

Table S1. Population and endometrial characteristics.

	Proliferative Phase Group (n = 8)	Secretory Phase Group (n = 6)	UPA Group (n = 7)	p
Age (years) median (IQR)	47.5 (45.3-50.5)	47.0 (46.0-49.3)	48.0 (45.0-50.0)	0.95 ¹
BMI kg/m ² mean (CI95%)	27.2 (23.2-31.2)	27.9 (22.1-33.7)	28.0 (21.9-34.0)	0.96 ²
Tobacco smoking n (%)	0 (0)	2 (40)	2 (29)	0.25 ³
Parity n (%)				
0	1 (12.5)	2 (33.3)	1 (14.3)	0.27 ³
1	1 (12.5)	2 (33.3)	4 (57.1)	
> 1	6 (75.0)	2 (33.3)	2 (28.6)	
FIGO classification				
1-2	1	3	2	0.57 ³
3-5	6	3	4	
6-7	0	0	0	
NA	1	0	1	
Myoma neighbouring to the analysed endometrium	3	3	2	0.73 ³
Presence of focal PAEC	NA	NA	2	NA

¹ Non-parametric Kruskal Wallis; ² ANOVA test variance analysis. ³ Chi² test; IQR – interquartile range; CI95% – 95% confidence interval.

Table S2. Selection of the top ten statistically most significant biological processes potentially involved in the physiopathology of human endometrium.

	Biological Processes	-log(p-value)	mRNA Participating in the Selected Biological Processes and Regulated by Identified miRNA
Superficial layer Different from proliferative	Quantity of connective tissue cells	5.47	AKT2,NFATC2,SFRP4
	Cell death of connective tissue cells	4.29	AKT2,NFATC2,SFRP4
	Migration of cancer cells	3.59	AKT2,NFATC2
	Metastasis of tumour cell lines	3.32	AKT2,NFATC2
	Remission of tumour	3.09	AKT2
	Transmigration of cancer cells	3.01	NFATC2
	Apoptosis of fibroblast cell lines	3.00	AKT2,NFATC2
	Binding of leukocytes	2.93	AKT2,NFATC2
	Migration of cells	2.89	AKT2,NFATC2,SFRP4
	Binding of DNA	2.85	AKT2,NFATC2
Down	Transcription of RNA	21.22	AHR,AHRR,AR,BCL6,BDNF,BTG3,CAV1,CCL2,CCND1,CDK2,CDK6,CEBPA,CREB1,CREB3L2,CTGF,DLL1,DLX2,E2F3,E2F5,E2F6,EGR1,ELF4,ELK3,ESR1,ETS1,FOXA2,GMCL1,GSK3B,HDAC1,HDAC4,HD

		AC5,HES1,HOXA1,HOXA11,INPPL1,JAG1,KLF15,LDLR,MAP2K1,MAPK14,MDFIC,MED1,MET,MYB,MYC,MYCN,NEUROD1,NFATC1,NFIC,NOTCH1,NOTCH2,PHF19,PPP1R13L,PRKCE,PRKD1,PTBP1,PTEN,RARG,RELA,SIRT1,SMAD5,SNAI2,SOX9,SP1,STAT3,TEAD1,TOM1L1,TP53,TRIM29,TRIP11,TRPS1,TWIST2,UHRF1,WNT1,ZBED3,ZEB1,ZEB2
G1/S phase transition	20.50	AHR,BCL2,CCND1,CDK2,CDK4,CDK6,CEBPA,E2F3,E2F5,ESR1,ITGB1,MAP2K1,MAPK14,MET,MYB,MYC,NFATC1,PTEN,PTK2,STAT3,TP53,VEGFA,WNT1,ZEB2
Interphase	20.32	AHR,ARAF,BCL2,CAV1,CCND1,CDK2,CDK4,CDK6,CEBPA,E2F3,E2F5,E2F6,EGR1,ESR1,HDAC1,HDAC4,ITGB1,MAD2L2,MAP2K1,MAP3K8,MAPK14,MET,MYB,MYC,MYCN,NEK9,NFATC1,NOTCH1,PTEN,PTK2,RELA,SIRT1,SOX9,STAT3,TP53,UHRF1,VEGFA,WNT1,ZEB2
Transcription	19.98	AHR,AHRR,AR,BCL6,BDNF,BTG3,CAV1,CCL2,CCND1,CDK2,CDK6,CEBPA,CREB1,CREB3L2,CTGF,DLL1,DLX2,E2F3,E2F5,E2F6,EGR1,ELF4,ELK3,ERBB3,ESR1,ETS1,FOXA2,GAS2L1,GMCL1,GSK3B,HDAC1,HDAC4,HDAC5,HES1,HOXA1,HOXA11,INPPL1,JAG1,KLF15,LDLR,MAP2K1,MAPK14,MDFIC,MED1,MET,MYB,MYC,MYCN,NEUROD1,NFATC1,NFIC,NOTCH1,NOTCH2,PHF19,PPP1R13L,PRKCE,PRKD1,PTBP1,PTEN,RARG,RELA,SIRT1,SMAD5,SNAI2,SOX9,SP1,STAT3,TEAD1,TOM1L1,TP53,TRIM29,TRIP11,TRPS1,TWIST2,UHRF1,VEGFA,WNT1,ZBED3,ZEB1,ZEB2
Differentiation of epithelial tissue	19.65	ABHD5,AR,BCL2,BLOC1S6,CAV1,CCND1,CEBPA,CTNND1,DLL1,FOX11R,FOXA2,HDAC1,HES1,ITGB1,JAG1,MAP2K1,MAPK14,MET,MYB,MYC,MYH9,NEUROD1,NFATC1,NOTCH1,NOTCH2,PLAU,PPP1R13L,PTEN,RDH10,RELA,SOX9,STAT3,TOM1L1,VEGFA,ZEB1,ZEB2
Apoptosis	19.17	AHR,AR,AXIN2,B4GALT1,BCL2,BCL6,BDNF,CAV1,CCL2,CCND1,CD164,CD47,CD59,CDK2,CDK4,CDK6,CEBPA,CERS2,CREB1,CREB3L2,CTGF,CYP1B1,DEPDC1,DFFB,DHCR24,DLL1,DLX2,DRAM1,E2F3,EGR1,ELF4,ERBB3,ESR1,ETS1,FOXA2,GMCL1,GSK3B,GSN,HDAC1,HDAC4,HDAC5,HEBP2,HES1,HOXA11,INPPL1,ITGB1,JAG1,LDLR,MAD2L2,MAN2A1,MAP2K1,MAP3K8,MAPK14,MCL1,MED1,MET,MTPN,MYB,MYC,MYCN,NEUROD1,NFATC1,NFIC,NOTCH1,NOTCH2,PGF,PLAU,PLP2,PLSCR3,PPP1R13L,PRKCE,PTEN,PTK2,RARG,RASSF5,RELA,SIRT1,SLC17A5,SMAD5,SNAI2,SOX9,SP1,STAT3,SWAP70,SYCP1,TEAD1,TJP2,TMEM109,TNFRSF21,TP53,TRIM29,TRPS1,VEGFA,WNT1,ZEB2,ZFP36L2
Expression of RNA	18.90	AHR,AHRR,AR,BCL6,BDNF,BTG3,CAV1,CCL2,CCND1,CDK2,CDK6,CEBPA,CREB1,CREB3L2,CTGF,DLL1,DLX2,DNAJC1,E2F3,E2F5,E2F6,EGR1,ELF4,ELK3,ERBB3,ESR1,ETS1,FOXA2,GAS2L1,GMCL1,GSK3B,HDAC1,HDAC4,HDAC5,HES1,HOXA1,HOXA11,INPPL1,JAG1,KLF15,LDLR,MAP2K1,MAPK14,MDFIC,MED1,MET,MYB,MYC,MYCN,NEUROD1,NFATC1,NFIC,NOTCH1,NOTCH2,PHF19,PPP1R13L,PRKCE,PRKD1,PTBP1,PTEN,RARG,RELA,SIRT1,SMAD5,SNAI2,SOX9,SP1,STAT3,TEAD1,TOM1L1,TP53,TRIM29,TRIP11,TRPS1,TWIST2,UHRF1,VEGFA,WNT1,ZBED3,ZEB1,ZEB2
Cell transformation	18.86	ARAF,ARHGEF1,BCL2,BCL6,CAV1,CCND1,CDK2,CDK4,CDK6,CEBPA,DFFB,EGR1,ERBB3,ESR1,ETS1,HES1,HTATIP2,ITGB1,MAP2K1,MAP3K8,MAPK14,MET,MYB,MYC,MYCN,NFATC1,NOTCH1,PPP1R13L,PRKCE,PTEN,PTK2,PTPN12,RELA,RHOG,SOX9,STAT3,TP53,

