = 3). Serum (b) TC level and (c) LDL-C levels. Data are presented as mean ±SD (n = 5). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S29.

Figure S17. Adhesion molecules, pro-inflammatory cytokines and p65 protein expression levels in HUVEC exposed to PCB29-pQ. HUVECs were treated with 5 μM PCB29-pQ for 1, 3, or 6 h. (**a**) IL-1β, IL-6, TNF-α, ICAM-1, and VCAM-1 expressions in cell lysates were analyzed by western blotting. (**b-f**) IL-1β, IL-6, TNF-α, ICAM-1, and VCAM-1 expressions were quantified by ImageJ software. Data are presented as mean ± Standard Deviation (SD) (n = 3). (**g**) Calcein-AM-loaded THP-1 cells (10^6 cells/ml) were added to HUVECs and then incubated for 3 h. The unbound cells were washed off, and attached fluorescent monocytes were visualized using an optical microscope. (Left panel) The fluorescence intensity of Calcein-AM was quantified using ImageJ software. Data are presented as mean ± SD (n = 3). P value was determined by unpaired Student's t-test. (**h**) HUVECs were treated with 5 μM PCB29-pQ for 1, 3, or 6 h. IκBα and p-p65 levels were analyzed by western blotting analysis. β-Actin was used as an internal loading control. (**i-j**) IκBα and p-p65 levels were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). (**k**) HUVECs were pretreated with 5 μM p65 inhibitor PDTC for 1 h, followed with 5 μM PCB29-pQ exposure for 6 h. IL-1β, IL-6, and TNF-α in cell lysates were analyzed by western blotting. β-Actin was used as an internal loading control. (**l-n**) IL-1β, IL-6, and TNF-α protein expression levels were quantified by ImageJ software. Data were presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S30.

Figure S18. Adhesion molecules, pro-inflammatory cytokines and p65 protein expression levels in HUVEC exposed to PCB29-pQ with *CAV1* siRNA. HUVECs were transfected with NC siRNA or 25 nM *CAV1* siRNA for 48 h and then treated with 5 μM PCB29-pQ for 6 h. (a) IL-1β, IL-6, TNF-α, ICAM-1 and VCAM-1 expressions were analyzed by western blotting. β-Actin was used as an internal loading control. (**b-f**) IL-1β, IL-6, TNF-α, ICAM-1 and VCAM-1 expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). (**g**) IκBα, p-p65, and p65 expressions were analyzed by western blotting. β-Actin was used as an internal loading control. (**h-i**) IκBα, p-p65, and p65 expression levels were quantified by ImageJ software. Data were presented as mean ± SD (n = 3). (**j**) (Left panel) Immunofluorescence analysis of p65. Green staining represents the location of p65. Nuclei shown in blue were stained with DAPI. Scale bar = 10 μm. (Right panel) Co-localization of p-CAV1 and DAPI was analyzed by Pearson's correlation coefficient. Data were presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's post hoc test. The exact mean and SD values are presented in Table S31.

Figure S19. Inflammatory factors and ROS levels in HUVEC exposed to PCB29-pQ. HUVECs were pretreated with 40 μM VC, 20 μM VE or 5 mM NAC for 1 h, followed with 5 μM PCB29-pQ exposure for 6 h. (n = 3). (**a**) p-p65, p65, IL-1β, IL-6, TNFα, ICAM-1 and VCAM-1 in cell lysates were analyzed by western blotting. (**b-g**) p-p65, p65, IL-1β, IL-6, TNFα, ICAM-1 and VCAM-1 expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). (**h**) ROS levels were detected by DCFH-DA (10 μM) probe. Data were presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. In all graphs, data is normalized to the control cell groups. The exact mean and SD values are presented in Table S32.

Figure S20. p-CAV1 and CAV1 levels in HUVEC exposed to PCB29-pQ and antioxidants. HUVECs were pretreated with 40 μM VC, 20 μM VE or 5 mM NAC for 1 h, followed by 5 μM PCB29-pQ exposure for 6 h. HUVECs were pretreated with (**a**) 40 μM VC, 20 μM VE or 5 mM NAC, (**b**) 200 U/ml PEG-SOD, 500 U/ml PEG-CAT and 5 mM GSH-MEE for 1 h, followed with 5 μM PCB29-pQ exposure for 6 h. (Left panel) p-CAV1 and CAV1 in cell lysates were analyzed by western blotting. β-Actin was used as an internal loading control. (Right panel) p-CAV1 and CAV1 expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. All data is graphed relative to the control cell groups. The exact mean and SD values are presented in Table S33.

Figure S21. Heatmap showing correlation scores between factors. Plasma RNA was extracted by TRNzol universal reagent. CHD group (n = 77) contains patients with > 50% coronary artery stenosis, and the control group (n = 50) contains subjects with < 50% coronary artery stenosis. RT-qPCR analysis of *HDAC7-AS1*, *MIR-7-5p*, *TGF-β2*, *PPME1*, *IL-1β*, *IL6* and *TNFα* expressions. Spearman's rank correlation coefficient was used to assess the correlation between the two indicated factors. P value of < 0.05 was considered significant. The size and color of circle represents the correlation between two factors. X's mean no significance. Summary data can be found in Table S11.

Table S1. Sources of antibodies using in this study.

Table S2. PCR primer sequences for *ApoE* and *CAV1* mice genotype.

Table S3. PCR program for *ApoE* and *CAV1* mice genotype.

Table S4. RT-qPCR primer sequences for lncRNAs and mRNAs.

Table S5. RT-qPCR primer sequences for miRNAs.

Table S6. RT-qPCR program.

Table S7. siRNAs, mimic, and inhibitor target sequences.

Table S8. Patient characteristics and clinical results.

Table S9. ***MIR-7-5p*** **binding sites for** ***HDAC7-AS1*** **as identified by Mireap, miRanda, and TargetScan.**

Table S10. Negatively correlated miRNA-gene pairs: ***MIR-7-5p*** **and its target genes.**

Table S11. Results of correlation analysis between two indicated factors.

Table S12. Univariable and multivariable logistic regression analysis for determining the independent risk factors of CHD.

Table S13. High-throughput lncRNA and miRNA sequence analysis and relevant qPCR results from HUVECs treated with 5 µM PCB29-pQ.

Table S14. The expression of ***HDAC7-AS1, MIR-7-5p*** **and** ***TGF-β2/PPME1*** **in HUVECs exposed to 5 µM PCB29-pQ.**

Table S15. Endothelial injury and atherogenesis in ***ApoE$^{-/-}$*** **mice exposed to PCB29-pQ, and apoptotic rate in HUVECs exposed to PCB29-pQ.**

Table S16. Measures of endothelial injury in cells and protein and mRNA expression of ***TGF-β2*** **and PPME1 in HUVECs transfected with a** ***HDAC7-AS1*** **overexpression vector or a** ***MIR-7-5p*** **mimic exposed to 5 µM PCB29-pQ.**

Table S17. Atherosclerosis and inflammation in ApoE-/- mice exposed to PCB29-pQ accompanied by AAV-*HDAC7-AS1* treatment.

Table S18. Inflammation and atherogenesis in ***ApoE$^{-/-}$*** **and** ***ApoE$^{-/-}$CAV1$^{-/-}$*** **mice exposed to PCB29-pQ.**

Table S19. Plasma ***HDAC7-AS1*** **(a),** ***MIR-7-5p*** **(b),** ***TGF-β2*** **(c),** ***PPME1*** **(d),** ***IL-1β*** **(e),** ***IL-6*** **(f), and** ***TNFα*** **(g) levels in patients with CHD.**

Table S20. The expression of select lncRNAs in HUVECs exposed to PCB29-pQ.

Table S21. The expression of ***HDAC7*** **level in HUVECs transfected with** ***HDAC7-AS1*** **siRNA or pEZ-M61-*HDAC7-AS1*.**

Table S22. Protein TGF-β2 and PPME1 levels in HUVECs exposed to PCB29-pQ with ***MIR-7-5p*** **inhibitor or** ***TGF-β2/PPME1*** **siRNA.**

Table S23. Luciferase analysis of the activity of ***MIR-7-5p*** **bind to** ***TGF-β2, PPME1,*** **and** ***HDAC7-AS1*** **in HUVECs transfected with NC mimic or** ***MIR-7-5p*** **mimic.**

Table S24. The tube forming ability in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor.

Table S25. *HDAC7-AS1, MIR-7-5p, TGF-β2, PPME1* levels and apoptosis or proliferation rates in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor or *HDAC7-AS1* siRNA.

Table S26. HE staining of aortic root cross-sections and total cholesterol (TC) and low-density lipoprotein (LDL) levels in *ApoE*$^{-/-}$ mice were *i.v.* injected with AAV-*HDAC7-AS1*.

Table S27. TGF-β2, PPME1, and inflammatory factors level in HUVECs exposed to PCB29-pQ with or without *CAV1* siRNA.

Table S28. Pearson's correlation coefficient for expression of **p-CAV1 and** CD31 **in *ApoE*$^{-/-}$ mice that *were i.v.* injected with AAV-*HDAC7-AS1*.**

Table S29. Immunohistochemistry staining of CD68, total cholesterol (TC), and low-density lipoprotein level (LDL) in *ApoE*$^{-/-}$ and *ApoE*$^{-/-}$/*CAV1*$^{-/-}$ mice.

Table S30. Adhesion molecules, pro-inflammatory cytokines and *p65* protein expression level in HUVEC exposed to PCB29-pQ.

Table S31. Adhesion molecules, pro-inflammatory cytokines and *p65* protein expression levels in HUVEC exposed to PCB29-pQ with *CAV1* siRNA.

Table S32. Protein expression of inflammatory factors and ROS levels in HUVEC exposed to PCB29-pQ.

Table S33. p-CAV1 protein expression relative to CAV1 total protein in HUVEC exposed to PCB29-pQ and antioxidants.

Additional File- Excel Document

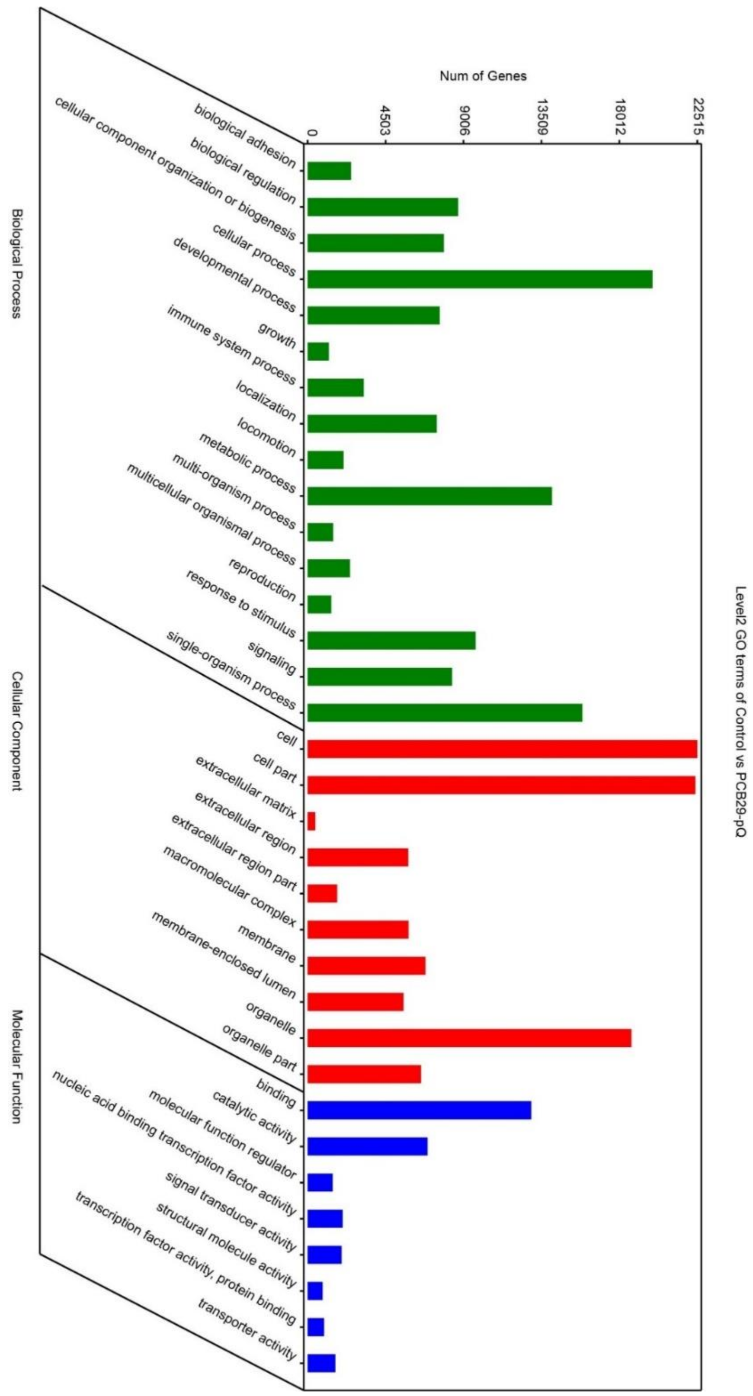


Figure S1. Functional analyses of genes targeted by differentially expressed miRNAs. High-throughput sequencing analysis of differentially expressed miRNAs after 5 μM PCB29-pQ treatment of HUVECs for 24 h (n = 3). Target gene of differentially expressed genes were screened and functional analyses performed. Gene ontology has three ontologies: molecular function, cellular component, and biological process. The exact data are presented in Excel Table S3.

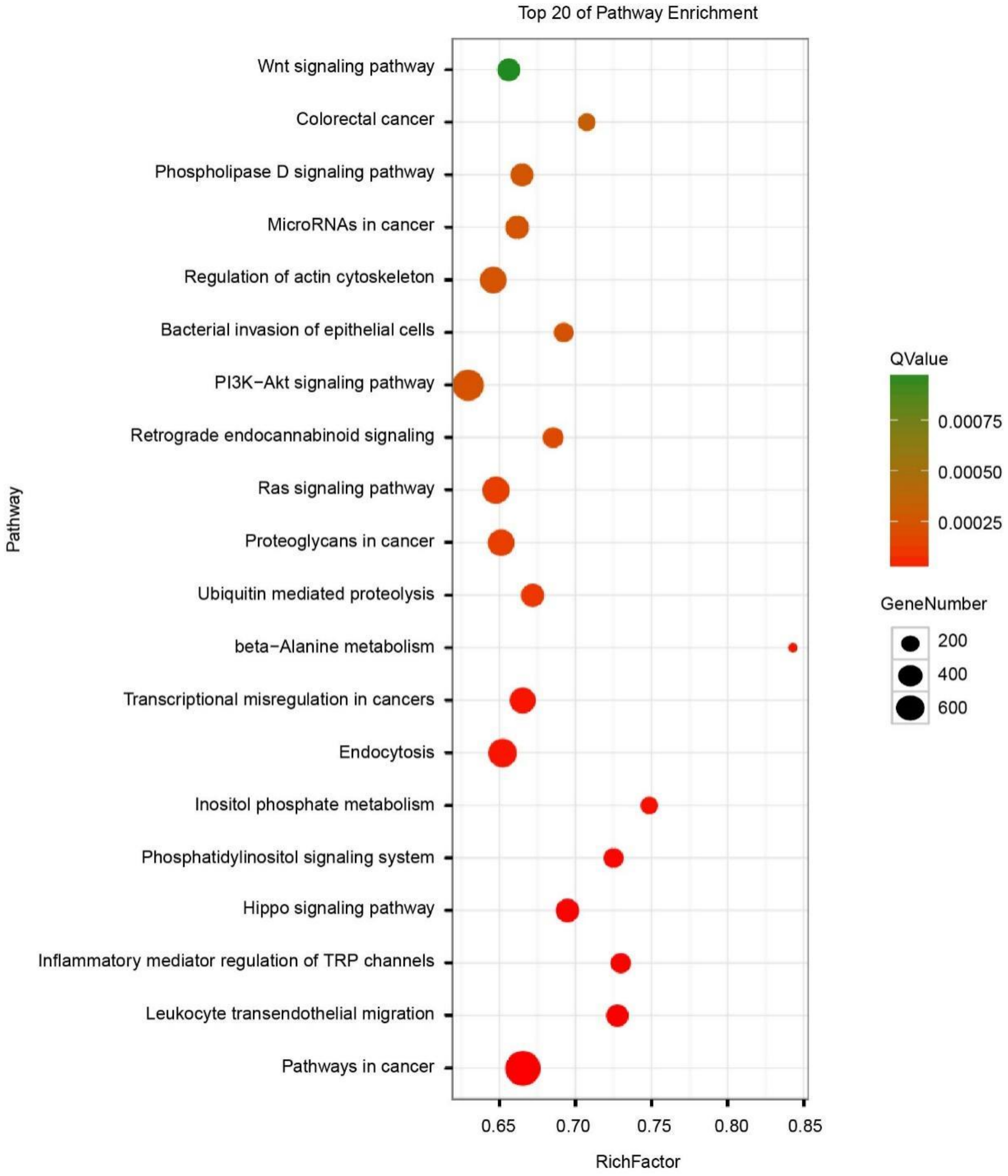
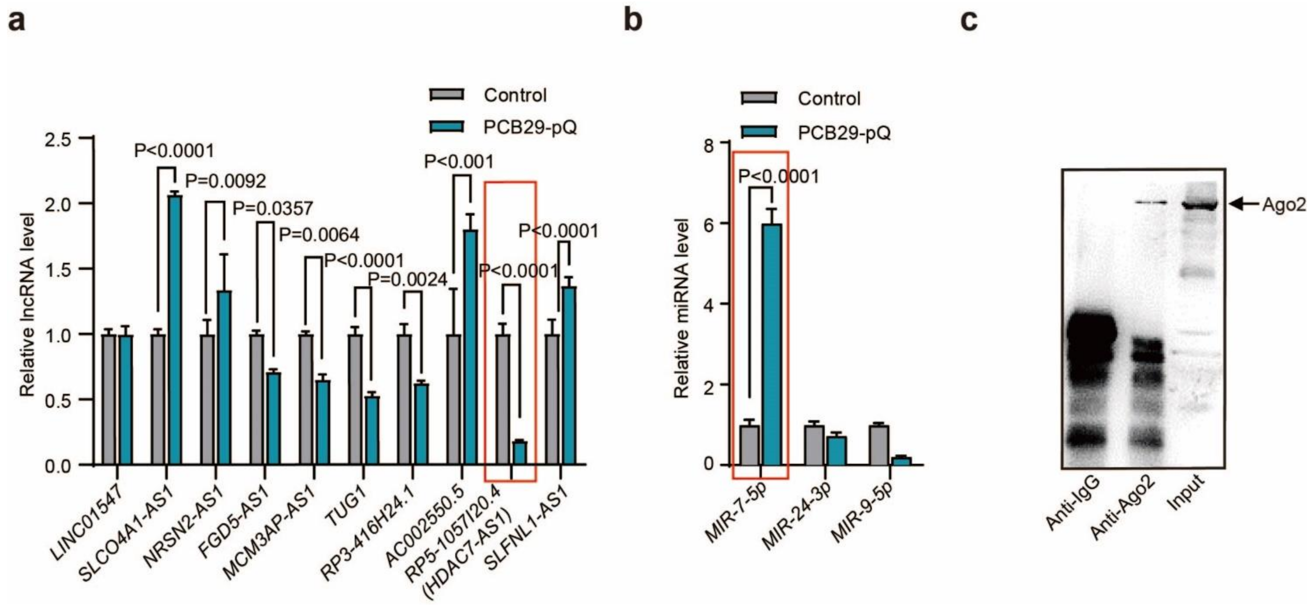


Figure S2. KEGG pathway analyses of genes targeted by differentially expressed miRNAs. High-throughput sequencing analysis of differentially expressed miRNAs in HUVECs with 5 μM PCB29-pQ treatment for 24 h (n = 3). KEGG pathway enrichment in miRNA, the rich factor represents the degree of enrichment. The node size shows the number of selected genes, and the color scale represents -log (P value). The exact data are presented in Excel Table S4.



