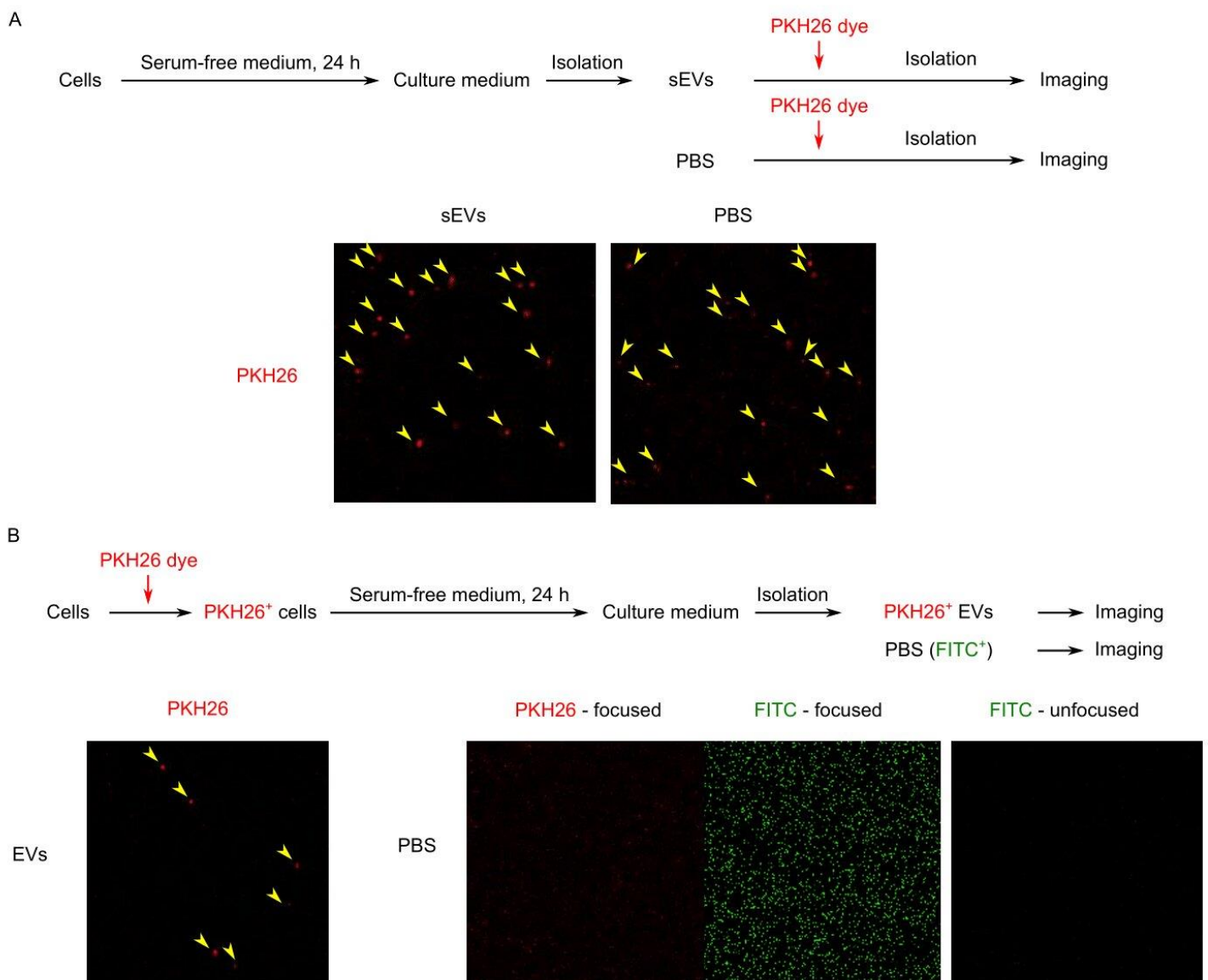


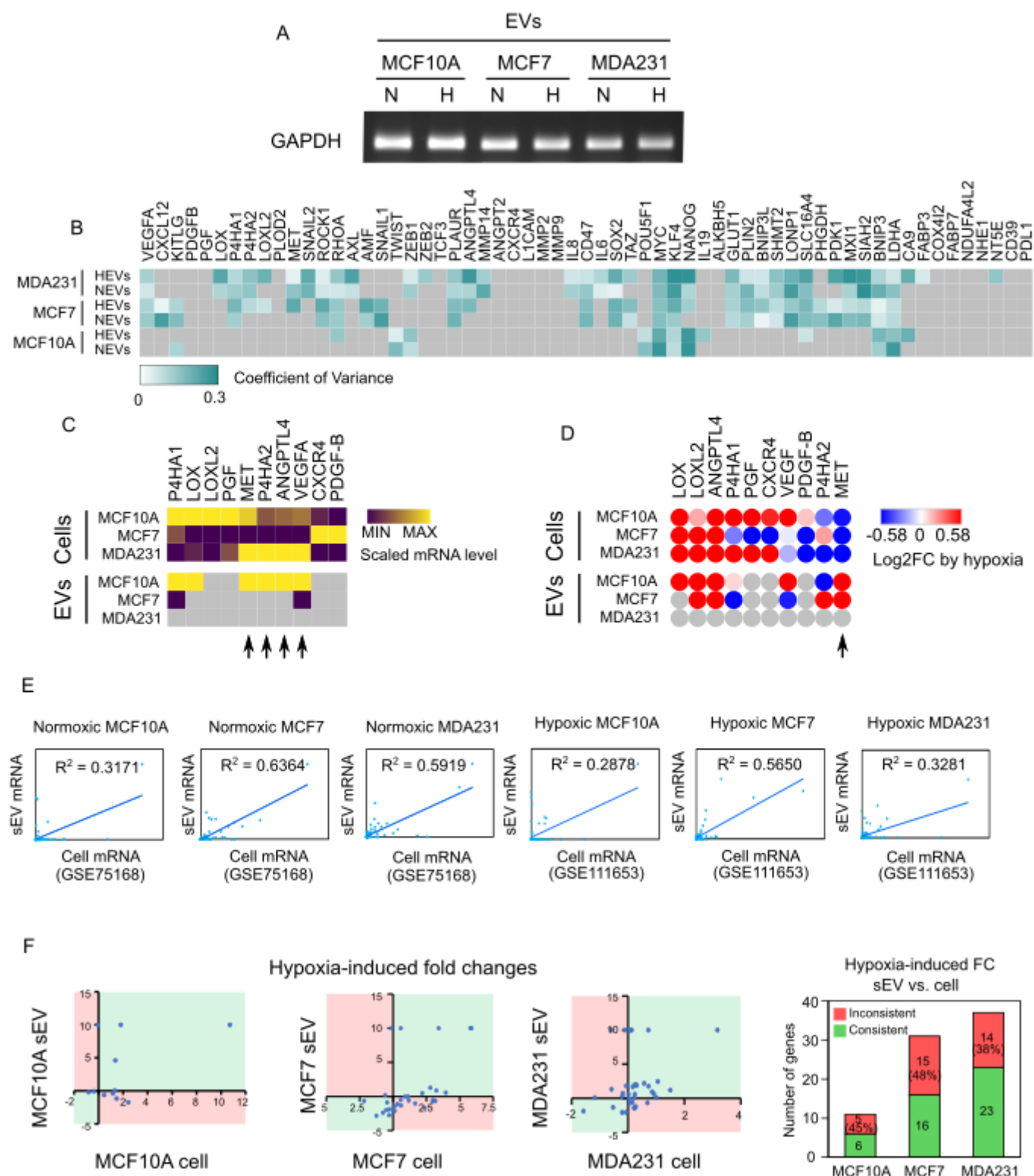
Article

# Supplementary Materials: Distinct mRNAs in Cancer Extracellular Vesicles Activate Angiogenesis