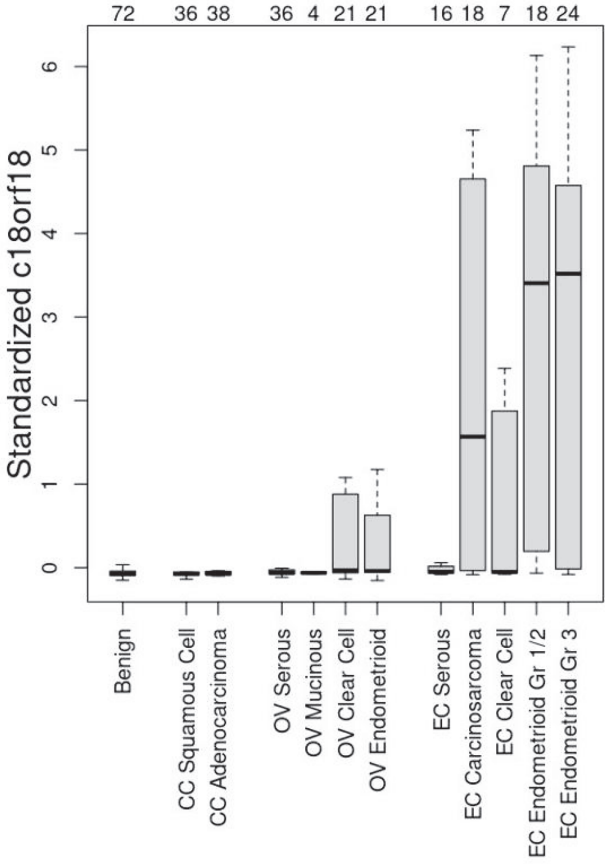
benign histologies. Twenty-five MDMs representing each organ site were selected as previously reported; DNA extracted from independent primary tissues was assayed by quantitative methylation specific PCR. MDMs were normalized to β-actin. MDM distributions were displayed using boxplots and intensity maps.

Results 82 EC (16 serous, 18 carcinosarcoma, 7 clear cell, 17 endometrioid grade 1/2, 24 endometrioid grade 3), 82 OC (36 serous, 21 clear cell, 4 mucinous, 21 endometrioid), and 64 CC (36 squamous cell, 28 adenocarcinoma) were compared to controls of benign epithelium (29 cervicovaginal, 29 fallopian tube, 14 benign endometrial tissues). While CDO1 discriminated any cancer type from benign control tissue, cancer specificity was evident for most MDMs (figure 1). Overlap of MDMs, such as c18orf18 among EC and OC clear cell and endometrioid histologies, is compatible with the origin of these OCs from endometriosis (figure 2).



Abstract 42/#466 Figure 2

Conclusions MDMs discovered and independently validated in EC, OC, and CC tissues discriminate among GC site origin. MDM testing in vaginal fluid and/or blood is warranted to assess GC detection and site-specificity via non-invasive liquid biopsy.

Poster rounds with the professors: Group 03

43/#512 ASSESSING ROBUSTNESS OF AN ARTIFICIAL INTELLIGENCE DERIVED HISTOLOGICAL BIOMARKER ACROSS DIFFERENT SITES OF DISEASE AND IN SERIAL SECTIONS IN TUBO-OVARIAN HIGH-GRADE SEROUS CARCINOMA

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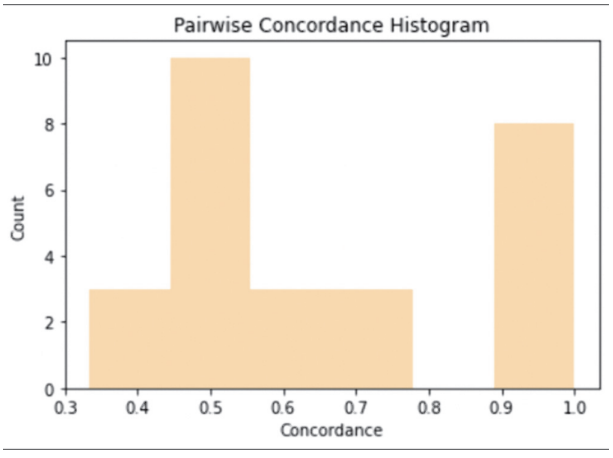
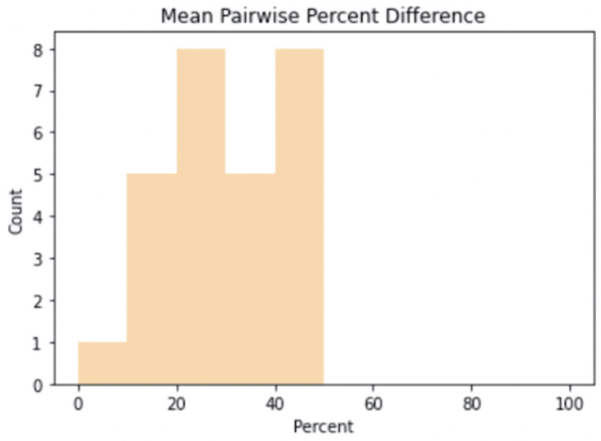
Objectives Histological biomarkers may produce different predictions for a single patient when using whole slide images of biopsies from different sites and even serial sections of the same tissue. Previous work had developed a signature of AI-derived morphologic features correlated with response to platinum-based chemotherapy in tubo-ovarian high-grade serous carcinoma (HGSC) specimens from The Cancer Genome Atlas (TCGA) (hazard ratio: 0.35). We aim to assess the robustness of this marker across different sites of disease and in serial sections.

