Supplementary

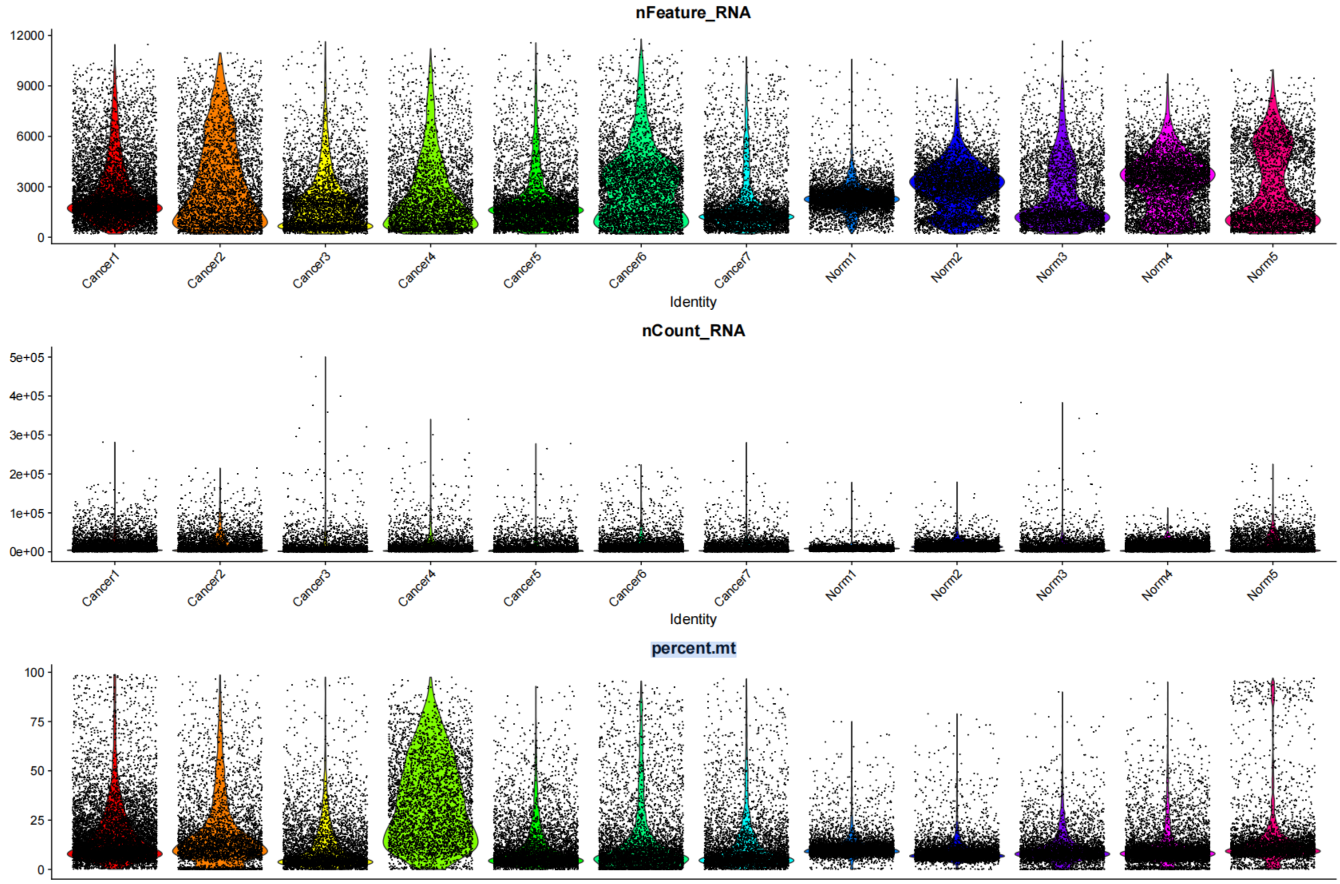

Figure S1 Violin plots of nFeature_RNA, nCount_RNA and percent mitochondrial transcript content in each sample before quality control.

