

Supplementary Material.

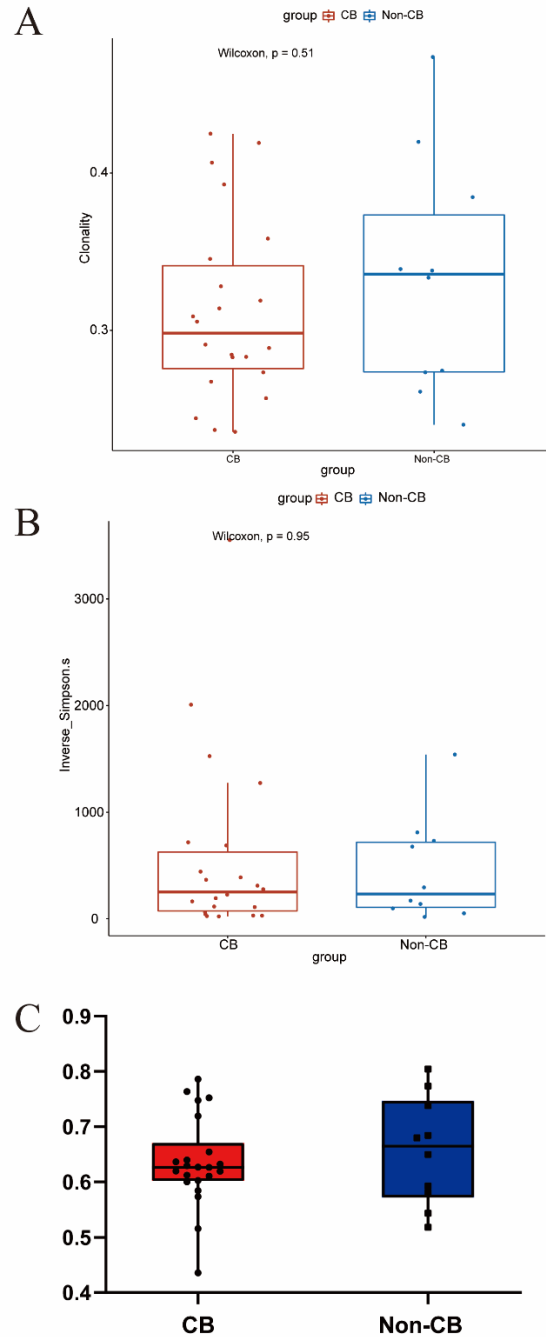


Fig. S1 Comparative analysis of pre-treatment TCR repertoire characteristics by clinical outcome. (A) Clonality index and (B) Inverse Simpson's diversity index in patients with (red) and without (blue) clinical benefit (CB). (C) Clonal space (cumulative frequency of top 10% abundant clones) comparison between groups. P-values were obtained using the Mann-Whitney test.

