

Figure S1. Correlations between 24hUP and UPCR in the derivation cohort. (A) 24hUP vs. mUPCR; (B) 24hUP vs. UPCR adjusted by m24hUCr ($eUPCR_0 = mUPCR \times m24hUCr$); (C-E) 24hUP vs. UPCR adjusted by e24hUCr using the Hellerstein ($eUPCR_1$), Ghazali-Barratt ($eUPCR_2$) and Cockcroft-Gault ($eUPCR_3$) equations. UPCR, urine protein-creatinine ratio; 24hUP, 24-h urine protein; 24hUCr, 24-h urine creatinine; m, measured; e, estimated.

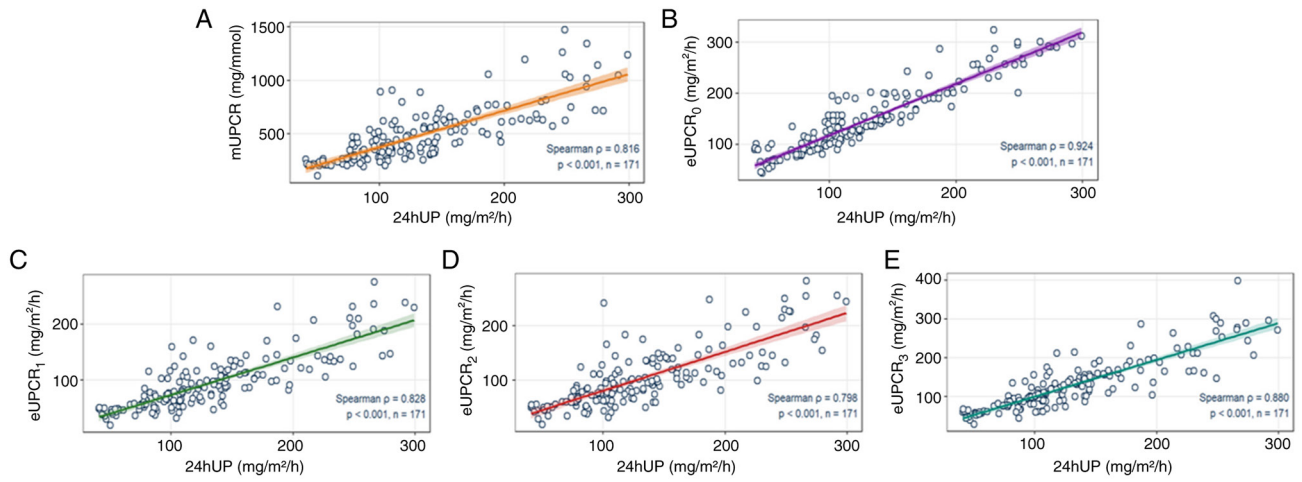


Figure S2. Bland-Altman agreements between 24hUP and UPcr in the derivation cohort. (A) 24hUP vs. mUPCR; (B) 24hUP vs. UPcr adjusted by m24hUCr ($eUPCR_0 = mUPCR \times m24hUCr$); (C-E) 24hUP vs. UPcr adjusted by e24hUCr using the Hellerstein ($eUPCR_1$), Ghazali-Barratt ($eUPCR_2$), and Cockcroft-Gault ($eUPCR_3$) equations. All values are \log_{10} -transformed. UPcr, urine protein-creatinine ratio; 24hUP, 24-h urine protein; 24hUCr, 24-h urine creatinine; m, measured; e, estimated.