and Alter Transcriptome of Vascular Endothelial Cells

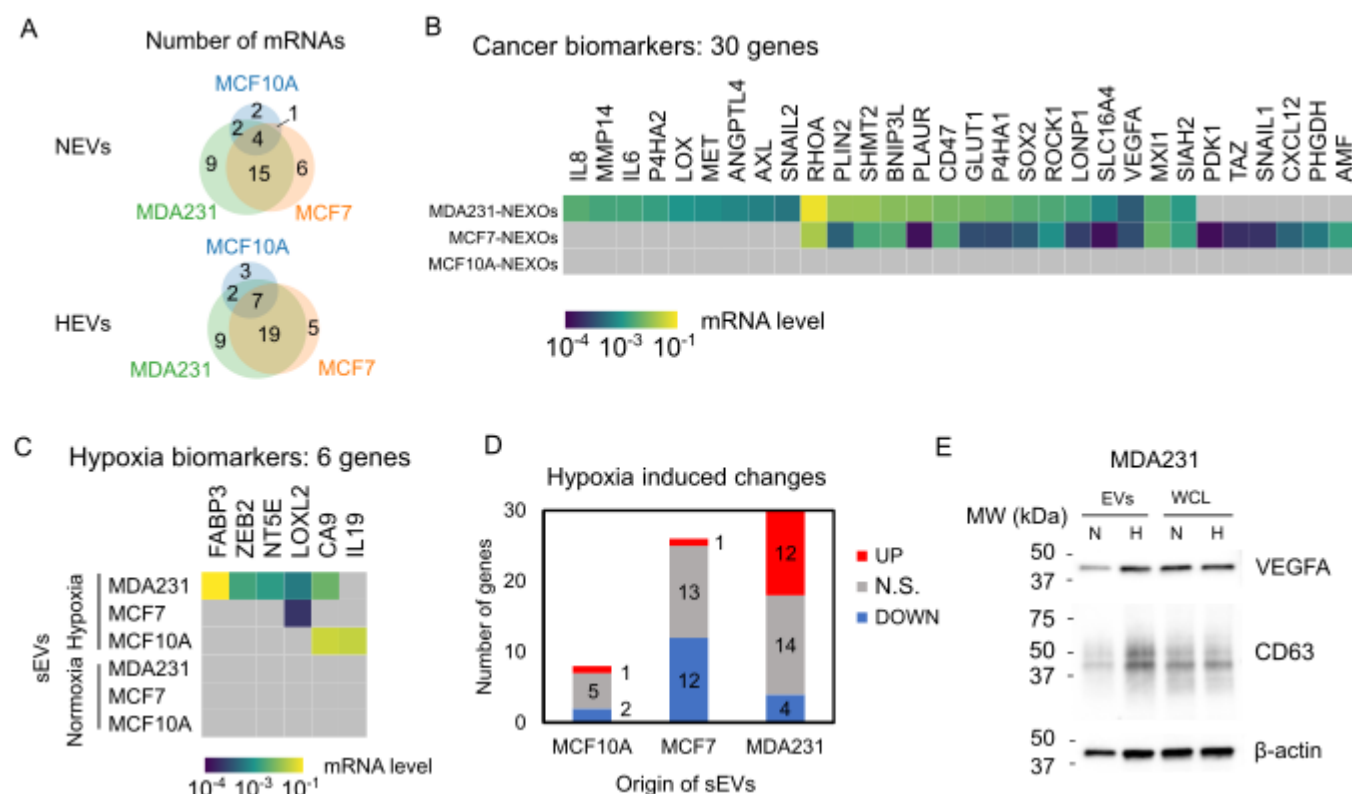
Pan Zhang, Su Bin Lim, Kuan Jiang, Ti Weng Chew, Boon Chuan Low and Chwee Teck Lim



