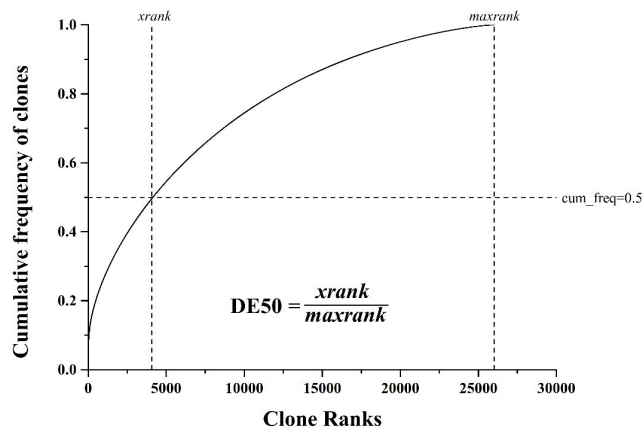
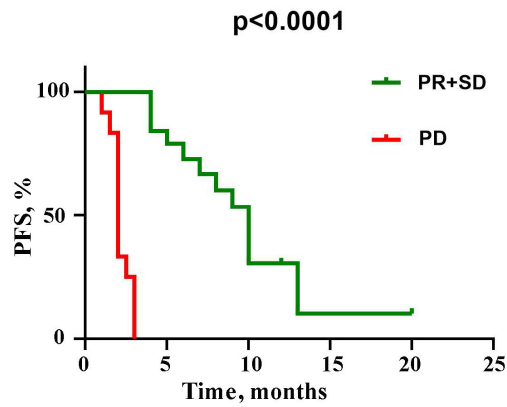


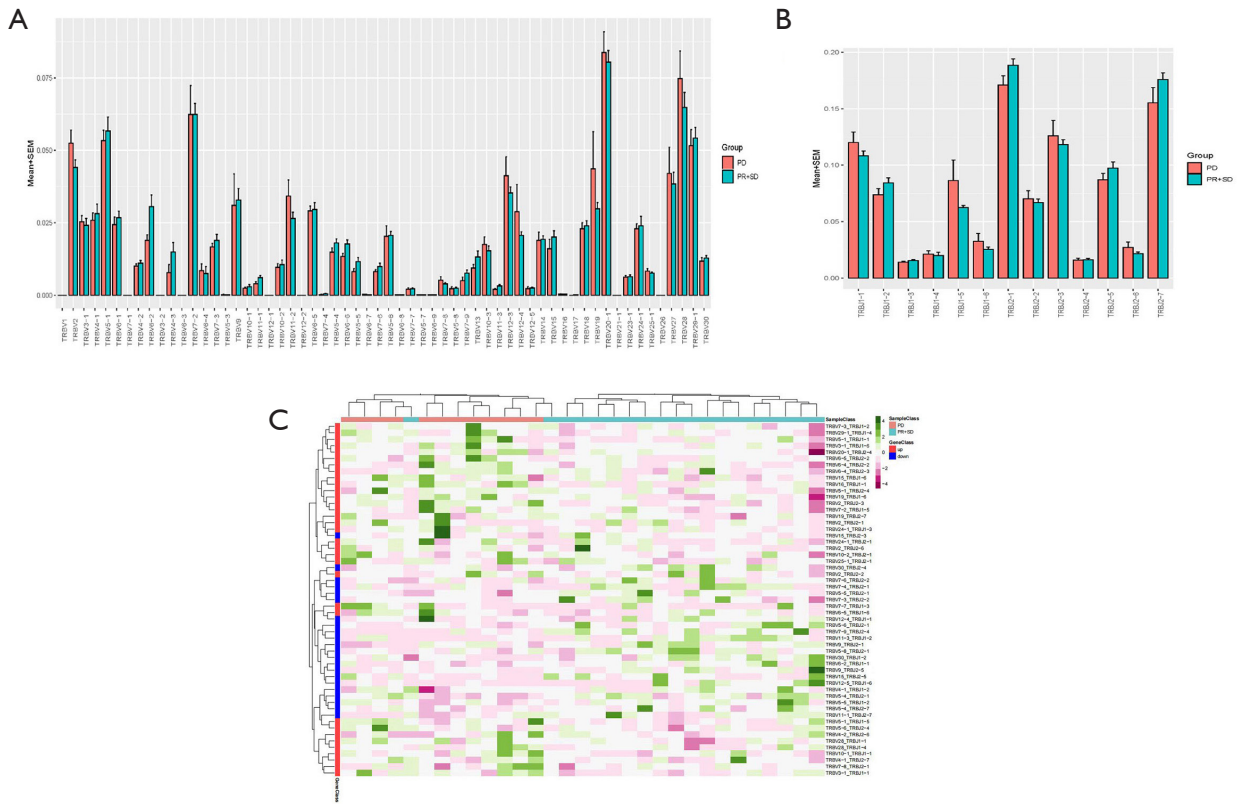
**Figure S1** The analysis process of TCR repertoire diversity. TCR, T-cell receptor.