		VEGFA,WNT1	
Different from secretory	Up-regulated		
	Cell cycle progression	18.22	AHR,ARAF,ARPC1B,B4GALT1,BCL2,BCL6,BTG3,CAV1,CCND1,CD59,CDK2,CDK4,CDK6,CEBPA,CREB1,DLX2,E2F3,E2F5,E2F6,EGR1,ERBB3,ESR1,ETS1,GAS2L1,GSK3B,HDAC1,ITGB1,MAD2L2,MAP2K1,MAPK14,MET,MYB,MYC,MYCN,NEK6,NEK9,NEUROD1,NFATC1,NOTCH1,PTEN,PTK2,RARG,RELA,SIRT1,STAT3,TP53,UHMK1,VEGFA,WNT1,ZEB1
	Solid tumour	17.61	AHR,ALDH9A1,AR,ARAF,BCL2,BCL6,BDNF,BTG3,CAV1,CCND1,CD47,CDCA7L,CDK2,CDK4,CDK6,CEBPA,CREB1,CTGF,CTNND1,CYP1B1,DLL1,DNM2,DVL2,E2F3,EGR1,ERBB3,ESR1,ETS1,FAM129B,FAM57A,GSK3B,HDAC1,HTATIP2,IQGAP1,ITGB1,MAP2K1,MAP3K8,MAPK14,MCL1,MET,MYB,MYC,MYCN,MYH9,NEUROD1,NFATC1,NOTCH1,NOTCH2,PGF,PGM1,PLAU,PPP1R13L,PRKCE,PTBP1,PTEN,PTK2,RASSF5,RELA,RHOG,SIRT1,SNAI2,STAT3,STX2,TLN1,TNFRSF21,TP53,TRIM29,UHRF1,VEGFA,WNT1,ZEB1,ZEB2
	Endometrial cancer	6.90	BAP1,ERRFI1,PTEN
	Quantity of cells	5.90	AKT2,ERBIN,ERRFI1,NFATC2,PLCG1,PTEN,PTPN12,PTPN13,RERE,SFRP4,ZEB1,ZEB2
	Migration of cells	5.80	AKT2,ELMO2,ERRFI1,NFATC2,PLCG1,PTEN,PTPN12,RERE,SFRP4,ZEB1,ZEB2
	Endometrial adenocarcinoma	5.48	BAP1,PTEN
	Metastasis of cells	4.80	AKT2,NFATC2,PTEN,ZEB1,ZEB2
	Hyperplasia of endometrium	4.51	ERRFI1,PTEN
	Migration of cancer cells	4.50	AKT2,NFATC2,PTEN,ZEB1
	Solid tumour	4.46	AKT2,BAP1,ERBIN,ERRFI1,NFATC2,PTEN,PTPN13,ZEB1,ZEB2
Differentiation of epithelial tissue	4.45	ERBIN,ERRFI1,PTEN,ZEB1,ZEB2	
Neoplasia of tumour cell lines	4.40	AKT2,BAP1,NFATC2,PTEN,ZEB2	
Down-regulated	Solid tumour	11.58	ABL1,ANPEP,ATP2A2,BCL6,BECN1,CDCP1,CTGF,CXCL14,E2F3,F2,GALNT1,GNAI2,IDH1,IL11,ITGA2,JUN,MAP4K4,MBNL1,MET,MLLT1,MNT,NEUROD1,NPTX1,NT5E,PGM1,PTPN1,RAD52,RUNX2,SDHD,SLC7A11,SLC9A3R2,SMAD4,SOCS3,SRC,STX1A,TNRC6A,TP53,TP63,WNT5A
	Malignant solid tumour	10.36	ABL1,ANPEP,ATP2A2,BCL6,BECN1,CTGF,CXCL14,E2F3,F2,GNAI2,IL11,ITGA2,JUN,MAP4K4,MBNL1,MET,MLLT1,NEUROD1,NPTX1,NT5E,PGM1,PTPN1,RAD52,RUNX2,SLC7A11,SMAD4,SOCS3,SRC,TNRC6A,TP53,TP63,WNT5A
	Cancer	10.01	ABL1,ANPEP,ATP2A2,BCL6,BECN1,CBFB,CDCP1,CTGF,CXCL14,E2F3,F2,GNAI2,HNRNPM,HOXA1,IL11,ISCU,ITGA2,JUN,MAP4K4,MBNL1,MET,MLLT1,NEUROD1,NPTX1,NT5E,PGM1,PNP,PTPN1,RAD52,RUNX2,SLC7A11,SMAD4,SOCS3,SRC,TNRC6A,TP53,TP63,UBE2I,WNT5A
	Cell viability	7.49	ABL1,BCL6,BECN1,CBFB,CTGF,E2F3,EFNA3,IL11,JUN,MET,MNT,NEUROD1,PPP3CA,PTPN1,RAD52,RUNX2,SMAD4,SOCS3,SRC,STX1A,TP53,TP63,WNT5A
	Tumorigenesis of malignant tumour	7.28	ABL1,BCL6,BECN1,GNAI2,JUN,MBNL1,MET,NEUROD1,RUNX2,SLC7A11,SMAD4,SOCS3,TNRC6A,TP53,TP63,WNT5A