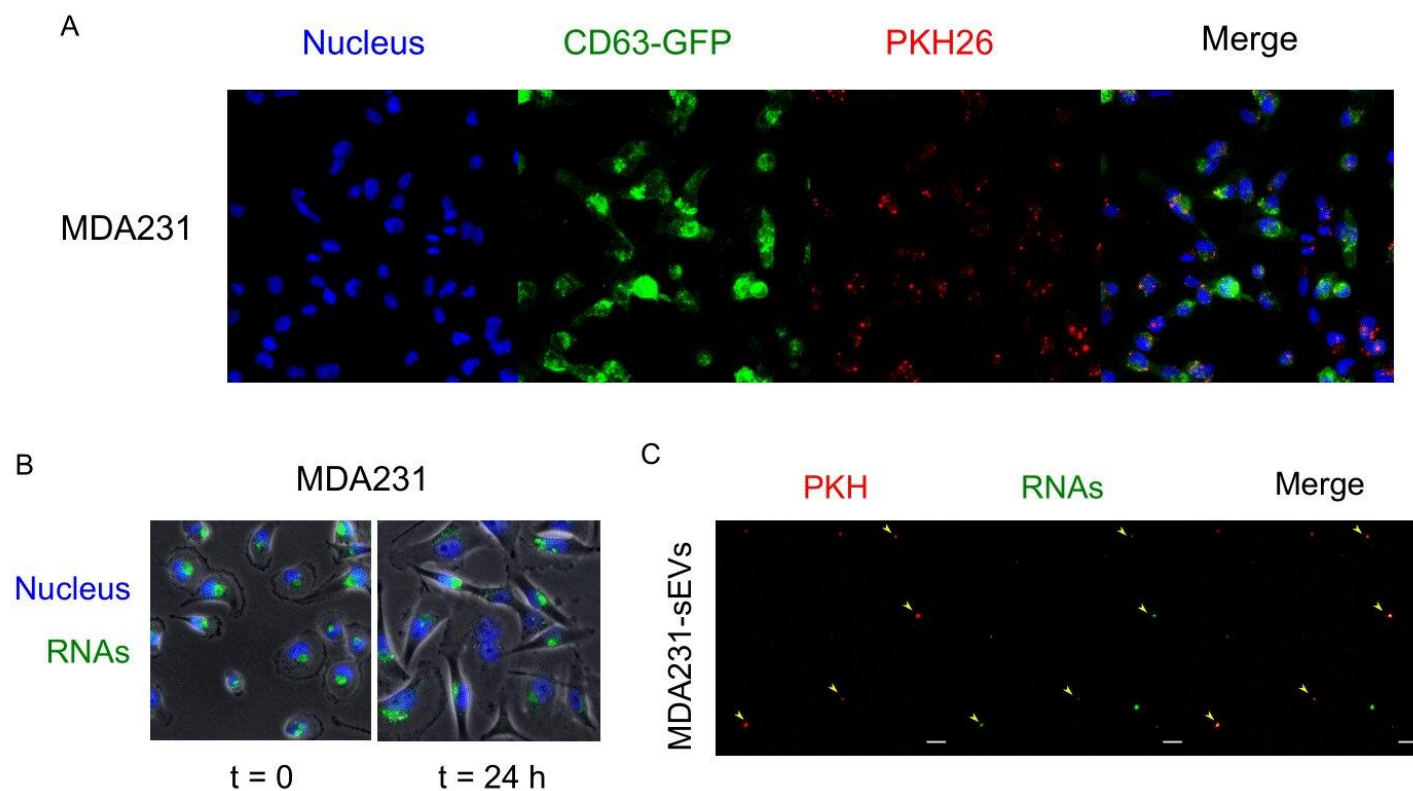
**Figure S1.** Comparison of two methods of EVs staining with PKH26. **(A)** Staining of EVs with direct mixing of EVs and PKH26 dye resulted in excessive dye that co-isolated with EVs and mimicked EVs in fluorescent imaging since abundant EV-like spots were identified in PBS control sample. **(B)** Cells that were stained with PKH26 dye generated PKH26<sup>+</sup> EVs. Excessive dye was thoroughly wash off after cell staining. PBS control showed no fluorescence.



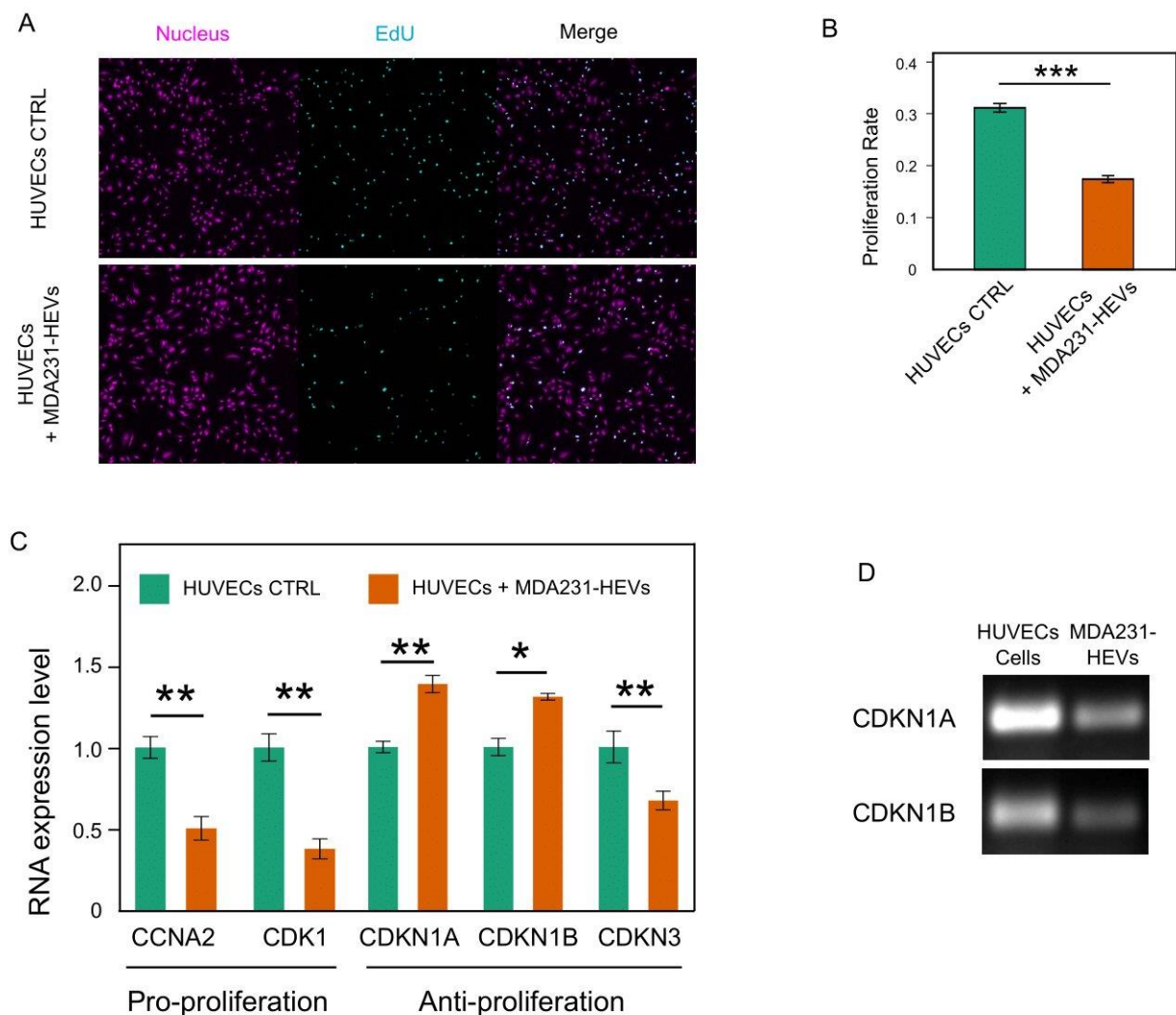
**Figure S2.** Comparison of mRNA profile between EVs and cells. (A) GAPDH mRNA was robustly present in all the quantified EVs. (B) The coefficient of variances of all gene expressions were less than 0.3, demonstrating that the exosomal mRNA levels were homeostatic, and the quantification of exosomal mRNA by RT-qPCR was reproducible. (C) Comparison of gene expressions in cells and EVs. The expression levels were normalized to GAPDH. (D) Comparison of hypoxia induced alterations of mRNA level in cells and EVs. (E) Expression correlation plot of hypoxia gene panel between EVs and cells. The R-squared values were calculated with linear regression. (F) The relationship of the hypoxia-induced gene expression fold change between EVs and cells.



