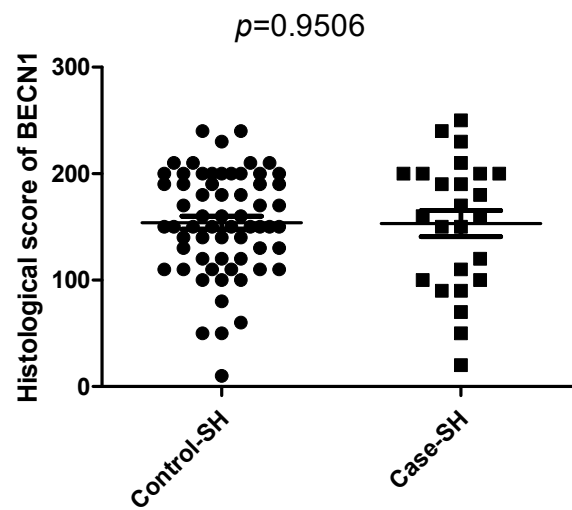


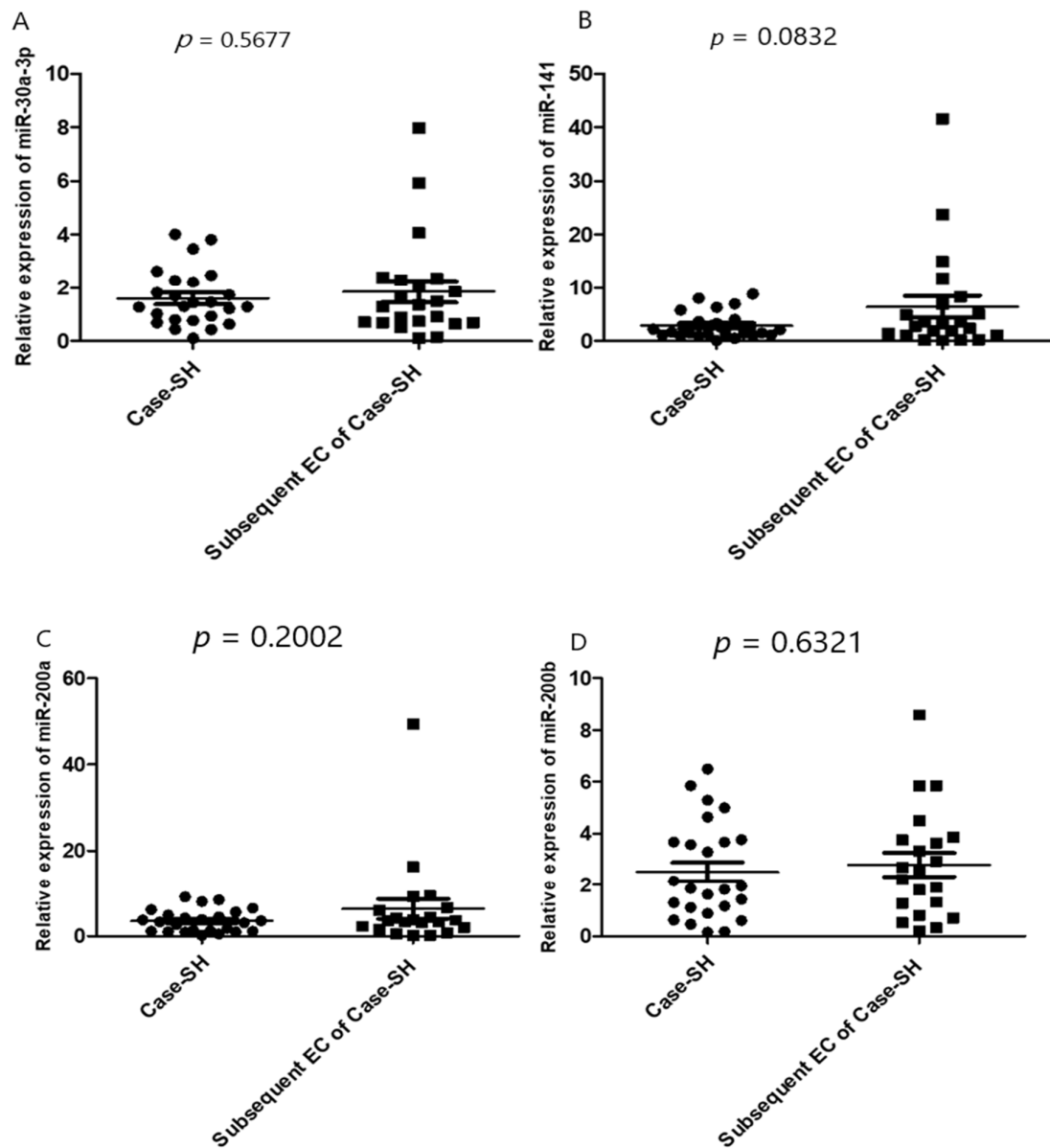
**Table S1.** Demographics and clinical features of patients whose SH /CH-nonA and subsequently progressing to EC.

