

Suppl. Figure S1

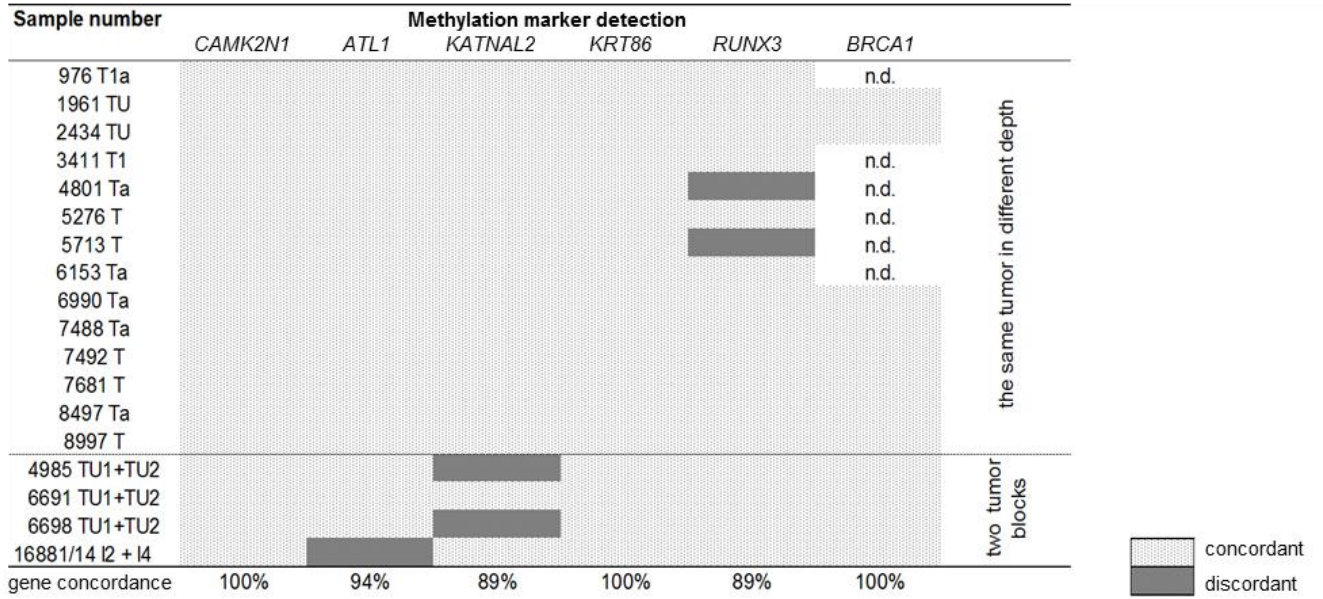


Figure S1: Validation of MSP assays. Different sections of the same tissue block (upper part) or different tumor blocks of the same patient (lower part) were analyzed for marker methylation by MSP. Concordant and discordant analyses are marked in grey and dar-grey, respectively. The gene-specific concordance ranges from 89%-100% and averages to 95% overall concordance (Cohen's Kappa = 0.881).