**Figure S3.** Analysis of exosomal mRNA profile of the hypoxia gene panel. **(A)** Venn diagram shows the presence of mRNAs of the hypoxia gene panel in normoxic EVs (NEVs) and hypoxic EVs (HEVs). **(B)** 30 genes from the hypoxia gene panel were potential cancer biomarker since their mRNAs were found present in cancer EVs while absent in MCF10A EVs. **(C)** 6 genes from the hypoxia gene panel can potentially reflect the hypoxic status of the tumor microenvironment as their mRNAs were only present in hypoxic EVs. **(D)** The number of mRNAs that were upregulated, downregulated or not significantly altered by hypoxic stress. Of the significantly regulated genes, most were downregulated in MCF7 and upregulated in MDA231. **(E)** Western blot shows that the VEGFA protein level in cells (normalized to  $\beta$ -actin) and in EVs (normalized to CD63) were not changes by the hypoxic stimulus.

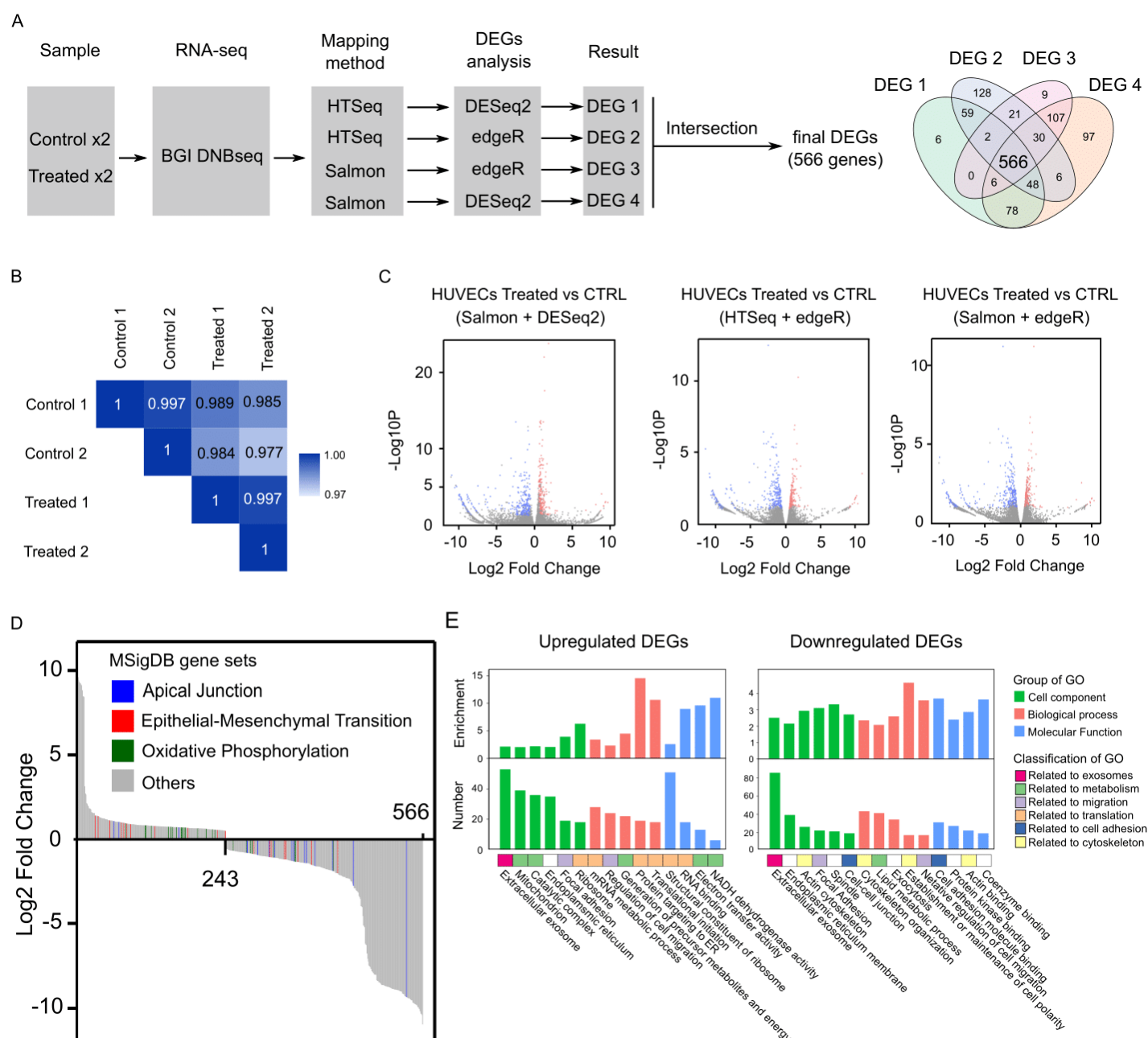


**Figure S4.** Fluorescent staining of CD63 and RNAs in MDA231 cell and EVs. (A) CD63-GFP and PKH26 efficiently label MDA231 cells. (B) The SYTO RNaselect specifically stained cell RNAs and lasted for more than 24 hours. (C) MDA231-derived PKH26<sup>+</sup> EVs carry RNAs as they can be stained by SYTO RNaselect.



