

Supplementary Information

Comprehensive analysis of lncRNA-mRNA co-expression patterns identifies immune-associated lncRNA biomarkers in ovarian cancer malignant progression

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Supplementary Table S1. Univariate analysis of lncRNAs expression in OV malignant progression.

Variable	Univariate analysis		
	HR (95%CI)	Coefficient	P-value
PSMB8-AS1	0.970(0.941-0.999)	-0.0308	0.04
AC104699.1.1	0.444(0.214-0.920)	-0.8117	0.02
GS1-124K5.11.1	1.135(1.017-1.267)	0.1265	0.02
GAS5	1.002(1.000-1.267)	0.0022	0.04
RP11-320G24.1.1	0.621(0.416-0.928)	-0.4756	0.02
ZFHX4-AS1	1.485(1.217-1.812)	0.3958	9.80E-05
AL928768.3.1	0.298(0.122-0.724)	-1.2117	7.50E-03
RP11-284N8.3.1	0.656(0.458-0.940)	-0.4211	0.02

Supplementary Table S2. Univariate analysis of lncRNAs expression for progression-free survival.

Variable	Univariate analysis		
	HR (95%CI)	Regression coefficient	P-value
RP11-284N8.3.1	0.649(0.461-0.914)	-0.4317	0.01
AC104699.1.1	0.424(0.215-0.836)	-0.8573	0.02

Supplementary Table S3. Multivariate analysis of clinicopathological factors and RP11-284N8.3.1 in OV malignant progression

Variable	Multivariate analysis		
	HR (95%CI)	Regression coefficient	P-value
Stage	1.165(0.861-1.576)	0.153	0.32
Age	1.016(1.004-1.029)	0.016	0.01
Histological grade	1.069(0.813-1.404)	0.066	0.63
Residual tumor diameter(cm)	1.326(1.103-1.595)	0.282	2.72E-03
RP11-284N8.3.1	0.658(0.456-0.951)	-0.418	0.03

Supplementary Table S4. Multivariate analysis of clinicopathological factors and AC104699.1.1 in OV malignant progression

Variable	Multivariate analysis		
	HR (95%CI)	Regression coefficient	P-value
Stage	1.177(0.869-1.593)	0.163	0.29
Age	1.015(1.003-1.028)	0.016	0.01
Histological grade	1.054(0.803-1.384)	0.053	0.7
Residual tumor diameter(cm)	1.314(1.092-1.581)	0.273	3.77E-03
AC104699.1.1	0.497(0.239-1.033)	-0.699	0.06

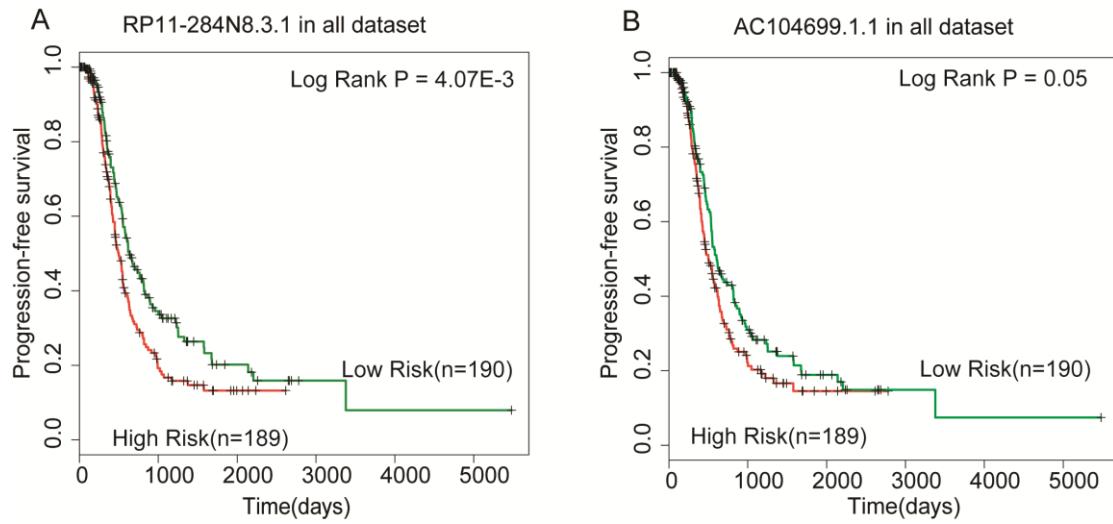


Figure S1. The use of lncRNAs to predict the progression-free survival of OV patients.

