

Supplementary Table S1. Sequences of primers used for RT-qPCR.

Gene	Forward primer	Reverse primer
<i>IL1R1</i>	GGCTGAAAAGCATAGAGGGAAC	CTGGGCTCACAATCACAGG
<i>TNFRSF1A</i>	CCAGGAGAAACAGAACACCGT	AAACCAATGAAGAGGAGGGATAA
<i>TNFRSF1B</i>	GTCCACACGATCCCAACAC	CACACCCACAATCAGTCCAA
<i>IL1B</i>	TGGCTTATTACAGTGGCAATG	GTGGTGGTCGGAGATTCTG
<i>IL6</i>	GGCACTGGCAGAAAAACAACC	GCAAGTCTCCTCATTGAATCC
<i>CXCL8</i>	CAGAGACAGCAGAGCACAC	AGTTCTTTAGCACTCCTTGGC
<i>CCL2</i>	TTCTGTGCCCTGCTGCTCATAG	AGGTGACTGGGGCATTGATTG
<i>ACTA2</i>	GTGTTGCCCCCTGAAGAGCAT	GCTGGGACATTGAAAGTCTCA
<i>SMTN</i>	GGGATCGTGTCCACAAGTTCA	GCTACTCCTCGTTGCTCCTT
<i>VIM</i>	CGCCAGATGCGTGAAATGG	ACCAGAGGGAGTGAATCCAGA
<i>COL1A1</i>	GTCACCCACCGACCAAGAAACC	AAGTCCAGGCTGTCCAGGGATG
<i>COL1A2</i>	CCCCTGGTATGACTGGTTTCCC	GTCACCACGAGGACCACGAA
<i>COL4A1</i>	GGACTACCTGGAACAAAAGGG	GCCAAGTATCTCACCTGGATCA
<i>MMP2</i>	CCGTGTTTGCCATCTGTTTTAG	AGGTTCTCTTGCTGTTTACTTTGGA
<i>RUNX2</i>	AGATGGACCTCGGGAACCCA	TGAGGCGGGACACCTACTCT
<i>SOX9</i>	ACCAGTACCCGCACTTGCACA	CGCTTCTCGCTCTCGTTCAGAAGT

Supplementary Table S2. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in cytosol of human coronary artery endothelial cells (HCAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Hydrolase (UniProtKB Keywords)	17	17.5	1.9	3.8×10^{-1}
Innate immune system (Reactome)	15	15.5	2.0	1.4×10^{-1}
Cytokine signaling in immune system (Reactome)	14	14.4	2.8	4.8×10^{-2}
Ubiquitin-dependent protein catabolic process (GO BP)	9	9.3	6.4	4.4×10^{-2}
Apoptosis (UniProtKB Keywords)	9	9.3	2.6	1.2×10^{-1}
Ubiquitin protein ligase binding (GO MF)	8	8.2	5.1	3.6×10^{-2}
Signaling by interleukins (Reactome)	8	8.2	2.4	2.7×10^{-1}
Protein ubiquitination (GO BP)	7	7.2	3.1	8.7×10^{-1}
Programmed cell death (Reactome)	6	6.2	4.1	1.6×10^{-1}
Signaling by VEGF (Reactome)	5	5.2	6.7	9.5×10^{-2}
Chemokine signaling pathway (KEGG)	5	5.2	3.7	3.1×10^{-1}
Ca-dependent events (Reactome)	4	4.1	14.8	5.2×10^{-2}
VEGFA-VEGFR2 pathway (Reactome)	4	4.1	5.8	2.3×10^{-1}
Positive regulation of cell migration involved in sprouting angiogenesis (GO BP)	3	3.1	17.3	8.7×10^{-1}
Intrinsic apoptotic signaling pathway (GO BP)	3	3.1	16.9	8.7×10^{-1}
Downregulated after CPP-P treatment				
Metabolism of RNA (Reactome)	39	16.6	3.5	8.0×10^{-9}
Cadherin binding (GO MF)	35	14.9	9.0	3.9×10^{-20}
Cell cycle, mitotic (Reactome)	19	8.1	2.2	1.7×10^{-2}
mRNA processing (UniProtKB Keywords)	17	7.2	3.5	3.7×10^{-4}
Negative regulation of apoptotic process (GO BP)	17	7.2	2.8	3.2×10^{-2}
mRNA splicing (UniProtKB Keywords)	15	6.4	4.0	3.7×10^{-4}
mRNA transport (UniProtKB Keywords)	14	6.0	10.0	7.4×10^{-8}
Mitotic metaphase and anaphase (Reactome)	14	6.0	3.8	2.0×10^{-3}
Eukaryotic translation initiation (Reactome)	11	4.7	5.9	7.3×10^{-4}

Eukaryotic translation elongation (Reactome)	8	3.4	5.5	8.6×10^{-3}
Eukaryotic translation termination (Reactome)	8	3.4	5.5	8.6×10^{-3}
Ribosome (KEGG)	8	3.4	3.2	1.8×10^{-1}
Cell-cell adhesion (GO BP)	8	3.4	3.5	2.9×10^{-1}
Tight junction (KEGG)	8	3.4	3.2	1.8×10^{-1}
Cadherin binding involved in cell-cell adhesion (GO MF)	3	1.3	13.6	2.4×10^{-1}