**Figure S5.** Cancer EVs suppress cell proliferation. **(A)** EdU proliferation assay of HUVECs in basal medium or treated with MDA231-HEVs for 24 h. **(B)** Proliferation rate of HUVECs were represented by the ratio of EdU+ cells to the Hoechst+ cells ( $n = 25$ ). **(C)** The expressions of proliferation-related genes that were significantly altered by the treatment of MDA231-HEVs ( $n = 3$ ). **(D)** The two upregulated CDK inhibitors, CDKN1A and CDKN1B, were carried by MDA231-HEVs. \*  $P < 0.05$ , \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$  based on Mann-Whitney U test for **(B)**, or Student's  $t$  test for **(C)**. Error bars indicate the standard error of the mean (SEM) for **(B)** and **(C)**.





**Figure S6.** RNA-seq of HUVECs treated with cancer EVs. **(A)** Workflow of the RNA-seq data analysis. The final list of DEGs comprising 566 genes were acquired by intersecting four list of DEGs. **(B)** Correlation of four samples based on the expression profile shows the samples within each group were similar, while the correlation between control and EV-treated sample is relatively lower. **(C)** Volcano plot shows RNA-seq data of HUVECs with or without the treatment of MDA231-HEVs processed by pipelines of Salmon + DESeq2, HTSeq + edgeR, or Salmon + edgeR. **(D)** The plot of EV-induced fold changes of DEGs. Genes that belongs to Apical junction gene set, EMT gene set, or OP gene set were highlighted in blue, red, or green color, respectively. **(E)** Gene ontology analysis of DEGs. GO terms with >2 enrichment factor were ranked in gene number.

**Table S1.** Hypoxia-targeted gene panel.

Gene Symbol in Paper	Official Gene Symbol	Official Full Name	Group of Function
VEGFA	VEGFA	vascular endothelial growth factor A	Angiogenesis
CXCL12	CXCL12	C-X-C motif chemokine ligand 12	Angiogenesis
KITLG	KITLG	KIT ligand	Angiogenesis
PDGFB	PDGFB	platelet derived growth factor subunit B	Angiogenesis
PGF	PGF	placental growth factor	Angiogenesis

LOX	LOX	lysyl oxidase	ECM stiffening
P4HA1	P4HA1	prolyl 4-hydroxylase subunit alpha 1	ECM stiffening
P4HA2	P4HA2	prolyl 4-hydroxylase subunit alpha 2	ECM stiffening
LOXL2	LOXL2	lysyl oxidase like 2	ECM stiffening
PLOD2	PLOD2	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2	ECM stiffening
MET	MET	MET proto-oncogene, receptor tyrosine kinase	Cell motility
SNAIL2	SNAIL2	snail family transcriptional repressor 2	Cell motility
ROCK1	ROCK1	Rho associated coiled-coil containing protein kinase 1	Cell motility
RHOA	RHOA	ras homolog family member A	Cell motility
AXL	AXL	AXL receptor tyrosine kinase	Cell motility
AMF	GPI	glucose-6-phosphate isomerase	Cell motility
SNAIL1	SNAIL1	snail family transcriptional repressor 1	Cell motility
TWIST	TWIST1	twist family bHLH transcription factor 1	Cell motility
ZEB1	ZEB1	zinc finger E-box binding homeobox 1	Cell motility
ZEB2	ZEB2	zinc finger E-box binding homeobox 2	Cell motility
TCF3	TCF3	transcription factor 3	Cell motility
PLAUR	PLAUR	plasminogen activator, urokinase receptor	Metastasis
ANGPTL4	ANGPTL4	angiopoietin like 4	Metastasis
MMP14	MMP14	matrix metalloproteinase 14	Metastasis
ANGPT2	ANGPT2	angiopoietin 2	Metastasis
CXCR4	CXCR4	C-X-C motif chemokine receptor 4	Metastasis
L1CAM	L1CAM	L1 cell adhesion molecule	Metastasis
MMP2	MMP2	matrix metalloproteinase 2	Metastasis
MMP9	MMP9	matrix metalloproteinase 9	Metastasis
IL8	CXCL8	C-X-C motif chemokine ligand 8	Cancer stem cell maintenance
CD47	CD47	CD47 molecule	Cancer stem cell maintenance
IL6	IL6	interleukin 6	Cancer stem cell maintenance
SOX2	SOX2	SRY-box transcription factor 2	Cancer stem cell maintenance
TAZ	TAZ	tafazzin	Cancer stem cell maintenance
POU5F1	POU5F1	POU class 5 homeobox 1	Cancer stem cell maintenance
MYC	MYC	MYC proto-oncogene, bHLH transcription factor	Cancer stem cell maintenance
KLF4	KLF4	Kruppel like factor 4	Cancer stem cell maintenance
NANOG	NANOG	Nanog homeobox	Cancer stem cell maintenance
IL19	IL19	interleukin 19	Cancer stem cell maintenance
ALKBH5	ALKBH5	alkB homolog 5, RNA demethylase	Cancer stem cell maintenance
GLUT1	SLC2A1	solute carrier family 2 member 1	Metabolism
PLIN2	PLIN2	perilipin 2	Metabolism
BNIP3L	BNIP3L	BCL2 interacting protein 3 like	Metabolism
SHMT2	SHMT2	serine hydroxymethyltransferase 2	Metabolism
LONP1	LONP1	lon peptidase 1, mitochondrial	Metabolism
SLC16A4	SLC16A4	solute carrier family 16 member 4	Metabolism
PHGDH	PHGDH	phosphoglycerate dehydrogenase	Metabolism
PDK1	PDK1	pyruvate dehydrogenase kinase 1	Metabolism
MXI1	MXI1	MAX interactor 1, dimerization protein	Metabolism
SIAH2	SIAH2	siah E3 ubiquitin protein ligase 2	Metabolism
BNIP3	BNIP3	BCL2 interacting protein 3	Metabolism
LDHA	LDHA	lactate dehydrogenase A	Metabolism
CA9	CA9	carbonic anhydrase 9	Metabolism
FABP3	FABP3	fatty acid binding protein 3	Metabolism
COX4I2	COX4I2	cytochrome c oxidase subunit 4I2	Metabolism
FABP7	FABP7	fatty acid binding protein 7	Metabolism
NDUFA4L2	NDUFA4L2	NDUFA4 mitochondrial complex associated like 2	Metabolism
NHE1	SLC9A1	solute carrier family 9 member A1	Metabolism
NT5E	NT5E	5'-nucleotidase ecto	Immune evasion
CD39	ENTPD1	ectonucleoside triphosphate diphosphohydrolase 1	Immune evasion
PDL1	CD274	CD274 molecule	Immune evasion

