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CORRECTION

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Correction to: Clinical implications of prospective genomic profiling of metastatic breast cancer patients

Courtney T. van Geelen^{1†}, Peter Savas^{1,2†}, Zhi Ling Teo¹, Stephen J. Luen^{1,2}, Chen-Fang Weng¹, Yi-An Ko¹, Keilly S. Kuykhoven³, Franco Caramia¹, Roberto Salgado¹, Prudence A. Francis^{2,5}, Sarah-Jane Dawson^{1,2,5}, Stephen B. Fox^{1,4,5}, Andrew Fellowes⁴ and Sherene Loi^{1,2,5*} 

Correction to: Breast Cancer Research (2020) 22:91

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Following publication of the original article [1], the authors identified some errors in Fig. 4. The correct figure is given below.

The original article [1] has been corrected.

The original article can be found online at <https://doi.org/10.1186/s13058-020-01328-0>.

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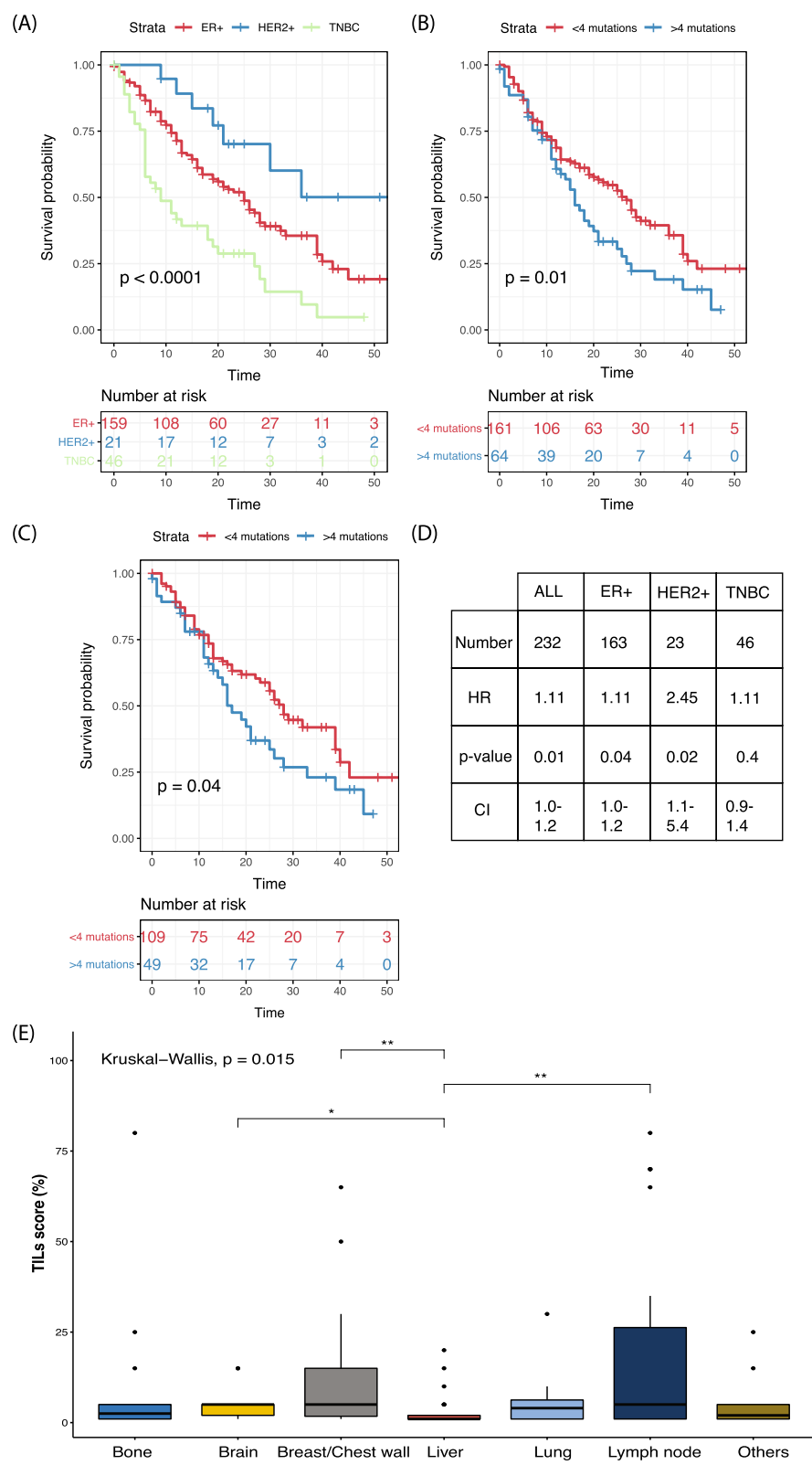


Fig. 4 (See legend on next page.)

(See figure on previous page.)

Fig. 4 Prognostic associations in this cohort of sequenced metastatic breast cancer patients. **a** Overall survival by subtype for all recruited patients ($n = 323$). **b** Overall survival of patients based on the mutational burden of 4 mutations (75th percentile) or more ($n = 234$). **c** Overall survival of ER + HER2 — patients based on the median mutation number of 4 or more ($n = 163$ patients). **d** Table of HR for all patients and all subtypes by mutation number per sample. Patients were excluded if there was incomplete survival information. **e** Spread of TILs across distant metastatic site ($n = 123$)

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1. van Geelen CT, Savas P, Teo ZL, Luen SJ, Weng C-F, Ko Y-A, Kuykhoven KS, Caramia F, Salgado R, Francis PA, Dawson S-J, Fox SB, Fellowes A, Loi S. Clinical implications of prospective genomic profiling of metastatic breast cancer patients. *Breast Cancer Res.* 2020;22:91. <https://doi.org/10.1186/s13058-020-01328-0>.

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