

Figure S1. Schoenfeld residual plots for the PH assumption test of the 14 candidate genes identified by univariate Cox regression. The figure is composed of 14 labelled panels (A-N) arranged in a 4x4 grid: (A) *CRBN*, (B) *HERC1*, (C) *KAT2B*, (D) *KCTD5*, (E) *MAP3K3*, (F) *RNF125*, (G) *RNF144B*, (H) *RNF180*, (I) *RWDD3*, (J) *TRAF7*, (K) *TRIM2*, (L) *TRIM27*, (M) *USP49* and (N) *USP54*. Each panel shows scaled Schoenfeld residuals over time. A non-significant trend ( $P>0.05$ ) in all panels indicates that the PH assumption is satisfied, confirming the suitability of these genes for the Cox proportional hazards model. PH, proportional hazards.

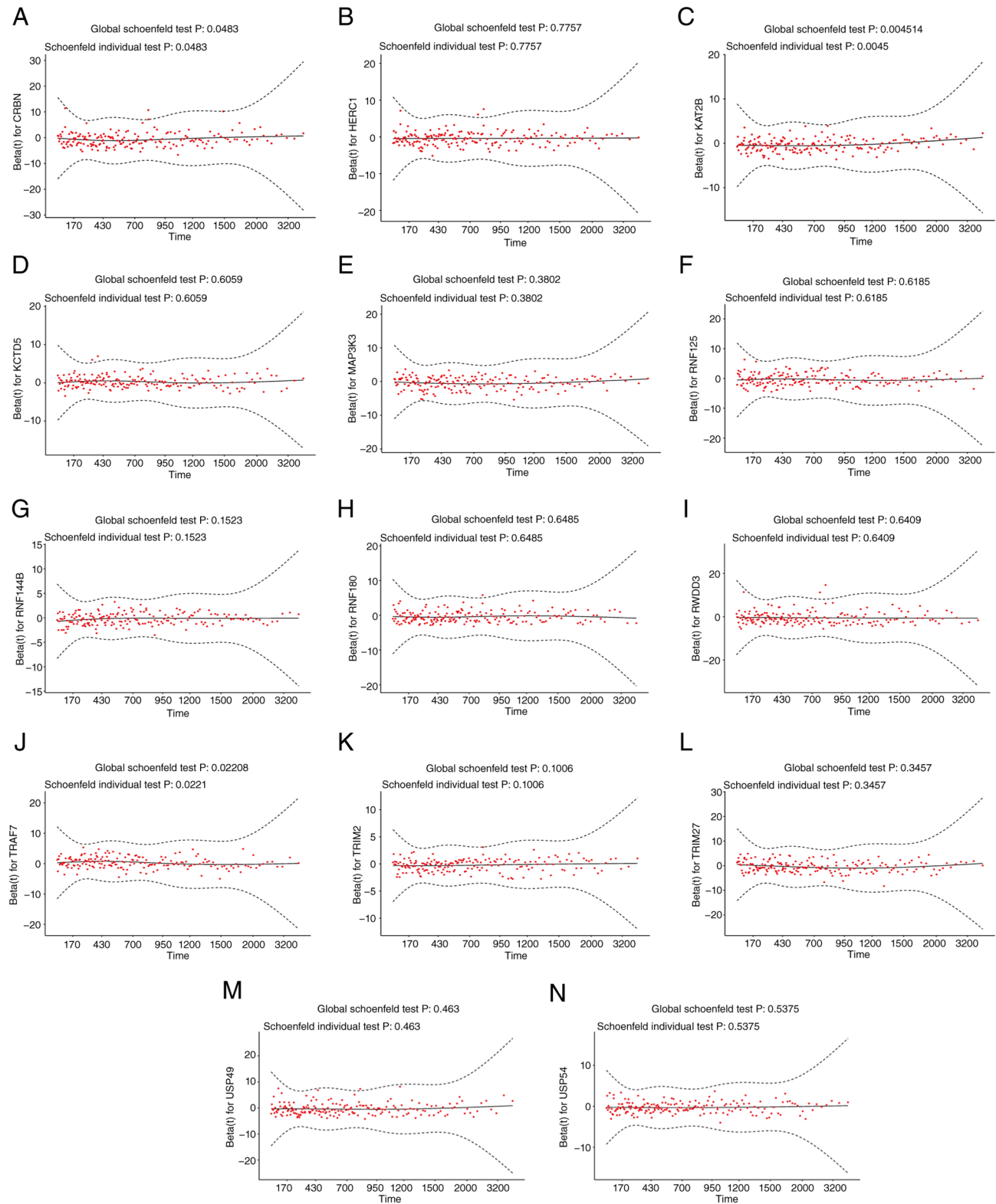


Figure S2. Schoenfeld residual plots for the PH assumption test of the independent prognostic factors (risk score and M stage). The figure contains four labelled panels (A-D) arranged in a 2x2 grid: (A) Univariate analysis of M stage, (B) univariate analysis of risk score, (C) multivariate analysis of M stage and (D) multivariate analysis of risk score. Each panel displays the residual distribution over time, confirming that both variables satisfy the PH assumption ( $P>0.05$ ) in both univariate and multivariate settings, justifying their inclusion in the multivariate Cox regression and the nomogram. PH, proportional hazards.

