Clinical Characteristics of Ovarian Cancer Classified by *BRCA1, BRCA2*, and *RAD51C* Status

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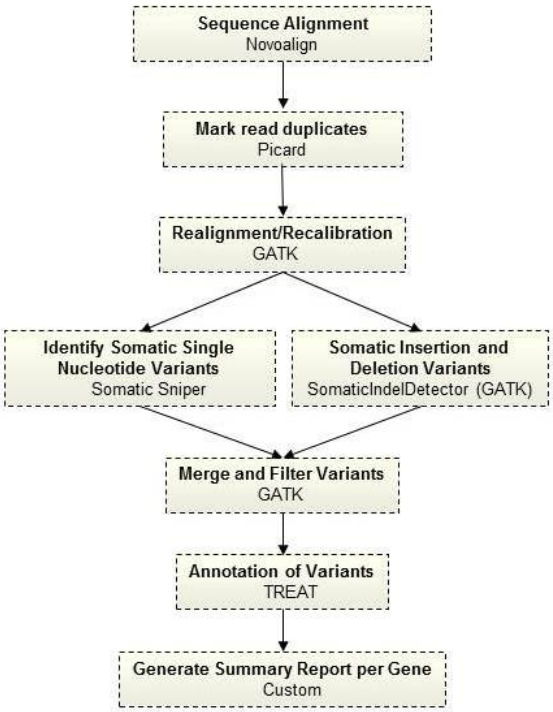
SUPPLEMENTAL FIGURES

Figure S1. Bioinformatics workflow for somatic sequences

Figure S1



Bold indicates process; non-bold indicates software.

