

CORRECTION

Open Access



# Correction to: Prevalence of *RECQL* germline variants in Pakistani early-onset and familial breast cancer patients

Muhammad Usman Rashid<sup>1,2\*</sup>, Noor Muhammad<sup>1</sup>, Faiz Ali Khan<sup>1</sup>, Umara Shehzad<sup>1</sup>, Humaira Naeemi<sup>1</sup>, Naila Malkani<sup>3</sup> and Ute Hamann<sup>2\*</sup>

**Correction to: *Hered Cancer Clin Pract* 18, 25 (2020)**  
<https://doi.org/10.1186/s13053-020-00159-6>

Following publication of the original article [1], a typesetting error was identified. Figure 1 was not published in full. The complete Fig. 1 is given in this correction article and the original article [1] has been corrected.

#### Author details

<sup>1</sup>Department of Basic Sciences Research, Shaukat Khanum Memorial Cancer Hospital and Research Centre (SKMCH&RC), 7A, Block R3, Johar Town, Lahore, Punjab 54000, Pakistan. <sup>2</sup>Molecular Genetics of Breast Cancer, German Cancer Research Center (DKFZ), Im Neuenheimer Feld 580, 69120 Heidelberg, Germany. <sup>3</sup>Department of Zoology, Government College University, Lahore, Pakistan.

Published online: 07 January 2021

#### Reference

1. Rashid MU, Muhammad N, Khan FA, et al. Prevalence of *RECQL* germline variants in Pakistani early-onset and familial breast cancer patients. *Hered Cancer Clin Pract.* 2020;18:25. <https://doi.org/10.1186/s13053-020-00159-6>.

The original article can be found online at <https://doi.org/10.1186/s13053-020-00159-6>.

\* Correspondence: [usmanr@skm.org.pk](mailto:usmanr@skm.org.pk); [u.hamann@dkfz-heidelberg.de](mailto:u.hamann@dkfz-heidelberg.de)