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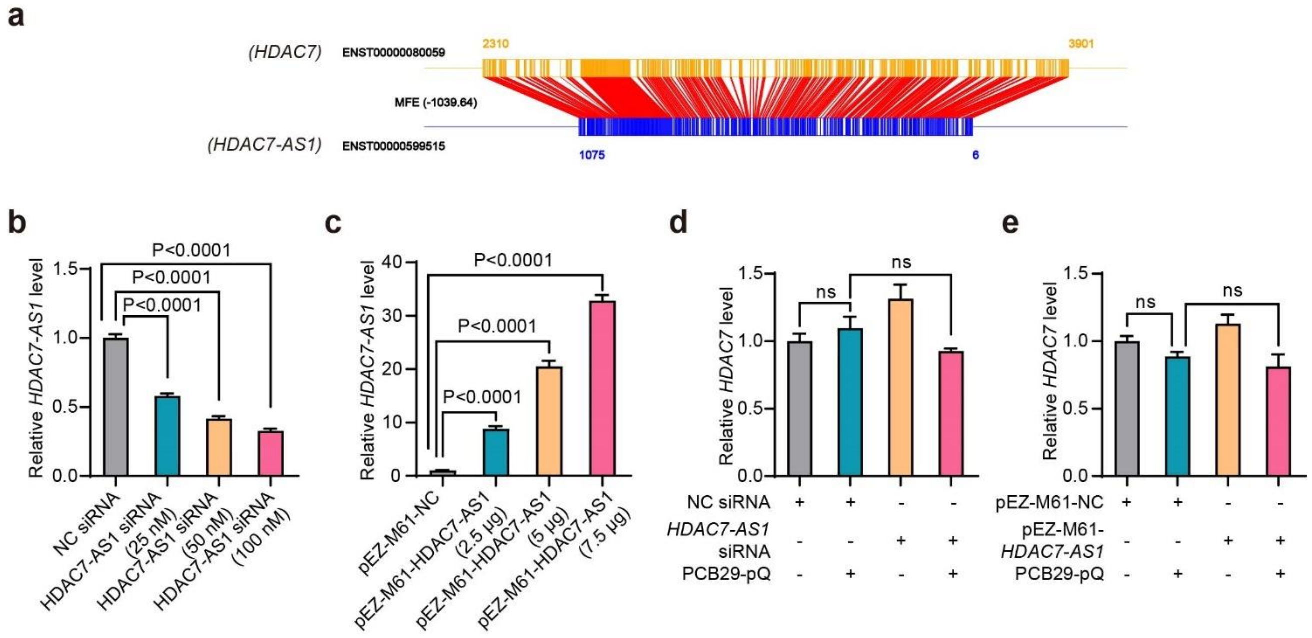

Figure S4. The expression of *HDAC7* level in HUVECs transfected with *HDAC7-AS1* siRNA or pEZ-M61-*HDAC7-AS1*. (**a**) Predicted relationship between ENST00000080059 (*HDAC7*) and ENST00000599515 (*HDAC7-AS1*) *via* RNAplex (http://www.tbi.univie.ac.at/RNA/RNAplex.1.html) (**b**) After transfection with NC siRNA or *HDAC7-AS1* siRNA (25, 50, or 100 nM) for 48 h, the silencing efficiency of *HDAC7-AS1* siRNA in HUVECs was determined by RT-qPCR. Data are presented as mean ± SD (n = 3). (**c**) After transfection with 2.5 μg pEZ-M61-NC or pEZ-M61-*HDAC7-AS1* (2.5, 5, or 7.5 μg) for 6 h, HUVECs were treated with 5 μM PCB29-pQ. *HDAC7-AS1* level was determined by RT-qPCR. Data are presented as mean ± SD (n = 3). *HDAC7* expression of PCB29-pQ-exposed cells or control after (**d**) transfection with 25 nM NC siRNA or 25 nM *HDAC7-AS1* siRNA for 24 h or (**e**) transfection with 2.5 μg pEZ-M61-NC or 2.5 μg pEZ-M61-*HDAC7-AS1* for 6 h. Data are presented as mean ± SD (n = 3). The housekeeping gene *β-actin* was used for quantification, and the primer information is shown Table S3. P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. For b and c, expression is shown relative to NC siRNA control and pEZ-M61-NC controls, respectively. The exact mean and SD values are presented in Table S21.

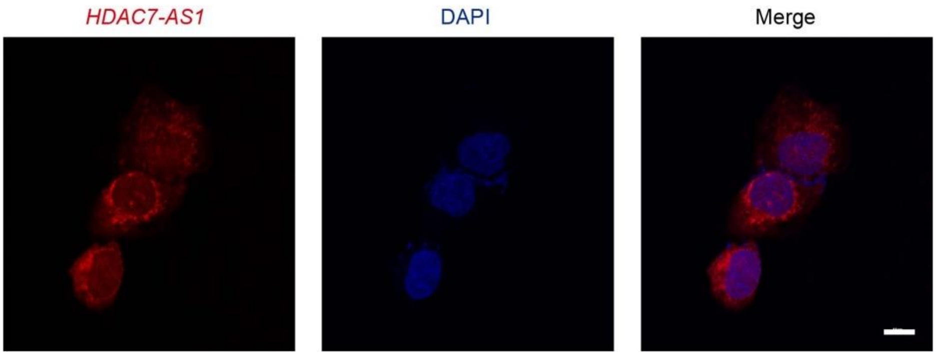

Figure S5. The localization of LncRNA *HDAC7-AS1* in HUVECs. HUVECs were treated with 5 μM PCB29-pQ for 24 h. (n = 3). Fluorescent *in situ* hybridization (FISH) assay was used to investigate the localization of *HDAC7-AS1* in in the cells. *HDAC7-AS1* was stained red using an RNA probe, and the nucleus was stained blue with DAPI. Scale bar = 10 μm.

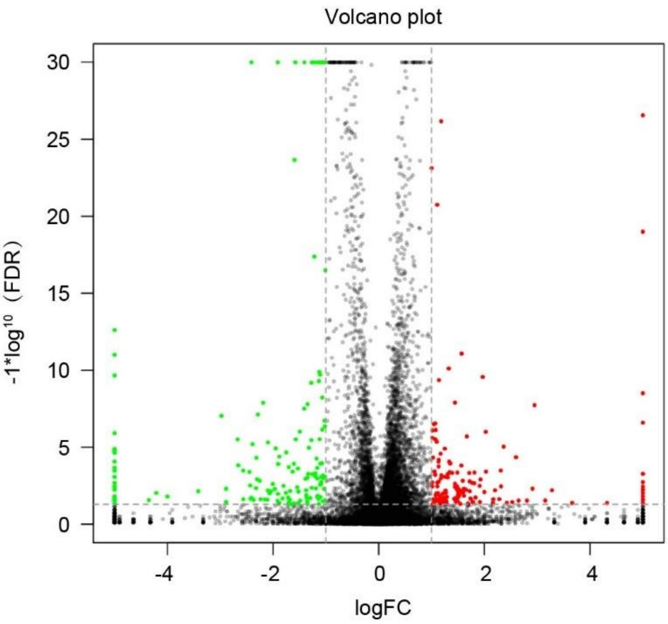

Figure S6. Volcano plots analyzing differential expression with mRNA sequencing (mRNA-Seq) in the control group and PCB29-pQ group. The abscissa represents the logarithmic values of two different groups, and the ordinate represents mRNAs differences (fold change⩾2 and P value < 0.05) between two groups. Red dots indicated PCB29-pQ group is higher relative to control group). Green dots indicated lower expression in PCB29-pQ group than control group (judgment standard is P value <0.05, and the difference multiple is more than 2). Black dots indicted no difference between two groups.

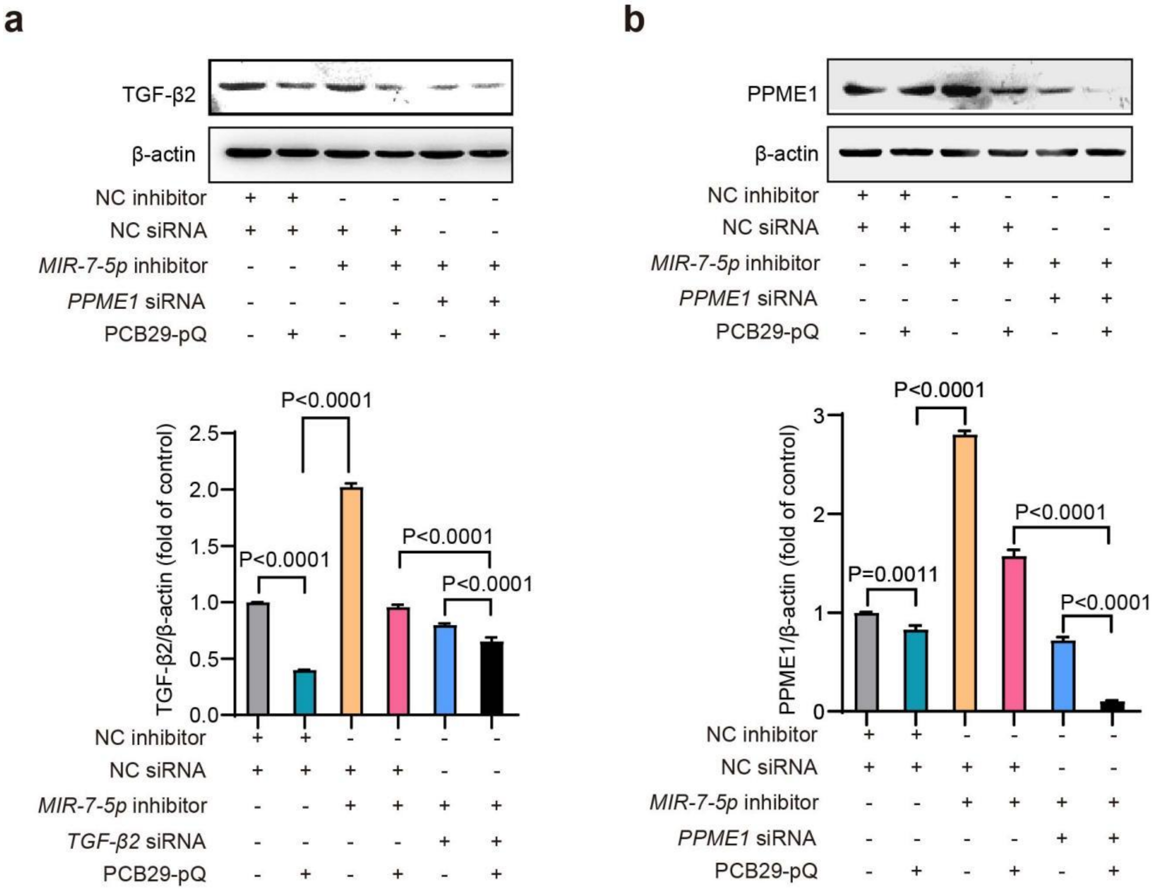

Figure S7. Target genes TGF-β2 and PPME1 protein levels in HUVECs exposed to PCB29-pQ with *MIR-7-5p* inhibitor or *TGF-β2/PPME1* siRNA. After co-transfection with 100 nM NC inhibitor or *MIR-7-5p* inhibitor and NC siRNA or *TGF-β2*/*PPME1* siRNA (25 nM) for 24 h, HUVECs were treated with 5 μM PCB29-pQ for 24 h. (n = 3). Protein levels of (**a**) PPME1 and (**b**) TGF-β2 were detected by western blotting (upper panel). The relative protein expression levels (lower panel) were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). β-Actin was used as an internal loading control. Data are graphed relative to the expression in cells exposed to the NC inhibitor and NC siRNA together. The exact mean and SD values are presented in Table S22.

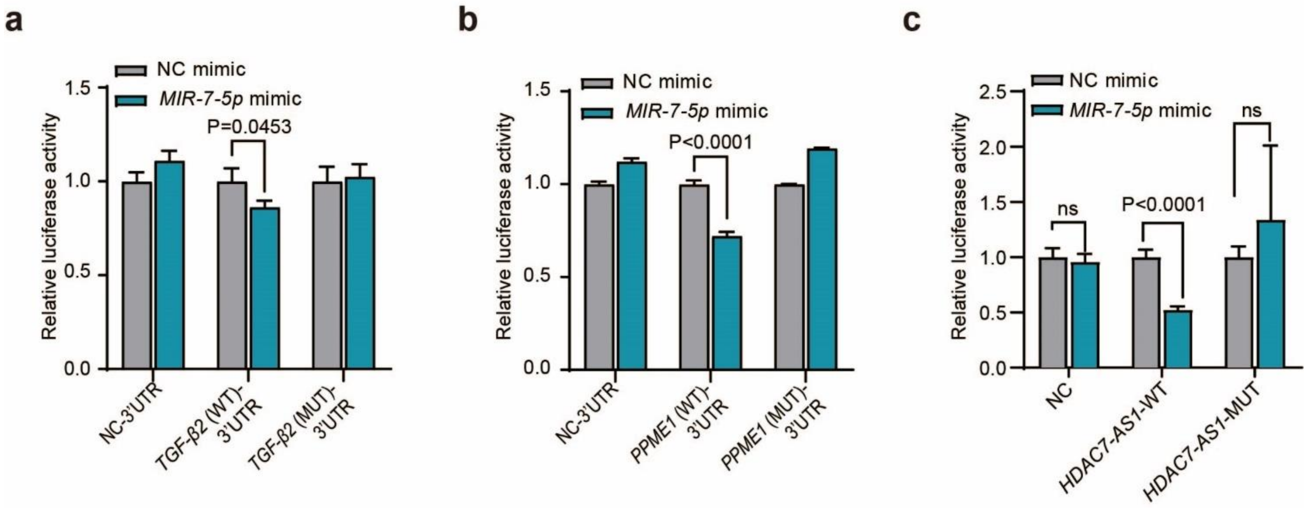

Figure S8. Luciferase analysis of the activity of *MIR-7-5p* bind to *TGF-β2*, *PPME1*, and *HDAC7-AS1* in HUVECs transfected with NC mimic or *MIR-7-5p* mimic. (**a**) HUVECs were transfected with NC mimic or *MIR-7-5p* mimic for 48 h, together with NC-3’UTR, *TGF-β2* (WT)-3’UTR, or *TGF-β2* (MUT)-3’UTR. (**b**) HUVECs were transfected with 50 nM NC mimic or 50 nM *MIR-7-5p* mimic for 48 h, together with NC-3’UTR, *PPME1* (WT)-3’UTR, or *PPME1* (MUT)-3’UTR. (**c**) HUVECs were transfected with 50 nM NC mimic or 50 nM *MIR-7-5p* mimic for 48 h, together with Luc-NC, Luc-*HDAC7-AS1*-WT, or Luc-*HDAC7-AS1*-MUT. For all panels, Gaussia luciferase activity was analyzed, corresponding to *TGF-β2*, *PPME1*, and *HDAC7-AS1* transcription. Data are presented as mean ± SD (n = 3). P values were determined by two-way ANOVA, followed by Tukey’s *post hoc* test. Data are graphed relative to the NC-mimic treated, NC-3’UTR controls. The exact mean and SD values are presented in Table S23.

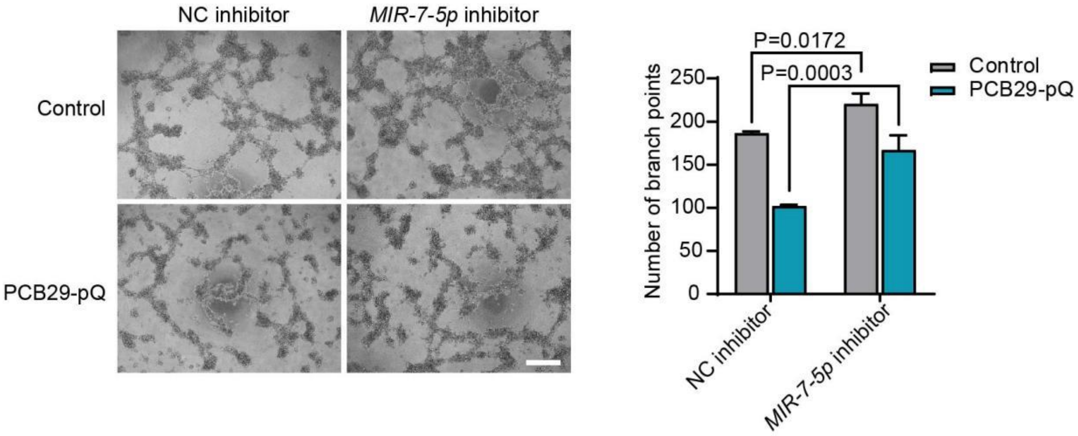

Figure S9. The tube forming ability in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor. (Left panel) After transfection with 100 nM NC inhibitor or 100 nM *MIR-7-5p* inhibitor for 48 h, followed by exposure to 5 μM PCB29-pQ for 24 h, cells were plated on Matrigel to conduct tube formation assay. Scale bar = 200 μm. (Right panel) Quantification of tube formation through measurement of branch point number with ImageJ software. Data were presented as mean ± SD (n = 3). P values were determined by two-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S24.

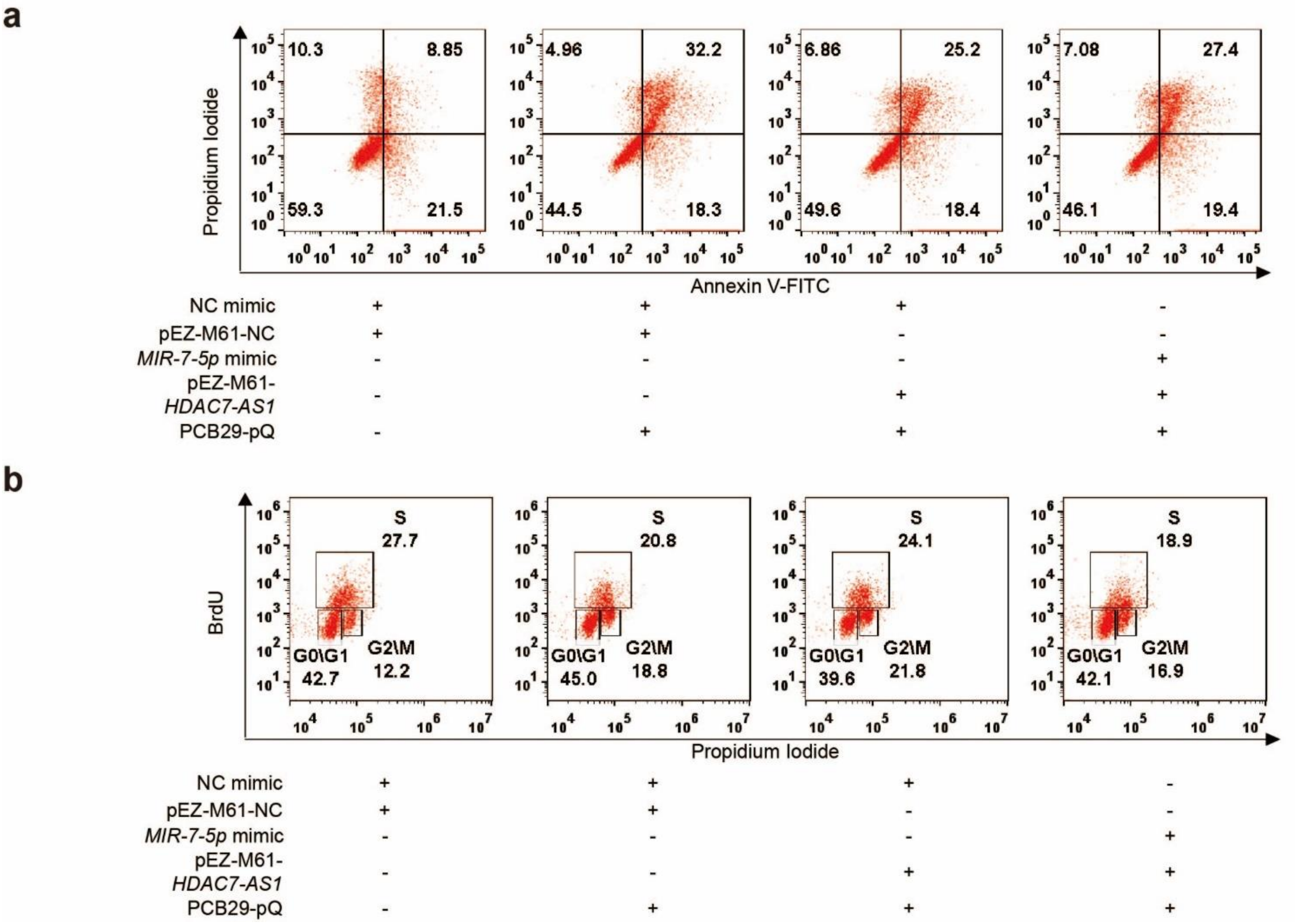

Figure S10. Apoptosis and proliferation rates in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* mimic or pEZ-M61-*HDAC7-AS1*. (**a**) Cell apoptosis was assessed by Annexin V-FITC/PI double staining with a flow cytometer. (n = 3). (**b**) Cell proliferation was measured by BrdU/PI double staining with a flow cytometer. (n = 3).

