Abstract 2022-RA-1697-ESGO Figure 1

Conclusion Low ALI was associated with higher perioperative complications and poorer survival in ovarian cancer. The utility of preoperative ALI as a prognostic marker in ovarian cancer should be assessed in prospective studies.

Introduction/Background More than 75% of individuals with ovarian cancer (OC) are diagnosed at an advanced stage, given that early-stage disease is usually asymptomatic. Epigenetics studies are emerging in cancer research and diagnostics with encouraging outcomes. Recent developments in large-scale DNA methylation profiling have shown that those changes are at the very early stage of carcinogenesis, indicating that the detection of such markers would drastically increase patient outcome. In OC, that would potentially represent early detection for the majority of patients. Here, we (1) investigated a large-scale methylation landscape of OC, (2) devised a predictive model based on the discovered targets, and (3) sought to validate its performance on independent external cohorts.

Methodology Fresh-frozen tissues were collected from 29 OC patients and 14 benign pelvic mass patients. Samples were submitted to global DNA methylation profiling, comprised of ~850,000 targets. For the design of the predictive model we performed: (1) univariate linear model; (2) LASSO-penalized multivariate analysis; (3) cross-validation; and (4) group assignment by centroid approach followed by principal component analysis (PCA). The predictive model was trained on our own samples and validated in 2 external cohorts.

Results We identified 21 targets that showed a clear distinction for the OC patient group, with clustering analysis showing two independent groups. Furthermore, the two main components explained 66% of the variance shown by PCA. The validation of our model in 2 independent cohorts showed classification concordance of 81.1% and 85.2%, respectively. Conclusion Our current findings showed that OC presents an unique methylation landscape represented by a signature of 21 targets. Our predictive model algorithm showed considerable concordance with external cohorts. Noteworthy, due to the relatively small cohort used to train our model, we are currently collecting more samples to further improve its prediction efficiency, which may be relevant in diagnostic settings.