Figure S1. (A) Amplification of angio-miRNAs. U6 was used as an internal control. (B) Amplification of target mRNAs of angio-miRNAs. GAPDH was used as an internal control. (C and D) Melting curves of angio-miRNAs. (E) Melting curves of target mRNAs of angio-miRNAs. Angio-miRNA, angiogenesis-regulatory microRNA. HGS, hepatocyte growth factor-regulated tyrosine kinase substrate; VEGFR2, vascular endothelial growth factor receptor 2; HUVEC, human umbilical vein endothelial cell; CM, conditioned medium; RASA1, RAS P21 protein activator 1. ΔRn indicates the fluorescence intensity minus reference dye (passive reporter) and –R indicates the derivatives of melt curves (fluorescence intensity).

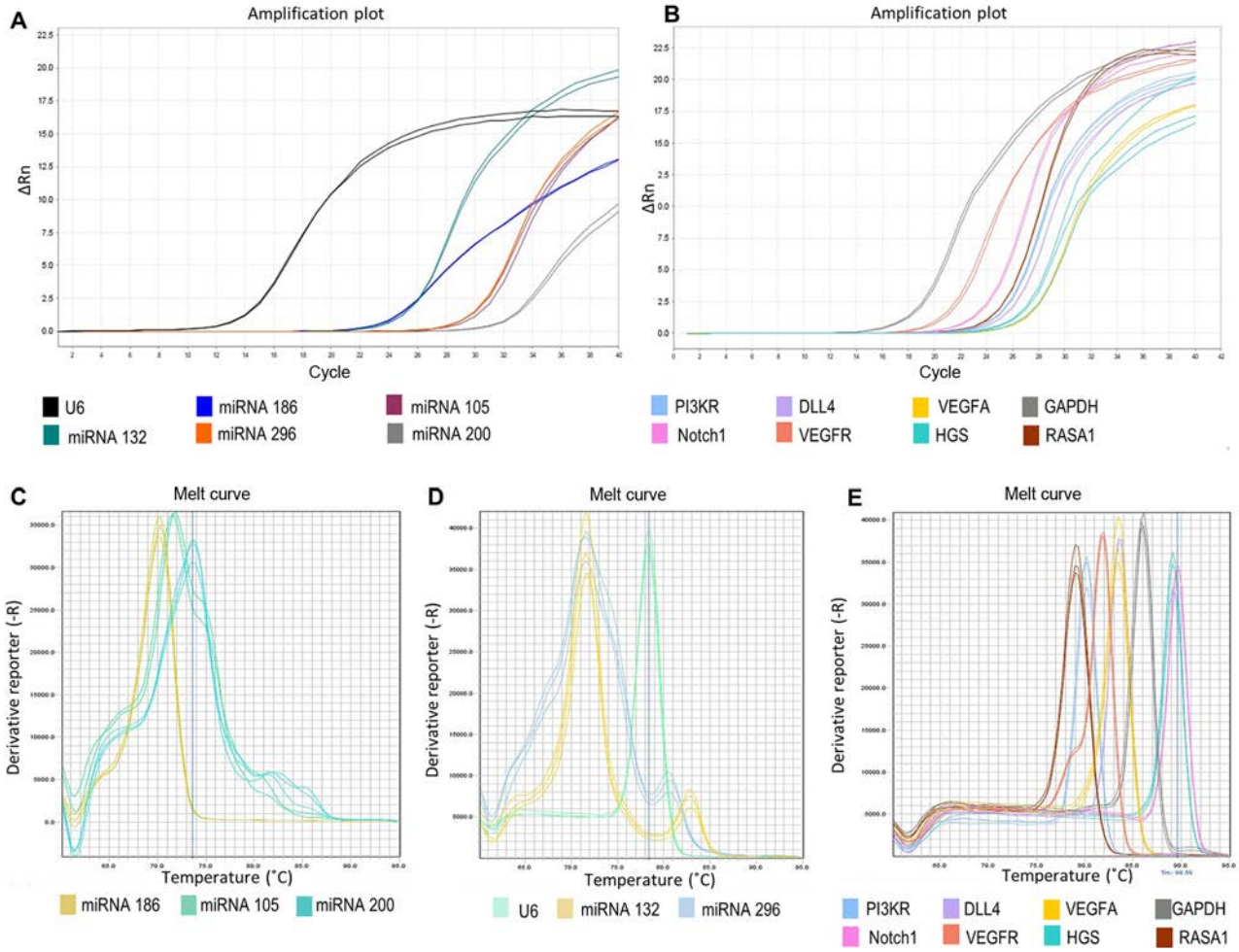
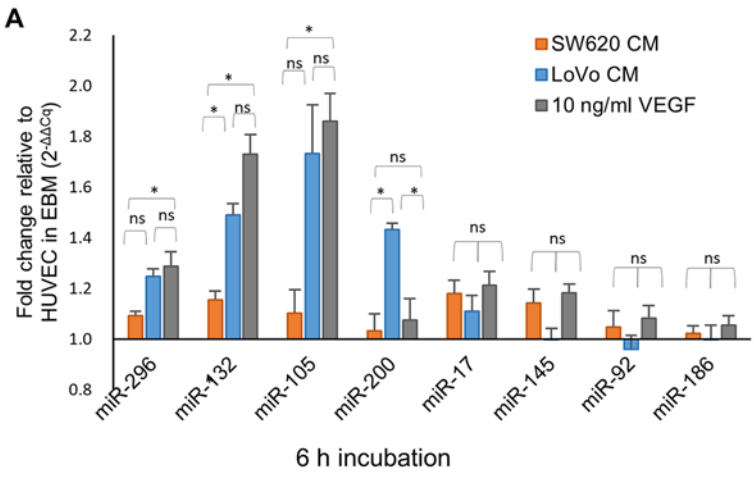
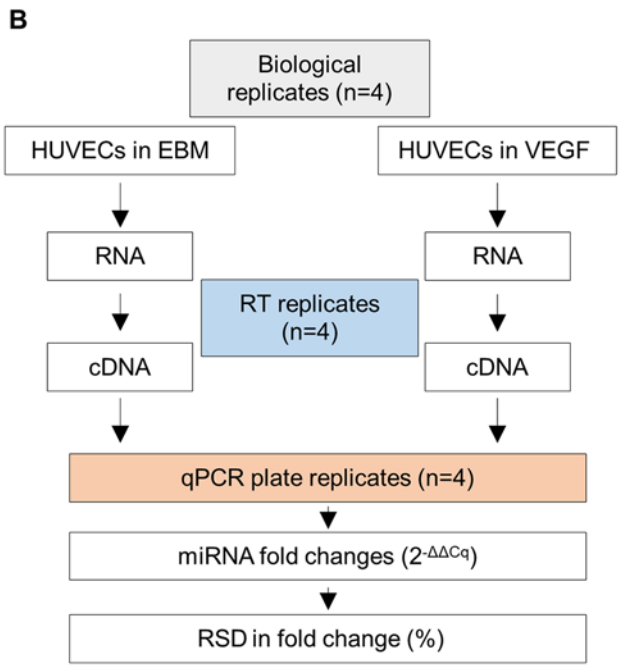


