

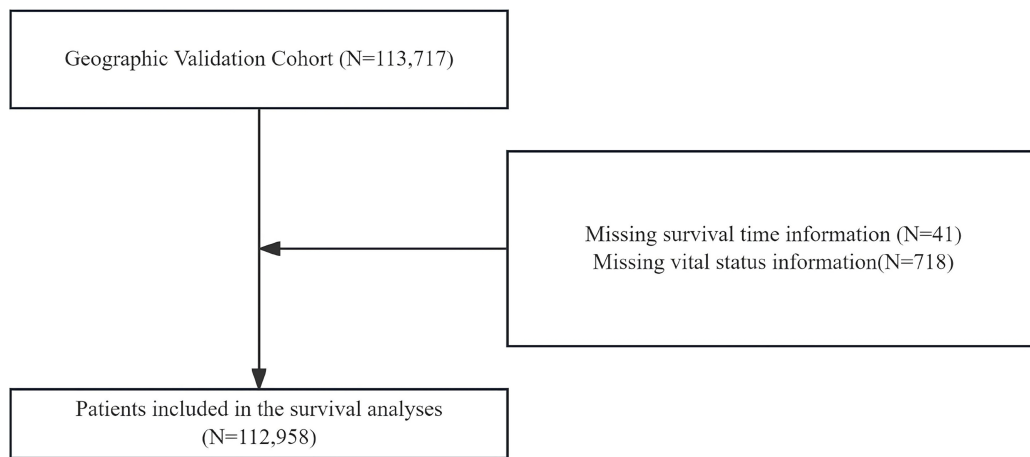


Fig. S1. Flowchart of patient selection for the survival analyses in the geographic validation cohort. Among 113,717 patients in the geographic validation cohort, 41 were excluded because of missing survival time and 718 were excluded because of missing vital status, leaving 112,958 patients with NSCLC for the survival analyses.

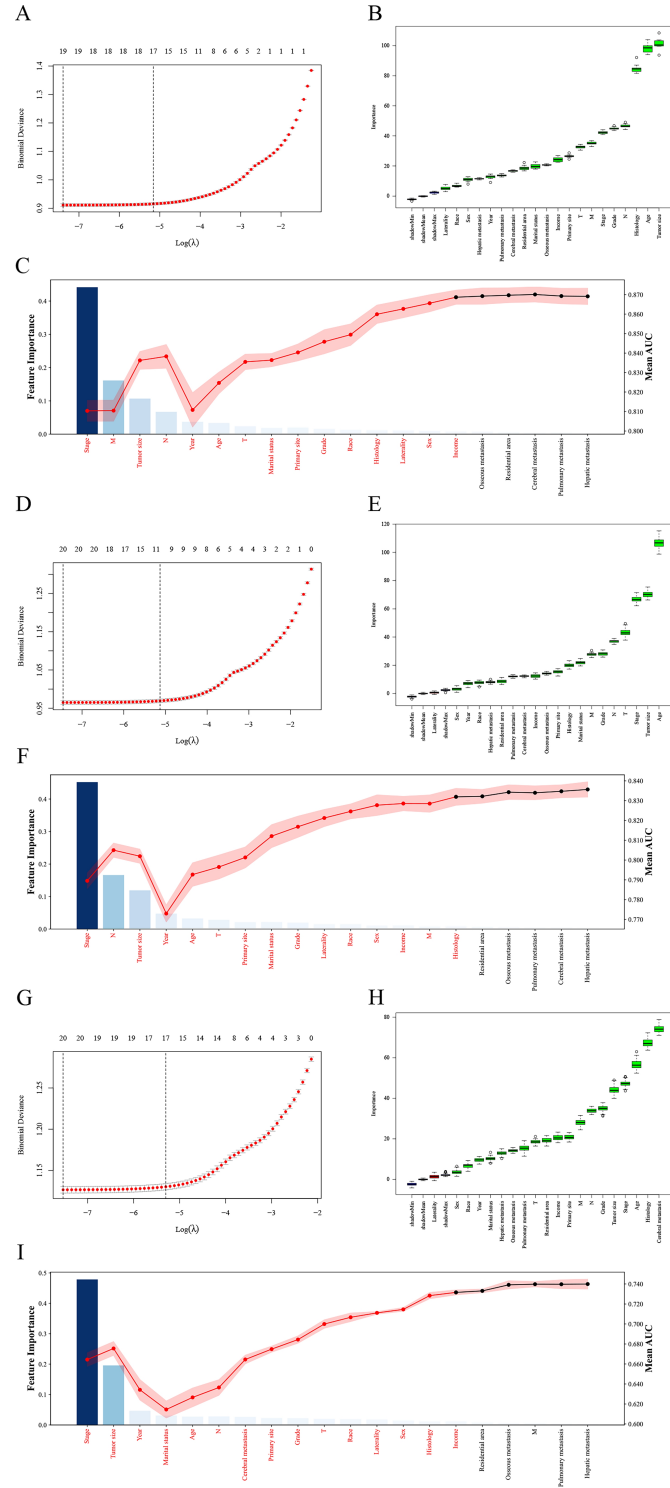


Fig. S2. Feature selection results for machine learning models predicting historical allocations of surgery, chemotherapy, and radiotherapy. Panels A-C, D-F, and G-I present results for the surgical, chemotherapy, and radiotherapy allocation models, respectively. Within each set, the panels show LASSO-based feature selection, Boruta feature importance assessment, and recursive feature elimination, respectively. LASSO, least absolute shrinkage and selection operator; RFE, recursive feature elimination.

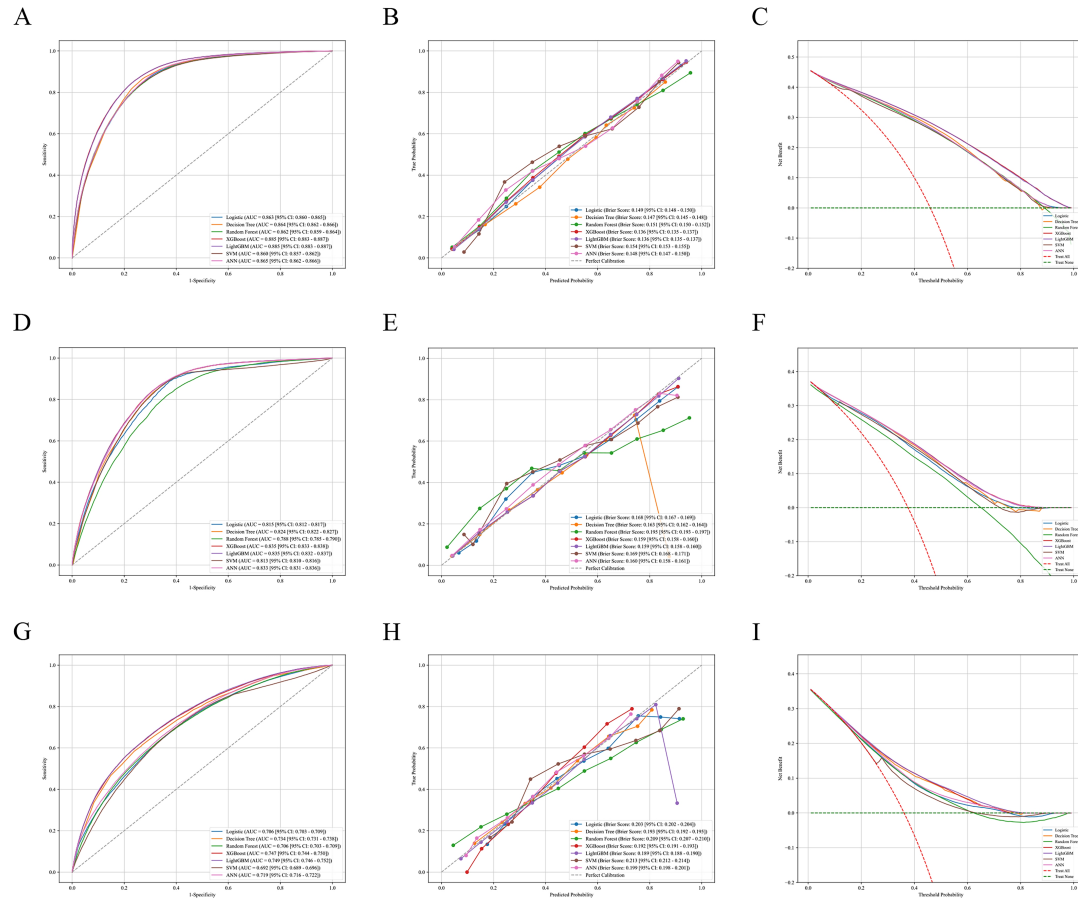


Fig. S3. Performance of seven candidate machine learning models for predicting historical allocations of surgery, chemotherapy, and radiotherapy in the geographic validation cohort. (A) ROC curves for the prediction of historical surgical allocation. (B) Calibration curves for the prediction of historical surgical allocation. (C) DCA curves for the prediction of historical surgical allocation. (D) ROC curves for the prediction of historical chemotherapy allocation. (E) Calibration curves for the prediction of historical chemotherapy allocation. (F) DCA curves for the prediction of historical chemotherapy allocation. (G) ROC curves for the prediction of historical radiotherapy allocation. (H) Calibration curves for the prediction of historical radiotherapy allocation. (I) DCA curves for the prediction of historical radiotherapy allocation. ROC, receiver operating characteristic; DCA, decision curve analysis.

