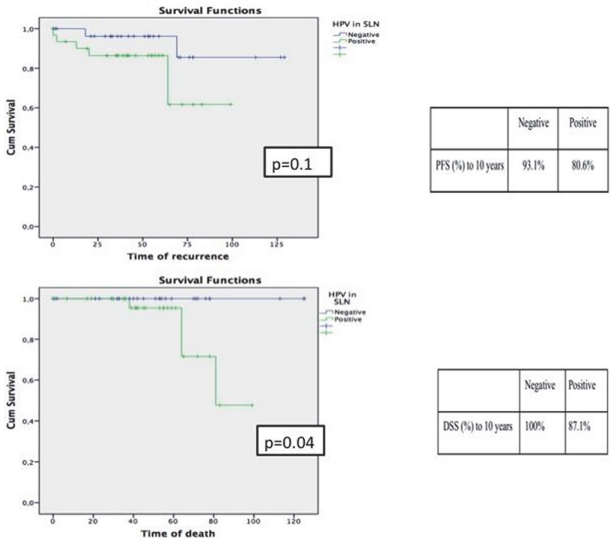
respectively 43.5 and 29.2 month, but, these differences are not statistical significant.However, all of the 4 deaths listed in our study occurred in the positive HPV DNA SLN group for which the 10 years Overall survival (OS) is thus significantly decreased.



	Negative	Positive
PFS (%) to 10 years	93.1%	80.6%

	Negative	Positive
DSS (%) to 10 years	100%	87.1%

Abstract 2022-RA-1480-ESGO Figure 1

Conclusion Our results show worst OS in patients with detected HPV DNA compared to patients without detected HPV DNA in their SLN and the same tendency is observed for PFS without significance. Thus, HPV DNA in SLN detected by ultrasensitive ddPCR could represent an interesting prognosis biomarker in N0 ECC.

2022-RA-1502-ESGO MULTIPLEXED BIOMARKER DETECTION USING THE QUANTIGENE ASSAY IN WOMEN LIVING WITH HIV FOR CERVICAL DYSPLASIA DETECTION

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Introduction/Background Cervical cancer (CxCa) and its precursor lesions are caused by persistent infection with a high-risk(HR) Human Papillomavirus (HPV). Women living with HIV (WLWH) have a higher risk for cervical dysplasia and CxCa development. The high HPV prevalence in WLWH makes a HPV-PCR based screening non-efficient. Biomarker detection could be a possibility, to find woman at risk. We evaluated the biomarker-based QuantiGene-Molecular-Profiling-Histology assay (QG-MPH) in WLWH.

Methodology We analysed a representative subset of samples (n=301) from the prospective 2H-study including HIV+ and HIV- women. A cervical sample was collected using a cyto-brush and fixed into ThinPrep/PreservCyt. The QG-MPH assay is based on the multiplexed Luminex bead-based technology platform (QuantiGene 2.0). It detects and quantifies the mRNA of 18 HR-HPV genotype-specific oncogenes, reference genes and cellular biomarkers including proliferation, tumour stem cell and tumour markers to predict the dysplasia stage, simultaneously.

Results HIV coinfection was significantly associated with increased mRNA expression of the following biomarkers in HR-HPV+ women without cervical lesions: leading HPV-E7 (p=0.0019), p16 (p=0.022), STMN1 (p=0.0039), MCM2 (p=0.015), KRT7 (p=0.0035) and KRT17 (p=0.014). In cervical cancer cases (HIV+=19, HIV-=18) only the expression of Nanog mRNA was different (p=0.022). Using the risk score developed on a HIV- cohort led to false positive detection (CIN3+) of 68.8% (n=22) in WLWH without lesions. Logistic regression analyses showed best markers for CxCa detection in HIV+ patients in our cohort were BIRC5, KRT17, MMP7 and p53 with a combined AUC of 0.93 (sensitivity=95%, specificity=82.0%).

Conclusion Viral oncogene expression is increased in HR-HPV + WLWH without cervical lesions. Biomarker evaluation has the potential to overcome problems of HPV PCR-based screening in WLWH. However, risk score adaptation is needed as biomarker expression varies between HIV+ and HIV- patients. Further studies with higher sample number are warranted to confirm the best markers and risk scores by QG-MPH analysis.

2022-RA-1558-ESGO A COMBINATION OF MOLECULAR AND CLINICAL PARAMETERS PROVIDES A NEW STRATEGY FOR HIGH-GRADE SEROUS OVARIAN CANCER PATIENT MANAGEMENT

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Introduction/Background High-grade serous carcinoma (HGSC) is the most common and deadly subtype of ovarian cancer. Although most patients will initially respond to first-line treatment with a combination of surgery and platinum-based chemotherapy, up to a quarter will be resistant to treatment. We aimed to identify a new strategy to improve HGSC patient management at the time of cancer diagnosis (HGSC-1LTR).

Methodology Ready-available formalin-fixed paraffin-embedded HGSC tissues obtained at the time of diagnosis were selected for proteomic analysis. Clinical data, treatment approach and outcomes were collected for all patients. Chemoresistant (TFIp < 6 m) and chemosensitive (TFIp > 6 m) groups were evaluated using discovery proteomics (discovery cohort, n=21). Protein candidates were verified in an independent cohort using targeted proteomics (verification cohort, n=88). Predictive analysis combined with a cross-validation was used to select those proteins able to correctly classify patients into chemoresistant and chemosensitive groups. The classification performance of the protein and clinical data combinations were assessed through the generation of receiver operating characteristic (ROC) curves.