

Edinburgh Research Explorer Exploring the clonal evolution of CD133/aldehyde-dehydrogenase-1 (ALDH1)-positive cancer stem-like cells from primary to recurrent high-grade serous ovarian cancer (HGSOC). A study of the Ovarian Cancer Therapy-Innovative Models Prolong Survival (OCTIPS) Consortium

Citation for published version:

Ruscito, I, Cacsire Castillo-tong, D, Vergote, I, Ignat, I, Stanske, M, Vanderstichele, A, Ganapathi, RN, Glajzer, J, Kulbe, H, Trillsch, F, Mustea, A, Kreuzinger, C, Benedetti Panici, P, Gourley, C, Gabra, H, Kessler, M, Sehouli, J, Darb-esfahani, S & Braicu, El 2017, 'Exploring the clonal evolution of CD133/aldehyde-dehydrogenase-1 (ALDH1)-positive cancer stem-like cells from primary to recurrent high-grade serous ovarian cancer (HGSOC). A study of the Ovarian cancer Therapy—Innovative Models Prolong Šurvival (OCTIPS) Consortium', European Journal of Cancer, vol. 79, pp. 214-225. https://doi.org/10.1016/j.ejca.2017.04.016

Digital Object Identifier (DOI):

10.1016/j.ejca.2017.04.016

Link:

Link to publication record in Edinburgh Research Explorer

Document Version:

Peer reviewed version

Published In:

European Journal of Cancer

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- 1 Exploring the clonal evolution of CD133/ALDH1-positive cancer
- 2 stem-like cells from primary to recurrent high-grade serous ovarian
- 3 cancer (HGSOC). A study of the OCTIPS Consortium.

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57 ABSTRACT

58 Background: High-grade serous ovarian cancer (HGSOC) causes 80% of all OC 59 deaths. In this setting, the role of cancer stem-like cells (CSCs) is still unclear. In 60 particular, the evolution of CSC biomarkers from primary (pOC) to recurrent (rOC) 61 HGSOCs is unknown. Aim of this study was to investigate changes in CD133 and 62 aldehyde dehydrogenase-1(ALDH1) CSC biomarker expression in pOC and rOC 63 HGSOCs. 64 Methods: 224 pOC and rOC intra-patient paired tissue samples derived from 112 65 HGSOC patients(pts) were evaluated for CD133 and ALDH1 expression using IHC. 66 pOCs and rOCs were compared for CD133 and/or ALDH1 levels. Expression profiles 67 were also correlated with patients' clinico-pathological and survival data. 68 **Results:**49.1%(55/112) and 37.5%(42/112) pOCs were CD133+ and ALDH1+, 69 respectively. CD133+ and ALDH1+ samples were detected in 33.9%(38/112) and 70 36.6%(41/112) rOCs. CD133/ALDH1 coexpression was observed in 23.2%(26/112) 71 and 15.2%(17/112) of pOCs and rOCs, respectively. Pairwise analysis showed a 72 significant shift of CD133 staining from higher (pOCs) to lower expression levels 73 (rOCs)(p<0.0001). Furthermore, all CD133+pOC pts were FIGO-stage III/IV 74 (p<0.0001) and had significantly worse PFI(p=0.04) and OS(p=0.02). On multivariate 75 analysis, CD133/ALDH1 coexpression in pOCs was identified as independent 76 (HR:1.64;95%CI:1.03-2.60;p=0.036) prognostic factor for PFI 77 (HR:1.71;95%CI:1.01-2.88;p=0.045). Analysis on 52 pts with known somatic BRCA 78 status revealed that BRCA mutations did not influence CSC biomarker expression. 79 Conclusions: The study showed that CD133/ALDH1 expression impacts HGSOC pts' 80 survival and firstly suggests that CSCs might undergo phenotypic change during the disease course similarly to non stem-like cancer cells, providing also a first evidence that there is no correlation between CSCs and BRCA status.

Key Words: Ovarian Cancer; CD133; ALDH1; Aldehyde dehydrogenase-1; cancer stem-like cell; BRCA; prognosis; survival.

INTRODUCTION

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Ovarian cancer (OC) remains the most lethal gynecologic malignancy[1]. Advances in cancer genomics, epigenomics and proteomics has led to the understanding that OC is a heterogeneous group of different tumors displaying distinct phenotypes and etiology[2,3]. The current dichotomous OC classification[4,5] groups these tumors in two distinct categories: Type I (low-grade serous-papillary, low-grade endometrioid, mucinous and clear-cell carcinomas) and Type II (high-grade serous-papillary, highgrade endometroid, carcinosarcomas and undifferentiated tumors). Type II OCs show a more aggressive biological behavior, are diagnosed at advanced stage and are chromosomally highly unstable. Among them, high-grade serous OC (HGSOC) accounts for around 80% of all OC deaths[3]. The identification of predictive biomarkers is pivotal for designing new treatment strategies able to reduce HGSOCrelated mortality. In this context, the cancer stem-like cell (CSC) theory represents one model to investigate OC heterogeneity. This hypothesis, supported by increased evidence acquired in the last decade, proposes that, within OC tissues, a small population of cells has an increased capacity for self-renewal, tumorigenesis and differentiation [6]. In multiple experimental studies CSCs showed to increase potential of tumorigenesis, metastasis/invasion, neoangiogenesis and chemoresistance [7,8] and have been often correlated with a poor prognosis [9-13]. Several potential CSC markers have been identified in OC samples [14-15]. Among them, aldehyde dehydrogenase-1 (ALDH1) and CD133 are currently the best characterized for ovarian CSCs. Their expression on the cell surface is associated with increased tumorigenesis and self-renewal capability [16-18]. Nevertheless, the clonal evolution of CSCs throughout the course of disease, from primary (pOC) to recurrent

- 112 (rOC) OC, has not been elucidated yet and information about the changes in CSC
- presence within the tumor after relapse is still lacking.
- The aim of this study was to investigate the evolution of CSC biomarkers CD133 and
- ALDH1 expression in a large series of paired primary and recurrent HGSOCs.

