

**Supplementary Table 1. Clinicopathological characteristics of ovarian cancer and controls**

Overall			
Variables	Case, n(%)	Control, n(%)	<i>P</i>
Age, mean (SD)	60.73(10.36)	60.30(10.71)	0.554
Race			
White	339( 81.3)	349( 83.7)	0.269
Hispanic	48( 11.5)	49( 11.8)	
Others	30( 7.2)	19( 4.6)	
Total	417	417	
White cases*			
Median survival time (months)	48.26		
Age, median (range)	61(26-88)		
Clinical stage			
Stage I	16( 5)		
Stage II	21( 7)		
Stage III	202(66)		
Stage IV	65(21)		
Total	304		
Histology			
Serous	197(62)		
Mixed	72(23)		
Others	50(16)		
Total	319		
Death			
No	173(54)		
Yes	146(46)		
Total	319		
Recurrence			
No	167(52)		
Yes	152(48)		
Total	319		
Nonresponder			
No	199(67)		
Yes	96(33)		
Total	295		

\* Restricted to patients treated with surgery and platinum-based therapy

**Supplementary Table 2. Haplotype analysis of *GEMIN4* SNPs and ovarian cancer risk**

Haplotype*	Case	Control	OR <sup>†</sup>	95% CI <sup>‡</sup>	P value
<i>GEMIN4</i>					
W_W_W_W_W_W	205	165	1(reference)		
M_M_W_W_M_M	155	183	0.69	(0.51-0.94)	0.018
M_M_M_W_W_W	106	142	0.63	(0.46-0.86)	0.004
W_W_W_M_W_M	112	111	0.84	(0.60-1.17)	0.304
W_W_W_W_M_W	74	69	0.87	(0.59-1.30)	0.506
Other	20	18	0.91	(0.46-1.80)	0.789

\* W- wildtype allele, M- variant allele

† Adjusted for age

‡ Confidence interval

Haplotype in the order of rs2740351 (A/G), rs7813 (A/G), rs2740349 (A/G), rs1062923 (A/G), rs2291778 (C/A), rs3087833 (G/A)

**Supplementary Table 3. Top SNPs in miRNA-related genes associated with ovarian cancer risk and clinical outcome**

SNP	Gene	Association	Locus	Function	P - value	q value <sup>‡</sup>
rs2740351	GEMIN4	Susceptibility Risk	17p13	Component of miRNP and spliceosome protein complex; required for pre-mRNA splicing	0.0014	0.112
rs5973822	ATG4A	Susceptibility Risk	Xq22	Cysteine protease involved in autophagy	0.0015	0.112
rs1425486	PDGFC	Survival	4q32	Mitogenic factor for mesenchymal cells	4.90 X 10 <sup>-5</sup>	0.004
rs1047920	SNAI1	Survival	20q13	Transcription factor involved in epithelial-mesenchymal transition; downregulates E-cadherin	0.001	0.056
rs7869402	TLR4	Survival	9q32	Toll-like receptor that mediates pathogen recognition and innate immunity	0.002	0.063
rs10771184	KRAS	Survival	12p12	Kirsten ras oncogene homolog; member of GTPase superfamily	0.005	0.095
rs12190214	ALDH5A1	Treatment Response	6p22	Aldehyde dehydrogenase; non-P450 enzyme metabolism	0.0062	0.167
rs1425486	PDGFC	Treatment Response	4q32	See above	0.007	0.167
rs7869402	TLR4	Treatment Response	9q32	See above	0.0071	0.167

‡ FDR-adjusted P-value

**Supplementary Table 4. Overall and stratified analysis of top 15 SNPs associated with ovarian cancer survival and treatment response**

