

PUBLISHER CORRECTION

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Publisher Correction: Ganglioglioma deep transcriptomics reveals primitive neuroectoderm neural precursor-like population

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<https://doi.org/10.1186/s40478-023-01548-3>

Following the publication of the original article [1], it was noted that due to a typesetting error Fig. 10 was

incorrect. A part of Fig. 6 was incorrectly included also as Fig. 10. The correct figure is given hereafter.

The publisher apologizes for the inconvenience caused.

The original article can be found online at <https://doi.org/10.1186/s40478-023-01548-3>.

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The incorrect Fig. 10 reads:

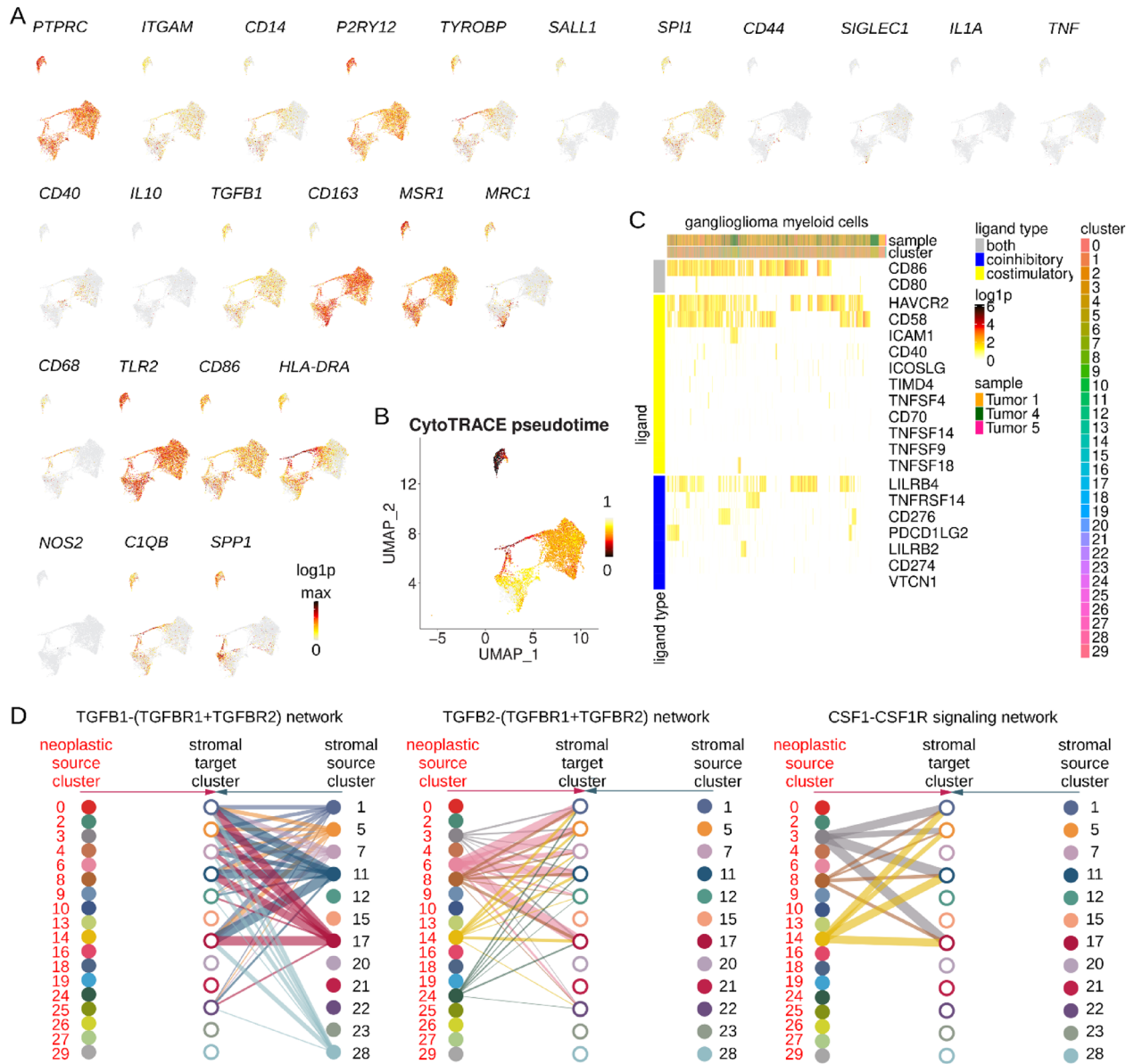


Fig. 10 Low grade glioma outcomes analysis. **A, B** Kaplan–Meier EFS (95% CI shaded, dotted line for median) for Bergthold et al. patients overall (**A**) and by resection status (**B**). **C** Kaplan–Meier EFS (95% CI shaded, dotted line for median) for Bergthold et al. patients by UCell score quartile for the gene signature of CD34, SOX2, CD99, and