	Apoptosis	7.17	ABL1,ANPEP,API5,ATRX,BCL6,BECN1,CASP8AP2,CBFB,CDCP1,CTGF,E2F3,F2,FGFRL1,GNAI2,IL11,JUN,MAP4K4,MET,MNT,NCEH1,NCL,NEUROD1,PAFAH1B2,PEX11B,PNP,PPP3CA,PTPN1,RUNX2,SLC4A7,SLC7A11,SMAD4,SOCS3,SRC,STX1A,TNFAIP2,TNRC6A,TP53,TP63,TRPS1,UBE2I,WNT5A
	Connective tissue tumour	6.76	ABL1,BECN1,IDH1,JUN,MAP4K4,MET,MLLT1,NT5E,RUNX2,SLC7A11,TP53,TP63
	Differentiation of tumour cell lines	6.52	ABL1,ACVR1,BCL6,CNOT9,IL11,JUN,NEUROD1,SMAD4,SOCS3,TP53
	Proliferation of connective tissue cells	6.46	ABL1,CTGF,F2,GNAI2,IDH1,JUN,MET,NPR3,PTPN1,RUNX2,SLC7A11,SMAD4,SOCS3,SRC,TP53,TP63,TRPS1,WNT5A
	Connective tissue cancer	6.39	JUN,MET,NT5E,RUNX2,TP53,TP63
Basal layer Different from proliferative Down-regulated	Interphase	26.35	AHR,ARAF,BCL2,CAV1,CCND1,CCND3,CCNE1,CDC25A,CDK2,CDK4,CDK6,CEBPA,CENPJ,CHEK1,DMTF1,E2F3,E2F5,EGR1,EIF4E,FGF2,FLT3,GRB10,GRB2,HDAC1,HDAC4,IGF1,IGF1R,ITGB1,JUN,KITLG,MAD2L2,MAP2K1,MAPK14,MAPK3,MET,MSH2,MYB,MYC,MYCN,NEK9,NFATC1,NOTCH1,PTEN,PTGS2,PURA,RAF1,RELA,SIRT1,SOX9,SPI1,STAT3,TP53,UHRF1,VEGFA,WNT1,ZEB2
	Cell transformation	25.93	ARAF,ARHGEF1,BCL2,CAV1,CCND1,CCND3,CCNE1,CDC25A,CDK2,CDK4,CDK6,CEBPA,DFFB,DMTF1,EGFR,EGR1,EIF4E,ERBB3,F2,FGF2,FGFR1,FLT3,GOLGA5,GRB10,GRB2,HES1,HMGA1,HTATIP2,IGF1,IGF1R,ITGB1,JUN,MAP2K1,MAP2K4,MAPK14,MET,MLLT1,MYB,MYC,MYCN,NFATC1,NOTCH1,ODC1,PDCD4,PISD,PPP1R13L,PRKCE,PTEN,PTPN12,RAF1,RELA,RHOG,SOX9,STAT3,TP53,TPM3,VEGFA,WNT1
	Cell cycle progression	25.59	AHR,ARAF,ARPC1B,B4GALT1,BCL2,BTG3,CAV1,CCND1,CCND3,CCNE1,CCNF,CD59,CDC25A,CDK2,CDK4,CDK6,CEBPA,CENPJ,CHEK1,CREB1,DLX2,DMTF1,E2F3,E2F5,EGFR,EGR1,ERBB3,F2,FGF2,FGF7,FGFR1,GAS2L1,GRB10,GRB2,GSK3B,GTF2H1,HDAC1,IGF1,IGF1R,ITGB1,JUN,KITLG,MAD2L2,MAP2K1,MAP2K4,MAPK14,MAPK3,MET,MSH2,MYB,MYC,MYCN,NEK6,NEK9,NEUROD1,NFATC1,NOTCH1,PLAG1,PLK1,PRIMPOL,PTEN,PTGS2,PURA,RAF1,RARG,RELA,SIRT1,STAT3,TP53,UBE2S,UHMK1,VEGFA,WEE1,WNT1,WNT3A,ZEB1
	Malignant solid tumour	25.51	AHR,ALDH9A1,ARHGDI1,ASXL2,BCL2,BTG3,CAV1,CCL2,CCND1,CCND3,CD47,CDCA7L,CDK2,CDK4,CDK6,CEBPA,CHEK1,CREB1,CTGF,CTNND1,CYP1B1,DMTF1,E2F3,EGFR,EGR1,ERBB3,F2,FGF2,FGF7,FGFR1,FNDC3B,GRB2,HACE1,HDAC1,HMGA1,HMOX1,HSP90B1,HTATIP2,IGF1,IGF1R,IQGAP1,ITGA2,ITGB1,JUN,KITLG,LAMTOR5,MAP2K1,MAPK14,MCL1,MET,MLLT1,MSH2,MYB,MYC,MYCN,MYH9,NEUROD1,NFATC1,NFIA,NOTCH1,NOTCH2,ODC1,PDCD4,PGF,PGM1,PLK1,PRKCE,PTBP1,PTEN,PTGS2,RAD51C,RAF1,RASSF5,RECK,RELA,RHOG,SIRT1,SKAP2,SNAI2,SPI1,SQSTM1,STAT3,STX2,TLN1,TNFRSF21,TP53,TPI1,TRIM29,TUSC2,UHRF1,VEGFA,WNT1,WNT3A,WT1,ZEB1,ZEB2,ZYX
	Solid tumour	24.46	AHR,ALDH9A1,ARAF,ARHGDI1,ASXL2,BCL2,BDNF,BTG3,CAV1,CCL2,CCND1,CCND3,CCNE1,CD47,CDC25A,CDCA7L,CDK2,CDK4,CDK6,CEBPA,CHEK1,CREB1,CSHL1,CTGF,CTNND1,CYP1B1,DLL1,DMTF1,DNM2,DVL2,E2F3,EGFR,EGR1,EIF4E,ERBB3,F2,FAM129B,FAM57A,FGF2,FGF7,FGFR1,FNDC3B,GRB2,GSK3B,HACE1,HDAC1,