Supplementary Table S3. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in cytosol of human coronary artery endothelial cells (HCAEC) treated with either secondary CPPs (CPP-S) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-S treatment				
Hydrolase (UniProtKB Keywords)	20	18.7	1.9	4.3×10^{-2}
Cytokine signaling in immune system (Reactome)	16	15.0	3.0	2.9×10^{-2}
Signaling by interleukins (Reactome)	10	9.3	2.9	1.5×10^{-1}
Ubiquitin-dependent protein catabolic process (GO BP)	7	6.5	4.4	7.7×10^{-1}
Ubiquitin protein ligase binding (GO MF)	6	5.6	3.4	7.6×10^{-1}
Chemokine signaling pathway (KEGG)	6	5.6	3.6	1.3×10^{-1}
Signaling by VEGF (Reactome)	5	4.7	6.3	1.5×10^{-1}
Toll like receptor 4 (TLR4) cascade (Reactome)	5	4.7	4.6	2.4×10^{-1}
Apoptosis (KEGG)	5	4.7	4.2	1.4×10^{-1}
Ca-dependent events (Reactome)	4	3.7	13.9	1.0×10^{-1}
MyD88 cascade initiated on plasma membrane (Reactome)	4	3.7	5.6	2.5×10^{-1}
VEGFA-VEGFR2 pathway (Reactome)	4	3.7	5.5	2.6×10^{-1}
MyD88 dependent cascade initiated on endosome (Reactome)	4	3.7	5.2	2.7×10^{-1}
Intrinsic apoptotic signaling pathway (GO BP)	3	2.8	15.1	9.5×10^{-1}
Cellular response to reactive oxygen species (GO BP)	3	2.8	10.9	9.7×10^{-1}
Downregulated after CPP-S treatment				
Metabolism of RNA (Reactome)	45	20.7	4.4	9.4×10^{-15}
Cadherin binding (GO MF)	30	13.8	8.4	3.1×10^{-16}
mRNA processing (UniProtKB Keywords)	24	11.1	5.3	3.1×10^{-9}
Negative regulation of apoptotic process (GO BP)	17	7.8	3.0	1.6×10^{-2}
Cell cycle, mitotic (Reactome)	17	7.8	2.1	2.1×10^{-2}
mRNA transport (UniProtKB Keywords)	13	6.0	10.0	1.6×10^{-7}
RNA splicing (GO BP)	13	6.0	5.8	5.4×10^{-4}
rRNA processing (Reactome)	12	5.5	4.1	1.8×10^{-3}
Mitotic metaphase and anaphase (Reactome)	12	5.5	3.6	4.9×10^{-3}
Eukaryotic translation initiation (Reactome)	10	4.6	5.9	8.3×10^{-4}
Eukaryotic translation termination (Reactome)	9	4.1	6.7	8.3×10^{-4}
Eukaryotic translation elongation (Reactome)	9	4.1	6.7	8.3×10^{-4}
Ribosome (KEGG)	9	4.1	4.0	4.2×10^{-2}
Mitotic prophase (Reactome)	7	3.2	3.5	4.3×10^{-2}
Cell-cell adhesion (GO BP)	7	3.2	3.3	5.6×10^{-1}

Supplementary Table S4. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in cytosol of human internal thoracic artery endothelial cells (HITAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Immune system (Reactome)	15	38.5	2.4	2.1×10^{-1}
Innate immune system (Reactome)	10	25.6	3.0	3.0×10^{-1}
Cytokine signaling in immune system (Reactome)	7	17.9	3.1	1.0×10^{-1}
Signaling by VEGF (Reactome)	4	10.3	11.9	3.0×10^{-1}
Angiogenesis (GO BP)	4	10.3	7.8	8.2×10^{-1}
Positive regulation of cell migration (GO BP)	4	10.3	7.6	8.2×10^{-1}
VEGF signaling pathway (KEGG)	3	7.7	21.5	3.9×10^{-1}
Regulation of cell shape (GO BP)	3	7.7	10.0	1.0×10^{-1}
VEGFA-VEGFR2 pathway (Reactome)	3	7.7	9.8	1.0×10^{-1}
Positive regulation of NF- κ B transcription factor activity (GO BP)	3	7.7	9.1	1.0×10^{-1}
Vascular endothelial growth factor binding (GO MF)	2	5.1	194.3	2.0×10^{-1}
Neutrophil interactions with VEGF and VEGFR (Reactome)	2	5.1	161.1	7.7×10^{-1}
Vascular endothelial growth factor-activated receptor activity (GO MF)	2	5.1	121.4	2.5×10^{-1}
Substrate-dependent cell migration, cell extension (GO BP)	2	5.1	110.6	8.4×10^{-1}
Cell migration involved in sprouting angiogenesis (GO BP)	2	5.1	47.4	1.0×10^{-1}
Calcium-mediated signaling using intracellular calcium source (GO BP)	2	5.1	43.3	1.0×10^{-1}
Downregulated after CPP-P treatment				
Cadherin binding (GO MF)	18	16.5	10.1	2.1×10^{-10}
Metabolism of RNA (Reactome)	12	11.0	2.6	1.0×10^{-1}
mRNA binding (GO MF)	11	10.1	7.8	7.9×10^{-5}
Actin-binding (UniProtKB Keywords)	10	9.2	5.5	1.3×10^{-3}
mRNA 3'-UTR binding (GO MF)	9	8.3	6.5	3.2×10^{-3}
Negative regulation of apoptotic process (GO BP)	9	8.3	3.2	8.5×10^{-1}
Cell adhesion (UniProtKB Keywords)	9	8.3	3.0	1.7×10^{-1}
mRNA transport (UniProtKB Keywords)	6	5.5	8.6	3.4×10^{-2}
Transcription cofactor activity (GO MF)	6	5.5	7.6	4.6×10^{-2}
Cell-cell adhesion (GO BP)	6	5.5	5.6	6.6×10^{-1}
Transcription, DNA-templated (GO BP)	6	5.5	5.6	6.6×10^{-1}
Negative regulation of translation (GO BP)	5	4.6	10.3	5.0×10^{-1}
Actin filament organization (GO BP)	5	4.6	5.9	8.5×10^{-1}
RNA splicing (GO BP)	5	4.6	4.4	1.0×10^{-1}
Regulation of mRNA stability (GO BP)	4	3.7	11.8	6.6×10^{-1}

