

Table S1: Demographic features of the subjects enrolled in the study (Recurrent Pregnancy Losses)

Demographic Features	Cases n=200 (%)	Controls n= 240 (%)	p value
Age			
< 30	112 (56)	125 (52.1)	Reference (Ref) 0.25
≥ 30	88 (44)	115 (47.9)	
Miscarriages			
<3	79 (39.5)	-	
≥ 3	121 (60.5)		
Consanguinity			
Yes	70 (35)	41 (17)	Ref <0.05
No	130 (65)	199 (83)	
Family History			
Yes	39 (19.5)	13 (5.4)	Ref <0.05
No	161 (80.5)	227 (94.6)	
TORCH			
Positive	4 (2.6)	0	
Negative	148 (97.3)	240 (100)	
APLA			
Positive	2 (2.5)	0	
Negative	77 (97.5)	240 (100)	
VDRL			
Positive	0	0	
Negative	152 (100)	240 (100)	
USG Findings			
Normal	101(78.3)	188 (98.4)	
Abnormal	28 (21.7)	3 (1.57)	

Ref, Reference

Table S2: The primers, polymerase chain reaction (PCR) conditions and a restriction enzyme used in this study

Primer Pairs		PCR conditions	Restriction Enzymes
PCR-RFLP rs12976445 C/T	5'-TTTTGGTCTTTCTGTCTCTGG -3' 5'-TGGAGGAAGGGTATGAGGAGT-3'	95°C for 5 min (94°C for 30 s, 58°C for 30 s, 72°C for 30 s) × 35 cycles72°C for 7 min	BaeGI
Sequencing rs12976445 C/T	5'-TTTTGGTCTTTCTGTCTCTGG -3' 5'-TGGAGGAAGGGTATGAGGAGT-3'	95°C for 5 min (94°C for 30 s, 58°C for 30 s, 72°C for 30 s) × 35 cycles72°C for 7 min	-
PCR-RFLP rs10404453 A/G	5'-CTGACTCCCTCTTATTCTGG-3' 5'-TAGAGACTGGCAACATGG-3'	95°C for 5 min (94°C for 30 s, 55°C for 30 s, 72°C for 30 s) × 35 cycles72°C for 7 min	MspI
miR-125a	F-5'GGTGTCCCTGAGACCCTTAA-3' R-5' GTGCAGGGTCCGAGGT		

RNU6	F-5' GCTTCGGCAGCACATATACTAAAAT R-5'AACGCTTCACGAATTTGCGT
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Table S3: Multivariate analysis of demographic characteristics, rs 12976445 genotypes and miR-125a expression in Recurrent Miscarriage patients

Parameter	Hazard (B)	95% CI	p Value
Age	1.260	0.78- 2.13	0.308
Family History	1.471	0.80- 3.20	0.183
Consanguinity	0.198	0.46-1.45	0.500
rs12976445 CT	1.266	0.14- 3.99	0.197
rs12976445 CC	1.788	0.39- 4.61	0.037
miR-125a	2.786	0.84- 5.33	0.008