		HMGA1,HMOX1,HSP90B1,HTATIP2,IGF1,IGF1R,IQGAP1,ITGA2,ITGB1,JUN,KITLG,LAMTOR5,MAP2K1,MAP2K4,MAPK14,MCL1,MET,MLLT1,MSH2,MYB,MYC,MYCN,MYH9,NEUROD1,NFATC1,NFIA,NOTCH1,NOTCH2,ODC1,PDCD4,PGF,PGM1,PISD,PLK1,PPP1R13L,PRKCE,PTBP1,PTEN,PTGS2,RAD51C,RAF1,RASSF5,RECK,RELA,RHOG,SIRT1,SKAP2,SNAI2,SPI1,SQSTM1,STAT3,STX2,TLN1,TNFRSF21,TP53,TPI1,TRIM29,TUSC2,UHRF1,VEGFA,WNT1,WNT3A,WT1,ZEB1,ZEB2,ZYX
Apoptosis	22.41	AHR,ATF6,AXIN2,B4GALT1,BCL2,BCL2L2,BDNF,CADM1,CAPRIN1,CAV1,CCL2,CCND1,CCND3,CCNE1,CD164,CD47,CD59,CDC25A,CDK2,CDK4,CDK6,CEBPA,CENPJ,CERS2,CHEK1,CREB1,CREB3L2,CREBL2,CTGF,CYP1B1,DEPDC1,DFFB,DHCR24,DLL1,DLX2,DRAM1,E2F3,EGFR,EGR1,EIF4E,ELF4,ERBB3,F2,FGF2,FGFR1,FLT3,FOXA2,GFPT1,GMCL1,GPAM,GRB10,GSK3B,GSN,HDAC1,HDAC4,HDAC5,HEBP2,HES1,HMGA1,HMOX1,IGF1,IGF1R,IGF2R,INPPL1,ITGB1,JAG1,JUN,KITLG,LDLR,MAD2L2,MAN2A1,MAP2K1,MAP2K4,MAPK14,MAPK3,MCL1,MED1,MET,MSH2,MTPN,MYB,MYC,MYCN,NEUROD1,NFATC1,NFIC,NOTCH1,NOTCH2,ODC1,OGT,OMA1,PAFAH1B2,PANX1,PDCD4,PDCD6IP,PGF,PLK1,PLP2,PLSCR3,PNP,PPP1R13L,PRKCE,PTEN,PTGS2,RAF1,RARG,RASSF5,RELA,RNASEL,RTN4,SERPINE2,SIRT1,SLC17A5,SMAD5,SNAI2,SOX9,SP1,SPI1,SQSTM1,STAT3,SWAP70,SYCP1,TEAD1,TIA1,TJP2,TMEM109,TNFRSF21,TP53,TRIM29,TRPS1,TXN2,UCP2,VEGFA,VTI1B,WEE1,WNT1,WNT3A,WT1,ZEB2,ZFP36L2
Tumorigenesis of tissue	22.29	AHR,ARAF,BCL2,BDNF,CAV1,CCL2,CCND1,CCND3,CCNE1,CDK2,CDK4,CDK6,CEBPA,CHORDC1,CREB1,CSHL1,CTGF,CTNND1,DLX1,E2F3,EGFR,EGR1,ERBB3,FAM57A,FGF2,FGF7,FGFR1,FLT3,GRB2,GSK3B,HMGA1,HMOX1,HTATIP2,IGF1,IGF1R,IQGAP1,ITGA2,ITGB1,JUN,LAMTOR5,MAP2K1,MAP2K4,MET,MSH2,MYC,MYCN,NFATC1,NOTCH1,NOTCH2,ODC1,PDCD4,PGF,PISD,PLK1,PRKCE,PTEN,PTGS2,RAD51C,RAF1,RASSF5,RECK,RELA,RHOG,SIRT1,SNAI2,SPI1,STAT3,STX2,TP53,TPI1,TRIM29,TUSC2,VEGFA,WNT1,WNT3A,WT1
Proliferation of fibroblast cell lines	21.87	AHR,ARHGEF1,ATG9A,BTG3,CAPRIN1,CAV1,CCND1,CDC14B,CDK4,CDK6,CEBPA,CREB1,DMTF1,E2F3,EGFR,EGR1,EIF4E,ERBB3,F2,FGF2,GRB2,HMGA1,IGF1,IGF1R,ITGB1,JAG1,JUN,LDLRAP1,MAD2L2,MAPK14,MAPK3,MET,MYC,NFATC1,NOTCH1,ODC1,PLAG1,PIF,PRKCE,PTEN,RAF1,RASSF5,RECK,RELA,RNASEL,RYK,SIRT1,SOX9,STAT3,SWAP70,TP53,TPM3,WNT3A,WT1
Cell survival	21.62	AHR,BCL2,BCL2L2,BDNF,CADM1,CAV1,CCL2,CD47,CD59,CDCA7L,CDK4,CHEK1,CREB1,CTGF,DLX2,E2F3,EGFR,EGR1,EIF4E,ELF4,ERBB3,FGF2,FGF7,FGFR1,FLT3,GRB10,GRB2,GSK3B,HDAC1,HDAC5,HES1,HMGA1,HMOX1,IGF1,IGF1R,IQGAP1,ITGB1,JAG1,JUN,KITLG,MAD2L2,MAP2K1,MAP2K4,MAPK14,MAPK3,MCL1,MET,MSH2,MYB,MYC,MYCN,NEUROD1,NOTCH1,NOTCH2,ODC1,OGT,PDCD4,PGF,PLK1,PPP1R13L,PRKCE,PRKD1,PTEN,PTGS2,RAD51C,RAF1,RARG,RELA,RNASEL,SIRT1,SNAI2,SOX9,STAT3,TP53,UCP2,UHRF1,VEGFA,WIPF1,WNT1,WT1,ZEB1,ZEB2
Cancer	21.30	AHR,ALDH9A1,ARHGDI1,ASXL2,BCL2,BTG3,CAV1,CCL2,CCND1,CCND3,CD47,CD59,CDC25A,CDCA7L,CDK2,CDK4,CDK6,CEBPA,CHEK1,CREB1,CSHL1,CTGF,CTNND1,CYP1B1,DFFB,DLX2,DMTF1,

