



B

References (PMID)	Number of genes in the model	1-, 3-, 5-year AUCs in CGGA301 cohort	C-index of the model	Validation in clinical samples
35756689(1)	7	0.749, 0.827, 0.770	0.697 (0.681-0.714)	No
35018108(2)	5	0.620, 0.728, 0.705	0.630 (0.611-0.650)	Yes (12 pairs, gene expression)
36161280(3)	3	0.632, 0.721, 0.687	0.624 (0.603-0.645)	Yes (12 pairs, gene expression)
34876094(4)	10	0.633, 0.746, 0.727	0.645 (0.625-0.666)	No
35023963(5)	9	0.726, 0.813, 0.779	0.687 (0.670-0.705)	No
Our risk model	3	0.657, 0.781, 0.747	0.668 (0.648-0.688)	Yes (43 paired samples, gene expression and risk model)

Supplementary Figure 5. Benchmarking prognostic models. (A) ROC curves of partially existing models and the model proposed in this study based on CGGA301 cohort. (B) AUCs and C-index showed that our three-gene prognostic model achieved similarly great prediction performance compared with existing models.

References

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3. Zhang M, Cheng Y, Xue Z, Sun Q, Zhang J. A novel pyroptosis-related gene signature predicts the prognosis of glioma through immune infiltration. *BMC Cancer*. 2021;21(1):1311.
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