Figure S2. Selection of BRCA1 methylation probes

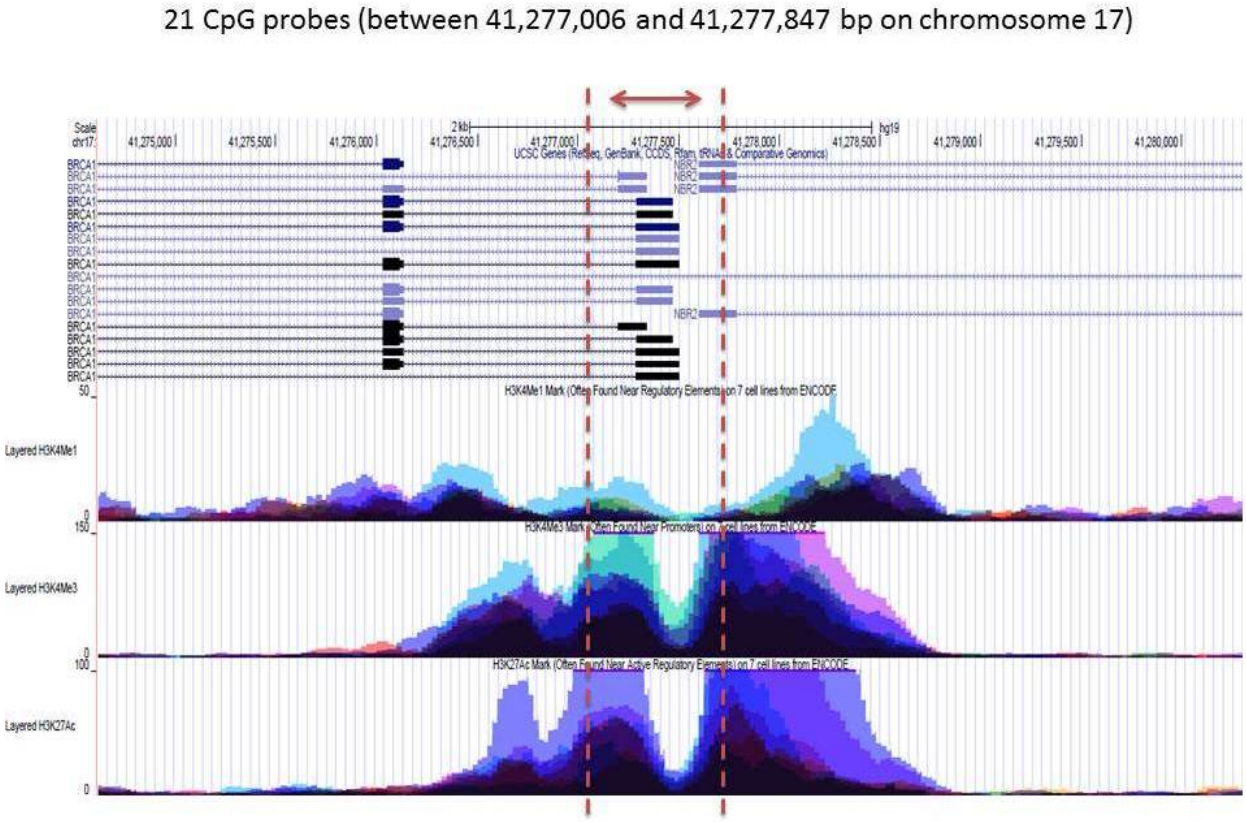


Figure S2.A.

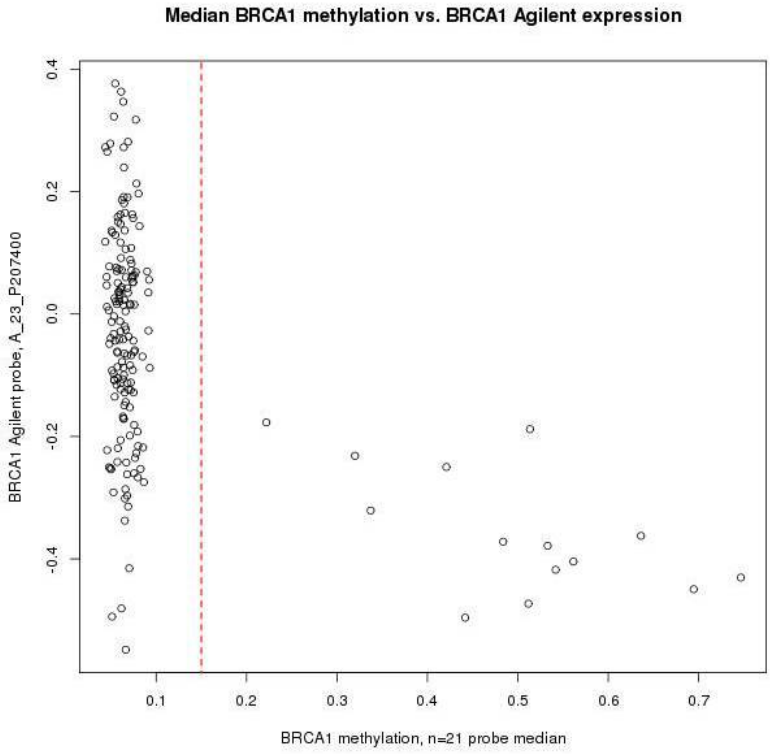


Figure S2.B.

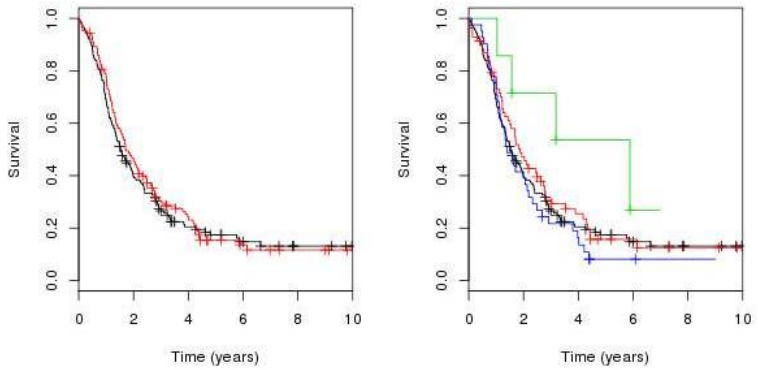
A. UCSC Genome Browser view of the 21 CpG probes around chromosome 17 BRCA1 region (41,277,006 bp to 41,277,847 bp).

The genomic range of CpG probes are indicated between red dashed lines. The three tracks show promoter- and regulatory element-associated histone marks identified in cell-line studies within the ENCODE project, supporting the likely regulation roles of this region.

B. Median BRCA1 Methylation versus BRCA1 Expression.

For 171 patients with methylation and expression data (Illumina Methylation 450k Array and Agilent Whole Human Genome 4x44K Expression Array, respectively), BRCA1 expression probe value is plotted against the mean of 21 CpG probes (between 41,277,006 and 41,277,847 bp on chromosome 17) which were found to correlate with expression. A threshold of median CpG beta of 0.15 (red line) was then applied to the overall patient set to define BRCA1 methylated tumors.

