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Author Correction: Genomic and transcriptomic correlates of immunotherapy response within the tumor microenvironment of leptomeningeal metastases

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This article contained errors in Fig. 1b and Supplementary Data 1. In Fig. 1b the sample P061_2 was incorrectly presented with an icon denoting "pre-treatment" status. In the "Results" section, the related sentence "We performed longitudinal high-throughput scRNA-Seq (Figure 1a) on 13 pre-treatment and 24 post-treatment low-input CSF samples" was also incorrect. The sentence should have read: "We performed longitudinal high-throughput scRNA-Seq (Figure 1a) on 12 pre-treatment and 25 post-treatment low-input CSF samples". The correct samples and treatment timing were used elsewhere in the manuscript. These errors have been corrected in the PDF and HTML versions of the Article.

The original version of Supplementary Data 1 showed "days since treatment" for sample P129_1 indicated as "350"; however, the sample was obtained 15 days prior to therapy. This error has been corrected in Updated Supplementary Data 1.

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Additional information

Supplementary information The online version contains supplementary material available at <https://doi.org/10.1038/s41467-021-27207-6>.

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