

CORRECTION

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Correction: Protein-based prognostic signature for predicting the survival and immunotherapeutic efficiency of endometrial carcinoma

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Correction: *BMC Cancer* 22, 325 (2022)
<https://doi.org/10.1186/s12885-022-09402-w>

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Following publication of the original article [1], an error was identified regarding the order of Figs. 5, 6, 7, 8, 9 and 10.

- Fig. S3 was incorrectly published as Fig. 5.
- Fig. 5 was incorrectly published as Fig. 6.
- Fig. 6 was incorrectly published as Fig. 7.
- Fig. 7 was incorrectly published as Fig. 8.
- Fig. 8 was incorrectly published as Fig. 9.
- Fig. 9 was incorrectly published as Fig. 10.
- We missed to upload the corrected version of Fig. 10 when we proofed this article. Fig. 10 has been corrected to maintain the integrity of our article.

The correct versions of Figs. 5, 6, 7, 8, 9 and 10 are given in this correction article. The original article [1] has been corrected.

Reference

1. Lai J, Xu T, Yang H. Protein-based prognostic signature for predicting the survival and immunotherapeutic efficiency of endometrial carcinoma. *BMC Cancer*. 2022;22:325. <https://doi.org/10.1186/s12885-022-09402-w>.

The original article can be found online at <https://doi.org/10.1186/s12885-022-09402-w>.

