

Supporting Information

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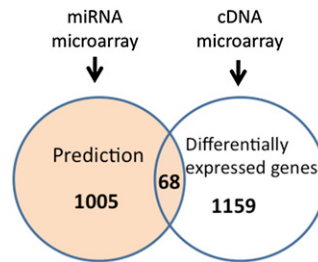


Fig. S1. Venn diagram of the overlap between differentially expressed genes from mRNA microarray data and putative miR targets.

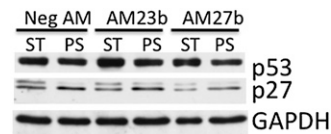


Fig. S2. Effects of miR-23b and -27b on cell cycle proteins. HUVECs were transfected with Neg. AM, AM23b, and AM27b. Twenty-four hours after transfection, cells were subjected to PS or ST for 24 h. Western blot analysis of p53 and p27^{kip} expressions on total cell extract with antibodies against p53 and p27_{kip} (Santa Cruz). Blots shown here are representative of three independent experiments with similar results.

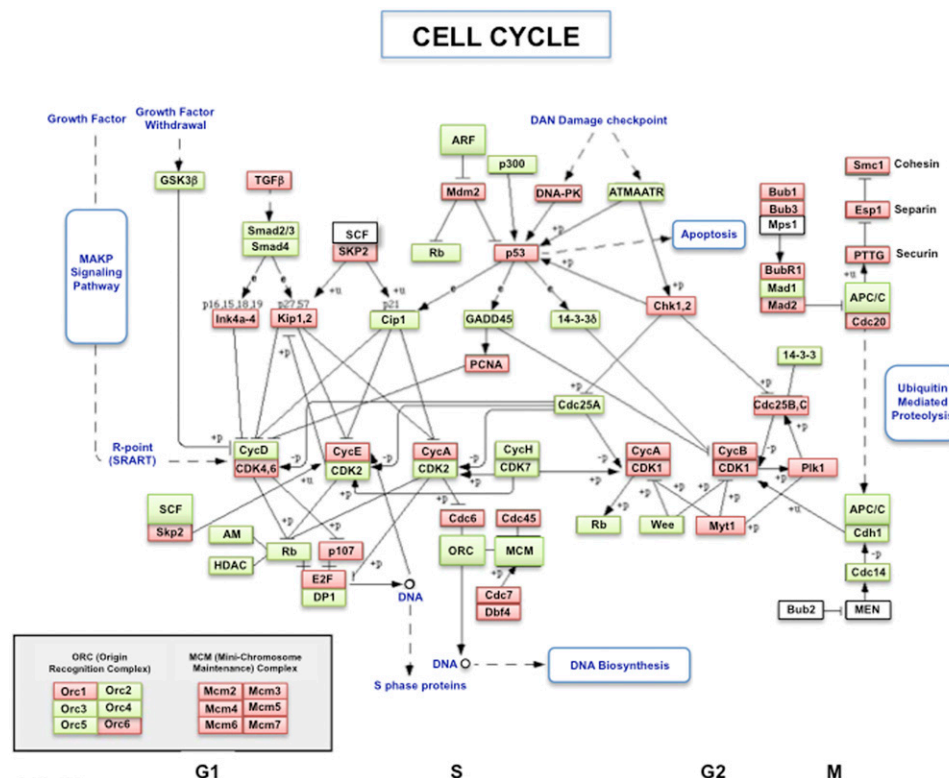


Fig. S3. Mapping of differentially expressed genes to "cell cycle" network. The figure of cell cycle network was obtained from KEGG pathway database. The boxes represent the components identified in human cell cycle regulations. The red boxes indicate that the corresponding mRNAs were differentially expressed in our PS vs. ST microarray data with the application of a 1.5-fold change cutoff. The green boxes represent the known molecules reported in the literature, and open boxes indicate the predicted molecules by the pathway finder.

Table S1. The top 10 gene ontology terms of up- and down-regulated genes in ECs under PS vs. ST

GO terms representing cellular compartment		
GO	Cellular compartment	P value
GO:0005694	Chromosome	3.60×10^{-16}
GO:0044427	Chromosomal part	3.20×10^{-15}
GO:0005819	Spindle	9.90×10^{-15}
GO:0000775	Chromosome, pericentric region	1.80×10^{-14}
GO:0015630	Microtubule cytoskeleton	2.40×10^{-11}
GO:0043232	Intracellular nonmembrane-bound organelle	$3.90E \times 10^{-7}$
GO:0043228	Nonmembrane-bound organelle	3.90×10^{-7}
GO:0044430	Cytoskeletal part	1.80×10^{-5}
GO:0005634	Nucleus	$2.30E \times 10^{-5}$
GO:0005815	Microtubule organizing center	$4.10E \times 10^{-5}$
GO terms representing molecular function		
GO	Molecular function	P value
GO:0005515	Protein binding	$1.10E \times 10^{-11}$
GO:0030554	Adenyl nucleotide binding	$1.00E \times 10^{-7}$
GO:0032559	Adenyl ribonucleotide binding	1.50×10^{-7}
GO:0005488	Binding	2.00×10^{-7}
GO:0005524	ATP binding	2.60×10^{-7}
GO:0017076	Purine nucleotide binding	1.40×10^{-6}
GO:0032555	Purine ribonucleotide binding	1.90×10^{-6}
GO:0032553	Ribonucleotide binding	1.90×10^{-6}
GO:0008094	DNA-dependent ATPase activity	2.30×10^{-5}
GO:0000166	Nucleotide binding	2.70×10^{-5}

Table S2. Validation of selected miRs with TaqMan RT-PCR

miR	Microarray	TaqMan PCR
miR-27b	2.3 ± 1.1	$2.6 \pm 0.4^*$
miR-23b	1.7 ± 0.4	$1.7 \pm 0.4^*$
miR-923	2.2 ± 0.1	$2.2 \pm 0.2^*$
miR-16	0.5 ± 0.1	$0.8 \pm 0.1^*$
miR-106a	0.6 ± 0.1	$0.6 \pm 0.1^*$
miR-19b	0.3 ± 0.1	1 ± 0.2
miR-221	0.7 ± 0.1	1.3 ± 0.1
miR-26b	—	$1.1 \pm 0.1^*$
let-7e	—	$1.1 \pm 0.1^*$

*indicates the PCR results are in agreement with microarray data.

Table S3. The overlapping GO terms between putative miR targets and differentially expressed genes

GO	Biological process	P value
GO:0000079	Regulation of cyclin-dependent protein kinase activity	2.84×10^{-6}
GO:0022402	Cell cycle process	6.82×10^{-5}
GO:0051329	Interphase of mitotic cell cycle	0.0001095
GO:0007017	Microtubule-based process	0.0002482
GO:0007001	Chromosome organization and biogenesis (sensu Eukaryota)	0.0027113
GO:0043549	Regulation of kinase activity	0.0066311
GO:0050790	Regulation of catalytic activity	0.0096842
GO:0007050	Cell cycle arrest	0.017707
GO:0007154	Cell communication	0.03393
GO:0048839	Inner ear development	0.0433963
GO:0006865	Amino acid transport	0.0472377