Figure S3. Time to recurrence for high grade serous EOC by HRD and type of alteration



A. Red: HRD; Black: NAD.

B. Red: germline deleterious mutation; Green: somatic deleterious mutation; Blue: somatic methylation; Black: no germline mutation, somatic mutation or methylation.

Table S1. Catalog of germline mutations found among N=912 epithelial ovarian cancer patients

Gene	Chr	Start	Stop	Reference Allele	Alternate Allele	Exon	Protein Change	Type	Rsid (dbSNP 132)	Classification
BRCA1	17	41197728	41197728	-	T	Exon24	Y1853_L1854delinsX	stopgain SNV	rs80357629	deleterious
		41197783	41197783	C	T	Exon24	R1835Q	nonsynonymous SNV		VUS
		41197784	41197784	G	A	Exon24	R1835X	stopgain SNV	rs41293465	deleterious
		41209079	41209079	-	G	Exon20	Q1756fs	frameshift insertion		deleterious
		41209133	41209133	C	T	Exon20	G1738E	nonsynonymous SNV	rs80357450	VUS
		41215363	41215366	TTTC	-	Exon19	1726_1727del	frameshift deletion	rs80357975	deleterious
		41215947	41215947	C	T	Exon18	R1699Q	nonsynonymous SNV	rs41293459	missense deleterious
		41219628	41219628	T	C	Exon17	T1691A	nonsynonymous SNV		VUS
		41219694	41219694	C	A	Exon17	A1669S	nonsynonymous SNV	rs80357087	VUS
		41222975	41222975	C	T	Exon16	M1652I	nonsynonymous SNV	rs1799967	polymorphic
		41223021	41223021	G	A	Exon16	P1637L	nonsynonymous SNV	rs80357048	VUS
		41223094	41223094	T	C	Exon16	S1613G	nonsynonymous SNV	rs1799966	polymorphic
		41223156	41223156	T	C	Exon16	N1592S	nonsynonymous SNV		VUS
		41226348	41226348	C	T	Exon15	E1559K	nonsynonymous SNV	rs80356988	VUS
		41226488	41226488	C	A	Exon15	S1512I	nonsynonymous SNV	rs1800744	polymorphic
		41242963	41242963	G	A	Exon12	Q1395X	stopgain SNV	rs80357260	deleterious
		41243014	41243014	C	G	Exon12	V1378L	nonsynonymous SNV	rs28897690	VUS
		41243017	41243017	T	G	Exon12	S1377R	nonsynonymous SNV		VUS
		41243480	41243483	TTGA	-	Exon11	1355_1356del	frameshift deletion	rs80357508	deleterious
		41243509	41243509	T	C	Exon11	R1347G	nonsynonymous SNV	rs28897689	VUS
		41243512	41243512	C	T	Exon11	E1346K	nonsynonymous SNV	rs80357407	VUS
		41243513	41243513	T	-	Exon11	E1345fs	frameshift deletion	rs80357711	deleterious
		41243789	41243792	AGAC	-	Exon11	1252_1253del	frameshift deletion	rs80357868	deleterious
		41243800	41243800	C	A	Exon11	E1250X	stopgain SNV	rs28897686	deleterious
		41243800	41243800	C	T	Exon11	E1250K	nonsynonymous SNV	rs28897686	polymorphic
		41243835	41243835	G	A	Exon11	P1238L	nonsynonymous SNV	rs28897688	VUS
		41243840	41243840	A	C	Exon11	N1236K	nonsynonymous SNV	rs28897687	VUS
		41243908	41243908	C	T	Exon11	E1214K	nonsynonymous SNV	rs80356923	VUS
		41244000	41244000	T	C	Exon11	K1183R	nonsynonymous SNV	rs16942	polymorphic
		41244252	41244252	G	A	Exon11	P1099L	nonsynonymous SNV	rs80357201	polymorphic
		41244429	41244429	C	T	Exon11	S1040N	nonsynonymous SNV	rs4986852	VUS
		41244435	41244435	T	C	Exon11	E1038G	nonsynonymous SNV	rs16941	polymorphic
		41244495	41244495	-	TCTCA	Exon11	N1018fs	frameshift insertion	rs80357856	deleterious

