

Pathogenic variants associated with prostate cancer ethnic disparities



Kazzem Gheybi¹, Jue Jiang¹, Pam Soh¹, Weerachai jaratlerdsiri¹, Riana Bornman², Vanessa Hayes^{1*}

¹ Ancestry and Health Genomics Laboratory, Charles Perkins Centre, School of Medical Sciences, University of Sydney, Australia ² School of Health Systems and Public Health, University of Pretoria, Pretoria, South Africa

Germline testing panels for prostate cancer are mainly based on studies on European ancestral populations, while African ancestry is a significant risk factor for advanced Prostate cancer. There is no agreement about prostate cancer germline testing of people with an African ancestry due to lack of data.

Black South African men are at 2.1fold increased risk for advanced disease compared with African Americans. Here we aimed to determine if current germline screening panels hold clinical benefit for men from southern Africa.



Germline testing was performed for 20 of the most common genes in available prostate cancer genetic testing panels on 113 southern African and 53 **European prostate** cancer cases and the results were compared

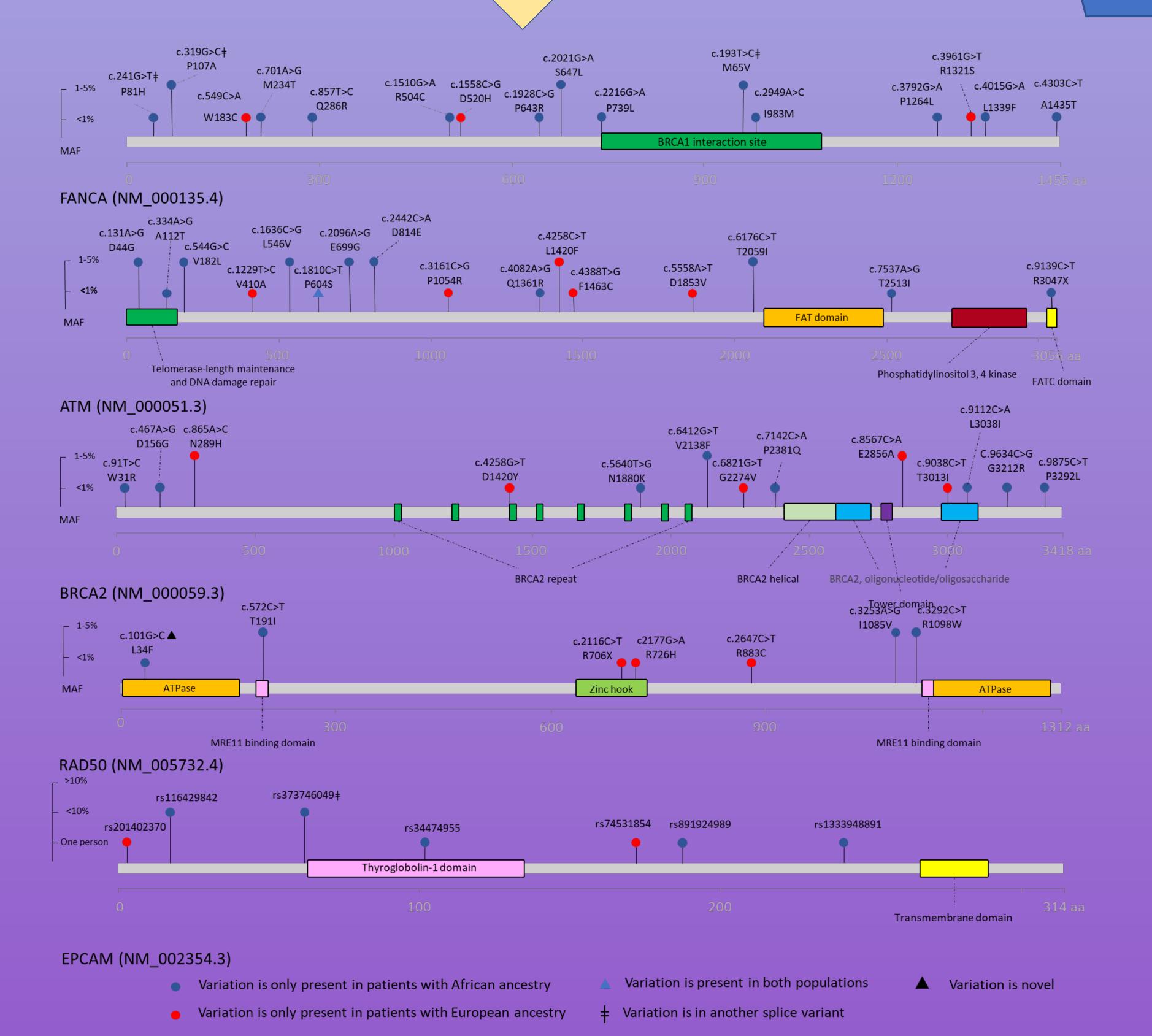
NBN APC **FANCA**

BRCA1 BRCA2 CHEK2 **EPCAM** HOXB13 MLH1 MSH2 MSH6 PMS2 *TP53* BRIP1 PALB2 RAD51C RAD51D **MUTYH** RAD50

ATM



Predicted deleterious variants (PDV) in genes with higher likelihood of harbouring a variant among Africans



Our findings showed that using the current germline testing panels for southern African patient has some merits. However, more studies need to be conducted among sub-Saharan Africans to develop germline testing panels which are more aligned to the genetic profile of this population

119 PDVs were found and only 2 were common between the two populations

Known pathogenic variants: 6 for the 53 European

VS

4 for the 113 Africans

Known pathogenic variants were found in ATM, TP53, BRCA2 and CHEK2 genes in Black southern African Patients

No potentially oncogenic variants in HOXB13, BRCA1, NBN and **MSH2** for Africans

> Several uncertain significance and 4 novel variant among Africans