Supplementary Table S5. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in cytosol of human internal thoracic artery endothelial cells (HITAEC) treated with either secondary CPPs (CPP-S) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-S treatment				
Hydrolase (GO MF)	10	21.3	2.5	2.6×10^{-1}
Cytokine signaling in immune system (Reactome)	8	17.0	3.3	1.0×10^{-1}

Necroptosis (KEGG)	4	8.5	10.6	3.4×10^{-1}
Programmed cell death (Reactome)	4	8.5	5.7	1.0×10^{-1}
Positive regulation of apoptotic process (GO BP)	4	8.5	5.3	9.1×10^{-1}
VEGF signaling pathway (KEGG)	3	6.4	21.5	3.4×10^{-1}
Macroautophagy (GO BP)	3	6.4	18.8	9.1×10^{-1}
Signaling by VEGF (Reactome)	3	6.4	8.5	1.0×10^{-1}
Regulation of early endosome to late endosome transport (GO BP)	2	4.3	95.9	9.1×10^{-1}
Substrate-dependent cell migration, cell extension (GO BP)	2	4.3	95.9	9.1×10^{-1}
Downregulated after CPP-S treatment				
RNA binding (GO MF)	32	34.4	4.4	2.0×10^{-10}
Metabolism of proteins (Reactome)	21	22.6	1.5	8.4×10^{-1}
Cadherin binding (GO MF)	14	15.1	9.0	4.5×10^{-7}
Metabolism of RNA (Reactome)	14	15.1	2.8	1.5×10^{-1}
Cell cycle (UniProtKB Keywords)	10	10.8	2.2	2.8×10^{-1}
Cell adhesion (UniProtKB Keywords)	9	9.7	2.7	2.5×10^{-1}
Positive regulation of transcription, DNA-templated (GO BP)	9	9.7	2.6	1.0×10^{-1}
Apoptosis (UniProtKB Keywords)	9	9.7	2.5	2.5×10^{-1}
Negative regulation of apoptotic process (GO BP)	8	8.6	3.2	1.0×10^{-1}
Mitosis (UniProtKB Keywords)	6	6.5	3.1	2.8×10^{-1}
Protein stabilization (GO BP)	5	5.4	4.6	1.0×10^{-1}
Transcription coactivator activity (GO MF)	5	5.4	3.8	5.7×10^{-1}
ER-Golgi transport (UniProtKB Keywords)	4	4.3	6.3	2.5×10^{-1}
Mitotic cell cycle (GO BP)	4	4.3	5.5	1.0×10^{-1}
Stem cell division (GO BP)	2	2.2	59.6	1.0×10^{-1}

Supplementary Table S6. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in cytosol of human internal thoracic artery endothelial cells (HITAEC) treated with either primary CPPs (CPP-P) or secondary CPPs (CPP-S).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Hydrolase (UniProtKB Keywords)	14	24.6	2.2	1.2×10^{-1}
Vesicle-mediated transport (Reactome)	10	17.5	3.5	6.9×10^{-2}
Ubiquitin-dependent protein catabolic process (GO BP)	6	10.5	7.1	1.6×10^{-1}
Deubiquitination (Reactome)	6	10.5	4.7	2.1×10^{-1}
Protease (UniProtKB Keywords)	6	10.5	3.0	3.4×10^{-1}
Ub-specific processing proteases (Reactome)	5	8.8	5.3	2.4×10^{-1}
Protein ubiquitination (GO BP)	5	8.8	3.7	9.3×10^{-1}
Cysteine-type endopeptidase activity (GO MF)	4	7.0	13.3	9.6×10^{-2}
ER to Golgi anterograde transport (Reactome)	4	7.0	6.1	3.7×10^{-1}
Transport to the Golgi and subsequent modification (Reactome)	4	7.0	5.0	4.7×10^{-1}
Monoubiquitinated protein deubiquitination (GO BP)	3	5.3	127.7	1.2×10^{-1}
Ubiquitinyl hydrolase activity (GO MF)	3	5.3	76.7	3.9×10^{-2}
Lys48-specific deubiquitinase activity (GO MF)	3	5.3	55.4	5.7×10^{-2}
Golgi associated vesicle biogenesis (Reactome)	3	5.3	12.5	3.3×10^{-1}
trans-Golgi network vesicle budding (Reactome)	3	5.3	9.7	4.7×10^{-1}
Upregulated after CPP-S treatment				
Metabolism of RNA (Reactome)	9	13.6	2.9	1.0×10^{-1}
mRNA splicing (UniProtKB Keywords)	6	9.1	6.6	6.5×10^{-2}
mRNA processing (UniProtKB Keywords)	6	9.1	5.1	9.8×10^{-2}
mRNA 3'-UTR binding (GO MF)	5	7.6	5.9	2.7×10^{-1}

mRNA binding (GO MF)	5	7.6	5.8	2.7×10^{-1}
Programmed cell death (Reactome)	5	7.6	5.5	1.0×10^{-1}
Positive regulation of apoptotic process (GO BP)	5	7.6	4.7	1.0×10^{-1}
Negative regulation of translation (GO BP)	4	6.1	13.8	5.5×10^{-1}
Apoptosis (Reactome)	4	6.1	5.2	1.0×10^{-1}
mRNA transport (UniProtKB Keywords)	3	4.5	10.7	1.0×10^{-1}