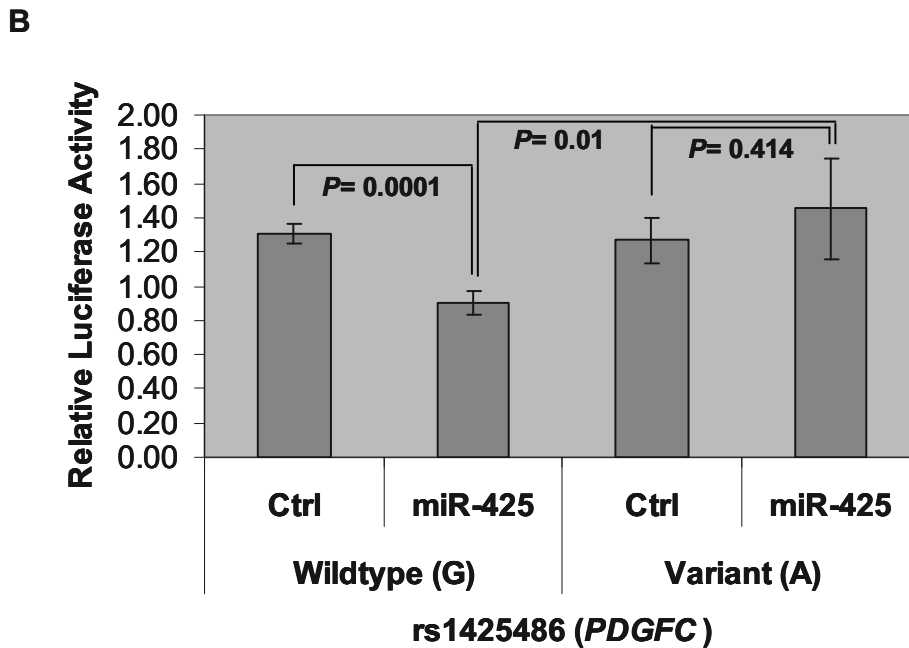
No.	SNP	Model <sup>‡</sup>	Overall Survival			
			All patients		Serous carcinoma	
			HR*(95% CI)	P smallest	HR*(95% CI)	P smallest
1	rs1425486	Rec	2.69( 1.67- 4.33)	0.00005	2.99( 1.73- 5.17)	0.00009
2	rs1047920	Dom	1.96( 1.30- 2.97)	0.00146	1.24( 0.68- 2.25)	0.47940
3	rs7869402	Dom	2.16( 1.31- 3.57)	0.00248	2.24( 1.21- 4.16)	0.01025
4	rs10771184	Dom	0.56( 0.38- 0.84)	0.00502	0.57( 0.32- 1.00)	0.05181
5	rs10518679	Dom	0.57( 0.38- 0.86)	0.00711	0.58( 0.34- 0.97)	0.03879
6	rs3757	Rec	2.76( 1.30- 5.84)	0.00804	2.47( 1.03- 5.91)	0.04198
7	rs3792830	Dom	0.39( 0.19- 0.79)	0.00864	0.39( 0.18- 0.85)	0.01783
8	rs1633445	Rec	2.67( 1.27- 5.64)	0.00984	2.34( 0.99- 5.58)	0.05381
9	rs720014	Rec	2.65( 1.26- 5.59)	0.01057	2.33( 0.98- 5.55)	0.05597
10	rs3087833	Add	1.48( 1.08- 2.03)	0.01380	1.54( 1.02- 2.32)	0.04010
11	rs2287584	Rec	0.39( 0.19- 0.84)	0.01610	0.43( 0.18- 1.02)	0.05426
12	rs9333555	Dom	2.49( 1.18- 5.24)	0.01627	1.81( 0.65- 5.04)	0.26001
13	rs17749202	Rec	1.66( 1.07- 2.58)	0.02442	1.84( 1.07- 3.17)	0.02846
14	rs12889916	Rec	0.42( 0.19- 0.91)	0.02791	0.35( 0.14- 0.87)	0.02389
15	rs8139591	Rec	0.20( 0.05- 0.84)	0.02840	0.17( 0.02- 1.24)	0.07998

No.	SNP	Model <sup>‡</sup>	Treatment Response			
			All patients		Serous carcinoma	
			OR*(95% CI)	P smallest	OR*(95% CI)	P smallest
1	rs12190214	Dom	2.60( 1.31- 5.14)	0.00619	2.65( 1.19- 5.92)	0.01749
2	rs1425486	Rec	3.38( 1.39- 8.19)	0.00703	3.40( 1.25- 9.23)	0.01643
3	rs7869402	Dom	3.49( 1.41- 8.67)	0.00705	2.78( 0.93- 8.33)	0.06801
4	rs2248718	Dom	2.12( 1.19- 3.78)	0.01089	2.66( 1.25- 5.68)	0.01151
5	rs12226697	Dom	3.30( 1.29- 8.45)	0.01278	4.89( 1.53-15.62)	0.00736
6	rs17408716	Dom	0.38( 0.17- 0.84)	0.01658	0.50( 0.20- 1.27)	0.14614
7	rs713065	Rec	2.28( 1.15- 4.53)	0.01893	1.81( 0.80- 4.11)	0.15519
8	rs16869269	Rec	7.67( 1.36-43.16)	0.02090	#	-
9	rs7695605	Dom	1.85( 1.09- 3.13)	0.02165	2.09( 1.08- 4.07)	0.02895
10	rs10900596	Rec	0.31( 0.11- 0.85)	0.02327	0.27( 0.07- 1.00)	0.05044
11	rs10771184	Dom	0.50( 0.27- 0.91)	0.02385	0.70( 0.31- 1.56)	0.38396
12	rs12900401	Dom	2.68( 1.13- 6.34)	0.02504	1.61( 0.50- 5.26)	0.42663
13	rs8065843	Rec	4.47( 1.17-17.02)	0.02839	12.04( 1.35-107.56)	0.02593
14	rs7957	Dom	1.75( 1.03- 2.97)	0.03741	1.90( 0.98- 3.68)	0.05597
15	rs1048691	Rec	0.11( 0.01- 0.90)	0.03916	#	-

\* Adjusted for age, clinical stage, histology, and treatment regimen; CI- confidence interval

‡ Rec- recessive, Dom- dominant, Add- additive

# Number of subjects with variant alleles too small for meaningful estimation



**Supplementary Figure 1.** Effect of the *PDGFC* variant allele on miR-425 targeting and luciferase reporter expression. *A*, schematic diagram of the luciferase reporter construct containing the entire *PDGFC* 3'UTR, including the wildtype or variant allele of rs1425486. *B*, relative luciferase reporter activity of the wildtype and variant *PDGFC* allele in the presence of control (Ctrl) or miR-425 RNA in OVCAR3 cells. Similar results were obtained with four replicates. *P* values were determined by two-sided Student's t-test.