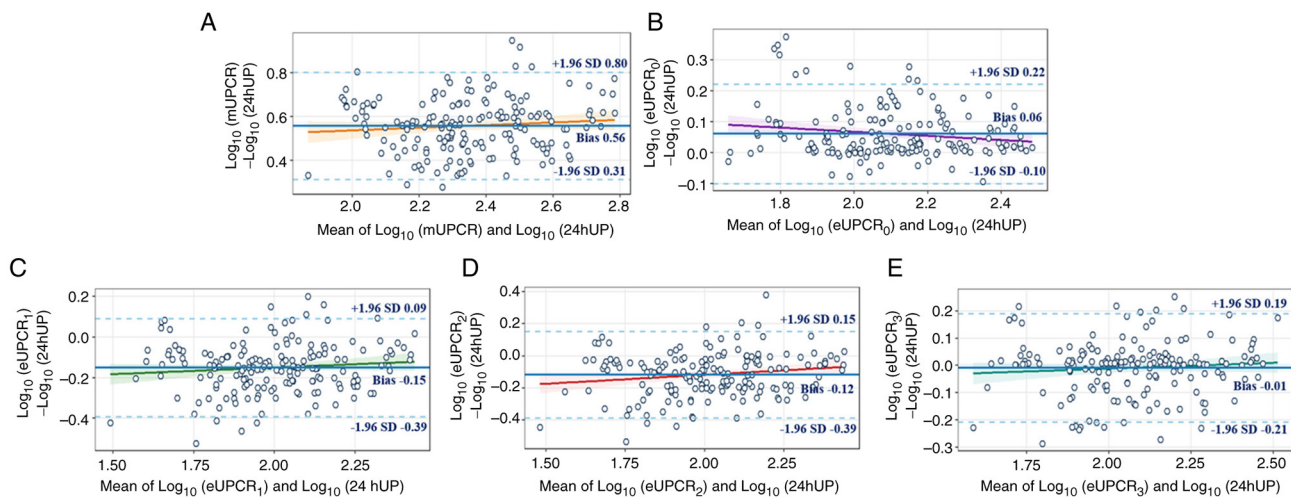


Figure S3. Residual diagnostics for model M_6 (Log_{10} -scale). (A) Residuals vs. fitted (log_{10} -scale). Points scatter around 0; the LOESS curve is essentially flat with slight curvature near the center, indicating no obvious model misspecification and small residual amplitude. (B) Normal Q-Q (standardized residuals). Points lie close to the 45° line with only mild tail departures, approximately normal. For conservative inference, HC3 robust standard errors are used. (C) Scale-location. $\sqrt{|\text{standardized residuals}|}$ decreases slightly and then stabilizes across fitted values, suggesting roughly constant variance; no clear ‘fan’ pattern, if heteroskedasticity exists, it is borderline. (D) Residuals vs. leverage (hat values). Most observations have leverage $< 2k/n=0.047$; a few exhibit higher leverage (~ 0.06) but small residuals, indicating no unduly influential observations. LOESS, locally weighted smoothing; SE (HC3), heteroskedasticity-consistent standard errors (type HC3).

