

**Table S1** Patient characteristics

Index	Age (year)	BMI (kg/m <sup>2</sup> )	Basal FSH levels (IU/L)	Basal LH levels (IU/L)	Number of retrieved oocytes (n)
Nonpregnant groups					
1	31	21.6	7.16	4.37	14
2	30	21.9	5.60	4.44	14
3	25	23.2	6.92	4.72	17
Pregnant groups					
1	34	22.6	8.17	4.36	15
2	32	20.6	7.46	5.27	10
3	28	23.5	8.85	4.2	8
4	29	21.9	6.6	4.94	16
5	33	22.6	7.89	5.28	17

BMI, body mass index; FSH, follicle-stimulating hormone; LH, luteinizing hormone.

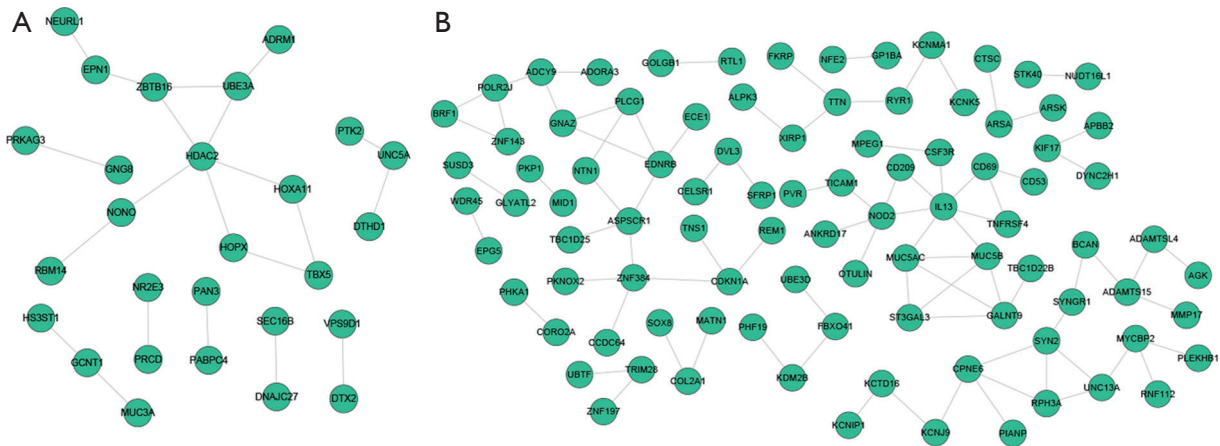
**Table S2** The primers used in qRT-PCR experiments

miRNA	Primer sequences
hsa-miR-483-5p	5'-AAGACGGGAGGAAAGAAGGGAG-3'
hsa-miR-199a-5p	5'-CCCAGTGTTCCAGACTACCTGTTC-3'
hsa-miR-199a-3p	5'-ACAGTAGTCTGCACATTGGTTA-3'
hsa-miR-379-5p	5'-TGGTAGACTATGGAACGTAGG-3'
hsa-miR-432-5p	5'-TCTTGGAGTAGGTCATTGGGTGG-3'
hsa-miR-99a-5p	5'-AACCCGTAGATCCGATCTTGTG-3'

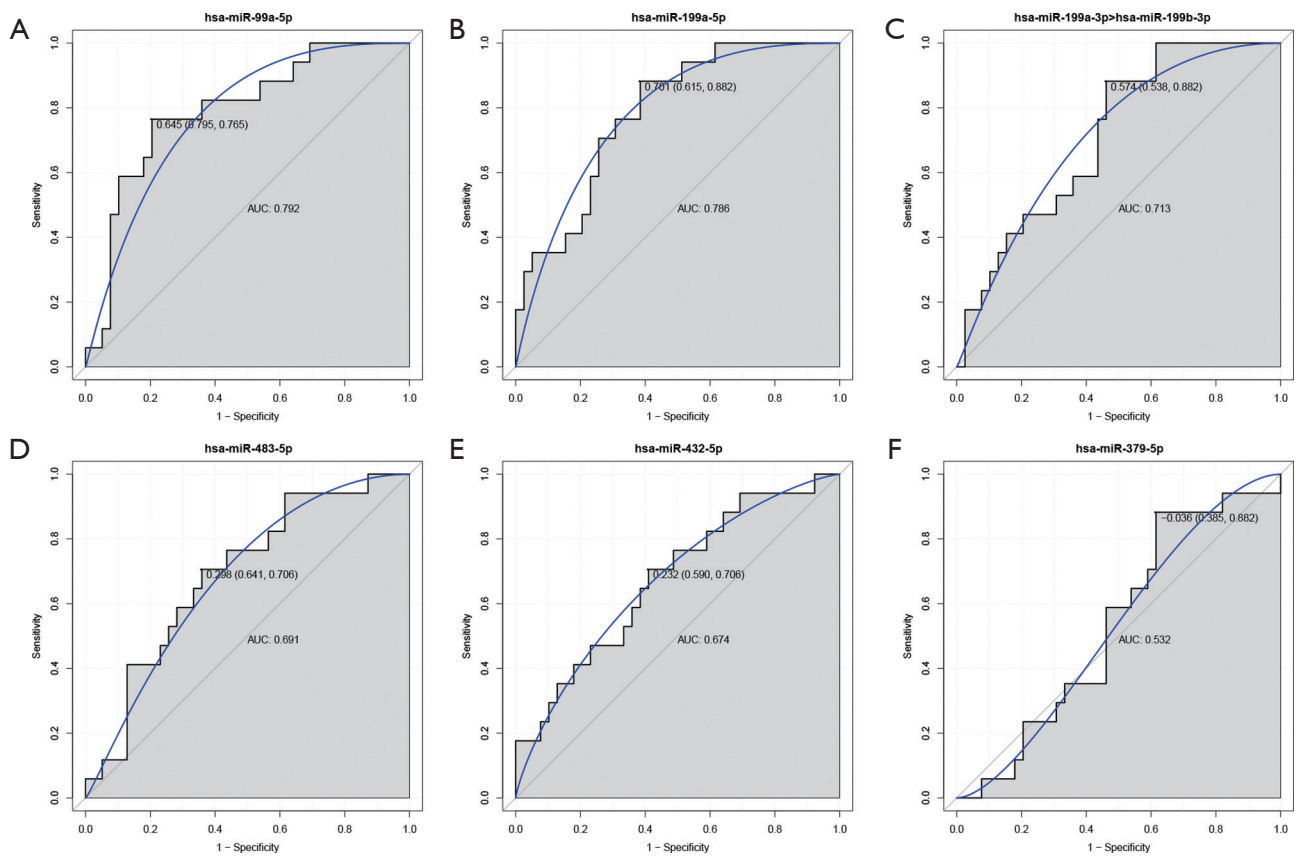
qRT-PCR, quantitative real-time polymerase chain reaction.

