Multi-gene Panel Testing for Prostate Cancer: What Have We Learned So Far?

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BACKGROUND

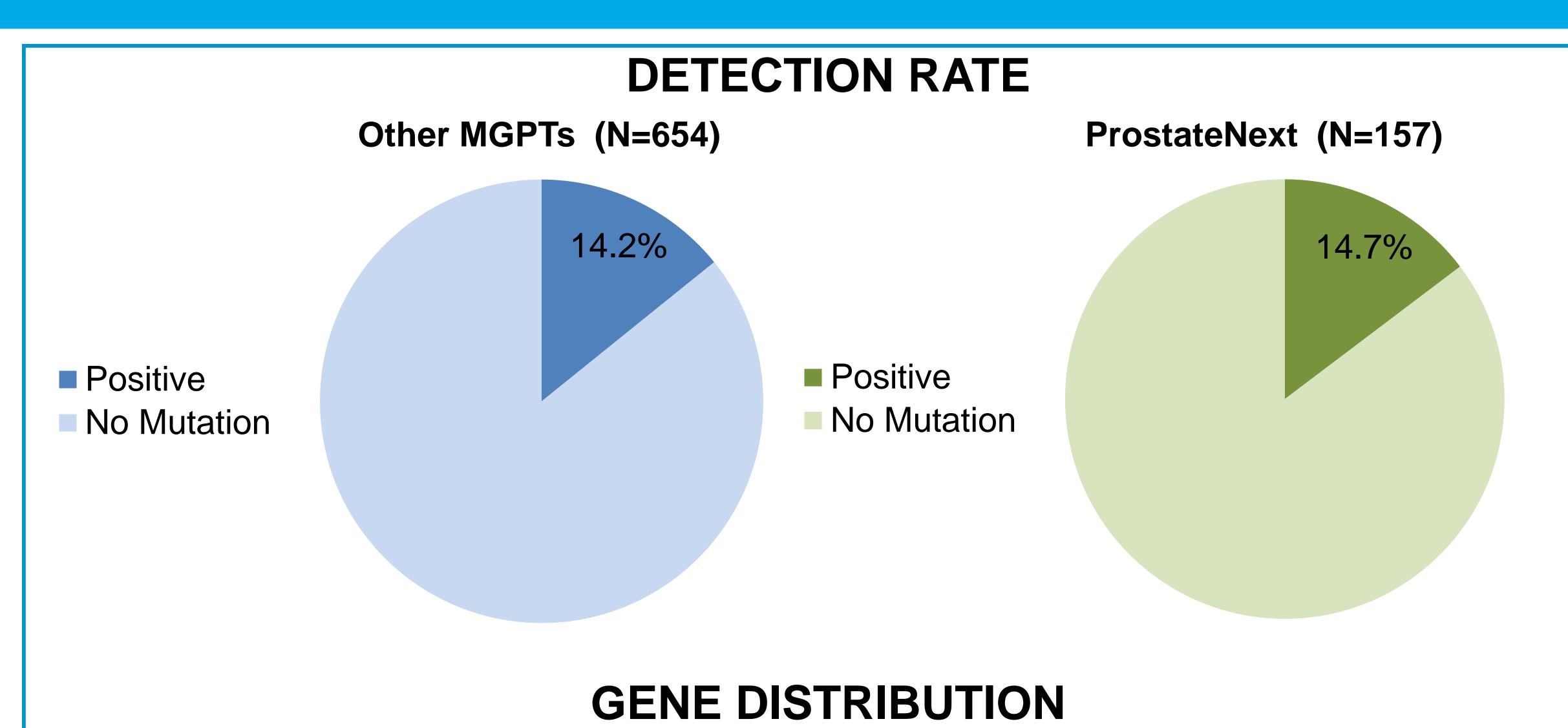
- Prostate cancer is the most common cancer in men
- Current genetic testing guidelines for prostate cancer are limited to BRCA1/2
- Recent studies have detected multiple germline mutations in prostate cancer patients¹⁻³
 - ➤ Including BRCA1/2, Lynch syndrome genes, HOXB13, ATM, CHEK2 and others
- This study aims to describe the findings of ProstateNext, a hereditary prostate cancer multi-gene panel test (MGPT) and compare them to the results of other MGPTs in prostate cancer patients