Supplementary Table S7. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclei of human coronary artery endothelial cells (HCAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Cytokine signaling in immune system (Reactome)	12	15.4	2.9	6.0×10^{-2}
DNA repair (Reactome)	10	12.8	5.4	1.6×10^{-2}
Ubiquitin-dependent protein catabolic process (GO BP)	9	11.5	7.9	7.6×10^{-3}
Ubiquitin protein ligase binding (GO MF)	9	11.5	7.0	1.7×10^{-3}
Protein ubiquitination (GO BP)	8	10.3	4.3	2.4×10^{-1}
Apoptosis (UniProtKB Keywords)	8	10.3	2.6	1.8×10^{-1}
DNA damage (UniProtKB Keywords)	7	9.0	3.0	1.8×10^{-1}
Apoptotic process (GO BP)	7	9.0	2.9	9.2×10^{-1}
Signaling by interleukins (Reactome)	7	9.0	2.7	3.7×10^{-1}
Chemokine signaling pathway (KEGG)	5	6.4	4.2	1.5×10^{-1}
Ubiquitin mediated proteolysis (KEGG)	5	6.4	5.6	9.2×10^{-2}
Ca-dependent events (Reactome)	4	5.1	18.4	5.0×10^{-2}
VEGFA-VEGFR2 pathway (Reactome)	4	5.1	7.3	2.0×10^{-1}
Signaling by VEGF (Reactome)	4	5.1	6.7	2.2×10^{-1}
Intrinsic apoptotic signaling pathway (GO BP)	3	3.8	21.0	4.6×10^{-1}
Downregulated after CPP-P treatment				
Metabolism of RNA (Reactome)	69	37.3	7.4	1.6×10^{-40}
mRNA processing (UniProtKB Keywords)	52	28.1	10.9	5.3×10^{-38}
mRNA splicing (UniProtKB Keywords)	46	24.9	12.5	5.3×10^{-36}
Gene expression (Transcription) (Reactome)	37	20.0	1.8	4.0×10^{-3}
Cell cycle, mitotic (Reactome)	18	9.7	2.5	1.1×10^{-2}
mRNA transport (UniProtKB Keywords)	17	9.2	12.3	7.4×10^{-12}
Positive regulation of transcription, DNA-templated (GO BP)	17	9.2	2.5	4.9×10^{-2}
Cadherin binding (GO MF)	13	7.0	4.2	2.9×10^{-3}
Negative regulation of apoptotic process (GO BP)	13	7.0	2.7	1.1×10^{-1}
Mitotic metaphase and anaphase (Reactome)	12	6.5	3.9	4.1×10^{-3}
mRNA surveillance pathway (KEGG)	11	5.9	9.8	4.8×10^{-6}
Mitotic prophase (Reactome)	9	4.9	4.9	6.7×10^{-3}
Cell cycle checkpoints (Reactome)	9	4.9	2.4	1.7×10^{-1}
Assembly of the pre-replicative complex (Reactome)	8	4.3	4.3	2.3×10^{-2}
DNA replication (Reactome)	8	4.3	3.3	7.7×10^{-2}

Supplementary Table S8. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclei of human coronary artery endothelial cells (HCAEC) treated with either secondary CPPs (CPP-S) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-S treatment				
Hydrolase (UniProtKB Keywords)	13	17.1	1.8	7.0×10^{-1}
Cytokine signaling in immune system (Reactome)	12	15.8	3.1	4.7×10^{-2}
Ubiquitin-dependent protein catabolic process (GO BP)	8	10.5	7.1	2.2×10^{-2}
Protein ubiquitination (GO BP)	8	10.5	4.4	1.8×10^{-1}
Signaling by interleukins (Reactome)	8	10.5	3.2	1.2×10^{-1}
Apoptosis (UniProtKB Keywords)	8	10.5	2.8	1.6×10^{-1}
Apoptotic process (GO BP)	7	9.2	2.9	8.5×10^{-1}
Chemokine signaling pathway (KEGG)	6	7.9	5.3	2.0×10^{-2}
Toll like receptor 4 (TLR4) cascade (Reactome)	5	6.6	6.5	1.0×10^{-1}
Positive regulation of apoptotic process (GO BP)	5	6.6	3.9	8.5×10^{-1}
Intrinsic apoptotic signaling pathway (GO BP)	4	5.3	28.4	4.9×10^{-2}
Ca-dependent events (Reactome)	4	5.3	19.4	4.5×10^{-2}
Signaling by VEGF (Reactome)	4	5.3	7.0	1.5×10^{-1}
Cellular response to reactive oxygen species (GO BP)	3	3.9	15.3	6.0×10^{-1}
Cellular response to hydrogen peroxide (GO BP)	3	3.9	11.8	7.9×10^{-1}
Downregulated after CPP-S treatment				
Metabolism of RNA (Reactome)	86	44.3	8.8	1.8×10^{-59}
mRNA processing (UniProtKB Keywords)	63	32.5	12.1	4.7×10^{-50}
mRNA splicing (UniProtKB Keywords)	55	28.4	13.6	4.5×10^{-46}
Gene expression (Transcription) (Reactome)	44	22.7	2.1	2.6×10^{-5}
Cell cycle, mitotic (Reactome)	21	10.8	2.7	5.5×10^{-4}
mRNA transport (UniProtKB Keywords)	17	8.8	11.2	2.2×10^{-11}
Mitotic metaphase and anaphase (Reactome)	14	7.2	4.3	1.9×10^{-4}
Cadherin binding (GO MF)	14	7.2	4.3	7.0×10^{-4}
Mitotic prophase (Reactome)	12	6.2	6.2	3.8×10^{-5}
Negative regulation of apoptotic process (GO BP)	12	6.2	2.3	2.9×10^{-1}
Cell cycle checkpoints (Reactome)	11	5.7	2.7	2.7×10^{-2}
mRNA surveillance pathway (KEGG)	10	5.2	8.0	1.0×10^{-4}
Assembly of the pre-replicative complex (Reactome)	7	3.6	3.6	4.2×10^{-2}
DNA replication (Reactome)	7	3.6	2.7	1.1×10^{-1}
mRNA export from nucleus (GO BP)	6	3.1	10.2	1.2×10^{-2}

