

Figure S1. Sensitivity analysis of overall survival after replacing the propensity score-matched estimate with the unmatched entire-cohort estimate, shown as a random-effects forest plot. HR, hazard ratio; IV, inverse variance; CI, confidence interval; SE, standard error; df, degrees of freedom.

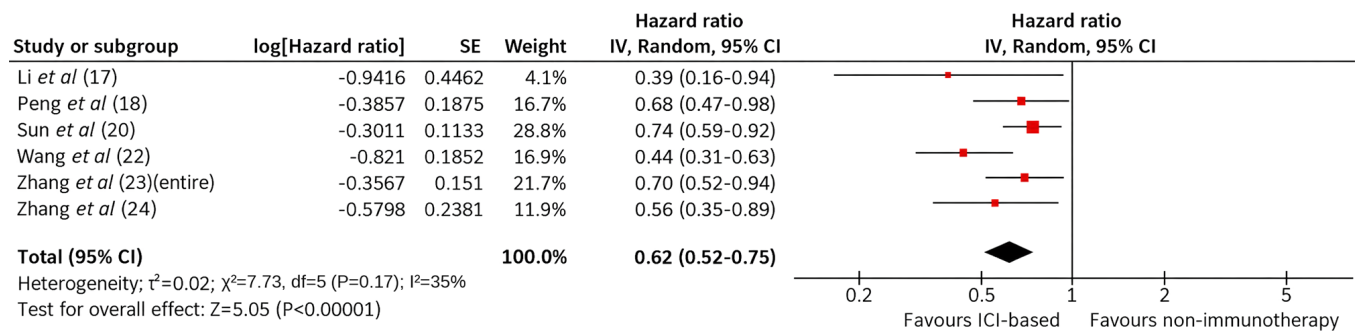


Figure S2. Sensitivity analysis of progression-free survival after replacing the propensity score-matched estimate with the unmatched entire-cohort estimate, shown as a random-effects forest plot. HR, hazard ratio; CI, confidence interval; IV, inverse variance; SE, standard error; df, degrees of freedom.

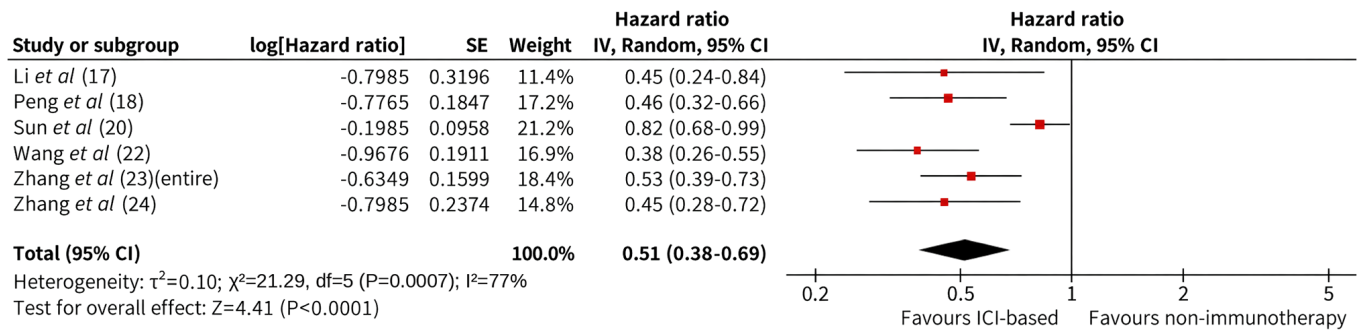


Figure S3. Sensitivity analysis of progression-free survival including additional studies with extractable or partially aligned post-progression ICI-based treatment data, shown as a random-effects forest plot. PSM, propensity score matching; ICI, immune checkpoint inhibitor; HR, hazard ratio; IV, inverse variance; CI, confidence interval; SE, standard error; df, degrees of freedom.

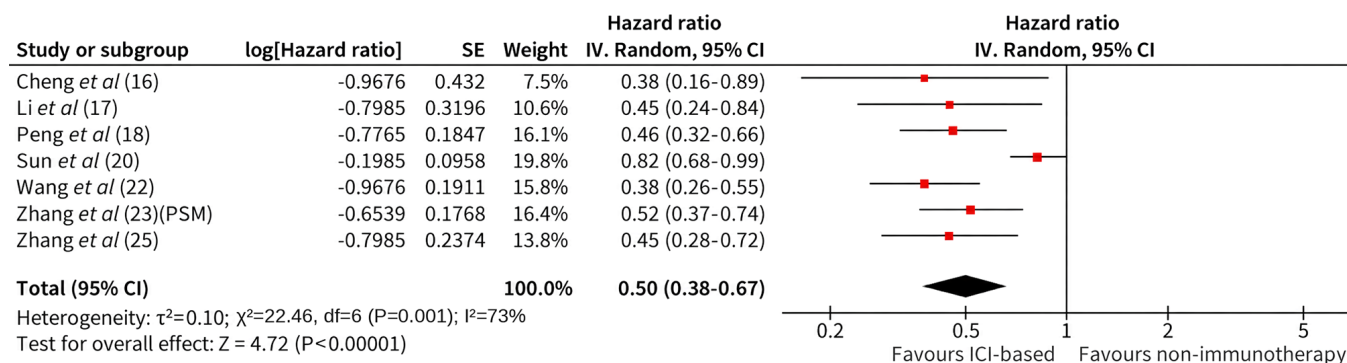


Figure S4. Conservative sensitivity analysis of PFS after excluding studies that used the label PFS2. The analysis was performed to examine whether the primary PFS estimate was dependent on PFS2-labelled endpoints. PFS, progression-free survival; PSM, propensity score matching; ICI, immune checkpoint inhibitor; HR, hazard ratio; CI, confidence interval; IV, inverse variance; SE, standard error; df, degrees of freedom.