https://dx.doi.org/10.21037/tcr-2025-1-2710

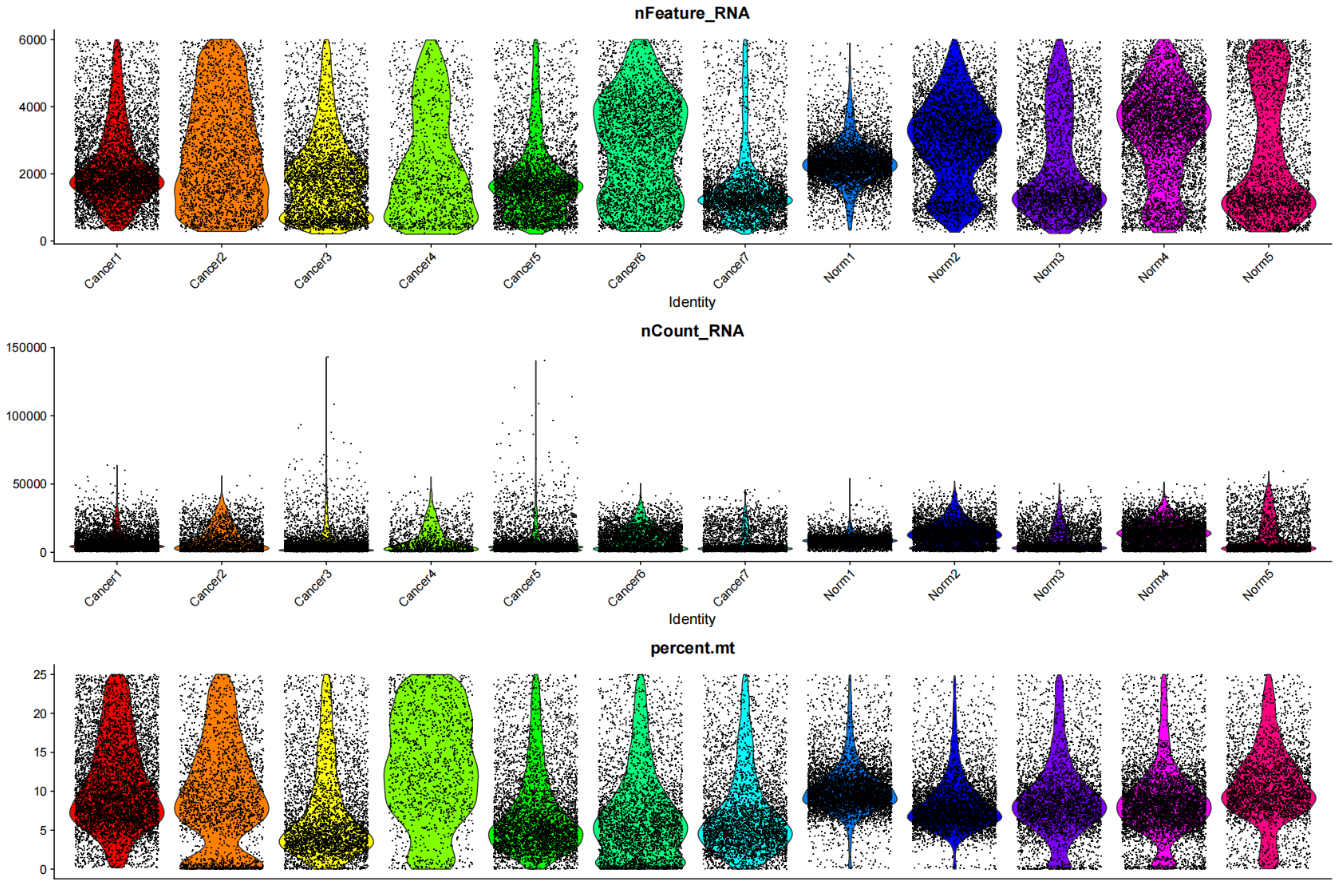

Figure S2 Violin plots of nFeature_RNA, nCount_RNA and percent mitochondrial transcript content in each sample after quality control.