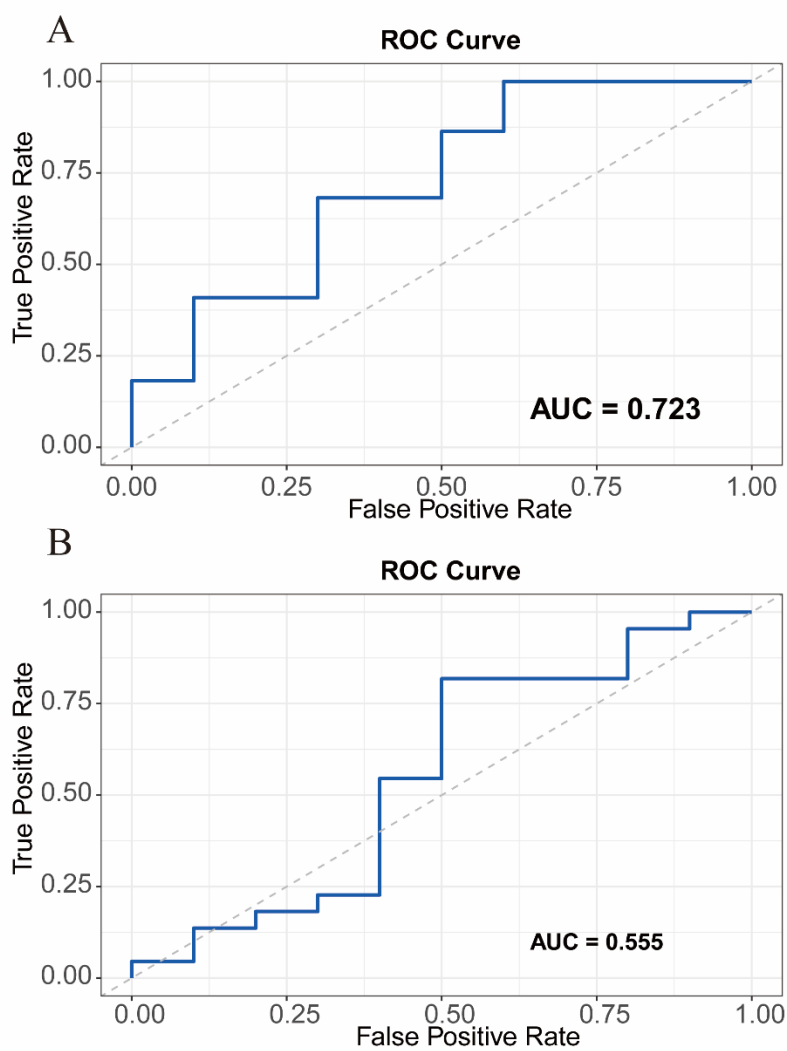


Fig. S2 Receiver operating characteristic curve for evaluating the predicting potential of richness (A) and Shannon index (B)

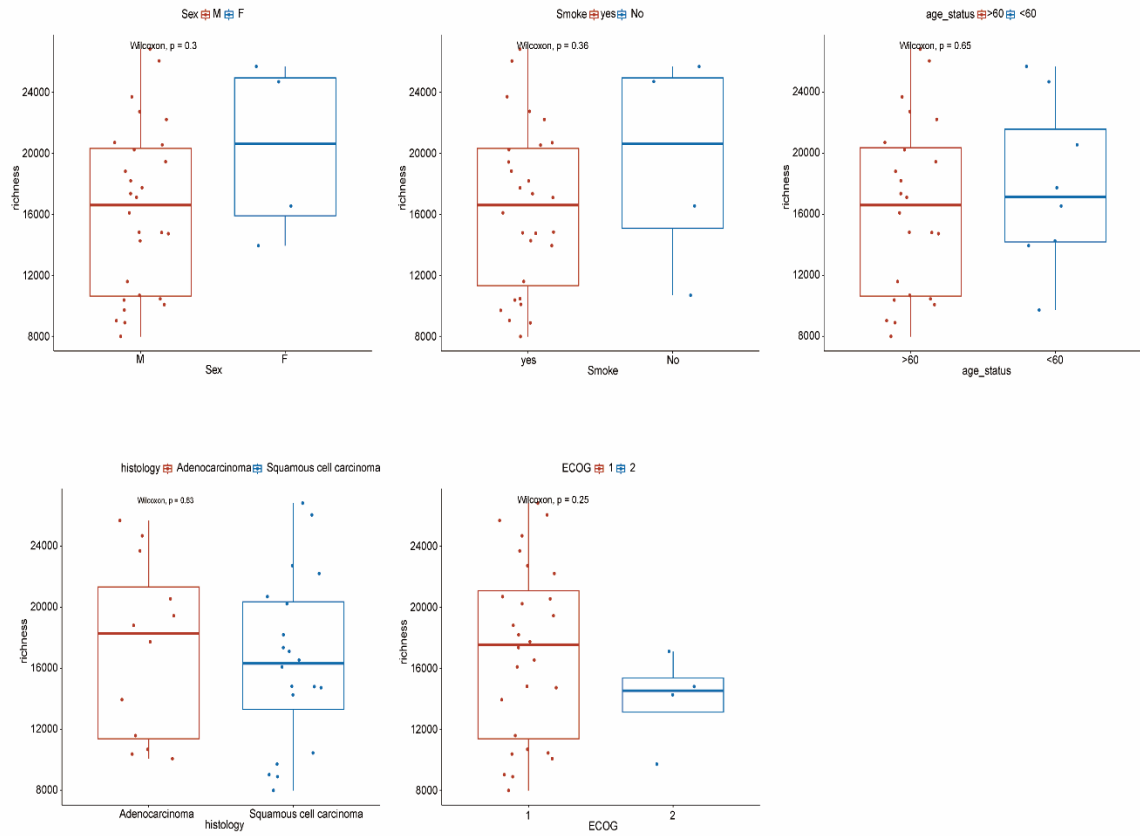


Fig. S3 Association between baseline TCR richness and clinical characteristics in NSCLC patients. Comparison of pre-treatment richness index (mean $\pm$ SEM) stratified by Sex (male/female), age (<60/ $\geq$ 60 years), Smoking status (yes/no), Histology (adenocarcinoma/squamous) or ECOG status (1 and 2).