Gene	Chr	Start	Stop	Reference Allele	Alternate Allele	Exon	Protein Change	Type	Rsid (dbSNP 132)	Classification
		41244524	41244524	C	T	Exon11	M1008I	nonsynonymous SNV	rs1800704	polymorphic
		41244526	41244526	T	C	Exon11	M1008V	nonsynonymous SNV	rs56321129	VUS
		41244557	41244557	-	TT	Exon11	N997fs	frameshift insertion	rs80357829	deleterious
		41244740	41244740	A	C	Exon11	D936E	nonsynonymous SNV		VUS
		41244787	41244787	G	A	Exon11	Q921X	stopgain SNV	rs80357377	deleterious
		41244936	41244936	G	A	Exon11	P871L	nonsynonymous SNV	rs799917	polymorphic
		41244951	41244951	C	T	Exon11	R866H	nonsynonymous SNV	rs80356911	VUS
		41245027	41245027	G	A	Exon11	R841W	nonsynonymous SNV	rs1800709	VUS
		41245073	41245073	G	-	Exon11	D825fs	frameshift deletion	rs80357970	deleterious
		41245091	41245091	G	-	Exon11	S819fs	frameshift deletion	rs80357669	deleterious
		41245120	41245120	T	A	Exon11	N810Y	nonsynonymous SNV	rs28897682	VUS
		41245233	41245233	A	G	Exon11	V772A	nonsynonymous SNV	rs80357467	VUS
		41245471	41245471	C	T	Exon11	D693N	nonsynonymous SNV	rs4986850	polymorphic
		41245477	41245477	T	-	Exon11	R691fs	frameshift deletion	rs80357688	deleterious
		41245513	41245513	T	A	Exon11	K679X	stopgain SNV	rs80357082	deleterious
		41245546	41245546	G	A	Exon11	L668F	nonsynonymous SNV	rs80357250	VUS
		41245683	41245683	G	C	Exon11	A622G	nonsynonymous SNV	rs56039126	VUS
		41245707	41245707	T	G	Exon11	K614T	nonsynonymous SNV		VUS
		41245722	41245725	TTCT	-	Exon11	608_609del	frameshift deletion	rs80357952	deleterious
		41245861	41245861	G	A	Exon11	Q563X	stopgain SNV	rs80356898	deleterious
		41245981	41245981	A	C	Exon11	L523V	nonsynonymous SNV		VUS
		41245992	41245992	T	-	Exon11	K519fs	frameshift deletion	rs80357662	deleterious
		41246061	41246061	C	T	Exon11	R496H	nonsynonymous SNV	rs28897677	polymorphic
		41246481	41246481	T	C	Exon11	Q356R	nonsynonymous SNV	rs1799950	polymorphic
		41246812	41246812	A	C	Exon11	L246V	nonsynonymous SNV	rs28897675	VUS
		41247911	41247911	T	G	Exon10	T208P	nonsynonymous SNV		VUS
		41256153	41256153	C	A	Exon7	E143X	stopgain SNV	rs80356991	deleterious
		41256155	41256155	G	T	Exon7	P142H	nonsynonymous SNV	rs55971303	VUS
		41258486	41258486	C	A	Exon5	D67Y	nonsynonymous SNV	rs80357102	VUS
		41258504	41258504	A	C	Exon5	C61G	nonsynonymous SNV	rs28897672	missense deleterious
		41276046	41276046	T	A	Exon2	E23V	nonsynonymous SNV		VUS
		41276080	41276080	G	A	Exon2	Q12X	stopgain SNV	rs80357134	deleterious
		41276113	41276113	T	C	Exon2	M1V	nonsynonymous SNV	rs80357287	missense deleterious
BRCA2	13	32893291	32893291	G	T	Exon3	E49X	stopgain SNV	rs80358435	deleterious
		32899275	32899275	G	-	Exon4	A127fs	frameshift deletion		deleterious