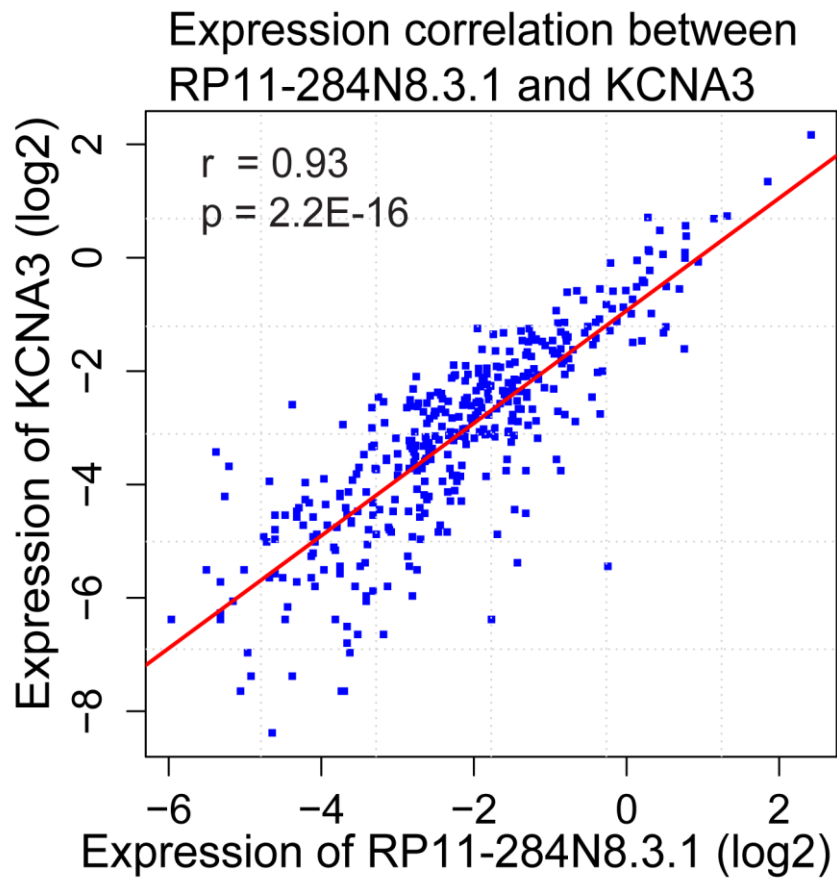


Figure S2. The expression illustration and correlation between RP11-284N8.3.1 and KCNA3.