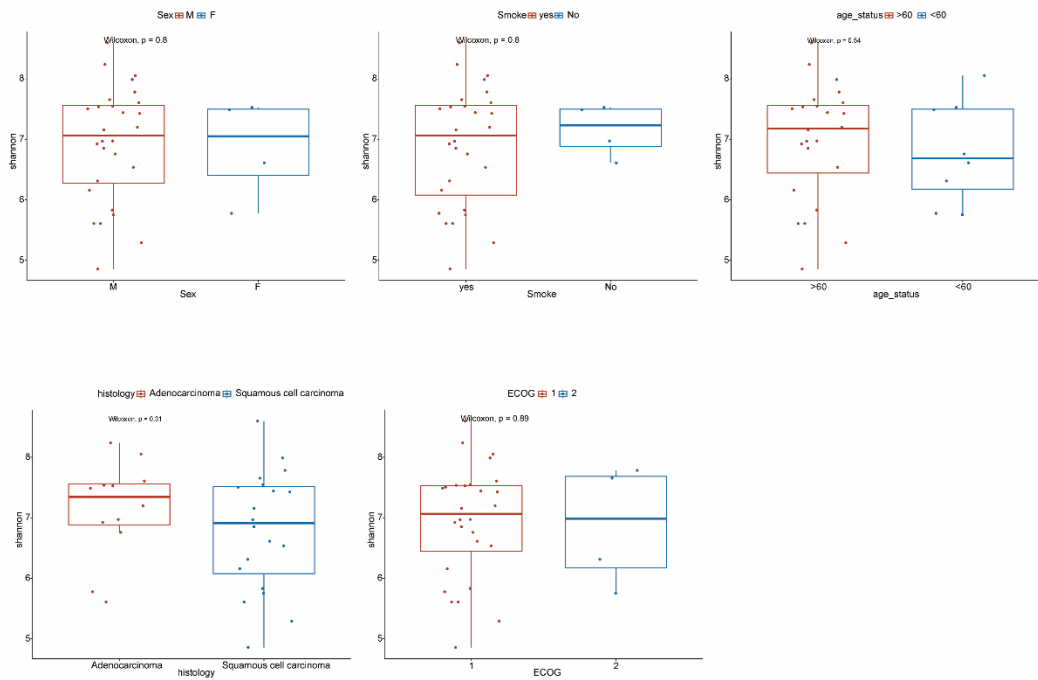


Fig. S4 Association between baseline TCR Shannon index and clinical characteristics in NSCLC patients. Comparison of pre-treatment richness index (mean $\pm$ SEM) stratified by Sex (male/female), age (<60/ $\geq$ 60 years), Smoking status (yes/no), Histology (adenocarcinoma/squamous) or ECOG status (1 and 2).