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MATERIALS AND METHODS

118 Sample Collection

- 224 paired samples from 112 HGSOC patients were collected during primary and
- secondary tumor debulking. Patients were included consecutively and have been
- treated between 1985 and 2013 through primary cytoreduction followed by platinum-
- based chemotherapy. Patients, retrospectively selected from the OCTIPS (Ovarian
- 123 Cancer Therapy–Innovative Models Prolong Survival, Agreement No.279113-2)
- 124 Consortium database, were treated for both pOC and rOC in one of the European
- 125 Gynecologic Oncology Referral Centers of the following Institutions: Charité
- 126 Universitätsmedizin Berlin, Germany; Katholieke Universiteit Leuven, Belgium;
- 127 Imperial College, London, UK; University of Edinburgh, UK.
- 128 Inclusion criteria were: having experienced at least one OC relapse for which having
- been subjected to at least one palliative surgery. Exclusion criterion was: no cancer
- tissue available from both pOC and rOC. Approval from each local ethics committee
- us obtained (EK207/2003,ML2524,05/Q0406/178,EK130113,06/S1101/16). OC
- tissue samples were collected during primary cytoreduction and at the surgery for
- relapse. All included samples underwent central histopathological assessment to
- 134 confirm the diagnosis of HGSOC and to evaluate the tissue quality and tumor contain.

135 *Immunohistochemistry*

136 Immunohistochemical staining was performed on tissue microarrays (TMAs).

- 137 Slides were deparaffinized in xylol, rehydrated in graded alcohol and boiled in a
- pressure cooker for 5 minutes in citrate buffer (pH=6) for ALDH1 staining or in
- 139 EDTA (pH=9) for CD133 staining. Mouse anti-human ALDH1-antibody (clone
- 140 44;BD Transduction Laboratories,Franklin Lakes, NJ,USA) and mouse anti-human
- 141 CD133/1-antibody (AC133 clone; Miltenyi-Biotech, BergischGladbach, Germany)
- were diluted 1:500 and incubated on the slides for 60 minutes at room temperature.
- Bound antibodies were visualized using DAKO Real Detection System and DAB+
- 144 (3,3' -diaminobenzidine;DAKO,Glostrup,Denmark) as a chromogen. Finally, the
- slides were co-stained with hematoxylin.
- 146 CD133 stained samples were assessed basing on the number of stained tumor cells.
- Samples were classified as "CD133-negative" (<10% CD133 positive tumor cells) and
- "CD133-positive"(>10% CD133-positive tumor cells)[19-20].
- 149 For ALDH1 staining evaluation, as previously published[21-22], the number of
- stained tumor cells (0%=0;1-10%=1;11-50%=2;>50%=3) was multiplied with the
- intensity of staining(negative=0; weak=1; moderate=2; strong=3), resulting in a
- semiquantitive immunoreactivity score(IRS) that ranged from 0 to 9. For further
- analysis, samples were classified "ALDH1-negative", for absent or weak focal
- staining(IRS=0-1), or "ALDH1-positive", for ALDH1-high tumor expression(IRS=2-
- 155 9).
- All samples were evaluated independently by two co-authors (IR and SDE).
- 157 Clinical Data and Follow-up
- Patients' clinical data and information on 52 patients' germline and/or somatic BRCA
- 159 status were retrieved from OCTIPS Consortium database[23-24]. Platinum-
- resistance and platinum-sensitivity were defined, according to GCIG, as relapse
- occurring before or after six months following the last platinum-based chemotherapy,

- respectively[25]. Recurrence was defined basing on RECIST Criteria[26]. A sole
- 163 CA125 serum elevation was not considered relapse[27].
- 164 Statistical Analysis
- Statistical analysis was performed using SPSS version 22.0(SPSS Inc, Chicago, IL,
- 166 USA). To assess the difference between pOCs and rOCs in terms of biomarker
- expression, the correlation test (Spearman coefficient, 2-tailed) and the "Wilcoxon
- signed rank" non-parametric test for related samples were applied. Correlation of
- 169 CD133 and ALDH1 tumor expression with patients' clinico-pathological categorical
- 170 data was assessed using the Fisher's exact test. Patients' progression-free
- interval(PFI), progression-free survival (PFS) and overall survival(OS) were
- determined by Kaplan-Meier analysis (Log-Rank test). PFI represented the time
- interval from the last adjuvant chemotherapy to relapse, whereas progression-free
- survival (PFS) was the time interval between first recurrence diagnosis and tumor
- progression. For univariate and multivariate survival analyses, the Cox regression
- model was used. Multivariable models were performed among variables reporting a
- p-value≤0.1 in univariate analysis. P values≤0.05 were considered statistically
- significant.

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- RESULTS
- Primary and recurrent intra-patient paired tumor samples derived from 112 HGSOC
- patients were analyzed for CD133 and ALDH1 expression. Patients' characteristics
- are listed in **Table 1**.
- 184 Immunohistochemistry staining showed that ALDH1 and CD133 proteins were
- localized to the cytoplasm(**Fig1,Fig.3**).

