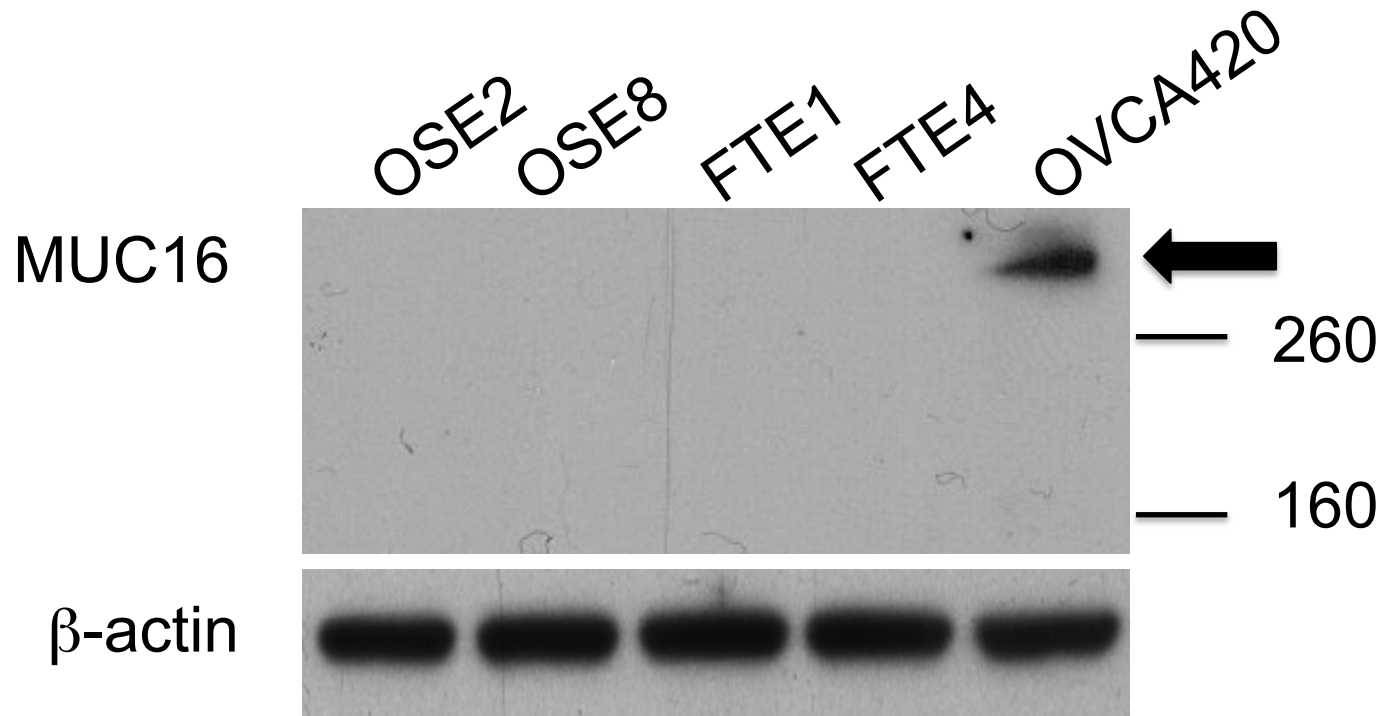


# **Supplemental Information**

**One Supplemental Figure and  
Five Supplemental Tables**



**Figure S1. Western blot analysis to show negligible expression of CA125 (MUC16) in OSE and FTE primary cultures.**

OVCA420 cancer cell line was used as the reference for MUC16 expression (block arrow).  $\beta$ -actin was used as loading control.

Table S1. Correlation analyses for the relationship between expression levels of miR-200 family and miR-205 and target genes.

	miR-200a	miR-200b	miR-200c	miR-141	miR-429	miR-205	ZEB1	ZEB2	TGFB1	TGFB2
miR-200a Pearson Correlation	1	.863**	.726**	.866**	.889**	.329**	-.268*	-.246*	-.178	-.242*
Sig. (2-tailed)		.000	.000	.000	.000	.003	.015	.027	.111	.029
miR-200b Pearson Correlation	.863**	1	.834**	.711**	.757**	.520**	-.474**	-.464**	-.208	-.297**
Sig. (2-tailed)	.000		.000	.000	.000	.000	.000	.000	.062	.007
miR-200c Pearson Correlation	.726**	.834**	1	.750**	.666**	.491**	-.409**	-.369**	-.281*	-.307**
Sig. (2-tailed)	.000	.000		.000	.000	.000	.000	.001	.011	.005
miR-141 Pearson Correlation	.866**	.711**	.750**	1	.886**	.330**	-.204	-.180	-.235*	-.211
Sig. (2-tailed)	.000	.000	.000		.000	.003	.067	.107	.035	.058
miR-429 Pearson Correlation	.889**	.757**	.666**	.886**	1	.397**	-.294**	-.295**	-.167	-.244*
Sig. (2-tailed)	.000	.000	.000	.000		.000	.008	.007	.136	.028
miR-205 Pearson Correlation	.329**	.520**	.491**	.330**	.397**	1	-.529**	-.483**	-.012	-.254*
Sig. (2-tailed)	.003	.000	.000	.003	.000		.000	.000	.919	.022
ZEB1 Pearson Correlation	-.268*	-.474**	-.409**	-.204	-.294**	-.529**	1	.709**	.507**	.537**
Sig. (2-tailed)	.015	.000	.000	.067	.008	.000		.000	.000	.000
ZEB2 Pearson Correlation	-.246*	-.464**	-.369**	-.180	-.295**	-.483**	.709**	1	.356**	.301**
Sig. (2-tailed)	.027	.000	.001	.107	.007	.000	.000		.001	.006
TGFB1 Pearson Correlation	-.178	-.208	-.281*	-.235*	-.167	-.012	.507**	.356**	1	.582**
Sig. (2-tailed)	.111	.062	.011	.035	.136	.919	.000	.001		.000
TGFB2 Pearson Correlation	-.242*	-.297**	-.307**	-.211	-.244*	-.254*	.537**	.301**	.582**	1
Sig. (2-tailed)	.029	.007	.005	.058	.028	.022	.000	.006	.000	

N=81 for all. \*\*. Correlation is significant at the 0.01 level (2-tailed). \*. Correlation is significant at the 0.05 level (2-tailed).