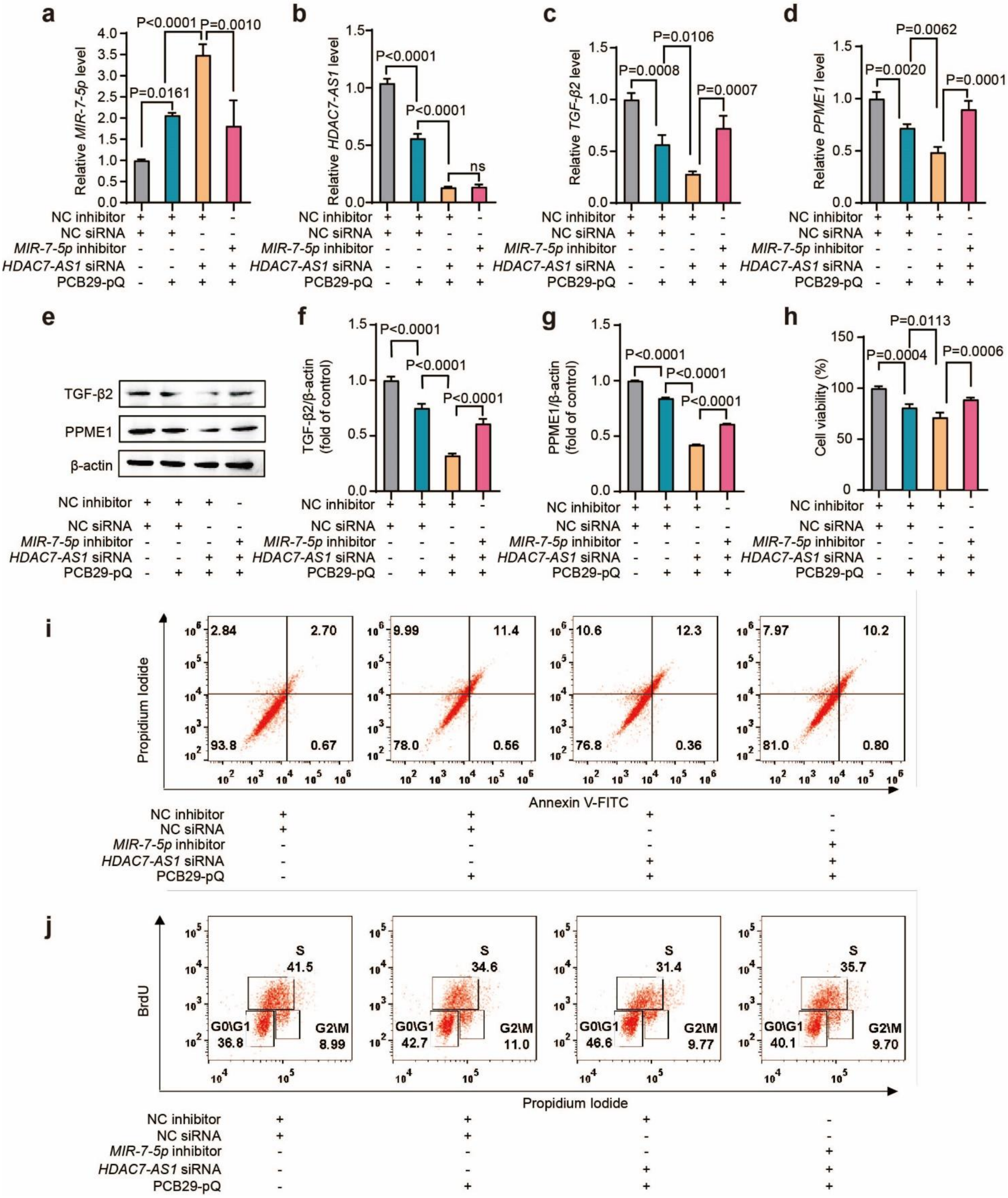

Figure S11. ***HDAC7-AS1*, *MIR-7-5p*, *TGF-β2*, *PPME1* mRNA levels, TGF-β2 and PPME1 protein levels, and apoptosis or proliferation rates in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor or *HDAC7-AS1* siRNA.** After co-transfection with 100 nM NC inhibitor or 100 nM *MIR-7-5p* inhibitor and NC siRNA or *HDAC7-AS1* siRNA (25 nM) for 24 h, HUVECs were treated with 5 μM PCB29-pQ for 24 h. RNAs expression of (**a**) *MIR-7-5p*, (**b**) *HDAC7-AS1*, (**c**) *TGF-β2* and (**d**) *PPME1* were detected by RT-qPCR. *β-actin* was used as a housekeeping gene, except U6 was used for *MIR-7-5p* quantification. The primer information is shown in Table S3-4. (**e**) Protein levels of TGF-β2 and PPME1 were detected by western blotting. β-Actin was used as an internal loading control. (**f**) TGF-β2, (**g**) PPME1 protein expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). (**h**) Cell viability was measured by CCK-8 kit. Data were presented as mean ± SD (n = 3). (**i**) Cell apoptosis was performed by Annexin V-FITC/PI assay with a flow cytometer. (**j**) Cell proliferation was performed by BrdU/PI staining. P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. Data are graphed relative to the cells exposed to NC inhibitor, NC siRNA, and vehicle control. The exact mean and SD values are presented in Table S25.

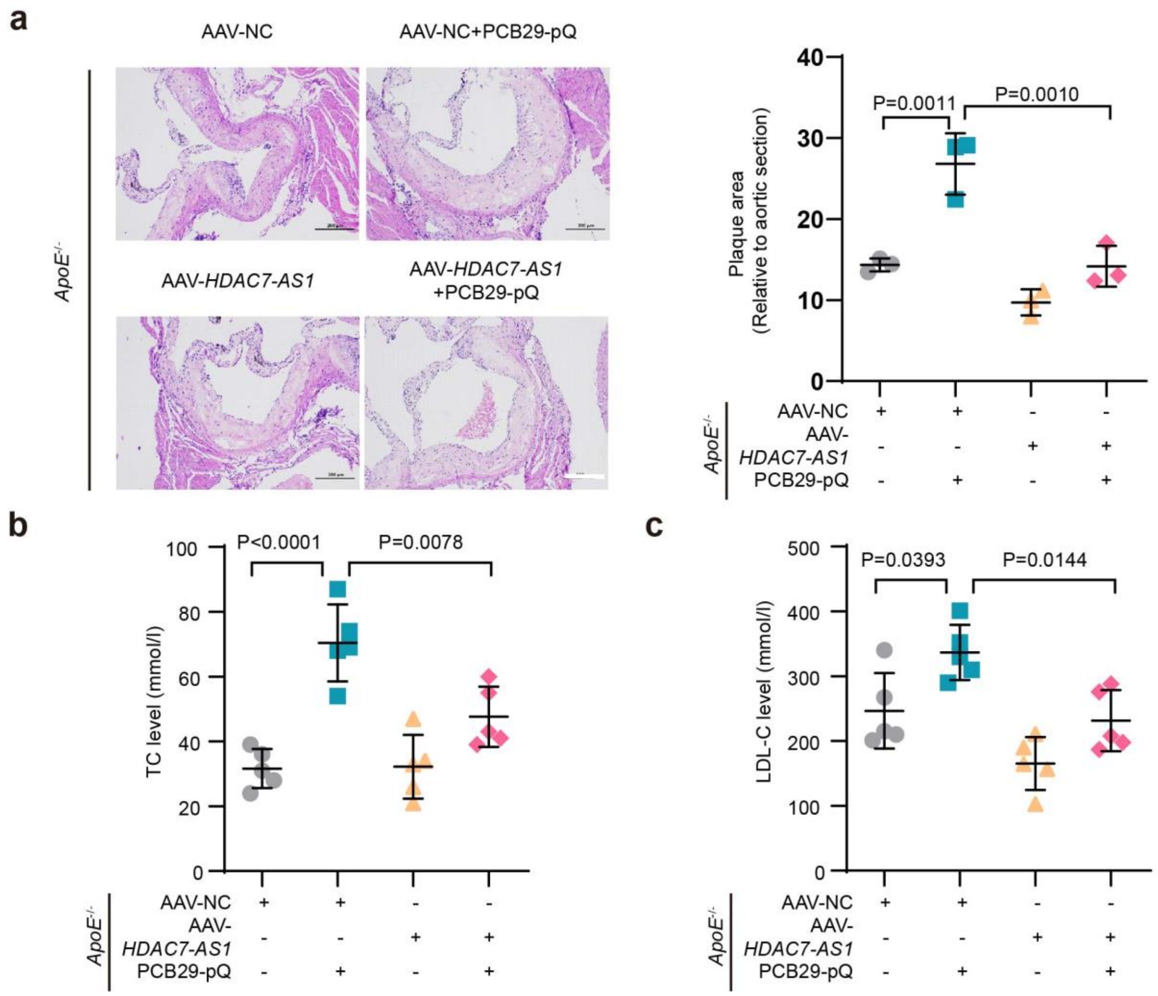

Figure S12. HE staining of aortic root cross-sections and TC and TG levels in *ApoE*$^{-/-}$ mice were intravenous (*i.v.*) injected with AAV-*HDAC7-AS1*. Male *ApoE*$^{-/-}$ mice were *i.v.* injected with AAV-*HDAC7-AS1 via* tail vein (4×10^{10} particles/mouse) to create an *HDAC7-AS1* overexpressed mice model. Male *ApoE*$^{-/-}$ mice that received the AAV vector were used as AAV control mice. Control and *HDAC7-AS1* overexpressed *ApoE*$^{-/-}$ mice were fed a western high-fat diet for 12 weeks and tap water *ad libitum*. Mice were injected with 5 mg/kg body weight of PCB29-pQ or equal volumes of corn oil by *i.p.* injection once a week for 12 continuous weeks with the first two injections during the 1st week (3 days apart). (**a**) (Left panel) HE of the aortic root (Right panel) plaque area in the aortic root was quantified by ImageJ software. Data are presented as mean ± Standard Deviation (SD). Scale bar = 200 μm. (**b**) TC level and (**c**) LDL-C level. Data are presented as mean ±SD (n = 5). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S26.

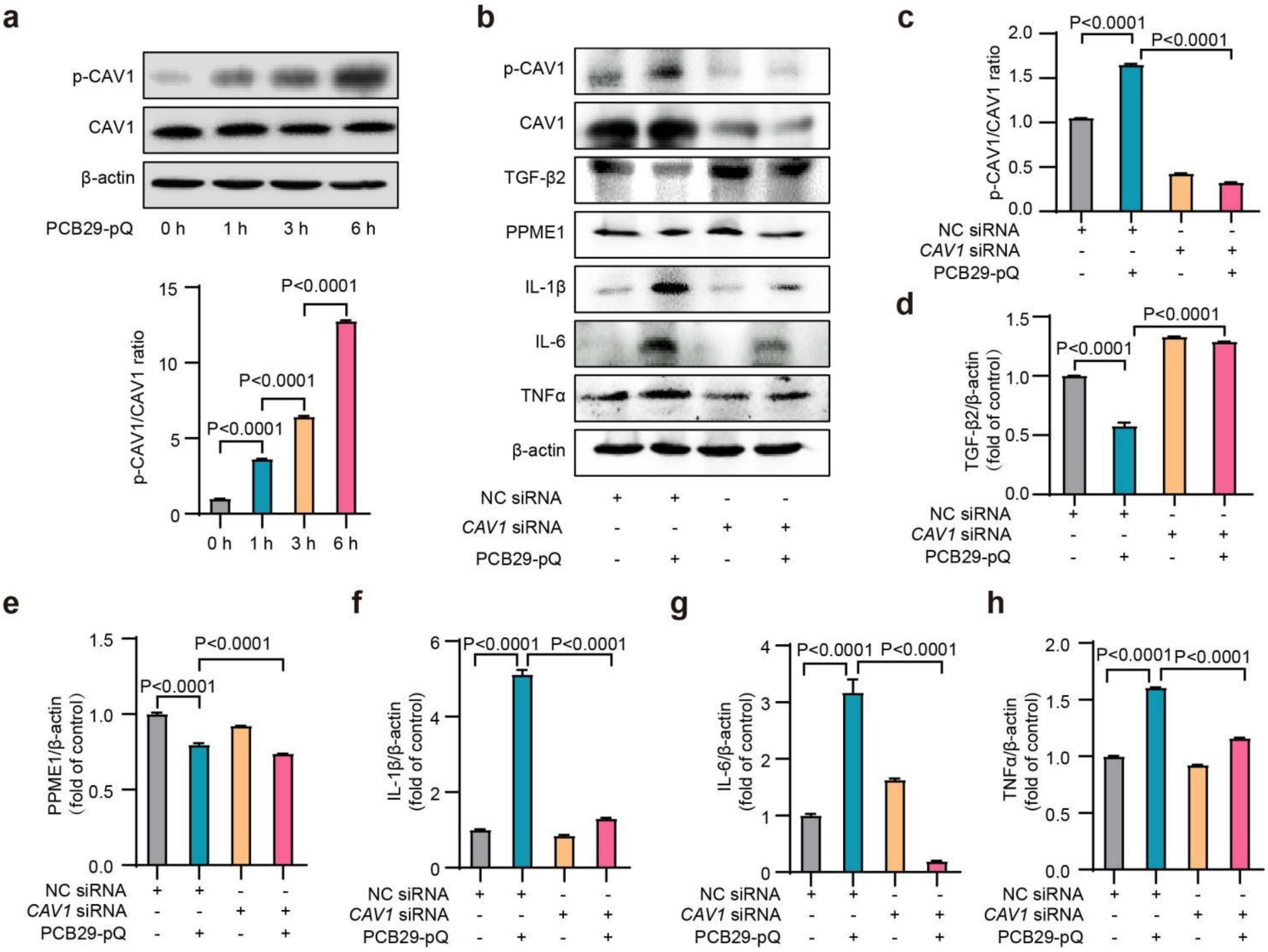

Figure S13. CAV1 phosphorylation and TGF-β, PPME1, and inflammatory factor levels in HUVECs exposed PCB29-pQ with *CAV1* siRNA. (**a**) HUVECs were treated with 5 μM PCB29-pQ for 1, 3, and 6 h. (upper panel) Protein levels of p-CAV1 and CAV1 were detected by western blotting. β-Actin was used as an internal loading control. The relative protein expression levels (lower panel) were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). After transfection with 25 nM NC siRNA or *CAV1* siRNA for 48 h, HUVECs were treated with 5 μM PCB29-pQ for 24 h. The siRNA information is shown in Table S6. (**b**) Protein levels of p-CAV1, CAV1, IL-1β, IL-6, and TNFα were detected by western blotting. β-Actin was used as an internal loading control. (**c-h**) p-CAV1, CAV1, IL-1β, IL-6, and TNFα were quantified by ImageJ software. Data are presented as mean

± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey’s *post hoc* test. Data are graphed relative to the NC siRNA group. The exact mean and SD values are presented in Table S27.

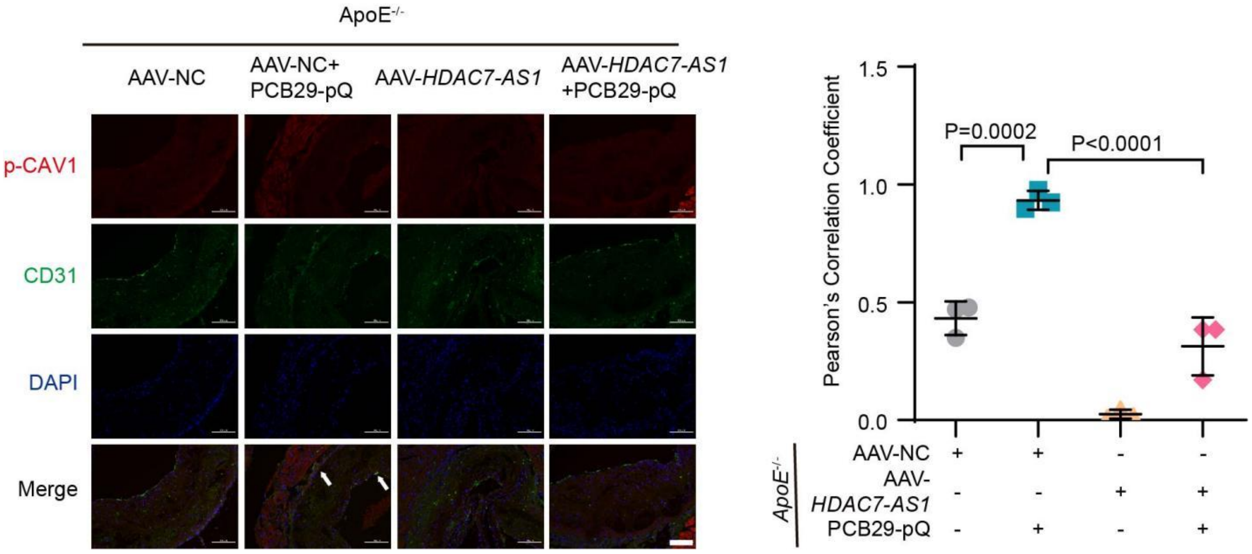

Figure S14. p-CAV1 level in *ApoE*$^{-/-}$ mice that were *i.v.* injected with AAV-*HDAC7-AS1*. Male *ApoE*$^{-/-}$ mice were *i.v.* injected with AAV-*HDAC7-AS1 via* tail vein (4×10^{10} particles/mouse) to create an *HDAC7-AS1* overexpressed mice model. Male *ApoE*$^{-/-}$ mice that received the AAV vector were considered as AAV control mice. Control and *HDAC7-AS1* overexpressed *ApoE*$^{-/-}$ mice were fed a Western high-fat diet for 12 weeks and tap water *ad libitum*. Mice were injected with 5 mg/kg body weight of PCB29-pQ or equal volumes of corn oil by *i.p.* injection once a week for 12 continuous weeks with the first two injections during the 1st week (3 days apart). (Left panel) The presence of p-CAV1 in aortic root cross-sections was detected by double immunostaining with the use of antibodies against p-CAV1 (red), endothelial cell marker CD31 (green), and nucleus marker DAPI (blue), respectively. Scale bar = 100 µm. White arrows represent the colocalization of p-CAV1 (red) and CD31 (green). (Right panel) Co-localization of p-CAV1 and CD31 was analyzed by Pearson's correlation coefficient. Data were presented as mean ± SD (n = 3). The exact mean and SD values are presented in Table S28.

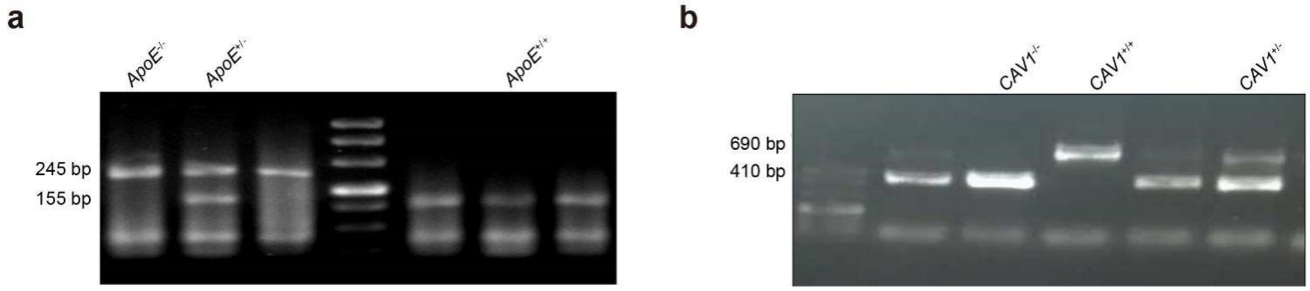

Figure S15. Gene type identification of *ApoE* and *CAV1* knockout mice. DNA from the tail of offspring mice was extracted and analyzed by PCR and agarose gel electrophoresis. (**a**) Homozygous of *ApoE*: 245 bp; Heterozygous of *ApoE*: 245 bp & 155 bp; WT of *ApoE*: 155 bp. (**b**) Homozygous of *CAV1*: 410 bp; Heterozygous of *CAV1*: 690 bp & 410 bp; WT of *CAV1*: 690 bp. The PCR primer sequences for *ApoE* and *CAV1* mice genotyping are shown in Table S2.