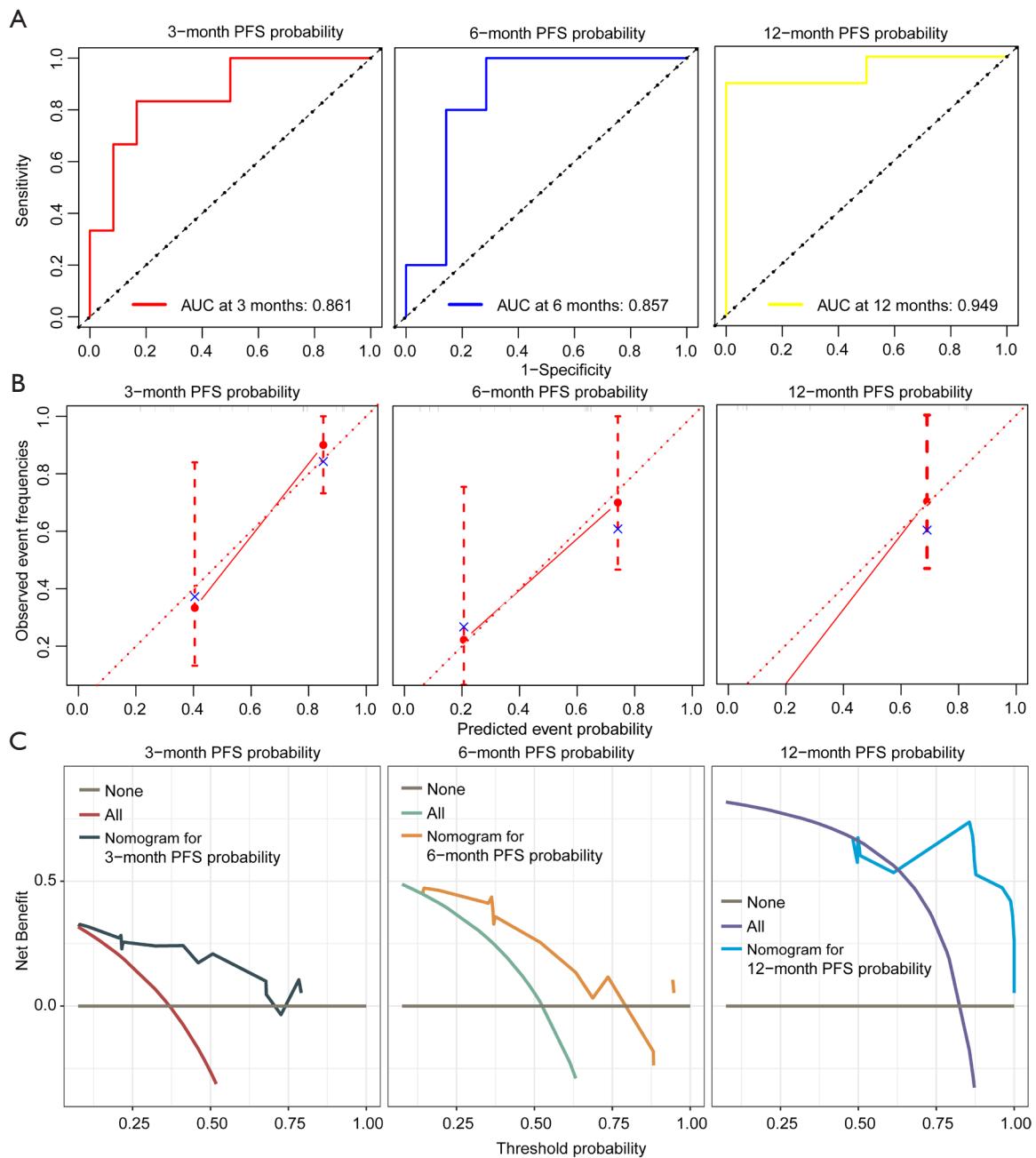
**Figure S2** Schematic graph for DE50 calculation. X-axis, clone ranks based on the frequency of each clone type in descending order; y-axis, cumulative frequency of each clone type.



**Figure S3** Kaplan-Meier plots showing PFS probability in responders and non-responders to anti-PD-1 treatment. PFS, progression-free survival; PD-1, programmed death 1.



**Figure S4** Usage frequency of V and J gene segments in PR + SD and PD group. Data are presented as mean ± SEM. PR, partial response; SD, stable disease; PD, progression disease; SEM, standard error of the mean.



**Figure S5** The internal validation of nomogram using ROC curves, calibration curve, and DCA curve analysis, respectively. (A) The ROC curves for the prediction of 3-, 6-, 12-month PFS rate of gastrointestinal cancer patients. (B) The calibration curve analysis of the nomogram compared for 3-, 6-, 12-month PFS. (C) DCA curve analysis of the nomogram compared for 3-, 6-, 12-month PFS. ROC, receiver operating characteristic; DCA, decision curve analysis; PFS, progression-free survival.