Molecular classification yielded 6 (9.1%) POLEmut, 17 (25.8%) MMR-D, 29 (43.9%) NSMP and 14 (21.2%) p53abn. Between POLEmut, 3 (50%) were low-grade endometrioid, while the rest were high-grade. 2 (14.3%) of p53abn were low-grade endometrioid, 2 (14.3%) high-grade endometrioid and 10 (71.4%) non-endometrioid histotype. Regarding MMR-D cases, loss of MLH1 and PMS2 expression was observed in 11/17 (64.7%), of those MLH1 promoter hypermethylation was identified in 7/11 (63.1%). Rest of cases were referred to germline testing, although no germline mutations have been identified yet.

According to final prognostic group, 25/66 (37.9%) were low risk, 9/66 (13.6%) intermediate risk, 7/66 (10.6%) high-intermediate risk, 17/66 (25.8%) high risk. Between low-risk patients, 3 would have classified as high risk if molecular classification had not been taken account, and 2 between high-risk would have classified as low-risk. Consequently, 7.6% of cases were reclassified and adjuvant therapy adjusted.

Conclusion Implementation of molecular classification is feasible in routine clinical practice. POLEmut and p53abn are identified not only in high-grade cases but also in low-grade. Molecular classification leads to a change in adjuvant therapy in a non-negligible proportion of cases.