Correlation coefficients that are  $\geq 4$  are highlighted in red, whereas the correlation coefficients that are  $\leq -4.0$  are highlighted in blue.



**Table S3: Differential expression of effector gene *MUC16* in different subtypes of ovarian tumors**

Effector gene	Ovarian cancer cells			
	Overall <i>P</i> -value	Clear cell	Endometrioid	Serous
		Difference in medians against Mucinous cancer cells ( <i>P</i> -value)		
MUC16	<0.016 <sup>†</sup>	7.979 (0.858)	7.819 (0.024*)	6.911 (0.012*)

<sup>†</sup> significant at the 0.05 level by Kruskal Wallis test

\* significant at the 0.05 level by Mann-Whitney test (corrected using the Bonferroni method for multiple comparisons)

**Table S4: Effects of microRNA on target gene expression in OSE and FTE cells**

	MicroRNA								
	miR-200a	miR-200b	miR-200c	miR-141	miR-429	miR-205	miR-200b + miR-205	miR-141 + miR-205	Five miR-200 members
Overall effect (OSE)	-1.010	-0.782	-0.452	-0.468	-0.629	-0.133	-0.472	-0.534	-0.587
<i>P</i> -value† (OSE)	<0.001*	<0.001*	0.029*	0.022*	0.001*	0.935	0.021*	0.007*	0.003*
Overall effect (FTE)	-0.419	-0.512	-0.578	-0.047	-0.454	0.156	-0.031	-0.088	-0.360
<i>P</i> -value† (FTE)	0.340	0.163	0.090	1.000	0.261	0.986	1.000	1.000	0.499
Target gene	Estimated marginal mean expression					<i>P</i> -value‡			
ZEB1 (OSE)	-0.389					<0.001*			
ZEB2 (OSE)	-0.854					<0.001*			
TGFB1 (OSE)	-0.338					<0.001*			
TGFB2 (OSE)	-0.449					<0.001*			
ZEB1 (FTE)	-0.252					0.016*			
ZEB2 (FTE)	-0.752					<0.001*			
TGFB1 (FTE)	-0.135					0.183			
TGFB2 (FTE)	0.204					0.048*			

† *p*-value of Dunnett's test to compare each microRNA versus Controls (two-sided)

‡ *p*-value for testing mean expressions not equal to zero (two-sided)

\* significant at the 0.05 level

**Table S5: Effects of microRNA on effector gene expression in OSE and FTE**

	MicroRNA								
	miR-200a	miR-200b	miR-200c	miR-141	miR-429	miR-205	miR-200b + miR-205	miR-141 + miR-205	Five miR-200 members
Overall effect (OSE)	1.493	1.684	1.351	0.935	0.835	-0.286	1.276	0.918	1.404
<i>P</i> -value† (OSE)	<0.001*	<0.001*	<0.001*	0.023*	0.055	0.941	0.001*	0.027*	<0.001*
Overall effect (FTE)	1.588	2.440	2.203	1.798	2.540	0.412	0.772	1.945	2.519
<i>P</i> -value† (FTE)	<0.001*	<0.001*	<0.001*	<0.001*	<0.001*	0.763	0.127	<0.001*	<0.001*
Effector gene	Estimated marginal mean expression (OSE)		<i>P</i> -value‡ (OSE)		Estimated marginal mean expression (FTE)		<i>P</i> -value‡ (FTE)		
CDH1	2.973		<0.001*		2.565		<0.001*		
CDH3	1.981		<0.001*		2.779		<0.001*		
CRB3	3.781		<0.001*		5.337		<0.001*		
LLGL2	0.608		0.059		0.875		0.011*		
CLDN7	-0.016		0.960		3.061		<0.001*		
SFN	1.856		<0.001*		0.894		0.009*		
PPL	1.303		<0.001*		0.774		0.024*		
EVA1	0.015		0.963		0.614		0.072		
EpCAM	1.774		<0.001*		1.946		<0.001*		
TSPAN1	1.744		<0.001*		4.470		<0.001*		
SCEL	0.027		0.933		0.411		0.227		

PKP3	0.847	0.009*	3.040	<0.001*
TMEM30B	-0.624	0.053	0.627	0.066
MAL2	1.468	<0.001*	0.830	0.015*
MUC1	0.362	0.259	0.136	0.689
CDH11	-0.057	0.859	-0.249	0.464
OCLN	0.158	0.622	0.212	0.532
PTAJ	1.237	<0.001*	0.549	0.107
SH3YL1	0.503	0.118	0.309	0.363
MUC16	0.163	0.611	4.496	<0.001*
HE4	0.081	0.800	0.380	0.264

† p-values of Dunnett's test to compare each microRNA versus Controls (two-sided)

‡ p-values for testing mean expressions not equal to zero (two-sided)

\* significant at the 0.05 level