Figure S2. (A) Fold-changes in angio-miRNA expression relative to EBM for SW620-CM, LoVo-CM and 10 ng/ml VEGF-treated HUVECs at 6 h. (B) Experimental design for assessing miRNA fold-change variance of each step in RT-qPCR. Four replicates were included in each step. (C) RSD in fold-changes of indicated miRNA. Average values were derived from the four miRNA. Angio-miRNA, angiogenesis-regulatory microRNA; miRNA, miR, microRNA; CM, conditioned medium; EBM, endothelial cell basal medium; HUVEC, human umbilical vein endothelial cell; VEGF, vascular endothelial growth factor; RT-qPCR, reverse transcription-quantitative PCR; RSD, relative standard deviation.





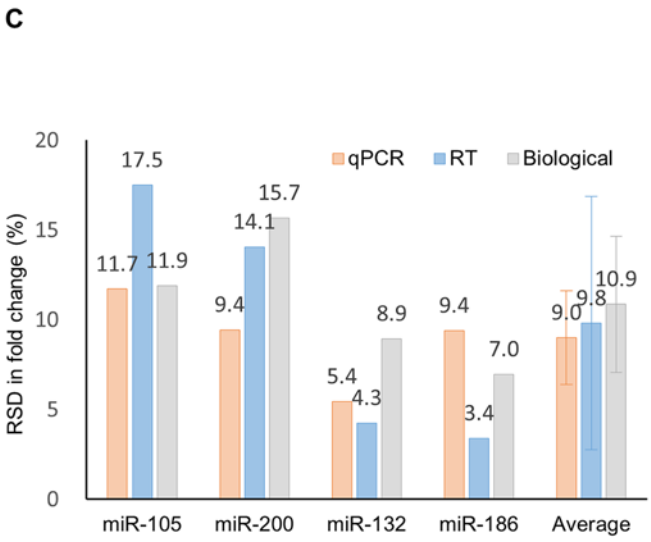


Table SI. Angio-miRNA primers in reverse transcription-quantitative PCR.

Primer name	miRNA primer sequence (5' to 3')
U6_F	CTCGCTTCGGCAGCACA
U6_R	AACGCTTCACGAATTTGCGT
miR296_F	CCCTCAATCCTGTTGTGCCT
miR132_F	GGTAACAGTCTACAGCCATG
miR105_F	TGTTTGCCTCCTTCTTCGTC
miR200_F	TGAGCATCTTACCGGACAGT
miR17_F	GAATAATGTCAAAGTGCTTACAGTG
miR145_F	GTCCAGTTTTCCCAGGAATCCCT
miR92_F	TATTGCACTTGTCCCGGCC
miR186_F	TTCCAAAGAATTCTCCTTTTGGG
miR185_F	GGGATTGGAGAGAAAGGCAG

Table SII. Target mRNA primers in reverse transcription-quantitative PCR.

Primer name	mRNA primer sequence (5' to 3')
HGS_F	CCACAATGGCGAGTCTGA
HGS_R	GAGGGCTGGTAGAGCACA
VEGFR2_F	GGGATTGACTTCAACTGG
VEGFR2_R	ATGGGATTGGTAAGGATG
PIK3R1_F	TGGACGGCGAAGTAAAGCATT
PIK3R1_R	AGTGTGACATTGAGGGAGTCG
RASA1_F	GGACGAAGGTGACTCTCTGGAT
RASA1_R	GGAGGAGCGGTCAACGGTAT
GAPDH_F	ACCACAGTCCATGCCATCAC
GAPDH_R	TCCACCACCCTGTTGCTGTA