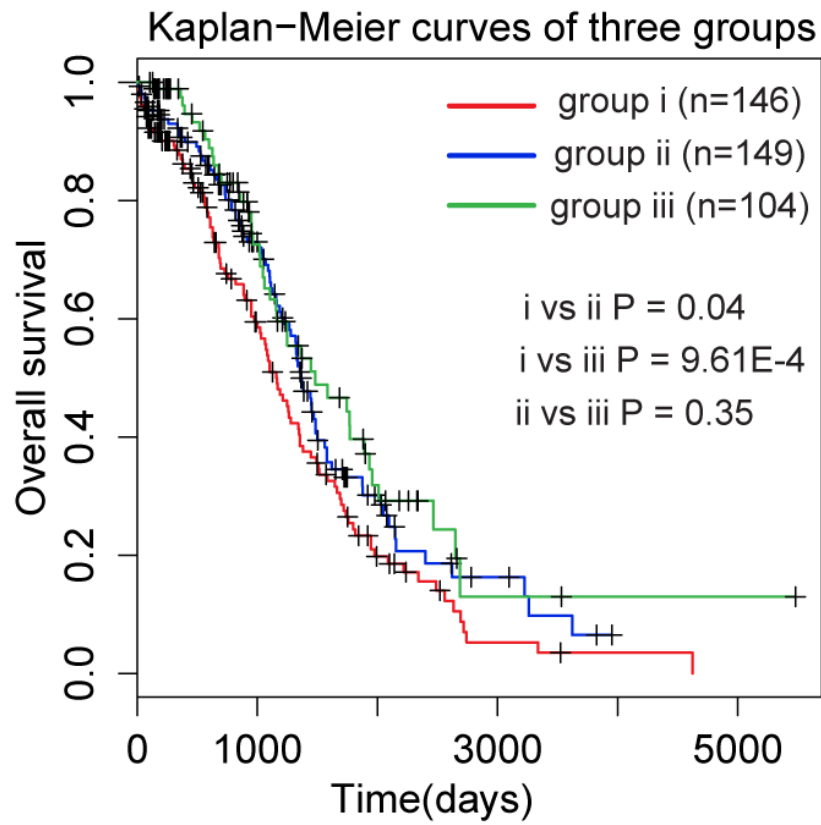


Figure S3. Detail information of survival rates for each of the three patient groups.

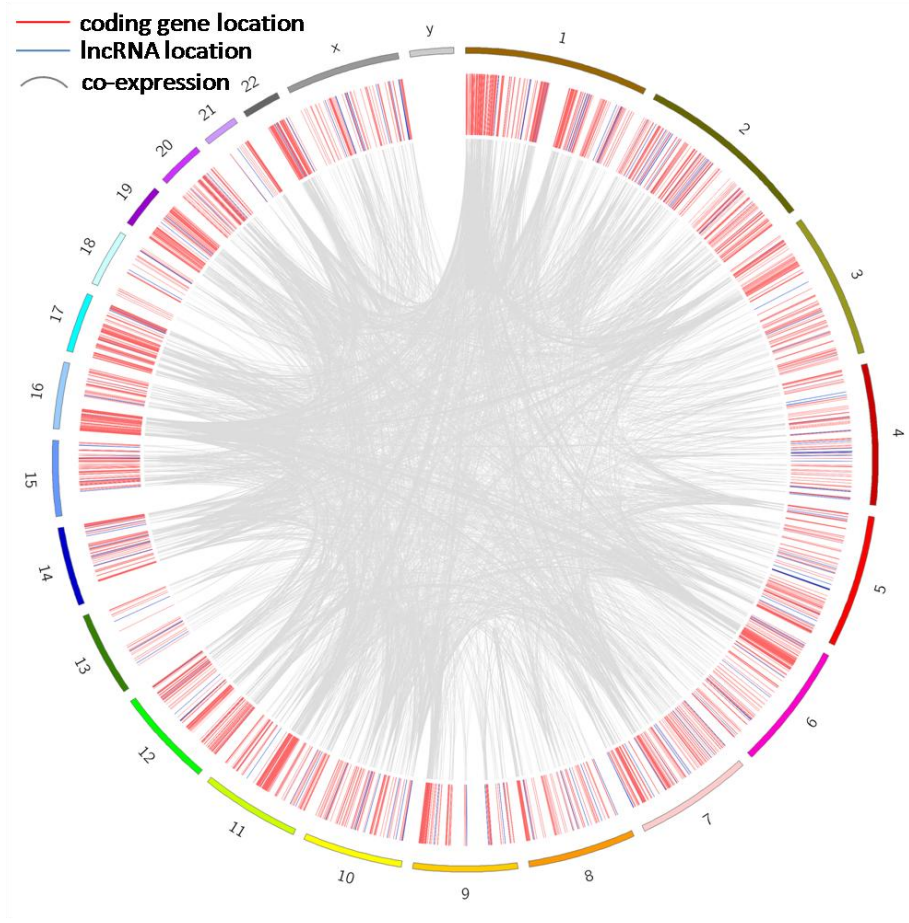


Figure S4. A genome-wide map of 8393 lncRNA-coding-gene pairs based on Circos-style visualization. Outer circles indicate human chromosomes. Genomic locations of lncRNAs and coding-genes were illustrated as blue and red bars. Grey arc lines within the circle denote pairs of co-expression interactions.