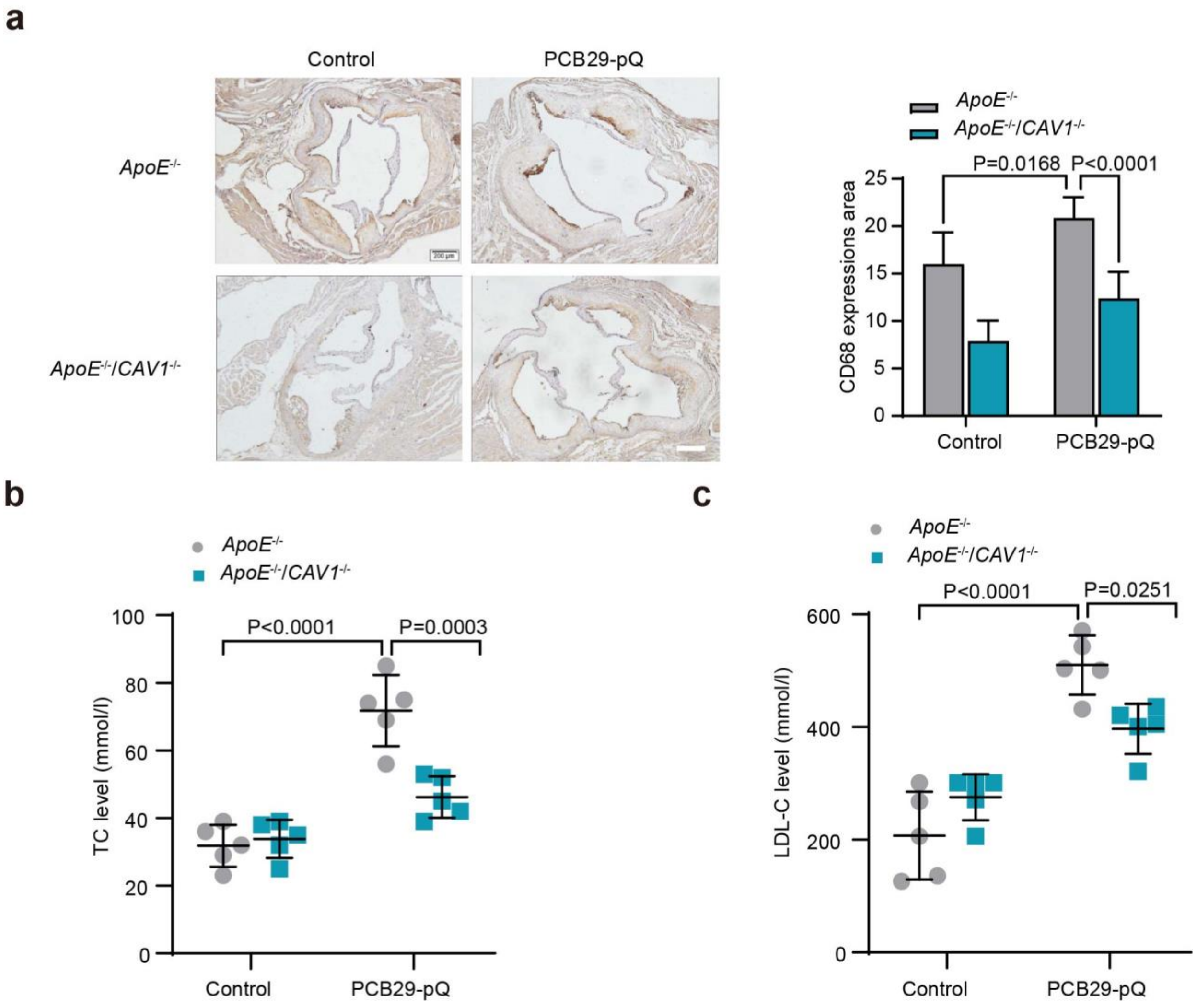

Figure S16. Immunohistochemistry staining of CD68 and TC and LDL-C levels in *ApoE*$^{-/-}$ and *ApoE*$^{-/-}$/*CAV1*$^{-/-}$ mice. *ApoE*$^{-/-}$ mice were crossed with *CAV1*$^{-/-}$ mice to generate *ApoE*$^{-/-}$/*CAV1*$^{-/-}$ mice. *ApoE*$^{-/-}$ or *ApoE*$^{-/-}$/*CAV1*$^{-/-}$ mice were fed a Western high-fat diet for 12 weeks and tap water *ad libitum*. Mice were treated with 5 mg/kg body weight of PCB29-pQ or equal volumes of corn oil by *i.p.* injection. (**a**) (Left panel) Immunohistochemistry staining of CD68 detected macrophage infiltration located at the aortic wall. Scale bar = 200 μm. (Right panel) Quantification proportion of positive CD68 expressions area to total aortic section using was performed by ImageJ software. Data are presented as mean ± SD (n = 3). Serum (**b**) TC level and (**c**) LDL-C levels. Data are presented as mean ±SD (n = 5). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S29.

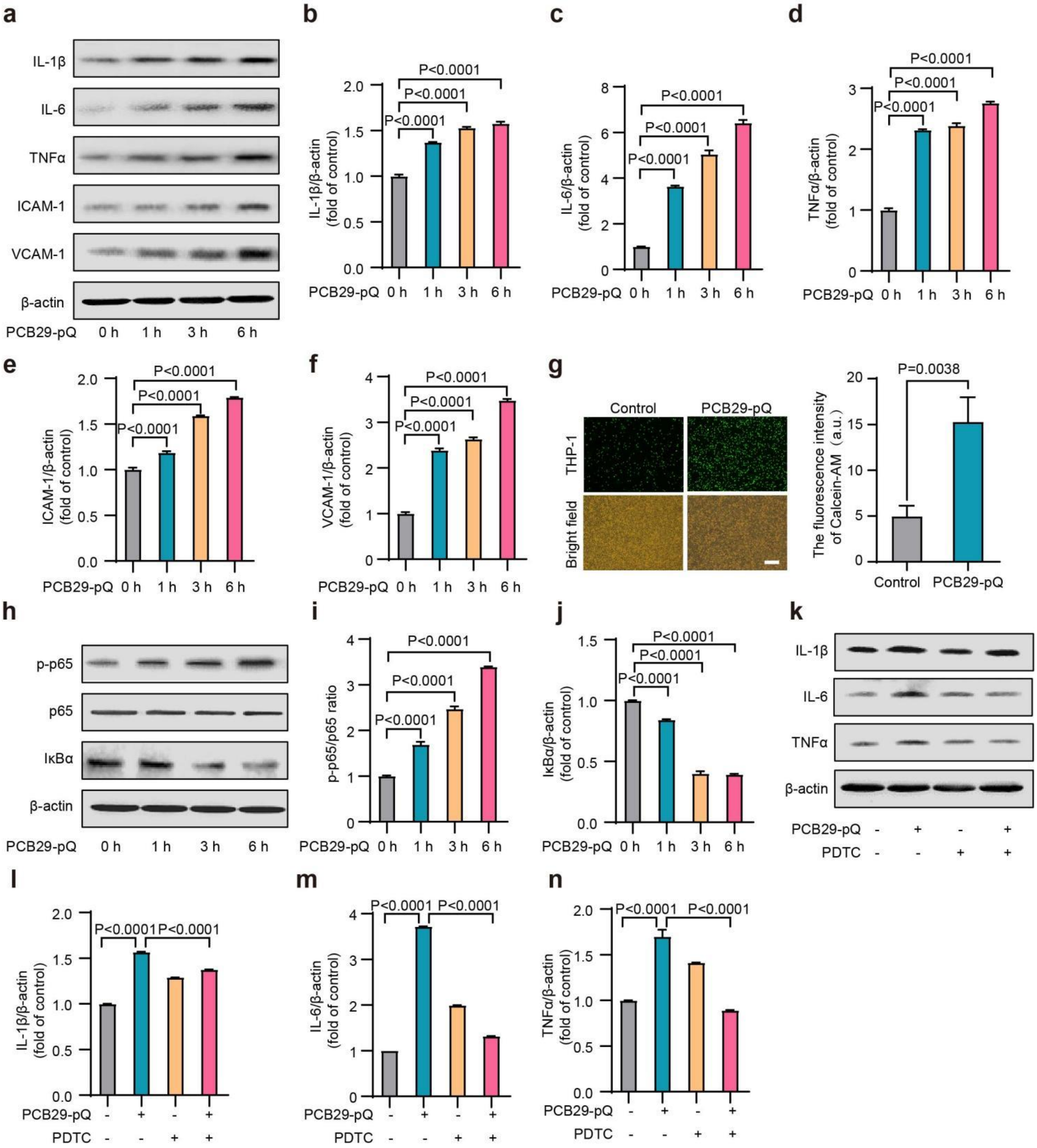

Figure S17. Adhesion molecules, pro-inflammatory cytokines and p65 protein expression levels in HUVEC exposed to PCB29-pQ. HUVECs were treated with 5 μM PCB29-pQ for 1, 3, or 6 h. (**a**) IL-1β, IL-6, TNF-α, ICAM-1, and VCAM-1 expressions in cell lysates were analyzed by western blotting. (**b-f**) IL-1β, IL-6, TNF-α, ICAM-1, and VCAM-1 expressions were quantified by ImageJ software. Data are presented as mean ± Standard Deviation (SD) (n = 3). (**g**) Calcein-AM-loaded THP-1 cells (10^6 cells/ml) were added to HUVECs and then incubated for 3 h. The unbound cells were washed off, and attached fluorescent monocytes were visualized using an optical microscope. (Left panel) The fluorescence intensity of Calcein-AM was quantified using ImageJ software. Data are presented as mean ± SD (n = 3). P value was determined by unpaired Student's *t*-test. (**h**) HUVECs were treated with 5 μM PCB29-pQ for 1, 3, or 6 h. IκBα and p-p65 levels were analyzed by western blotting analysis. β-Actin was used as an internal loading control. (**i-j**) IκBα and p-p65 levels were quantified by ImageJ software. Data are presented as mean ± SD (n = 3). (**k**) HUVECs were pretreated with 5 μM p65 inhibitor PDTC for 1 h, followed with 5 μM PCB29-pQ exposure for 6 h. IL-1β, IL-6, and TNF-α in cell lysates were analyzed by western blotting. β-Actin was used as an internal loading control. (**l-n**) IL-1β, IL-6, and TNF-α protein expression levels were quantified by ImageJ software. Data were presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S30.

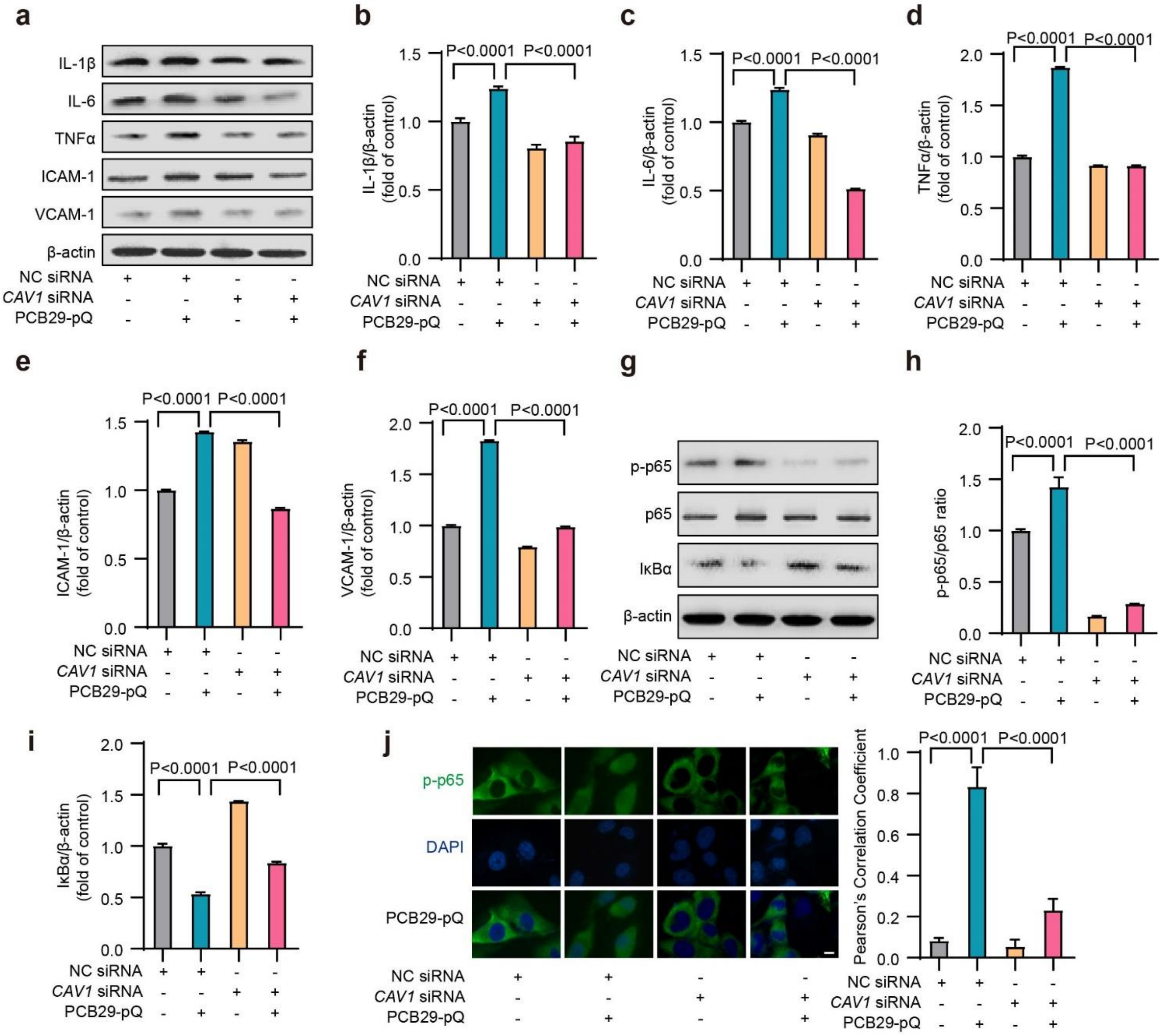

Figure S18. Adhesion molecules, pro-inflammatory cytokines and p65 protein expression levels in HUVEC exposed to PCB29-pQ with *CAV1* siRNA. HUVECs were transfected with NC siRNA or 25 nM *CAV1* siRNA for 48 h and then treated with 5 μM PCB29-pQ for 6 h. (**a**) IL-1β, IL-6, TNF-α, ICAM-1 and VCAM-1 expressions were analyzed by western blotting. β-Actin was used as an internal loading control. (**b-f**) IL-1β, IL-6, TNF-α, ICAM-1 and VCAM-1 expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). (**g**) IκBα, p-p65, and p65 expressions were analyzed by western blotting. β-Actin was used as an internal loading control. (**h-i**) IκBα, p-p65, and p65 expression levels were quantified by ImageJ software. Data were presented as mean ± SD (n = 3). (**j**) (Left panel) Immunofluorescence analysis of p65. Green staining represents the location of p65. Nuclei shown in blue were stained with DAPI. Scale bar = 10 μm. (Right panel) Co-localization of p-CAV1 and DAPI was analyzed by Pearson's correlation coefficient. Data were presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. The exact mean and SD values are presented in Table S31.

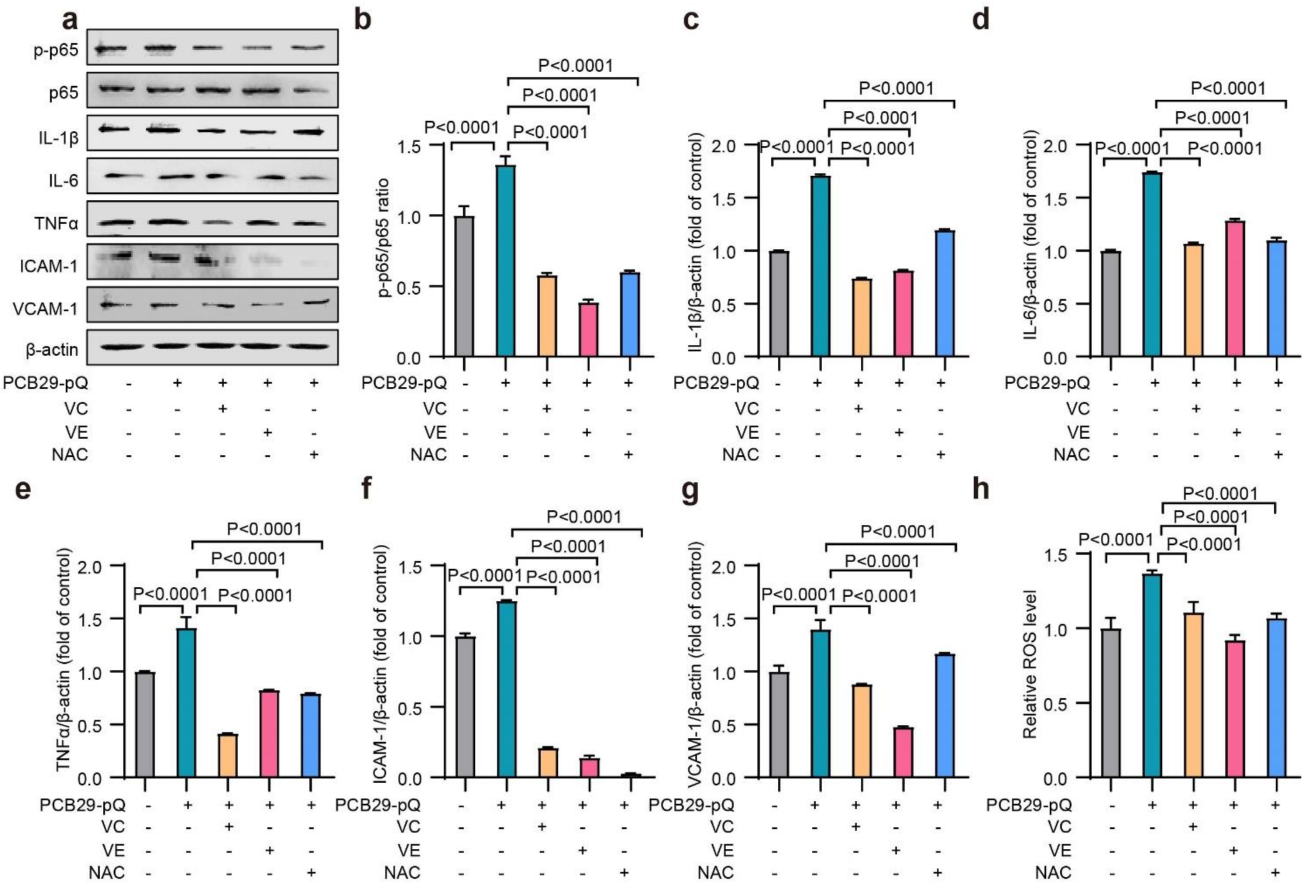

Figure S19. Inflammatory factors and ROS levels in HUVEC exposed to PCB29-pQ. HUVECs were pretreated with 40 μM VC, 20 μM VE or 5 mM NAC for 1 h, followed with 5 μM PCB29-pQ exposure for 6 h. (n = 3). (**a**) p-p65, p65, IL-1β, IL-6, TNFα, ICAM-1 and VCAM-1 in cell lysates were analyzed by western blotting. (**b-g**) p-p65, p65, IL-1β, IL-6, TNFα, ICAM-1 and VCAM-1 expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). (**h**) ROS levels were detected by DCFH-DA (10 μM) probe. Data were presented as mean ± SD (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. In all graphs, data is normalized to the control cell groups. The exact mean and SD values are presented in Table S32.