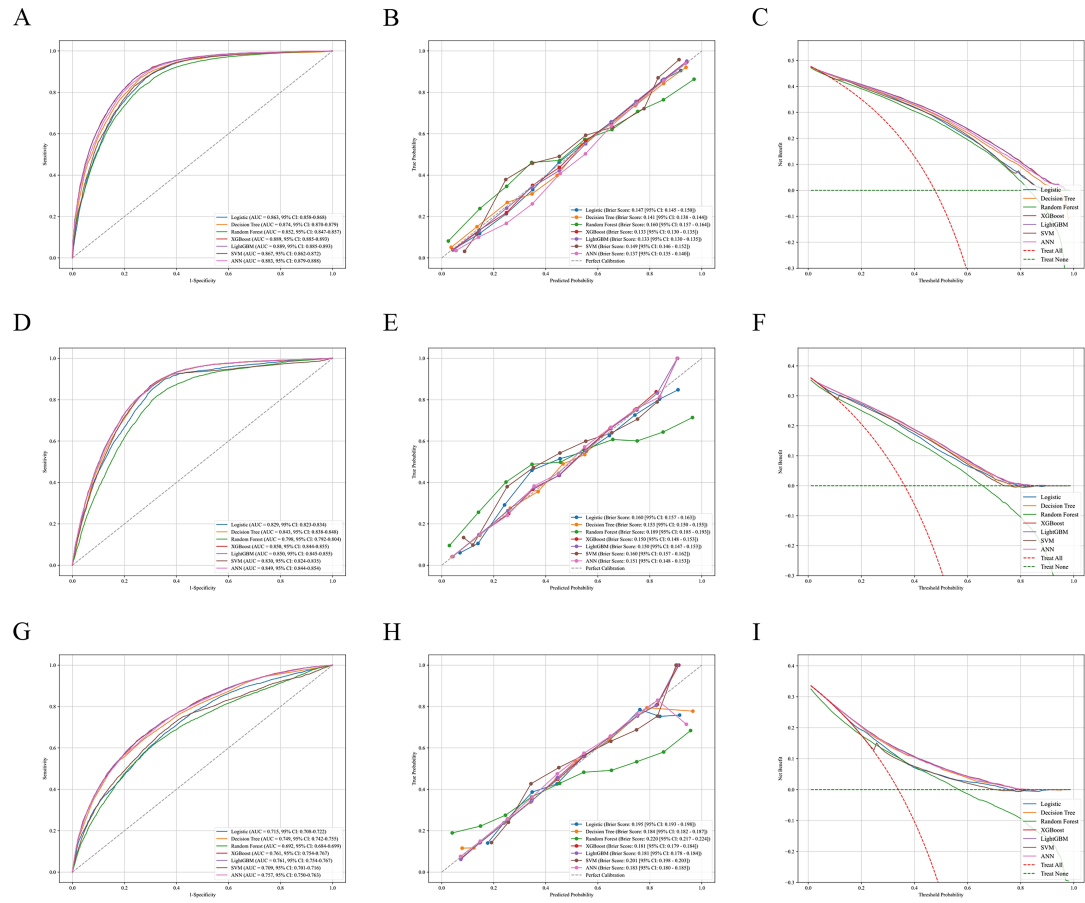


Fig. S4. Performance of machine learning models predicting historical allocations of surgery, chemotherapy, and radiotherapy after exclusion of prespecified sociodemographic variables in the internal testing cohort. (A) ROC curves for the prediction of historical surgical allocation using seven candidate machine learning models. (B) Calibration curves for the prediction of historical surgical allocation. (C) DCA curves for the prediction of historical surgical allocation. (D) ROC curves for the prediction of historical chemotherapy allocation using seven candidate machine learning models. (E) Calibration curves for the prediction of historical chemotherapy allocation. (F) DCA curves for the prediction of historical chemotherapy allocation. (G) ROC curves for the prediction of historical radiotherapy allocation using seven candidate machine learning models. (H) Calibration curves for the prediction of historical radiotherapy allocation. (I) DCA curves for the prediction of historical radiotherapy allocation. ROC, receiver operating characteristic; DCA, decision curve analysis.

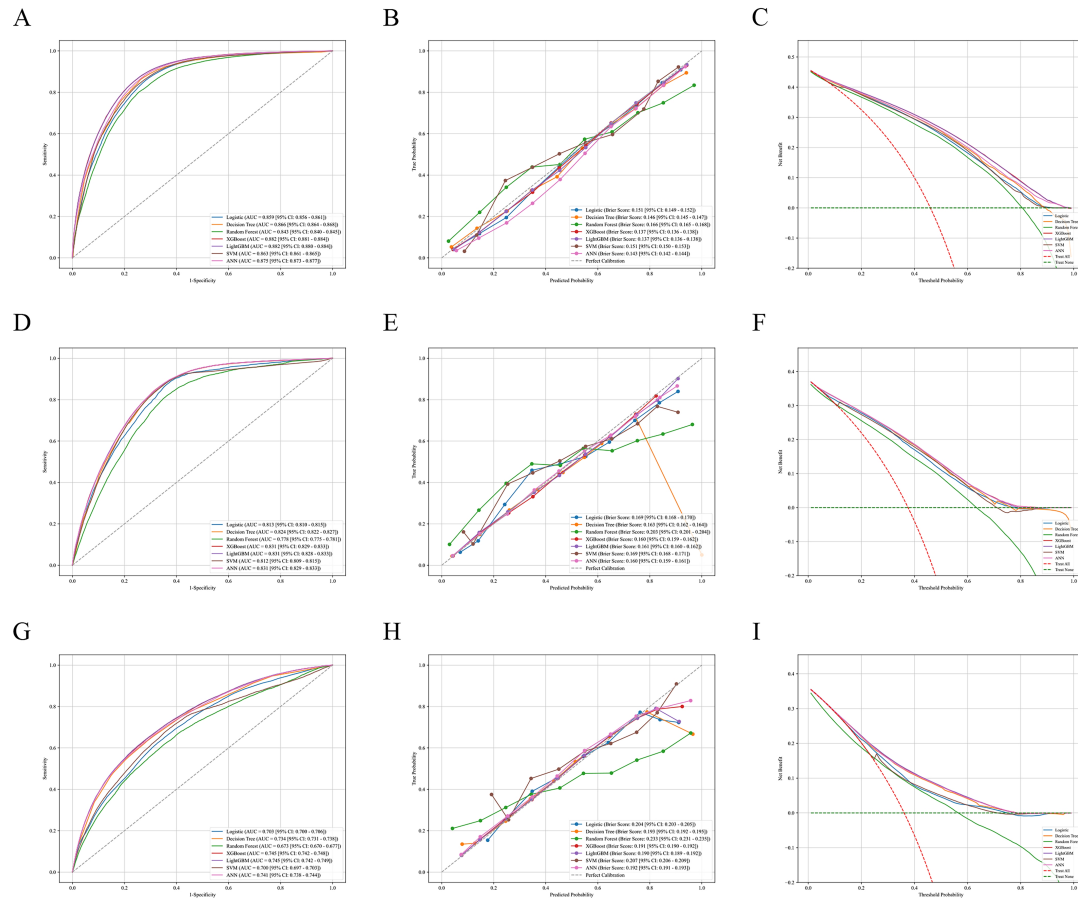


Fig. S5. Performance of machine learning models predicting historical allocations of surgery, chemotherapy, and radiotherapy after exclusion of prespecified sociodemographic variables in the geographic validation cohort. (A) ROC curves for the prediction of historical surgical allocation using seven candidate machine learning models. (B) Calibration curves for the prediction of historical surgical allocation. (C) DCA curves for the prediction of historical surgical allocation. (D) ROC curves for the prediction of historical chemotherapy allocation using seven candidate machine learning models. (E) Calibration curves for the prediction of historical chemotherapy allocation. (F) DCA curves for the prediction of historical chemotherapy allocation. (G) ROC curves for the prediction of historical radiotherapy allocation using seven candidate machine learning models. (H) Calibration curves for the prediction of historical radiotherapy allocation. (I) DCA curves for the prediction of historical radiotherapy allocation. ROC, receiver operating characteristic; DCA, decision curve analysis.