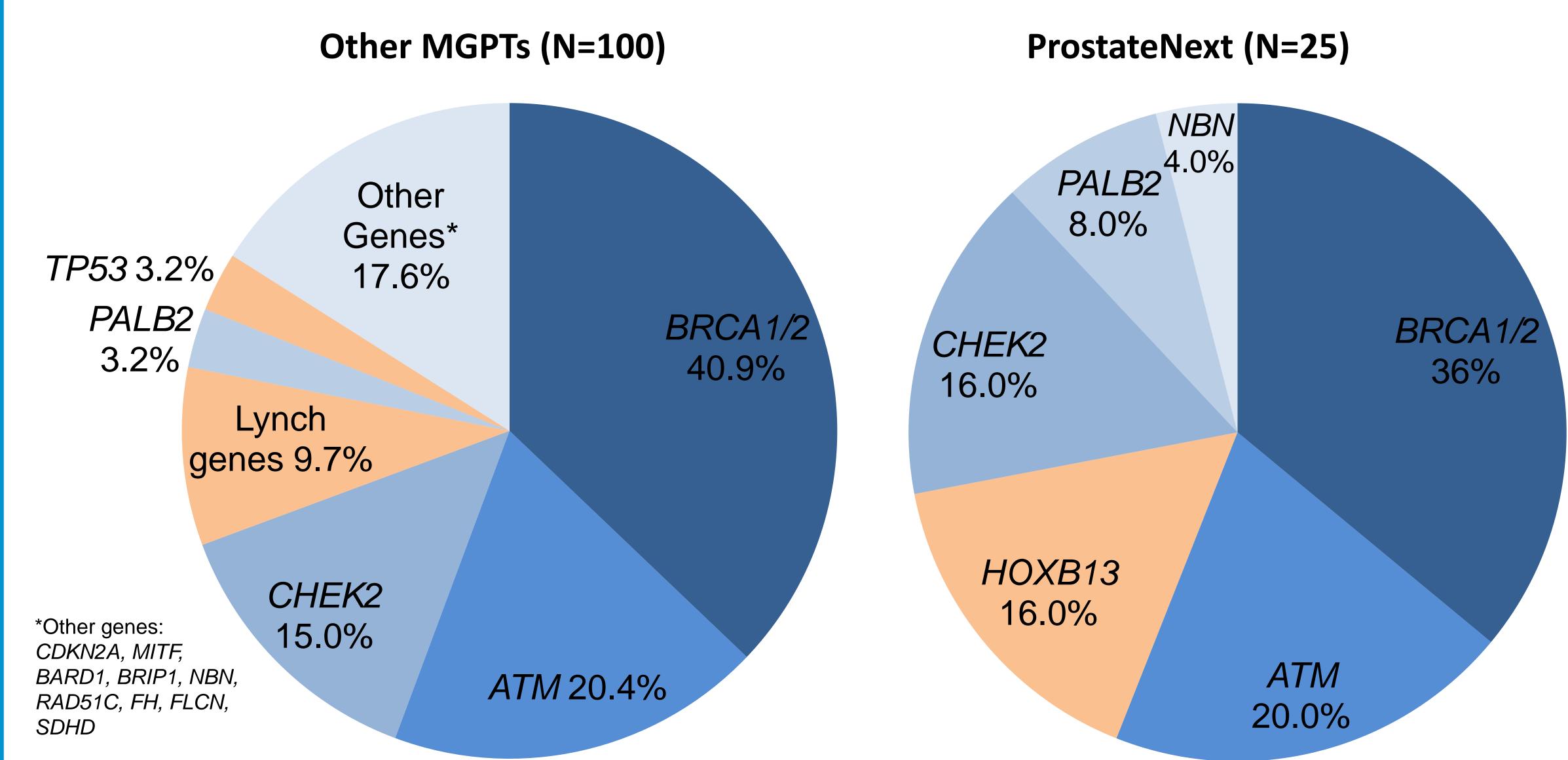
METHODS

- Clinical histories and molecular results for cases submitted for ProstateNext from 09/2016-03/2017 were retrospectively reviewed
- Comparisons were made to prostate cancer cases tested with other MGPTs from 06/2013-05/2016

DEMOGRAPHICS

- 8 females and 149 males underwent genetic testing with ProstateNext
- 143 individuals diagnosed with ≥1 type of cancer; 138 with prostate cancer
- Average age of prostate cancer was
 58y; 55y for those who tested positive