Methods 489 sections from 10 tissue microarrays (TMA) corresponding to 44 patients with HGSC from Stanford Hospital were included in this study. Using the digitally scanned histologic images, we computed geometric features of nuclei extracted from tissue regions using segmentation models. TMA sections were stratified into low and high responder groups by the histologic signature previously associated with platinum-based chemotherapy response. Concordance (c-index (C)) and mean pairwise percent difference (MPPD) across all cores for a given patient were calculated to assess the robustness of the signature.



Abstract 43/#512 Figure 1



Abstract 43/#512 Figure 2

Results The prediction of the morphologic signature is consistent when computed across all cores/slides per patient (C:0.66, MPPD:30%). When stratified by site, the signature is similar across serial sections for samples from the ovary (C:0.71, MPPD:22%) and the omentum (C:0.70, MPPD:25%). The signature is also consistently robust irrespective of anatomic site (C:0.62, MPPD:26%).

Conclusions The artificial intelligence derived histological biomarker associated with response to platinum-based chemotherapy is generalizable across both ovarian and omental sites and consistent between serial sections in patients with HGSC.

44/#219 PREDICTING RESPONSE TO PLATINUM-BASED CHEMOTHERAPY FOR TUBO-OVARIAN HIGH-GRADE SEROUS CARCINOMA USING AN ARTIFICIAL INTELLIGENCE HISTOPATHOLOGY PLATFORM

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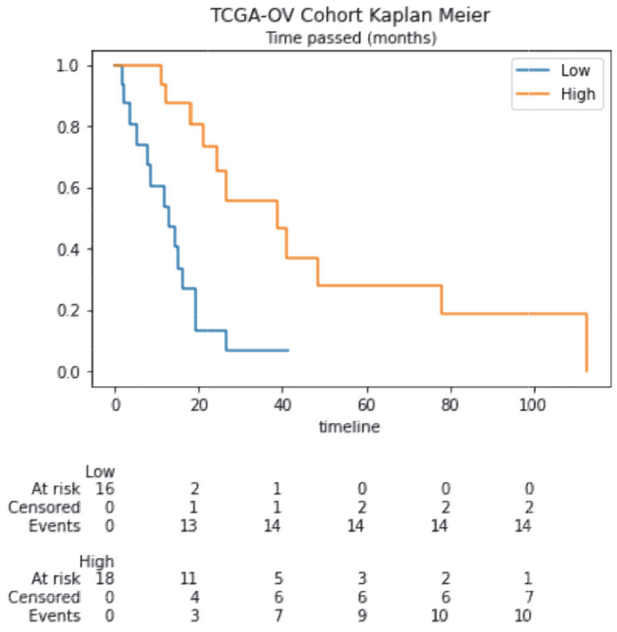
10.1136/ijgc-2022-igcs.88

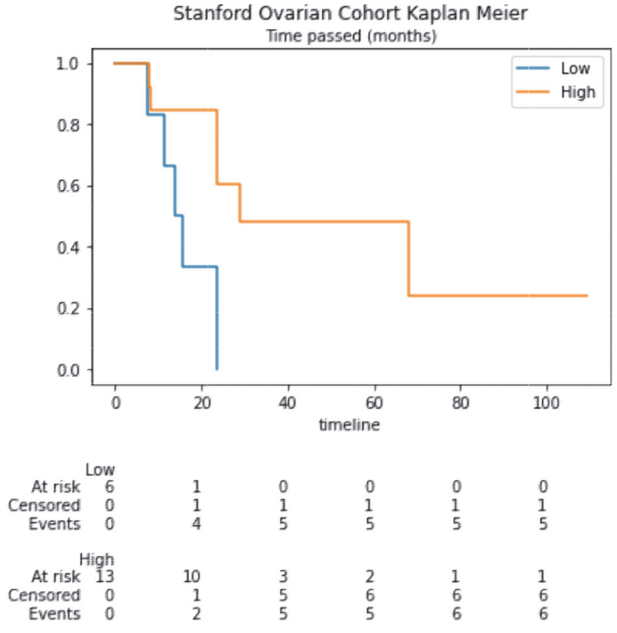
Objectives Platinum-based chemotherapy is the standard of care first-line systemic treatment for patients diagnosed with advanced stages of tubo-ovarian high-grade serous carcinoma (HGSC). While the majority of patients respond, roughly 15% of patients are platinum-resistant. We aimed to develop an artificial intelligence-based platform leveraging routine pre-treatment histopathology specimens to predict platinum-based chemotherapy response.

Methods 87 patients from The Cancer Genome Atlas (TCGA) and 19 patients from Stanford Hospital with HGSC who received platinum-based chemotherapy post resection were included in this study. Using scanned hematoxylin and eosin-stained (H&E) images, we extracted nuclei images from tissue regions using segmentation models and computed geometric features of these nuclei. In the TCGA cohort, quantitative features of the nuclear geometry were correlated with Progression Free Survival (PFS) using a multivariable Cox Proportional Hazards (CPH) model in order to construct a signature associated with platinum treatment benefit. The signature was assessed with a Kaplan Meier Estimator and log rank test by comparing the PFS between the high and low cohorts stratified by the signature in the internal TCGA and external Stanford cohorts.

Results The artificial intelligence derived histological biomarker is able to stratify patients into high and low responders to platinum-based chemotherapy with statistical significance (log-rank test – internal: p=0.000556, external: p=0.00571), achieving hazard ratios of 0.227 (95% CI: 0.092,0.559) on



Abstract 44/#219 Figure 1



Abstract 44/#219 Figure 2