Suppl. Figure S2

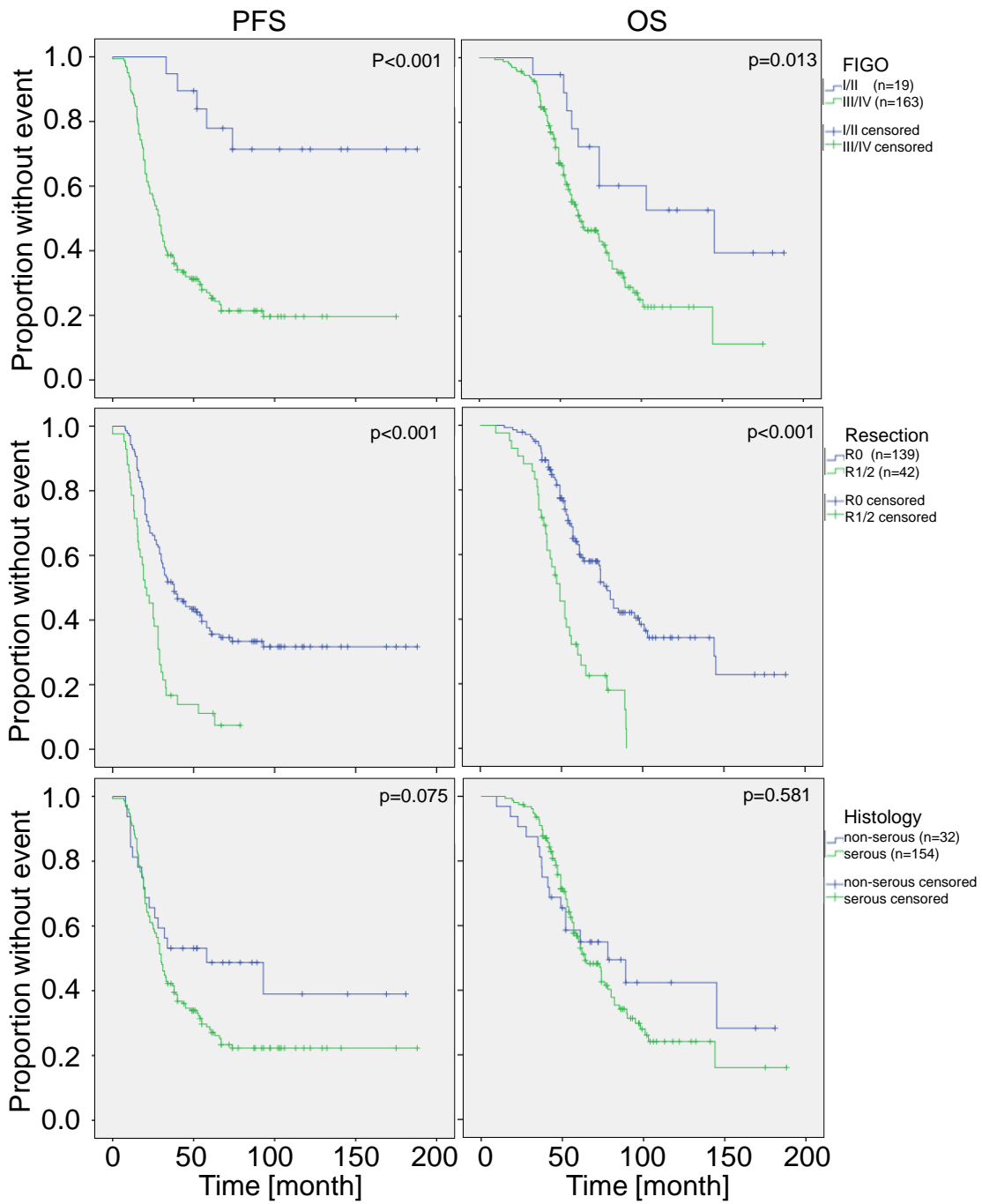


Figure S2: Kaplan-Meier plots for PFS and OS for 188 EOC patients stratified by FIGO stage, resection status and histology. LogRank test was utilized for statistical evaluation.

