


CORRECTION

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

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**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.

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

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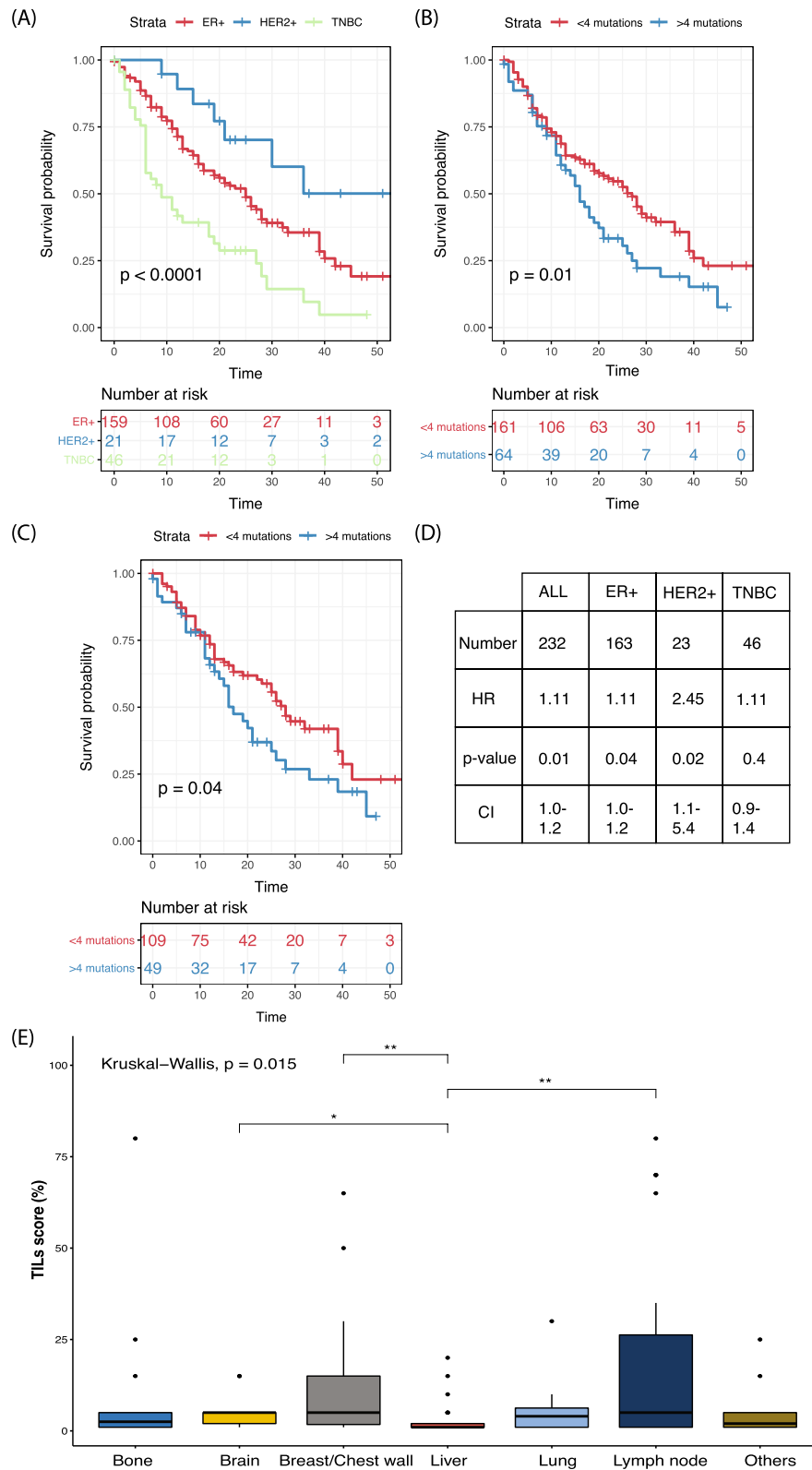
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**Fig. 4** (See legend on next page.)

(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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