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# Correction: Whole-exome sequencing of *BRCA*-negative breast cancer patients and case–control analyses identify variants associated with breast cancer susceptibility

Ning Yuan Lee<sup>1†</sup>, Melissa Hum<sup>1†</sup>, Aseervatham Anusha Amali<sup>1</sup>, Wei Kiat Lim<sup>1</sup>, Matthew Wong<sup>1</sup>, Matthew Khine Myint<sup>1</sup>, Ru Jin Tay<sup>2</sup>, Pei-Yi Ong<sup>3</sup>, Jens Samol<sup>4,5</sup>, Chia Wei Lim<sup>6</sup>, Peter Ang<sup>7</sup>, Min-Han Tan<sup>2</sup>, Soo-Chin Lee<sup>3,8,9</sup> and Ann S. G. Lee<sup>1,10,11\*</sup>

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Following publication of the original article [1], the authors reported Fig. 1 is not the updated version. The

correct Fig. 1 has been provided in this Correction.

The original article [1] has been corrected.

The original article can be found online at https://doi.org/10.1186/s40246-022-00435-7.

<sup>†</sup>Ning Yuan Lee and Melissa Hum these authors contributed equally

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

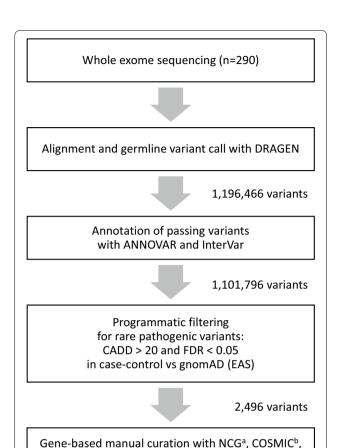


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<sup>\*</sup>Correspondence: gmslimsg@nus.edu.sg

<sup>&</sup>lt;sup>1</sup> Division of Cellular and Molecular Research, Humphrey Oei Institute of Cancer Research, National Cancer Centre Singapore, 11 Hospital Crescent, Singapore 169610, Singapore

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Case-control analysis of 49 variants with an external case cohort (dbGaP)

and other cancer driver gene databases<sup>c,d</sup> for variants in three or more patients

and two external control cohorts
(gnomAD, SG10K)

Fig. 1 Study design for the selection of variants and genes. <sup>a</sup>List of known or candidate cancer genes in the Network of Cancer Genes

49 variants

known or candidate cancer genes in the Network of Cancer Genes [9]. bThe Cancer Gene Census list of the Catalogue of Somatic Mutations in Cancer (COSMIC) [10]. cList of cancer driver genes from Bailey et al. [38]. dList of cancer driver genes inferred with nucleotide context from Dietlein et al. [11]

### **Author details**

<sup>1</sup> Division of Cellular and Molecular Research, Humphrey Oei Institute of Cancer Research, National Cancer Centre Singapore, 11 Hospital Crescent, Singapore 169610, Singapore. <sup>2</sup>Lucence Diagnostics Pte Ltd, 211 Henderson Road, Singapore 159552, Singapore. <sup>3</sup>Department of Hematology-Oncology, National University Cancer Institute, Singapore (NCIS), National University

Health System, 5 Lower Kent Ridge Road, Singapore 119074, Singapore.

<sup>4</sup>Medical Oncology Department, Tan Tock Seng Hospital, 11 Jalan Tan Tock Seng, Singapore 308433, Singapore.

<sup>5</sup>Johns Hopkins University, Baltimore, MD 21218, USA.

<sup>6</sup>Department of Personalised Medicine, Tan Tock Seng Hospital, 11 Jalan Tan Tock Seng, Singapore 308433, Singapore.

<sup>7</sup>Oncocare Cancer Centre, Gleneagles Medical Centre, 6 Napier Road, Singapore 258499, Singapore.

<sup>8</sup>Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, 10 Medical Dr, Singapore 117597, Singapore.

<sup>9</sup>Cancer Science Institute, Singapore (CSI), National University of Singapore, 14 Medical Dr, Singapore 117599, Singapore.

<sup>10</sup>Department of Physiology, Yong Loo Lin School of Medicine, National University of Singapore, 2 Medical Drive, Singapore 117593, Singapore.

<sup>11</sup>SingHealth Duke-NUS Oncology Academic Clinical Programme (ONCO ACP), Duke-NUS Graduate Medical School, 8 College Road, Singapore 169857, Singapore.

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