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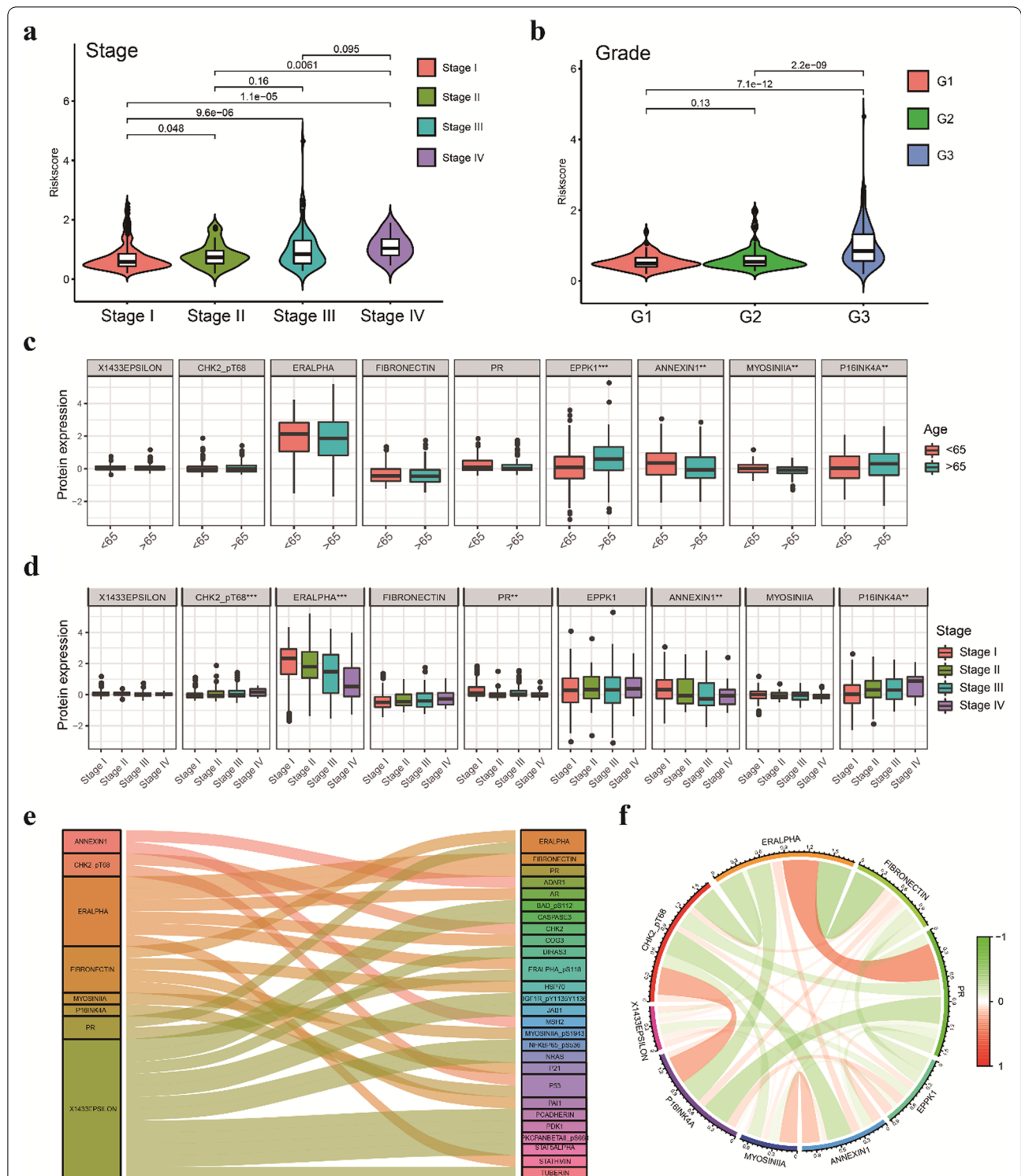
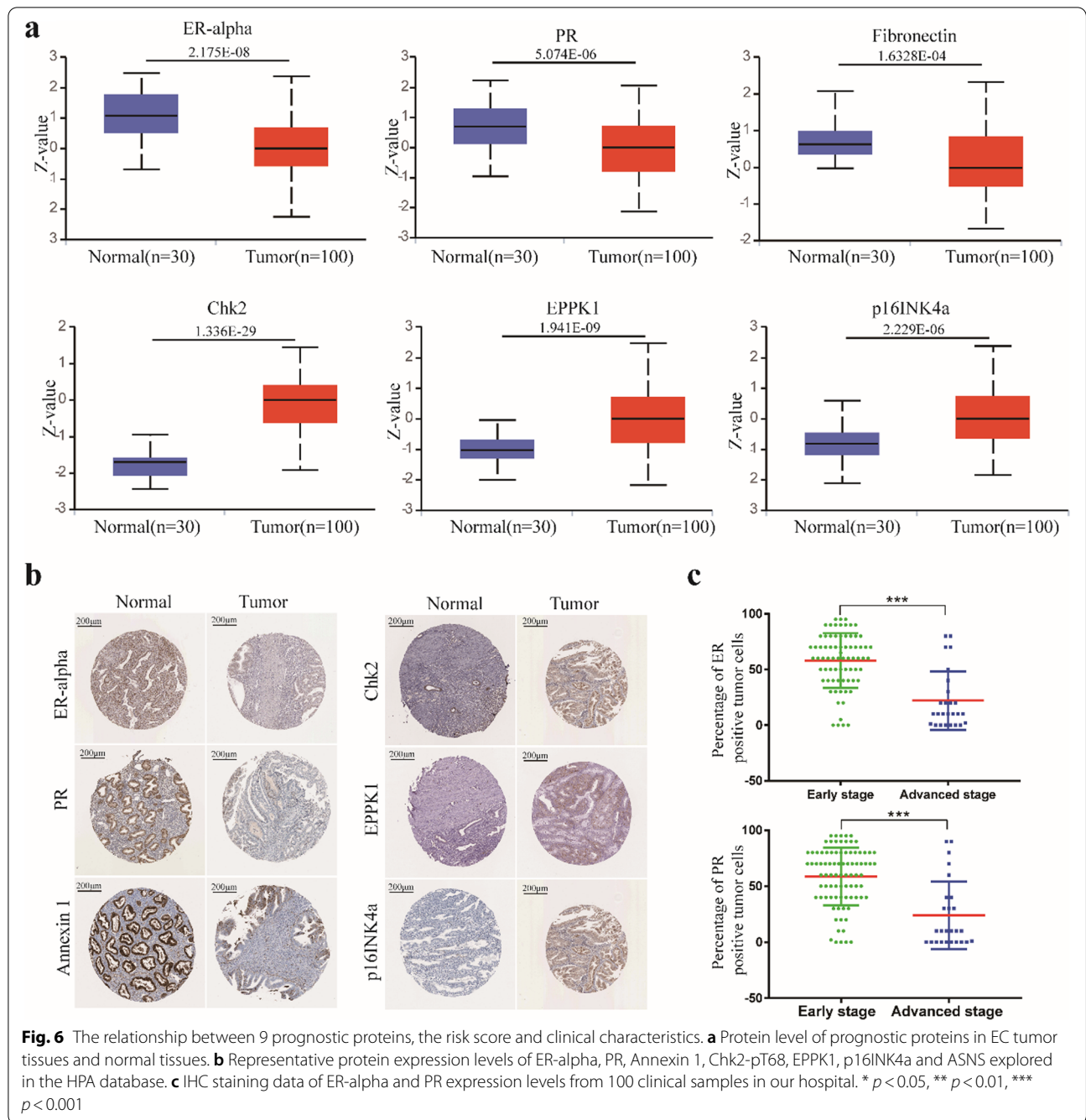


