Supplementary Tables

Supplementary Table 1 | Demographic and disease characteristics of BriTROC-1 patients

Characteristic	**Platinum-sensitive (*N*=109)**	**Platinum-resistant (*N*=33)**	**Total (*N*=142)**
Median age (range), years	70 (37–90)	67 (25–83)	69.5 (25–90)
Median time since diagnosis (range), months	33.5 (10.2–127.9)	27.3 (7.6–184.2)	32.5 (7.6–184.2)
Germline *BRCA1/2* mutation, *N* (%)*			
BRCA1	5 (4.6)	1 (3.0)	6 (4.2)
BRCA2	4 (3.7)	5 (15.2)	9 (6.3)
Histology, *N* (%)			
High grade serous	105 (96.3)	33 (100)	138 (97.2)
G3 Endometrioid	3 (2.8)	0	3 (2.1)
Missing	1 (0.9)	0	1 (0.7)
Number of prior treatment regimens			
Median number of regimens (range)	1 (1–5)	2 (1–12)	1 (1–12)
1, *N* (%)	72 (66.1)	11 (33.3)	83 (58.5)
2, *N* (%)	28 (25.7)	15 (45.5)	43 (30.3)
3, *N* (%)	6 (5.5)	1 (3.0)	7 (4.9)
>3, *N* (%)	2 (1.8)	6 (18.1)	8 (5.6)
Data missing	1 (1.2)	0	1 (0.7)

* Mutation status as recorded at time of study entry.

Supplementary Table 2 | Correlations of CN signature components across three sample sets

	CN signature 1	CN signature 2	CN signature 3	CN signature 4	CN signature 5	CN signature 6	CN signature 7
ICGC correlation	0.78	0.91	0.95	0.88	0.93	0.73	0.84
ICGC p-value	1.00E-43	6.00E-15	3.00E-21	2.00E-15	5.00E-26	9.00E-05	2.00E-09
TCGA correlation	0.73	0.84	0.89	0.93	0.71	0.56	0.92
TCGA p-value	5.00E-41	8.00E-14	4.00E-15	3.00E-11	1.00E-08	3.00E-08	1.00E-21

Supplementary Table 3 | Means of CN signature components

Component	Mean	SD
bp1	6.47E-05	NA
bp2	1.25529082	NA
bp3	4.07458306	NA
cn1	0.99799839	0.10280125
cn2	1.98135508	0.12149214
cn3	2.56168152	1.00230467
cn4	2.99108879	0.1440896
cn5	3.97051928	0.17145688
cn6	4.27164691	1.58429331
cn7	8.39260927	3.50149434
cn8	30.8672269	23.15811
cp1	0.49452648	0.15645341
cp2	0.96834666	0.15629395
cp3	1.17859816	0.22669911
cp4	1.82240751	0.39907792
cp5	3.00685766	1.03958107
cp6	7.3149416	3.45921997
cp7	28.7346654	22.0551593
ct1	0.06154321	NA
ct2	2.62256735	NA
ct3	7.77720192	NA
ct4	17.5464903	NA
ct5	33.5306827	NA
os1	0.33948439	NA
os2	2.62714528	NA
os3	9.58714514	NA
ss1	426861.918	186924.872
ss2	1081858.4	407302.128
ss3	2233029.82	749092.036
ss4	4303321.09	1115831.53
ss5	7304340.04	1644306.83
ss6	10479327.2	2972413.84
ss7	16419124.1	5226151.49
ss8	29508322.4	9703791.44
ss9	58638899	20499001.4
ss10	118310989	45210595

Supplementary Table 4 | SNVs in BriTROC-1, PCAWG-OV and TCGA samples

As a separate excel file

Supplementary Table 5 | Amplifications and deletions in BriTROC-1, PCAWG-OV and TCGA samples

As a separate excel file

Supplementary Table 6 | Differences in CN signature exposures for the selected genes

Gene	**CN signature**	**Median difference**	**p-value**	**Adjusted p-value**
NF1	s1	0.26217944	0.00434335	0.03040345
BRCA1	s3	0.20048675	0.00899089	0.04495445
BRCA2	s3	0.24255108	0.00542057	0.03252342
CDK12	s2	0.11998113	0.0002275	0.00204746
CDK12	s4	0.17920597	8.69E-05	0.00086864
CCNE1	s4	0.08524036	1.76E-11	2.12E-10
CCNE1	s6	0.17989992	7.39E-27	1.03E-25
PTEN	s3	0.3382558	0.0002489	0.00204746
MYC	s4	0.10009799	7.17E-13	9.32E-12
MYC	s7	0.08059432	9.70E-08	1.07E-06

Supplementary Table 7 | Differences in CN signature exposures for the selected 9 pathways