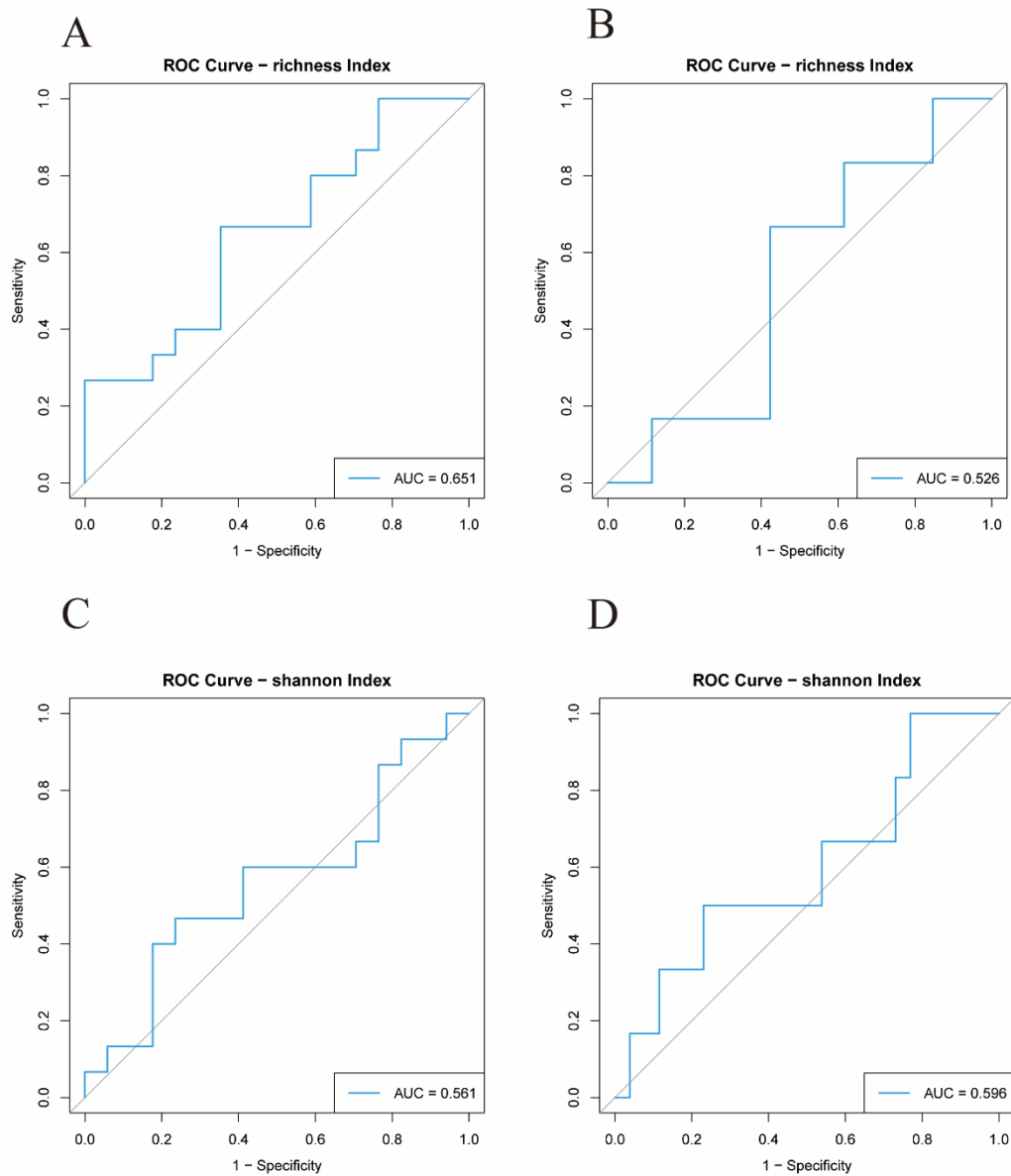


Fig. S5 Optimal threshold determination for TCR diversity metric dichotomization in survival prediction. ROC analysis for richness index stratification (A) Progression-free survival (PFS) prediction (AUC = 0.651) and (B) Overall survival (OS) prediction (AUC = 0.526). ROC analysis for Shannon index stratification (C) PFS prediction (AUC = 0.561) and (D) OS prediction (AUC = 0.596).

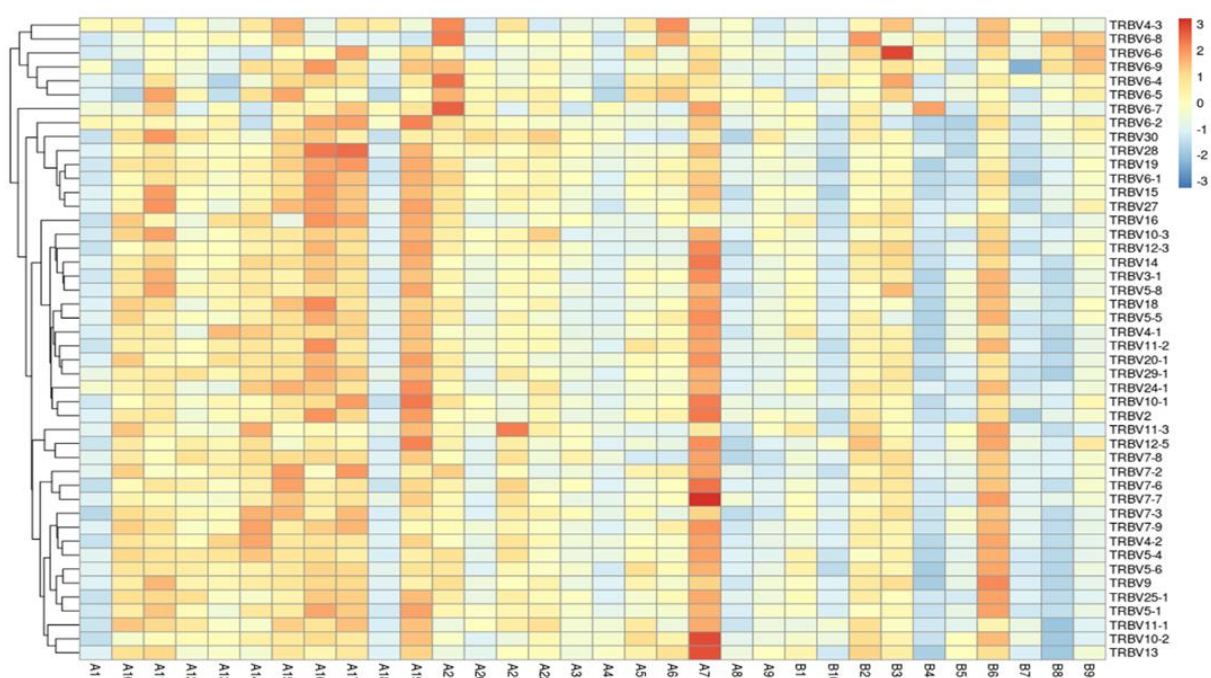


Fig. S6 Heatmap of the TRBV gene segment usage of patients with NSCLC in each sample.