**Table S2.** Primer sequences for RT-qPCR.

Gene Symbol	Forward	Reverse	Product Length (bp)
<b>Hypoxia-targeted gene panel</b>			
ALKBH5	5'-CGGCGAAGGCTACACTTACG-3'	5'-CCACCAGCTTTTGGATCACCA-3'	128
AMF	5'-CCGCGTCTGGTATGTCTCC-3'	5'-CCTGGGTAGTAAAGGTCTTGA-3'	113
ANGPT2	5'-ACCCCACTGTTGCTAAAGAAGA-3'	5'-CCATCCTCACGTCGCTGAATA-3'	184
ANGPTL4	5'-GGCTCAGTGGACTTCAACCG-3'	5'-CCGTGATGCTATGCACCTTCT-3'	103
AXL	5'-CCGTGGACCTACTCTGGCT-3'	5'-CCTTGGCGTTATGGGCTTC-3'	132
BNIP3	5'-CAGGGCTCCTGGGTAGAACT-3'	5'-CTACTCCGTCCAGACTCATGC-3'	131
BNIP3L	5'-TTGGATGCACAACATGAATCAGG-3'	5'-TCTTCTGACTGAGAGCTATGGTC-3'	140
CA9	5'-GGATCTACCTACTGTTGAGGCT-3'	5'-CATAGCGCCAATGACTCTGGT-3'	98
CD39	5'-AGGTGCCTATGGCTGGATTAC-3'	5'-CCAAAGCTCCAAAGGTTTCCT-3'	116
CD47	5'-TCCGGTGGTATGGATGAGAAA-3'	5'-ACCAAGGCCAGTAGCATTCTT-3'	129
COX4I2	5'-CCGTCGCTCCAATGAGTGG-3'	5'-CGTCCGTCAAGGTGATCGG-3'	125
CXCL12	5'-ATTCTCAACACTCCAACTGTGC-3'	5'-ACTTTAGCTTCGGGTCAATGC-3'	88
CXCR4	5'-ACGCCACCAACAGTCAGAG-3'	5'-AGTCGGGAATAGTCAGCAGGA-3'	96
FABP3	5'-TGGAGTTCGATGAGACAACAGC-3'	5'-CTCTTGCCCGTCCCATTTCTG-3'	101
FABP7	5'-GCACATTCAAGAACACGGAGA-3'	5'-CACATCACCAAAAGTAAGGGTCA-3'	203
GLUT1	5'-ATTGGCTCCGGTATCGTCAAC-3'	5'-GCTCAGATAGGACATCCAGGGTA-3'	174
IL19	5'-TCCTGGCGTTCTACGTGGA-3'	5'-TGACATTGCCGCAGAGTTTTC-3'	124
IL6	5'-ACTCACCTCTTCAGAACGAATTG-3'	5'-CCATCTTTGGAAGGTTTCAAGTTG-3'	149
IL8	5'-ACTGAGAGTGATTGAGAGTGGAC-3'	5'-AACCTCTGCACCCAGTTTTC-3'	112
KITLG	5'-AATCCTCTCGTCAAACTGAAGG-3'	5'-CCATCTCGCTTATCCAACAATGA-3'	163
KLF4	5'-CGGACATCAACGACGTGAG-3'	5'-GACGCCTTCAGCACGAACT-3'	139
L1CAM	5'-TGTCATCACGGAACAGTCTCC-3'	5'-CTGGCAAAGCAGCGGTAGAT-3'	246
LDHA	5'-TTGACCTACGTGGCTTGAAG-3'	5'-GGTAACGGAATCGGGCTGAAT-3'	91
LONP1	5'-GACGATCCCCGATGTGTTTCC-3'	5'-GGGCGAGACGAACTTTCCTT-3'	137
LOX	5'-CGGCGGAGGAAAACCTGTCT-3'	5'-TCGGCTGGGTAAGAAATCTGA-3'	128
LOXL2	5'-GGGTGGAGGTGTACTATGATGG-3'	5'-CTTGCCGTAGGAGGAGCTG-3'	137
MET	5'-AGCAATGGGGAGTGTAAGAGG-3'	5'-CCCAGTCTTGTAAGTCAAGCAAC-3'	198
MMP14	5'-CATCTGTGACGGGAACCTTTGA-3'	5'-GGCAGTGTTGATGGACGCA-3'	163
MMP2	5'-GATACCCCTTTGACGGTAAGGA-3'	5'-CCTTCTCCCAAGGTCCATAGC-3'	112
MMP9	5'-GGGACGCAGACATCGTCATC-3'	5'-TCGTCATCGTCGAAATGGGC-3'	139
MXI1	5'-GCGCCTTTGTGTTAGAACGCTT-3'	5'-AATGCTGTCCATTCGTATTCGT-3'	235
MYC	5'-GGCTCCTGGCAAAAGGTCA-3'	5'-CTGCGTAGTTGTGCTGATGT-3'	119
NANOG	5'-TTTGTGGGCTGAAGAAAACCT-3'	5'-AGGGCTGTCTCTGAATAAGCAG-3'	116
NDUFA4L2	5'-ATGATCGGCTTAATCTGCCTG-3'	5'-TCCGGGTGTTCTTTCTGTCC-3'	104
NHE1	5'-ACCACGAGAACGCTCGATTG-3'	5'-ACGTGTGTGTAGTCGATGCC-3'	144
NT5E	5'-CCAGTACCAGGGCACTATCTG-3'	5'-TGGCTCGATCAGTCCTTCCA-3'	136
P4HA1	5'-CCAAAGCTCTGTTACGTCTCC-3'	5'-AGTCTCAGCCGTTAGAAAAGA-3'	108
P4HA2	5'-CAAAGTGGTGAAGCGGCTAAA-3'	5'-GCACAGAGAGGTTGGCGATA-3'	95
PDGFB	5'-CTCGATCCGCTCCTTTGATGA-3'	5'-CGTTGGTGGGCTCTATGAG-3'	239
PDK1	5'-GAGAGCCACTATGGAACACCA-3'	5'-GGAGGTCTCAACACGAGGT-3'	187
PDL1	5'-TGGCATTTGCTGAACGCATTT-3'	5'-TGCAGCCAGGTCTAATTGTTTT-3'	120
PGF	5'-GAACGGCTCGTCAGAGGTG-3'	5'-ACAGTGCAGATTCTCATCGCC-3'	187
PHGDH	5'-CTGCGGAAAGTGCTCATCAGT-3'	5'-TGGCAGAGCGAACAATAAGGC-3'	154
PLAUR	5'-TGTAAGACCAACGGGGATTGC-3'	5'-AGCCAGTCCGATAGCTCAGG-3'	166
PLIN2	5'-TTGCAGTTGCCAATACCTATGC-3'	5'-CCAGTCACAGTAGTCGTCACA-3'	148
PLOD2	5'-TTATTGAGCAACCAACCCCTTT-3'	5'-GGCTTCCGCTTGACTTAGATTT-3'	206
POU5F1	5'-GGGAGATTGATAACTGGTGTGTT-3'	5'-GTGTATATCCCAGGGTGATCCTC-3'	144
RHOA	5'-GGAAAGCAGGTAGAGTTGGCT-3'	5'-GGCTGTGATGGAAGAAACACAT-3'	118
ROCK1	5'-GGTGGTTCGGTTGGGGTATTTT-3'	5'-CGCCCTAACCTCACTTCCC-3'	196
SHMT2	5'-CCCTTCTGCAACCTCACGAC-3'	5'-TGAGCTTATAGGGCATAGACTCG-3'	135
SIAH2	5'-CGCCAGAAGTTGAGCTGCT-3'	5'-TGGTGGCATACTTACAGGGAA-3'	115
SLC16A4	5'-AGGTATCCTTGAGACGGTCAG-3'	5'-CAAGCAGGTTAGTGATGCCG-3'	119
SNAIL1	5'-TCGGAAGCCTAACTACAGCGA-3'	5'-AGATGAGCATTGGCAGCGAG-3'	140