Gene	Chr	Start	Stop	Reference Allele	Alternate Allele	Exon	Protein Change	Type	Rsid (dbSNP 132)	Classification
		32903605	32903606	TG	-	Exon8	219_220del	frameshift deletion		deleterious
		32906640	32906640	A	-	Exon10	E342fs	frameshift deletion		deleterious
		32907487	32907488	TT	-	Exon10	624_625del	frameshift deletion		deleterious
		32911298	32911301	AAAC	-	Exon11	936_937del	frameshift deletion	rs80359351	deleterious
		32911389	32911390	CT	-	Exon11	966_966del	frameshift deletion		deleterious
		32911562	32911563	AT	-	Exon11	1024_1024del	frameshift deletion		deleterious
		32912090	32912091	TG	-	Exon11	1200_1200del	frameshift deletion	rs80359391	deleterious
		32912338	32912339	TG	-	Exon11	1282_1283del	frameshift deletion		deleterious
		32912702	32912706	TCAAA	-	Exon11	1404_1405del	frameshift deletion		deleterious
		32912887	32912891	ATTAC	-	Exon11	1465_1467del	frameshift deletion		deleterious
		32912964	32912967	TGAA	-	Exon11	1491_1492del	frameshift deletion	rs80359452	deleterious
		32913703	32913706	TACT	-	Exon11	1737_1738del	frameshift deletion		deleterious
		32913729	32913729	-	T	Exon11	S1746fs	frameshift insertion		deleterious
		32913778	32913779	TC	-	Exon11	1762_1763del	frameshift deletion		deleterious
		32913837	32913838	AA	-	Exon11	1782_1782del	frameshift deletion		deleterious
		32914356	32914356	C	A	Exon11	S1955X	stopgain SNV	rs80358815	deleterious
		32914529	32914529	A	T	Exon11	K2013X	stopgain SNV	rs80358840	deleterious
		32929058	32929059	TC	-	Exon14	2356_2357del	frameshift deletion		deleterious
		32932023	32932023	A	-	Exon16	I2588fs	frameshift deletion	rs80359679	deleterious
		32937672	32937672	T	C	Exon18		splicing		deleterious
		32954222	32954222	C	T	Exon24	Q3066X	stopgain SNV	rs80359180	deleterious
		32969001	32969002	TG	-	Exon25	3144_3145del	frameshift deletion		deleterious
		32972626	32972626	A	T	Exon27	K3326X	stopgain SNV	rs11571833	polymorphic
		32893271	32893271	A	G	Exon3	Y42C	nonsynonymous SNV	rs4987046	VUS
		32906480	32906480	A	C	Exon10	N289H	nonsynonymous SNV	rs766173	polymorphic
		32906480	32906480	A	G	Exon10	N289D	nonsynonymous SNV	rs766173	polymorphic
		32906593	32906593	C	A	Exon10	S326R	nonsynonymous SNV	rs28897706	VUS
		32906655	32906655	A	G	Exon10	Q347R	nonsynonymous SNV	rs55800493	VUS
		32906729	32906729	A	C	Exon10	N372H	nonsynonymous SNV	rs144848	polymorphic
		32906934	32906934	T	G	Exon10	L440R	nonsynonymous SNV		VUS
		32906949	32906949	C	T	Exon10	S445F	nonsynonymous SNV		VUS
		32907000	32907000	A	G	Exon10	E462G	nonsynonymous SNV	rs56403624	VUS
		32907129	32907129	T	C	Exon10	I505T	nonsynonymous SNV	rs28897708	VUS
		32910812	32910812	A	G	Exon11	T774A	nonsynonymous SNV	rs55968715	VUS
		32911246	32911246	C	G	Exon11	N918K	nonsynonymous SNV		VUS