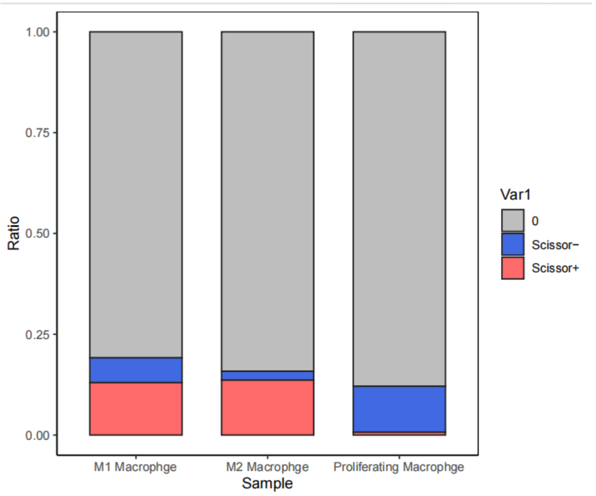

Figure S3 The proportion of Scissor+ cells in M1, M2 and Proliferating macrophage subtypes.

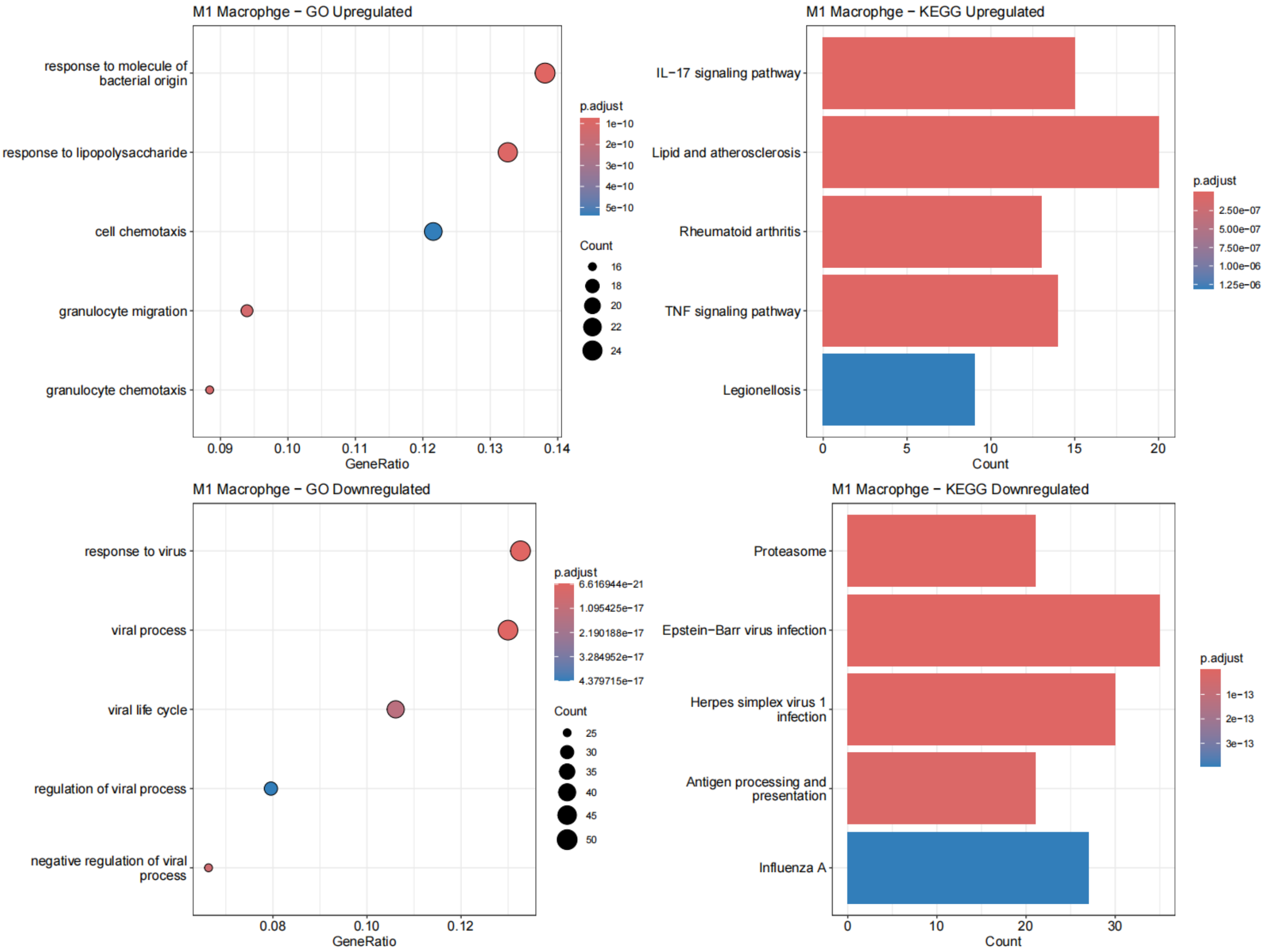

Figure S4 GO and KEGG enrichment analyses of up- and down-regulated genes in Scissor+ *vs.* Scissor− cells of M1 macrophages. GO, Gene Ontology; KEGG, Kyoto Encyclopedia of Genes and Genomes.