<b>SNAIL2</b>	5'-TGTGACAAGGAATATGTGAGCC-3'	5'-TGAGCCCTCAGATTTGACCTG-3'	203
<b>SOX2</b>	5'-GCCGAGTGGAACCTTTGTGCG-3'	5'-GGCAGCGTGACTTATCCTTCT-3'	155
<b>TAZ</b>	5'-CACCGTGTCCAATCACCAGTC-3'	5'-TCCAACGCATCAACTTCAGGT-3'	95
<b>TCF3</b>	5'-ACGAGCGTATGGGCTACCA-3'	5'-GTTATTGCTTGAGTGATCCGGG-3'	233
<b>TWIST</b>	5'-GTCCGCAGTCTTACGAGGAG-3'	5'-GCTTGAGGGTCTGAATCTTGCT-3'	156
<b>VEGFA</b>	5'-AGGGCAGAATCATCACGAAGT-3'	5'-AGGGTCTCGATTGGATGGCA-3'	75
<b>ZEB1</b>	5'-CAGCTTGATACCTGTGAATGGG-3'	5'-TATCTGTGGTCGTGTGGGACT-3'	106
<b>ZEB2</b>	5'-CAAGAGGCGCAAACAAGCC-3'	5'-GGTTGGCAATACCGTCATCC-3'	128
<b>Cell cycle-related genes</b>			
<b>CCNA1</b>	5'-ACATGGATGAACTAGAGCAGGG-3'	5'-GAGTGTGCCGGTGTCTACTT-3'	95
<b>CCNA2</b>	5'-CGCTGGCGGTACTGAAGTC-3'	5'-GAGGAACGGTGACATGCTCAT-3'	120
<b>CCNB1</b>	5'-CCTGCCTGCAACAGTACCC-3'	5'-CCAACACGATCTCTGGTCGC-3'	115
<b>CCND1</b>	5'-GCTGCGAAGTGGAACCATC-3'	5'-CCTCCTTCTGCACACATTTGAA-3'	135
<b>CCND2</b>	5'-ACCTTCCGCAGTGCTCCTA-3'	5'-CCCAGCCAAGAAACGGTCC-3'	161
<b>CCND3</b>	5'-TACCCGCCATCCATGATCG-3'	5'-AGGCAGTCCACTTCAGTGC-3'	128
<b>CCNE1</b>	5'-ACTCAACGTGCAAGCCTCG-3'	5'-GCTCAAGAAAGTGCTGATCCC-3'	141
<b>CCNE2</b>	5'-TCAAGACGAAGTAGCCGTTTAC-3'	5'-TGACATCCTGGGTAGTTTTCTC-3'	115
<b>CDK1</b>	5'-AAACTACAGGTCAAGTGGTAGCC-3'	5'-TCCTGCATAAGCACATCCTGA-3'	148
<b>CDK2</b>	5'-CCAGGAGTTACTTCTATGCCTGA-3'	5'-TTCATCCAGGGGAGGTACAAC-3'	90
<b>CDK4</b>	5'-ATGGCTACCTCTCGATATGAGC-3'	5'-CATTGGGGACTCTCACACTCT-3'	124
<b>CDK6</b>	5'-CCAGATGGCTCTAACCTCAGT-3'	5'-AACTTCCACGAAAAAGAGGCTT-3'	152
<b>CDK7</b>	5'-ATGGCTCTGGACGTGAAGTCT-3'	5'-GCGACAATTTGGTTGGTGTTT-3'	116
<b>CDKN1A</b>	5'-TGTCCGTCAGAACCCATGC-3'	5'-AAAGTCGAAGTTCCATCGCTC-3'	139
<b>CDKN1B</b>	5'-TAATTGGGGCTCCGGCTAACT-3'	5'-TGCAGGTCGCTTCCTTATTCC-3'	116
<b>CDKN1C</b>	5'-ACGAGGAGCTGAGTCGTGAG-3'	5'-CTGTCCACCTCGGTCCACT-3'	136
<b>CDKN2A</b>	5'-ATGGAGCCTTCGGCTGACT-3'	5'-GTAAGTATTCGGTGCGTTGGG-3'	108
<b>CDKN2B</b>	5'-GAATGCGCGAGGAGAACA-3'	5'-CATCATCATGACCTGGATCGC-3'	170
<b>CDKN2C</b>	5'-GGGGACCTAGAGCAACTTACT-3'	5'-CAGCGCAGTCCTTCCAAAT-3'	81
<b>CDKN2D</b>	5'-AGTCCAGTCCATGACGCAG-3'	5'-ATCAGGCACGTTGACATCAGC-3'	87
<b>CDKN3</b>	5'-GGACTCTGACATAGCCAGC-3'	5'-CTGTATTGCCCCGGATCCTC-3'	209
<b>Angiogenesis pathway-related genes</b>			
<b>ANGPT1</b>	5'-TCGTGAGAGTACGACAGACCA-3'	5'-TCTCCGACTTCATGTTTTCCAC-3'	173
<b>ANGPT2</b>	5'-ACCCCACTGTTGCTAAAGAAGA-3'	5'-CCATCCTCACGTCGCTGAATA-3'	184
<b>TIE1</b>	5'-AAGCAGACAGACGTGATCTGG-3'	5'-GCACGATGAGCCGAAAGAAG-3'	184
<b>TIE2</b>	5'-CAGGATACGAACCATGAAGATGC-3'	5'-GGGGCACTGAATGGATGAAG-3'	167
<b>VEGFA</b>	5'-AGGGCAGAATCATCACGAAGT-3'	5'-AGGGTCTCGATTGGATGGCA-3'	75
<b>VEGFR1</b>	5'-GAAAACGCATAATCTGGGACAGT-3'	5'-GCGTGGTGTGCTTATTTGGA-3'	173
<b>VEGFR2</b>	5'-GTGATCGGAAATGACACTGGAG-3'	5'-CATGTTGGTCACTAACAGAAGCA-3'	124
<b>Other genes</b>			
<b>ATP5F1E</b>	5'-GGCTGGACTCAGCTACATCC-3'	5'-TTACGTTGCTGCCAGAAGTCT-3'	110
<b>ATP5PF</b>	5'-GTTCTCCTCTGTCAATTCGGTCA-3'	5'-TCCAGATGTCTGTCGCTTAGAT-3'	151
<b>CALD1</b>	5'-TGGAGGTGAATGCCCAGAAC-3'	5'-GAAGGCGTTTTTGGCGTCTTT-3'	138
<b>COL4A1</b>	5'-GGGATGCTGTTGAAAGGTGAA-3'	5'-GGTGGTCCGGTAAATCCTGG-3'	113
<b>COL5A2</b>	5'-GACTGTGCCGACCCTGTAAC-3'	5'-CCTGGACGACCACGTATGC-3'	155
<b>COX6A1</b>	5'-AGTTGGTGTGTCTCGGTTTC-3'	5'-GTGAGAGTCTTCCACATGCGA-3'	117
<b>COX6C</b>	5'-CCAAAACCTCGGATGCGTG-3'	5'-AAATCTGCGTATGCCTTCTTCT-3'	137
<b>COX7A2</b>	5'-CTCGGAGGTAGTTCCGGTTC-3'	5'-TCTGCCCAATCTGACGAAGAG-3'	122
<b>COX7B</b>	5'-CTTGGTCAAAAGCGCACTAAATC-3'	5'-AAAATCAGGTGTACGTTTCTGGT-3'	91
<b>COX7C</b>	5'-GGTCCGTAGGAGCCACTATGA-3'	5'-GTGTCTTACTACAAGGAAGGGTG-3'	136
<b>CTHRC1</b>	5'-CAATGGCATTCCGGGTACAC-3'	5'-GTACACTCCGCAATTTCCCAA-3'	168
<b>ETFA</b>	5'-GTTTTCTGTCCGTGGAACATCC-3'	5'-ATTTCTGGTCAAGCCACTCTG-3'	116
<b>GFP</b>	5'-TCTATATCATGGCCGACAAGC-3'	5'-GGTGTCTGCTGGTAGTGG-3'	110
<b>HTRA1</b>	5'-TCCCAACAGTTTGCGCCATAA-3'	5'-CCGGCACCTCTCGTTTAGAAA-3'	119
<b>IL32</b>	5'-TGGCGGCTTATTATGAGGAGC-3'	5'-CTCGGCACCGTAATCCATCTC-3'	78
<b>ITGAV</b>	5'-ATCTGTGAGGTGGAACAGGA-3'	5'-TGGAGCATACTCAACAGTCTTG-3'	136
<b>LGALS1</b>	5'-CTGTGCCTGCACTTCAACC-3'	5'-CATCTGGCAGCTTGACGGT-3'	187

