

# Multigene Panel Testing in Gynaecological Malignancies: A study in a Cohort of over 1000 patients

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## INTRODUCTION

Gynaecological malignancies, specifically ovarian and endometrial cancer, are often attributed to an inherited predisposition. A variety of genes has been associated with oncogenesis; thus, **multigene panel testing** is recommended to patients. Detecting pathogenic alterations can lead to proactive measures such as improved screening and preventive actions, or redefinition of their **clinical management** through personalized health care.

## MATERIALS & METHODS

Between 2020 and 2025, over **1000 women** were referred for genetic testing at GeneKor Medical S.A., with a diagnosis of ovarian and/or endometrial cancer. Next Generation Sequencing was performed in DNA extracted from all patients' peripheral blood, targeting 52 genes. Analysis was performed for both single nucleotide variations (**SNVs**) and copy number variations (**CNVs**), to detect pathogenic/likely pathogenic variants in cancer susceptibility genes.

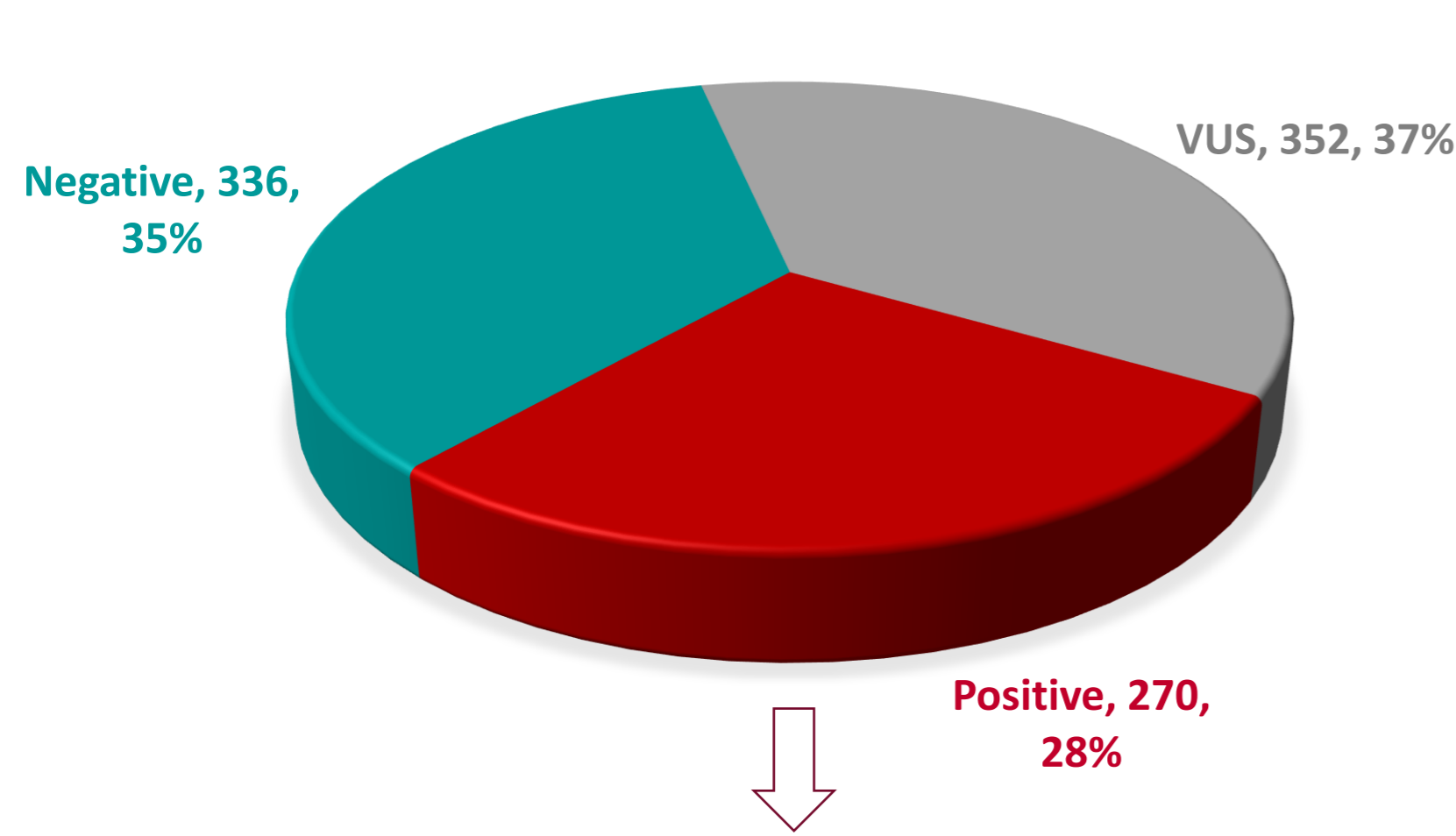
## AIM

Detection of pathogenic/likely pathogenic variants in cancer susceptibility genes.