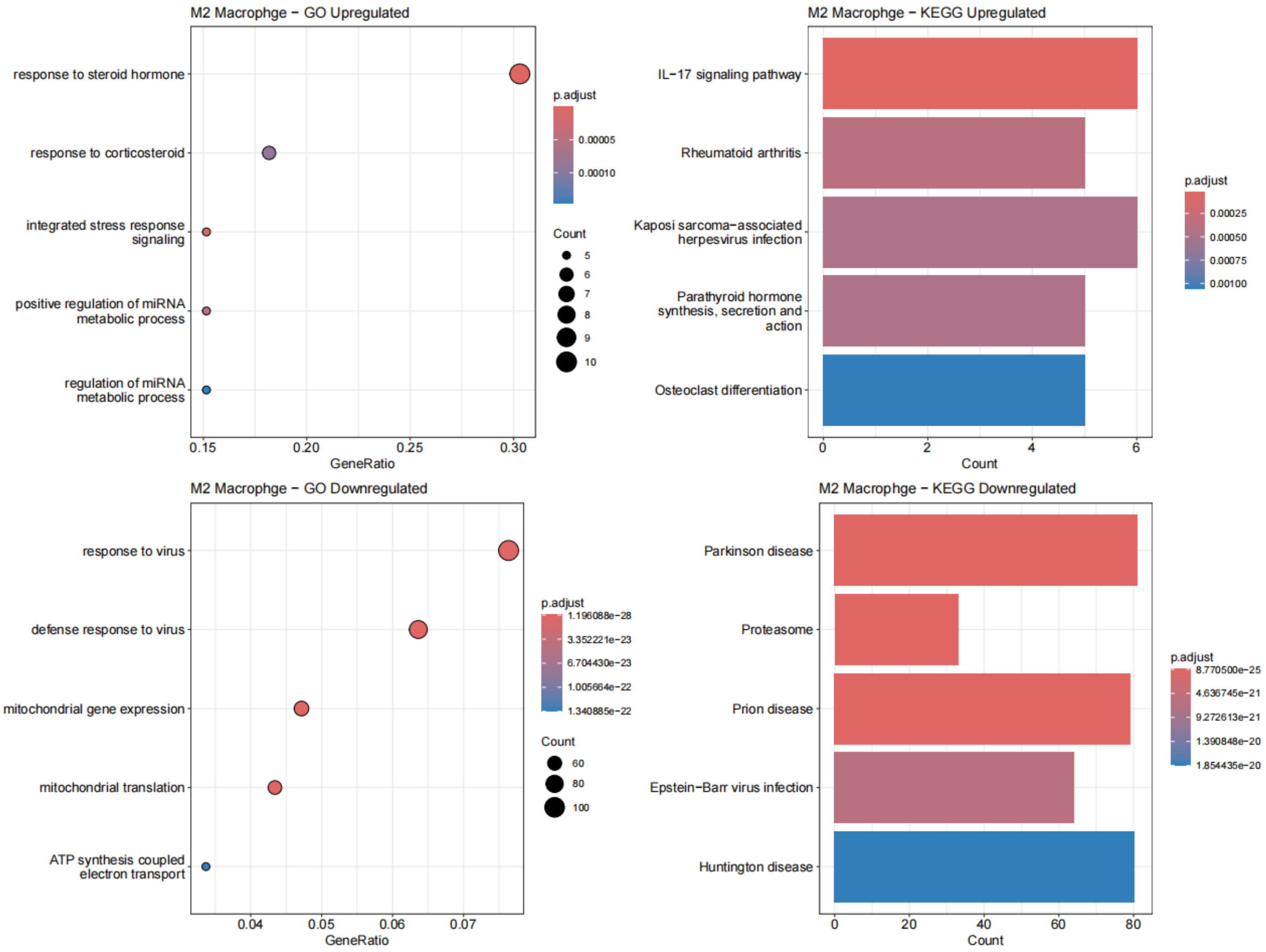

Figure S5 GO and KEGG enrichment analyses of up- and down-regulated genes in Scissor+ *vs.* Scissor– cells of M2 macrophages. KEGG, Kyoto Encyclopedia of Genes and Genomes