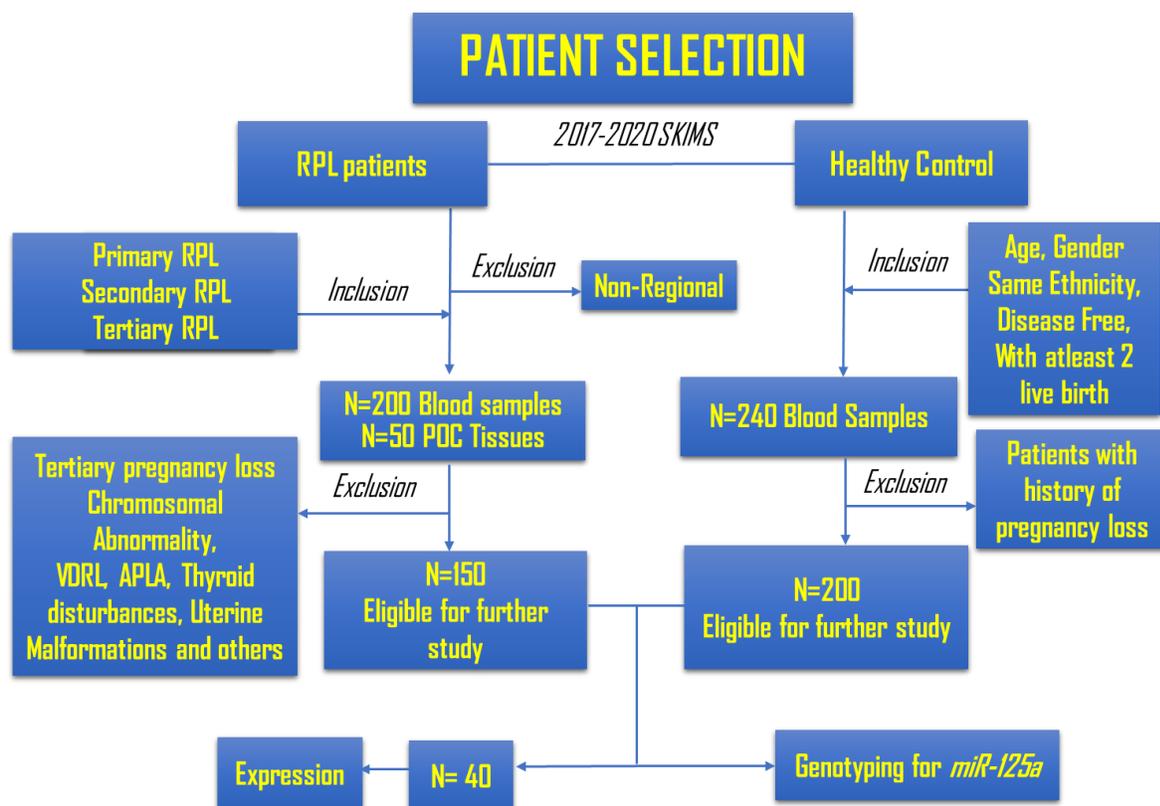


Figure S1: Path map showing the selection of patient with recurrent pregnancy loss and control group.

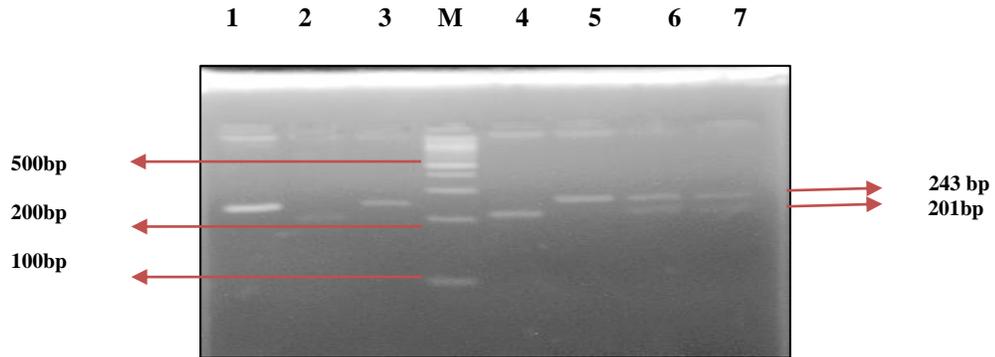


Figure S2 (a): RFLP picture of *miR-125a* rs 12976445 C/T after restriction digestion with *BaeGI* (3%) agarose gel electrophoresis
 Lane M: 100bp marker, Lane 2,4 : homozygous variant CC genotype
 Lane 1,3,5: homozygous wild TT genotype
 Lane 6,7 : heterozygous CT genotype

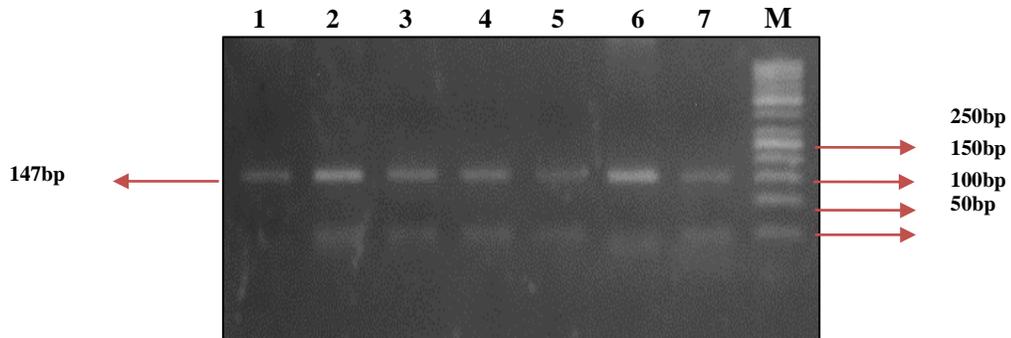


Figure S2 (b): RFLP picture of *miR-125a* 10404453 A/G after restriction digestion with *MspI* (3%) agarose gel electrophoresis
 Lane M: 50bp marker, Lane1-7 : homozygous CC genotype