- 188 *CD133 expression*.
- 189 CD133-positive (CD133⁺) staining was significantly more frequent among
- 190 pOCs[55/112(49.1%)] compared to rOCs[38/112(33.9%)], p=0.030(Fisher's exact
- test, Fig. 1a,1c). Investigation of sequential changes in CD133+ expression in paired
- tumors, with a correlation test (Spearman coefficient) between pOCs and rOCs,
- demonstrated a significant correlation (p=0.001,Spearman coefficient 0.306).
- 194 Furthermore, pairwise testing revealed a significant shift from higher frequency of
- 195 CD133⁺ cells in pOCs to lower levels in the paired recurrent samples (p<0.0001,
- Wilcoxon test; Fig.2), thus indicating significantly higher rates of CD133⁺ cells in
- pOCs compared to rOCs.
- 198 ALDH1 expression.
- 199 Distribution of ALDH1 IRS in pOCs and rOCs is shown in Fig.3a,3d. ALDH-1
- 200 positive tumors were found in 37.5%(42/112) and 36.6%(41/112) of primary and
- recurrent samples, respectively (p=1,Fisher's exact test,Fig.3b,3e). A trend for
- significant correlation between pOCs and rOCs ALDH1-expression levels was seen
- 203 (p=0.059,Spearman coefficient 0.179). Pairwise analysis showed no tendency towards
- a change of IRS values to higher or lower levels in recurrences (p=0.988, Wilcoxon
- 205 test; **Fig.4**).
- 206 <u>CD133/ALDH1 co-expression.</u>
- 207 Co-expression of both CSCs biomarkers was detected in 23.2%(26/112) of pOCs and
- in 15.2%(17/112) of rOCs(p=0.174,Fisher's exact test). Among 26 patients reporting
- 209 CD133/ALDH1 co-expression in pOCs, 22(84.6%) lost this pathological
- 210 characteristic in relapse situation. Of the 17 patients presenting biomarker co-
- expression in rOC, 13(76.5%) showed no co-expression in pOC. Consequently, 4/112

- patients (3.6%) showed CD133/ALDH1 co-expression in both pOC and rOC: two of
- them were platinum-resistant and two were platinum-sensitive.
- 214 <u>CSCs biomarkers and clinico-pathological factors</u>
- We analyzed the correlation of ALDH1 and/or CD133 tumor expression patterns in
- pOCs with patients' clinico-pathological characteristics. All primary CD133⁺ patients
- 217 were diagnosed at FIGO III/IV stage (p=0.006). No correlation was observed between
- 218 other clinico-pathological factors and ALDH1 and/or CD133 tumor
- 219 expression(Tab.2).
- 220 Survival
- 221 CD133 positivity in pOCs was significantly associated with poor PFI and OS
- 222 (Fig.5a,5b). In particular, CD133⁺ and CD133⁻ patients reported median OS of 51 and
- 223 71 months (HR:1.713;95%CI:1.076-2.727;p=0.02) and median PFI of 9 and 17
- 224 months (HR:1.477;95%CI:1.006-2.170;p=0.04). PFS after recurrence was not
- significantly different (p=0.868, Fig. 5c) between patients with CD133+ and CD133-
- or between (p=0.252,**Fig.5f**) patients with ALDH1+ and ALDH1rOC.
- Median OS for ALDH1⁺ and ALDH1⁻ patients was 52 and 64 months, respectively
- 228 (p=0.402) and median PFI-1 was 9 and 17 months, respectively (p=0.199)(Fig.5d,5e).
- 229 ALDH1/CD133 co-expression in pOCs was found to significantly affect HGSOC
- patients' outcome. A significant decrease in OS and PFI has been found in patients
- co-expressing ALDH1/CD133 in primary tissue (46 and 9 months, respectively)
- 232 compared to patients without biomarker co-expression (68 and 17 months,
- respectively) (p=0.019,**Fig.5g**;p=0.015,**Fig.5h**). No significant difference in PFS after
- relapse was observed between patients who reported CD133/ALDH1 co-expression or
- no co-expression in rOC(p=0.898, Fig.5i).

- On multivariate analysis, the co-expression of ALDH1 and CD133 in pOC, rather
- than the single expression of one biomarker, was identified to be an independent
- 238 prognostic factor for both PFI (HR:1.638;95%CI:1.033-2.598;p=0.036) and OS
- 239 (HR:1.707;95%CI:1.012-2.881;p=0.045) in HGSOC(**Tab.3,4**).
- 240 Outliers' sub-analysis
- 241 "Outliers" were considered patients for whom the highest difference between pOC
- and rOC could be detected in CD133+cell rate. Three patients were identified: two
- reported a difference in CD133+cell rate of -90%(from 90% of CD133+cells at pOC
- 244 to 0% at rOC); the first one was a platinum-resistant patient with PFI of 2 months and
- OS of 14 months; the second one was a platinum-sensitive patient with PFI of 7
- 246 months and OS of 9 months. The third patient showed a difference in CD133+cell
- rate of +70%(from 0% of CD133+ at pOC cells to 70% in rOC) with PFI of 15
- 248 months (platinum-sensitive) and OS of 44 months.
- 249 CSC biomarker expression and BRCA status
- 250 In order to investigate if BRCA mutations could influence CSC biomarker expression,
- a subgroup analysis was carried out among 52 patients, whose germline and/or
- somatic BRCA status (assessed on pOC and rOC) was available [24]. 40.4% of tested
- patients (21/52) had a somatic BRCA mutation in both pOCs and rOCs: 16/52(30.8%)
- were BRCA1-mutated (mBRCA1) and 5/52(9.6%) were BRCA2-mutated
- 255 (mBRCA2)(**Tab.5**).
- No significant difference in CD133 and/or ALDH1 expression was found between
- BRCA-wild type (BRCA-WT) and BRCA-mutant (mBRCA1/2) tumors(**Tab.6**).
- Among BRCA-WT patients, no correlation between pOCs and rOCs in CD133+
- expression was observed (p=0.088,Spearman coefficient 0.312). Furthermore, in
- accordance with results observed in the whole population, paired testing revealed a