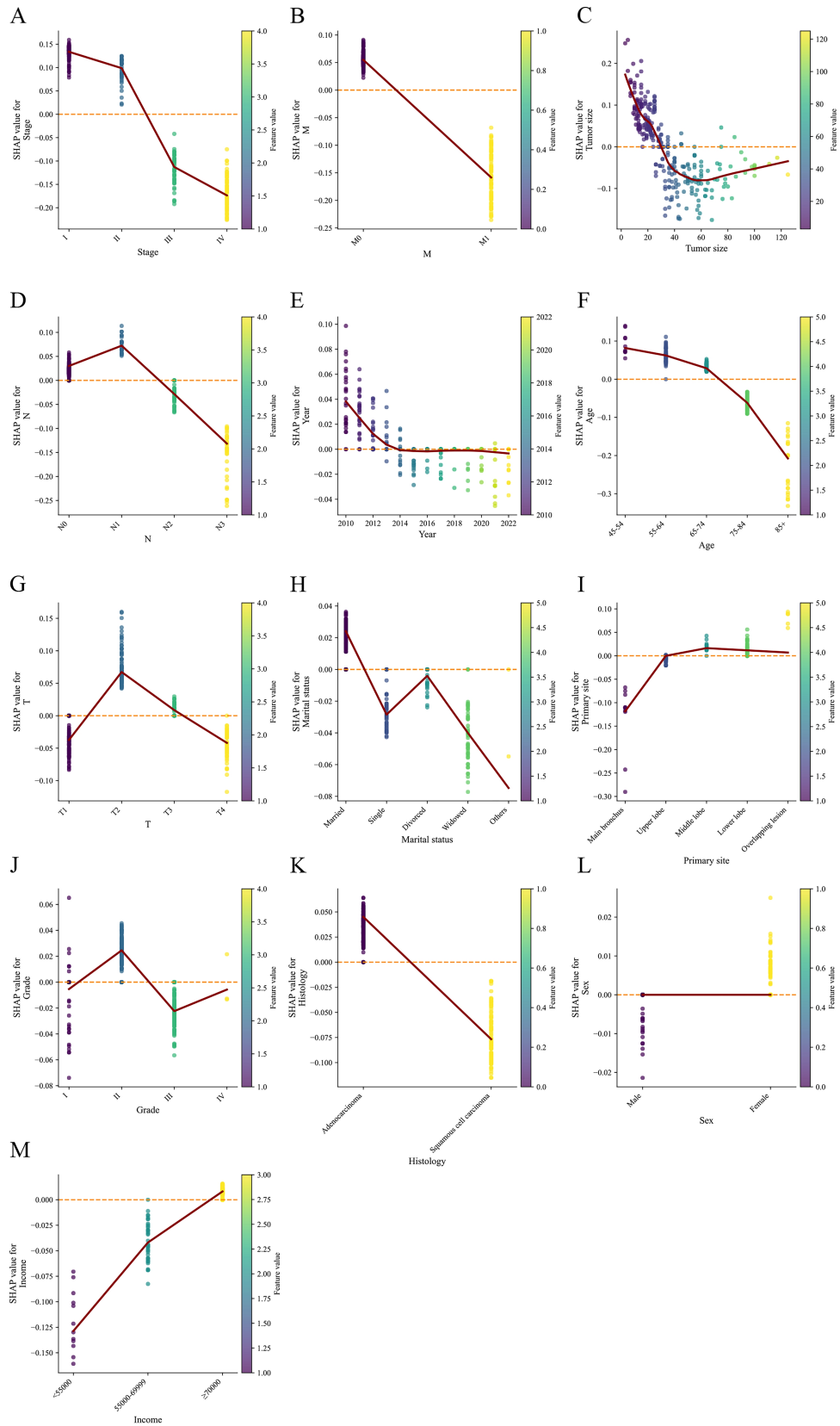


Fig. S6. SHAP dependence plots illustrating the non-linear associations of individual features in the model predicting historical surgical treatment allocation. (A) Stage, (B) M stage, (C) Tumor size, (D) N stage, (E) Year of diagnosis, (F) Age, (G) T stage, (H) Marital status, (I) Primary site, (J) Grade, (K) Histology, (L) Sex, (M) Income.

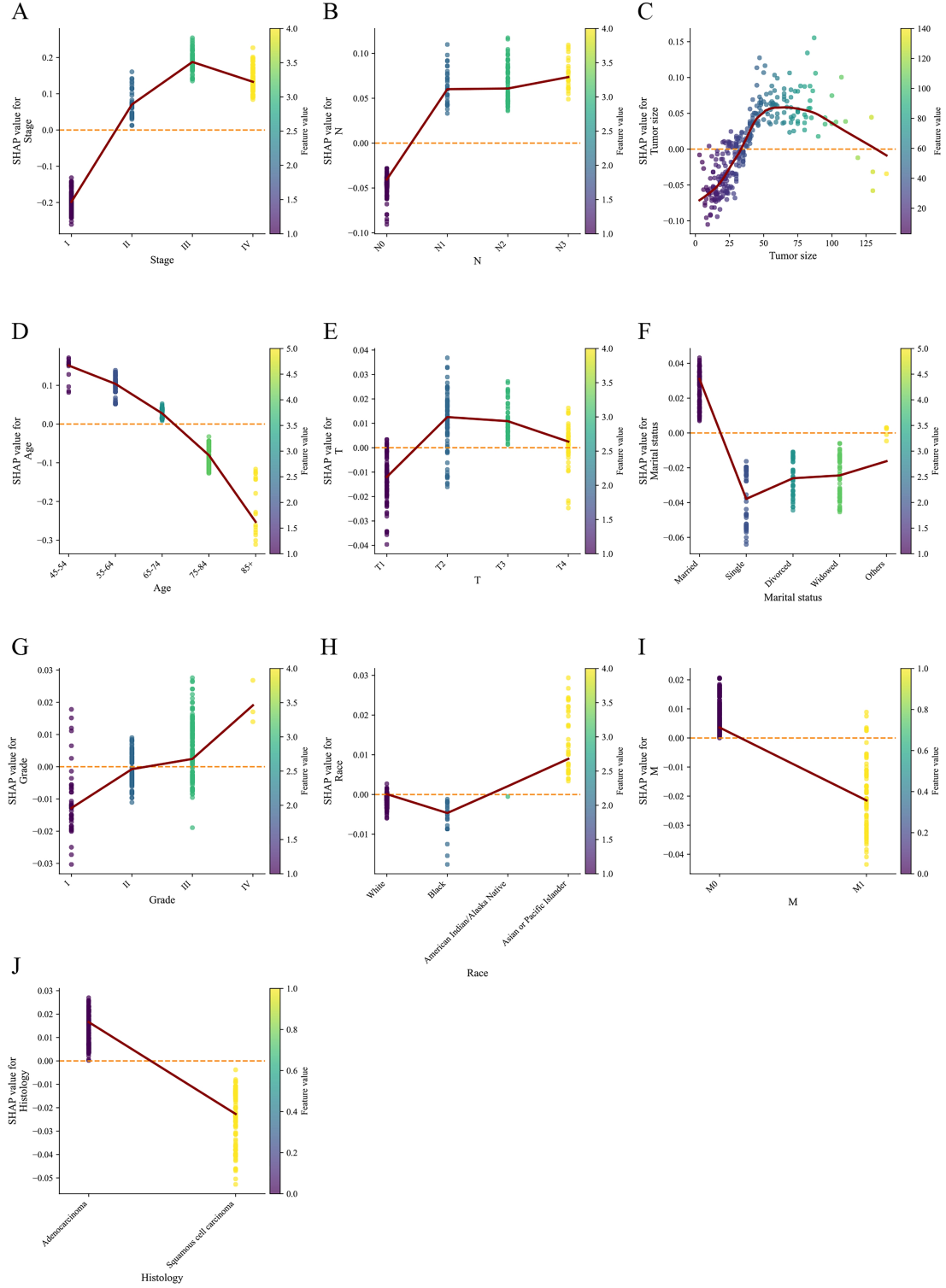


Fig. S7. SHAP dependence plots illustrating the non-linear associations of individual features in the model predicting historical chemotherapy allocation. (A) Stage, (B) N stage, (C) Tumor size, (D) Age, (E) T stage, (F) Marital status, (G) Grade, (H) Race, (I) M stage, (J) Histology.