https://dx.doi.org/10.21037/tcr-2025-1-2710

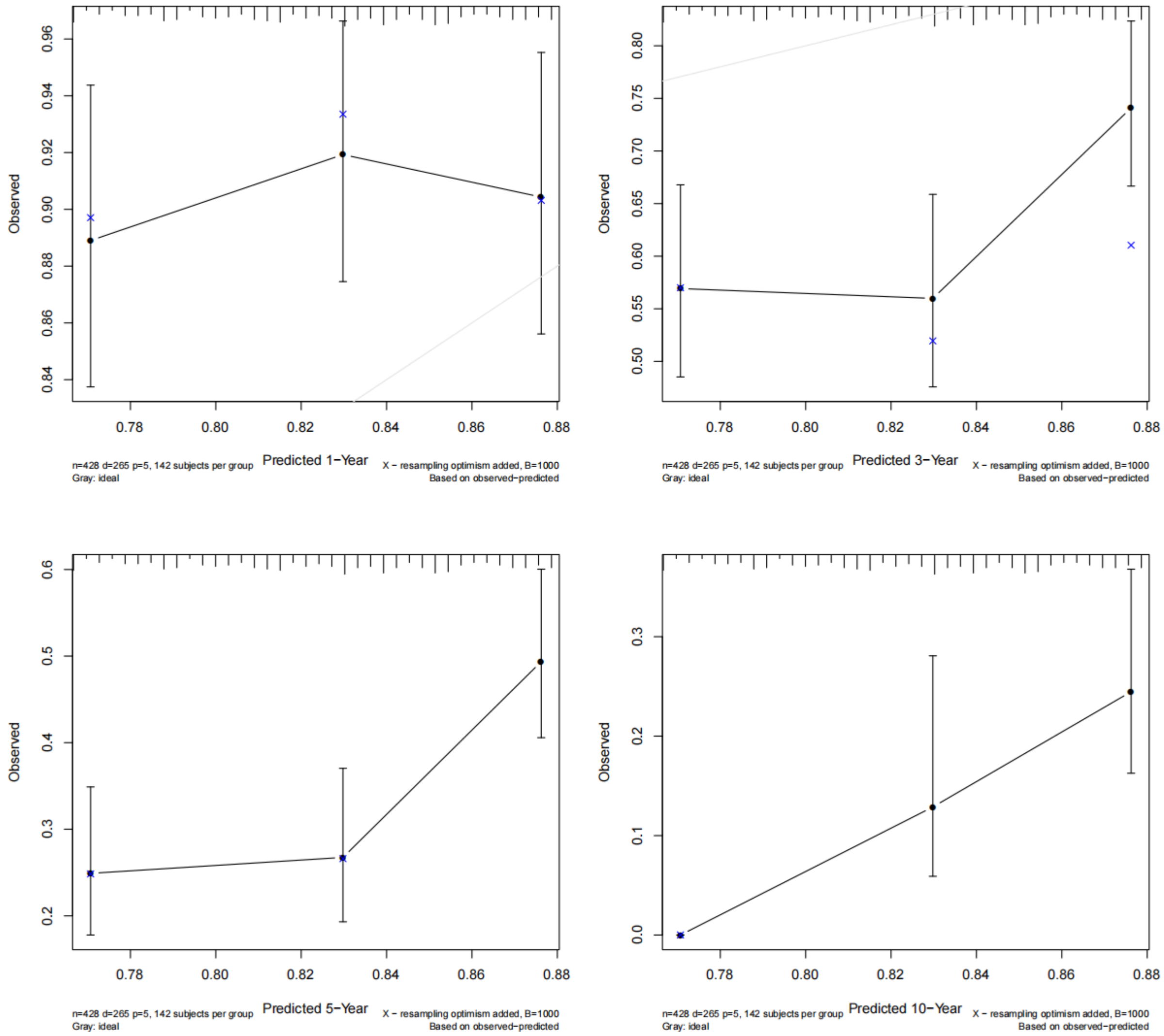

Figure S6 Calibration curves of the prognostic model for predicting 1-, 3-, 5- and 10-year OS in ovarian cancer patients. OS, overall survival.