Gene	Chr	Start	Stop	Reference Allele	Alternate Allele	Exon	Protein Change	Type	Rsid (dbSNP 132)	Classification
		32911295	32911295	G	A	Exon11	D935N	nonsynonymous SNV	rs28897716	polymorphic
		32911539	32911539	A	C	Exon11	E1016A	nonsynonymous SNV		VUS
		32911547	32911547	C	G	Exon11	L1019V	nonsynonymous SNV	rs55638633	VUS
		32911565	32911565	A	G	Exon11	K1025E	nonsynonymous SNV	rs80358550	VUS
		32912060	32912060	C	T	Exon11	R1190W	nonsynonymous SNV	rs80358604	VUS
		32912361	32912361	G	A	Exon11	C1290Y	nonsynonymous SNV	rs41293485	polymorphic
		32912553	32912553	C	T	Exon11	T1354M	nonsynonymous SNV	rs80358656	VUS
		32912703	32912703	C	T	Exon11	S1404L	nonsynonymous SNV	rs41293489	VUS
		32912733	32912733	C	T	Exon11	T1414M	nonsynonymous SNV	rs70953664	VUS
		32912750	32912750	G	T	Exon11	D1420Y	nonsynonymous SNV	rs28897727	polymorphic
		32912829	32912829	T	C	Exon11	I1446T	nonsynonymous SNV		VUS
		32913077	32913077	G	A	Exon11	G1529R	nonsynonymous SNV	rs28897728	VUS
		32913154	32913154	T	G	Exon11	S1554R	nonsynonymous SNV		VUS
		32913562	32913562	A	C	Exon11	K1690N	nonsynonymous SNV	rs56087561	VUS
		32913804	32913804	G	A	Exon11	G1771D	nonsynonymous SNV	rs80358755	polymorphic
		32913962	32913962	A	C	Exon11	N1824H	nonsynonymous SNV		VUS
		32914127	32914127	G	A	Exon11	E1879K	nonsynonymous SNV	rs55996097	VUS
		32914163	32914163	G	A	Exon11	A1891T	nonsynonymous SNV		VUS
		32914196	32914196	G	A	Exon11	D1902N	nonsynonymous SNV	rs4987048	polymorphic
		32914218	32914218	A	G	Exon11	D1909G	nonsynonymous SNV	rs80358798	VUS
		32914236	32914236	C	T	Exon11	T1915M	nonsynonymous SNV	rs4987117	VUS
		32914592	32914592	C	T	Exon11	R2034C	nonsynonymous SNV	rs1799954	VUS
		32914668	32914668	G	A	Exon11	S2059N	nonsynonymous SNV		VUS
		32914814	32914814	C	T	Exon11	R2108C	nonsynonymous SNV	rs55794205	VUS
		32914815	32914815	G	A	Exon11	R2108H	nonsynonymous SNV	rs35029074	VUS
		32915105	32915105	G	A	Exon11	V2205M	nonsynonymous SNV	rs80358889	VUS
		32915198	32915198	G	A	Exon11	E2236K	nonsynonymous SNV	rs41293503	VUS
		32929387	32929387	T	C	Exon14	V2466A	nonsynonymous SNV	rs169547	polymorphic
		32930634	32930634	G	A	Exon15	R2502H	nonsynonymous SNV	rs56070345	VUS
		32930673	32930673	C	T	Exon15	T2515I	nonsynonymous SNV	rs28897744	polymorphic
		32930694	32930694	C	T	Exon15	S2522F	nonsynonymous SNV	rs80358985	VUS
		32936757	32936757	G	A	Exon17	E2635K	nonsynonymous SNV		VUS
		32936778	32936778	T	G	Exon17	F2642V	nonsynonymous SNV		VUS
		32937488	32937488	G	T	Exon18	A2717S	nonsynonymous SNV	rs28897747	polymorphic
		32937489	32937489	C	T	Exon18	A2717V	nonsynonymous SNV		VUS