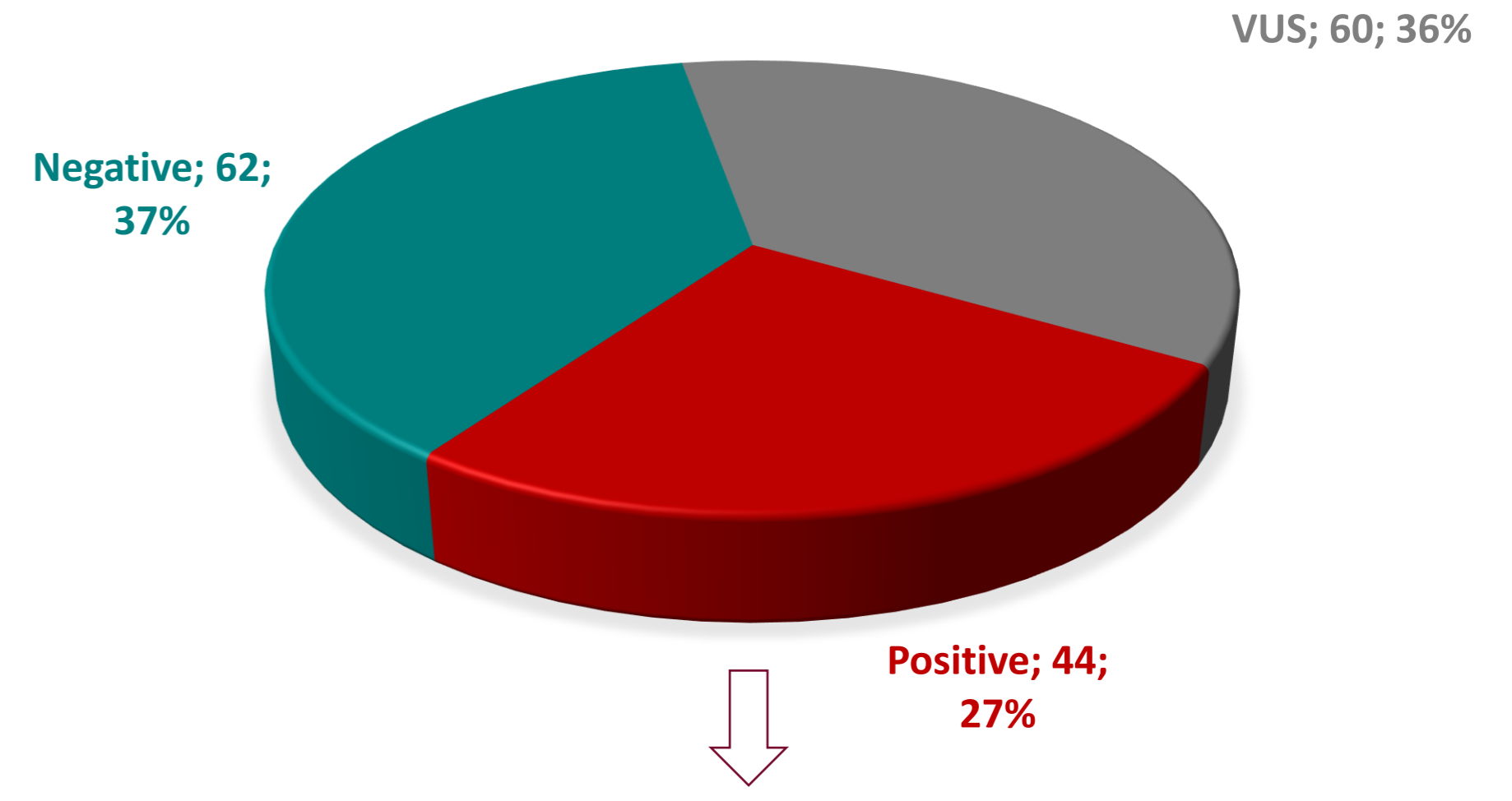
## RESULTS

- Among patients tested, **958** had malignancy of the **ovaries**, while **166** were diagnosed with **endometrial cancer**. In **28%** and **27%** of cases, respectively, a pathogenic/likely pathogenic variant was identified.