ProstateNext Detection Rate by Referral Indication

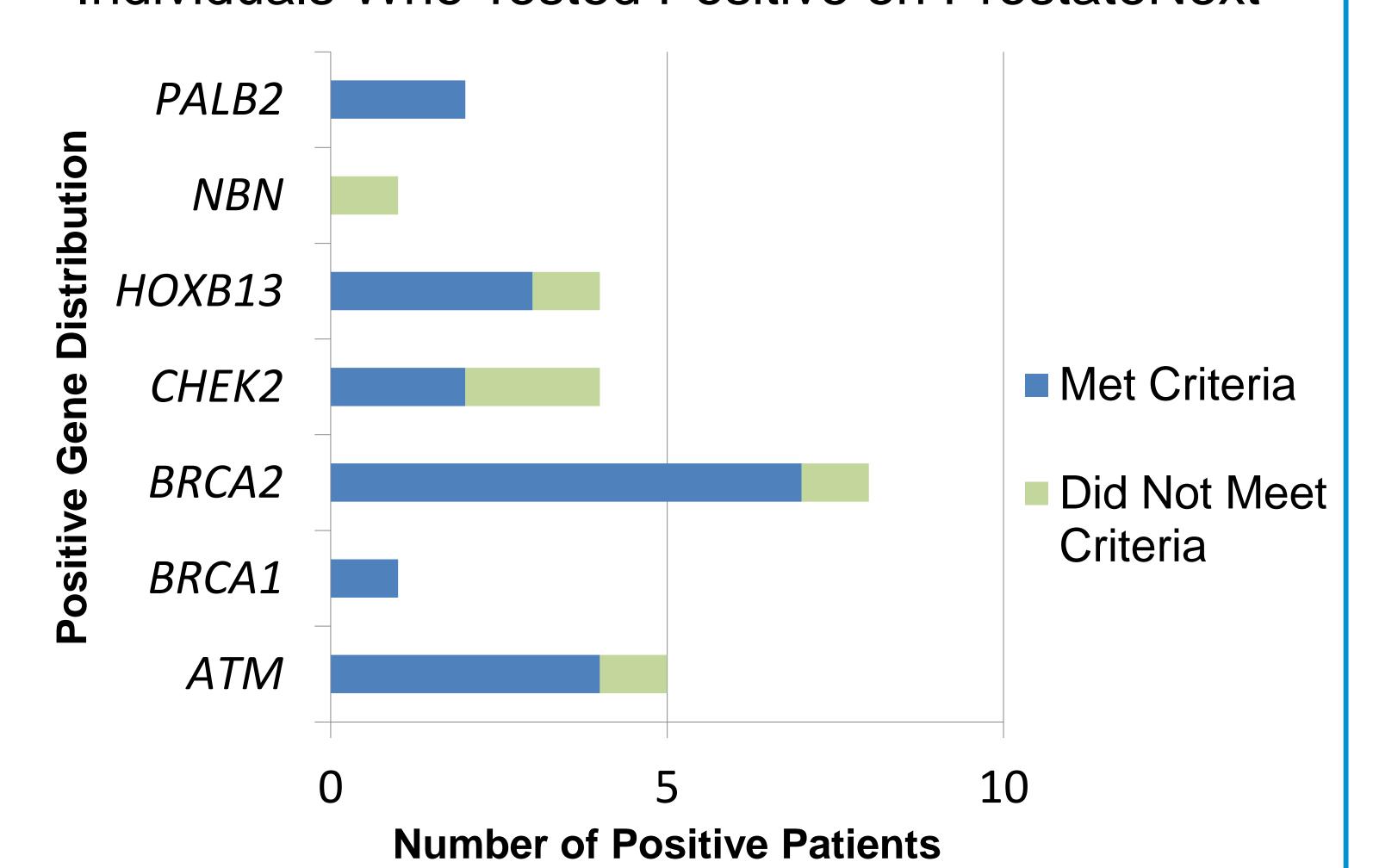
	Personal History of Prostate Cancer Only (N=16)	Family History of Prostate and/or Other Cancer Only (N=16)	Personal and Family History of Prostate and/or Other Cancer (N=125)
Positive	25.0% (N=4)	18.7% (N=3)	13.6% (N=17)
Negative	56.3% (N=9)	75.0% (N=12)	72.8% (N=91)
VUS	18.7% (N=3)	6.3% (N=1)	13.6% (N=17)

Gleason Score and Metastatic Disease Status Of Men With Prostate Cancer Who Underwent ProstateNext

	Average Gleason Score (N=113)	Known Metastatic Disease (N=37)
Positive (N=22)	8.0 (N=20)	31.8% (N=7)
Negative (N=97)	7.6 (N=79)	25.8% (N=25)
VUS (N=19)	7.4 (N=14)	26.3% (N=5)

*Gleason score and metastatic disease status were only available for a subset of cases in each group as denoted by the Ns.

Evaluating NCCN® Criteria for BRCA1/2 Testing In Individuals Who Tested Positive on ProstateNext



TAKE-HOME POINTS

- The mutation detection rate was >14% in both groups
- HOXB13 accounted for 16% of positive patients; 2.5% of all patients tested with ProstateNext
- Lynch genes and *TP53* weren't identified with ProstateNext, most likely due to smaller numbers and mutations in these genes being more rare in prostate cancer patients
- Gleason score and metastatic disease were highest in the positive patients, which is consistent with previous reports
- As 25% of positive patients did not meet NCCN® testing criteria for *BRCA1/*2, expansion of guidelines should be considered

REFERENCES

- 1. Pritchard CC, et al. N Engl J Med., 2016.
- 2. Giri VN, *et al.* <u>Semin Oncol</u>., 2016.

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3. Giri VN , *et al.* 2017. <u>Precis Oncol</u>., 2017.