CORRECTION

BMC Cancer

Open Access

Correction to: A genome-wide association study identifies single nucleotide polymorphisms associated with time-to-metastasis in colorectal cancer



Michelle E. Penney¹, Patrick S. Parfrey², Sevtap Savas^{1,3} and Yildiz E. Yilmaz^{1,2,4*}

Correction to: Penney et al. BMC Cancer (2019) 19:133 https://doi.org/10.1186/s12885-019-5346-5

Following publication of the original article [1], the authors reported that Fig. 3 was mistakenly replaced by Fig. 4. The correct Fig. 3 is given below:

Author details

¹Discipline of Genetics, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada. ²Discipline of Medicine, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada. ³Discipline of Oncology, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada. ⁴Department of Mathematics and Statistics, Faculty of Science, Memorial University of Newfoundland, St. John's, Canada.

Received: 3 May 2019 Accepted: 3 May 2019 Published online: 10 May 2019

Reference

 A genome-wide association study identifies single nucleotide polymorphisms associated with time-to-metastasis in colorectal cancer. Penney et al BMC Cancer. 2019;19:133 https://doi.org/10.1186/s12885-019-5346-5.

* Correspondence: yyilmaz@mun.ca
¹Discipline of Genetics, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada
²Discipline of Medicine, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada

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



© The Author(s). 2019 **Open Access** This article is distributed under the terms of the Creative Commons Attribution 4.0 International License (http://creativecommons.org/licenses/by/4.0/), which permits unrestricted use, distribution, and reproduction in any medium, provided 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 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.



Fig. 3 Kaplan-Meier survival function for the most significant SNPs in the multivariable analysis under the (**a**) mixture cure model and (**b**) Cox proportional hazards regression model. n: number of patients in that genotype category; d: number of metastasis in that genotype category. **a** rs5749032 was the only SNP maintaining genome-wide significance after the multivariable analysis using the mixture cure model. In the rs5749032 GG genotype subgroup, the clear plateau at approximately 80% metastasis-free survival probability indicates the existence of a large proportion of long-term metastasis-free survivors. **b** In the rs2327990 TT genotype subgroup, all the patients experienced metastasis within approximately the first two years. Therefore, a standard survival analysis method is appropriate