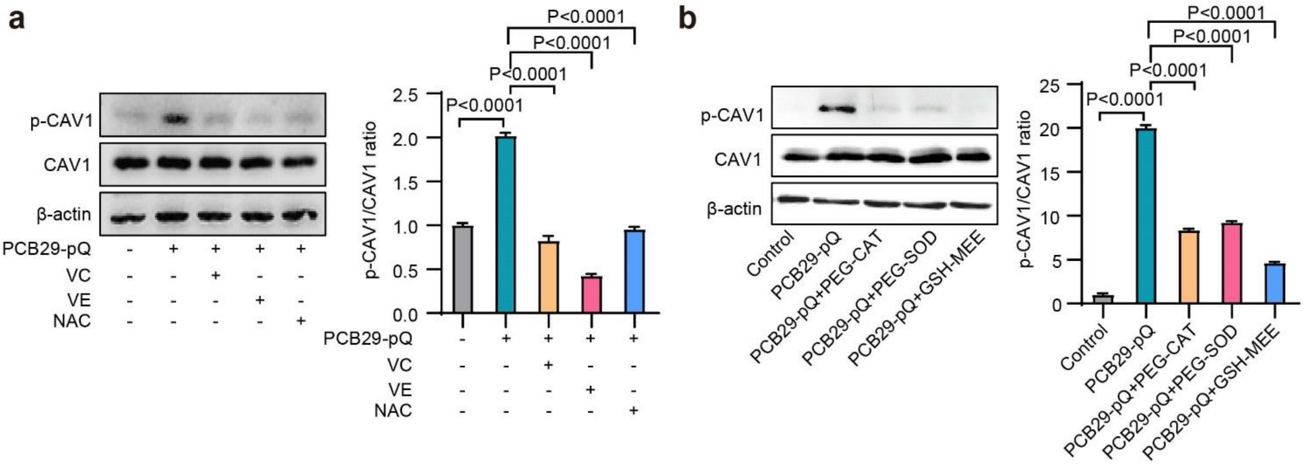

Figure S20. p-CAV1 and CAV1 levels in HUVEC exposed to PCB29-pQ and antioxidants. HUVECs were pretreated with 40 μM VC, 20 μM VE or 5 mM NAC for 1 h, followed by 5 μM PCB29-pQ exposure for 6 h. HUVECs were pretreated with (**a**) 40 μM VC, 20 μM VE or 5 mM NAC, (**b**) 200 U/ml PEG-SOD, 500 U/ml PEG-CAT and 5 mM GSH-MEE for 1 h, followed with 5 μM PCB29-pQ exposure for 6 h. (Left panel) p-CAV1 and CAV1 in cell lysates were analyzed by western blotting. β-Actin was used as an internal loading control. (Right panel) p-CAV1 and CAV1 expression levels were quantified by ImageJ software. Data were presented as mean ± Standard Deviation (SD) (n = 3). P values were determined by one-way ANOVA, followed by Tukey's *post hoc* test. All data is graphed relative to the control cell groups. The exact mean and SD values are presented in Table S33.

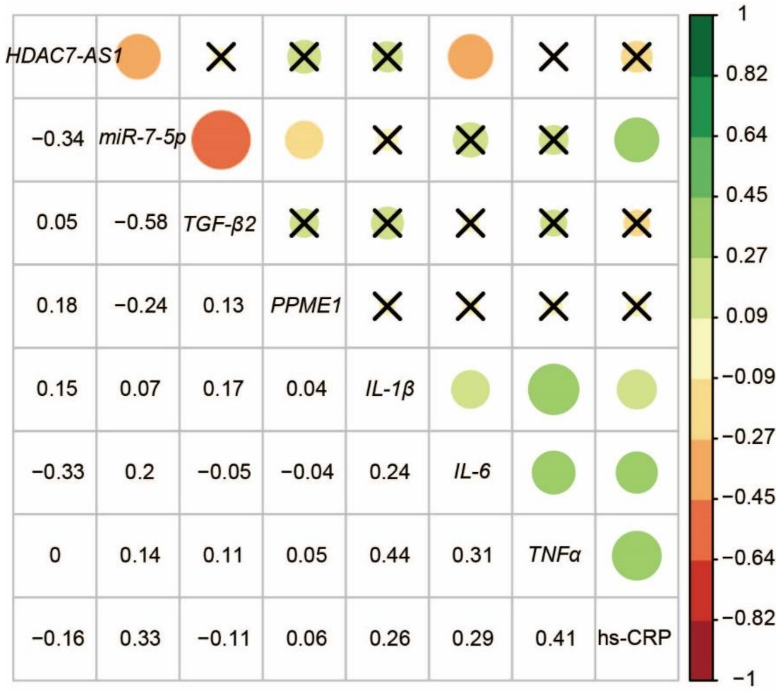

Figure S21. Heatmap showing correlation scores between factors. Plasma RNA was extracted by TRNzol universal reagent. CHD group (n = 77) contains patients with > 50% coronary artery stenosis, and the control group (n = 50) contains subjects with < 50% coronary artery stenosis. RT-qPCR analysis of *HDAC7-AS1*, *MIR-7-5p*, *TGF-β2*, *PPME1*, *IL-1β*, *IL6* and *TNFα* expressions. Spearman's rank correlation coefficient was used to assess the correlation between the two indicated factors. P value of < 0.05 was considered significant. The size and color of circle represents the correlation between two factors. X's mean no significance. Summary data can be found in Table S11.

Table S1. Sources of antibodies using in this study.

Producers	Antibodies (Item No.)	Dilution
Proteintech Group, Inc. (Wuhan, China)	Goat anti-rabbit IgG (H+L), oralite 488 conjugate (# SA00013-2)	1:500 (IF)
	Mouse TNF-α monoclonal antibody (# 60291-1-lg)	1:1000 (WB)
	Rabbit ICAM-1 monoclonal antibody (# 60299-1-lg)	1:1000 (WB) 1:500 (IF)
	Rabbit VCAM-1 monoclonal antibody (# 66294-1-lg)	1:1000 (WB) 1:500 (IF)
	Rabbit CAV1 polyclonal primary antibody (#66067-1-lg)	1:1000 (WB)
	Rabbit Ago2 polyclonal antibody (# 10686-1-AP)	1:500 (RIP)
Sangon Biotech Co. Ltd. (Wuhan, China)	HRP-conjugated Goat Anti-Rabbit IgG secondary antibody (# D11058)	1:2000 (WB)
	HRP-conjugated Rabbit Anti-mouse IgG secondary antibody (# D110098)	1:2000 (WB)
	Rabbit β-actin polyclonal antibody (# D110001)	1:5000 (WB)
	Rabbit TGF-β2 antibody (# D262351)	1:1000 (WB) 1:500 (IF)
Wanlei Co. Ltd. (Shenyang, China)	Rabbit IL-6 polyclonal antibody (# WL02841)	1:1000 (WB)

	Rabbit IL-1β polyclonal antibody (# WL00891)	1:1000 (WB)
	Rabbit IκBα antibody (# WL00148)	1:1000 (WB)
Bioss Biotech Co. Ltd. (Beijing, China)	Rabbit p65 antibody (# bs-20159R)	1:1000 (WB)
	Rabbit p-p65 (pSer536) antibody (# bs-0982R)	1:1000 (WB) 1:500 (IF)
Servicebio (Wuhan, China)	Rabbit vWF polyclonal antibody (# GB11020)	1:500 (IF)
	CD31 polyclonal antibody (# GB11063-2)	1:500 (IF)
Cell Signaling Technology (Boston, USA)	Rabbit p-CAV1 (Tyr14) antibody (# 3251)	1:1000 (WB) 1:500 (IF)
CUSABIO (Wuhan, China)	Rabbit PPME1 antibody (# CSB-PA018501LA01HU)	1:1000 (WB) 1:500 (IF)
Abcam (Cambridge, MA, USA)	Rabbit CD68 antibody (#ab283654)	1:500 (IHC)

Table S2. PCR primer sequences for *ApoE* and *CAV1* mice genotype.

	Primer Type	**5’ - 3’**
ApoE	Common	GCCTAGCCGAGGGAGAGCCG
	Wild type Forward	TGTGACTTGGGAGCTCTGCAGC
	Mutant Forward	GCCGCCCCGACTGCATCT
CAV1	Common	CTTGAGTTCTGTTAGCCCAG
	Wild type Forward	GTGTATGACGCGCACACCAAG
	Mutant Forward	CTAGTGAGACGTGCTACTTCC

Sequences are mouse unless otherwise specified.

Table S3. PCR program for *ApoE* and *CAV1* mice genotype.

Step	**1**	**2**			**3**
	CYCLE (1 cycle)	CYCLE (35 cycles)			CYCLE (1 cycle)
Temp.	94 ℃	94 ℃	55-65 ℃	72 ℃	72 ℃
Time	2 min	30 sec	30 sec	30 sec	2 min

Table S4. RT-qPCR primer sequences for lncRNAs and mRNAs.

Gene	**Sequence (5’ to 3’)**
LINC01547-F	AGGCCAAGAGACAACAGCGATTAC
LINC01547-R	GCCAAGTGTGGACTCAGAGCTTC
SLCO4A1-AS1- F	CTGTCAGCCGCCTTCTTGCC
SLCO4A1-AS1- R	GCGAGGAGCATGTAGAACCTGTC
NRSN2-AS1-F	AATGAGCGGAGATTGTGCCACTG
NRSN2-AS1-R	CGACAGTACCTACAACAGCCACAC
FGD5-AS1-F	GTTGGACCAAGAGGCAGCTC
FGD5-AS1-R	AGACCACCGAACAGTGACCA
MCM3AP-AS1-F	AGAAGCTCCTCGCATCAGATCCTC
MCM3AP-AS1-R	CACATGCACCGTAACTGGAAGAGG
TUG1-F	TAGCAGTTCCCCAATCCTTG
TUG1-R	CACAAATTCCCATCATTCCC
_RP3-416H24.1_-F	GGCTTCATTGGCACCACCTACTC
_RP3-416H24.1_-R	GCAGAGCCAGAACTGGAACATAGG
_AC002550.5_-F	CTGTCAGCCGCCTTCTTGCC
_AC002550.5_-R	GCGAGGAGCATGTAGAACCTGTC
HDAC7-AS1-F	GCCTTCTAGCCACAAGCACACTC
HDAC7-AS1-R	GCGAAGCGGAAGCCTCTGTTC
SLFNL1-AS-F	AACTGAAGCACAGAGGCATAGCAC
SLFNL1-AS-R	CCAGGAGGCAGAGGACAGACC
HDAC7-F	TGCACCACCACCTCTTCCTAGC
HDAC7-R	ACTTCGCTTGCTCTTGTCCTTGTG
TGF-β2-F	GTGCCTGAACAACGGATTGA
TGF-β2-R	AAGGAGAGCCATTCGCCTTC
(mouse) TGF-β2-F	TCGACATGGATCAGTTTATGCG
(mouse) TGF-β2-R	CCCTGGTACTGTTGTAGATGGA
PPME1-F	CAGTCCTGCTCCTTCTGCAT
PPME1-R	TTTCACCATGACTTCGCAGA
(mouse) PPME1-F	AGTCAGAGCGGAGCCAAGAT
(mouse) PPME1-R	TCGAAAAGTATCCTTGCCAGTTT
_IL-1β_-F	TTCGACACATGGGATAACGAGG
_IL-1β_-R	TTTTTGCTGTGAGTCCCGGAG
(mouse) IL-1β-F	GCAACTGTTCCTGAACTCAACT
(mouse) IL-1β-R	ATCTTTTGGGGTCCGTCAACT
_IL-6_-F	ACTCACCTCTTCAGAACGAATTG
_IL-6_-R	CCATCTTTGGAAGGTTCAGGTTG
(mouse) _IL-6_-F	TAGTCCTTCCTACCCCAATTTCC

(mouse) *IL-6*-R	TTGGTCCTTAGCCACTCCTTC
***TNF-α*-F**	GAGGCCAAGCCCTGGTATG
***TNF-α*-R**	CGGGCCGATTGATCTCAGC
(mouse) *TNF-α*-F	CAGGCGGTGCCTAGTTCTC
(mouse) *TNF-α*-R	CGATCACCCCGAAGTTCAGTAG
***β-actin*-F**	CATGTACGTTGCTATCCAGGC
***β-actin*-R**	CTCCTTAATGTCACGCACGAT
(mouse) *β-actin*-F	GGCTGTATTCCCCTCCATCG
(mouse) *β-actin*-R	CCAGTTGGTAACAATGCCATGT
***18s*-F**	GTAACCCGTTGAACCCCATT
***18s*-R**	CCATCCAATCGGTAGTAGCG

Sequences are human unless otherwise specified.

Table S5. RT-qPCR primer sequences for miRNAs.

miRNA	**Forward (5’ to 3’)**
MIR-7-5p	UGGAAGACUAGUGAUUUUGUUGU
MIR-24-3p	UGGCUCAGUUCAGCAGGAACAG
MIR-9-5p	UCUUUGGUUAUCUAGCUGUAUGA

Sequences are human unless otherwise specified.

Table S6. RT-qPCR program.

RT-qPCR program (For mRNA and lncRNA)

Step	**1**	**2**			**3**		
	Hot-Start DNA Polymerase Activation	**PCR**			**Melt Curve**		
	HOLD	CYCLE (40 cycles)			CYCLE (1 cycle)		
		Denature	Anneal	Extend			
Temp.	95 ℃	95 ℃	50-60 ℃	72 ℃	95 ℃	60 ℃	95 ℃
Time	10 min	15 sec	30 sec	30 sec	15 sec	60 sec	15 sec

RT-qPCR program (For miRNA)

<table>
<tr><th rowspan="2">Step</th><th>1</th><th colspan="3">2</th><th colspan="2">3</th><th colspan="3">4</th></tr>
<tr><th>Hot-Start DNA Polymerase Activation</th><th colspan="3">Enrich low-abundance miRNA</th><th colspan="2">PCR</th><th colspan="3">Melt Curve</th></tr>
<tr><td rowspan="2"></td><td rowspan="2">HOLD</td><td colspan="3" rowspan="2">CYCLE (5 cycles)</td><td colspan="2">CYCLE (40-45 cycles)</td><td colspan="3" rowspan="2">CYCLE (1 cycle)</td></tr>
<tr><td>Denature</td><td>Anneal, Extend</td></tr>
<tr><td>Temp.</td><td>95 ℃</td><td>94 ℃</td><td>63-65 ℃</td><td>72 ℃</td><td>94 ℃</td><td>60 ℃</td><td>94 ℃</td><td>60 ℃</td><td>95 ℃</td></tr>
<tr><td>Time</td><td>15 min</td><td>20 sec</td><td>30 sec</td><td>34 sec</td><td>20 sec</td><td>34 sec</td><td>15 sec</td><td>60 sec</td><td>15 sec</td></tr>
</table>

Table S7. siRNAs, mimic, and inhibitor target sequences.

Producers	Item No.	Gene	Target sequences
Shanghai Gene Pharma Co., Ltd. (Shanghai, China)	# A01001	*TGF-β2* siRNA	5’-GCGGCCUAUUCGUUUAGAA-3’
			3’-UUCUAAAGCAAUAGGCCGC-5’
	# A01001	*PPME1* siRNA	5’-GAAUGAAACUGGCAAGGAU-3’
			3’-AUCCUUGCCAGUUUCAUUC-5’
	# A01001	*HDAC7-AS*1 siRNA	5’-GATGTTGAGTTGAAGTTGA-3’
			3’-TCAACTTCAACTCAACATC-5’
	# A01001	*CAV1* siRNA	5’-CGACGACGUGGUCAACAUU-3’
			3’-AAUCUUGACCACGUCGUCG-5’
	# B01001	*MIR-7-5p* mimic	5’-UGGAAGACUAGUGAUUUUGUUG-3’
			3’-CAACAAAAUCACUAGUCUUCCA-5’
	# B03001	*MIR-7-5p* inhibitor	5’-AACAACAAAAUCACUAGUCUUCCA-3’

Sequences are human unless otherwise specified.

Table S8. Patient characteristics and clinical results.

	Control (n=50)	CHD (n=77)	P
Male, n (%)	27 (54.0)	59 (76.6)	0.011
Age, years, mean ± SD	62.18 ± 10.78	64.08 ± 7.769	0.252
Cardiovascular risk factors			
Diabetes, n (%)	17 (34.0)	32 (41.6)	0.457
Hypertension, n (%)	33 (66.0)	56 (74.7)	0.319
Hyperlipidemia, n (%)	41 (82.0)	68 (88.3)	0.435

Current smoke, n (%)	20 (40.0)	43 (55.8)	0.103
Body mass index, kg/m^2, mean ± SD	25.94 ± 3.433	25.88 ± 3.082	0.917
Blood biochemical analysis			
TG (mM), mean ± SD	4.017 ± 0.814	4.112 ± 1.113	0.610
TC (mM), mean ± SD	1.900 ± 1.608	1.910 ± 1.483	0.971
LDL-C (mM), mean ± SD	2.207 ± 0.532	2.430 ± 0.994	0.151
HDL-C (mM), mean ± SD	1.065 ± 0.423	1.019 ± 0.374	0.523
FBG (mM), mean ± SD	5.644 ± 1.325	6.298 ± 2.154	0.061
HbA1c (%), mean ± SD	6.312± 0.157	6.626 ± 1.493	0.231
hs-CRP (mg/L), mean ± SD	2.622 ± 3.526	8.418 ± 16.30	0.036
ALT(U/L), mean ± SD	25.55 ± 16.97	23.46 ± 16.64	0.498
AST(U/L), mean ± SD	24.92 ± 11.78	29.03 ± 44.01	0.524
Albumin (g/L), mean ± SD	39.37 ± 2.737	38.58 ± 2.640	0.112
T-BIL (μM), mean ± SD	15.31 ± 6.063	14.05 ± 6.475	0.279
Urea (mM), mean ± SD	4.954 ± 1.323	5.498 ± 1.880	0.081
Creatinine (μM), mean ± SD	64.91 ± 13.32	70.38 ± 17.20	0.061
Uric acid (μM), mean ± SD	361.3 ± 88.16	348.4 ± 95.36	0.452

Data are presented as Mean ± SD or n (%). CHD, coronary heart disease; TC, total cholesterol; TG, total triglyceride; LDL-C, low-density lipoprotein cholesterol; HDL-C, high-density lipoprotein cholesterol; FBG, fasting blood glucose; hs-CRP, high-sensitivity C-reactive protein; ALT, alanine aminotransferase; AST, aspartate aminotransferase; T-BIL, total bilirubin. To compare the differences between two groups with normally distributed variables, Student's *t* test was used. To test for differences between two groups with skewed variables, the nonparametric Mann-Whitney *U* test was used. In addition, categorical variables were showed as number with percent and analyzed by the $\chi 2$ test.

Table S9. ***MIR-7-5p*** **binding sites for** ***HDAC7-AS1*** **as identified by Mireap, miRanda, and TargetScan.**

<table>
<tr><th>miRNA</th><th>Target Gene</th><th>Score</th><th>Energy (kcal/mol)</th><th>3’-miRNA-5’-alignment-5’-utr-3’</th></tr>
<tr><td><i>HSA-MIR-7-5p</i></td><td><i>HDAC7-AS1</i></td><td>119</td><td>-13.6</td><td>3’ uuGUUG-UUUUAGUGAUCAGAAGGu 5’
:||| ::| || || |||||
5’ ccTAACTTGGAACA-GAGGCTTCCg 3’</td></tr>
<tr><td><i>HSA-MIR-7-5p</i></td><td><i>HDAC7-AS1</i></td><td>117</td><td>-15.34</td><td>3’ uuGUUGUUUUAGUGA-UCAGAaggu 5’
|| |||:||| :| |||||
5’ acCACCAAGATCCTTCAGTCTgagc 3’</td></tr>
<tr><td><i>HSA-MIR-7-5p</i></td><td><i>HDAC7-AS1</i></td><td>115</td><td>-16.82</td><td>3’ uuguUGU-UUUAGUGAUCAGAAGGu 5’
||| |: ||| |||||:|
5’ cagtACATCAGCCACCAGTCTCTCa 3’</td></tr>
<tr><td><i>HSA-MIR-7-5p</i></td><td><i>HDAC7-AS1</i></td><td>114</td><td>-7.86</td><td>3’ uuguuguuuUAGUGAU-CAGAAGGu 5’
|| ||: ||||||
5’ ctgttctctACCCCTGTGGCTTCCc 3’</td></tr>
<tr><td><i>HSA-MIR-7-5p</i></td><td><i>HDAC7-AS1</i></td><td>111</td><td>-11.1</td><td>3’ uuguuGUUUUAGUGAUCAGAAGGu 5'
||::: || || ||||:
5’ cacccCAGGGGCCCCAGCCTTCTa 3'</td></tr>
</table>

Mireap (v2.0) (http://sourceforge.net/projects/mireap/);

miRanda (v3.3a) (http://cbio.mskcc.org/microrna_data/miRanda-aug2010.tar.gz);

TargetScan (v7.0) (http://www.targetscan.org/vert_71/).

Table S10. Negatively correlated miRNA-gene pairs: ***MIR-7-5p*** **and its target genes.**

miRNA	Gene	P value	asso_sign (miRNA-Target gene)
MIR-7-5p	*CTSK*	0.000142241	UP-DOWN
	CSMD3	1.89E-06	UP-DOWN
	HSPBAP1	9.02E-05	UP-DOWN
	YPEL2	0.000112022	UP-DOWN
	GLS	6.58E-20	UP-DOWN
	FAM110C	0.000660921	UP-DOWN
	PPME1	1.12E-53	UP-DOWN
	IFITM10	0.009667697	UP-DOWN
	ABL2	7.28E-39	UP-DOWN
	TGFB2	6.75E-12	UP-DOWN
	SH2D5	2.27E-65	UP-DOWN

	PTCH1	3.89E-09	UP-DOWN
	SLC5A3	2.57E-119	UP-DOWN
	KLHDC7A	0.000498548	UP-DOWN
	SLC23A3	0.00724907	UP-DOWN
	TRIML2	1.47E-81	UP-DOWN

The R package edgeR (http://www.bioconductor.org/packages/release/bioc/html/edgeR.html) was used to identify differentially expressed transcripts across the samples or groups as evaluated using RNA-seq. mRNA and miRNA with a fold change ≥ 2 and $P < 0.05$ were considered as significant differentially expressed genes (DEGs).

