node metastases in high-risk endometrial cancer were 0.66 (95% CI: 0.59-0.73), 0.93 (95% CI: 0.87-0.96) and 0.72 respectively.

Conclusion* Despite the widespread use of 18F-FDG PET or PET/CT for imaging staging in patients with high-risk endometrial cancer, this study shows the moderate sensitivity of this technique to diagnose lymph node metastases. Therefore, the actual usefulness of this technique for the diagnosis of lymph node metastases is limited, especially nowadays, with the arrival and implementation of the sentinel node.

615 ABSTRACT WITHDRAWN

619 VALIDATION OF MODEPLEX TECHNOLOGY FOR THE DETERMINATION OF POLE MUTATIONS IN ENDOMETRIAL CARCINOMA SAMPLES

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Introduction/Background* The current molecular classification of endometrial cancer recognizes 4 subtypes with prognostic and therapeutic implications: 1) Copy-Number-High, 2) Hypervariable, 3) Ultramutated (POLE-mutated) and 4) Copy-Number-Low.

To extrapolate this classification into clinical practice, some authors have proposed a simplified scheme using three immunohistochemical markers and a molecular test (POLE mutation analysis). The mutational determination can be carried out
through massive sequencing techniques or using Single-Gene strategies such as Sanger sequencing.

The lack of a cost-effective Gold-Standard has prompted the development of new techniques so that this determination can be carried out routinely in most centers.

In this study we intend to explore the diagnostic accuracy of a novel technology called MODAPLEX that combines multiplex-qPCR and capillary-electrophoresis in order to study POLE mutations in endometrial carcinomas.

**Methodology** A total of 76 patients diagnosed with endometrial cancer with available histological and molecular classification, were selected, obtaining a paraffin block with adequate viability and tumor representation. From each case, eight sections of 10 μm thickness were obtained, subsequently isolating DNA. Those samples with a concentration over 10ng/μl were tested by MODAPLEX. Any positive result was reconfirmed by Sanger sequencing.

**Result(s)** A total of 76 samples were finally submitted to the test: 10 were POLE mutated, 20 CNL, 29 CNH and 20 MSI. MODAPLEX identified a total of 11 samples with mutations in POLE: V411L(4), P286R(3), S297F(1), A456P(1), T278M(1) and L424V(1). All these mutations were located in the exonuclease domain and had a functional impact on the protein. Ten mutations were confirmed afterwards by Sanger sequencing, except one sample harboring the T278M mutation, which were considered a false positive result of MODAPLEX.

MODAPLEX demonstrated a sensitivity of 100%, a specificity of 98.5%, a Positive Predictive Value of 90.9% and a Negative of 100%.

**Conclusion** MODAPLEX is a promising technology still in development that allows the determination of the main ‘Hot-spot’ mutations in POLE gene in a fast, practical and efficient way.

Following a Single-Gene approach and in this clinical context, this technology could compete with Sanger sequencing for the study of POLE mutations.

This test could emerge as a valid and fast alternative to Next – Generation Sequencing, especially in those centers where they do not have access to massive sequencing techniques.