	Predicted consequential pairing of target region (top) and miRNA (bottom)	Site type	Context++ score	Context++ score percentile	Weighted context++ score	Conserved branch length	PCT
Position 277-283 of ASPSCR1 3' UTR <i>hsa-miR-432-5p</i>	5' ...AGUUAUUUACACUUC <u>CUCCAAG</u> ...                 3' GGUGGGUACUGGAUG <u>GAGGUUCU</u>	7mer-m8	-0.13	80	-0.01	0.016	N/A
Position 963-969 of ASPSCR1 3' UTR <i>hsa-miR-432-5p</i>	5' ...CCCACAGCCUGCGU <u>CUCCAAG</u> ...                 3' GGUGGGUACUGGAUG <u>GAGGUUCU</u>	7mer-m8	-0.02	34	0.00	0.031	N/A
Position 1297-1303 of ZNF384 3' UTR <i>hsa-miR-432-5p</i>	5' ...GUAUUUGGGGAGAUG <u>UCAAGAA</u> ...                 3' GGUGGGUACUGGAUG <u>GAGGUUCU</u>	7mer-A1	-0.16	87	-0.05	0.073	N/A
Position 404-410 of GALNT9 3' UTR <i>hsa-miR-432-5p</i>	5' ...CGCAGGCCUCC <u>AUGCUCCAAG</u> ...                 3' GGUGGGUACUGGAUG <u>GAGGUUCU</u>	7mer-m8	-0.11	75	-0.11	0.145	N/A
Position 4940-4946 of ZBTB16 3' UTR <i>hsa-miR-483-5p</i>	5' ...UCCUCCUCUGGCUC <u>CCCGUCUC</u> ...                 3' GAGGGAAGAAAGG <u>GGCAGAA</u>	7mer-m8	-0.16	67	-0.15	0	N/A
Position 1762-1769 of HDAC2 3' UTR <i>hsa-miR-483-5p</i>	5' ...CCUCCACCAUGCC <u>CCCGUCUA</u> ...                 3' GAGGGAAGAAAGG <u>GGCAGAA</u>	8mer	-0.36	96	-0.01	0	N/A

**Figure S1** Targeted relationship validation of *hsa-miR-432-5p*-*ASPSCR1*/*ZNF384*/*GALNT9* and *hsa-miR-483-5p*-*ZBTB16*/*HDAC2* by TargetScan software. The TargetScanHuman page for the 3' UTR of the *ASPSCR1*, *ZNF384*, *GALNT9*, *ZBTB16*, and *HDAC2* gene. Boxed are predicted *hsa-miR-432-5p* and *hsa-miR-483-5p* sites. The multiple sequence alignment shows that orthologous sites can be detected (red highlighting) between the miRNA and targeted mRNAs. The position, site type, context++ score, context++ score percentile, weighted context++ score, branch-length score, and PCT score are also shown for each site. miRNA, microRNA; mRNA, messenger RNA.



**Figure S2** PPI networks of the targets of known DEmiRNAs. (A) D3 cleavage, (B) D5 blastocyst. PPI, protein-protein interaction; DEmiRNAs, differentially expressed miRNAs; D3 cleavage, cleavage on day 3; D5 blastocyst, blastocyst stages on day 5.



**Figure S3** ROC curves of known DE miRNAs. (A) hsa-miR-99a-5p, (B) hsa-miR-199a-5p, (C) hsa-miR-199a-3p>hsa-miR-199b-3p, (D) hsa-miR-483-5p, (E) hsa-miR-432-5p, and (F) hsa-miR-379-5p. ROC, receiver operating characteristic; DE miRNAs, differentially expressed miRNAs.