Type	**Signature**	**Mean difference**	**p-value**	**q-value**	**Description**	**Gene ID**
R-HSA-5658442	1	0.25038405	7.88E-06	9.21E-06	RAS signaling	*NF1/KRAS/RASA1/RASA2/CUL3/NRAS*
R-HSA-5685942	3	0.21108933	0.0010908	0.00118685	HDR through Homologous Recombination (HRR)	*BARD1/PALB2/BRCA1/ATR/BLM/ATM/NBN/MRE11/BRCA2*
R-HSA-168164	4	0.12397634	1.99E-08	2.75E-08	Toll-Like Receptor Cascades	*PPP2R1A/JUN/MAP2K4/IRF7/IKBKB/CUL1/MEF2C/DHX9/ATF1*
R-HSA-69202	6	0.12701651	5.00E-32	1.24E-30	Cyclin E associated events during G1/S transition	*MYC/CCNE1/AKT2/RB1/CCND1/CDK4/CDK2/CUL1*
R-HSA-2559583	6	0.14745787	2.83E-30	5.44E-29	Cellular Senescence	*TP53/CDK6/CCNE1/RB1/JUN/MDM2/HIST1H3B/MAP2K4/CDK4/MDM4/CDK2/CDKN2A/CDKN2B/HIST1H3F/CDC27/ATM/TFDP1/HIST1H3I/NBN/MRE11/POT1/CDKN2C/STAT3*
R-HSA-2219528	6	0.17711275	1.74E-28	2.31E-27	PI3K/AKT Signaling in Cancer	*PIK3CA/EGFR/MET/RICTOR/FGFR4/AKT2/FGFR1/MDM2/FRS2/ERBB2/HGF/FGFR2/FGF3/FGF4/PDPK1/IRS2/PDGFRA/FGFR3/KIT/ERBB4/PIK3R1/PIK3CB/PIK3R2*
R-HSA-69231	6	0.15513127	2.70E-21	1.42E-20	Cyclin D associated events in G1	*CDK6/CCND3/PPP2R1A/RB1/CCND2/CCND1/CDK4/CDKN2A/CDKN2B/TFDP1/CUL1/CDKN2C*
R-HSA-6785807	7	0.12578358	5.23E-19	2.26E-18	Interleukin-4 and 13 signaling	*TP53/JAK2/MYC/SOX2/BCL2/HGF/CCND1/HSP90AA1/JAK3/STAT6/PIK3R1/VIM/MMP2/STAT3*
R-HSA-195721	7	0.12631054	3.31E-18	1.36E-17	Signaling by Wnt	*MYC/SOX2/TERT/AKT2/PPP2R1A/HIST1H3B/SMARCA4/CREBBP/KMT2D/CTNNB1/HIST1H3F/AXIN1/AXIN2/TRRAP/APC/CUL3/RNF43/CHD8/HIST1H3I/CUL1/CDC73/CSNK2A1/EP300/RHOA/LRP6/TCF7L2*

Supplementary Table 8 | Summary of mutated cases by gene in each pathway

As a separate excel file

Supplementary Table 9 | Cox proportional hazards model

CN signature	**HR**	**Lower**	**Higher**	**P value**
s1	1.15	1.06	1.25	0.001
s2	1.12	1.01	1.23	0.029
s3	0.91	0.83	1	0.049
s4	1	0.91	1.1	0.97
s6	1.01	0.93	1.1	0.734
s7	0.88	0.81	0.97	0.006

Supplementary Table 10 | Difference in CN signature exposures of platinum sensitive vs. resistant cases

CN signature	term	estimate	Standard error	statistic	p-value	Adjusted p-value
s5	(Intercept)	1.16114215	0.58473805	1.98574755	0.04706136	0.14118409
s5	diagnosis_exposure	4.84957051	5.6784812	0.85402599	0.39309059	0.39309059
s5	centered_AGE	-0.5361215	0.4853387	-1.1046336	0.26931837	0.39309059
s1	(Intercept)	4.2003331	1.36910422	3.06794257	0.00215538	0.00646614
s1	diagnosis_exposure	-7.698947	3.0920139	-2.4899458	0.01277626	0.01916439
s1	centered_AGE	-1.1173441	0.66809127	-1.6724422	0.09443715	0.09443715
s2	(Intercept)	-0.4280877	0.80787705	-0.5298922	0.5961867	0.5961867
s2	diagnosis_exposure	51.7371557	23.7491136	2.17848786	0.02936974	0.08810921
s2	centered_AGE	-2.0850188	1.11917136	-1.8630023	0.06246194	0.09369291
s3	(Intercept)	1.34496518	0.66653014	2.01786101	0.04360574	0.13081722
s3	diagnosis_exposure	1.64792166	4.102203	0.40171626	0.68789285	0.68789285
s3	centered_AGE	-0.6022419	0.49284101	-1.2219802	0.22171512	0.33257269
s4	(Intercept)	0.81162853	0.64294595	1.26235888	0.20681968	0.20681968
s4	diagnosis_exposure	5.12356758	3.52869049	1.45197421	0.14650878	0.20681968
s4	centered_AGE	-0.9239388	0.55719803	-1.6581874	0.09727964	0.20681968
s6	(Intercept)	2.23199636	0.73610117	3.03218695	0.00242789	0.00728366
s6	diagnosis_exposure	-6.127137	4.26538457	-1.4364794	0.15086598	0.22629897
s6	centered_AGE	-0.4218361	0.52380542	-0.8053297	0.42062943	0.42062943
s7	(Intercept)	1.33605223	0.6670159	2.00302905	0.04517417	0.13552251
s7	diagnosis_exposure	1.75264219	4.16080913	0.42122629	0.67358985	0.67358985
s7	centered_AGE	-0.6779965	0.48600033	-1.3950535	0.1629997	0.24449955