			E2F3,EGFR,EGR1,ERBB3,F2,FGF2,FGF7,FGFR1,FLT3,FNDC3B,FOXA2,GRB2,GSK3B,GSN,HACE1,HDAC1,HES1,HMGA1,HMOX1,HSP90B1,HTATIP2,IGF1,IGF1R,IGF2R,IQGAP1,ITGA2,ITGB1,JUN,KITLG,LAMTOR5,LITAF,MAD2L2,MAP2K1,MAP2K4,MAPK14,MCL1,MET,MLLT1,MSH2,MYB,MYC,MYCN,MYH9,NEUROD1,NFATC1,NFIA,NOTCH1,NOTCH2,ODC1,PDCD4,PGF,PGM1,PLK1,PNP,PPP1R13L,PRKCE,PTBP1,PTEN,PTGS2,RAD51C,RAF1,RARG,RASSF5,RECK,RELA,RHOG,SIRT1,SKAP2,SNAI2,SPI1,SQSTM1,STAT3,STX2,TLN1,TFNRSF21,TP53,TPI1,TRIM29,TUSC2,UHRF1,VEGFA,WNT1,WNT3A,WT1,ZEB1,ZEB2,ZYX	
	Expression of RNA	5.67	AR,HOXA7,HOXB8,HOXC8,HOXD8,IKBKB,LCOR,S100A9	
	Transcription of RNA	4.96	AR,HOXA7,HOXB8,HOXC8,HOXD8,IKBKB,LCOR	
	Activation of DNA endogenous promoter	4.90	AR,HOXA7,HOXB8,HOXC8,HOXD8,LCOR	
Up-regulated	Regeneration of epithelial tissue	4.48	AR,IKBKB	
	Cell death of cancer cells	4.35	ANXA1,AR,HOXA7,IKBKB	
	Fibrosis of secretory structure	4.32	AR,IKBKB	
	Migration of tumour cell lines	4.10	ANXA1,IKBKB,S100A9	
	Morphology of tumour	3.86	ANXA1,AR,IKBKB	
	Chemotaxis	3.83	ANXA1,HOXA7,IKBKB,S100A9	
	Growth of tumour	3.64	ANXA1,AR,HOXA7,IKBKB,S100A9	
	Different from secretory	Inflammation of organ	17.98	ABL1,BLMH,CAMP,CD1D,CD40,CFH,CHUK,CRP,DMBT1,E2F3,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL36RN,IRAK1,IRF5,LBP,LTB,MNT,MR1,NOS2,PGLYRP1,PGLYRP2,PTAFR,PTPN1,SFTPD,SMAD4,SOCS3,STAT1,TLR4,TLR9,TP63,TRAF6
		Quantity of leukocytes	16.65	ABL1,CAMP,CCR3,CD1D,CD40,CFH,CHUK,CRP,CXCL14,CXCR4,FADD,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL36A,IL36RN,IRAK1,IRF5,LTB,MNT,MR1,NOS2,PGLYRP1,PTAFR,RAD52,RUNX2,SFTPD,SOCS3,STAT1,TLR4,TLR9,TRAF6
Inflammatory response		15.93	CAMP,CCR3,CD1D,CD40,CFH,CHUK,CRP,CXCR4,IFNB1,IL10,IL11,IL1R1,IL1RL2,IL36A,IRAK1,LBP,LTB,MCPH1,NOS2,PGLYRP1,PGLYRP2,PTAFR,SFTPD,SOCS3,STAT1,TLR1,TLR4,TLR9	
Down-regulated		Quantity of mononuclear leukocytes	15.75	ABL1,CAMP,CCR3,CD1D,CD40,CHUK,CRP,CXCL14,CXCR4,FADD,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL36A,IRAK1,IRF5,LTB,MNT,MR1,NOS2,PGLYRP1,PTAFR,RUNX2,SFTPD,SOCS3,STAT1,TLR4,TLR9,TRAF6
		T cell development	15.53	ABL1,BRCA1,CD1D,CD40,CHUK,CRP,CXCR4,FADD,IFNB1,IL10,IL12RB2,IL1R1,IL1RL2,IL36B,IRAK1,IRF5,LTB,MNT,PGLYRP2,RAD52,RUNX2,SOCS3,STAT1,TLR4,TP63,TRAF6
		Haematopoiesis of mononuclear leukocytes	15.49	ABL1,BRCA1,CAMP,CD1D,CD40,CHUK,CRP,CXCR4,FADD,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL1RL2,IL36B,IRAK1,IRF5,LTB,MNT,PGLYRP2,RAD52,RUNX2,SOCS3,STAT1,TLR4,TLR9,TP63,TRAF6
		Quantity of cells	15.42	ABL1,BRCA1,CAMP,CCR3,CD1D,CD40,CFH,CHUK,CRP,CXCL14,CXCR4,DMBT1,EFNA3,FADD,FGFRL1,HOXA1,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL1RAP,IL36A,IL36RN,IRAK1,IRF5,LTB,MCPH1,MNT,MR1,NLGN1,NOS2,PGLYRP1,PTAFR,RAD52,RUNX2,SFTPD,SMAD4,SOCS3,STAT1,TLR4,TLR9,TP63,TRAF6

