**Results** Among 700 patients randomized, 508 (73% of expected) and 432 (86% of expected) completed respectively baseline QOL and SHA. Compliance post-baseline was 56% to 69% for QOL and 63% to 79% for SHA with 58% of patients reporting QOL and 63% responding to the SHA at 36 months. Mean baseline scores were high for all EORTC QLQ-C30 functional scales. EORTC symptoms with the highest (worst) mean baseline scores were fatigue (24.5 on SH and 24.1 on RH) and sleep (29.9 on SH and 32.0 on RH). Mean baseline FSFI and FSDS-R total scores were respectively 27.1 and 10.9 on SH and 27.6 and 10.1 on RH; all were in the non-clinical range. Significant differences in favor of treatment with SH was found for the following domains: EORTC QLQ-C30 pain scale; EORTC QLQ-CX24 symptom experiences, body image, sexual-vaginal functioning, and sexual worry, sexual activities, and sexual enjoyment scales; FSFI desire, arousal, lubrication, pain scales and total score; and FSDS-R total score.

**Conclusion** Better quality of life and sexual health were observed with SH compared to RH.

**#630 LOWER-LIMB LYMPHEDEMA AFTER SENTINEL LYMPH NODE BIOPSY IN CERVICAL CANCER PATIENTS: FINAL RESULTS OF THE SENTIX PROSPECTIVE INTERNATIONAL STUDY (CEEGOG 01-ENGOT-CX2)**

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Abstract #630 Figure 1 Postoperative cumulative incidence of LLL in the SLN and PLND cohorts. LLL: limb lymphedema defined as a limb volume increase black (LVI); black (LVI >40%); dark grey: moderate LLL (LVI 20–39%); light grey: mild LLL (LVI 10–19%)

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Conclusion Severe persistent LLL occurred rarely after surgical pelvic LN staging in cervical cancer patients. Contrary to our expectations, de-escalation from systematic PLND to SLN biopsy was not associated with a significantly decreased risk of mild-to-moderate LLL.

11. Translational research/biomarkers

HOMOLOGOUS RECOMBINATION DEFICIENCY (HRD) TESTING ON CELL-FREE TUMOR DNA FROM PERITONEAL FLUID OF PATIENT WITH EPITHELIAL OVARIAN CANCER

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Introduction/Background Knowledge regarding homologous recombination deficiency (HRD) status at diagnosis is essential to manage patients with advanced epithelial ovarian cancer (EOC). These genomic tests are performed on tumor samples and unfortunately the analysis of tumor DNA are missing 15–19% of cases.

Methodology We collected ascites or peritoneal washings (20ml) from 53 patients undergoing primary or secondary laparoscopy for suspicion of EOC, or therapeutic paracentesis. A Cancer Gene Panel (CGP) was analyzed by Next generation sequencing (NGS) for TP53 genes and HR genes and shallow Whole Genome Sequencing (sWGS) on cftDNA and provided a contributive result for all patients (86%) had a TP53 pathogenic variant, all cases werediscordant with acfDNA compared with tumor testing for prognostic features includi ng residual disease, age, grade, FIGO stage, primary site, and BRCA type (BRCA1 vs BRCA2) could not explain short survival in BRCA-mutants –it could be explained by the homologous recombination DNA repair deficiency (HRD) score. The homologous recombination DNA repair deficiency (HRD) score was significantly higher in BRCA-mutants with long survival compared to those with shorter survival. Somatic mutation and neoantigen burden were equivalent between the two survival groups of BRCA-mutants, however the homologous recombination DNA repair deficiency (HRD) score was significantly higher in BRCA-mutants with long survival compared to those with shorter survival (73.6 vs 65.5, p=0.007). T-cell (PD1+CD4+) density was associated with good outcomes in BRCA-mutants (p=0.003). Mutation signature clustering identified a group of BRCA-mutants characterised by short survival, low HRD-scores, and DNA copy number signature CN9 which is associated with increased leucocyte fraction and poor disease-specific survival. PIK3CA alterations were enriched in BRCA2-mutants with short survival (5/10, 50%, p=0.061).

Conclusion Survival in BRCA-mutants with HGSOCC was associated with different mutational signatures, differential immune responses, somatic gene alterations, and differences in the extent of HRD. Integration of multi-omic data with clinical variables can enhance the accuracy of predictive models and