https://dx.doi.org/10.21037/tcr-2025-1-2710

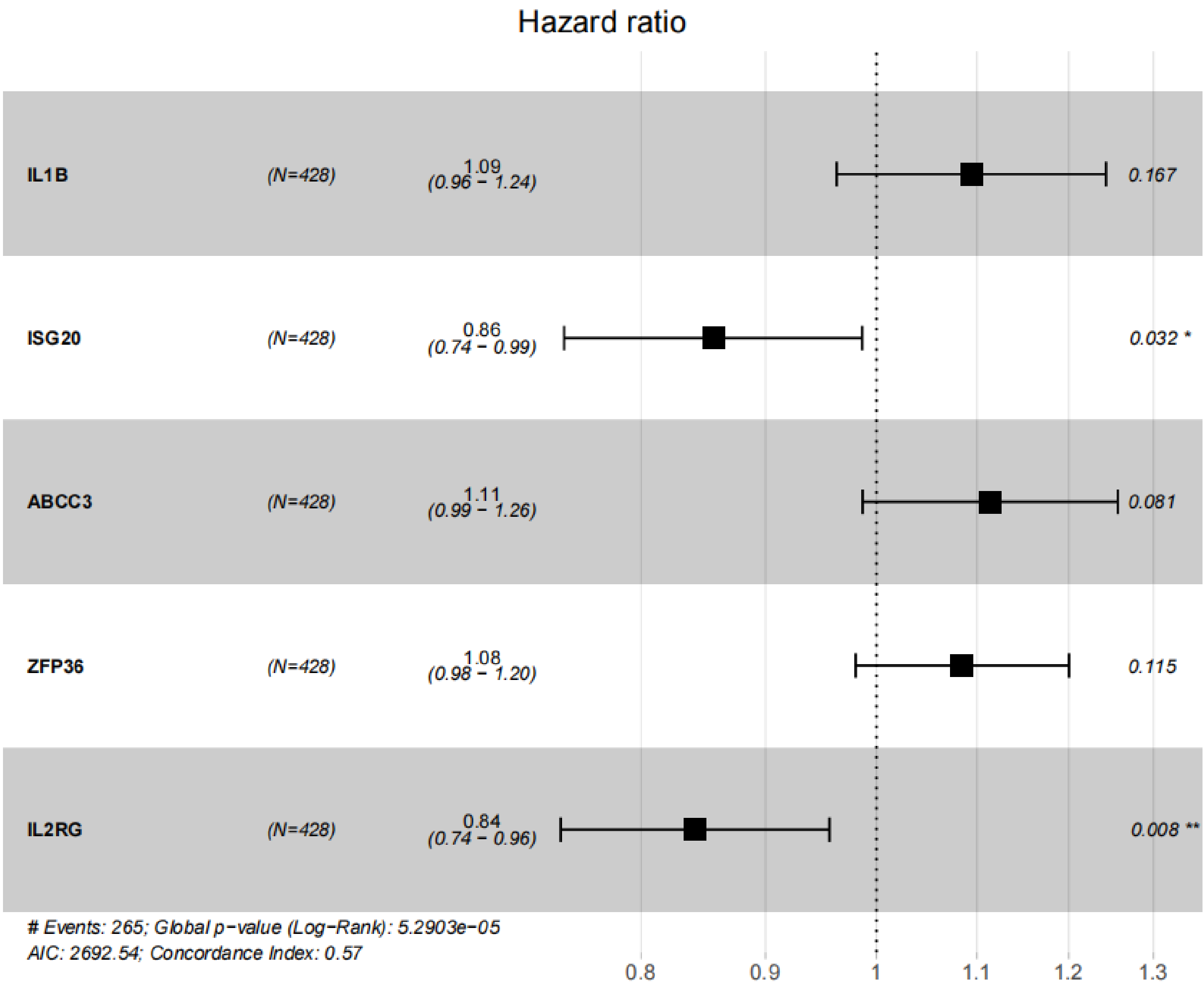

Figure S7 Forest plot of multivariate Cox regression analysis for the core genes in the prognostic model. *, P<0.05; **, P<0.01.

