Conclusion MLH1 promoter methylation analysis would play a valuable role as a clinical biomarker.

**Reference**
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**Methodology** For 240 patients with endometrial cancer who underwent hysterectomy at Seoul National University Bundang Hospital from 2006 to 2013, POLE gene sequencing and IHC for hMLH1, hMSH2, hMSH6, PMS2 and p53 were performed. For 155 patients with POLE or CN-low subtype, clinicopathologic factors were abstracted from medical records, and cyclin B1 IHC was performed using primary monoclonal antibody (RBT-B1, 1:50; LSBio, Seattle, WA, USA). Cyclin B1 expression level (cyclin B1 score) was determined by intensity of staining. Decision tree classifiers encompassing clinicopathologic factors and cyclin B1 IHC were constructed using accuracy from 5-fold cross-validation. Hyperparameters (max_depth, min_samples_leaf) were tuned using GridSearch.

**Results** 24 with POLE and 131 with CN-low were included. Median age was 56 and median weight was 61.6kg. Number of patients with stage 3, 4 were 14 and those with LVSI were 41. In the final model, weight (cutoff 54.3kg) and cyclin B1 IHC (cutoff score 1.5) were selected. With the POLE subtype, the mean validation accuracy were 84%. The model divided the whole cohort into 3 groups. Of 25 patients with weight > 54.3 kg and cyclin B1 score > 1.5 (group 2), 8 patients of POLE or CN-low subtype were included (40%); Of 51 patients with weight > 54.3 kg and cyclin B1 score > 1.5 (group 2), 8 patients with POLE subtype were included (16%); Of 48 patients with weight > 54.3 kg and cyclin B1 score ≤ 1.5 (group 3), 1 patients with POLE subtype were included (2%).

**Conclusion** POLE vs. CN-low cannot be distinguished but can be enriched using clinicopathologic factors and cyclin B1 IHC.