Introduction/Background: The detection of gBRCA1/2 mutations in patients(pts) with epithelial ovarian cancer (EOC) provides information regarding family risk and influences clinical management, e.g. use of PARP inhibitors. The availability of next generation sequencing (NGS) allows for simultaneous sequencing of multiple cancer risk genes including BRCA1/2. Our aim was to evaluate the prevalence and clinical outcome of deleterious germline mutations in EOC patients.

Methodology: EOC patients treated between 2011 and 2020 at our institution and with germline TruRisk® gene panel testing were included in this retrospective analysis. Based on the genetic test result three cohorts were considered: A) no mutation, B) gBRCA1/2, and C) mutations in other risk genes. Demographic and clinicopathological characteristic were retrieved from the prospective database. To evaluate survival outcome in FIGO III/IV EOC univariate and multivariate logistic regression was performed.

Result(s): In total 702 EOC pts underwent germline panel testing. Median age was 59 years, 74.5% of patients underwent primary debulking surgery, 83.9% were FIGO III/IV, and complete macroscopic resection was achieved in 74.0%. No mutation was detected in 76.6% (n=538), pathogenic gBRCA1/2 mutations in 17.4% (n=122), and mutations in other risk genes in 6.0% (n=42), respectively (tbl.1). Significant differences between the cohorts were detected for age, previous history of malignancies, personal/familial breast/ovarian cancer history, and histology.

For FIGO III/IV patients median PFS was significantly different for cohort A, B, and C with 23, 37, and 34 months (p=0.039/multivariate 0.015), respectively. 3-years-OS was 70%, 83%, and 87% for cohorts A, B, and C (p=0.003), respectively.

In multivariate analysis type of surgery (IDS: HR 2.79 (1.86-4.19), p<0.001), ascites >500mL (HR 1.75(1.14-2.68), p=0.010), and residual disease (RD>0mm: HR 2.87(1.99-4.14), p<0.001), were identified as worse prognostic factors for OS. Patients from cohorts B and C showed significantly better OS than those from cohort A (B: HR 0.49(0.31-0.80), p=0.004; C: HR 0.34(0.14-0.83), p=0.021) (table 1, figure 1).

Conclusion: The detection rate of germline mutations in EOC is 23.4%. Our findings underline the necessity to offer germline panel testing in EOC to identify families at risk. Further, our findings underscore the prognostic value of germline mutations towards a better prognosis.