

Table S1. Mutational status of four cancer driver genes (*TP53*, *BRCA1*, *BRCA2*, and *KRAS*) and carboplatin response of selected cell lines and its carboplatin-resistant counterparts.

Cell line	Mutation status			Carboplatin IC ₅₀ (μM)
	<i>TP53</i>	<i>BRCA1/2</i>	<i>KRAS</i>	
IGROV1	p.Y126C	<i>BRCA1</i> p.K654fs*47 <i>BRCA2</i> p.P3150T	wt	14.0 ± 1.1
IGROV1-R1	p.Y126C	<i>BRCA1</i> p.K654fs*47 <i>BRCA2</i> p.P3150T	wt	44.4 ± 8.2
OVCAR3	p.R248Q	wt	wt	4.8 ± 2.1
OVCAR3-R1	p.R248Q	wt	wt	28.6 ± 2.6
OVCAR3-R2	p.R248Q	wt	wt	31.4 ± 2.1
OVCAR4	p.L130V	<i>BRCA2</i> p.P2505L	wt	8.8 ± 4.2
OVCAR5	wt	wt	p.Gly12Val	17.2 ± 4.0
OVCAR5-R1	wt	wt	p.Gly12Val	47.4 ± 7.4
OVCAR8	c.376-1G>A (splice variant)	wt	wt	33.0 ± 2.6
Ovc316	-	wt	wt	77.8 ± 2.8

R1 and R2 carboplatin-resistant derived counterparts;
wt: wild type, no predicted deleterious mutation identified.

Table S2. Clinical and pathological features of 39 patients with high-grade serous ovarian carcinoma included in this study.

Variable	Cases (N=39)
Age at diagnosis (years)	
Mean (\pm Std. Deviation)	69.4 \pm 9.4
Median	69.1
Range	min 46 - max 83
FIGO stage	
III	31
IV	8
CA-125 baseline level, U/L*	
Median	803
Range	min 179 - max 17096
Progression-free survival (months)	
0-6	11
7-11	9
>12	19
Overall survival (months)	
<12	12
>12	27

(*) data available on 22 out of 39 cases.

Table S3. Pathway enrichment analysis of differentially expressed genes between carboplatin-sensitive and carboplatin resistant OC derived cells.

Pathway name	Entities				Reactions	
	found	ratio	p-value	FDR*	found	ratio
Up-regulated genes						
Glutathione conjugation	4/67	0.006	0.003	0.268	1/14	0.001
Activation of PUMA and translocation to mitochondria	2/10	6.97e-04	0.003	0.268	5/5	3.78e-04
Formyl peptide receptors bind formyl peptides and many other ligands	2/11	7.47e-04	0.004	0.268	2/3	2.27e-04
Signaling by TGFB family members	4/114	0.008	0.016	0.47	11/107	0.008
FOXO-mediated transcription of cell death genes	2/23	0/002	0.016	0.47	2/15	0.001
TP53 regulates transcription of genes involved in cytochrome C release	2/33	0.002	0.032	0.47	2/25	0.002
Antagonism of activin by follistatin	1/4	2.72e-04	0.033	0.47	2/2	1.51e-04
TGFBRI LED mutants in cancer	1/4	2.72e-04	0.033	0.47	1/1	7.56e-05
Signaling by TGF-beta receptor complex	3/85	0.006	0.035	0.47	4/82	0.006
Activation of BH3 only proteins	2/36	0.002	0.037	0.47	5/19	0.001
SMAD2/SMAD3:SMAD4 heterotrimer regulates transcription	2/39	0.003	0.043	0.47	1/17	0.001
BMAL1:CLOCK, NPAS2 activates circadian gene expression	2/42	0.003	0.049	0.47	2/20	0.002
Down-regulated genes						
RUNX1 regulates genes involved in megakaryocyte differentiation and platelets function	11/73	0.005	1.13e-07	6.70e-05	21/33	0.002
RNA Polymerase I promoter opening	8/34	0.002	1.43e-07	6.70e-05	2/2	1.51e-04
IGF1R signaling cascade	10/72	0.005	4.92e-07	1.30e-04	9/17	0.001
Activated PEN1 stimulates transcription of AR (androgen receptor) regulated genes KLK2 and KLK3	8/49	0.003	2.15e-06	4.02e-04	9/11	8.32e-04
DNA methylation	7/36	0.002	3.04e-06	4.74e-04	7/7	5.29e-04
NoRC negatively regulates rRNA expression	9/80	0.005	9.89e-05	0.001	5/7	5.29e-04
PRC2 methylates histones and DNA	7/44	0.003	1.11e-05	0.001	4/4	3.02e-04
SIRT1 negatively regulates rRNA expression	7/45	0.003	1.28e-05	0.001	3/5	3.78e-04
Unfolded protein response (UPR)	12/15 5	0.011	1.44e-05	0.001	13/94	0.007
RNA Polymerase I promoter escape	8/64	0.004	1.47e-05	0.001	2/2	1.51e-04
Signaling by FGFR	10/10 7	0.007	1.56e-05	0.001	777/142	0.011
ERCC2 (CSB) and EHMT2 (G9a) positively regulate rRNA expression	7/48	0.003	1.92e-05	0.001	2/4	3.02e-04

Table S4. Differentially expressed lncRNAs and overlapping differentially methylated positions in ovarian cancer cell lines relative to its carboplatin-resistant counterparts.

lncRNA	Chr	Nucleotide position		Gene expression analysis		DNA methylation analysis		
		Start	End	log FC	p-value	Probe ID	$\Delta\beta$	p-value
<i>SNHG12</i>	1	28578538	28583132	0.41	0.010	cg08625918	-0.08	0.03
<i>LINC01781</i>	1	80535755	80646791	-1.65	0.003	cg22327746	0.24	0.03
<i>AC010894.3</i>	2	174547141	174776720	-1.15	0.047	cg17095939	0.16	0.02
						cg14797460	0.04	0.00
						cg08213000	0.17	0.01
						cg15174367	0.05	0.03
<i>LINC01811</i>	3	33956972	34677247	1.48	0.004	cg17661563	0.36	0.05
<i>AC025470.2</i>	5	57395060	57534504	1.49	0.002	cg00325378	0.24	0.04
<i>LINC01277</i>	6	142966293	143059682	0.75	0.009	cg19979228	0.22	0.03
						cg23117546	0.35	0.02
						cg03616157	0.20	0.01
<i>EMX2OS</i>	10	117473215	117545068	-0.54	0.034	cg04556008	0.39	0.03
<i>AP002807.1</i>	11	68050740	68053762	0.90	0.001	cg00387390	0.12	0.04
						cg14774134	0.07	0.00
						cg15085109	0.08	0.02
<i>AP002518.2</i>	11	114210616	114356571	0.81	0.047	cg03409036	0.11	0.04
<i>AC244502.1</i>	14	22197446	22482959	1.09	0.009	cg21875948	0.37	0.03
						cg10268229	0.21	0.01
<i>AC087612.1</i>	15	63091085	63110589	4.06	8.93e-12	cg06828657	0.17	0.02

Chr: chromosome; logFC: log Fold-Change