Supplementary Table S9. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclei of human internal thoracic artery endothelial cells (HITAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Metabolism of RNA (Reactome)	7	20.0	3.7	8.5×10^{-1}
mRNA splicing (UniProtKB Keywords)	5	14.3	7.7	1.2×10^{-1}
mRNA processing (UniProtKB Keywords)	5	14.3	6.0	1.3×10^{-1}
Nucleocytoplasmic transport (KEGG)	4	11.4	18.4	1.0×10^{-1}
Spliceosome (KEGG)	4	11.4	9.2	3.7×10^{-1}
Regulation of mRNA processing (GO BP)	3	8.6	107.1	5.9×10^{-2}

mRNA export from nucleus (GO BP)	3	8.6	28.6	3.0×10^{-1}
Positive regulation of epithelial to mesenchymal transition (GO BP)	3	8.6	31.7	3.0×10^{-1}
mRNA transport (GO BP)	3	8.6	19.9	3.7×10^{-1}
mRNA 3'-end processing (Reactome)	3	8.6	19.2	8.5×10^{-1}
RNA polymerase II transcription termination (Reactome)	3	8.6	16.7	8.5×10^{-1}
mRNA surveillance pathway (KEGG)	3	8.6	15.4	4.8×10^{-1}
Positive regulation of NF- κ B transcription factor activity (GO BP)	3	8.6	10.4	9.5×10^{-1}
Response to elevated platelet cytosolic Ca^{2+} (Reactome)	3	8.6	8.5	1.0×10^{-1}
Calcium-mediated signaling using intracellular calcium source (GO BP)	2	5.7	49.7	9.9×10^{-1}
Downregulated after CPP-P treatment				
Metabolism of RNA (Reactome)	21	25.0	5.2	2.7×10^{-7}
mRNA processing (UniProtKB Keywords)	18	21.4	7.8	2.1×10^{-9}
mRNA splicing (UniProtKB Keywords)	16	19.0	9.0	2.8×10^{-9}
Gene expression (Transcription) (Reactome)	15	17.9	1.7	8.1×10^{-1}
Transcription cofactor activity (GO MF)	8	9.5	12.7	1.2×10^{-4}
mRNA transport (UniProtKB Keywords)	8	9.5	12.0	6.0×10^{-5}
Transcription, DNA-templated (GO BP)	8	9.5	9.5	2.8×10^{-3}
Nuclear envelope reassembly (Reactome)	5	6.0	11.8	4.6×10^{-2}
Nucleocytoplasmic transport (KEGG)	5	6.0	10.9	2.7×10^{-2}
Mitotic metaphase and anaphase (Reactome)	5	6.0	3.7	8.1×10^{-1}
mRNA export from nucleus (GO BP)	4	4.8	15.6	1.9×10^{-1}
Nuclear envelope breakdown (Reactome)	4	4.8	13.6	1.2×10^{-1}
mRNA surveillance pathway (KEGG)	4	4.8	9.7	1.1×10^{-1}
Mitotic prophase (Reactome)	4	4.8	5.0	8.1×10^{-1}
Stem cell division (GO BP)	2	2.4	66.8	7.6×10^{-1}

Supplementary Table S10. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclei of human internal thoracic artery endothelial cells (HITAEC) treated with either secondary CPPs (CPP-S) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-S treatment				
Metabolism of RNA (Reactome)	10	33.3	6.7	1.7×10^{-3}
mRNA splicing (UniProtKB Keywords)	7	23.3	11.8	4.7×10^{-4}
mRNA processing (UniProtKB Keywords)	7	23.3	9.1	1.0×10^{-3}
RNA polymerase II transcription (Reactome)	7	23.3	2.4	8.0×10^{-1}
Calcium ion binding (GO MF)	5	16.7	4.2	3.6×10^{-1}
Nucleocytoplasmic transport (KEGG)	4	13.3	24.1	1.9×10^{-2}
Regulation of mRNA processing (GO BP)	3	10.0	121.3	4.6×10^{-2}
mRNA export from nucleus (GO BP)	3	10.0	32.4	3.3×10^{-1}
mRNA transport (GO BP)	3	10.0	22.6	3.7×10^{-1}
Regulation of translation (GO BP)	3	10.0	22.3	3.7×10^{-1}
mRNA surveillance pathway (KEGG)	3	10.0	20.1	1.8×10^{-1}
RNA polymerase II transcription termination (Reactome)	3	10.0	21.0	3.6×10^{-1}
tRNA processing (Reactome)	3	10.0	13.4	4.5×10^{-1}
Response to elevated platelet cytosolic Ca^{2+} (Reactome)	3	10.0	10.7	4.9×10^{-1}
Spliceosome (KEGG)	3	10.0	9.0	5.6×10^{-1}
Downregulated after CPP-S treatment				
Metabolism of RNA (Reactome)	24	36.4	6.8	1.6×10^{-11}

Gene expression (Transcription) (Reactome)	16	24.2	2.1	4.4×10^{-2}
mRNA processing (UniProtKB Keywords)	11	16.7	5.6	2.9×10^{-4}
mRNA splicing (UniProtKB Keywords)	10	15.2	6.6	2.9×10^{-4}
Negative regulation of apoptotic process (GO BP)	8	12.1	4.5	9.2×10^{-2}
Nucleocytoplasmic transport (KEGG)	7	10.6	13.1	2.0×10^{-3}
Cadherin binding (GO MF)	7	10.6	6.3	2.9×10^{-2}
Cell adhesion (UniProtKB Keywords)	7	10.6	2.9	1.0×10^{-1}
tRNA processing (Reactome)	6	9.1	11.4	3.2×10^{-3}
mRNA transport (UniProtKB Keywords)	6	9.1	10.6	2.6×10^{-3}
DNA repair (GO BP)	6	9.1	5.9	1.3×10^{-1}
mRNA export from nucleus (GO BP)	4	6.1	19.6	6.9×10^{-2}
rRNA processing (GO BP)	4	6.1	8.7	3.3×10^{-1}
Ribosome biogenesis (UniProtKB Keywords)	4	6.1	8.3	4.4×10^{-2}
Positive regulation of translation (GO BP)	3	4.5	10.5	6.5×10^{-1}