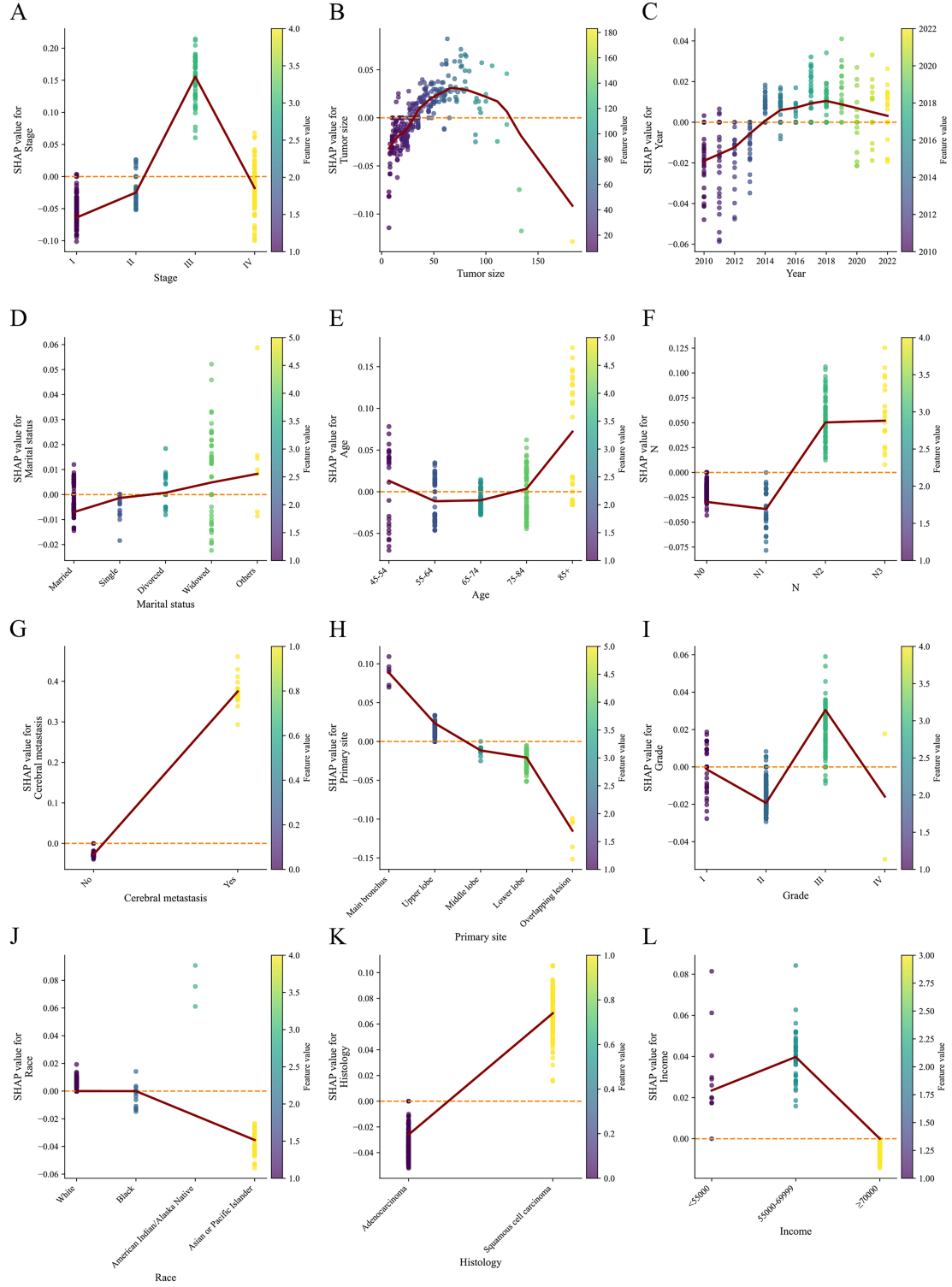


Fig. S8. SHAP dependence plots illustrating the non-linear associations of individual features in the model predicting historical radiotherapy allocation. (A) Stage, (B) Tumor size, (C) Year of diagnosis, (D) Marital status, (E) Age, (F) N stage, (G) Cerebral metastasis, (H) Primary site, (I) Grade, (J) Race, (K) Histology, and (L) Income.

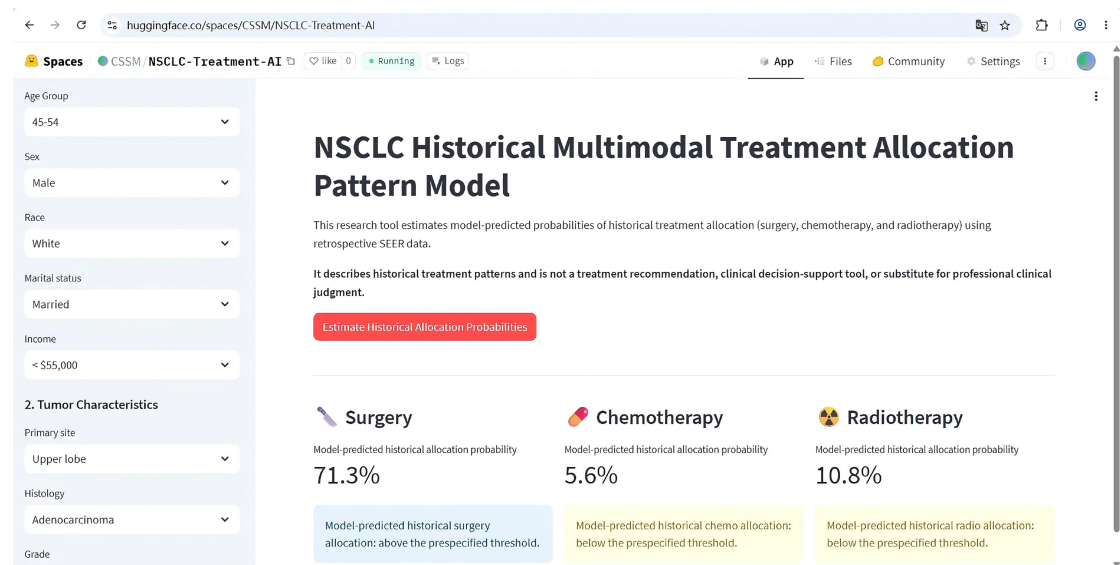


Fig. S9. Web-based interface displaying model-predicted probabilities of historical treatment allocation for patients with NSCLC.

