

AUTHOR CORRECTION OPEN

Author Correction: Breast-cancer-specific mortality in patients treated based on the 21-gene assay: a SEER population-based study

Valentina I Petkov¹, Dave P Miller², Nadia Howlader¹, Nathan Gliner², Will Howe³, Nicola Schussler³, Kathleen Cronin¹, Frederick L Baehner^{2,4}, Rosemary Cress⁵, Dennis Deapen⁶, Sally L Glaser^{7,8}, Brenda Y Hernandez⁹, Charles F Lynch¹⁰, Lloyd Mueller¹¹, Ann G Schwartz¹², Stephen M Schwartz¹³, Antoinette Stroup^{14,15}, Carol Sweeney¹⁶, Thomas C Tucker¹⁷, Kevin C Ward¹⁸, Charles Wiggins¹⁹, Xiao-Cheng Wu²⁰, Lynne Penberthy¹ and Steven Shak²

npj Breast Cancer (2018)4:17; doi:10.1038/s41523-018-0069-3

Correction to: *npj Breast Cancer*; https://doi.org/10.1038/npjbcancer.2016.17, Published online 8 June 2016

In the original version of the published article, line three of the third paragraph of the methods stated "Excluding patients with micrometastatic disease, the 5-year BCSM for patients with Recurrence Score results <18 and 1–3 positive nodes (n=2,617) was 1.3% (95% CI, 0.6–2.9%)." To improve clarity this statement has been replaced with "Excluding patients with micrometastatic disease, there were 2,617 patients with 1–3 positive nodes. Of these, 1,487 also had Recurrence Score results <18 with 5-year BCSM of 1.3% (95% CI, 0.6–2.9%)." The original version of the published article also contained an error in the second sentence of the Figure 2 legend describing the mutation status of the patient population examined. The sentence in the original published version of the Article stated "Patients with HR+, HER2-positive, node-negative..." this has been changed to "Patients with HR+,

HER2-negative, node-negative...". This has been corrected in the PDF and HTML versions of this paper.

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 license, and indicate if changes were made. The images or other third party material in this article are included in the article's Creative Commons license, unless indicated otherwise in a credit line to the material. If material is not included in the article's Creative Commons license 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 license, visit http://creativecommons.org/licenses/by/4.0/.

© The Author(s) 2018

¹National Cancer Institute, Bethesda, MD, USA; ²Genomic Health, Inc., Redwood City, CA, USA; ³IMS, Inc., Calverton, MD, USA; ⁴University of California, San Francisco, CA, USA; ⁵Public Health Institute, Cancer Registry of Greater California, Sacramento, CA, USA; ⁶University of Southern California, Los Angeles, CA, USA; ⁷Cancer Prevention Institute of California, Fremont, CA, USA; ⁸Stanford Cancer Institute, Stanford, CA, USA; ⁹University of Hawaii Cancer Center, Honolulu, HI, USA; ¹⁰Department of Epidemiology, University of Iowa, Iowa City, IA, USA; ¹¹Connecticut Tumor Registry, Connecticut Department of Public Health, Hartford, CT, USA; ¹²Karmanos Cancer Institute, Wayne State University, Detroit, MI, USA; ¹³Cancer Surveillance System, Fred Hutchinson Cancer Research Center, Seattle, WA, USA; ¹⁴Rutgers School of Public Health, Piscataway, NJ, USA; ¹⁵Cancer Institute of New Bersey, New Brunswick, NJ, USA; ¹⁶Utah Cancer Registry, Department of Internal Medicine, and Huntsman Cancer Institute, University of Utah, Salt Lake City, UT, USA; ¹⁷University of Kentucky, Markey Cancer Center, Lexington, KY, USA; ¹⁸Emory University, Atlanta, GA, USA; ¹⁹New Mexico Tumor Registry, University of New Mexico Comprehensive Cancer Center, Albuquerque, NM, USA and ²⁰Louisiana State University Health Sciences Center, New Orleans, LA, USA

Published online: 06 July 2018



