

# 3053eP-High-Risk cancer susceptibility genes mutation carriers' compliance with surgical risk reduction for breast and ovarian cancer

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## Background

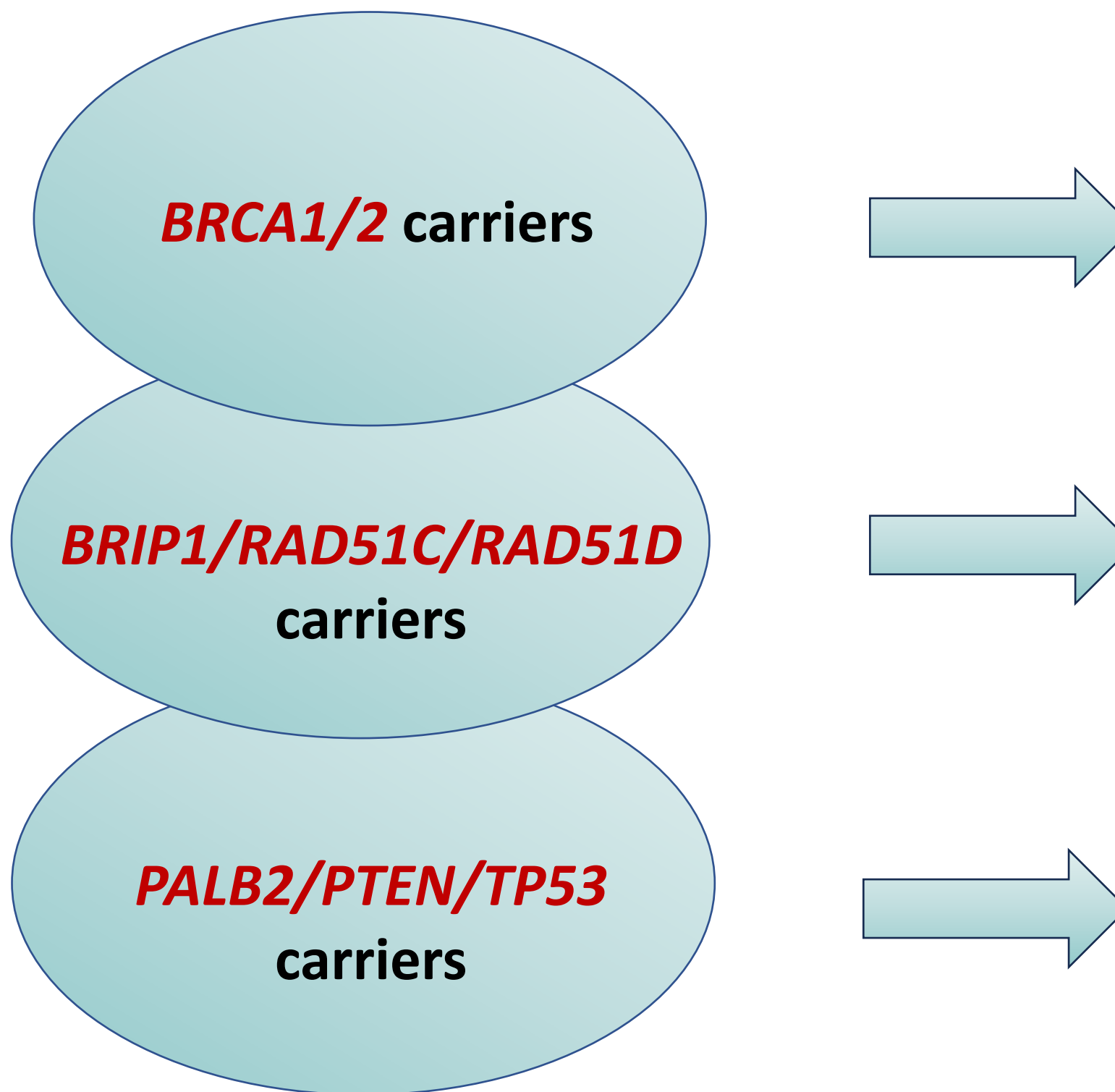
Identifying pathogenic/likely pathogenic variants in high-risk cancer genes is key to cancer risk management. Prophylactic surgeries like RRM and RRSO are guideline-recommended options. This study aims to provide real-world evidence on their clinical implementation.

## Methods

Between 2020 and 2025, 203 women referred for genetic testing at Genekor Medical S.A., were detected with P/LP variants in cancer susceptibility genes, for which risk-reducing surgical options are either recommended or considered for discussion. Referring clinicians were invited to complete a questionnaire to assess whether prophylactic surgical options had been discussed, if the patients had agreed to undergo such procedures, and whether the surgeries have already been performed or postponed.

## Results

Among the individuals referred for genetic testing, 168(83%) were referred following a cancer diagnosis, while 35(17%) were unaffected individuals referred due to a family history.



	Discussed	Agreed
RRM	113/153 (74%)	73/113 (65%)
RRSO	78/153 (51%)	60/78 (77%)
RRSO+Hysterectomy	16/78 (21%)	10/16 (63%)

	Discussed	Agreed
RRM	5/19 (26%)	2/5 (40%)
RRSO	9/19 (47%)	7/9 (78%)

	Discussed	Agreed
RRM	21/31 (68%)	9/21 (43%)
RRM/RRSO	5/31 (16%)	3/5 (60%)

In all cases, 22 individuals although agreed to proceed with RRM and/or RRSO, decided to postpone the procedure

## Conclusions

This study highlights the high awareness and acceptance of surgical management demonstrating the adherence to the recommendations. Age under 35 years and receiving therapy at the time of genetic testing were significant factors in lowering risk reduction strategies (RRSO and hysterectomy) performance rates. **Stage IV cancer (45%), comorbidities (15%) and preceded surgical operations (6%)** were the main reasons for not discussing surgical intervention.

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**Figure 1.** Clinically important pathogenic/Likely pathogenic findings on DNA level identified in 203 patients who underwent hereditary genetic testing in 52 cancer associated genes