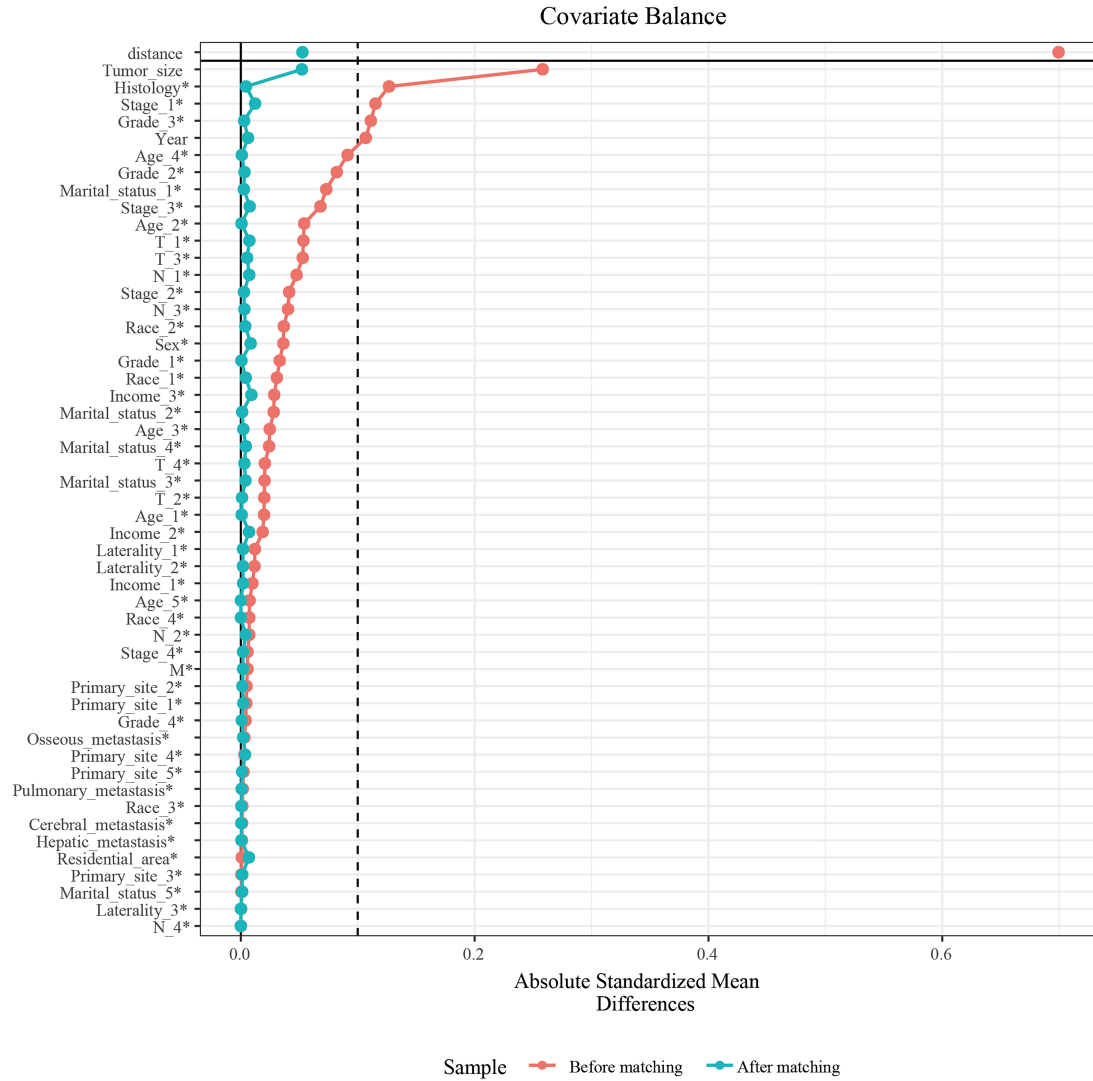


Fig. S10. Covariate balance before and after propensity score matching in the surgery cohort. The Love plot shows the absolute standardized mean differences in the propensity score and baseline covariates between the groups concordant and discordant with the model-predicted historical surgical allocation. The dashed vertical line indicates the prespecified balance threshold of 0.10. Values closer to zero indicate better covariate balance. PSM, propensity score matching; SMD, standardized mean difference.

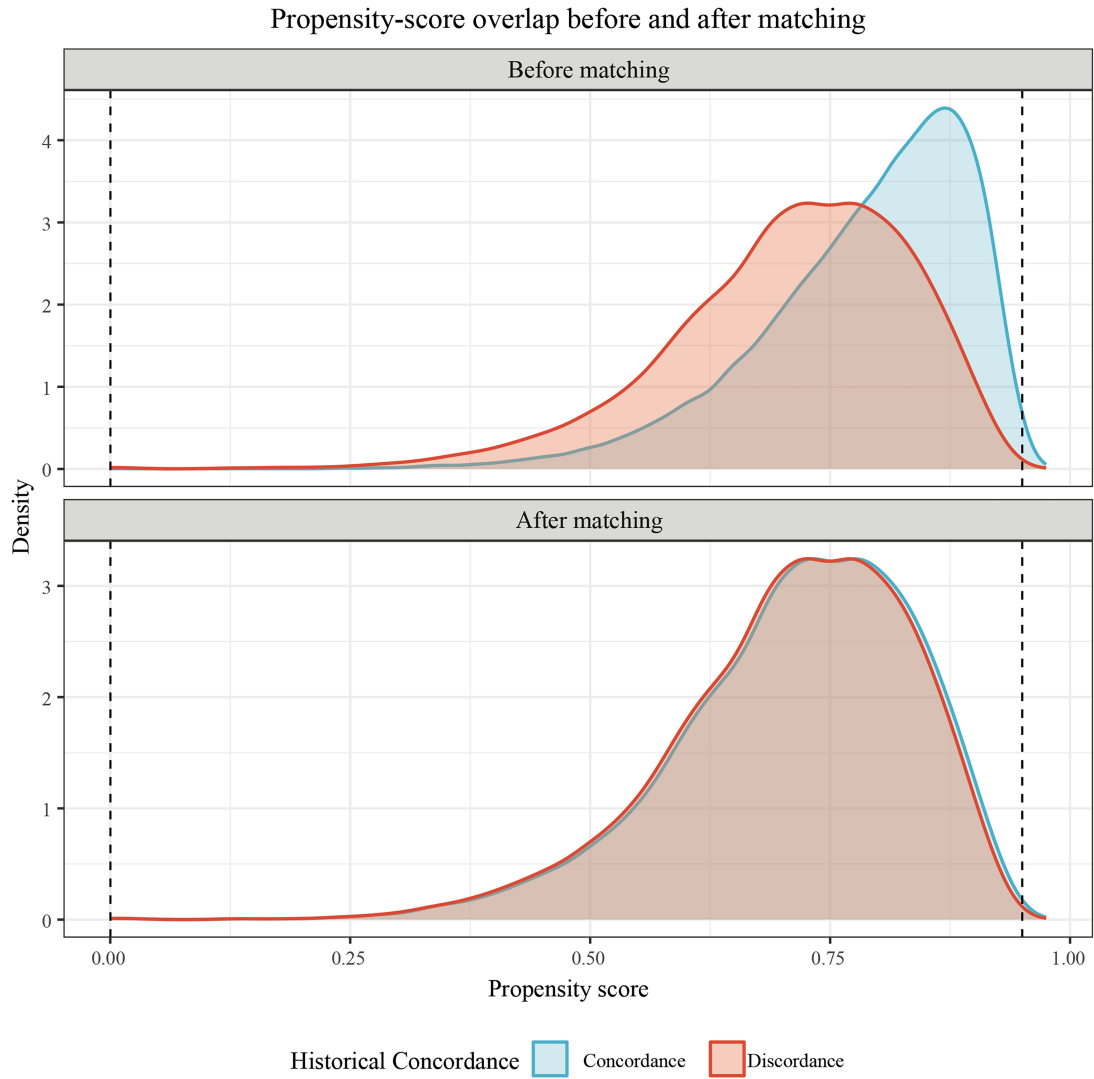


Fig. S11. Propensity score overlap before and after matching in the surgery cohort. Kernel density distributions of propensity scores are shown for the groups concordant and discordant with the model-predicted historical surgical allocation. The upper and lower panels present the distributions before and after propensity score matching, respectively. The dashed vertical lines indicate the boundaries of the region of common support.

