

CORRECTION

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Correction: A longer time to relapse is associated with a larger increase in differences between paired primary and recurrent IDH wild-type glioblastomas at both the transcriptomic and genomic levels

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Following the publication of the original article [1], the wrong figure appeared as Fig. 7; the figure should have appeared as shown below.

The original article has been corrected.

The original article can be found online at <https://doi.org/10.1186/s40478-024-01790-3>.

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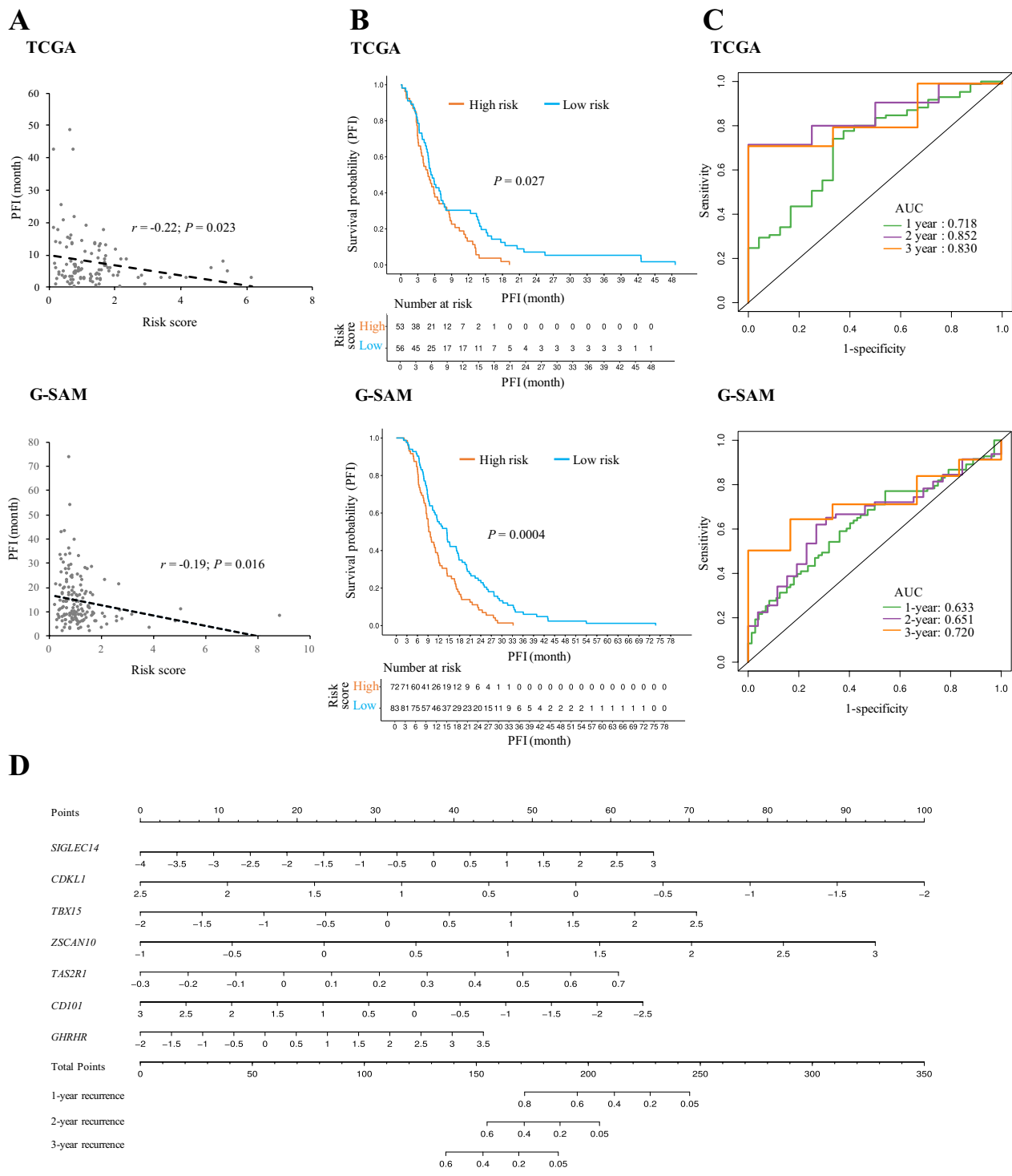


Fig. 7 Verification of the constructed prognostic model for PFS prediction in two testing sets (the TCGA and G-SAM datasets). **A** Correlation between the PFI values and the risk scores estimated by the constructed model for the primary IDH-wt GBM cases in the TCGA and G-SAM cohorts. **B** Kaplan–Meier analyses of PFS for the groups with low- or high-risk scores in the TCGA and G-SAM cohorts. **C** Time-dependent ROC analyses of 1-, 2-, and 3-year PFS for the constructed model in the TCGA and G-SAM cohorts. **D** Construction of a nomogram for quantitatively predicting 1-, 2-, and 3-year PFS of primary IDH-wt GBM patients

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Reference

1. Ho WM, Chen CY, Chiang TW et al (2024) A longer time to relapse is associated with a larger increase in differences between paired primary and recurrent IDH wild-type glioblastomas at both the transcriptomic and genomic levels. *Acta Neuropathol Commun* 12:77. <https://doi.org/10.1186/s40478-024-01790-3>

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