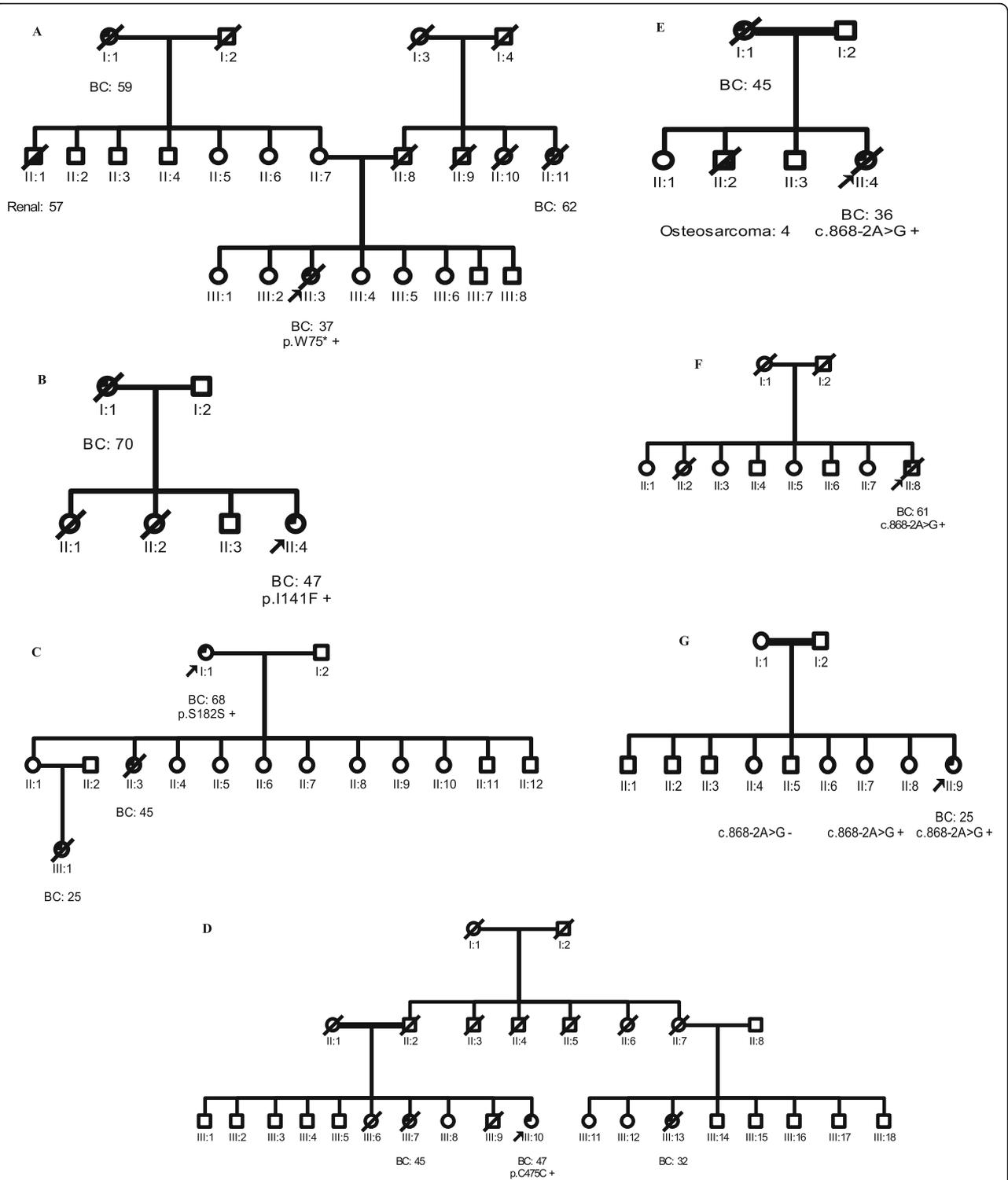
<sup>1</sup>Department of Basic Sciences Research, Shaukat Khanum Memorial Cancer Hospital and Research Centre (SKMCH&RC), 7A, Block R3, Johar Town, Lahore, Punjab 54000, Pakistan

<sup>2</sup>Molecular Genetics of Breast Cancer, German Cancer Research Center (DKFZ), Im Neuenheimer Feld 580, 69120 Heidelberg, Germany

Full list of author information is available at the end of the article



© The Author(s). 2021 **Open Access** This article is licensed under a Creative Commons Attribution 4.0 International License, which permits use, sharing, adaptation, distribution and reproduction in any medium or format, as long as you give appropriate credit to the original author(s) and the source, provide a link to the Creative Commons licence, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons licence, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons licence and your intended use is not permitted by statutory regulation or exceeds the permitted use, you will need to obtain permission directly from the copyright holder. To view a copy of this licence, visit <http://creativecommons.org/licenses/by/4.0/>. The Creative Commons Public Domain Dedication waiver (<http://creativecommons.org/publicdomain/zero/1.0/>) applies to the data made available in this article, unless otherwise stated in a credit line to the data.



**Fig. 1** Pedigrees of breast cancer patients with *RECQL* variants. **a** Family 282 carrying the pathogenic variant p.W75\*. **b-d** Families 565, 649, and 625 carrying the VUS p.I141F, p.S182S, and p.C475C, respectively. **e-g** Families 471, 577 and 595 carrying the benign variant c.868-2A > G. Circles are females, squares are males, and a diagonal slash indicates a deceased individual. Symbols with filled left upper quadrant: unilateral breast cancer. Symbols with filled right lower quadrant: cancer other than breast, the name of that cancer is indicated. Double line between spouses: consanguineous marriage. Identification numbers of individuals are below the symbols. The index patient is indicated by an arrow. BC: breast cancer. The numbers following these abbreviations indicate age at cancer diagnosis. +: carrier, -: non-carrier