261	significant shift from higher levels in pOCs to lower levels in the rOCs
262	(p<0.0001,Wilcoxon test; Fig.6a). In contrast, among mBRCA1/2 patients, no
263	correlation between pOCs and rOCs (p=0.493,Spearman coefficient 0.158), or a
264	tendency towards a change in CD133+ expression was observed (p=0.167,Wilcoxon
265	test;Fig.6b).
266	Regarding ALDH1 expression, among BRCA-WT patients no correlation between
267	pOCs and rOCs in ADH1 IRS was found (p=0.986,Spearman coefficient 0.003), as
268	well as no change in paired testing (p=0.895,Wilcoxon test;Fig.7a); also for
269	mBRCA1/2 patients no difference was observed in ALDH1-IRS between primary and
270	recurrent patients (p=0.410,Spearman coefficient 0.190;p=0.385,Wilcoxon
271	test;Fig.7b).
272	Among BRCA-WT patients, only 1/31 patient (3.2%) showed CD133/ALDH1 co-
273	expression in both pOCs and rOCs. In $3/31(9.7\%)$ patients the co-expression was
274	evidenced in rOCs but not in pOCs. 90% of patients (9/10) reporting CD133/ALDH1
275	co-expression in pOC lost biomarker co-expression at tumor relapse.
276	Also for mBRCA1/2 patients, only 1/21(4.8%) patient showed CD133/ALDH1 co-
277	expression in both pOC and rOC. Two patients (9.5%) had co-expression at recurrent
278	rather than at primary disease. The difference between BRCA-WT and $mBRCA1/2$
279	patients in terms of co-expression loss at rOC was not significant (4/5 vs 9/10,p=1,
280	Fisher's exact test).
281	Considering patients who were CD133+ and/or ALDH1+ at pOC, no significant
282	difference could be detected in PFI and OS among BRCA-WT vs mBRCA1/2
283	cases(Fig.8).

DISCUSSION

286 In the Era of Precision Medicine, huge steps have been taken in the understanding of 287 HGSOC biology. In this tumor setting, the role of CSC and its clonal evolution during 288 subsequent disease relapse has been relatively unexplored. 289 This study investigated the changes in CSC biomarkers CD133 and ALDH1 290 expression in primary and recurrent HGSOCs and showed that CD133+CSCs are 291 significantly more represented in pOCs rather than rOCs, whereas no significant 292 changes in terms of ALDH1 expression levels occurred at disease relapse. 293 Furthermore, CD133 positivity in pOCs significantly correlates with poor survival, 294 while co-expression of both CD133 and ALDH1 in primary samples independently 295 predicted poor PFI and OS in HGSOC patients. 296 In 2015, Zhou published a meta-analysis [28], which investigated the prognostic value 297 of immunohistochemical CD133 expression in OC. Pooled data derived from 1050 298 patients from 8 studies showed that CD133 positivity significantly correlates with 299 advanced FIGO stage at diagnosis and with worse OS, in accordance with our 300 findings, although our population was restricted to HGSOC. 301 Other recent meta-analysis demonstrated that also ALDH1 is a promising prognostic 302 biomarker for breast[9], head/neck[10], lung[11] and colorectal cancer[12] but its 303 predictive or prognostic role in OC is still controversial [13,29-31]. In contrast to 304 CD133, ALDH1 expression is usually low or negative in serous OC compared to 305 other cancer histotype and more frequent in low FIGO stage tumors [13,29]. 306 Previously, Liebscher[21] investigated the prognostic impact of ALDH1 expression 307 in a homogeneous group of primary HGSOC patients and demonstrated that ALDH1 308 was an independent prognostic factor for OS. These results differ from our findings, 309 since in our population ALDH1 did not have an impact on patients' survival. 310 Nevertheless, in Liebscher's population the frequency of FIGO Stage I-II cases was

311 higher than in our population (11.5% vs 7.2%), while the number of optimally 312 cytoreduced patients was lower (66.3% vs 80.4%). 313 Silva[32] showed that the co-expression of CD133 and ALDH1 correlated with 314 significant worse PFI and OS in a small cohort of 56 ovarian cancer patients. These 315 results were in accordance with our findings in a larger HGSOC population. 316 To our knowledge, this is the first study analyzing the evolution of CSC markers in 317 the largest cohort of primary and recurrent HGSOC patients. Furthermore, the 318 subanalysis on patients with known BRCA status increases the value of the findings 319 by taking into consideration the genetic influence of BRCA status on patients' 320 survival[33-34] and provides a first evidence of the correlation between tumor-321 initiating cells and homologous recombination deficieny. Limitation of the study was 322 the lack of information regarding BRCA1/2 status on all enrolled patients. The 323 analysis on a cohort of 52 patients could not provide definitive conclusions for this 324 issue. 325 Interestingly, we observed that 84.6% of our patients' cohort reporting 326 CD133/ALDH1 co-expression in pOC lost this pathological characteristic at relapse. 327 Nevertheless, while CSC biomarker expression is significantly correlated with poor 328 prognosis, it is enigmatic why in a recurrent setting, which represents a more 329 aggressive step of the disease compared to primary disease, CSCs are less frequently 330 encountered. Theoretically, CSCs were expected to be much more frequent in rOC 331 than in the pOC. We hypothesize that the reduction in CSC biomarker expression 332 does not represent a reduction in CSC number within the tumor sample, but might be 333 the result of cellular reprogramming occurring in the CSC itself, which might lead to 334 the loss of CSC biomarker expression. Studies on this issue are still lacking.

This study shows that CD133 and ALDH1 as biomarkers can have influence on HGSOC patients' survival and for the first time suggests that they might be caused by a phenotypical change during the course of the disease similarly to non stem-like cancer cells. However, the need for recurrent tumor tissue to be analyzed implied that this cohort of samples might be not the most representative one for ovarian cancer patients, due to the fact that most of patients had a platinum sensitive relapse, and surgical approach at relapse was feasible. For this reason, general conclusion for the whole recurrent ovarian cancer setting cannot currently be drawn.

