

**Supplementary Table S1. Genotype frequencies of miRNA gene polymorphisms in control subjects and recurrent pregnancy loss patients.**

Genotype	Controls (n=281)	RPL patients (n=381)	AOR (95% CI)	<i>P</i>	FDR- <i>P</i>
<i>miR-10aA&gt;T</i>					
AA	230 (81.9)	285 (74.8)	1.000 (reference)		
AT	50 (17.8)	88 (23.1)	1.420 (0.963–2.094)	0.077	0.584
TT	1 (0.4)	8 (2.1)	6.476 (0.804–52.176)	0.079	0.237
Dominant (AA vs. AT+TT)			1.520 (1.038–2.227)	<b>0.032</b>	0.709
Recessive (AA+AT vs. TT)			6.003 (0.746–48.285)	0.092	0.276
HWE <i>P</i>	0.318	0.695			
<i>miR-30cA&gt;G</i>					
AA	106 (37.7)	163 (42.8)	1.000 (reference)		
AG	144 (51.2)	182 (47.8)	0.821 (0.591–1.139)	0.237	0.237
GG	32 (11.0)	36 (9.4)	0.742 (0.432–1.276)	0.281	0.422
Dominant (AA vs. AG+GG)			0.810 (0.591–1.111)	0.191	0.191
Recessive (AA+AG vs. GG)			0.842 (0.506–1.400)	0.507	0.606
HWE- <i>p</i>	0.104	0.144			
<i>miR-181aT&gt;C</i>					
TT	198 (70.5)	247 (64.8)	1.000 (reference)		
TC	78 (27.8)	125 (32.8)	1.286 (0.916–1.805)	0.147	0.221
CC	5 (1.8)	9 (2.4)	1.483 (0.488–4.509)	0.487	0.487
Dominant (TT vs. TC+CC)			1.294 (0.929–1.803)	0.128	0.191
Recessive (TT+TC vs. CC)			1.337 (0.443–4.037)	0.606	0.606
HWE- <i>p</i>	0.393	0.137			
<i>miR-499bA&gt;G</i>					
AA	188 (66.9)	221 (58.0)	1.000 (reference)		
AG	87 (31.0)	139 (36.5)	1.361 (0.977–1.896)	0.068	0.204
GG	6 (2.1)	21 (5.5)	2.956 (1.168–7.482)	<b>0.022</b>	0.066
Dominant (AA vs. AG+GG)			1.465 (1.062–2.020)	<b>0.020</b>	0.060
Recessive (AA+AG vs. GG)			2.677 (1.066–6.725)	<b>0.036</b>	0.108
HWE- <i>p</i>	0.263	0.888			

Abbreviations: AOR, adjusted odds ratio; CI, confidence interval; FDR-*P*, false-positive discovery rate-corrected; PL, pregnancy loss; RPL, recurrent pregnancy loss.

**Supplementary Table S2. Four allele combination analysis of miRNA polymorphisms in recurrent pregnancy loss patients and control subjects.**

Allele combination	Control (n= 281)	Case (n=381)	OR(95% CI)	<i>P</i> <sup>a</sup>	FDR- <i>P</i>
<i>miR-10aA&gt;T/miR 181a T&gt;C/miR-30cA&gt;G/miR-499A&gt;G</i>					
A-T-A-A	236	272	1.000 (reference)		
A-T-A-G	39	66	1.468 (0.953 - 2.263)	0.085	0.128
A-T-G-A	129	139	0.935 (0.695 - 1.257)	0.705	0.705
A-T-G-G	28	63	1.952 (1.210 - 3.149)	<b>0.006</b>	0.036
A-C-A-A	44	59	1.163 (0.759 - 1.784)	0.516	0.619
A-C-A-G	10	27	2.343 (1.111 - 4.942)	<b>0.026</b>	0.056
A-C-G-A	13	32	2.136 (1.095 - 4.165)	<b>0.028</b>	0.056
A-C-G-G	12	0	0.035 (0.002 - 0.590)	<b>0.0001</b>	0.0001
T-T-A-A	11	44	3.471 (1.752 - 6.874)	<b>0.0001</b>	0.0001
T-T-A-G	7	23	2.851 (1.202 - 6.764)	<b>0.014</b>	0.056
T-T-G-A	21	11	0.455 (0.215 - 0.962)	<b>0.044</b>	0.088
T-T-G-G	4	2	0.434 (0.079 - 2.391)	0.425	0.425
T-C-A-A	9	18	1.735 (0.765 - 3.937)	0.235	0.313
T-C-A-G	0	0	-	-	
T-C-G-A	0	7	13.020 (0.739 - 229.300)	<b>0.017</b>	0.017
T-C-G-G	0	0	-	-	

Abbreviations: CI, confidence interval; FDR, false-discovery rate; OR, odds ratio; RPL, recurrent pregnancy loss. ORs and 95% CIs for each allele combination were calculated with reference to frequencies of all others using Fisher's exact test.