CTSC. **D** Forest plot of COXPH EFS HR for Bergthold et al. patients with continuous variables kept continuous. Includes HR for Z-score for the gene signature of CD34, SOX2, CD99, and CTSC. EFS = event-free survival, NR = none reported, GTR = gross total resection, NTR = near total resection, G/NTR = gross or near total resection, STR = subtotal resection, WT = wild-type. DA = diffuse astrocytoma, GG = ganglioglioma, ODG = oligodendroglioma, DNT = dysplastic neuroepithelial tumor, NOS or LGG = low-grade glioma, not otherwise specified. PA = pilocytic astrocytoma

The correct Fig. 10 should read:

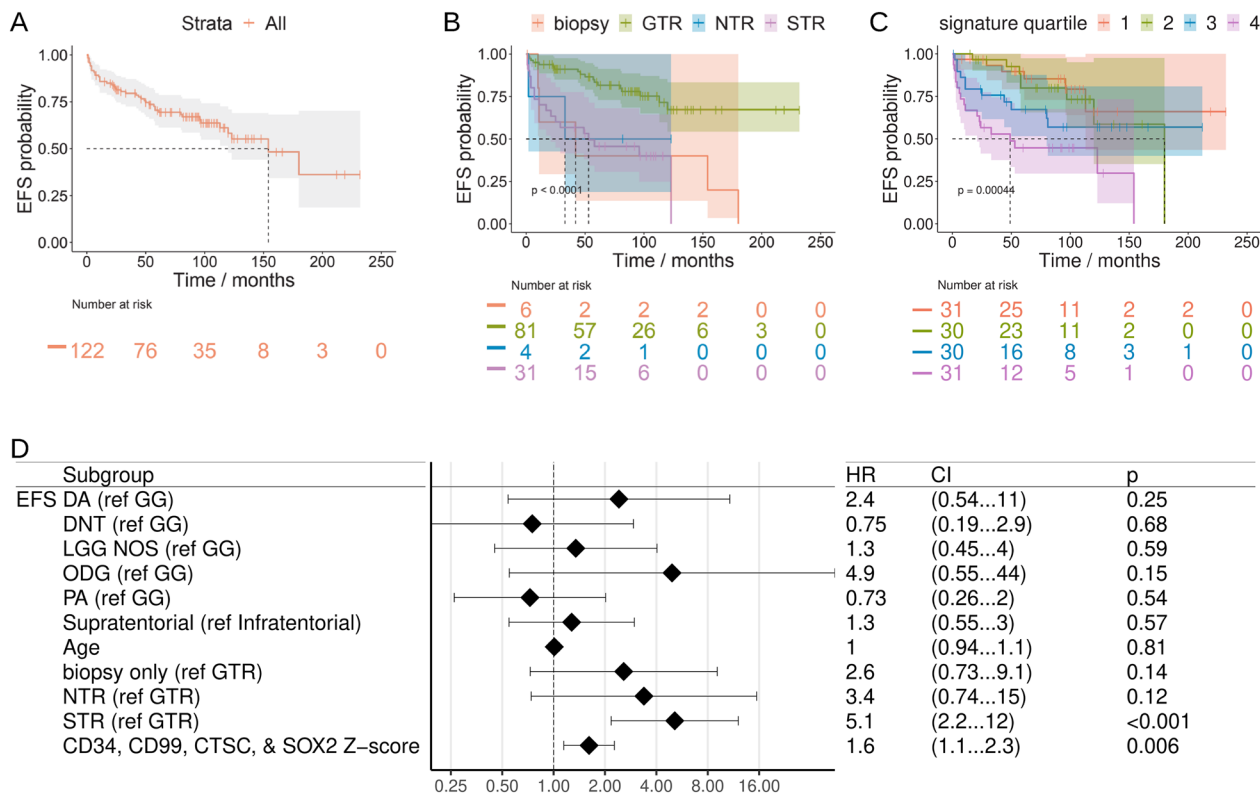


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The correct figure has been included in this correction, and the original article [1] has been corrected.

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Reference

1. Regal JA, Guerra García ME, Jain V et al (2023) Ganglioglioma deep transcriptomics reveals primitive neuroectoderm neural precursor-like population. *Acta Neuropathol Commun* 11:50. <https://doi.org/10.1186/s40478-023-01548-3>

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