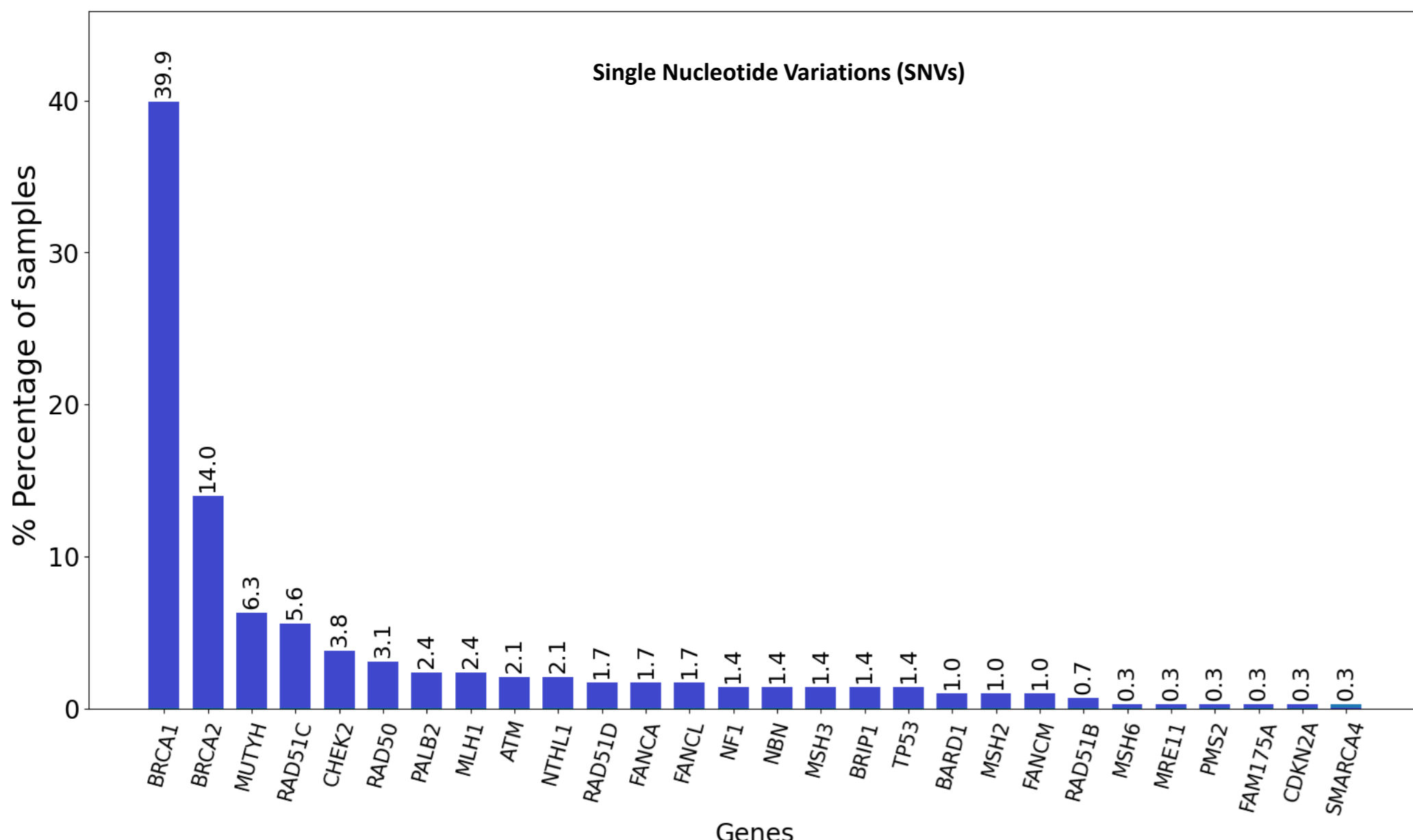
Ovarian Cancer Cases