<b>MGP</b>	5'-TCCGAGAACGCTCTAAGCCT-3'	5'-GCAAAGTCTGTAGTCATCACAGG-3'	65
<b>NDUFA1</b>	5'-GCGTACATCCACAGGTTCACT-3'	5'-GCGCCTATCTCTTTCCATCAGA-3'	90
<b>NDUFA4</b>	5'-ATGCTCCGCCAGATCATCG-3'	5'-TGCCAGACGCAAGAGATACAG-3'	111
<b>NDUFB4</b>	5'-ATGTCGTTCCCAAAGTATAAGCC-3'	5'-GAAGCAGGTACTCTCGTTTCAG-3'	148
<b>NDUFS6</b>	5'-TTCGGTTTGTAGGTCGTCAGA-3'	5'-CCATCGCACGCTATCACCC-3'	106
<b>SUCLA2</b>	5'-GCTGCCTAGTAAATGGTGCTG-3'	5'-GTTGACCAGAATAGCCAGTACC-3'	173
<b>TIMM8B</b>	5'-TCACTTCATGGAGTTATGTTGGG-3'	5'-AGACAATTTTCAGTGCGAGAGTC-3'	78
<b>TPM1</b>	5'-GCCGACGTAGCTTCTCTGAAC-3'	5'-TTTGGGCTCGACTCTCAATGA-3'	160
<b>UQCRB</b>	5'-GGTAAGCAGGCCGTTTCAG-3'	5'-AGGTCCAGTGCCCTCTTAATG-3'	200
<b>UQCRH</b>	5'-GAGGACGAGCAAAAGATGCTT-3'	5'-CGAGAGGAATCACGCTCATCA-3'	170
<b>UQCRQ</b>	5'-ATCCGCACGTCTTCACTAAAG-3'	5'-TGGATCTCTCGAACTCTTCAGTC-3'	132
<b>VIM</b>	5'-GACGCCATCAACACCGAGTT-3'	5'-CTTTGTCGTTGGTTAGCTGGT-3'	238

**Dataset S1 (separate file).** RT-qPCR quantification results of cellular and exosomal mRNAs.