Gene	Chr	Start	Stop	Reference Allele	Alternate Allele	Exon	Protein Change	Type	Rsid (dbSNP 132)	Classification
		32937516	32937516	A	T	Exon18	Y2726F	nonsynonymous SNV	rs80359064	VUS
		32937521	32937521	G	A	Exon18	V2728I	nonsynonymous SNV	rs28897749	VUS
		32937663	32937663	T	G	Exon18	M2775R	nonsynonymous SNV	rs80359073	VUS
		32937672	32937672	T	C	Exon18		splicing		deleterious
		32945172	32945172	A	C	Exon20	E2856A	nonsynonymous SNV	rs11571747	polymorphic
		32953549	32953549	G	T	Exon22	K2950N	nonsynonymous SNV	rs28897754	VUS
		32953550	32953550	G	A	Exon22	A2951T	nonsynonymous SNV	rs11571769	polymorphic
		32954180	32954180	C	T	Exon24	R3052W	nonsynonymous SNV	rs45580035	missense deleterious
		32954275	32954275	A	T	Exon24	K3083N	nonsynonymous SNV	rs80359191	VUS
		32972471	32972471	T	G	Exon27	L3274W	nonsynonymous SNV		VUS
		32972739	32972739	A	G	Exon27	I3363M	nonsynonymous SNV	rs80358390	VUS
		32972804	32972804	G	A	Exon27	R3385H	nonsynonymous SNV	rs80358398	VUS
		32972852	32972852	C	T	Exon27	T3401M	nonsynonymous SNV	rs55853199	VUS
		32972884	32972884	A	G	Exon27	I3412V	nonsynonymous SNV	rs1801426	VUS
RAD51C	17	56787288	56787288	T	-	Exon5	R258fs	frameshift deletion		deleterious
		56772522	56772522	G	A	Exon2	A126T	nonsynonymous SNV	rs61758784	VUS
		56772540	56772540	A	C	Exon2	T132P	nonsynonymous SNV		VUS
		56772543	56772543	C	A	Exon2	Q133K	nonsynonymous SNV		VUS
		56774110	56774110	A	G	Exon3	E154G	nonsynonymous SNV		VUS
		56774116	56774116	T	G	Exon3	V156G	nonsynonymous SNV		VUS
		56774121	56774121	A	T	Exon3	I158F	nonsynonymous SNV		VUS
		56774124	56774124	G	T	Exon3	D159Y	nonsynonymous SNV		VUS
		56787298	56787298	T	G	Exon5	L262V	nonsynonymous SNV		VUS
		56787304	56787304	G	A	Exon5	G264S	nonsynonymous SNV		missense deleterious
		56798128	56798128	A	G	Exon6	T287A	nonsynonymous SNV	rs28363317	missense deleterious

Some mutations occurred in multiple patients, but are noted only once in this table.

Table S2. Catalog of somatic variants found among N=279 epithelial ovarian cancer patients

Gene	Chr	Start	Stop	Reference Allele	Alternate Allele	Exon	Protein Change	Function (GVS)Type	rsid (dbSNP 132)	Classification
BRCA1	17	41223094	41223094	T	C	Exon 9	S430G	NON-SYNONYMOUS CODING	rs1799966	polymorphic
		41226402	41226402	C	A	Exon 10	E358*	STOP GAINED	rs80357248	deleterious
		41243941	41243941	G	A	Exon 14	R1203*	STOP GAINED	rs62625308	deleterious
		41244000	41244000	T	C	Exon 14	K1183R	NON-SYNONYMOUS CODING	rs16942	polymorphic
		41244429	41244429	C	T	Exon 14	S1040N	NON-SYNONYMOUS CODING	rs4986852	VUS
		41244435	41244435	T	C	Exon 14	E1038G	NON-SYNONYMOUS CODING	rs16941	polymorphic
		41244936	41244936	G	A	Exon 14	P871L	NON-SYNONYMOUS CODING	rs799917	polymorphic
		41244936	41244936	G	A	Exon 14	P871L	NON-SYNONYMOUS CODING	rs799917	polymorphic
		41245467	41245467	C	T	Exon 14	S694N	NON-SYNONYMOUS CODING	-	polymorphic
		41258471	41258471	A	G	-		SPLICE SITE DONOR	rs80358026	deleterious
		41245278	41245279	AC	A	Exon 14		FRAME SHIFT	rs80357583	deleterious
		41245990	41245991	TC	T	Exon 14		FRAME SHIFT	-	deleterious
		41246824	41246825	TG	T	Exon 14		FRAME SHIFT	-	deleterious
BRCA2	13	32905116	32905116	G	A	Exon 9	A248T	NON-SYNONYMOUS CODING	rs55854959	VUS
		32906729	32906729	A	C	exon10	N372H	NON-SYNONYMOUS CODING	rs144848	polymorphic
		32906729	32906729	A	C	Exon 10	N372H	NON-SYNONYMOUS CODING	rs144848	polymorphic
		32911247	32911247	G	A	Exon 11	E919K	NON-SYNONYMOUS CODING	-	polymorphic
		32911325	32911325	A	C	Exon 11	K945Q	NON-SYNONYMOUS CODING	-	polymorphic
		32912381	32912381	A	G	Exon 11	N1297D	NON-SYNONYMOUS CODING	-	missense deleterious
		32914236	32914236	C	T	Exon 11	T1915M	NON-SYNONYMOUS CODING	rs4987117	VUS
		32914542	32914542	A	T	Exon 11	K2017I	NON-SYNONYMOUS CODING	-	missense deleterious
		32918697	32918697	G	T	Exon 12	E2282*	STOP GAINED	-	deleterious
		32936688	32936688	C	T	Exon 17	P2612S	NON-SYNONYMOUS CODING	-	polymorphic
		32937582	32937582	G	A	Exon 18	G2748D	NON-SYNONYMOUS CODING	rs80359071	missense deleterious
RAD51C	17	56809843	56809844	AG	A	-	-	SPLICE SITE ACCEPTOR	-	deleterious

Some mutations occurred in multiple patients, but are noted only once in this table.