Suppl. Figure S3

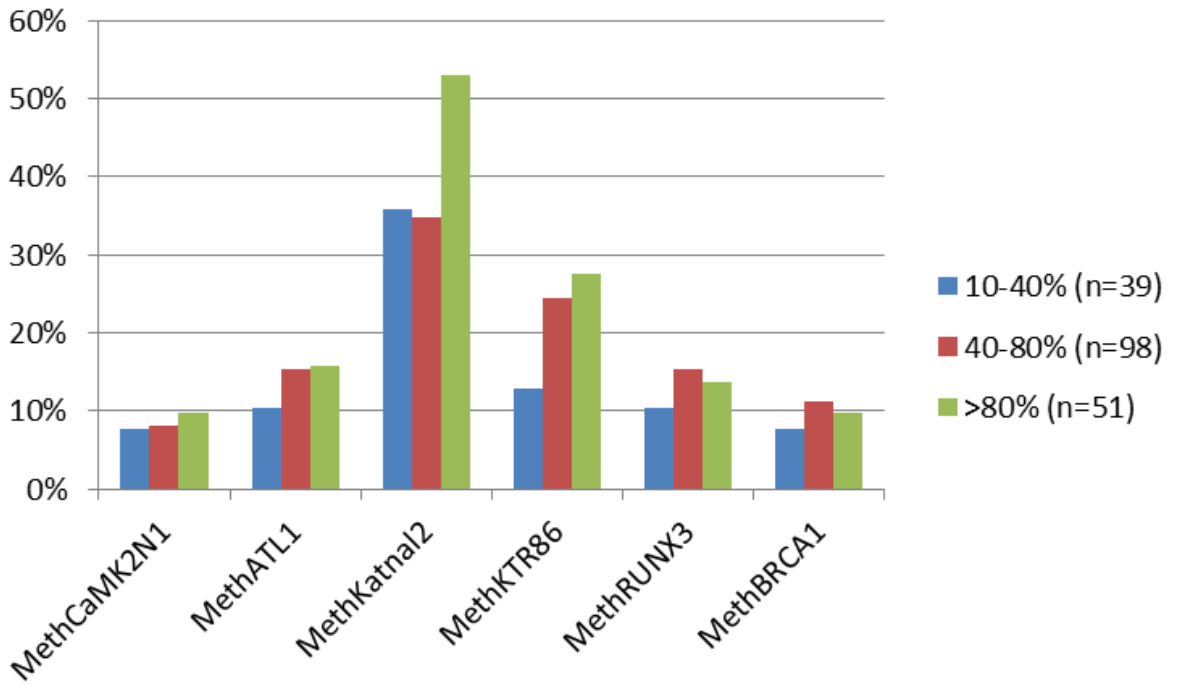


Figure S3: Methylation frequency of candidate genes depending on tumor cell fraction of tissues.

Suppl. Table S1. Data from EOC patients with HRD mutations

sample	age	histo	pT	pN	pM	FIGO	G	R	mutation
3325	39	serous	1c	0	x	IC	1	0	BRCA1 c.1319T>C ^{S#}
8265	48	mucinous	3c	1	1	IV	3	0	BRCA1 truncated ^S
8644	27	mucinous	1a	1	0	IA	1	0	BRCA1 truncated ^S
8861	49	serous	3c	x	0	IIIC	3	2	BRCA1 c.5503C>T ^H
9473	48	serous	3c	0	1	IIIC	3	0	BRCA1 c.3627 ins A ^S
9877	36	serous	3b	1	0	IIIC	2	0	BRCA1 c.1067A>G ^{S#}
10003	63	serous	3b	1	0	IIIC	3	0	BRCA1 mut
10080	73	serous	3c	x	0	IVA	3	2	BRCA2 c.5238dupT ^H
10163	53	mucinous	3c	1	1	IIIC	3	0	BRCA2 mut ^H
10196	44	serous	3c	x	1	IIIC	3	2	BRCA2 c.1953_1956del ^H
16881/14	60	serous	3c	0	0	IIIC	3	0	BRCA1 c.1953_1956del ^H
17571/15	49	serous	3c	1	0	IIIC	3	0	BRCA1 c.5062G>T ^S
2878/16	45	serous	3c	1	0	IIIC	2	0	BRCA1 c.5266depC ^H
14009/17	46	serous	1c	0	0	IC	1	0	RAD51C ^H , CHEK2 ^H
14426/17	49	serous	3c	1	0	IIIC	3	0	BRCA1 c.5080G>A ^H

H heterozygote, # unknown pathogenicity, S somatic mutation determined via exon analysis

Table S2 Overview of applied primer for MSP and *BRCA1* mutation analysis.