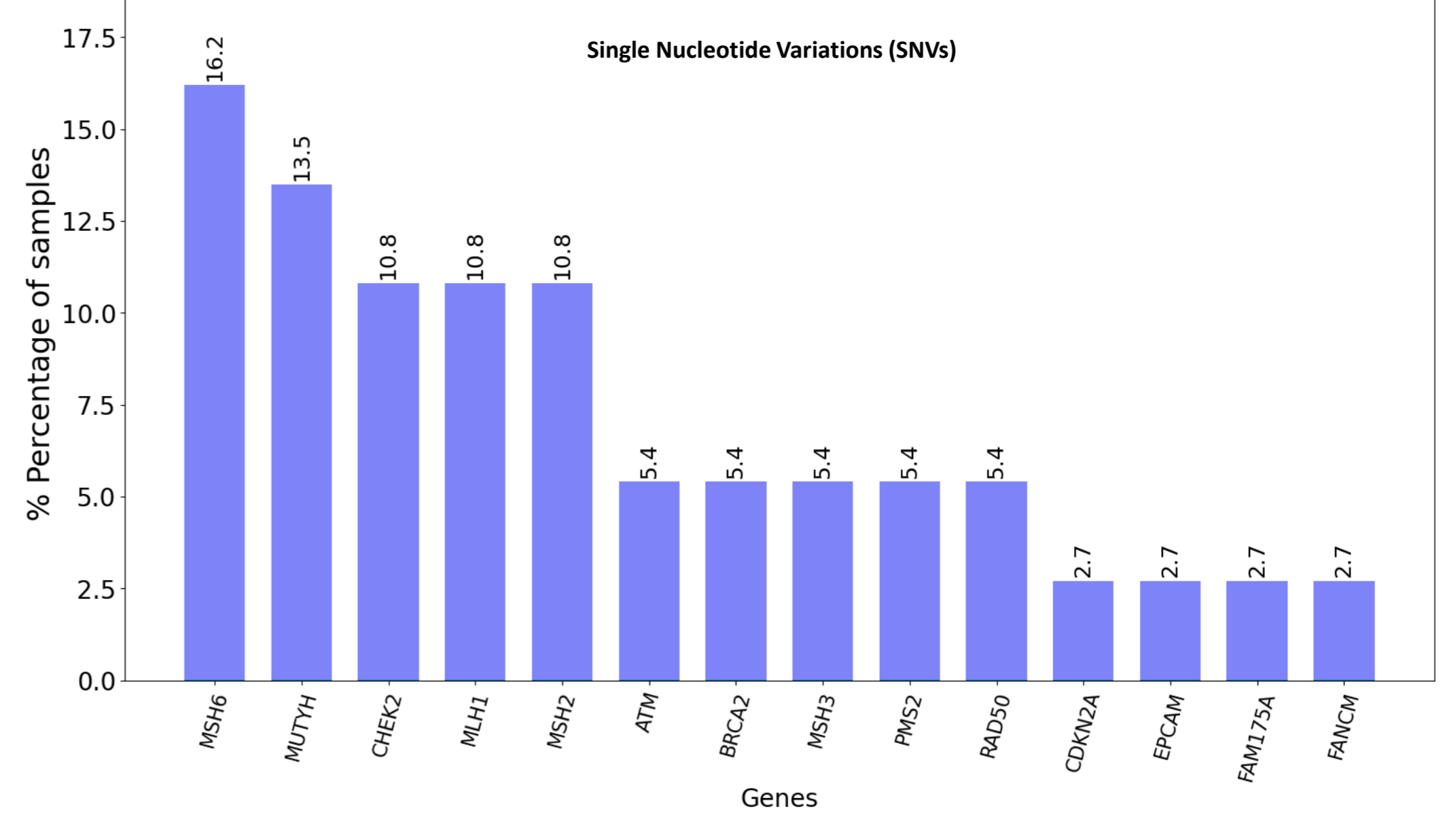
Endometrial Cancer Cases



