

CORRECTION

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# Correction to: Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data

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## Correction to: *Genome Med*

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It was highlighted that the original article [1] contained a typesetting mistake in the name of Noel Filipe da Cunha Carvalho de Miranda. This was incorrectly captured as Noel Filipe da Cunha Carvahlo de Miranda. It was also highlighted that in Fig. 3c the Y-axes of the left panels were cropped and in Fig. 5c, the CD8 bar was cropped. This Correction article shows the correct Figs. 3 and 5. The original article has been updated.

The Publisher apologises to the readers and the authors for any inconvenience caused.

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### Reference

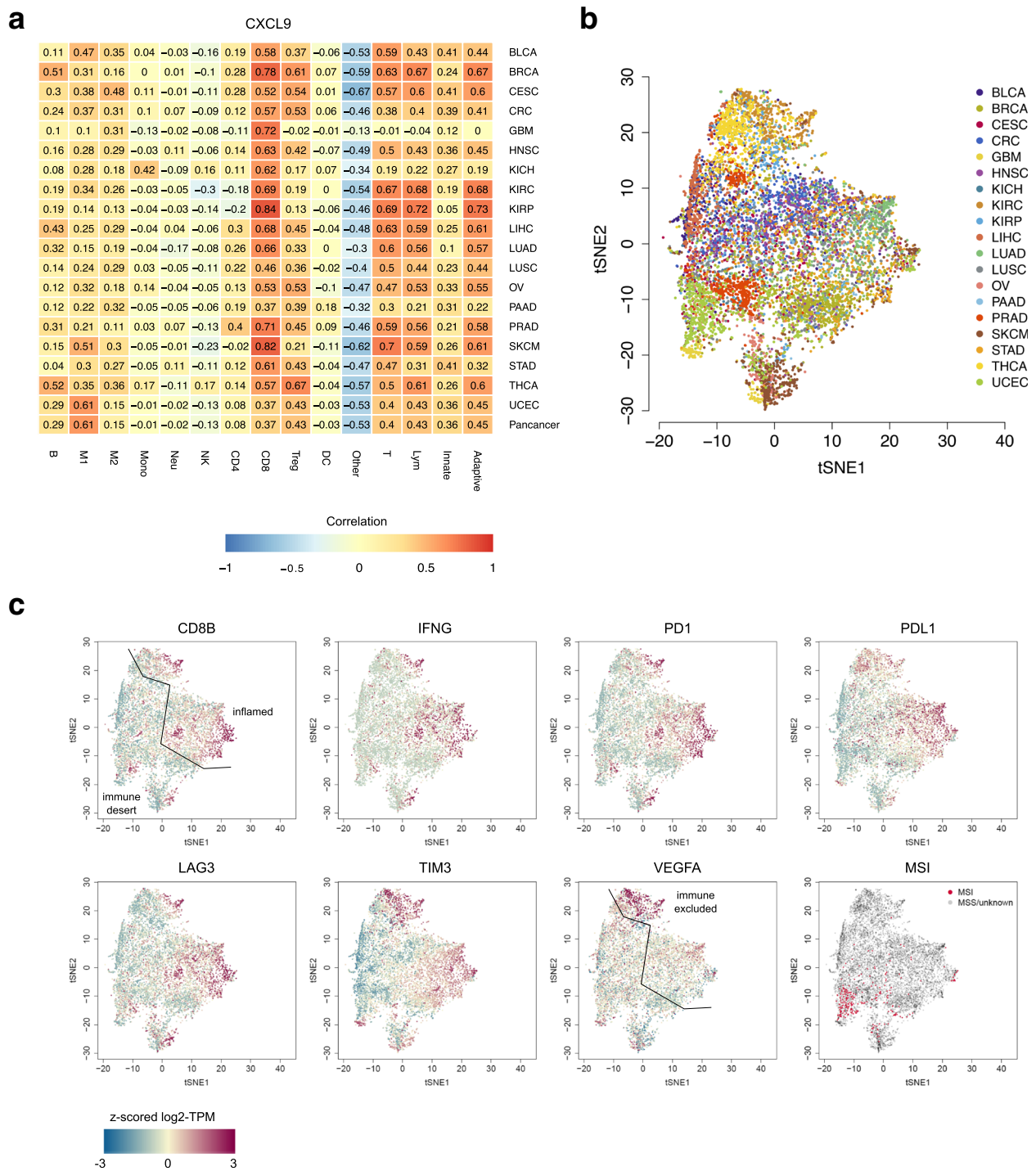
1. Finotello, et al. Molecular and pharmacological modulators of the tumor immune contexture revealed by deconvolution of RNA-seq data. *Genome Med.* 2019;11:34. <https://doi.org/10.1186/s13073-019-0638-6>.

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**Fig. 3** quantile analysis of RNA-seq data from 19 TCGA solid cancers. **a** Pearson's correlation between cell proportions estimated by quanTiseq and expression in TPM of the CXCL9 chemokine. t-SNE plot of the immune contexts of 8243 TCGA cancer patients, colored by **b** cancer type or **c** expression of immune-related genes and microsatellite instability state. The line in the t-SNE plots qualitatively indicates the separation of the putative inflamed, immune-desert, and immune-excluded phenotypes. Adaptive, total adaptive immune cells; B, B cells; CD4, total CD4<sup>+</sup> T cells (including also CD4<sup>+</sup> regulatory T cells); CD8, CD8<sup>+</sup> T cells; DC, dendritic cells; Innate, total innate immune cells; Lym, total lymphocytes; M1, classically activated macrophages; M2, alternatively activated macrophages; Mono, monocytes; MSI, microsatellite instable; MSS, microsatellite stable; Neu, neutrophils; NK, natural killer cells; Other, uncharacterized cells; T, T cells; Treg, regulatory T cells