Table S11. Results of correlation analysis between two indicated factors.

		r	**P**
HDAC7-AS1	*MIR-7-5p*	-0.3389	0.0026
	TGF-β2	0.04843	0.6758
	PPME1	0.1826	0.1119
	IL-1β	0.1533	0.1833
	IL-6	-0.3336	0.003
	TNF-α	0.002393	0.9835
	hs-CRP	-0.1602	0.1953
MIR-7-5p	*TGF-β2*	-0.5835	0.001
	PPME1	-0.24	0.0353
	IL-1β	0.07496	0.5171
	IL-6	0.201	0.0796
	TNF-α	0.1395	0.2264
	hs-CRP	0.3304	0.0063
TGF-β2	*PPME1*	0.1337	0.2463
	IL-1β	0.172	0.1346
	IL-6	-0.04524	0.696
	TNF-α	0.113	0.3277
	hs-CRP	-0.1098	0.3763
PPME1	*IL-1β*	0.03938	0.7338
	IL-6	-0.04292	0.7109
	TNF-α	0.04688	0.6856
	hs-CRP	0.06204	0.618
IL-1β	*IL-6*	0.2419	0.0341
	TNF-α	0.4351	0.0001
	hs-CRP	0.2608	0.0331
IL-6	*TNF-α*	0.313	0.0056
	hs-CRP	0.2887	0.0178
TNFα	hs-CRP	0.4069	0.0006

Spearman's rank correlation coefficient was used to assess the correlation between two indicated mRNAs.

Table S12. Univariable and multivariable logistic regression analysis for determining the independent risk factors of CHD.

Variables	OR	95% CI	P	Adjusted OR[a]	95% CI	P
Gender (male)	2.647	1.233-5.683	0.013	2.266	0.343-14.961	0.396
Age	1.028	0.987-1.027	0.180			
Diabetes	2.020	0.981-4.159	0.056	1.397	0.266-7.325	0.692
Hypertension	1.527	0.708-3.793	0.280			
Hyperlipidemia	1.263	0.606-2.632	0.533			
Current smoker	2.020	0.981-4.159	0.056	0.897	0.195-4.134	0.890
BMI	1.009	0.947-1.076	0.781			
TG	1.016	0.801-1.288	0.898			
TC	1.163	0.810-1.668	0.413			
LDL-C	1.557	0.922-2.628	0.098	2.090	0.735-5.944	0.167
HDL-C	0.779	0.314-1.937	0.592			
FBG	1.235	0.984-1.550	0.068	1.277	0.834-1.955	0.261
HbA1c	1.063	0.917-1.213	0.415			
hs-CRP	1.211	1.085-1.351	0.011	1.169	0.999-1.368	0.052
ALT	0.993	0.972-1.014	0.506			
AST	1.005	0.991-1.019	0.517			
Albumin	0.885	0.770-1.016	0.083	0.869	0.679-1.112	0.264
T-BIL	0.973	0.919-1.030	0341			
Urea	1.286	0.982-1.686	0.068	1.313	0.756-2.292	0.331
Creatinine	1.027	1.002-1.052	0.035	1.019	0.957-1.085	0.549
Uric acid	1.000	0.996-1.003	0.912			
HDAC7-AS1	0.238	0.125-0.451	0.032	0.430	0.157-1.177	0.101
MIR-7-5p	1.551	1.223-1.966	0.003	2.168	1.060-4.434	0.034
TGF-β2	0.553	0.357-0.857	0.008	0.651	0.265-1.599	0.349
PPME1	0.644	0.438-0.947	0.025	0.379	0.193-0.743	0.005
IL-1β	2.722	1.677-4.416	0.001	1.599	0.928-1.756	0.091
TNFα	1.179	0.961-1.446	0.114			
IL6	1.223	1.006-1.487	0.043	1.095	0.771-1.555	0.613

OR, Odds ratio; CI, confidence interval; CHD, coronary heart disease; TC, total cholesterol; TG, total triglyceride; LDL-C, low-density lipoprotein cholesterol; HDL-C, high-density lipoprotein cholesterol;

FBG, fasting blood glucose , fasting blood glucose; hs-CRP, high-sensitivity C-reactive protein; ALT, alanine aminotransferase; AST, aspartate aminotransferase.

[a] Corresponds to adjustment for gender, diabetes, current smoker, LDL-C, FBG, albumin, hs-CRP, urea, creatinine, Uric acid, *HDAC7-AS1*, *MIR-7-5p*, *TGF-β2*, *PPME1*, *IL-1β* and *IL-6*.

Table S13. High-throughput lncRNA and miRNA sequence analysis and relevant qPCR results from HUVECs treated with 5 µM PCB29-pQ.

		Control			PCB29-pQ		
		Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure 1c	*HDAC7-AS1*	21.70	1.00	0.02	19.71	3.57	0.61
		21.68			19.88		
		21.64			19.40		
	RP3-416H24.1	21.74	1.00	0.05	22.53	0.52	0.08
		21.60			22.62		
		21.70			22.21		
	LINC01547	21.57	1.00	0.07	19.81	2.20	1.00
		21.48			21.28		
		21.69			20.06		
	TUG1	21.81	1.00	0.04	21.74	0.93	0.06
		21.77			21.73		
		21.70			21.57		
	MCM3AP-AS1	21.86	1.00	0.01	21.59	0.97	0.08
		21.83			21.72		
		21.85			21.83		
	FGD5-AS1	21.86	1.00	0.02	24.44	0.17	0.02
		21.92			24.34		
		21.87			24.09		

	Bio-NC			Bio-*MIR-7-5p*		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure 1d	21.89	1.00	0.01	17.98	15.31	3.72
	21.89			17.97		
	21.87			17.40		

Mean and SD values are the ones presented in Figure 1c-d. Data reported relative to control or Bio-NC.

Table S14. The expression of *HDAC7-AS1*, *MIR-7-5p* and *TGF-β2*/*PPME1* in HUVECs exposed to 5 μM PCB29-pQ.

		Control			PCB29-pQ		
		Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure 2a	*TGF-β2*	21.91	1.00	0.01	22.76	0.48	0.06
		21.93			23.02		
		21.92			22.68		
	PPME1	22.17	1.00	0.03	22.46	0.71	0.04
		22.09			22.36		
		22.13			22.50		

		Control			PCB29-pQ		
		Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure 2b (Right panel)	TGF-β2	49800.52	1.00	0.30	13613.11	0.23	0.05
		49779.34			13624.50		
		49799.71			13598.56		
	PPME1	63958.41	1.00	0.20	43513.44	0.54	0.09

		63928.43			43484.88		
		63944.37			43491.22		

		NC mimic			*MIR-7-5p* mimic		
		Cq	Mean (normalized)	SD (normalized)	Cq	Mean (normalized)	SD (normalized)
Figure 2c	*TGF-β2*	25.54	1.00	0.03	26.88	0.49	0.06
		25.45			27.13		
		25.53			27.20		
	PPME1	25.69	1.00	0.03	26.90	0.68	0.04
		25.77			26.73		
		25.70			26.79		

		NC mimic			*MIR-7-5p* mimic		
		Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure 2d (Right panel)	TGF-β2	60469.01	1.00	0.20	29146.83	0.41	0.08
		60473.45			29101.17		
		60443.78			29128.81		
	PPME1	52334.05	1.00	0.17	52342.9	0.32	0.06
		52312.78			52253.98		
		52288.09			52338.05		

	NC mimic + pEZ-M61-NC			pEZ-M61-NC + *MIR-7-5p* mimic			*MIR-7-5p* mimic + pEZ-M61-HDAC7-AS1		
	luciferase activity	Mean	SD	luciferase activity	Mean	SD	luciferase activity	Mean	SD
Figure 2f	29.48	29.81	0.30	25.60	25.34	0.28	30.35	31.46	1.38
	29.86			25.05			33.00		
	30.08			25.37			31.02		

	NC mimic + pEZ-M61-NC			pEZ-M61-NC + *MIR-7-5p* mimic			*MIR-7-5p* mimic + pEZ-M61-HDAC7-AS1		
	luciferase activity	Mean	SD	luciferase activity	Mean	SD	luciferase activity	Mean	SD
Figure 2g	8.11	7.81	0.30	5.26	5.36	0.09	6.22	6.35	0.12
	7.52			5.36			6.38		
	7.80			5.45			6.45		

Mean and SD values are the ones presented in Figure 2a, b, c, d and f. Expression is relative to control or NC mimic for data from 2a, b, c, and d. For Figure 2F, data is expressed as luciferase activity (a.u.)

Table S15. Endothelial injury and atherogenesis in *ApoE*$^{-/-}$ mice exposed to PCB29-pQ, and apoptotic rate in HUVECs exposed to PCB29-pQ.

		Control			PCB29-pQ		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure 3a (Right panel; % plaque area)		13.01	14.89	1.80	54.48	45.47	11.17
		15.08			48.96		
		16.59			32.98		
Figure 3b (Right panel; Pearson’s correlation coefficient)		0.50	0.33	0.18	0.94	0.98	0.03
		0.15			0.99		
		0.33			1.00		
Figure 3d (cell viability, %)	NC inhibitor + NC siRNA	99.07	100.00	5.85	84.14	81.21	5.21
		109.28			75.19		
		91.65			84.30		
	NC siRNA + *MIR-7-5p* inhibitor	115.81	111.17	5.40	95.23	97.03	5.85
		105.25			92.29		
		112.46			103.57		
	MIR-7-5p inhibitor + *TGF-β*2 siRNA	63.92	60.10	3.36	49.93	50.27	5.01
		57.62			55.44		
		58.76			45.44		

	MIR-7-5p inhibitor + *PPME1* siRNA	64.33	57.59	5.86	45.79	48.14	3.87
		54.74			52.60		
		53.70			46.03		

Mean and SD values are the ones presented in Figure 3a, b and d.

Table S16. Measures of endothelial injury in cells and protein and mRNA expression of *TGF-β2* and *PPME1* in HUVECs transfected with a *HDAC7-AS1* overexpression vector or a *MIR-7-5p* mimic exposed to 5 µM PCB29-pQ.

	NC mimic + pEZ-M61-NC			NC mimic + pEZ-M61-NC + PCB29-pQ			NC mimic + pEZ-M61-*HDAC7-AS1* + PCB29-pQ			*MIR-7-5p* mimic + pEZ-M61-*HDAC7-AS1* + PCB29-pQ		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure 4a	23.01	1.00	0.03	21.70	2.11	0.24	25.50	0.29	0.02	16.74	102.90	11.57
	23.09			21.67			25.60			16.46		
	23.06			21.41			25.70			16.73		
Figure 4b	23.17	1.00	0.09	23.38	0.60	0.02	20.23	11.72	0.29	19.76	12.25	0.44
	22.92			23.38			20.27			19.71		
	23.06			23.45			20.30			19.66		
Figure 4c	22.92	1.00	0.02	23.59	0.47	0.00	24.30	0.63	0.03	24.35	0.51	0.07
	22.95			23.63			24.42			24.17		
	22.90			23.63			24.35			23.98		
Figure 4d	23.12	1.00	0.02	23.01	0.78	0.02	23.93	0.94	0.02	23.99	0.66	0.10
	23.07			23.10			23.97			23.76		
	23.09			23.06			23.94			24.20		

	NC mimic + pEZ-M61-NC			NC mimic + pEZ-M61-NC + PCB29-pQ			NC mimic + pEZ-M61-*HDAC7-AS1* + PCB29-pQ			*MIR-7-5p* mimic + pEZ-M61-*HDAC7-AS1* + PCB29-pQ		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure 4f	26963.37	1.00	0.20	16137.55	0.61	0.12	28054.02	1.03	0.11	4054.58	0.15	0.03

	26947.55			16115.34			28059.10			4076.37		
	26987.28			16118.57			28038.02			4068.09		
Figure 4g	34607.94	1.00	0.25	2472.08	0.07	0.01	79170.54	0.40	0.08	4518.18	0.13	0.03
	34653.02			2490.17			79273.68			4527.56		
	34649.21			2488.51			79264.95			4534.10		

	NC mimic + pEZ-M61-NC			NC mimic + pEZ-M61-NC + PCB29-pQ			NC mimic + pEZ-M61-*HDAC7-AS1* + PCB29-pQ			*MIR-7-5p* mimic + pEZ-M61-*HDAC7-AS1* + PCB29-pQ		
	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)
Figure 4h	98.67	100.00	1.77	73.49	72.17	4.00	90.16	93.44	6.10	78.20	76.38	1.69
	99.32			75.34			100.47			76.08		
	102.01			67.68			89.69			74.85		

Mean and SD values are the ones presented in Figure 4a (relative *MIR-7-5p* mRNA level), b (relative *HDAC7-AS1* mRNA level), c (relative *TGF-β2* mRNA level), d (relative *PPME1* mRNA level), f (relative TGF-β2/β-actin protein level), g (relative PPME1/β-actin protein level), and h (cell viability, %). Results presented relative to NC mimic + pEZ-M61-NC.

Table S17. Atherosclerosis and inflammation in ApoE$^{-/-}$ mice exposed to PCB29-pQ accompanied by AAV-*HDAC7-AS1* treatment.

	AAV-NC			AAV-NC + PCB29-pQ			AAV-*HDAC7-AS1*			AAV-*HDAC7-AS1* + PCB29-pQ		
	Individual values	Mean	SD	Individual values	Mean	SD	Individual values	Mean	SD	Individual values	Mean	SD
Figure 5a (Right panel)	10.87	12.63	1.79	21.48	25.78	3.93	10.69	9.64	1.90	6.61	8.35	1.57
	12.58			26.69			10.79			8.77		
	14.44			29.17			7.45			9.65		
Figure 5c	0.67	0.70	0.06	0.27	0.26	0.02	0.95	0.93	0.01	0.71	0.78	0.07
	0.66			0.23			0.92			0.78		
	0.76			0.27			0.93			0.86		

	AAV-NC			AAV-NC + PCB29-pQ			AAV-*HDAC7-AS1*			AAV-*HDAC7-AS1* + PCB29-pQ		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure 5d	24.72	1.00	0.29	26.83	0.25	0.10	22.80	17.06	4.81	24.16	7.19	2.05
	25.47			27.68			22.30			24.78		
	24.86			27.83			21.96			24.88		
Figure 5e	25.56	1.00	0.29	22.63	5.79	1.81	28.07	0.29	0.05	27.65	0.96	0.45
	24.70			23.57			28.21			28.35		
	25.09			22.71			28.53			26.97		
Figure 5f	24.46	1.00	0.24	28.62	0.14	0.05	25.99	2.59	1.29	27.41	1.34	0.42
	24.87			27.88			24.62			26.66		
	25.20			27.62			24.33			26.46		
Figure 5g	24.56	1.00	0.27	26.09	0.33	0.02	24.60	2.65	1.27	26.84	0.93	0.22
	24.24			26.22			23.50			26.31		
	23.76			26.00			24.60			26.91		
Figure 5h	24.74	1.00	0.71	21.78	4.57	1.52	28.29	0.24	0.14	26.04	1.13	0.55

	23.31			22.76			26.74			25.84		
	24.25			22.25			27.92			27.46		
Figure 5i	24.01	1.00	0.14	22.69	3.72	1.54	28.17	0.32	0.15	26.14	1.18	0.13
	24.14			23.26			26.68			26.44		
	24.39			22.05			27.09			26.33		
Figure 5j	23.25	1.00	0.70	23.05	4.65	1.83	30.36	0.90	0.88	26.23	0.74	0.58
	25.77			22.58			25.97			27.98		
	24.07			21.93			24.86			28.05		
	AAV-NC			AAV-NC + PCB29-pQ			AAV-*HDAC7-AS1*			AAV-*HDAC7-AS1* + PCB29-pQ		
	Individual values	Mean	SD	Individual values	Mean	SD	Individual values	Mean	SD	Individual values	Mean	SD
Figure 5k	0.57	0.43	0.13	0.94	0.95	0.02	0.17	0.17	0.02	0.77	0.71	0.08
	0.42			0.94			0.19			0.72		
	0.31			0.98			0.16			0.62		

Mean and SD values are the ones presented in Figure 5a (plaque area, % of whole aorta), c (Pearson's correlation coefficient), d (relative *HDAC7-AS1* mRNA level), e (relative *MIR-7-5p* mRNA level), f (relative *TGF-β2* mRNA level), g (relative *PPME1* mRNA level), h (relative *IL-1β* mRNA level), i (relative *IL6* mRNA level), (relative *TNFα* mRNA level), and k (Pearson's correlation coefficient). Data in panels 5d through 5J are normalized to AAV-NC.

Table S18. Inflammation and atherogenesis in $ApoE^{-/-}$ and $ApoE^{-/-}CAV1^{-/-}$ mice exposed to PCB29-pQ.

Figure 6a (Right panel)		$ApoE^{-/-}$			$ApoE^{-/-}/CAV1^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD

	Control	18.02	18.86	0.84	7.57	6.78	1.97
		18.86			4.54		
		19.70			8.24		
	PCB29-pQ	22.60	25.78	2.76	10.90	10.94	0.94
		27.59			10.03		
		27.15			11.90		

		$ApoE^{-/-}$			$ApoE^{-/-}/CAV1^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure 6b (Right panel)	Control	16.00	14.88	2.53	10.00	9.13	1.73
		14.00			9.00		
		20.00			11.00		
		15.00			8.00		
		16.00			12.00		
		12.00			8.00		
		13.00			8.00		
		13.00			7.00		
	PCB29-pQ	25.00	23.50	4.38	16.00	13.25	2.66
		20.00			12.00		
		19.00			11.00		
		17.00			18.00		
		28.00			10.00		
		29.00			13.00		
		24.00			14.00		
		26.00			12.00		

Figure 6c (p-p65/p65 ratio)		$ApoE^{-/-}$		$ApoE^{-/-}/CAV1^{-/-}$	
		Mean	SD	Mean	SD
	Control	1.00	0.16	0.23	0.09
	PCB29-pQ	2.33	0.86	0.96	0.17

Figure 6c (p-CAV1/CAV1 ratio)		*ApoE*$^{-/-}$		*ApoE*$^{-/-}$/*CAV1*$^{-/-}$	
		Mean	SD	Mean	SD
	Control	1.00	0.11	0.08	0.02
	PCB29-pQ	3.75	0.92	0.07	0.01

	Control				PCB29-pQ			
	ApoE$^{-/-}$		*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		*ApoE*$^{-/-}$		*ApoE*$^{-/-}$/*CAV1*$^{-/-}$	
Figure 6c (p-p65) Grayscale values	18025.72	15823.21	7120.71	7710.74	17526.13	17479.45	8560.24	9882.45
	18017.23	15808.01	7137.93	7726.64	17416.06	17442.11	8593.80	9883.14
	17994.76	15840.00	7124.79	7711.38	17585.55	17606.18	8572.30	9853.36
Figure 6c (p65) Grayscale values	21915.41	17645.41	18709.33	17144.99	13269.30	10481.24	11373.95	11423.09
	21890.29	17623.68	18726.23	17160.83	13420.54	10315.40	11402.96	11403.68
	21920.01	17614.19	18723.14	17145.52	13415.86	10358.81	11403.80	11389.21
Figure 6c (p-CAV1) Grayscale values	9486.03	8721.17	484.76	840.55	21084.55	25457.17	1837.09	507.38
	9484.11	8723.01	516.13	880.38	21127.93	25430.59	1824.28	422.53
	9504.05	8703.10	478.96	857.29	21099.89	25474.25	2003.54	621.80
Figure 6c (CAV1) Grayscale values	19233.40	13857.08	3048.81	5964.90	20226.02	20341.42	4573.50	5367.20
	19238.14	13878.08	3088.71	6004.51	20239.88	20364.73	4463.46	5460.55
	19217.17	13861.90	3071.12	5979.90	20269.11	20407.64	4663.11	5260.69

Figure 6d (Right panel)		*ApoE*$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
	Control	0.29	0.19	0.10	0.09	0.09	0.06
		0.19			0.15		
		0.10			0.04		
	PCB29-pQ	0.96	0.86	0.09	0.59	0.58	0.02
		0.84			0.57		

		0.78			0.59		

		ApoE$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure 6e (Right panel)	Control	0.18	0.23	0.15	0.05	0.13	0.13
		0.10			0.28		
		0.40			0.06		
	PCB29-pQ	0.99	0.93	0.11	0.53	0.49	0.04
		1.00			0.45		
		0.81			0.49		

		ApoE$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure 6f	Control	440.40	365.54	157.76	263.67	272.87	60.05
		183.36			202.68		
		296.01			364.26		
		312.06			244.65		
		595.89			289.08		
	PCB29-pQ	639.27	760.11	174.41	563.34	523.07	39.67
		942.63			501.93		
		594.96			487.67		
		702.90			493.50		
		470.79			568.89		

		ApoE$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
Figure 6g		Individual values	Mean	SD	Individual values	Mean	SD
	Control	1468.8	1336.34	408.68	878.90	919.93	205.04
		986.7			675.60		

		1042.9			1214.60		
		1196.8			815.50		
		1986.5			1015.05		
	PCB29-pQ	2130.9	2135.64	135.701	1775.85	1791.71	142.14
		2056.95			1877.80		
		1983.00			1673.90		
		2343.9			1645.00		
		2163.45			1986.00		

Mean and SD values are the ones presented in Figure 6a (plaque area, % of whole aorta), b (plaque area, % of whole aorta), c (ratio of p-p65/p65 and pCAV1/CAV1 protein), d (Pearson's correlation coefficient), e (Pearson's correlation coefficient), f (*IL-6* (pg/ml)), and g (TNFα (pg/ml)). Data in figure 6c normalized to control ApoE$^{-/-}$ mice.