Another limitation of the study is that these biomarkers, in particular ALDH1, are broadly expressed, not only by CSCs. The identification of CSC is actually sure only based on the capacity to build spheroids, on tumor xenograft assay and on serial transplantation assay, which require fresh tumor tissue. Nevertheless, IHC allowed to analyze a large cohort of paired tumor tissues and to observe that there is a change in CSC–associated biomarker expression between primary and relapse disease.

Further investigations on larger cohort of paired pOC and rOC samples are warranted,

Acknowledgements.

This work was supported by European Community's Seventh Framework Program under grant agreement No. 279113-2 (OCTIPS). The documentation of clinical and patient's data was managed with "AlcedisTRIAL the web based documentation system" of Alcedis GmbH, Winchesterstr. 3, 35394 Giessen, Germany.

potentially expanding the scope with inclusion of further candidate CSC markers and

with evaluation of CSCs behavior following neoadjuvant chemotherapy[31,35-36],

in order to reduce mortality of one of the most deadly malignancies of our time.

359	Elena Ioana Braicu, MD, PhD is participant in the BIH Charité Clinician Scientist
360	Program funded by the Charité Universitätsmedizin Berlin and the Berlin Institute of
361	Health.
362	Role of the Funding Source
363	European Community's Seventh Framework Program supported this study under the
364	grant agreement No. 279113-2 (OCTIPS).
365	
366	Conflict of interest statement.
367	All Authors declare no conflict of interest.

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516 LEGEND TO TABLES AND FIGURES

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Figure 1 b d

Figure 2

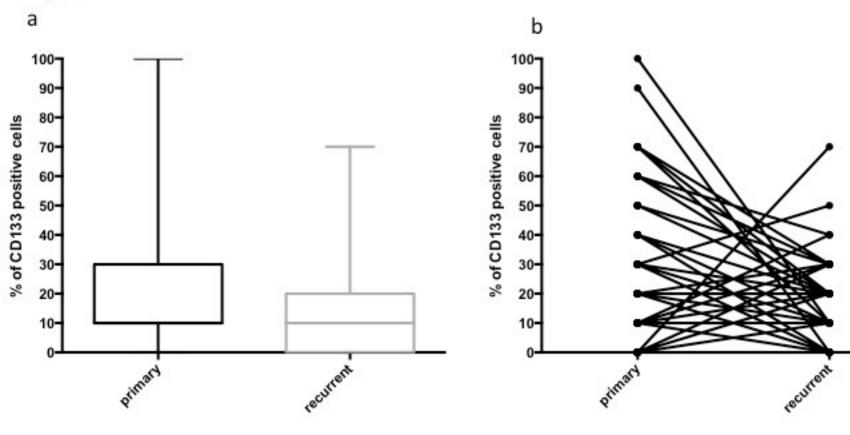


Figure 3

ALDH1 IRS recurrent

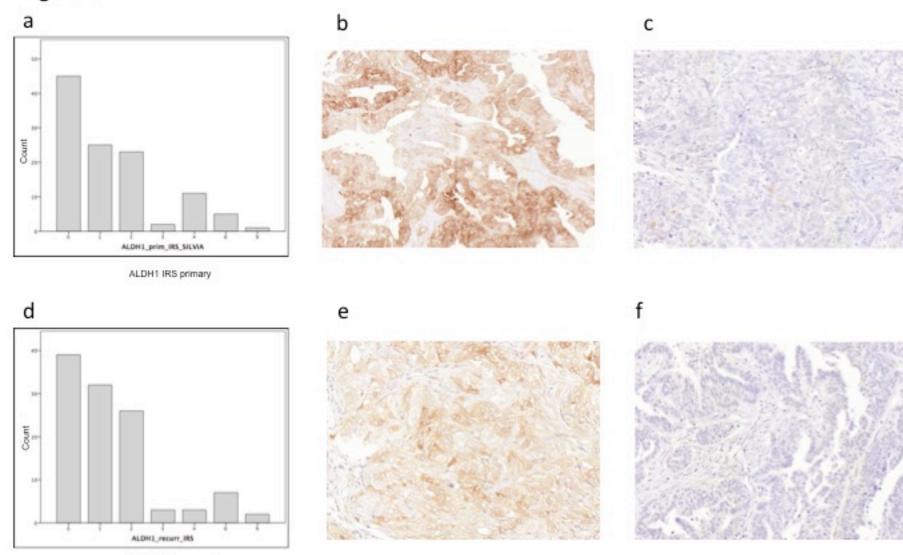
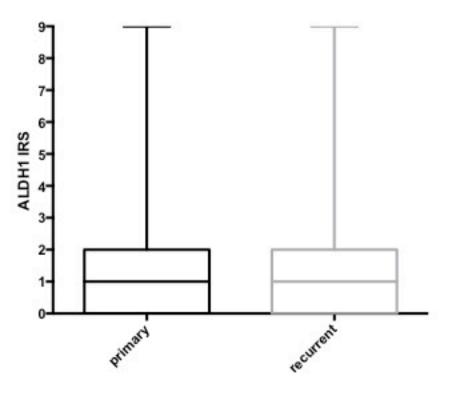