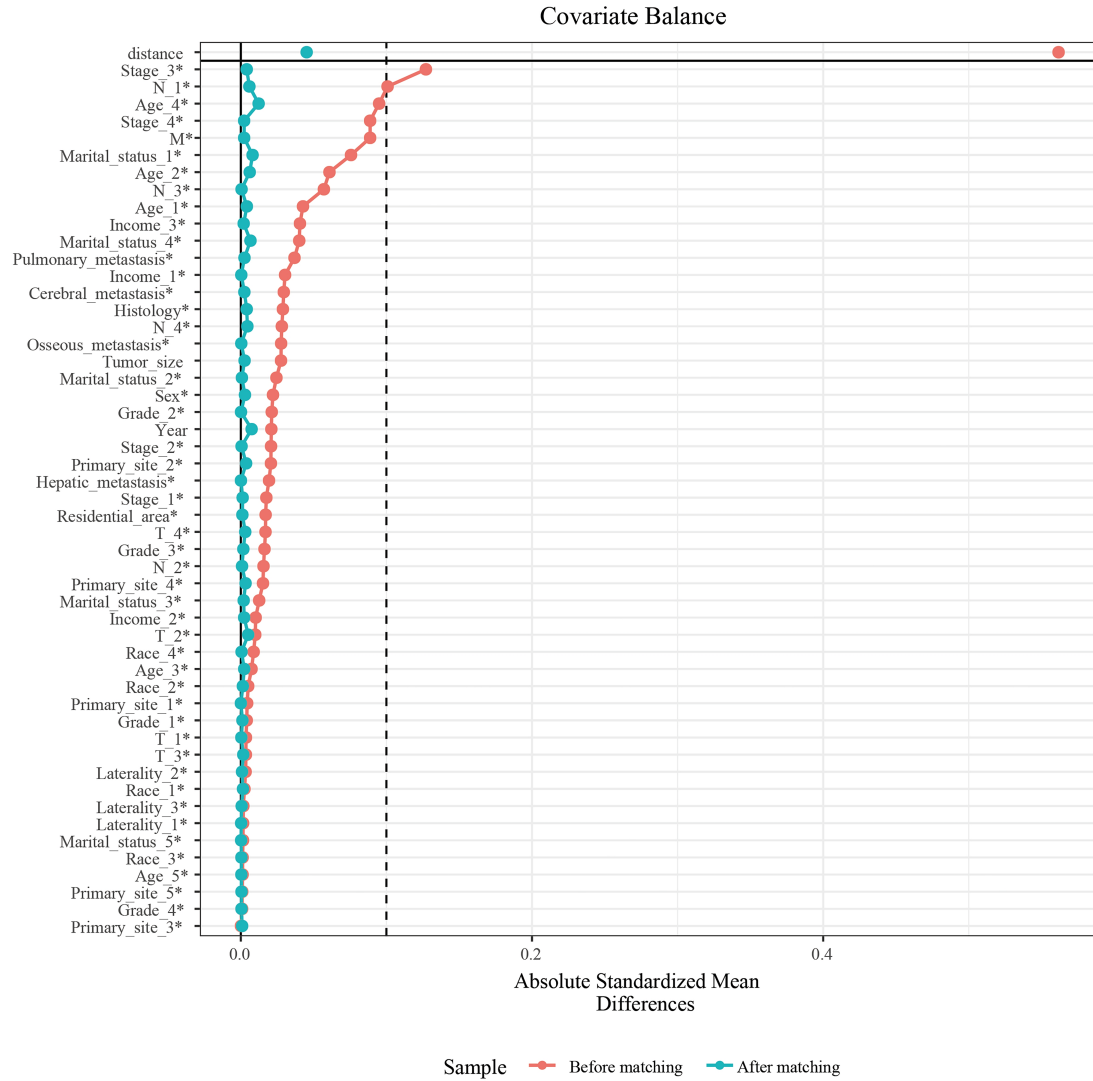


Fig. S12. Covariate balance before and after propensity score matching in the chemotherapy cohort. The Love plot shows the absolute standardized mean differences in the propensity score and baseline covariates between the groups concordant and discordant with the model-predicted historical chemotherapy allocation. The dashed vertical line indicates the prespecified balance threshold of 0.10. Values closer to zero indicate better covariate balance. PSM, propensity score matching; SMD, standardized mean difference.

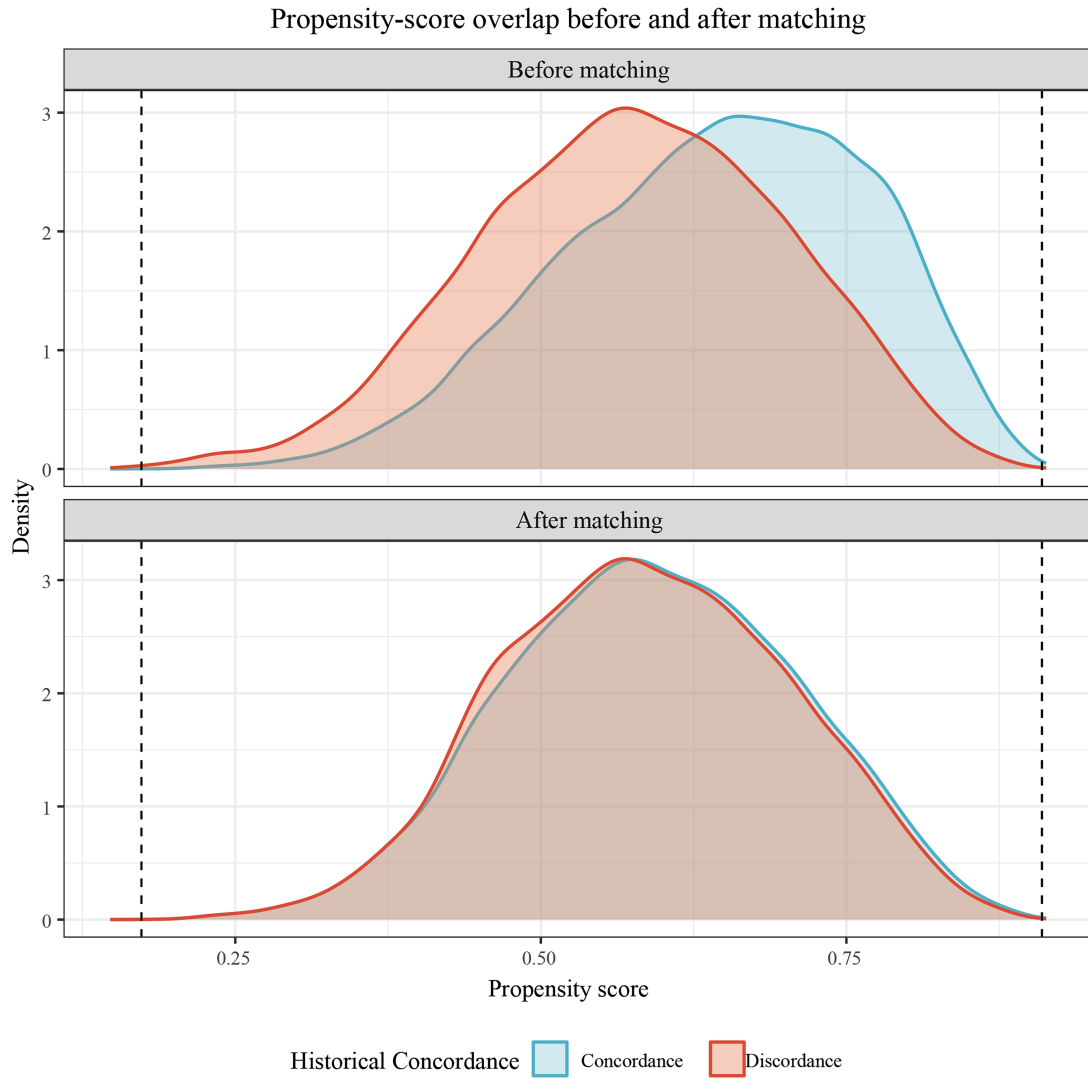


Fig. S13. Propensity score overlap before and after matching in the chemotherapy cohort. Kernel density distributions of propensity scores are shown for the groups concordant and discordant with the model-predicted historical chemotherapy allocation. The upper and lower panels present the distributions before and after propensity score matching, respectively. The dashed vertical lines indicate the boundaries of the region of common support.