Study Code	SH Date	SH/CH Dx	Em. ca. Date	Histological Dx	Stage	Grade	MiRNA array/ QPCR/
SH-01P	1989/4/13	Focal polypoid hyperplasia	2004/5/11	endometrioid	IIIC2	3	MiRNA array/ QPCR
SH-02P	1998/4/27	SH without atypia	2004/2/27	endometrioid	IA	2	QPCR
SH-03P	2000/10/9	SH without atypia	2003/8/23	endometrioid	IA	1	MiRNA array/ QPCR
SH-06P	2008/9/26	SH without atypia	2009/4/14	endometrioid	IA	1	QPCR
SH-07P	1992/11/20	CH without atypia	2005/8/23	endometrioid	IA	2	MiRNA array/ QPCR
SH-08P	2008/8/26	SH without atypia	2012/4/24	endometrioid	IA	2	MiRNA array/ QPCR
SH-012P	2001/10/29	SH/CH without atypia	2009/6/15	endometrioid	IA	1	QPCR
SH-013P	2005/7/6	SH without atypia	2015/9/8	endometrioid	IA	1	MiRNA array/ QPCR
SH-014P	2011/4/1	SH/CH without atypia	2015/5/26	endometrioid	IA	1	MiRNA array
SH-15P	1996/5/14	SH without atypia	2005/7/27	endometrioid	IA	2	QPCR
SH-16P	2002/6/22	SH without atypia	2014/10/29	endometrioid	IB	1	QPCR
SH-17P	1996/4/17	SH without atypia	2004/12/31	endometrioid	IA	1	QPCR
SH-18P	2011/3/24	SH/CH without atypia	2017/4/25	endometrioid	IIIA	1	QPCR
SH-19P	2000/10/11	SH without atypia	2015/4/2	endometrioid	IA	1	QPCR
SH-20P	2003/10/23	SH without atypia	2012/11/15	endometrioid	IA	1	QPCR
SH-21P	1998/12/31	SH without atypia	2002/12/28	endometrioid	NA	1	QPCR
SH-22P	2002/11/9	SH/CH without atypia	2008/6/19	endometrioid	1A	2	QPCR
SH-27P	2010/2/10	SH without atypia	2015/1/22	endometrioid	IA	1	QPCR
SH-29P	1995/9/16	SH without atypia	2015/7/18	endometrioid	IA	1	QPCR
SH-30P	2007/5/11	SH without atypia	2012/12/5	endometrioid	IIIA	2	QPCR
SH-32P	1993/2/6	SH/CH without atypia	2004/11/29	endometrioid	IIIA	2	QPCR
SH-35P	2002/10/4	SH without atypia	2019/4/25	endometrioid	IA	1	QPCR
SH-36P	2002/11/9	SH without atypia	2020/6/23	endometrioid	IA	1	QPCR
SH-37P	2005/6/17	SH/CH without atypia	2021/1/22	endometrioid	1A	1	QPCR
SH-38P	2017/3/27	SH without atypia	2020/6/23	endometrioid	IA	1	QPCR
SH-39P	2012/7/4	SH without atypia	2021/1/22	endometrioid	IB	1	QPCR

Em. ca.: endometrial cancer; Dx: diagnosis; SH: simple hyperplasia; CH: complex hyperplasia; NA: not available.



**Figure S1.** Histoscores of BECN1 in patients with control EH and case EH tissues. The protein levels of BECN1 were analyzed through IHC in the tissue samples from SH/CH-nonA progressed to EC (Case-SH) and those whose did not (Control-SH).



**Figure S2.** Differential expression of miRNAs in EC tissue and EH tissue in case with SH/CH-nonA. (A–D) The expression levels of miR-30a-3p, miR-141, miR-200a and miR-200b were not significantly different between the EH tissue in case with SH/CH-nonA (Case-SH) and EC tissue (Subsequent EC of Case-SH) by using RT-qPCR. The expression of miRNAs was normalized to endogenous control miR-16.

(A)

GO.term.accession	GO.term.name	GO.domain	num_genes	num_intersection	p.value	adj.p.value
GO:0019835	cytolysis	biological_process	20	3	0.000176467485933474	0.365385791674339
GO:0019369	arachidonic acid metabolic process	biological_process	23	3	0.000270846354012866	0.365385791674339
GO:0000096	sulfur amino acid metabolic process	biological_process	5	2	0.000301388571020689	0.365385791674339
GO:0015793	glycerol transport	biological_process	6	2	0.00045044478118883	0.365385791674339
GO:0042426	choline catabolic process	biological_process	6	2	0.00045044478118883	0.365385791674339

(B)

GO.term.accession	GO.term.name	GO.domain	num_genes	num_intersection	p.value	adj.p.value
GO:0070125	mitochondrial translational elongation	biological_process	88	9	0.0000547996588868838	0.168899279325252
GO:0019369	arachidonic acid metabolic process	biological_process	23	5	0.0000694059089070276	0.168899279325252
GO:0009642	response to light intensity	biological_process	7	3	0.000243444898412104	0.394948773523903
GO:0070126	mitochondrial translational termination	biological_process	89	8	0.000348203049183704	0.423676060094272
GO:0032835	glomerulus development	biological_process	9	3	0.00056749367031661	0.552398338686188

**Figure S3.** A prediction of biological processes targeted by (A) 20 miRNAs or (B) 4 miRNAs by using the data from a website (<https://fadeel.shinyapps.io/miRNA-GO-analysis/>)