

TableS1. Summary of sample location for TCR sequencing

ID	Tumor	PBMC	2	3	4	5	6	7	8	9	10	11	12
P01	√	√	√	√	√			√		√	√	√	
P02	√	√	√	√	√			√	√	√	√	√	
P03	√	√				√	√	√		√	√	√	√
P04	√	√	√	√	√			√	√	√	√	√	
P05	√		√		√			√	√	√	√	√	
P06	√	√	√		√			√				√	
P07	√	√	√		√			√		√		√	
P08	√	√			√	√		√		√		√	
P09	√	√					√	√		√	√	√	√
P10	√	√	√		√			√			√	√	√
P11	√	√				√		√		√	√		
P12	√	√						√		√	√	√	
P13	√	√				√		√		√	√	√	
P14	√	√				√		√			√	√	
P15	√	√	√		√			√			√	√	
P16	√	√		√	√			√				√	
P17	√	√	√		√			√	√		√	√	
P18	√	√				√		○		√	○	√	
P19	√	√				√	√	○		√	√	√	
P20	√	√	○		○			○		√	○	○	
P21	√	√	√	○	√			√			√	√	
P22	√					√		○		○	√	√	√
P23	√		√		√			○			√	√	
P24	√		○	√	○			√					

√ : Tumor or PBMC or negative LN samples

○: Positive LN samples

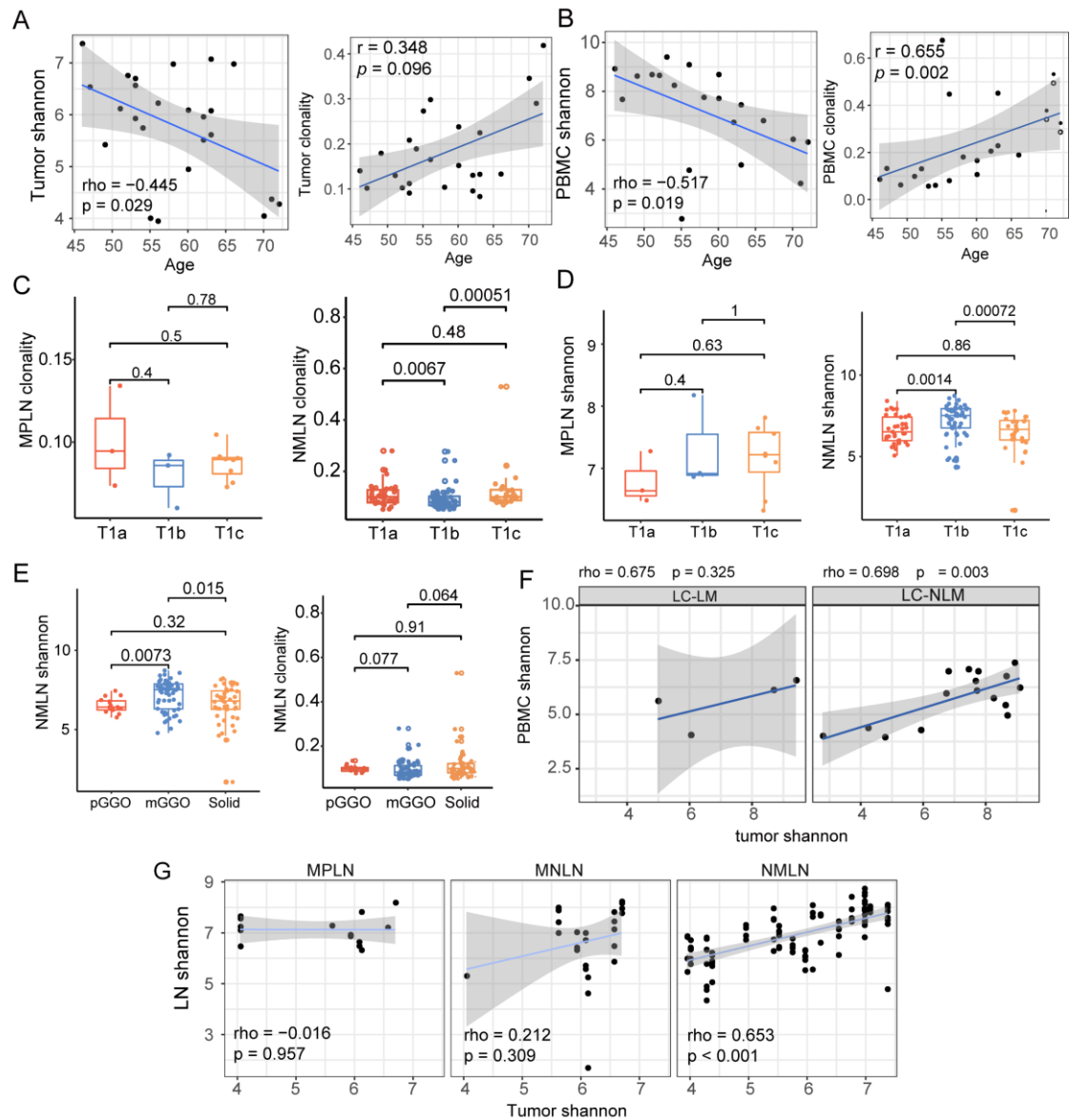