Activation of cells	14.99	CAMP,CD1D,CD40,CFH,CHUK,CRP,CXCR4,FADD,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL36A,IL36B,IL36G,IL36RN,IRAK1,IRF5,LBP,LTF,MR1,NOS2,PGLYRP2,RUNX2,SMAD4,SRC,STAT1,TLR4,TLR9,TRAF6
Quantity of T lymphocytes	14.84	ABL1,CAMP,CD1D,CD40,CHUK,CRP,CXCL14,CXCR4,FADD,IFNB1,IL10,IL12RB2,IL1R1,IRAK1,LTB,MNT,MR1,NOS2,PGLYRP1,PTAFR,RUNX2,SOCS3,STAT1,TLR4,TLR9,TRAF6
Quantity of lymphocytes	14.36	ABL1,CAMP,CD1D,CD40,CHUK,CRP,CXCL14,CXCR4,FADD,IFNB1,IL10,IL11,IL12RB2,IL1R1,IL36A,IRAK1,IRF5,LTB,MNT,MR1,NOS2,PGLYRP1,PTAFR,RUNX2,SOCS3,STAT1,TLR4,TLR9,TRAF6

The first three columns specify endometrial layers and expression of identified miRNA in the UPA group as compared to proliferative and secretory phase groups. The next three columns specify the biological processes identified using IPA in which mRNAs regulated by the identified miRNA participate.

Table S3. Selection of top ten canonical pathways regulated by the miRNA identified in Table1.

	Canonical Pathway IPA	$-\log(p\text{-value})$	mRNA Participating in the Selected Canonical Pathways and Regulated by Identified miRNA
Up-regulated	Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	5.75	SFRP4,AKT2,NFATC2
	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	5.37	SFRP4,AKT2,NFATC2
	IL-4 Signalling	4.23	AKT2,NFATC2
	RANK Signalling in Osteoclasts	4.07	AKT2,NFATC2
	iCOS-iCOSL Signalling in T Helper Cells	3.94	AKT2,NFATC2
	CD28 Signalling in T Helper Cells	3.88	AKT2,NFATC2
	PI3K Signalling in B Lymphocytes	3.85	AKT2,NFATC2
	Gαq Signalling	3.67	AKT2,NFATC2
	Wnt/β-catenin Signalling	3.62	SFRP4,AKT2
	Role of NFAT in Regulation of the Immune Response	3.58	AKT2,NFATC2
Down-regulated	Cell Cycle: G1/S Checkpoint Regulation	11.5	MYC,TP53,E2F6,HDAC4,HDAC1,CDK6,CDK4,E2F5,GSK3B,E2F3,CCND1,CDK2,HDAC5
	Aryl Hydrocarbon Receptor Signalling	11.3	TP53,TRIP11,RELA,NFIC,MED1,CDK6,CDK4,RARG,CCND1,CYP1B1,ALDH9A1,AHRR,MYC,SP1,ESR1,CDK2,AHR
	Molecular Mechanisms of Cancer	9.77	RELA,CDK4,ARHGEF1,SMAD5,E2F3,CCND1,BCL2,PTK2,MYC,E2F6,RHOG,E2F5,PRKCE,GSK3B,MAP2K1,PRKD1,ITGB1,TP53,CDK6,GNAI3,MAPK14,NOTCH1,CDK2,WNT1,CTNND1
	p53 Signalling	9.56	TP53,SNAI2,MED1,HDAC1,CDK4,CCND1,PTEN,BCL2,MAPK14,SIRT1,GSK3B,TRIM29,CDK2,DRAM1
	Cyclins and Cell Cycle Regulation	9.17	TP53,E2F6,HDAC4,HDAC1,CDK6,CDK4,E2F5,GSK3B,E2F3,CCND1,CDK2,HDAC5
	Pancreatic Adenocarcinoma Signalling	8.99	TP53,RELA,CDK4,STAT3,E2F3,CCND1,BCL2,PGF,VEGFA,E2F6,E2F5,NOTCH1,MAP2K1,CDK2
	Regulation of the Epithelial-Mesenchymal Transition Pathway	8.93	ETS1,RELA,TWIST2,SNAI2,EGR1,ZEB1,STAT3,MET,DVL2,NOTCH2,ARAF,ZEB2,GSK3B,JAG1,NOTCH1,MAP2K1,WNT1
	Estrogen-mediated S-phase Entry	8.8	MYC,E2F6,CDK4,E2F5,E2F3,ESR1,CCND1,CDK2
Chronic Myeloid Leukaemia Signalling	8.62	MYC,TP53,RELA,E2F6,HDAC4,HDAC1,CDK6,CDK4,E2F5,	