Fig. 5 The relationship between 9 prognostic proteins, the risk score and clinical characteristics. **a** The scatter plot shows the correlation between the risk score and tumor stages. **b** The scatter plot shows the correlation between risk score and tumor grade. **c** The expression of EPPK1, p16INK4a, Annexin 1 and Myosin IIA was related to age in EC patients. **d** The expression of ER-alpha, Annexin 1, Chk2-pT68 and p16INK4a was significantly associated with cancer stage. **e** Sankey diagram of all proteins related to 9 proteins in the TCPA database (correlation coefficient > 0.4) ($p < 0.001$). (F) The relationship of 9 proteins in the prognostic signature. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$



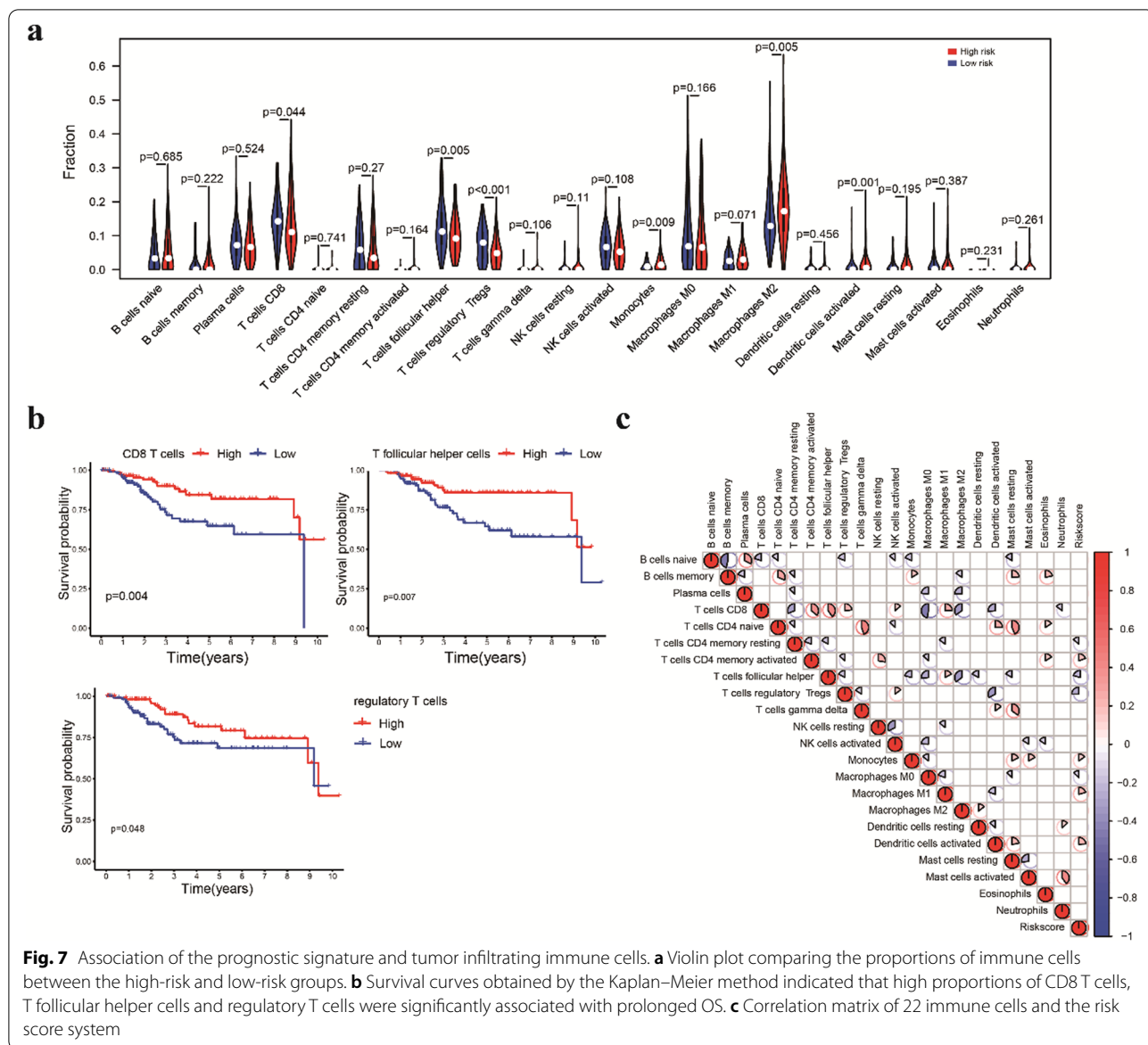


Fig. 7 Association of the prognostic signature and tumor infiltrating immune cells. **a** Violin plot comparing the proportions of immune cells between the high-risk and low-risk groups. **b** Survival curves obtained by the Kaplan–Meier method indicated that high proportions of CD8 T cells, T follicular helper cells and regulatory T cells were significantly associated with prolonged OS. **c** Correlation matrix of 22 immune cells and the risk score system