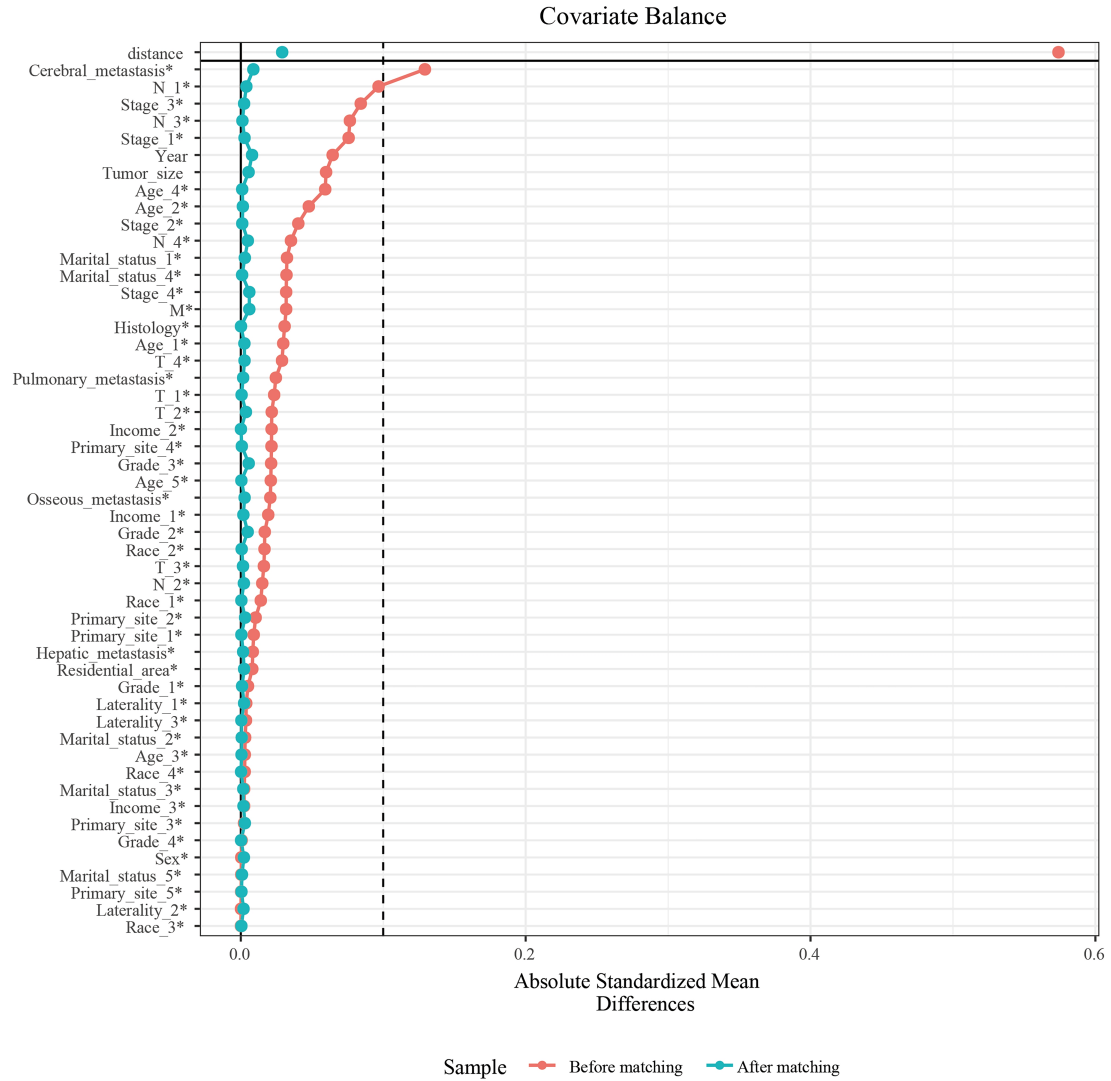


Fig. S14. Covariate balance before and after propensity score matching in the radiotherapy cohort. The Love plot shows the absolute standardized mean differences in the propensity score and baseline covariates between the groups concordant and discordant with the model-predicted historical radiotherapy allocation. The dashed vertical line indicates the prespecified balance threshold of 0.10. Values closer to zero indicate better covariate balance. PSM, propensity score matching; SMD, standardized mean difference.

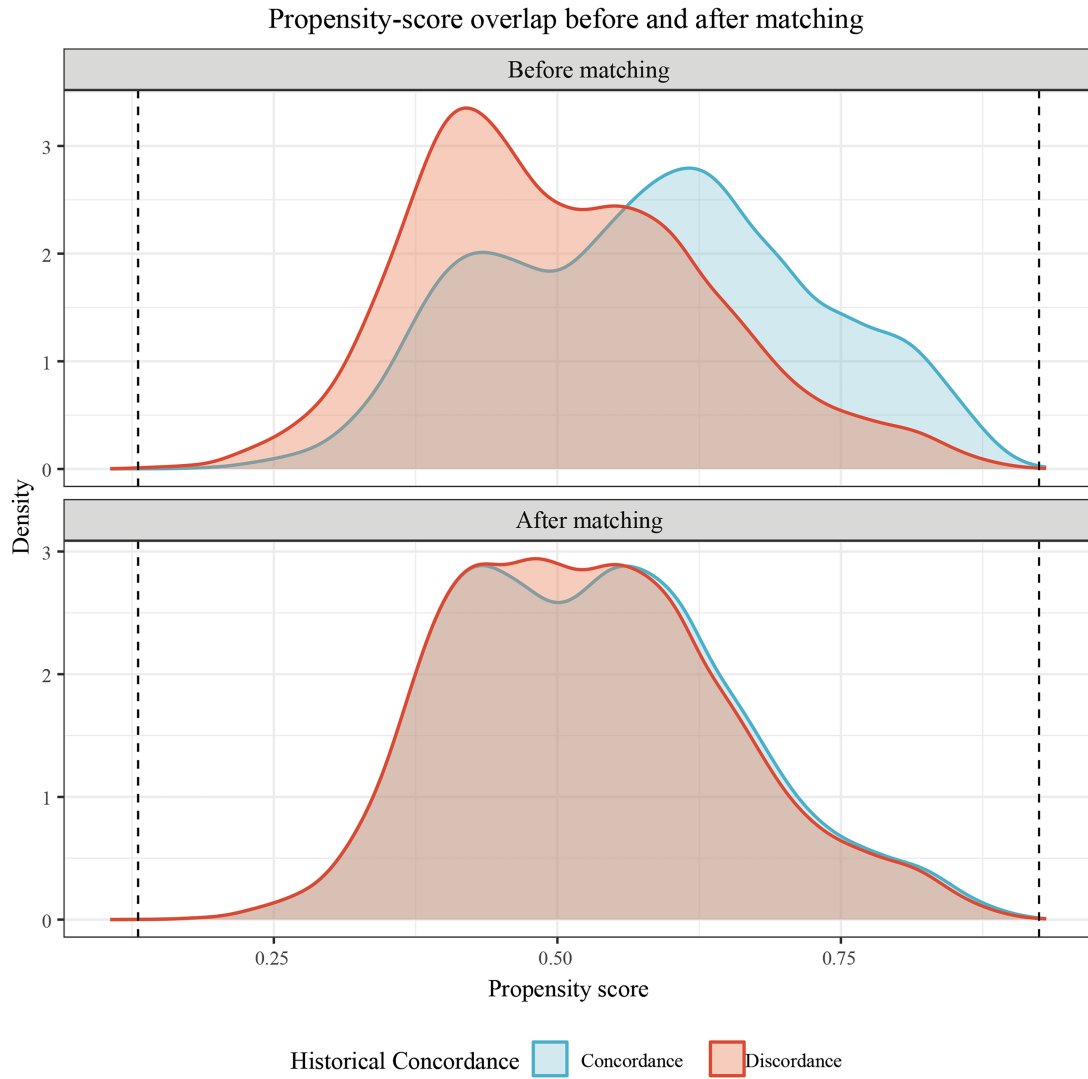


Fig. S15. Propensity score overlap before and after matching in the radiotherapy cohort. Kernel density distributions of propensity scores are shown for the groups concordant and discordant with the model-predicted historical radiotherapy allocation. The upper and lower panels present the distributions before and after propensity score matching, respectively. The dashed vertical lines indicate the boundaries of the region of common support.

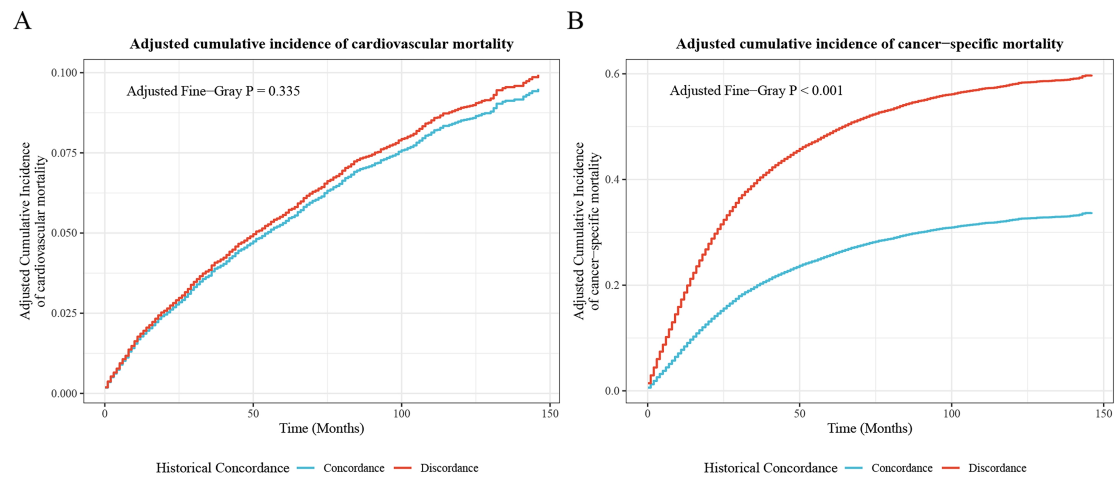


Fig. S16. Adjusted cumulative incidence functions for mortality outcomes in the propensity score-matched surgery cohort. (A) Cardiovascular mortality. (B) Cancer-specific mortality. The curves compare patients concordant and discordant with the model-predicted historical surgical allocation. P values were derived from covariate-adjusted Fine-Gray competing-risk models.

