BMC Cancer

CORRECTION

Open Access

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

Michelle E. Penney[1], Patrick S. Parfrey[2], 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
[1]Discipline of Genetics, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada. [2]Discipline of Medicine, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada. [3]Discipline of Oncology, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada. [4]Department 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

1. 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
[1]Discipline of Genetics, Faculty of Medicine, Memorial University of Newfoundland, St. John's, Canada
[2]Discipline 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

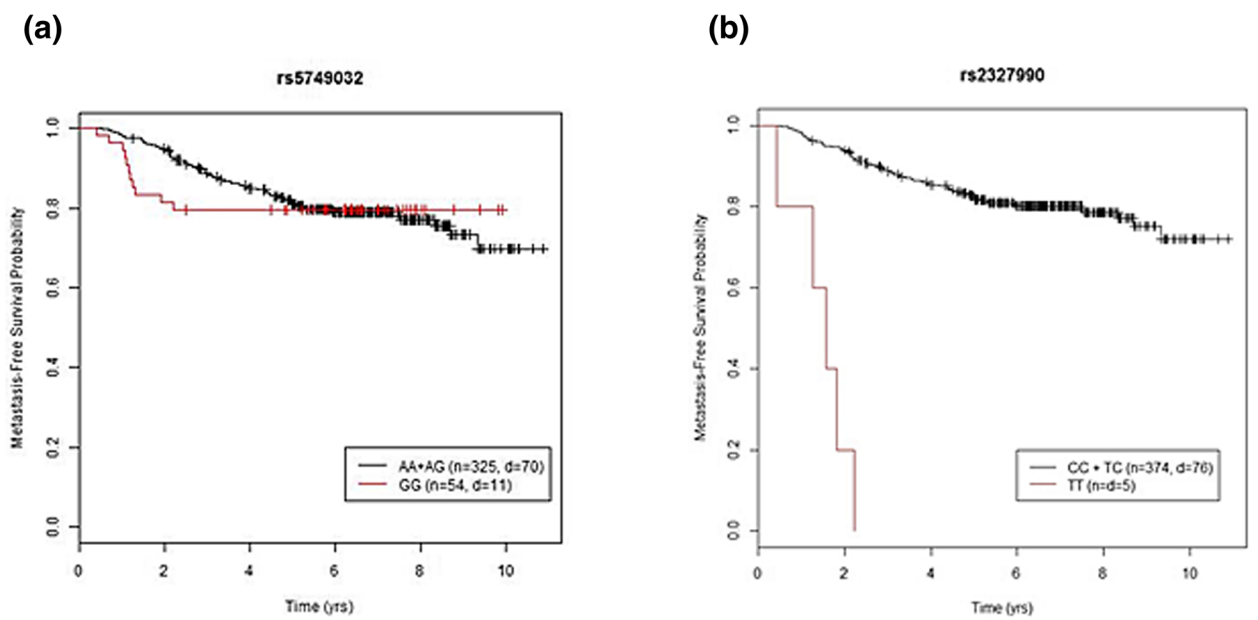

Fig. 3 Kaplan-Meier survival function for the most significant SNPs in the multivariable analysis under the (**a**) mixture cure model and (**b**) Cox proportional hazards regression model. n: number of patients in that genotype category; d: number of metastasis in that genotype category. **a** rs5749032 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