Primer	Oligo sequence	product size	melting temp.	Localization*
Actin beta-BS-F	TGGTGATGGAGGAGGTTTAGTAAGT	125bp	60 °C	no CpG island, 1500nt upstream 1st exon
Actin-beta BS-R	AACCAATAAAACCTACTCCTCCCTTAA			
ATL1-M-F	AATTGCGTTTAGCGCGGGTAC	89bp	61 °C	CpG island (CpG:52); promoter+1st exon
ATL1-M-R	CGATAAACGCTATCACTACGCTCG			
BRCA1-M-F	GCGAGTTTACGTCGCGTAGTC	84bp	60 °C	CpG island; promoter+1st exon
BRCA1-M-R	AATTTCGTAACAACGAAAAAACG			
Katnal2-M-F	TTATTGTTGTTGCGGGACGATTTTC	109bp	61 °C	CpG island (CpG:23); 1st exon
Katnal2-M-R	AAATTTAACACCTCGACCGAACG			
KRT86-M-F	TTTAGTTACGGGGGTTTCGGC	256bp	62 °C	CpG island (CpG:63); last exon
KRT86-M-R	GCCACCGCGAAAACACTACTAACG			
CAMK2N1-M-F	TAGTCGTTGGTCGATTGATTC	184bp	60 °C	CpG island (CpG:245); promoter+1st exon
CAMK2N1-M-R	AACCTCGATCGACTACCG			
RUNX3-M-F	GTGTTTCGATTTTCGGTTTAGCGTC	353bp	64 °C	CpG island (CpG:311); promoter+1st exon
RUNX3-M-R	CGCTCGACTCCGAAACCTCG			
RUNX3-Pa-M-F	TTAGCGTCGTTTCGGTAAAAATTC	127bp	60 °C	CpG island (CpG:311); promoter+1st exon
RUNX3-Pa-M-R	ACCGCGAATAAAATACGAACG			
BRCA1-ORF1-F	CACCCTCTGCTCTGGGTA	893bp	56 °C	
BRCA1-ORF1-R	GCTGTAATGAGCTGGCATGA			
BRCA1-ORF2-F	AGCTGAGAGGCATCCAGAAA	864bp	56 °C	
BRCA1-ORF2-R	TGCTCCGTTTGGTTAGTTCC			
BRCA1-ORF3-F	AAAGCAGATTTGGCAGTTCAA	883bp	56 °C	
BRCA1-ORF3-R	GTCCCTTGGGGTTTTCAAAT			
BRCA1-ORF4-F	GGAAGGCCAAAACAGAACCA	902bp	56 °C	
BRCA1-ORF4-R	CTCAGGTTGCAAACCCCTA			
BRCA1-ORF5-F	CAGAGGGCCAAAATTGAATG	900bp	56 °C	
BRCA1-ORF5-R	TCACTCTCACACCCAGATGC			
BRCA1-ORF6-F	CAAGAAGAGCAAAGCATGGA	901bp	56 °C	
BRCA1-ORF6-R	CAGACACCACCATGGACATT			
BRCA1-ORF7-F	TGCTGGGTATAATGCAATGG	775bp	56 °C	
BRCA1-ORF7-R	AAGCTCATTCTTGGGGTCTCT			

* UCSC CpG island names parenthesized if available

Suppl. Tab. S3 BRCA1 immunohistochemistry results depending on BRCA1 aberrations*

		BRCA1 aberration			total	
		wt	mut	meth		
BRCA1_IHC	negativ	n	2	3	2	7
		% of samples	8%	23%	67%	17%
	weak positive	n	6	6	1	13
		% of samples	24%	46%	33%	32%
	positive	n	17	4	0	21
		% of samples	68%	31%	0%	51%
total	n	25	13	3	41	
	% of samples	100%	100%	100%	100%	

* Chi² test p<0.05