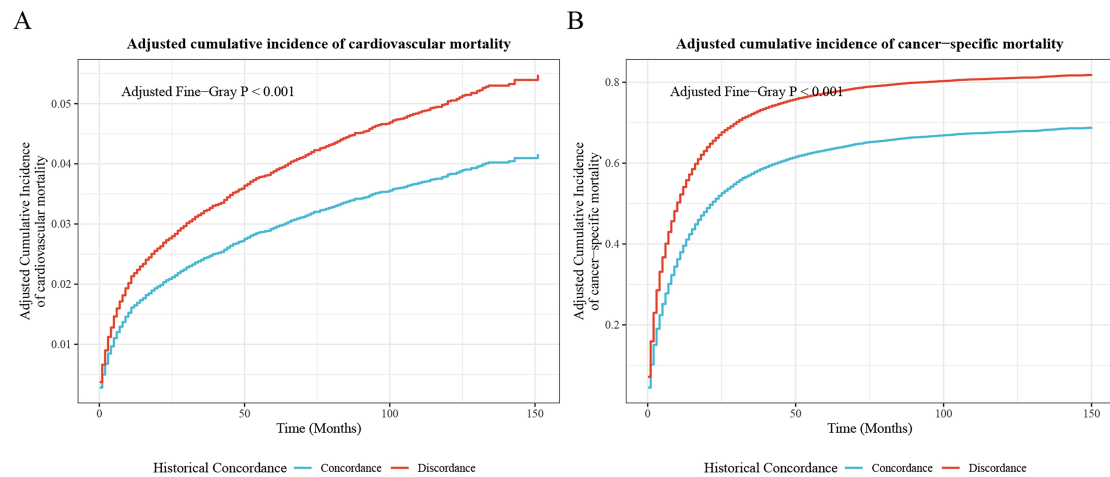


Fig. S17. Adjusted cumulative incidence functions for mortality outcomes in the propensity score-matched chemotherapy cohort. (A) Cardiovascular mortality. (B) Cancer-specific mortality. The curves compare patients concordant and discordant with the model-predicted historical chemotherapy allocation. P values were derived from covariate-adjusted Fine-Gray competing-risk models.

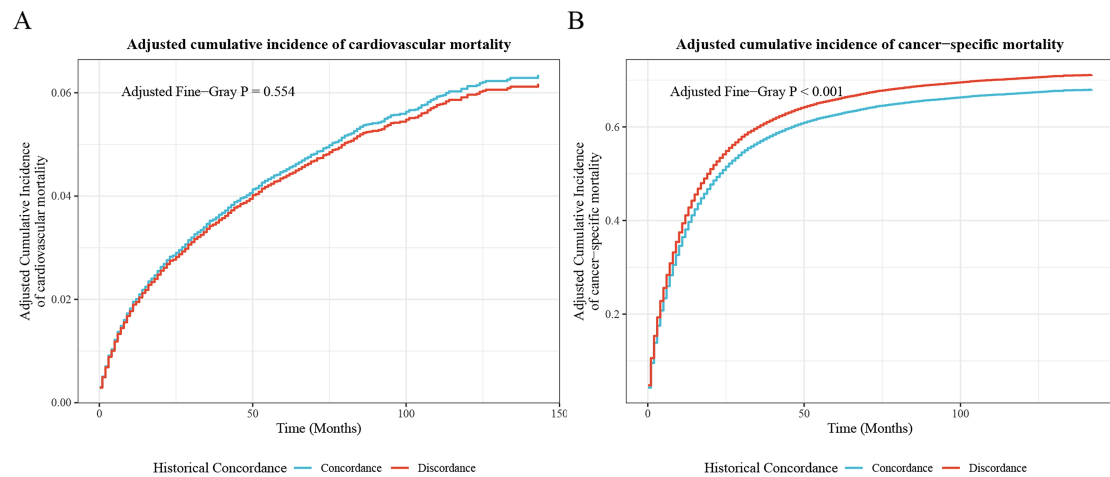


Fig. S18. Adjusted cumulative incidence functions for mortality outcomes in the propensity score-matched radiotherapy cohort. (A) Cardiovascular mortality. (B) Cancer-specific mortality. The curves compare patients concordant and discordant with the model-predicted historical radiotherapy allocation. P values were derived from covariate-adjusted Fine-Gray competing-risk models.

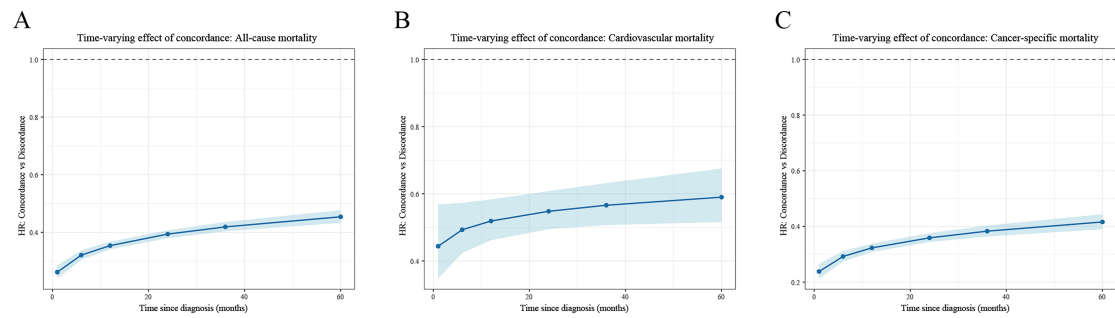


Fig. S19. Time-varying associations between concordance with the model-predicted historical surgical allocation and mortality outcomes in the propensity score-matched surgery cohort. (A) All-cause mortality. (B) Cardiovascular mortality. (C) Cancer-specific mortality. Solid lines represent time-specific hazard ratios comparing the concordant group with the discordant group, and shaded areas represent 95% confidence intervals. Horizontal dashed lines indicate a hazard ratio of 1.0.

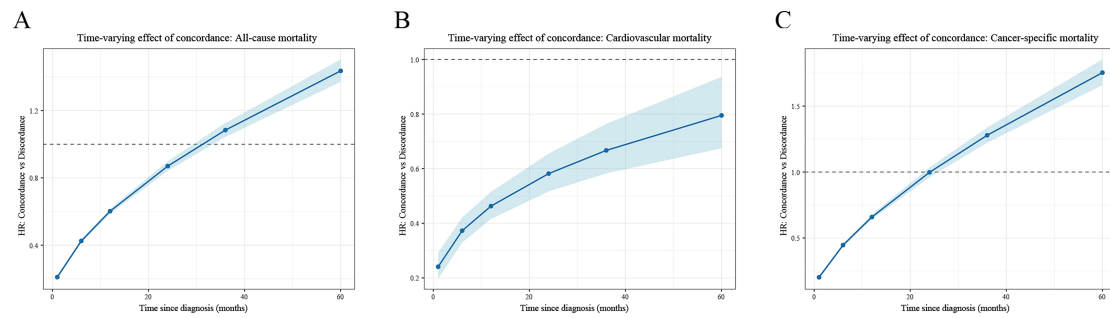


Fig. S20. Time-varying associations between concordance with the model-predicted historical chemotherapy allocation and mortality outcomes in the propensity score-matched chemotherapy cohort. (A) All-cause mortality. (B) Cardiovascular mortality. (C) Cancer-specific mortality. Solid lines represent time-specific hazard ratios comparing the concordant group with the discordant group, and shaded areas represent 95% confidence intervals. Horizontal dashed lines indicate a hazard ratio of 1.0.

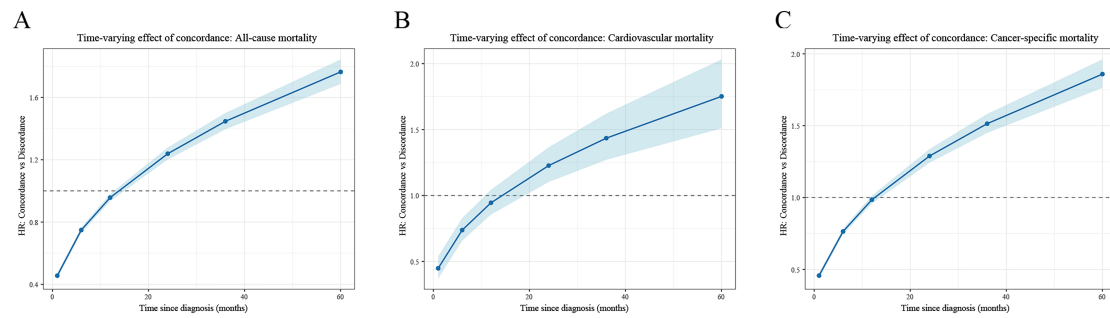


Fig. S21. Time-varying associations between concordance with the model-predicted historical radiotherapy allocation and mortality outcomes in the propensity score-matched radiotherapy cohort. (A) All-cause mortality. (B) Cardiovascular mortality. (C) Cancer-specific mortality. Solid lines represent time-specific hazard ratios comparing the concordant group with the discordant group, and shaded areas represent 95% confidence intervals. Horizontal dashed lines indicate a hazard ratio of 1.0.