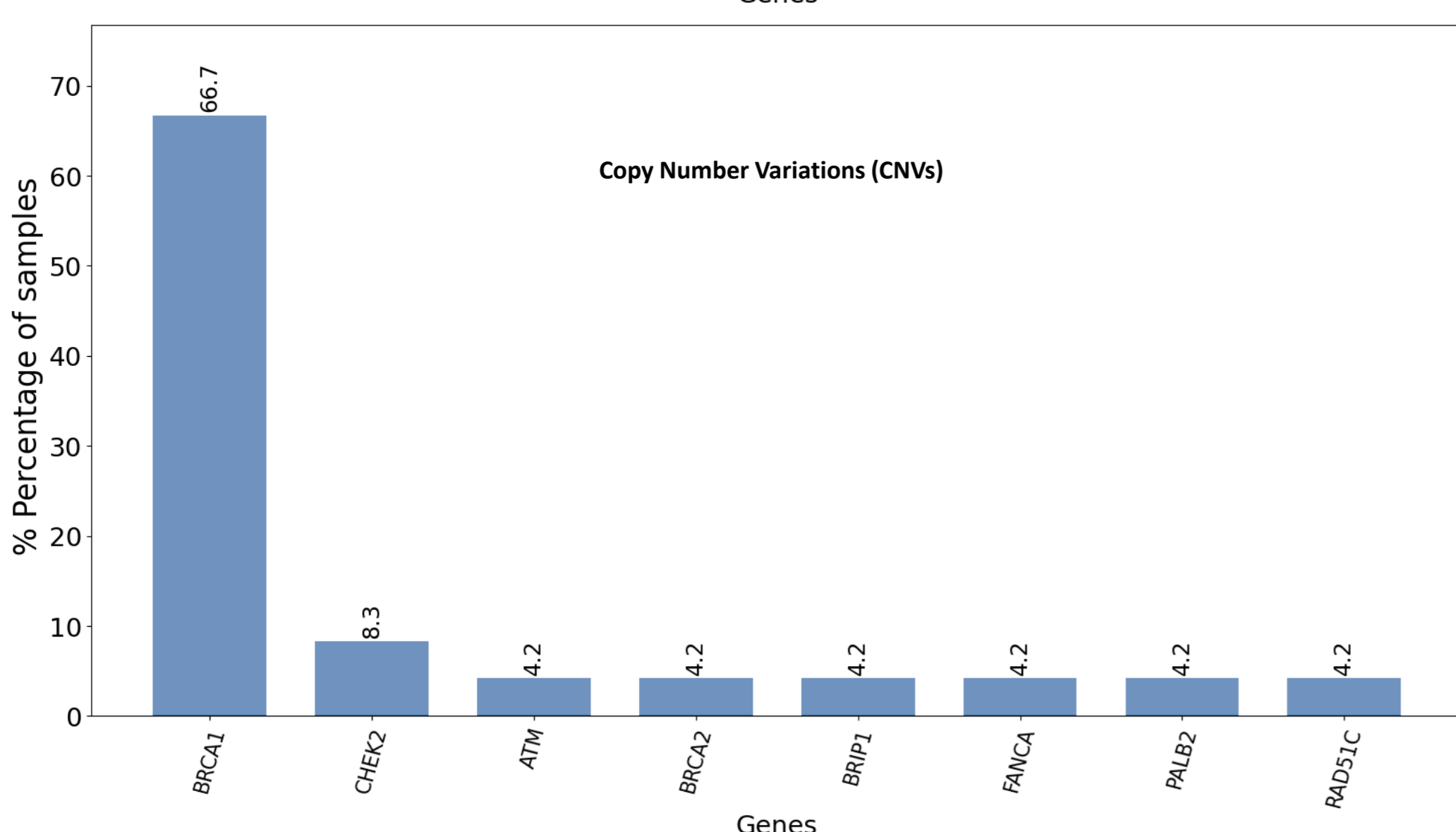
Single Nucleotide Variations (SNVs)