Supplementary Table S11. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclei of human internal thoracic artery endothelial cells (HITAEC) treated with either primary CPPs (CPP-P) or secondary CPPs (CPP-S).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Metabolism of proteins (Reactome)	17	32.7	2.4	2.7×10^{-2}
Metabolism of RNA (Reactome)	16	30.8	6.1	2.8×10^{-6}
Gene expression (Transcription) (Reactome)	13	25.0	2.3	6.9×10^{-2}
Hydrolase (UniProtKB Keywords)	12	23.1	2.1	1.6×10^{-1}
DNA repair (GO BP)	7	13.5	9.0	2.9×10^{-2}
mRNA processing (UniProtKB Keywords)	7	13.5	4.9	2.1×10^{-2}
Protein transport (UniProtKB Keywords)	7	13.5	3.0	1.1×10^{-1}
Nucleocytoplasmic transport (KEGG)	6	11.5	13.8	6.8×10^{-3}
mRNA splicing (Reactome)	6	11.5	7.6	2.7×10^{-2}
DNA damage (UniProtKB Keywords)	6	11.5	3.9	7.9×10^{-2}
mRNA transport (UniProtKB Keywords)	5	9.6	12.0	1.2×10^{-2}
Cellular response to DNA damage stimulus (GO BP)	5	9.6	6.5	3.2×10^{-1}
tRNA processing in the nucleus (Reactome)	4	7.7	19.2	2.7×10^{-2}
Ribosome biogenesis (UniProtKB Keywords)	3	5.8	8.5	1.6×10^{-1}
rRNA processing (GO BP)	3	5.8	8.4	7.9×10^{-1}
Upregulated after CPP-S treatment				
Metabolism of RNA (Reactome)	15	34.1	7.2	5.8×10^{-7}
mRNA splicing (Reactome)	12	27.3	13.1	1.2×10^{-8}
mRNA processing (Reactome)	12	27.3	10.1	8.8×10^{-8}
Gene expression (Transcription) (Reactome)	12	27.3	2.7	9.2×10^{-2}
RNA polymerase II Transcription (Reactome)	10	22.7	2.5	2.9×10^{-1}
Regulation of transcription, DNA-templated (GO BP)	7	15.9	3.1	6.1×10^{-1}
Spliceosome (KEGG)	6	13.6	11.7	2.7×10^{-3}
mRNA transport (UniProtKB Keywords)	5	11.4	14.5	2.5×10^{-3}
mRNA export from nucleus (GO BP)	3	6.8	22.6	2.9×10^{-1}
Nucleocytoplasmic transport (KEGG)	3	6.8	11.8	2.4×10^{-1}

Supplementary Table S12. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in mitochondria of human internal thoracic artery endothelial cells (HITAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Transmembrane transporter activity (GO MF)	3	15.0	19.1	3.4×10^{-1}
Ubiquitin protein ligase binding (GO MF)	3	15.0	9.6	6.8×10^{-1}
Mitochondrial transmembrane transport (GO BP)	2	10.0	204.4	1.0×10^{-1}
Ion transmembrane transporter activity (GO MF)	2	10.0	142.4	3.4×10^{-1}
Inner mitochondrial membrane organization (GO BP)	2	10.0	97.3	1.0×10^{-1}
Downregulated after CPP-P treatment				
Metabolism (Reactome)	10	55.6	3.7	4.2×10^{-3}
Oxidoreductase (UniProtKB Keywords)	6	33.3	7.7	7.5×10^{-3}
Metabolism of amino acids and derivatives (Reactome)	4	22.2	8.3	2.0×10^{-1}
Amino-acid biosynthesis (UniProtKB Keywords)	3	16.7	92.8	4.6×10^{-3}
Cellular response to oxidative stress (GO BP)	3	16.7	34.8	1.7×10^{-1}

Supplementary Table S13. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in lysosomes of human coronary artery endothelial cells (HCAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Hydrolase (UniProtKB Keywords)	9	45.0	4.2	9.5×10^{-4}
Innate immune system (Reactome)	8	40.0	5.1	5.0×10^{-3}
Glycosidase (UniProtKB Keywords)	5	25.0	50.6	1.7×10^{-5}
Dipeptidyl-peptidase activity (GO MF)	2	10.0	199.4	2.2×10^{-1}
Keratan sulfate degradation (Reactome)	2	10.0	105.4	1.0×10^{-1}
Downregulated after CPP-P treatment				
Hydrolase (UniProtKB Keywords)	5	50.0	6.6	4.2×10^{-3}
Innate immune system (Reactome)	4	40.0	4.1	7.2×10^{-1}
Glycosaminoglycan degradation (KEGG)	2	20.0	127.3	1.0×10^{-1}
Autophagosome maturation (GO BP)	2	20.0	100.3	7.8×10^{-1}
Endosome to lysosome transport (GO BP)	2	20.0	86.3	7.8×10^{-1}

Supplementary Table S14. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in lysosomes of human coronary artery endothelial cells (HCAEC) treated with either secondary CPPs (CPP-S) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-S treatment				
Hydrolase (UniProtKB Keywords)	4	36.4	3.8	1.9×10^{-1}
Hydrolase activity (GO MF)	3	27.3	20.9	2.6×10^{-1}
Glycosaminoglycan degradation (KEGG)	2	18.2	99.0	2.2×10^{-1}
Glycosidase (UniProtKB Keywords)	2	18.2	40.4	1.9×10^{-1}
Protein processing (GO BP)	2	18.2	41.5	1.0×10^{-1}
Downregulated after CPP-S treatment				