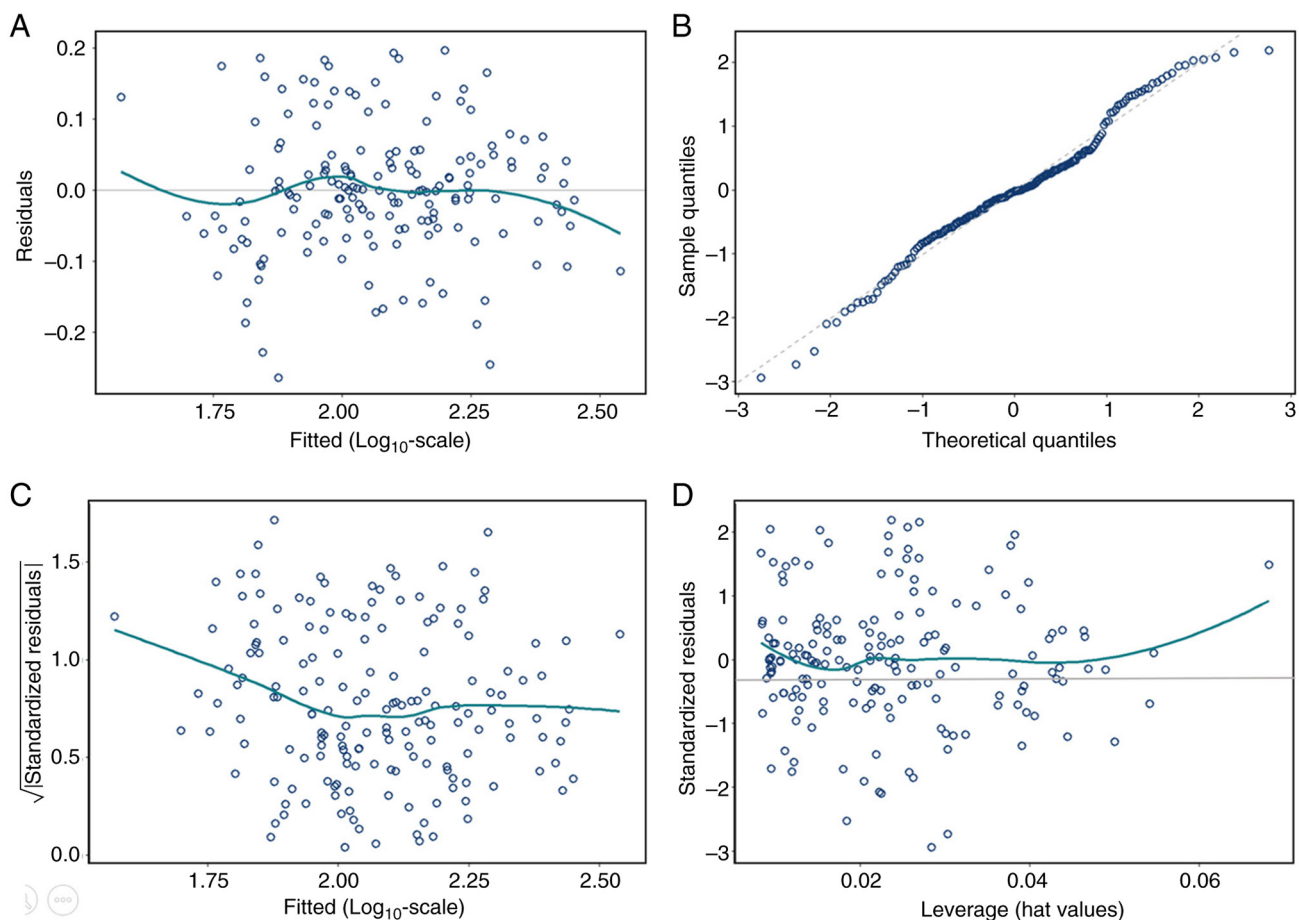


Figure S4. Component-plus-Residual (partial residual) plots for model M_6 . (A) $\text{Log}_{10}(\text{adjusted UPCR})$: Linear pattern, LOESS overlaps the fitted line. (B) Age: Mild downward linear trend, no systematic curvature. (C) Sex: Upward shift for girls and no evidence of sex-specific heteroskedasticity. LOESS, locally weighted smoothing; UPCR, urine protein/creatinine ratio; 24hUP, 24-h urine protein.