Table S19. Plasma *HDAC7-AS1* (a), *MIR-7-5p* (b), *TGF-β2* (c), *PPME1* (d), *IL-1β* (e), *IL-6* (f), and *TNFα* (g) levels in patients with CHD.

Figure 7a		Figure 7b		Figure 7c		Figure 7d		Figure 7e		Figure 7f		Figure 7g	
Control	CHD	Control	CHD	Control	CHD	Control	CHD	Control	CHD	Control	CHD	Control	CHD
24.40	17.03	26.95	21.46	17.38	32.35	23.17	22.83	28.05	26.75	26.46	26.33	25.47	28.40
24.38	16.70	21.71	18.75	27.06	31.23	25.94	21.26	26.89	27.72	26.31	25.75	25.08	29.54
24.73	17.50	23.92	19.60	27.22	27.76	21.96	20.26	27.59	26.80	26.93	24.60	26.37	27.09
26.39	18.01	24.19	21.27	25.71	30.52	25.84	22.09	30.89	26.19	27.07	26.05	26.03	29.10
26.66	18.62	23.32	20.38	26.91	27.98	22.52	32.47	25.92	27.88	23.76	25.85	26.42	25.02

24.63	29.38	24.02	18.65	22.69	28.15	22.00	32.32	29.56	23.34	26.87	23.90	26.55	23.10
20.82	26.60	24.21	19.90	26.20	28.91	22.73	31.89	27.86	29.65	24.99	26.18	24.61	28.84
23.75	27.35	26.49	20.30	21.52	32.17	24.02	28.22	29.81	26.42	29.28	26.11	26.27	27.15
23.73	25.62	25.65	20.36	26.50	30.99	21.59	31.79	25.57	26.88	29.21	27.14	28.76	29.10
23.48	27.79	25.69	21.38	21.88	28.96	24.75	31.06	30.67	29.34	26.95	24.87	26.84	27.30
21.54	17.03	22.34	22.38	24.32	28.93	24.20	31.08	28.53	26.98	26.79	25.66	25.37	27.99
25.02	18.47	27.15	18.97	22.97	30.76	25.56	33.10	28.05	26.14	26.17	22.90	27.85	29.56
25.71	27.46	26.63	22.45	22.97	27.62	24.36	31.48	27.66	27.62	28.52	24.70	26.99	23.61
27.24	24.41	22.03	19.47	23.41	29.54	24.97	33.91	28.62	22.97	25.47	20.60	25.51	21.46
26.00	26.54	22.93	21.68	27.37	22.61	22.12	31.18	28.34	24.86	27.30	23.71	26.18	24.04
25.59	27.31	23.93	21.62	19.07	21.69	22.73	33.09	28.44	27.58	24.79	23.96	27.19	21.28
22.93	26.28	23.83	19.80	24.84	20.37	24.34	28.62	29.27	27.66	28.34	25.85	25.64	24.52
24.91	24.47	23.21	19.05	24.31	20.61	24.50	27.25	29.48	27.54	25.62	25.07	25.77	19.55
27.63	28.80	24.73	21.78	24.79	21.91	23.89	33.00	27.57	26.11	25.50	22.57	27.13	22.91
25.98	27.10	26.02	20.82	24.55	20.34	24.25	30.97	29.76	28.82	25.57	25.63	25.43	24.42
24.31	25.62	26.22	20.33	23.14	31.55	21.64	29.10	29.07	29.52	26.27	24.04	25.36	26.40

24.56	26.77	22.76	19.64	24.07	21.17	23.40	27.67	29.37	28.93	27.40	23.99	27.00	25.65
25.97	25.95	23.12	18.46	26.98	19.34	24.75	29.08	28.37	25.95	26.61	23.82	27.34	22.43
22.61	26.23	25.47	16.88	21.48	31.40	24.52	30.81	25.08	27.64	27.63	23.43	27.00	23.91
23.53	28.28	26.95	17.52	28.94	30.97	23.50	31.62	30.07	25.54	25.23	24.00	25.12	23.47
20.89	26.15	31.41	19.84	30.12	27.30	23.47	28.22	28.83	27.22	25.25	24.97	24.37	25.65
25.70	26.94	28.53	21.62	25.47	30.87	24.79	32.74	27.76	28.90	24.64	28.41	26.23	24.63
23.08	18.17	25.56	22.58	22.05	30.14	21.02	20.98	26.73	27.65	23.51	25.26	24.57	21.11
24.53	17.10	27.49	18.32	21.63	30.16	22.93	20.44	24.76	28.33	25.76	25.69	26.09	25.41
22.56	16.96	21.82	20.76	25.13	32.18	23.42	19.50	29.77	29.08	25.28	26.64	26.62	26.56
24.80	17.17	25.41	22.99	27.80	30.56	21.78	19.56	26.22	27.77	28.06	24.81	28.60	24.76
23.42	16.98	28.78	21.06	26.59	32.99	24.27	19.06	30.13	28.13	26.37	25.42	24.48	23.35
24.93	17.58	25.71	21.40	25.39	30.26	25.43	17.99	28.87	25.10	24.59	25.31	26.69	25.76
24.80	16.43	23.40	22.40	24.45	32.17	25.03	20.08	26.36	28.20	24.82	25.48	27.06	24.72
21.34	18.70	23.48	22.66	21.98	27.70	25.80	19.72	29.34	27.89	26.37	24.72	27.92	24.73
23.56	18.01	18.09	18.42	23.86	26.33	24.45	20.57	26.82	28.16	26.79	24.88	27.88	24.41
23.84	18.62	21.36	18.37	23.75	32.08	21.80	23.20	28.89	29.05	24.64	22.85	27.09	25.68
23.78	29.38	22.55	18.47	20.19	30.05	25.88	20.93	28.22	28.18	26.81	25.03	27.07	22.59

24.61	26.60	24.64	17.85	22.25	28.18	23.52	20.19	28.08	26.65	26.81	25.67	25.28	23.95
24.43	27.35	24.50	18.46	28.17	26.75	26.83	30.58	26.96	26.85	26.04	24.18	26.43	19.96
24.17	25.62	23.62	19.98	24.66	28.16	23.29	30.42	25.06	28.19	23.88	24.73	28.14	23.87
25.59	27.79	23.61	20.76	20.29	29.89	23.20	29.99	27.17	29.17	24.94	26.37	25.59	25.67
24.24	17.03	24.86	19.84	27.33	30.70	24.03	26.32	30.90	26.86	27.18	25.30	23.76	22.52
24.80	18.47	28.15	17.52	26.22	27.30	22.84	29.89	29.40	27.64	26.81	24.49	27.41	20.09
24.22	27.46	22.87	21.62	26.29	31.82	23.52	29.16	28.27	28.14	28.09	25.03	29.05	22.80
25.07	24.41	31.84	22.58	28.20	20.06	22.68	29.18	29.66	26.93	27.23	25.27	26.13	25.30
25.53	26.54	19.78	22.99	26.37	19.52	23.43	31.21	26.81	27.03	26.17	26.15	26.30	25.38
22.12	27.31	15.95	18.32	22.16	20.61	20.88	29.58	30.93	21.96	28.98	23.39	26.28	20.07
25.14	26.28	18.64	16.88	23.59	24.97	24.95	32.02	30.59	27.74	26.02	26.37	25.63	19.47
24.55	24.47	22.69	21.06	17.99	25.51	23.72	29.29	31.18	29.14	28.14	25.12	26.25	22.92
	28.80		21.40		21.83		31.20		27.67		23.81		26.54
	27.10		22.40		25.91		26.72		24.95		25.28		24.98
	25.62		22.66		22.55		25.35		26.42		24.18		23.85
	26.77		22.78		28.39		31.10		26.48		25.32		25.19

	25.95		22.53		26.76		29.08		27.60		24.06		23.24
	26.23		18.47		25.04		27.20		24.20		21.22		19.64
	28.28		17.85		25.60		25.77		25.13		27.01		23.34
	26.15		19.98		25.56		27.18		21.71		24.07		20.92
	26.94		20.36		24.00		28.92		20.16		25.66		24.19
	18.17		21.38		24.10		29.72		24.06		24.33		24.80
	17.10		22.38		25.80		26.32		24.95		26.94		26.30
	16.96		18.97		24.15		30.84		27.50		26.60		24.20
	17.17		22.45		28.67		19.08		25.90		24.91		23.42
	16.98		19.47		28.12		18.54		22.59		25.61		25.06
	17.58		21.68		27.74		21.27		26.42		24.18		24.29
	18.70		21.62		23.58		21.19		22.78		25.95		24.94
	19.07		19.80		23.18		28.50		24.59		29.75		23.96
	20.22		19.05		21.90		28.33		24.62		26.11		23.12
	26.62		21.78		24.63		28.35		20.44		28.57		22.86
	26.54		25.50		23.31		28.33		20.87		26.74		25.48

	18.63		24.72		22.90		29.86		25.99		25.41		24.00
	18.34		18.42		28.97		29.74		20.77		32.32		22.35
	18.34		18.37		28.83		30.04		24.53		26.12		21.75
	18.34		24.85		29.06		28.80		23.03		27.66		23.66
	20.06		21.93		29.07		27.53		24.04		26.57		23.34
	25.70		19.08		28.96		27.53		23.73		22.95		22.93
	25.59		22.20		29.18		27.51		22.36		24.15		21.04

Cq values are the ones presented in Figure 7a-g.

	Control		CHD	
	Mean	SD	Mean	SD
Figure 7a	1.00	0.88	0.29	0.49
Figure 7b	1.00	1.60	4.52	5.65
Figure 7c	1.00	1.24	0.40	0.95
Figure 7d	1.00	1.45	0.44	1.07
Figure 7e	1.00	1.67	3.34	8.17
Figure 7f	1.00	1.35	2.55	4.55
Figure 7g	1.00	1.66	4.37	8.01

Mean and SD values are the ones presented in Figure 7a-g.

Table S20. The expression of select lncRNAs in HUVECs exposed to PCB29-pQ.

		Control			PCB29-pQ		
		Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure S3a	*LINC01547*	26.22	1.00	0.04	26.75	1.00	0.07
		26.28			26.86		
		26.16			26.67		
	SLCO4A1-AS1	25.42	1.00	0.04	24.96	2.07	0.02
		25.52			24.93		
		25.43			24.93		
	NRSN2-AS1	27.58	1.00	0.11	27.27	1.34	0.27
		27.27			27.69		
		27.52			27.82		
	FGD5-AS1	26.39	1.00	0.03	27.44	0.71	0.02
		26.32			27.36		
		26.39			27.42		
	MCM3AP-AS1	26.52	1.00	0.02	27.77	0.65	0.04
		26.58			27.73		
		26.54			27.60		
	TUG1	25.44	1.00	0.05	26.86	0.53	0.03
		25.41			27.00		
		25.55			26.92		
	RP3-416H24.1	27.29	1.00	0.08	28.63	0.62	0.02
		27.52			28.65		
		27.41			28.56		
	AC002550.5	24.52	1.00	0.34	24.81	1.80	0.12
		25.36			24.75		
		25.24			24.63		
	RP5-1057I20.4 (HADC7-AS1)	24.46	1.00	0.08	27.49	0.18	0.01
		24.52			27.57		

		24.68			27.57		
	SLFNL1-AS1	24.95	1.00	0.11	25.06	1.37	0.07
		24.95			25.20		
		25.22			25.11		

		Control			PCB29-pQ		
		Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure S3b	*MIR-7-5p*	22.29	1.00	0.12	20.63	6.00	0.35
		22.46			20.50		
		22.11			20.47		
	MIR-24-3p	22.09	1.00	0.09	23.05	0.72	0.08
		21.85			23.32		
		21.88			23.35		
	MIR-9-5p	21.89	1.00	0.04	24.81	0.21	0.02
		21.79			25.01		
		21.89			24.94		

Mean and SD values are the ones presented in Figure S3a-b. All data reported relative to control treated cells.

Table S21. The expression of *HDAC7* level in HUVECs transfected with *HDAC7-AS1* siRNA or pEZ-M61-*HDAC7-AS1*.

	NC siRNA			*HDAC7-AS1* siRNA (25 nm)			*HDAC7-AS1* siRNA (50 nm)			*HDAC7-AS1* siRNA (100 nm)		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure S4b	23.74	1.00	0.03	24.89	0.58	0.02	25.36	0.41	0.02	25.71	0.33	0.02

	23.66			24.79			25.46			25.80		
	23.74			24.84			25.32			25.67		

	pEZ-M61-NC			pEZ-M61-*HDAC7-AS1* (2.5 µg)			pEZ-M61-*HDAC7-AS1* (5 µg)			pEZ-M61-*HDAC7-AS1* (7.5 µg)		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure S4c	23.72	1.00	0.05	20.77	8.79	0.53	19.77	20.51	1.07	18.98	32.83	1.04
	23.58			20.94			19.68			19.01		
	23.67			20.88			19.62			19.07		

	NC siRNA			NC siRNA + PCB29-pQ			*HDAC7-AS1* siRNA			*HDAC7-AS1* siRNA + PCB29-pQ		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure S4d	23.59	1.00	0.06	23.89	1.10	0.09	23.71	1.31	0.10	24.13	0.93	0.02
	23.69			23.68			23.48			24.09		
	23.51			23.85			23.60			24.09		
Figure S4e	24.90	1.00	0.04	25.35	0.89	0.03	25.11	1.13	0.07	25.51	0.81	0.09
	24.84			25.45			25.04			25.51		
	24.95			25.42			25.20			25.79		

Mean and SD values are the ones presented in Figure S4b-e. All data is *HDAC1-AS1* mRNA levels reported relative to levels in NC siRNA or pEZ-M61-NC.

Table S22. Protein TGF-β2 and PPME1 levels in HUVECs exposed to PCB29-pQ with *MIR-7-5p* inhibitor or *TGF-β2/PPME1* siRNA.

	NC inhibitor + NC siRNA	NC inhibitor + NC siRNA + PCB29-pQ	NC siRNA + *MIR-7-5p* inhibitor	NC siRNA + *MIR-7-5p* inhibitor + PCB29-pQ	*MIR-7-5p* inhibitor + *TGF-β2* siRNA	*MIR-7-5p* inhibitor + *TGF-β2* siRNA + PCB29-pQ
Figure S7a (Lower panel)	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	13486.08	4773.18	24453.20	9189.13	9331.76	6005.81
	13486.08	4807.88	23710.78	9553.25	9037.81	6698.18
	13508.49	4833.88	24159.95	9516.47	9203.93	6424.71
Figure S7b (Lower panel)	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	12610.66	13479.47	28440.61	14589.18	5921.18	1069.50
	12527.00	13590.42	28704.73	13716.52	6436.83	1139.45
	12510.71	13746.54	27936.61	14791.59	6066.13	1023.26

Figure S7a (Lower panel)	NC inhibitor + NC siRNA		NC inhibitor + NC siRNA + PCB29-pQ		NC siRNA + *MIR-7-5p* inhibitor		NC siRNA + *MIR-7-5p* inhibitor + PCB29-pQ		*MIR-7-5p* inhibitor + *TGF-β2* siRNA		*MIR-7-5p* inhibitor + *TGF-β2* siRNA + PCB29-pQ	
	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)
	1.00	0.00	0.40	0.00	2.02	0.03	0.96	0.02	0.80	0.01	0.65	0.04

Figure S7b (Lower panel)	NC inhibitor + NC siRNA		NC inhibitor + NC siRNA + PCB29-pQ		NC siRNA + *MIR-7-5p* inhibitor		NC siRNA + *MIR-7-5p* inhibitor + PCB29-pQ		*MIR-7-5p* inhibitor + *PPME1* siRNA		*MIR-7-5p* inhibitor + *PPME1* siRNA + PCB29-pQ	
	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)
	1.00	0.00	0.83	0.04	2.80	0.04	1.57	0.06	0.72	0.03	0.10	0.01

Mean and SD values are the ones presented in Figure S7a-b (Lower panel). All data is presented as fold difference relative to NC inhibitor + NC siRNA.

Table S23. Luciferase analysis of the activity of *MIR-7-5p* bind to *TGF-β2*, *PPME1*, and *HDAC7-AS1* in HUVECs transfected with NC mimic or *MIR-7-5p* mimic.

		NC mimic			*MIR-7-5p* mimic		
		luciferase activity	Mean (normalized)	SD (normalized)	luciferase activity	Mean (normalized)	SD (normalized)
Figure S8a	NC-3'UTR	2.95	1.00	0.05	3.07	1.11	0.05
		2.90			3.07		
		2.67			3.32		
	TGF-β2 (WT)- 3'UTR	0.55	1.00	0.07	0.48	0.86	0.03
		0.57			0.51		
		0.63			0.51		
	TGF-β2 (MUT)- 3'UTR	0.16	1.00	0.08	0.18	1.03	0.07
		0.16			0.16		

		0.18			0.18		

		NC mimic			*MIR-7-5p* mimic		
		luciferase activity	Mean	SD	luciferase activity	Mean	SD
Figure S8b	NC-3’UTR	3.00	1.00	0.01	3.35	1.12	0.02
		3.03			3.35		
		3.02			3.44		
	PPME1 (WT)- 3’UTR	0.67	1.00	0.02	0.50	0.72	0.02
		0.66			0.49		
		0.69			0.47		
	PPME1 (MUT)- 3’UTR	0.19	1.00	0.00	0.23	1.19	0.00
		0.19			0.23		
		0.19			0.23		

		NC mimic			*MIR-7-5p* mimic		
		luciferase activity	Mean	SD	luciferase activity	Mean	SD
Figure S8c	NC	3.03	1.00	0.08	2.56	0.96	0.07
		2.73			2.53		
		2.58			2.89		
	HDAC7-AS1-WT	0.65	1.00	0.07	0.32	0.52	0.03
		0.57			0.35		
		0.65			0.31		
	HDAC7-AS1-MUT	0.16	1.00	0.10	0.16	1.34	0.67
		0.15			0.31		
		0.13			0.12		

Mean and SD values are the ones presented in Figure S8a-c. All data presented as fold difference relative to NC mimic. All data is expressed as luciferase activity (a.u.).

Table S24. The tube forming ability in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor.

		Control			PCB29-pQ		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure S9 (Right panel)	NC inhibitor	188.48	186.50	2.12	103.11	102.00	1.41
		186.73			102.49		
		184.29			100.41		
	MIR-7-5p inhibitor	208.41	220.50	12.02	186.33	167.00	16.97
		220.68			160.12		
		232.41			154.55		

Mean and SD values are the ones presented in Figure S9 (Right panel). Number of branch points is presented.

Table S25. *HDAC7-AS1*, *MIR-7-5p*, *TGF-β2*, *PPME1* levels and apoptosis or proliferation rates in HUVECs exposed to PCB29-pQ and transfected with a *MIR-7-5p* inhibitor or *HDAC7-AS1* siRNA.