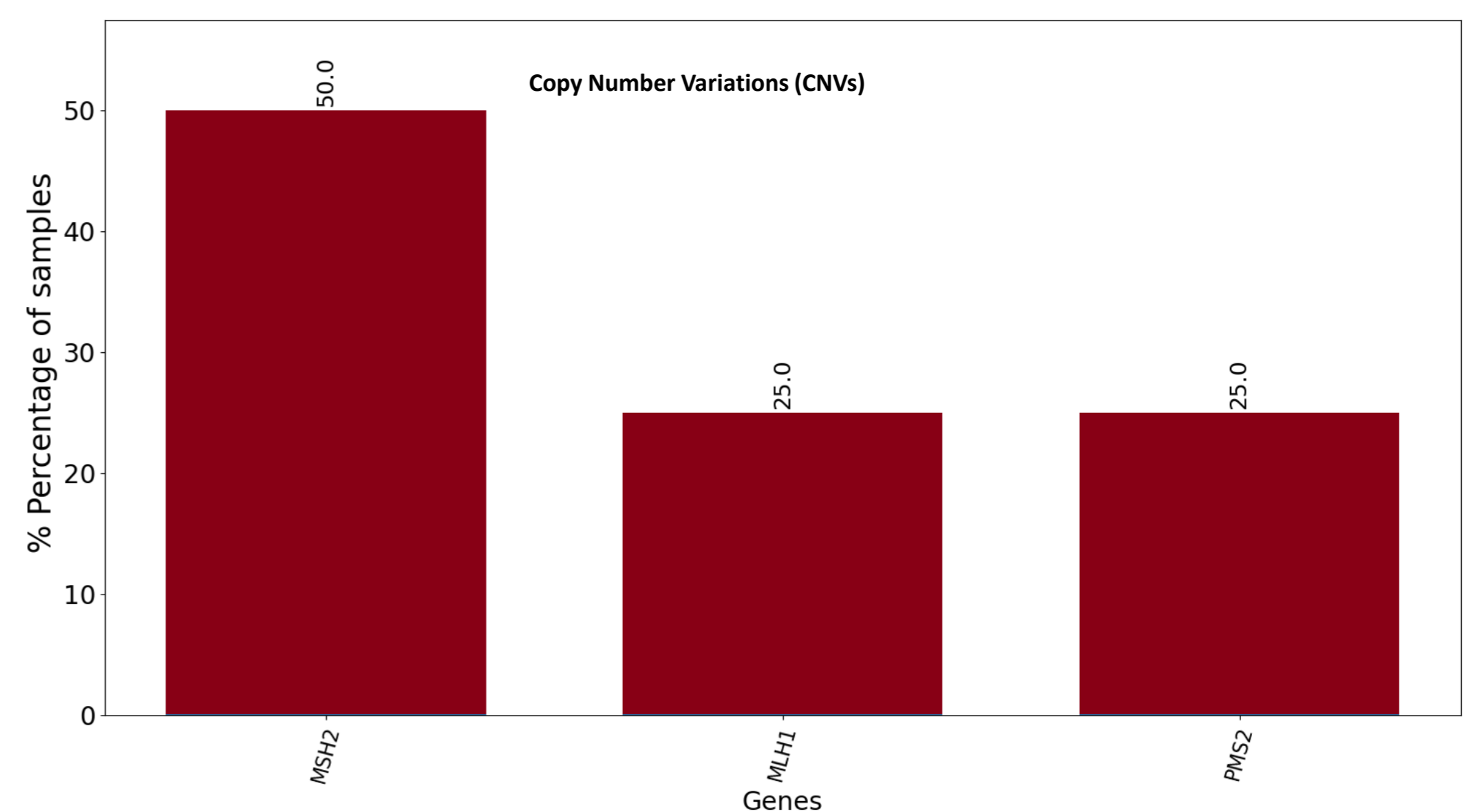
Single Nucleotide Variations (SNVs)



Copy Number Variations (CNVs)



Copy Number Variations (CNVs)



In ovarian malignancies, among patients harboring pathogenic/likely pathogenic alterations, the most common altered genes were **BRCA1** (39.9%), **BRCA2** (14.0%), **RAD51C** (5.6%), **PALB2** (2.4%), **MLH1** (2.4%), **RAD51D** (1.7%), **BRIP1** (1.4%) for SNVs and **BRCA1** for CNVs.

- Alterations were also identified in **clinically important genes** that have not yet been associated with the development of gynaecological tumors (e.g. **TP53**, **CDH1**, **CDKN2A**).

In endometrial cancer cases, among patients harboring pathogenic/likely pathogenic alterations, SNVs were identified in clinically important genes like **MSH6** (16.2%), **MLH1** (10.8%), **MSH2** (10.8%), **BRCA2** (5.4%), **PMS2** (5.4%), **EPCAM** (2.7%). CNVs were mainly found in **MSH2**, followed by **MLH1** and **PMS2**.

## CONCLUSIONS

Comprehensive multigene genetic testing is necessary for appropriate clinical management of pathogenic variants' carriers. Alterations detected in gynaecological tumors may be associated with other malignancies as well, thus giving the opportunity to physicians to manage patients holistically.

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## ACKNOWLEDGEMENTS



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