Superficial layer
Different from proliferative

Down-regulated

			E2F3,CCND1,MAP2K1,HDAC5	
	HGF Signalling	8.27	ETS1,ITGB1,STAT3,CCND1,PTK2,MET,ELF4,PRKCE,MAP3K8,MAP2K1,ELK3,CDK2,PRKD1	
	Neuregulin Signalling	7.56	AKT2,ERBIN,PLCG1,ERRFI1,PTEN	
	D-myo-inositol-5-phosphate Metabolism	6.28	PTPN13,PLCG1,PPM1F,PTPN12,PTEN	
	Superpathway of Inositol Phosphate Compounds	5.46	PTPN13,PLCG1,PPM1F,PTPN12,PTEN	
Up-regulated	iCOS-iCOSL Signalling in T Helper Cells	5.19	AKT2,PLCG1,NFATC2,PTEN	
	PI3K Signalling in B Lymphocytes	5.02	AKT2,PLCG1,NFATC2,PTEN	
	D-myo-inositol (1,4,5,6)-Tetrakisphosphate Biosynthesis	4.91	PTPN13,PPM1F,PTPN12,PTEN	
	D-myo-inositol (3,4,5,6)-tetrakisphosphate Biosynthesis	4.91	PTPN13,PPM1F,PTPN12,PTEN	
	3-phosphoinositide Degradation	4.74	PTPN13,PPM1F,PTPN12,PTEN	
	Protein Kinase A Signalling	4.39	PTPN13,PLCG1,NFATC2,PTPN12,PTEN	
	3-phosphoinositide Biosynthesis	4.32	PTPN13,PPM1F,PTPN12,PTEN	
	Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	4.73	SRC,JUN,RUNX2,PPP3R1,ITGA2,SMAD4,PPP3CA,WNT5A,IL11	
	Guanosine Nucleotides Degradation III	4.24	NT5C3A,NT5E,PNP	
	Urate Biosynthesis/Inosine 5'-phosphate Degradation	4.13	NT5C3A,NT5E,PNP	
Down-regulated	DNA Double-Strand Break Repair by Homologous Recombination	4.02	ATRX,RAD52,ABL1	
	Adenosine Nucleotides Degradation II	4.02	NT5C3A,NT5E,PNP	
	Wnt/ β -catenin Signalling	3.92	TP53,SRC,JUN,PTPA,ACVR1,ACVR1B,WNT5A	
	Purine Nucleotides Degradation II (Aerobic)	3.76	NT5C3A,NT5E,PNP	
	Clathrin-mediated Endocytosis Signalling	3.63	MET,SRC,AP2M1,AP2A1,PPP3R1,F2,PPP3CA	
	TGF- β Signalling	3.62	JUN,RUNX2,ACVR1,SMAD4,ACVR1B	
	Virus Entry via Endocytic Pathways	3.35	SRC,AP2M1,AP2A1,ITGA2,ABL1	
Basal layer	Down-regulated	Aryl Hydrocarbon Receptor Signalling	14.50	TP53,TRIP11,RELA,NFIC,MED1,CDK6,CDK4,RARG,CCND1,CYP1B1,ALDH9A1,CHEK1,MYC,AHRR,CCNE1,HSP90B1,JUN,SP1,CCND3,MAPK3,NFIA,GSTM4,AHR,CDK2
		Pancreatic Adenocarcinoma Signalling	13.70	MAP2K4,TP53,RELA,RAF1,GRB2,FGFR1,CDK4,STAT3,E2F3,CCND1,BCL2,PGF,VEGFA,HMOX1,CCNE1,MAPK3,E2F5,PTGS2,NOTCH1,MAP2K1,CDK2,EGFR
		Molecular Mechanisms of Cancer	13.70	MAP2K4,RELA,RAF1,CDK4,ARHGEF1,SMAD5,E2F3,CCND1,CHEK1,BCL2,MYC,LAMTOR3,RHOG,JUN,CCND3,SUFU,RHOT1,MAPK3,E2F5,PRKCE,GSK3B,MAP2K1,PRKD1,CD25A,ITGB1,TP53,GRB2,FGFR1,ITGA2,CDK6,GNAI3,CCNE1,MAPK14,WNT3A,NOTCH1,WNT1,CDK2,CTNND1
		p53 Signalling	12.50	TP53,WT1,SNAI2,GRB2,MED1,FGFR1,HDAC1,CDK4,CCND1,CHEK1,BCL2,PTEN,SERPINE2,JUN,MAPK14,SIRT1,GSK3B,TRIM29,CDK2,DRAM1
		Regulation of the Epithelial-Mesenchymal Transition Pathway	12.00	MAP2K4,RELA,RAF1,TWIST2,SNAI2,FGF2,GRB2,EGR1,FGFR1,ZEB1,STAT3,MET,NOTCH2,DVL2,WNT3A,ARAF,MAPK3,ZEB2,GSK3B,JAG1,FGF7,NOTCH1,MAP2K1,WNT1,EG