Figure 4





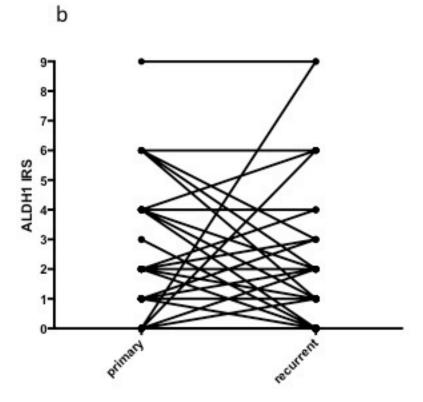


Figure 5

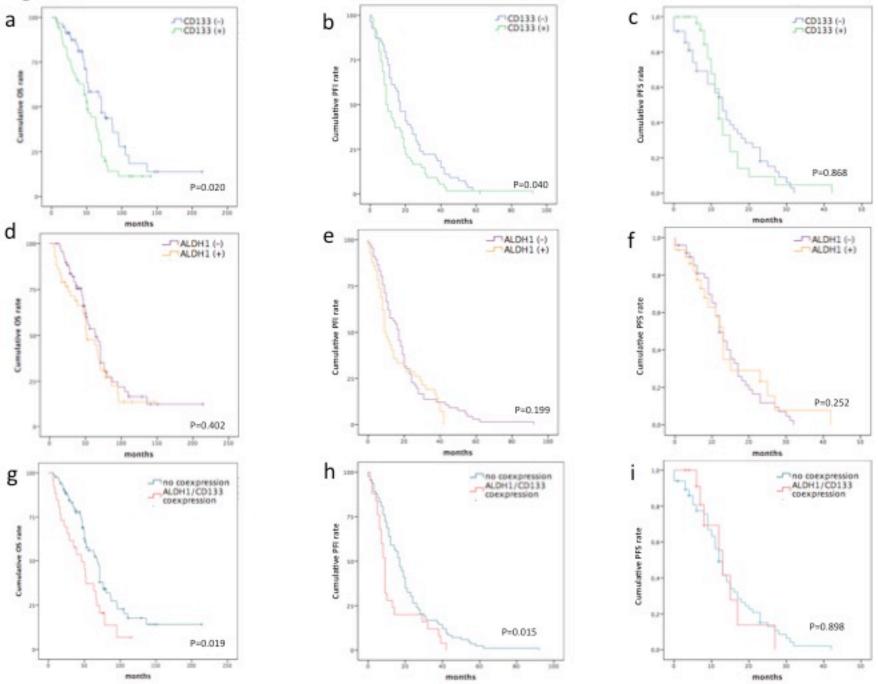
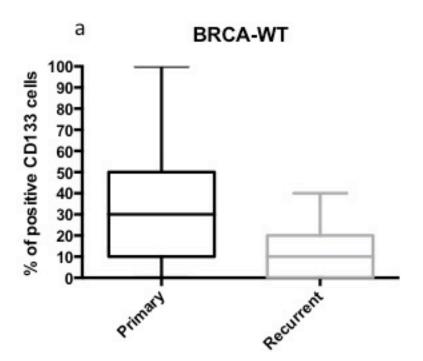


