Objectives The study aimed to evaluate factors associated with 30-day severe post-operative morbidity classified by Clavien-Dindo classification (CDC) ≥ grade IIIa and time to adjuvant chemotherapy (TTC) after cytoreductive surgery for primary advanced stage epithelial ovarian cancer (AEOC).

Methods Patients undergoing cytoreductive surgery for primary AEOC were enrolled from February 2018 to September 2020. Ten post-operative complications were graded according to the CDC. Logistic regression models were used to evaluate risk factors for the following complications: ICU admission, readmission and time to chemotherapy (TTC). Area under the receiver operating characteristic (AUC) was used to establish the diagnostic performance of each classification.

Results Totally, 300 patients were included from February 2018 to September 2020. Thirty days post-operative complications occurred in 146 patients of whom 30% had multiple complications (range 2–6 events). Severe complications were diagnosed in 17% of patients when using the CDC while the percentage increased to 30% when using the CCI. In regression analysis, both CDC and CCI presented as predictors for PLOS (>9 days), TTC >42 days, ICU admission and readmission (all p < 0.05). AUC demonstrated that CCI (0.843, 95% CI 0.79–0.90) performed better than CDC (0.813, 95% CI 0.75–0.88) for PLOS. Both systems equally showed a fair diagnostic performance for TTC >42 days (both AUC 0.630, 95% CI 0.55–0.71).

Conclusions The cumulative score of CCI had shown a superior diagnostic performance for PLOS than CDC in AEOC. The use of the CCI should be considered in other gynecological evaluations.

Objectives The comprehensive complication index (CCI) is an instrument for reporting the cumulative post-operative complications while Clavien-Dindo classification (CDC) reports the most serious event. This study aims to validate the CCI for advanced stage epithelial ovarian cancer (AEOC) after cytoreductive surgery and compare its diagnostic performance with CDC.

Methods Complications after cytoreductive surgery for primary AEOC were classified using CDC and CCI. Logistic regression was used to determine the association between CDC and CCI with prolonged length of hospital stays (PLOS), intensive care unit (ICU) admission, readmission and time to chemotherapy (TTC). Area under the receiver operating characteristic (AUC) was used to establish the diagnostic performance of each classification.

Results Totally, 300 patients were included from February 2018 to September 2020. Thirty days post-operative complications occurred in 146 patients of whom 30% had multiple complications (range 2–6 events). Severe complications were diagnosed in 17% of patients when using the CDC while the percentage increased to 30% when using the CCI. In regression analysis, both CDC and CCI presented as predictors for PLOS (>9 days), TTC >42 days, ICU admission and readmission (all p < 0.05). AUC demonstrated that CCI (0.843, 95% CI 0.79–0.90) performed better than CDC (0.813, 95% CI 0.75–0.88) for PLOS. Both systems equally showed a fair diagnostic performance for TTC >42 days (both AUC 0.630, 95% CI 0.55–0.71).

Conclusions The cumulative score of CCI had shown a superior diagnostic performance for PLOS than CDC in AEOC. The use of the CCI should be considered in other gynecological evaluations.

Objectives Despite the substantial clinical use of PARP inhibitors, the development of resistance contributes to mortality. Thus, we aimed to discover protein signatures associated with response to PARP inhibitors in high-grade serous ovarian carcinoma (HGSOC) through proteomic analysis.

Methods We conducted an in-depth proteomic analysis of FFPE tissues of patients with platinum-sensitive recurrent HGSOC who received PARP inhibitor maintenance therapy (n = 24). The proteomic strategy was as follows: removal of paraffin, isolation of tumor via examination by a pathologist, high-resolution quadruple Orbitrap LC-MS/MS. Patient samples were assigned to the poor prognosis group (n = 9). Dysregulated proteins between the good and poor response groups were identified.

Results In total, 7,825 proteins were quantified. There were 56 proteins significantly expressed in the good response group compared with the poor response group.