	NC inhibitor + NC siRNA			NC inhibitor + NC siRNA + PCB29-pQ			NC inhibitor + *HDAC7-AS1* siRNA + PCB29-pQ			*MIR-7-5p* inhibitor + *HDAC7-AS1* siRNA + PCB29-pQ		
	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)	Cq values	Mean (normalized)	SD (normalized)
Figure S11a	24.00	1.00	0.02	22.95	2.07	0.05	20.55	3.50	0.25	23.43	1.82	0.60
	24.03			22.90			20.35			22.51		
	23.97			22.88			20.40			23.06		
Figure S11b	24.06	1.04	0.04	24.90	0.56	0.04	25.23	0.13	0.01	26.81	0.14	0.02
	24.11			24.75			25.23			26.51		
	23.99			24.90			25.12			26.81		
Figure S11c	24.04	1.00	0.06	24.96	0.57	0.09	24.26	0.28	0.02	24.48	0.73	0.12

	24.11			24.56			23.99			24.05		
	23.93			24.93			24.04			24.41		
Figure S11d	23.83	1.00	0.06	24.32	0.72	0.04	23.28	0.49	0.05	23.89	0.90	0.08
	23.95			24.32			23.05			23.77		
	24.00			24.44			23.28			24.02		

	NC inhibitor + NC siRNA			NC inhibitor + NC siRNA + PCB29-pQ			NC inhibitor + *HDAC7-AS1* siRNA + PCB29-pQ			*MIR-7-5p* inhibitor + *HDAC7-AS1* siRNA + PCB29-pQ		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S11f	26471.34	1.00	0.03	19404.29	0.75	0.04	8350.731	0.32	0.02	24470.19	0.61	0.04
	25571.42			18907.89			7680.765			23380.91		
	24789.01			17650.91			7690.97			21457.98		
Figure S11g	35445.87	1.00	0.00	29143.95	0.84	0.00	14331.22	0.42	0.00	31926.00	0.61	0.00
	35402.05			28836.87			14263.22			32072.82		
	35530.12			28979.22			14351.63			31968.29		

	NC inhibitor + NC siRNA			NC inhibitor + NC siRNA + PCB29-pQ			NC inhibitor + *HDAC7-AS1* siRNA + PCB29-pQ			*MIR-7-5p* inhibitor + *HDAC7-AS1* siRNA + PCB29-pQ		
	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)
Figure S11h	100.92	100.00	1.91	79.83	81.03	3.32	76.57	71.42	4.65	87.85	88.99	1.81

	97.81			84.78			67.54			91.08		
	101.27			78.47			70.15			88.04		

Mean and SD values are the ones presented in Figure S11a (mRNA expression of *MIR-7-5p*), b (mRNA expression of *HDAC7-AS1*), c (mRNA expression of *TGFβ-2*), and d (mRNA expression of *PPME1*), and f (protein expression of TGF-β2), g (protein expression of PPME1), and h (% cell viability). All data presented relative to NC inhibitor + NC siRNA.

Table S26. HE staining of aortic root cross-sections and total cholesterol (TC) and low-density lipoprotein (LDL) levels in *ApoE*$^{-/-}$ mice were *i.v.* injected with AAV-*HDAC7-AS1*.

	AAV-NC		AAV-NC + PCB29-pQ		AAV-*HDAC7-AS1*		AAV-*HDAC7-AS1* + PCB29-pQ	
	Mean	SD	Mean	SD	Mean	SD	Mean	SD
Figure S12a (Right panel)	14.35	0.81	26.81	3.78	9.71	1.62	14.17	2.52
	Individual values		Individual values		Individual values		Individual values	
	13.49		22.44		11.18		17.05	
	14.46		29.09		9.96		13.09	
	15.09		28.89		7.98		12.38	
Figure S12b	31.60	6.03	70.40	11.89	32.20	9.83	47.60	9.32
	Individual values		Individual values		Individual values		Individual values	
	36		68		26		43	
	39		69		34		41	
	28		74		47		55	
	24		87		21		60	
	31		54		33		39	
Figure S12c	246.6	58.22	336.6	42.74	165.2	40.77	231.4	46.98

	Individual values	Individual values	Individual values	Individual values
	267	310	211	187
	210	330	103	198
	201	352	190	208
	340	401	165	288
	215	290	157	276

Mean and SD values are the ones presented in Figure S12a (Right panel) and Figure S12a (plaque area relative to aortic section), b (TC; mmol/l), and c (LDL; mmol/l).

Table S27. TGF-β2, PPME1, and inflammatory factors level in HUVECs exposed to PCB29-pQ with or without *CAV1* siRNA.

	0 h			1 h			3 h			6 h		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S13a (p-CAV1)	3549.91	1.00	0.01	14419.75	3.63	0.01	21891.17	6.43	0.06	41060.31	12.76	0.05
	3551.91			14458.87			22463.19			40411.36		
	3544.50			14511.00			22130.58			40784.65		
Figure S13a (CAV1)	35207.65			39533.43			34135.36			31824.58		
	35245.36			39410.19			34430.60			31567.80		
	35224.65			39808.55			34124.48			31747.80		

	NC siRNA			NC siRNA + PCB29-pQ			*CAV1* siRNA			*CAV1* siRNA + PCB29-pQ		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S13c (p-CAV1)	20472.92	1.05	0.00	29074.26	1.65	0.01	8883.024	0.42	0.01	6454.782	0.32	0.01
	20411.51			29425.33			8531.782			6442.782		
	20471.34			29228.50			8789.317			6219.468		
Figure S13c (CAV1)	36333.41			38767.5			16916.46			10561.56		
	36998.02			38129.48			17327.41			10408.2		
	36895.19			38340.43			17230.58			10447.02		
Figure S13d	24553.22	1.00	0.00	12233.54	0.55	0.01	34677.92	1.33	0.01	31960.07	1.29	0.00
	24553.22			12233.54			34618.22			31996.07		
	24478.97			12233.54			34383.39			32146.77		
Figure S13e	28310.29	1.00	0.01	20444.51	0.80	0.01	27711.29	0.92	0.00	21154.87	0.74	0.00
	27989.63			20778.41			27671.17			21232.24		
	28526.24			20288.1			27720.41			21147.29		
Figure S13f	6365.974	1.00	0.02	29456.14	5.12	0.12	5738.782	0.85	0.02	8396.974	1.30	0.03
	6527.317			30621.72			6009.317			8674.924		

	6636.388			30772.26			5790.782			8691.338		
Figure S13g	12188.66	1.00	0.03	32999.77	3.17	0.23	21290.05	1.63	0.02	2204.359	0.19	0.01
	12851.49			37559.54			21818.55			2515.648		
	12532.95			37660.01			21875.55			2496.406		
Figure S13h	24172.53	1.00	0.00	35359.97	1.61	0.00	23666.02	0.92	0.00	28610.48	1.16	0.00
	24116.24			35383.38			23714.26			28470.24		
	24332.89			35253.43			23805.09			28493.41		

Mean and SD values are the ones presented in Figure S13a (Lower panel; p-CAV1/CAV1 ratio after treatment with PCB29-pQ for 0, 1, 3, or 6h, no *CAV1* siRNA) and Figure c (p-CAV/CAV ratio), d (TGF-β2), e (PPME1), f (IL-1β), g (IL-6), and h (TNF-α). Data for c-h were normalized to β-actin expression and presented as fold difference compared to NC siRNA.

Table S28. Pearson's correlation coefficient for expression of **p-CAV1** and CD31 **in *ApoE*$^{-/-}$ mice that were *i.v.* injected with AAV-*HDAC7-AS1*.**

	AAV-NC			AAV-NC + PCB29-pQ			AAV-*HDAC7-AS1*			AAV-*HDAC7-AS1* + PCB29-pQ		
	Individual values	Mean	SD	Individual values	Mean	SD	Individual values	Mean	SD	Individual values	Mean	SD
Figure S14 (Right panel)	0.35	0.43	0.07	0.92	0.93	0.04	0.02	0.02	0.02	0.17	0.31	0.12
	0.47			0.98			0.01			0.38		
	0.48			0.90			0.05			0.38		

	12943.66			20477.39			28475.48			37683.36		
	12634.66			20457.39			28444.24			37516.89		

Mean and SD values are the ones presented in Figure S14 (Right panel).

Table S29. Immunohistochemistry staining of CD68, total cholesterol (TC), and low-density lipoprotein level (LDL) in *ApoE*$^{-/-}$ and *ApoE*$^{-/-}$/*CAV1*$^{-/-}$ mice.

		ApoE$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure S16a (Right panel)	Control	19.85	16.00	3.35	6.33	7.88	2.17
		14.40			6.94		
		13.75			10.35		
	PCB29-pQ	21.76	20.86	2.19	15.48	12.38	2.83
		22.45			11.70		
		18.36			9.95		

		ApoE$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure S16b	Control	39.00	31.80	6.22	25.00	33.80	5.63
		32.00			39.00		
		29.00			32.00		
		23.00			38.00		
		36.00			35.00		
	PCB29-pQ	69.00	71.80	10.57	42.00	46.20	6.14
		74.00			39.00		
		85.00			45.00		

		56.00			52.00		
		75.00			53.00		

		ApoE$^{-/-}$			*ApoE*$^{-/-}$/*CAV1*$^{-/-}$		
		Individual values	Mean	SD	Individual values	Mean	SD
Figure S16c	Control	268.00	207.40	77.72	301.00	275.60	40.937
		126.00			301.00		
		206.00			206.00		
		136.00			299.00		
		301.00			271.00		
	PCB29-pQ	543.00	510.20	52.47	405.00	396.80	44.59
		571.00			321.00		
		432.00			401.00		
		501.00			436.00		
		504.00			421.00		

Mean and SD values are the ones presented in Figure S16a (Right panel;), b (TC, mmol/l), and c (LDL, mmol/l).

Table S30. Adhesion molecules, pro-inflammatory cytokines and *p65* protein expression level in HUVEC exposed to PCB29-pQ.

	0 h			1 h			3 h			6 h		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S17b	21710.31	1.00	0.02	32831.89	1.37	0.00	35262.31	1.53	0.01	34571.68	1.58	0.02
	22002.72			33634.02			35212.19			34389.10		
	22448.72			33584.48			34742.26			34622.68		

Figure S17c	5039.54	1.00	0.01	18047.31	3.63	0.04	26252.14	5.05	0.16	37682.02	6.42	0.13
	5142.37			17668.19			26381.60			38094.14		
	5138.37			17703.19			27830.45			36646.00		
Figure S17d	13157.73	1.00	0.03	29704.43	2.31	0.02	31683.31	2.39	0.04	41349.53	2.76	0.02
	13400.10			29558.07			31253.95			41482.58		
	12635.20			30513.92			31385.89			40789.29		
Figure S17e	16167.24	1.00	0.02	17999.00	1.19	0.01	26253.14	1.59	0.01	32660.29	1.79	0.00
	16070.17			18002.41			26429.67			32522.17		
	15514.68			18385.89			26264.26			32662.29		
Figure S17f	9014.22	1.00	0.03	20417.84	2.39	0.04	24193.53	2.63	0.04	35338.87	3.48	0.03
	8564.20			19950.19			24735.14			35652.00		
	9080.63			20655.31			24087.82			34981.51		
Figure S17i	12851.66	1.00	0.01	20475.39	1.69	0.06	28455.95	2.47	0.06	37633.19	3.40	0.01
	12943.66			20477.39			28475.48			37683.36		
	12634.66			20457.39			28444.24			37516.89		
Figure S17j	31806.92	1.00	0.00	25913.87	0.84	0.00	11533.10	0.40	0.02	11508.73	0.39	0.00

	31920.92			25681.92			11297.73			11025.27		
	31736.92			25889.75			11409.44			10419.42		

	Control			PCB29-pQ		
	Individual values	Mean (normalized)	SD (normalized)	Individual values	Mean (normalized)	SD (normalized)
Figure S17g (Right panel)	6.15	4.94	1.18	17.99	15.27	2.71
	4.89			15.26		
	3.79			12.56		

	Control			PCB29-pQ			PDTC			PDTC + PCB29-pQ		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S17l	24902.37	1.00	0.00	37563.55	1.57	0.00	25411.1	1.29	0.00	33129.51	1.38	0.00
	24895.37			37531.84			25381.39			33175.92		
	24917.2			37384.19			25371.63			33020.92		
Figure S17m	7863.196	1.00	0.00	28066.72	3.72	0.00	12419.56	2.00	0.00	10033.95	1.32	0.00
	7853.782			28090.14			12406.85			9969.246		
	7863.196			28115.67			12380.32			10031.95		

Figure S17n	18254.39	1.00	0.00	30108.24	1.70	0.08	20426.8	1.41	0.00	15814.39	0.89	0.01
	18289.8			30100.24			20369.1			15725.15		
	18234.56			30089.24			20425.51			15602.02		

Mean and SD values are the ones presented in Figure S17b (IL-1β), c (IL-6), d (TNFα), e (ICAM-1), f (VCAM-1), g (The fluorescence intensity of Calcein-AM) (a.u.), i (p-p65/p65 ratio), j (IκBα), l (IL-1β), m (IL-6), and n (TNF-α). Data in b-e normalized to β-actin and presented as fold difference compared to 0 h control. Data in i presented as fold difference compared to 0 h. Data in j normalized to β-actin and presented as fold difference compared to 0 h. Data in l-n normalized to β-actin and presented as fold difference compared to control.

Table S31. Adhesion molecules, pro-inflammatory cytokines and p65 protein expression levels in HUVEC exposed to PCB29-pQ with *CAV1* siRNA.

	NC siRNA			NC siRNA + PCB29-pQ			*CAV1* siRNA			*CAV1* siRNA + PCB29-pQ		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S18b	30214.87	1.00	0.02	37211.05	1.24	0.02	23534.58	0.81	0.03	23260.63	0.86	0.03
	30368.41			38160.58			24974.92			24800.87		
	31474.41			38190.24			24898.73			24913.41		

Figure S18c	27480.92	1.00	0.01	33946.92	1.24	0.01	25009.53	0.91	0.01	13017.08	0.51	0.00
	27800.12			33688.38			24770.82			13238.20		
	27472.05			34324.87			24471.58			13060.37		
Figure S18d	16321.92	1.00	0.01	30156.51	1.87	0.00	14698.73	0.92	0.00	13659.00	0.91	0.01
	16318.75			30156.51			14738.73			13695.71		
	16022.02			30156.51			14686.73			13699.00		
Figure S18e	24843.80	1.00	0.00	34943.65	1.43	0.00	33345.68	1.36	0.01	19715.92	0.87	0.00
	24493.92			35010.12			33010.68			19912.63		
	24677.87			35044.12			32993.15			19799.51		
Figure S18f	16432.29	1.00	0.01	29701.36	1.83	0.00	16065.10	0.79	0.00	14917.08	0.99	0.01
	16188.22			29686.65			16100.63			15005.20		
	16438.29			29721.77			16100.63			14972.78		
Figure S18h	3963.368	1.00	0.01	7330.66	1.42	0.10	25073.10	0.17	0.00	28151.45	0.29	0.00
	4098.439			7178.832			24649.32			28219.50		
	4134.196			7261.953			24475.80			27942.84		
Figure S18j	21031.05	1.00	0.02	12072.82	0.53	0.02	30701.04	1.44	0.00	18197.58	0.84	0.01

	21909.72			11440.39			30541.67			18714.48		
	21875.14			11506.80			30697.50			18468.00		

	0 h			1 h			3 h			6 h		
	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)	Grayscale values	Mean (normalized)	SD (normalized)
Figure S18j (Right panel)	0.07	0.08	0.01	0.72	0.83	0.09	0.01	0.05	0.03	0.17	0.23	0.06
	0.08			0.88			0.07			0.28		
	0.10			0.90			0.08			0.24		

Mean and SD values are the ones presented in Figure S18b (IL-1β), c (IL-6), d (TNF-α), e (ICAM-1), f (VCAM-1), h (p-p65/p65 ratio), I (IκBα), and j (Pearson's coefficient). Data in c-f and i normalized to β-actin and presented as fold difference compared to NC siRNA. Data in h presented as fold difference compared to NC siRNA.

Table S32. Protein expression of inflammatory factors and ROS levels in HUVEC exposed to PCB29-pQ.

	Control	PCB29-pQ	PCB29-pQ + VC	PCB29-pQ + VE	PCB29-pQ + NAC
Figure S19b	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	13974.88	14314.47	6892.91	4899.10	6949.18
	12348.40	14314.47	6892.91	4899.10	6954.59
	13750.64	14314.47	6892.91	4899.10	6949.18
Figure S19c	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	15912.10	21827.13	11045.47	12279.83	16616.30
	15863.28	22036.83	11003.47	12345.83	16551.59
	15839.98	21941.25	11018.93	12351.83	16497.59

Figure S19d	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	16573.56	23407.17	16591.27	20362.92	15709.90
	16479.90	23292.87	16712.22	20046.56	16281.73
	16693.39	23259.34	16577.97	20474.51	15738.20
Figure S19e	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	24377.20	27848.27	9483.76	19209.90	16895.78
	24422.78	27853.27	9527.47	19147.08	16898.95
	24457.78	27858.27	9443.76	19198.78	16931.78
Figure S19f	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	20508.34	3491.42	24095.95	22248.27	506.34
	20143.15	3515.83	24081.41	22567.15	494.34
	20916.39	3403.59	23976.77	22010.61	506.34
Figure S19g	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	8957.13	11376.25	7745.71	4248.71	9647.69
	9396.02	10545.05	7818.54	4345.42	9577.69
	9970.21	10050.10	7784.83	4246.42	9650.40

	Control	PCB29-pQ	PCB29-pQ + VC	PCB29-pQ + VE	PCB29-pQ + NAC
Figure S19h	Fluorescence values	Fluorescence values	Fluorescence values	Fluorescence values	Fluorescence values
	1001.23	1391.82	1121.46	961.25	1041.36
	1001.37	1361.78	1171.53	901.18	1081.41
	1001.31	1351.76	1031.35	901.18	1091.42

	Control		PCB29-pQ		PCB29-pQ + VC		PCB29-pQ + VE		PCB29-pQ + NAC	
	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)
Figure S19b	1.00	0.07	1.36	0.06	0.58	0.02	0.39	0.02	0.60	0.01

Figure S19c	1.00	0.00	1.71	0.01	0.74	0.00	0.82	0.00	1.20	0.00
Figure S19d	1.00	0.01	1.74	0.01	1.07	0.00	1.29	0.01	1.10	0.02
Figure S19e	1.00	0.00	1.41	0.10	0.41	0.00	0.83	0.00	0.79	0.00
Figure S19f	1.00	0.02	1.25	0.00	0.21	0.00	0.14	0.01	0.03	0.00
Figure S19g	1.00	0.05	1.40	0.09	0.88	0.00	0.48	0.01	1.17	0.01
Figure S19h	1.00	0.07	1.37	0.02	1.11	0.07	0.92	0.03	1.07	0.03

Mean and SD values are the ones presented in Figure S19b (p-65/p65 ratio), c (IL-1β), d (IL-6), e (TNF-α), f (ICAM-1), g (VCAM-1), and h (ROS level). Data in c-g are normalized to β-actin. All data presented as fold difference relative to control.

Table S33. p-CAV1 protein expression relative to CAV1 total protein in HUVEC exposed to PCB29-pQ and antioxidants.

	Control		PCB29-pQ		PCB29-pQ + VC		PCB29-pQ + VE		PCB29-pQ + NAC	
	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)
Figure	1.00	0.03	2.02	0.03	0.82	0.06	0.42	0.02	0.95	0.03

S20a (Right panel)										

	Control		PCB29-pQ		PCB29-pQ + PEG-CAT		PCB29-pQ + PEG-SOD		PCB29-pQ + GSH-MEE	
	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)	Mean (normalized)	SD (normalized)
Figure S20b (Right panel)	1.00	0.17	20.01	0.32	8.35	0.16	9.23	0.16	4.64	0.11

	Control	PCB29-pQ	PCB29-pQ + VC	PCB29-pQ + VE	PCB29-pQ + NAC
Figure S20a (p-CAV1)	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	13410.85	27941.75	11037.39	4832.47	10080.42
	13993.92	27406.58	10979.39	5269.59	9641.52
	13638.61	28534.65	9943.78	5056.23	9682.05
Figure S20a (CAV1)	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	30972.85	31152.49	28496.59	27020.02	22916.02
	30766.20	30912.78	29202.61	26508.83	23050.15
	30282.13	31115.78	29372.49	26523.42	23198.27

	Control	PCB29-pQ	PCB29-pQ + PEG-CAT	PCB29-pQ + PEG-SOD	PCB29-pQ + GSH-MEE
Figure S20b (p-CAV1)	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	1181.16	30552.43	11266.49	12159.02	6742.50

	981.63	31232.09	11089.49	12099.44	6548.62
	1374.41	30331.07	10787.42	12484.56	6891.33
Figure S20b (CAV1)	Grayscale values	Grayscale values	Grayscale values	Grayscale values	Grayscale values
	22054.73	28945.39	24954.80	24981.15	27437.22
	22386.22	28874.73	24947.92	24977.61	27180.97
	22204.80	28874.44	24811.39	24980.73	27335.80

Mean and SD values are the ones presented in Figure S20a and b. Data presented as fold difference relative to control.