Figure 6



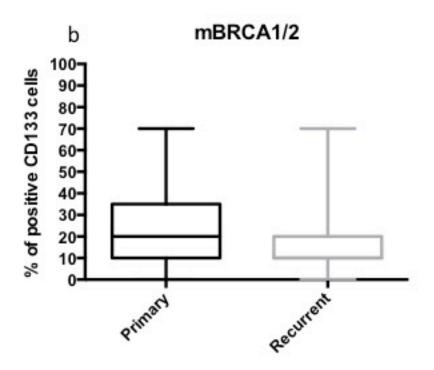


Figure 7

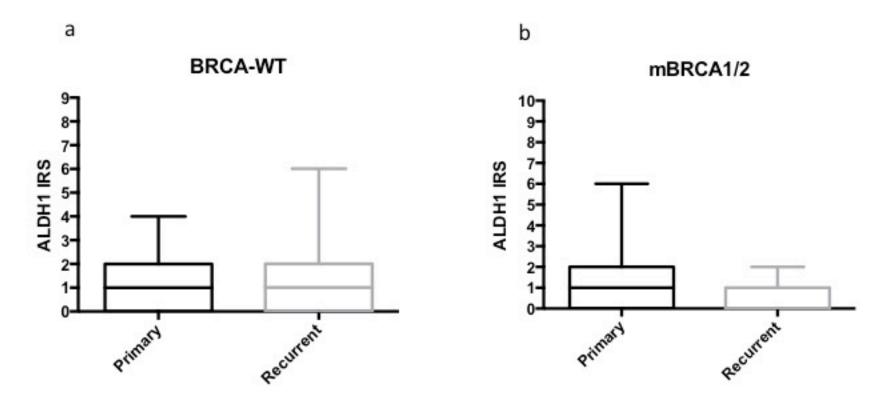


Figure 8

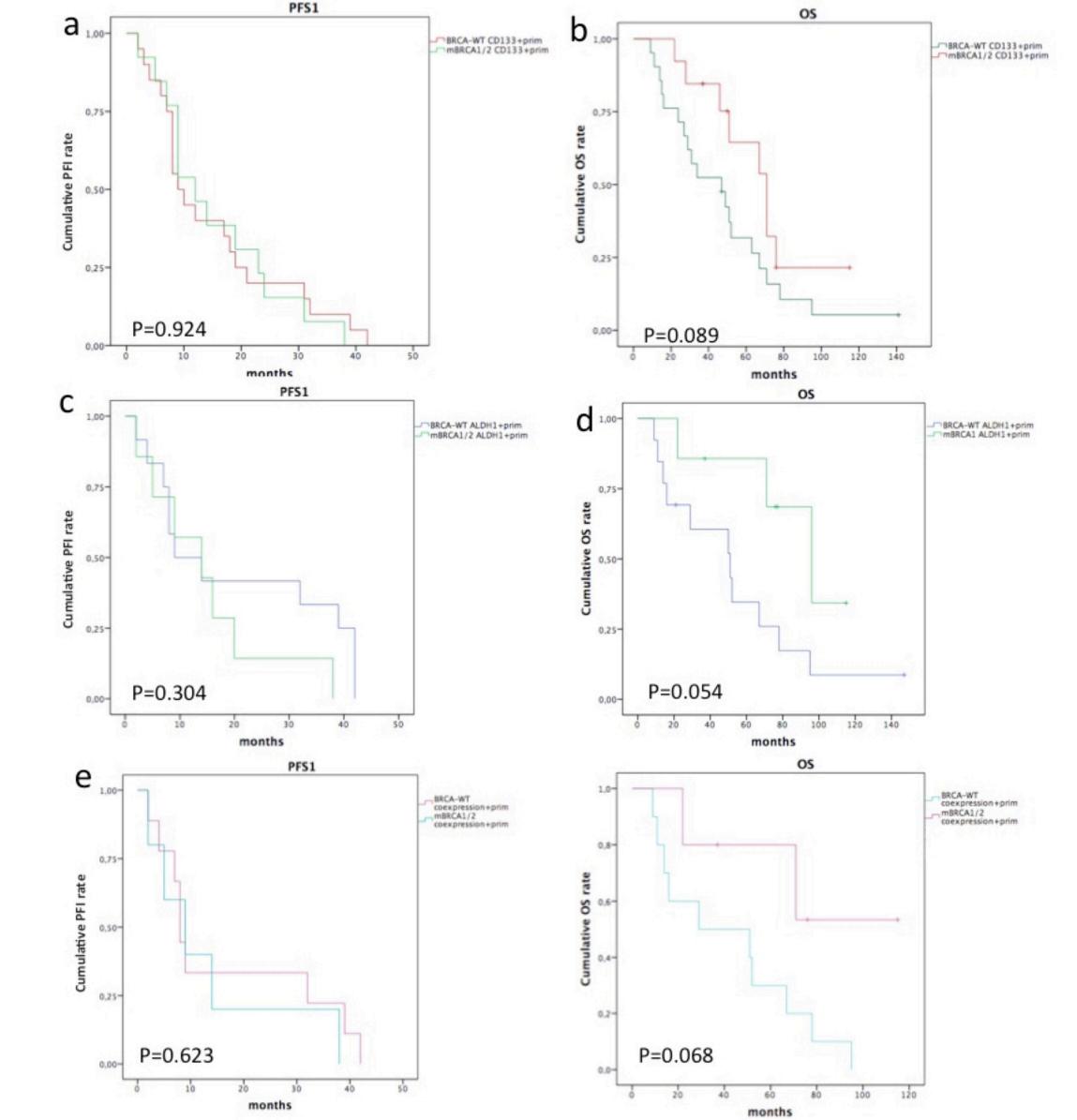


Table 1

PARAMETER	
PATIENTS (n.)	112
AGE Median (range)	56y (33-77y)
FIGO STAGE (%) - I - II - III - IV	2 (1.8%) 6 (5.4%) 93 (83%) 11 (9.8%)
RESIDUAL TUMOR AFTER PRIMARY DEBULKING SURGERY: - No residual tumor - Residual Tumor	90 (80.4%) 22 (19.6%)
PLATINUM SENSITIVITY STATUS AFTER PRIMARY TREATMENT - Platinum sensitive - Platinum resistant - Missing	90 (80.4%) 18 (16.1%) 4 (3.5%)
PLATINUM SENSITIVITY STATUS AFTER TREATMENT FOR DISEASE RELAPSE - Platinum sensitive - Platinum resistant - Missing	59 (52.7%) 12 (10.7%) 41(36.6%)

Table 2

N°	CD1	CD133 ALDH1			CD133 and ALDH1 coexpression				
	Positive (%)	Negative (%)	Р	Positive (%)	Negative (%)	Р	Positive (%)	Negative (%)	Р
54 58	27 (50%) 28 (48%)	27 (50%) 30 (52%)	0.855	18 (33%) 25 (43%)	36 (67%) 33 (57%)	0.288	11 (20%) 15 (26%)	43 (80%) 43 (74%)	0.492
8 104	0 55 (53%)	8 (100%) 49 (47%)	0.006	3 (38%) 40 (39%)	5 (62%) 64 (61%)	1.000	0 26 (25%)	8 (100%) 78 (75%)	0.194
90 22	42 (47%) 13 (59%)	48 (53%) 9 (41%)	0.346	35 (39%) 8 (36%)	55 (61%) 14 (64%)	1.000	20 (22%) 6 (27%)	70 (78%) 16 (73%)	0.586
90	43 (48%)	47 (52%)	0.439	33 (37%)	57 (63%)	0.303	19 (21%)	71 (79%)	0.357
	58 8 104 90 22	(%) 54	(%) (%) 54	(%) (%) (%) P 54	(%) (%) P (%) 54 27 (50%) 27 (50%) 0.855 18 (33%) 58 28 (48%) 30 (52%) 25 (43%) 8 0 8 (100%) 0.006 3 (38%) 104 55 (53%) 49 (47%) 40 (39%) 90 42 (47%) 48 (53%) 0.346 35 (39%) 22 13 (59%) 9 (41%) 8 (36%)	(%) (%) (%) (%) 54 27 (50%) 27 (50%) 0.855 18 (33%) 36 (67%) 58 28 (48%) 30 (52%) 25 (43%) 33 (57%) 8 0 8 (100%) 0.006 3 (38%) 5 (62%) 40 (39%) 64 (61%) 90 42 (47%) 48 (53%) 0.346 35 (39%) 55 (61%) 22 13 (59%) 9 (41%) 8 (36%) 14 (64%) 90 43 (48%) 47 (52%) 0.439 33 (37%) 57 (63%)	(%) (%) P (%) (%) P 54 27 (50%) 27 (50%) 0.855 18 (33%) 36 (67%) 0.288 58 28 (48%) 30 (52%) 25 (43%) 33 (57%) 8 0 8 (100%) 0.006 3 (38%) 5 (62%) 1.000 104 55 (53%) 49 (47%) 40 (39%) 64 (61%) 64 (61%) 90 42 (47%) 48 (53%) 0.346 35 (39%) 55 (61%) 1.000 22 13 (59%) 9 (41%) 8 (36%) 14 (64%)	(%) (%) (%) (%) P (%) 54 27 (50%) 27 (50%) 0.855 18 (33%) 36 (67%) 0.288 11 (20%) 58 28 (48%) 30 (52%) 25 (43%) 33 (57%) 15 (26%) 8 0 8 (100%) 0.006 3 (38%) 5 (62%) 1.000 0 104 55 (53%) 49 (47%) 48 (53%) 0.346 35 (39%) 55 (61%) 1.000 20 (22%) 22 13 (59%) 9 (41%) 8 (36%) 14 (64%) 6 (27%) 90 43 (48%) 47 (52%) 0.439 33 (37%) 57 (63%) 0.303 19 (21%)	(%) (