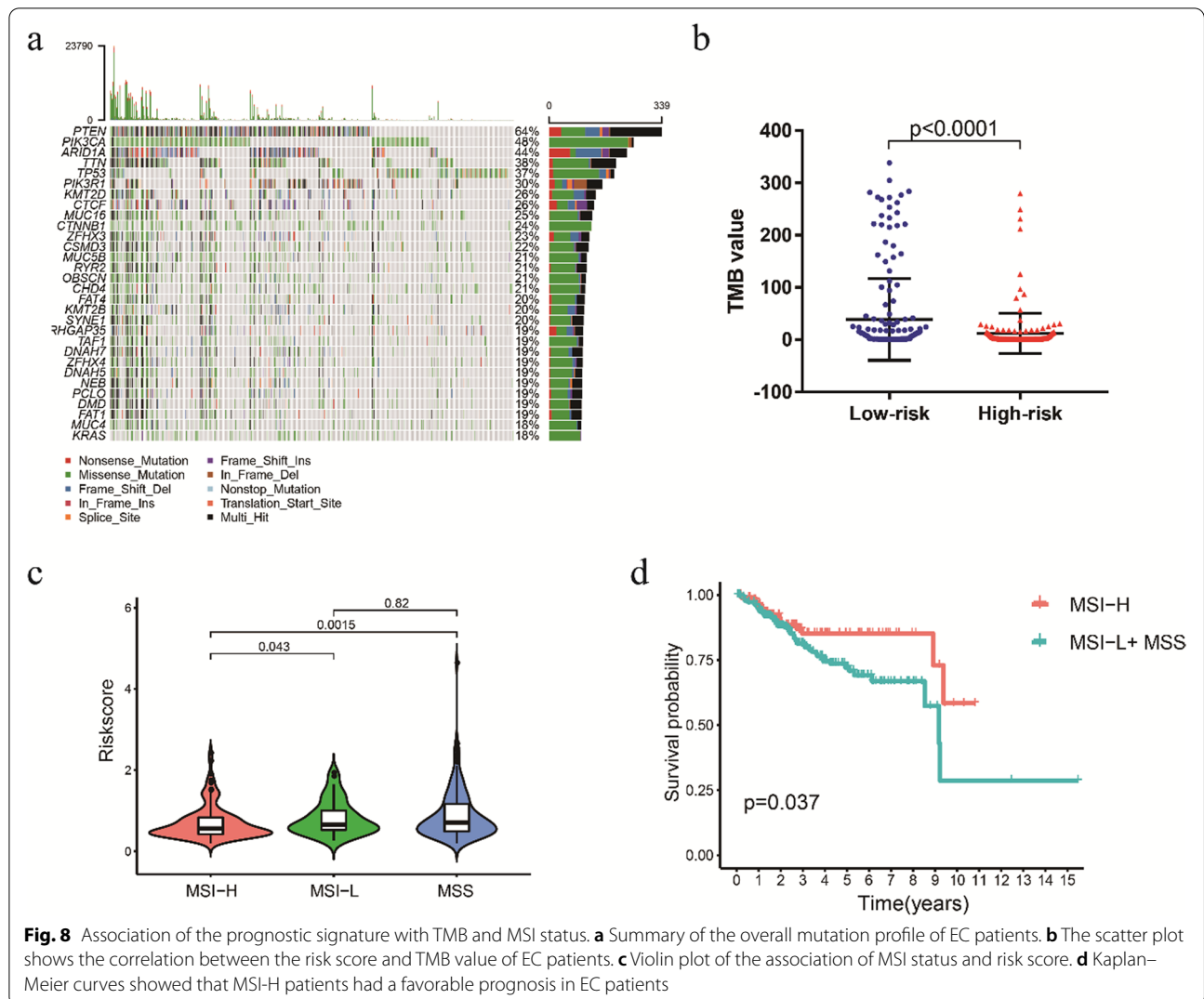


Fig. 8 Association of the prognostic signature with TMB and MSI status. **a** Summary of the overall mutation profile of EC patients. **b** The scatter plot shows the correlation between the risk score and TMB value of EC patients. **c** Violin plot of the association of MSI status and risk score. **d** Kaplan–Meier curves showed that MSI-H patients had a favorable prognosis in EC patients