Supplementary Table 11 | Difference in CN signature exposures in paired primary-relapse BriTROC-1 samples

CN signature	term	estimate	Standard error	statistic	p-value	Adjusted p-value
s5	(Intercept)	0.05430768	0.04052521	1.34009625	0.18995445	0.65879573
s5	log(diagnosis_exposure + 1)	0.16730291	0.17505777	0.95570112	0.34661719	0.65879573
s5	time_to_relapse	2.02E-05	2.34E-05	0.86205421	0.39527744	0.65879573
s5	centered_AGE	0.00966981	0.019155	0.5048193	0.61725574	0.72606165
s5	prior_lines_chemo	-0.0069177	0.01956574	-0.3535604	0.72606165	0.72606165
s1	(Intercept)	0.09502383	0.05740794	1.65523845	0.10796682	0.19466625
s1	log(diagnosis_exposure + 1)	0.71569037	0.14569089	4.91238923	2.76E-05	0.00013802
s1	time_to_relapse	-4.53E-05	2.81E-05	-1.6133674	0.11679975	0.19466625
s1	centered_AGE	0.00516766	0.02174027	0.23770004	0.8136778	0.91236298
s1	prior_lines_chemo	-0.0025952	0.02338889	-0.1109605	0.91236298	0.91236298
s2	(Intercept)	0.04351759	0.03678519	1.18301922	0.24579521	0.46586727
s2	log(diagnosis_exposure + 1)	0.52868796	0.1534013	3.44643736	0.00165369	0.00826847
s2	time_to_relapse	-5.70E-06	1.90E-05	-0.2994408	0.76660227	0.76660227
s2	centered_AGE	-0.0160833	0.01461252	-1.1006548	0.27952036	0.46586727
s2	prior_lines_chemo	0.01402005	0.01634427	0.85779596	0.39758877	0.49698596
s3	(Intercept)	0.05831058	0.03392091	1.71901565	0.09558396	0.2389599
s3	log(diagnosis_exposure + 1)	0.63254469	0.15185422	4.1654731	0.00023015	0.00115076
s3	time_to_relapse	1.87E-05	1.92E-05	0.97565791	0.33678656	0.4209832
s3	centered_AGE	-0.0230171	0.01550174	-1.4848055	0.14769389	0.24615648
s3	prior_lines_chemo	-0.0122262	0.01645885	-0.7428375	0.46317245	0.46317245
s4	(Intercept)	0.02733762	0.04726737	0.57836142	0.56719848	0.88422905
s4	log(diagnosis_exposure + 1)	0.54392473	0.14326478	3.79663949	0.0006407	0.00320348
s4	time_to_relapse	4.29E-05	2.27E-05	1.88660637	0.06861058	0.17152645
s4	centered_AGE	0.00678539	0.01791059	0.37884791	0.70738324	0.88422905
s4	prior_lines_chemo	0.00266658	0.01863326	0.14310867	0.88713053	0.88713053
s6	(Intercept)	0.05950631	0.03368539	1.76653204	0.08715307	0.21788267
s6	log(diagnosis_exposure + 1)	0.50029307	0.14794439	3.38162917	0.00196466	0.00982328
s6	time_to_relapse	-2.14E-05	1.66E-05	-1.2880421	0.20726324	0.34543874
s6	centered_AGE	0.01416556	0.01377867	1.02807887	0.31186806	0.38983508
s6	prior_lines_chemo	-0.0035647	0.01367493	-0.2606741	0.79606772	0.79606772
s7	(Intercept)	0.03699964	0.0287341	1.28765635	0.20739585	0.51848964
s7	log(diagnosis_exposure + 1)	0.62527933	0.13922491	4.49114533	9.18E-05	0.000459
s7	time_to_relapse	-6.99E-06	1.73E-05	-0.404366	0.68872001	0.68872001
s7	centered_AGE	-0.0061395	0.01288602	-0.476445	0.63709857	0.68872001
s7	prior_lines_chemo	0.01247864	0.01415476	0.88158612	0.38478526	0.64130877