Table 3

PROGRESSION FREE INTERVAL							
	UNIVARIATE ANALY	/SIS	MULTIVARIATE ANALYSIS				
	HR (95% CI) P		HR (95% CI)	Р			
Age	1.003 (0.983-1.024)	0.774					
FIGO Stage (III/IV vs I/II)	2.019 (0.907-4.496)	0.085	1.856 (0.826-4.169)	0.134			
Residual Tumor (any residual)	1.026 (0.625-1.684)	0.919					
CD133/ALDH1 coexpression (positive vs negative)	1.729 (1.093-2.733)	0.019	1.638 (1.033-2.598)	0.036			

Table 4

Table 4						
OVERALL SURVIVAL						
	UNIVARIATE ANAL	YSIS	MULTIVARIATE ANALYSIS			
	HR (95% CI)	Р	HR (95% CI)	Р		
Age	1.011 (0.985-1.038)	0.404				
FIGO Stage (III/IV vs I/II)	1.465 (0.533-4.020)	0.459				
Residual Tumor (any residual)	1.632 (0.973-2.736)	0.063	1.272 (0.725-2.231)	0.401		
Platinum sensitivity status after primary treatment (platinum resistant vs platinum sensitive)	3.394 (1.927-5.978)	<0.001	2.907 (1.594-5.302)	<0.001		
CD133/ALDH1 coexpression (positive vs negative)	1.799 (1.089-2.971)	0.022	1.707 (1.012-2.881)	0.045		

Table 5

I able 5								
PATIENT ID	GERMLINE BRCA STATUS	SOMATIC BRCA STATUS – PRIMARY TUMOR	SOMATIC BRCA STATUS – RECURRENT TUMOR					
B001	mBRCA1	mBRCA1	mBRCA1					
B002	WT	WT	WT					
B003	WT	WT	WT					
B006	N/A	WT	WT					
B007	N/A	WT	WT					
B009	N/A	WT	WT					
B012	N/A	WT	WT					
B015	N/A	WT	WT					
B019	WT	mBRCA2	mBRCA2					
B021	N/A	WT	WT					
B022	N/A	WT	WT					
B024	mBRCA1	mBRCA1	mBRCA1					
B025	N/A	WT	WT					
B026	N/A	WT	WT					
B028	mBRCA1	mBRCA1	mBRCA1					
B029	mBRCA1	mBRCA1	mBRCA1					
B030	N/A	WT	WT					
B032	WT	WT	WT					
B037	N/A	WT	WT					
B041	mBRCA1	mBRCA1	mBRCA1					
B044	N/A	WT	WT					
B045	N/A	mBRCA1	mBRCA1					
B048	WT	WT	WT					
B050	WT	WT	WT					
B051	N/A	mBRCA2	mBRCA2					
B052	WT	WT	WT					
B053	N/A	WT	WT					
B054	N/A	WT	WT					
B062	N/A	WT	WT					
B063	N/A	mBRCA2	mBRCA2					
B065	WT	WT	WT					
B068	N/A	mBRCA1	mBRCA1					
B069	N/A	WT	WT					
B071	N/A	mBRCA1	mBRCA1					
B077	mBRCA2	mBRCA2	mBRCA2					
B080	mBRCA2	mBRCA2	mBRCA2					
B081	WT	mBRCA1	mBRCA1					
B082	N/A	mBRCA1	mBRCA1					
B085	N/A	mBRCA1	mBRCA1					
B087	mBRCA1	mBRCA1	mBRCA1					
B088	N/A	WT	WT					
B090	N/A	mBRCA1	mBRCA1					
B093	N/A	WT	WT					
B094	N/A	mBRCA1	mBRCA1					
B097	N/A	mBRCA1	mBRCA1					
B098	N/A	WT	WT					
B099	N/A	WT	WT					
B100	N/A	WT	WT					
L007	WT	WT	WT					
L010	WT	WT	WT					
L017	WT	WT	WT					
L020	mBRCA1	mBRCA1	mBRCA1					
	I							

Table 6

BRCA status	Total N°	C	D133		А	LDH1			33 and ALD expression	
		Positive (%)	Negative (%)	Р	Positive (%)	Negative (%)	Р	Positive (%)	Negative (%)	Р
BRCA-WT mBRCA1/2	31 21	21 (68%) 13 (62%)	10 (32%) 8 (38%)	0.769	13 (42%) 7 (33%)	18 (58%) 14 (67%)	0.575	10 (32%) 5 (24%)	21 (68%) 16 (76%)	0.551