<sup>a</sup>Fisher's exact test. <sup>b</sup>FDR-adjusted *P*-value.

**Supplementary Table S3. Three allele combination analysis of miRNA polymorphisms in recurrent pregnancy loss patients and control subjects.**

Allele combination	Control (n= 281)	Case (n=381)	OR(95% CI)	<i>P</i> <sup>a</sup>	FDR- <i>P</i>
<b><i>miR-10aA&gt;T/miR-181aT&gt;C/miR-30cA&gt;G</i></b>					
A-T-A	275	340	1.000 (reference)		
A-T-G	156	201	1.042 (0.801 - 1.355)	0.789	1.000
A-C-A	53	84	1.282 (0.878 - 1.872)	0.216	0.432
A-C-G	26	33	1.027 (0.599 - 1.758)	1.000	1.000
T-T-A	19	64	2.724 (1.594 - 4.658)	0.0001	0.000
T-T-G	24	13	0.438 (0.219 - 0.877)	0.026	0.039
T-C-A	9	20	1.797 (0.805 - 4.011)	0.181	0.181
T-C-G	0	7	12.140 (0.690 - 213.600)	0.020	0.039
<b><i>miR-181aT&gt;C/miR-30cA&gt;G/miR-499A&gt;G</i></b>					
T-A-A	242	316	1.000 (reference)		
T-A-G	45	89	1.515 (1.020 - 2.250)	0.041	0.090
T-G-A	154	150	0.746 (0.564 - 0.987)	0.045	0.090
T-G-G	32	64	1.532 (0.971 - 2.417)	0.073	0.097
C-A-A	60	77	0.983 (0.674 - 1.433)	0.924	0.924
C-A-G	8	26	2.489 (1.107 - 5.596)	0.031	0.031
C-G-A	7	38	4.157 (1.825 - 9.473)	0.000	
C-G-G	13	3	0.177 (0.050 - 0.627)	0.004	0.008

Abbreviations: CI, confidence interval; FDR, false-discovery rate; OR, odds ratio; RPL, recurrent pregnancy loss. ORs and 95% CIs for each allele combination were calculated with reference to frequencies of all others using Fisher's exact test.

<sup>a</sup>Fisher's exact test. <sup>b</sup>FDR-adjusted *P*-value.

**Supplementary Table S4. Two allele combination analysis of miRNA polymorphisms in recurrent pregnancy loss patients and control subjects.**

Allele combination	Control (n= 281)	Case (n=381)	OR(95% CI)	<i>P</i> <sup>a</sup>	FDR- <i>P</i>
<b><i>miR-10aA&gt;T/miR-181aT&gt;C</i></b>					
A-T	430	541	1.000 (reference)		
A-C	80	117	1.162 (0.851 - 1.587)	0.386	0.386
T-T	44	78	1.409 (0.953 - 2.083)	0.099	0.149
T-C	8	26	2.583 (1.158 - 5.764)	<b>0.021</b>	0.063
<b><i>miR-10aA&gt;T/miR-30cA&gt;G</i></b>					
A-A	329	424	1.000 (reference)		
A-G	181	234	1.003 (0.788 - 1.277)	1.000	1.000
T-A	27	84	2.414 (1.529 - 3.813)	<b>0.0001</b>	0.0001
T-G	25	20	0.621 (0.339 - 1.137)	0.125	0.125
<b><i>miR-181aT&gt;C/miR-30cA&gt;G</i></b>					
T-A	289	405	1.000 (reference)		
T-G	185	214	0.825 (0.644 - 1.058)	0.145	0.435
C-A	66	103	1.114 (0.790 - 1.571)	0.601	0.601
C-G	22	40	1.297 (0.755 - 2.230)	0.419	0.601

Abbreviations: CI, confidence interval; FDR, false-discovery rate; OR, odds ratio; RPL, recurrent pregnancy loss. ORs and 95% CIs for each allele combination were calculated with reference to frequencies of all others using Fisher's exact test.

<sup>a</sup>Fisher's exact test. <sup>b</sup>FDR-adjusted *P*-value.