https://dx.doi.org/10.21037/tcr-2025-1-2710

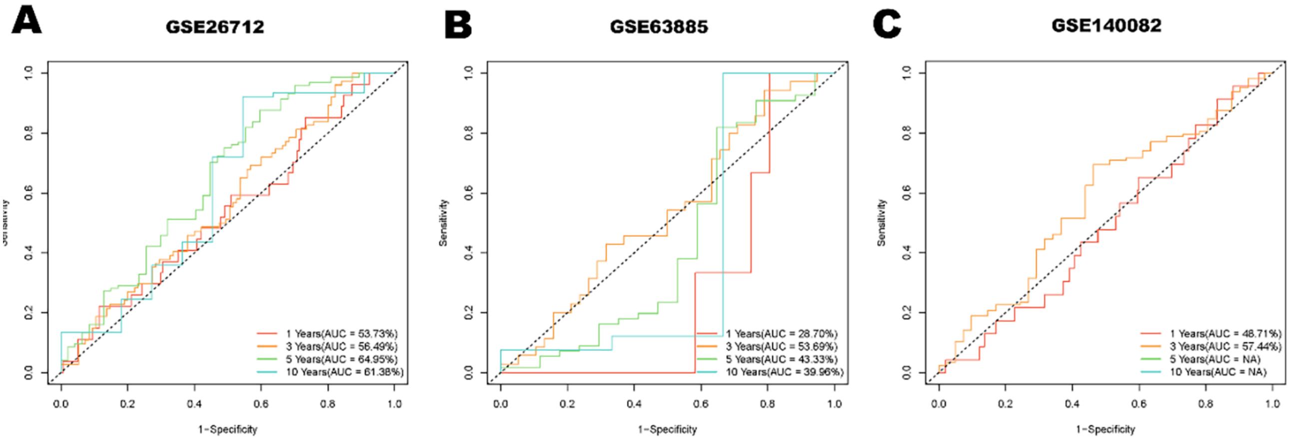

Figure S8 Time-dependent ROC curves of the prognostic model in each cohort. AUC, area under the curve; ROC, receiver operating characteristic.