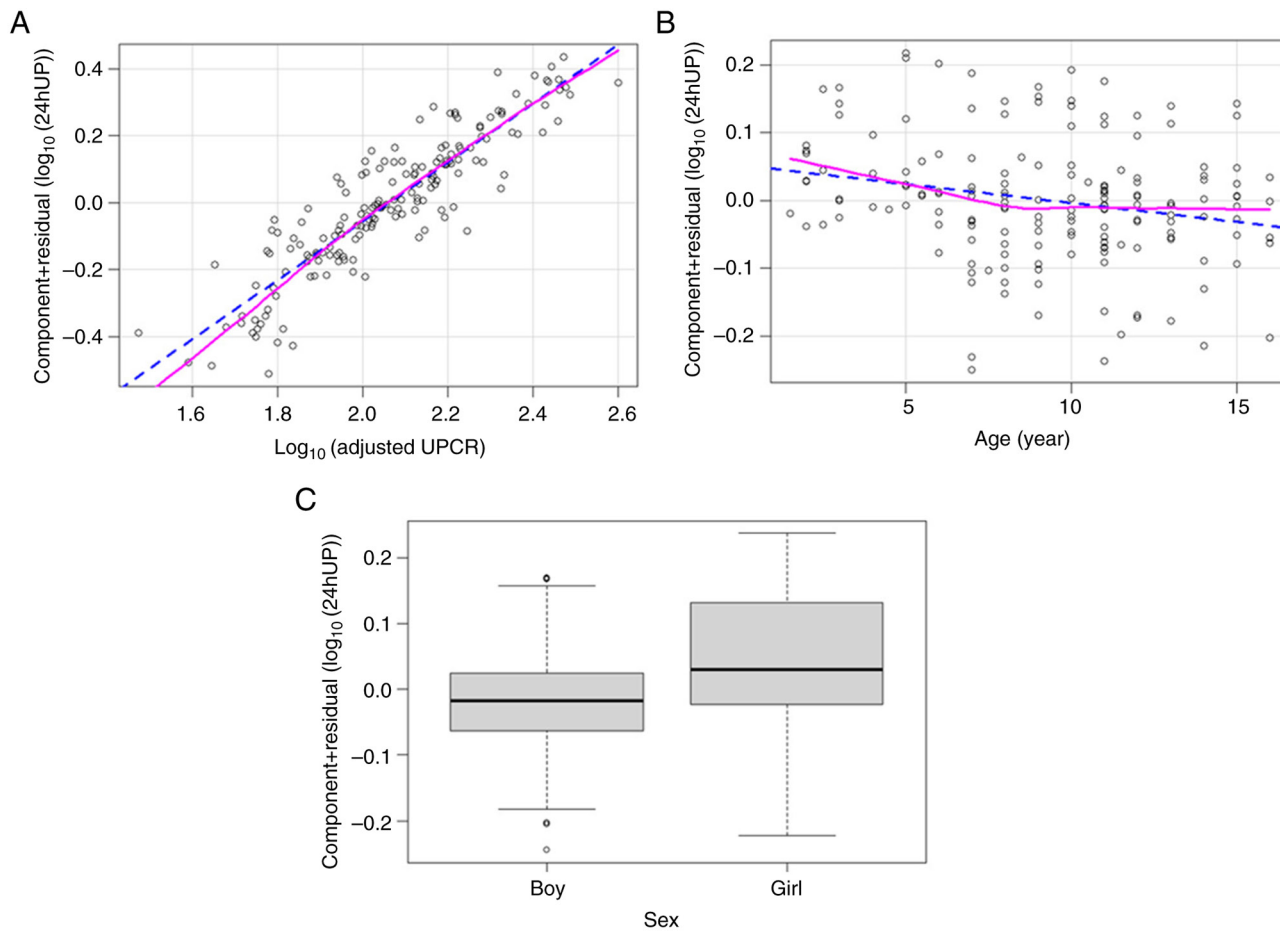


Figure S5. Decision curve analysis for the original M6 (external validation). (A) Threshold $T=100 \text{ mg/m}^2/\text{h}$; (B) Threshold $T=150 \text{ mg/m}^2/\text{h}$. Events were defined as $24\text{hUP} \geq T$, with predicted risk derived from the original M_6 model. Curves display net benefit per patient of the model, compared with treat-all and treat-none strategies, across a range of risk thresholds ($pt=0.05-0.80$). The model consistently provided higher net benefit over both reference strategies across clinically relevant thresholds, supporting its potential clinical utility for guiding 24h urine collection decisions. DCA, decision-curve analysis; pt , risk threshold; 24hUP, 24-h urine protein.