Table S3. Comparison of the clinical characteristics of HRD patients

	Germline (n=82)	Somatic (n=9)	Methylated (n=50)
Age at Diagnosis, years			
Mean (SD)	**58.3 (10.4)**	**60.0 (9.3)**	**58.4 (11.3)**
Histology			
High grade serous	**68 (83%)**	**7 (78%)**	**41 (82%)**
High grade endometrioid	**3 (4%)**	**2 (22%)**	**5 (10%)**
Low grade endometrioid	**1 (1%)**	**0**	**1 (2%)**
Clear Cell	**4 (5%)**	**0**	**1 (2%)**
Low grade Serous	**0**	**0**	**2 (4%)**
Mucinous	**0**	**0**	**0**
Other/Unknown	**6 (7%)**	**0**	**0**
Grade			
High	**77 (98%)**	**9 (100%)**	**47 (94%)**
Low	**2 (3%)**	**0**	**3 (6%)**
Unknown	**3**	**0**	**0**
First Degree Family History of Breast or Ovarian Cancer			
No	**49 (60%)**	**7 (78%)**	**46 (92%)**
Yes	**33 (40%)**	**2 (22%)**	**4 (8%)**
First Degree Family History of Ovarian Cancer			
No	**73 (89%)**	**9 (100%)**	**48 (96%)**
Yes	**9 (11%)**	**0**	**2 (4%)**

Table S4. Analysis of time to recurrence by HRD phenotypes

	All patients						High grade serous					
					Covariate-adjusted						Covariate adjusted	
	N	N (%) events	HR (95% CI)	P value	HR (95% CI)	P value	N	N(%)events	HR (95% CI)	P value	HR (95%CI)	P value
By HRD												
NAD	213	150 (70%)	ref	0.71	ref	0.30	146	118 (81)	ref		ref	0.55
HRD	142	106 (75%	1.05 (0.82,1.13)		0.87 (0.66, 1.13)		117	95 (81)	0.93 (0.71,1.21)	0.58	0.92 (0.69,1.22)	
By Type of Alteration												
None	213	150 (70%)	ref	0.31	ref	0.44	146	118 (81)	Ref	0.27	Ref	0.34
Germline mutation	81	57 (70%)	0.98 (0.72, 1.33)		0.83 (0.60, 1.15)		67	53 (79)	0.90 (0.65,1.24)		0.87 (0.62,1.23)	
Somatic mutation	9	5 (56%)	0.63 (0.26, 1.54)		0.58 (0.23, 1.43)		7	4 (57)	0.45 (0.16,1.21)		0.49 (0.18,1.34)	
Methylation	50	43 (86%)	1.29 (0.92, 1.81)		1.01 (0.69, 1.47)		41	37 (90)	1.15 (0.80,1.67)		1.14 (0.76,1.69)	
By Germline Mutation												
Non-carrier	801	544 (68%)	ref	0.55	Ref	0.06	541	428 (79)	Ref	0.66	Ref	0.54
BRCA1	29	23 (79%)	1.16 (0.77, 1.77)		1.11 (0.72, 1.70)		26	21 (81)	0.88 (0.57,1.36)		1.02 (0.65,1.60)	
BRCA2	27	17 (63%)	0.80 (0.49, 1.30)		0.58 (0.35, 0.94)		23	17 (74)	0.78 (0.48,1.26)		0.73 (0.45, 1.19)	
RAD51C	23	15 (65%)	0.80 (0.48, 1.33)		0.66 (0.39, 1.11)		18	15 (83)	0.86 (0.51,1.44)		0.82 (0.49,1.38)	

Women with VUS in any of the three genes were included in the non-HRD , non-carrier groups; results did not differ when these individuals were excluded from the analyses; adjusted results were adjusted for age at diagnosis, debulking status, stage, grade (low/high), ascites present at surgery, and menopausal status including categories for patients with missing data.