Supplementary Table S15. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in endoplasmic reticulum of human internal thoracic artery endothelial cells (HITAEC) treated with either primary CPPs (CPP-P) or secondary CPPs (CPP-S).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Protein processing in endoplasmic reticulum (GO BP)	6	15.0	11.7	5.1×10^{-3}
Ubiquitin-mediated endoplasmic-reticulum-associated protein degradation pathway (GO BP)	4	10.0	24.0	1.0×10^{-1}
Response to calcium ion (GO BP)	3	7.5	27.0	3.5×10^{-1}
Response to endoplasmic reticulum stress (GO BP)	3	7.5	17.3	6.2×10^{-1}
Metalloexopeptidase activity (GO MF)	2	5.0	48.6	9.5×10^{-1}
Upregulated after CPP-S treatment				
None				

Supplementary Table S16. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in mitochondrial lysate of human coronary artery endothelial cells (HCAEC) treated with either primary CPPs (CPP-P) or secondary CPPs (CPP-S).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Cellular responses to stress (Reactome)	31	55.4	8.3	1.8×10^{-21}
Cellular responses to stimuli (Reactome)	31	55.4	8.1	3.0×10^{-21}
Cellular senescence (Reactome)	29	51.8	31.2	9.4×10^{-36}
Diseases of programmed cell death (Reactome)	28	50.0	56.7	1.7×10^{-41}
Senescence-associated secretory phenotype (Reactome)	27	48.2	51.3	7.5×10^{-39}
Oxidative stress-induced senescence (Reactome)	27	48.2	45.9	1.5×10^{-37}
DNA damage/Telomere stress-induced senescence (Reactome)	19	33.9	50.7	2.5×10^{-26}
Depurination (Reactome)	17	30.4	65.1	2.7×10^{-25}
Depyrimidination (Reactome)	17	30.4	59.7	1.2×10^{-24}
Apoptotic execution phase (Reactome)	3	5.4	12.2	3.8×10^{-2}
Upregulated after CPP-S treatment				
None				

Supplementary Table S17. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclear lysate of human coronary artery endothelial cells (HCAEC) treated with either primary CPPs (CPP-P) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Cellular responses to stress (Reactome)	43	26.9	4.1	2.9×10^{-14}
Protein folding (GO BP)	13	8.1	8.7	9.7×10^{-6}
Unfolded protein binding (GO MF)	12	7.5	11.0	5.5×10^{-7}
Chaperone (UniProtKB Keywords)	10	6.2	4.0	5.3×10^{-3}
Chaperonin-mediated protein folding (Reactome)	10	6.2	8.2	2.6×10^{-5}
Angiogenesis (GO BP)	9	5.6	4.3	5.2×10^{-2}

Chemical carcinogenesis - reactive oxygen species (KEGG)	9	5.6	2.5	2.1×10^{-1}
Nuclear envelope reassembly (Reactome)	7	4.4	7.0	2.1×10^{-3}
Cellular senescence (KEGG)	7	4.4	2.8	2.2×10^{-1}
Necroptosis (KEGG)	7	4.4	2.8	2.3×10^{-1}
Sealing of the nuclear envelope (NE) by ESCRT-III (Reactome)	6	3.8	14.5	3.1×10^{-4}
Chaperone-mediated protein folding (GO BP)	6	3.8	18.9	1.6×10^{-3}
Response to oxidative stress (GO BP)	5	3.1	5.0	3.8×10^{-1}
Positive regulation of cysteine-type endopeptidase activity involved in apoptotic process (GO BP)	4	2.5	9.6	2.3×10^{-1}
Response to unfolded protein (GO BP)	4	2.5	8.5	2.8×10^{-1}
Downregulated after CPP-P treatment				
Transcription regulation (UniProtKB Keywords)	15	33.3	2.0	7.6×10^{-2}
mRNA processing (UniProtKB Keywords)	12	26.7	9.6	2.3×10^{-7}
mRNA splicing (UniProtKB Keywords)	11	24.4	11.4	2.3×10^{-7}
mRNA splicing, via spliceosome (GO BP)	9	20.0	20.3	2.1×10^{-6}
Cell cycle, mitotic (Reactome)	6	13.3	4.0	1.2×10^{-1}
Positive regulation of transcription, DNA-templated (GO BP)	6	13.3	3.7	5.8×10^{-1}
mRNA binding (GO MF)	5	11.1	8.6	1.0×10^{-1}
Chromatic modifying enzymes (Reactome)	5	11.1	6.9	6.7×10^{-2}
Homology directed repair (Reactome)	4	8.9	11.0	6.7×10^{-2}
DNA double-strand break repair (Reactome)	4	8.9	9.0	8.9×10^{-2}
Transcription coactivator activity (GO MF)	4	8.9	6.5	3.1×10^{-1}
Cell cycle checkpoints (Reactome)	4	8.9	5.2	2.0×10^{-1}
Base excision repair (Reactome)	3	6.7	12.5	1.5×10^{-1}
Transcription cofactor activity (GO MF)	3	6.7	9.1	4.3×10^{-1}
mRNA transport (UniProtKB Keywords)	3	6.7	8.2	1.5×10^{-1}