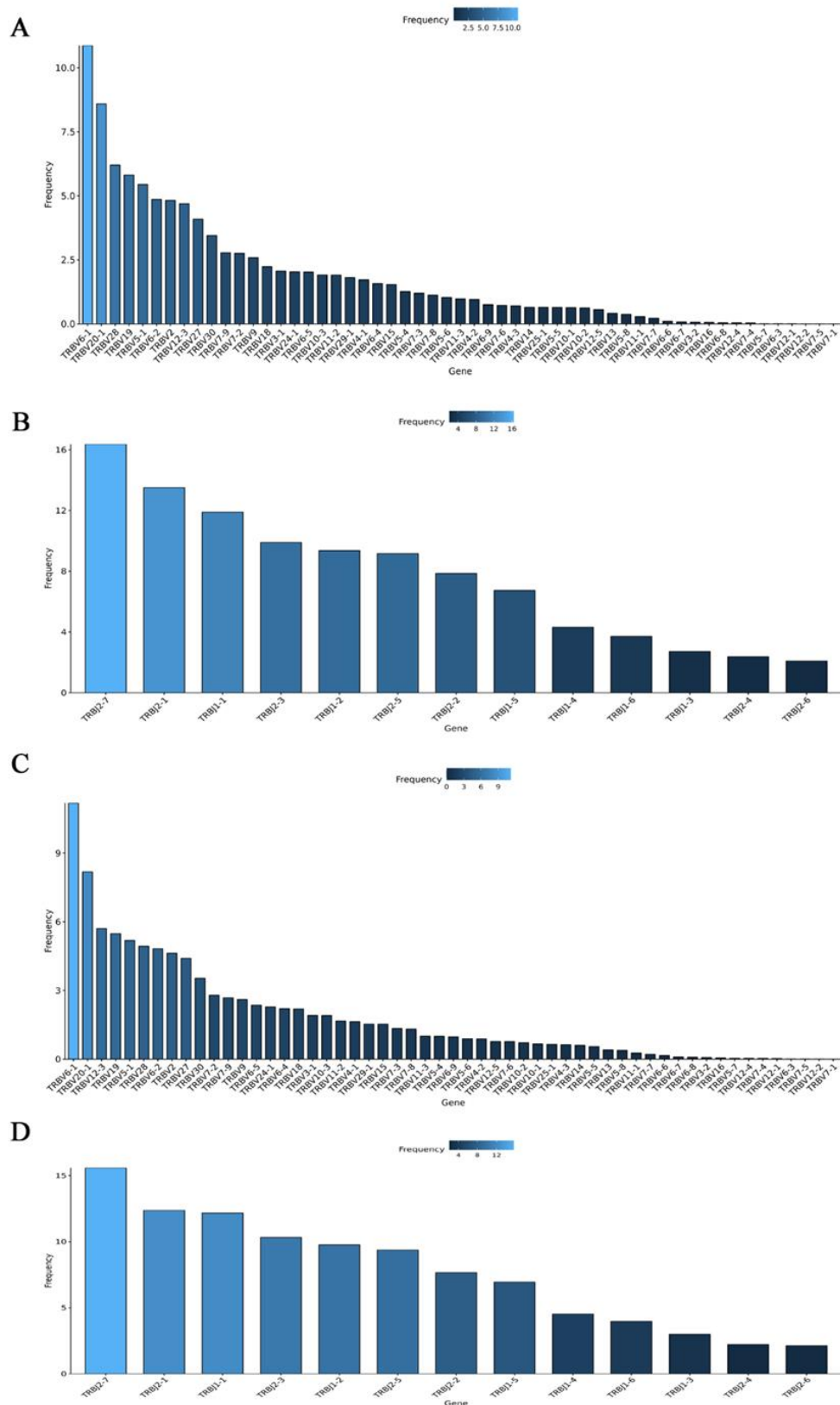


Fig. S7 TRBV/TRBJ gene usage in pre-treated patients with NSCLC. (A, B) Frequencies of the V and J genes in samples from patients with clinical benefit. (C, D) Frequencies of the V and J genes in samples from patients without clinical benefit.