

Table S1. Primer sequences.**(a) miR-9 quantitative MSP**

Gene	Primers (5'-3')	Size (bp)
<i>miR-9-1</i>	F: GAAATGTCGTTCTGAATTAGTGAG R: GAAAAAAACCGACCTCACGA P: GGTGTTGGTTAGTTTTCGCGTTTTAGTTTTTC -6FAM	123
<i>miR-9-2</i>	F: CGTTGTCGGAGATTATTTGTTG R: ATACCGAAAAATAATCGTCCA P: ATTTTGAAGGTAATAGATTTTCGTTTGGATGTTTTAGTCGC -YY	177
<i>miR-9-3</i>	F: TGTGCGTGTGTTTGTATT R: CTTAACCAATACCGCTACCG P: TTCGGGTACGGCGTTCTGTTTAGGTTTTTCG -DFO	135
<i>ACTB</i>	F: TGGTGATGGAGGAGTTTAGTAAGT R: AACCAATAAAACCTACTCCTCCCTTAA P: ACCACCACCCAACACACAATAACAAACACA -CY5	133

bp, base pairs; F, Forward primer; R, Reverse primer; P, probe

(b) TaqMan quantitative RT-PCR

Gene	Primers (5'-3')	Size (bp)
<i>CDH1</i>	F: TTGACGCCGAGAGCTACAC R: GACCGGTGCAATCTTCAAA P: GCGTCCTGGGCAGAGT -6FAM	93
<i>CDH2</i>	F: CCACCTTAAAATCTGCAGGC R: GTGCATGAAGGACAGCCTCT P: GGAAAAAGAAAAGTACAATATGAGAGCAGT -6FAM	100
<i>snRNP U1A</i>	F: TCCTCACCAACCTGCCAGA R: TGAAGCCAGGGAAGTACTGATTGA P: AGACCAACGAGCTCATGCTGTCCATG -6FAM	72
<i>TWIST1</i>	F: GTCCGCGTCCCCTAGC R: TCCATTTTCTCCTTCTCTGGAA P: GCAGGGCCGGAGACCTA -6FAM	90

bp, base pairs; F, Forward primer; R, Reverse primer; P, probe

(c) TWIST 3'UTR cloning & mutagenesis

Gene	Primers (5'-3')
3'UTR-TWIST1	F: TCGAGAGCTCTA GCCGGAGACCTAGATGTCATTGTTTC R: ACTGCTCGAGTA GCCCGTCTGGGAATCACTGTC
3'UTR-TWIST1_mut	F: tctTTTTCTTGGAATTAGAAGAGC R: aaccCATATATTTTTATTTTTAGTTATCCAG

bp, base pairs; F, Forward primer; R, Reverse primer; restriction site (F: SacI, R: XhoI); lower case: induced mutation

Table S2. Expression of miR-9-5p in whole miRNome sequencing data from the TCGA depository [32]. Data of 211 cervical carcinomas, which were either positive for HPV16 or HPV18, were included. * $p < 0.05$.

Comparison	p-value	Direction
<u>by HPV type:</u>		
HPV16: SCC (n=145) vs AC (n=27)	0.001 *	higher in SCC
HPV18: SCC (n=28) vs AC (n=11)	0.386	higher in SCC
<u>by histotype:</u>		
SCC: HPV16 (n=145) vs HPV18 (n=28)	0.209	higher in HPV18
AC: HPV16 (n=27) vs HPV18 (n=11)	0.021 *	higher in HPV18

Table S3. Correlation of miR-9-5p expression with expression of TWIST1, CDH1, and CDH2 per histotype. 200 cervical carcinomas were included, for which both whole miRNome and whole transcriptome sequencing data from the TCGA depository was available [32]. Spearman correlation coefficient rho and the associated p-value were assessed. # $p < 0.1$, * $p < 0.05$.

Spearman correlation	TWIST1		CDH1		CDH2	
	Rho	p-value	Rho	p-value	Rho	p-value
SCC (n=161)	-0.138	0.082 #	0.031	0.696	-0.167	0.035 *
AC (n=39)	0.367	0.022 *	-0.117	0.478	0.281	0.083 #

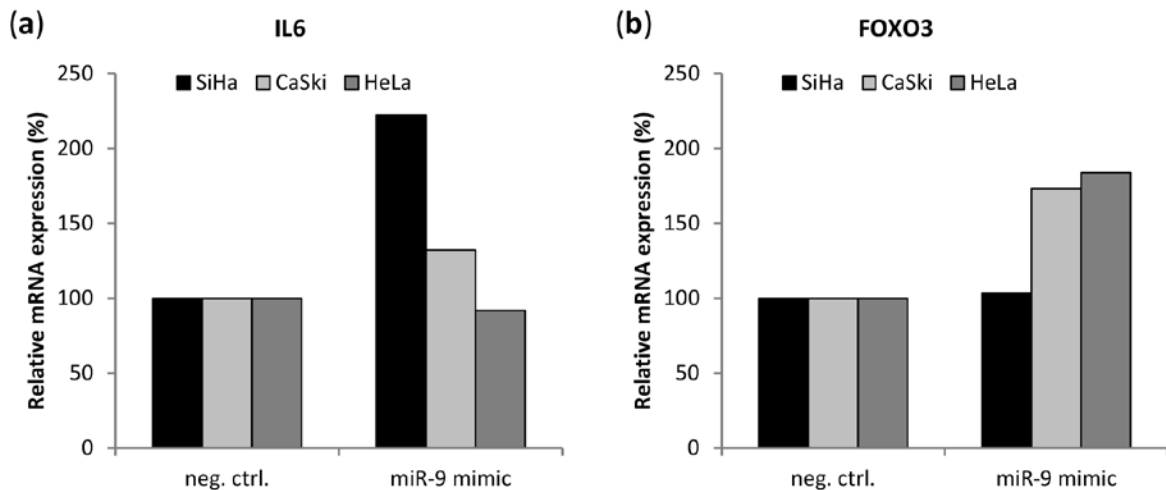


Figure S1. Effect of miR-9-5p on IL6 and FOXO3 in cervical cancer cell lines. Expression of (a) IL6 and (b) FOXO3 mRNAs upon overexpression of miR-9-5p in cervical cancer cell lines SiHa, CaSki, and HeLa relative to the respective negative control. FOXO3 melting curve analysis indicated aspecific products and FOXO3 expression data should therefore be interpreted with caution.