Supplementary Table S18. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclear lysate of human coronary artery endothelial cells (HCAEC) treated with either secondary CPPs (CPP-S) or control phosphate-buffer saline (PBS).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-S treatment				
Protein binding involved in protein folding (GO MF)	8	5.6	20.6	3.2×10^{-6}
Cellular responses to stress (Reactome)	41	28.5	4.2	4.0×10^{-13}
Unfolded protein binding (GO MF)	14	9.7	14.2	1.1×10^{-9}
Chaperone (UniProtKB Keywords)	12	8.3	5.4	1.3×10^{-4}
Response to elevated cytosolic Ca ²⁺ (Reactome)	10	6.9	6.0	2.5×10^{-4}
Angiogenesis (GO BP)	10	6.9	5.3	8.3×10^{-3}
Protein folding (Reactome)	9	6.2	7.5	1.7×10^{-4}
Chaperonin-mediated protein folding (Reactome)	9	6.2	8.0	1.1×10^{-4}
Apoptosis (Reactome)	9	6.2	4.0	7.6×10^{-3}
Programmed cell death (Reactome)	9	6.2	3.4	1.9×10^{-2}
Nuclear envelope reassembly (Reactome)	9	6.2	9.7	3.0×10^{-5}
Cellular response to heat stress (Reactome)	7	4.9	6.3	3.9×10^{-3}
Fluid shear stress and atherosclerosis (KEGG)	7	4.9	3.4	9.3×10^{-2}
Sealing of the nuclear envelope by ESCRT-III (Reactome)	6	4.2	15.6	2.2×10^{-4}
Stress response (UniProtKB Keywords)	6	4.2	6.7	2.2×10^{-2}
Chaperone-mediated protein folding (GO BP)	5	3.5	17.3	1.2×10^{-2}
Response to unfolded protein (GO BP)	5	3.5	11.6	3.7×10^{-2}
Apoptotic execution phase (Reactome)	5	3.5	7.7	1.6×10^{-2}
Apoptotic cleavage of cellular proteins (Reactome)	4	2.8	8.5	4.2×10^{-2}

Cellular response to unfolded protein (GO BP)	3	2.1	14.4	3.4×10^{-4}
Downregulated after CPP-S treatment				
Gene expression (Transcription) (Reactome)	22	33.8	3.3	4.2×10^{-7}
Cell cycle, mitotic (Reactome)	19	29.2	7.9	7.4×10^{-12}
Transcriptional regulation by small RNAs (Reactome)	17	26.2	37.7	5.0×10^{-20}
Chromatic modifying enzymes (Reactome)	17	26.2	14.6	2.6×10^{-14}
mRNA transport (UniProtKB Keywords)	7	10.8	22.3	1.7×10^{-5}
Transport of mature mRNA derived from an intron-containing transcript (Reactome)	6	9.2	18.7	2.3×10^{-5}
Transport of mature transcript to cytoplasm (Reactome)	6	9.2	16.7	3.8×10^{-5}
Transport of mature mRNA derived from an intronless transcript (Reactome)	4	6.2	22.7	7.2×10^{-4}
mRNA export from nucleus (GO BP)	4	6.2	20.5	1.8×10^{-2}
snRNP assembly (Reactome)	4	6.2	17.6	1.4×10^{-3}
Metabolism of non-coding RNA (Reactome)	4	6.2	17.6	1.4×10^{-3}
tRNA processing in the nucleus (Reactome)	4	6.2	17.6	1.7×10^{-3}
Base excision repair (Reactome)	4	6.2	10.2	6.5×10^{-3}
Homology directed repair (Reactome)	4	6.2	6.8	2.0×10^{-2}
DNA double-strand break repair (Reactome)	4	6.2	5.6	3.3×10^{-2}

Supplementary Table S19. Fold enrichment (observed-versus-expected) analysis of differentially expressed proteins in nuclear lysate of human coronary artery endothelial cells (HCAEC) treated with either primary CPPs (CPP-P) or secondary CPPs (CPP-S).

Molecular term	Total proteins	Percent from differentially expressed proteins	Fold enrichment	FDR-corrected P value
Upregulated after CPP-P treatment				
Cellular responses to stress (Reactome)	34	68.0	10.3	3.4×10^{-28}
Gene expression (Transcription) (Reactome)	28	56.0	4.3	5.4×10^{-12}
Cellular senescence (Reactome)	28	56.0	34.0	5.4×10^{-36}
Transcriptional regulation by small RNAs (Reactome)	27	54.0	61.3	3.7×10^{-41}
Cell cycle, mitotic (Reactome)	27	54.0	11.5	3.1×10^{-22}
Diseases of programmed cell death (Reactome)	25	50.0	57.3	2.9×10^{-37}
Senescence-associated secretory phenotype (SASP) (Reactome)	25	50.0	53.6	1.3×10^{-36}
Oxidative stress induced senescence (Reactome)	25	50.0	48.0	2.1×10^{-35}
Assembly of the pre-replicative complex (Reactome)	25	50.0	41.9	6.6×10^{-34}
DNA replication (Reactome)	25	50.0	31.8	7.1×10^{-31}
DNA damage/Telomere stress induced senescence (Reactome)	18	36.0	54.3	1.4×10^{-25}
Base excision repair (Reactome)	15	30.0	39.3	6.1×10^{-19}
Homology directed repair (Reactome)	15	30.0	25.9	2.5×10^{-16}
DNA double-strand break repair (Reactome)	15	30.0	21.3	4.0×10^{-15}
Cell cycle checkpoints (Reactome)	15	30.0	12.2	8.3×10^{-12}
Eukaryotic translation termination (Reactome)	4	8.0	10.1	8.1×10^{-3}
Eukaryotic translation elongation (Reactome)	4	8.0	10.1	8.1×10^{-3}
Eukaryotic translation initiation (Reactome)	4	8.0	7.9	1.4×10^{-2}
Apoptosis induced DNA fragmentation (Reactome)	3	6.0	55.0	1.7×10^{-3}
Apoptotic execution phase (Reactome)	3	6.0	13.7	2.1×10^{-2}
Upregulated after CPP-S treatment				
mRNA binding (GO MF)	3	33.3	25.2	8.8×10^{-2}
mRNA splicing (Reactome)	3	33.3	21.8	1.1×10^{-1}
Processing of capped intron-containing pre-mRNA (Reactome)	3	33.3	16.5	1.5×10^{-1}

Regulation of alternative mRNA splicing, via spliceosome (GO BP)	2	22.2	67.4	1.0×10^{-1}
Double-stranded RNA binding (GO MF)	2	22.2	56.9	3.7×10^{-1}