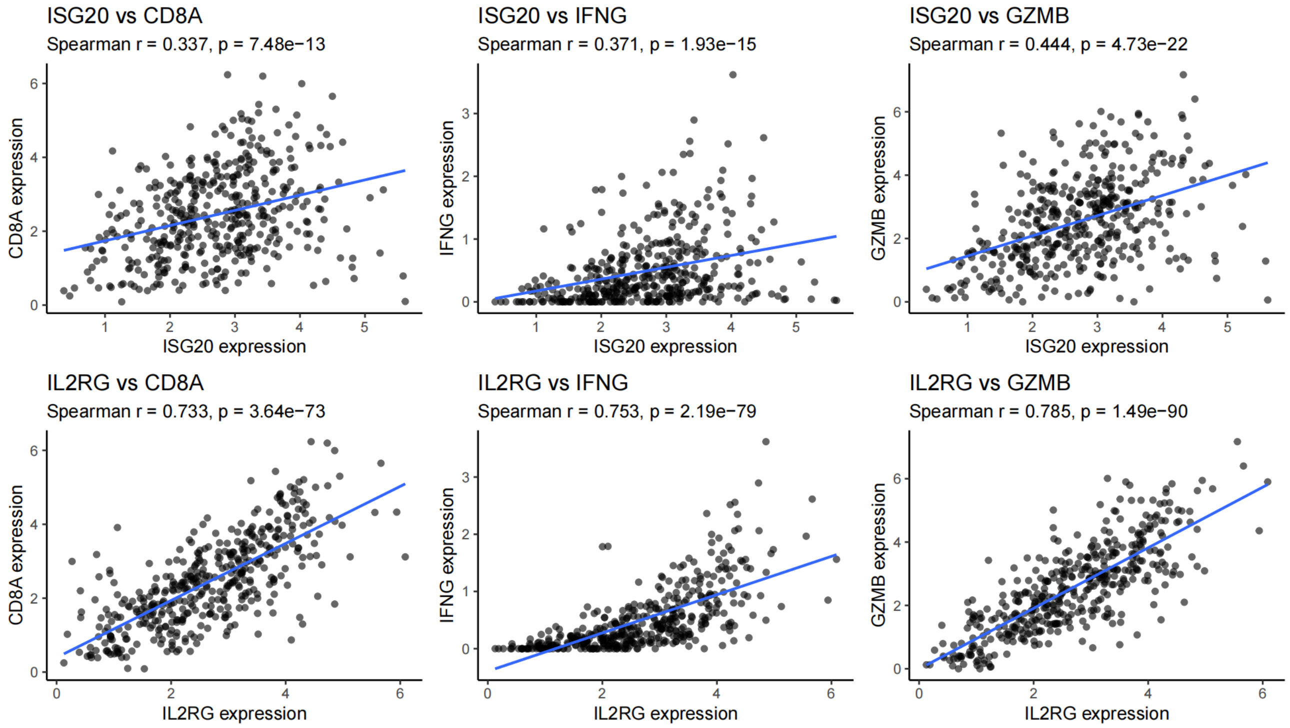

Figure S9 Scatter plots showing the correlations of *ISG20* and *IL2RG* with *CD8A*, *IFNG* and *GZMB* (Spearman correlation).

https://dx.doi.org/10.21037/tcr-2025-1-2710