			FR
	Glioblastoma Multiforme Signalling	11.80	TP53,RAF1,GRB2,FGFR1,CDK6,CDK4,E2F3,CCND1,PTEN,MYC,CCNE1,WNT3A,RHO,IGF1,RHOT1,MAPK3,IGF1R,E2F5,GSK3B,MAP2K1,CDK2,WNT1,EGFR
	Cell Cycle: G1/S Checkpoint Regulation	11.10	TP53,HDAC4,HDAC1,CDK6,CDK4,E2F3,CCND1,HDAC5,MYC,CCNE1,CCND3,E2F5,GSK3B,CDK2,CDC25A
	IL-8 Signalling	11.00	MAP2K4,RELA,RAF1,GRB2,FGFR1,IQGAP1,CCND1,BCL2,GNG10,PGF,VEGFA,HMOX1,GNAI3,RHO, JUN,ARAF,CCND3,RHOT1,MAPK3,PRKCE,PTGS2,MAP2K1,PRKD1,EGFR
	Cyclins and Cell Cycle Regulation	10.90	TP53,RAF1,HDAC4,WEE1,HDAC1,CDK6,CDK4,E2F3,CCND1,HDAC5,CCNE1,CCND3,E2F5,GSK3B,CDK2,CDC25A
	HGF Signalling	10.20	MAP2K4,ITGB1,RAF1,GRB2,FGFR1,ITGA2,STAT3,CCND1,MET,ELF4,JUN,MAPK3,PRKCE,PTGS2,ELK3,MAP2K1,PRKD1,CDK2
Up-regulated	Glucocorticoid Receptor Signalling	4.6	IKBKB,AR,ANXA1,KRT5
	Role of IL-17A in Psoriasis	2.33	S100A9
	TNFR2 Signalling	1.75	IKBKB
	4-1BB Signalling in T Lymphocytes	1.74	IKBKB
	IL-17A Signalling in Fibroblasts	1.73	IKBKB
	Role of RIG1-like Receptors in Antiviral Innate Immunity	1.71	IKBKB
	TWEAK Signalling	1.69	IKBKB
	April Mediated Signalling	1.64	IKBKB
	Role of PKR in Interferon Induction and Antiviral Response	1.63	IKBKB
	B Cell Activating Factor Signalling	1.62	IKBKB
Down-regulated	IL-10 Signalling	18.8	TRAF6,SOCS3,IL36G,IL1RL2,IL1RAPL2,IL10,IL36RN,IL36A,IL1R1,IL1F10,LBP,CHUK,IL1RAP,IL36B
	Role of Macrophages, Fibroblasts and Endothelial Cells in Rheumatoid Arthritis	17.7	SRC,SOCS3,IL1RAPL2,IL10,IL36A,LTB,IL1F10,IL1R1,TLR9,IRAK1,IL36B,TRAF6,TLR4,IL36G,IL1RL2,IL36RN,TLR1,CHUK,NOS2,IL1RAP,IRAK2
	Toll-like Receptor Signalling	16.5	TRAF6,TLR4,IL36G,IL36RN,TLR1,IL36A,IL1F10,LBP,CHUK,TLR9,IRAK2,IL36B,IRAK1
	Hepatic Cholestasis	16.3	IL1RAPL2,IL36A,IL1F10,IL1R1,IRAK1,IL36B,TRAF6,TLR4,IL36G,IL1RL2,IL36RN,CHUK,LBP,IL1RAP,IRAK2,IL11
	IL-6 Signalling	16.2	TRAF6,SOCS3,IL36G,IL1RL2,IL1RAPL2,IL36RN,CRP,IL36A,IL1R1,IL1F10,LBP,CHUK,TLR9,IL1RAP,IL36B
	Dendritic Cell Maturation	15.6	IL10,IFNB1,IL36A,LTB,IL1F10,TLR9,IL36B,TRAF6,TLR4,CD1D,IL36G,CD40,IL1RL2,IL36RN,CHUK,STAT1
	p38 MAPK Signalling	15.3	IL1RAPL2,IL36A,IL1F10,IL1R1,IRAK1,IL36B,TRAF6,FADD,IL36G,IL1RL2,IL36RN,STAT1,IL1RAP,IRAK2
	Role of Osteoblasts, Osteoclasts and Chondrocytes in Rheumatoid Arthritis	14.8	SRC,IL1RAPL2,IL10,IL36A,IL1F10,IL1R1,TLR9,IL36B,TRAF6,IL36G,IL1RL2,RUNX2,IL36RN,SMAD4,CHUK,IL1RAP,IL11
	Altered T Cell and B Cell Signalling in Rheumatoid Arthritis	14.1	TLR4,IL36G,CD40,IL10,IL36RN,TLR1,IL36A,LTB,IL1F10,CHUK,TLR9,IL36B
	NF- κ B Signalling	14.1	IL36A,IL1F10,IL1R1,TLR9,IRAK1,IL36B,TRAF6,FADD,TLR4,IL36G,CD40,IL36RN,TLR1,CHUK,FGFRL1

The first three columns specify endometrial layers and expression state of identified miRNA as compared to the proliferative and secretory phase. The next three columns specify the canonical pathways identified using IPA in which participate the mRNA regulated by the identified miRNA.