Figure S1 Correlation and comparison of TCR diversity among tumor, LNs, and blood. (A) The association of Shannon and clonality between tumor and age using Pearson coefficient. (B) The correlation of Shannon and clonality between blood and age using Pearson coefficient. Comparison of clonality (C) and Shannon (D) at different tumor stages. (E) TCR diversity on different pathological tumors. (F) Pearson coefficient of Shannon between tumor and blood at metastasis and non-metastatic patients. (G) The correlation of Shannon between LNs and tumor or LNs at MPLN, MNLN, and NMLN.

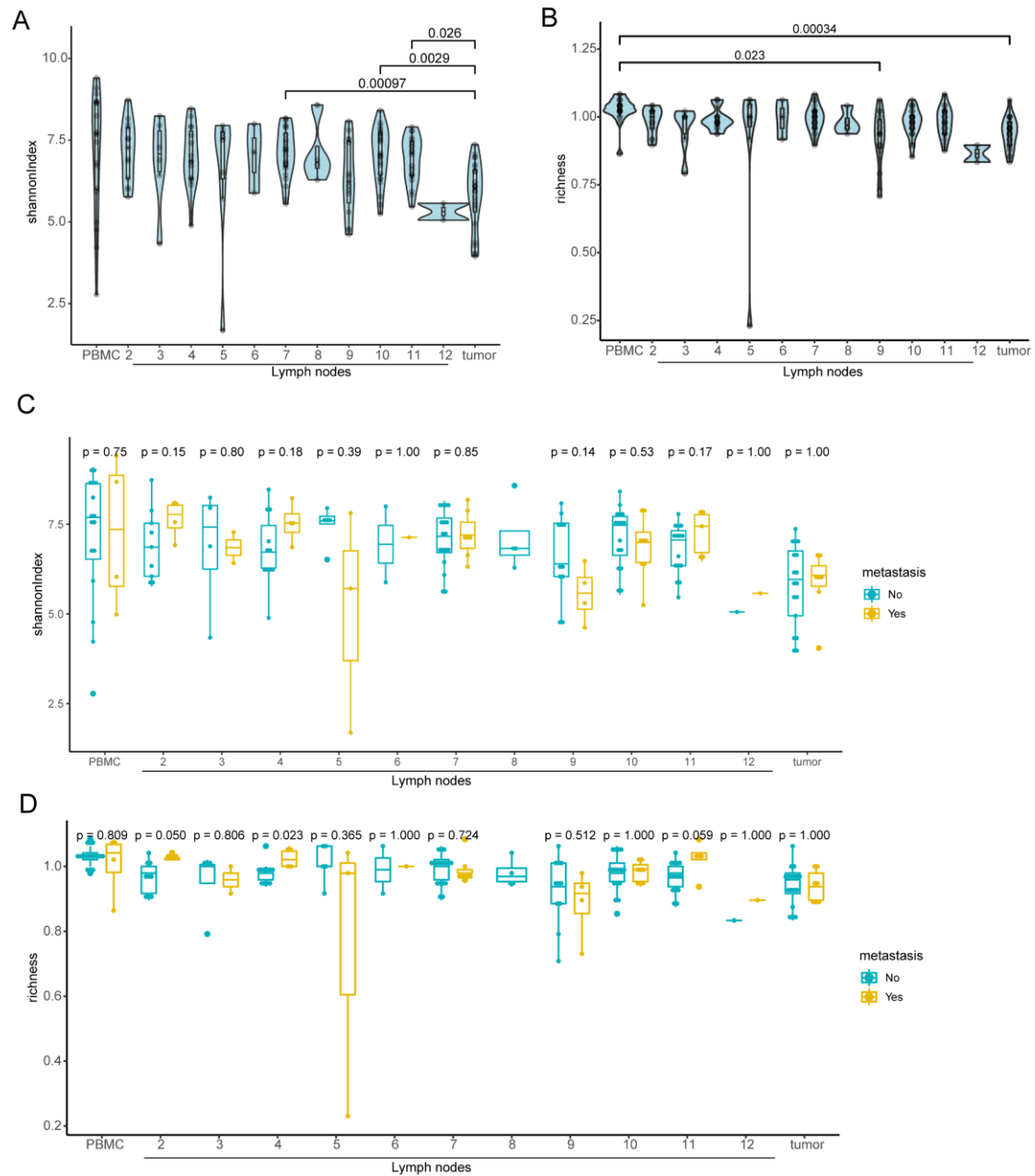


Figure S2 Comparison of Shannon and richness among LNs, tumor, and blood. The violin plots showing Shannon index (A) and richness (B) among blood, LNs and tumor. Two sided Mann-Whitney U test was performed to test the significance between groups. The box plots depicting Shannon index (C) and richness (D) of tumor, LNs, and blood between metastatic and non-metastatic patients.

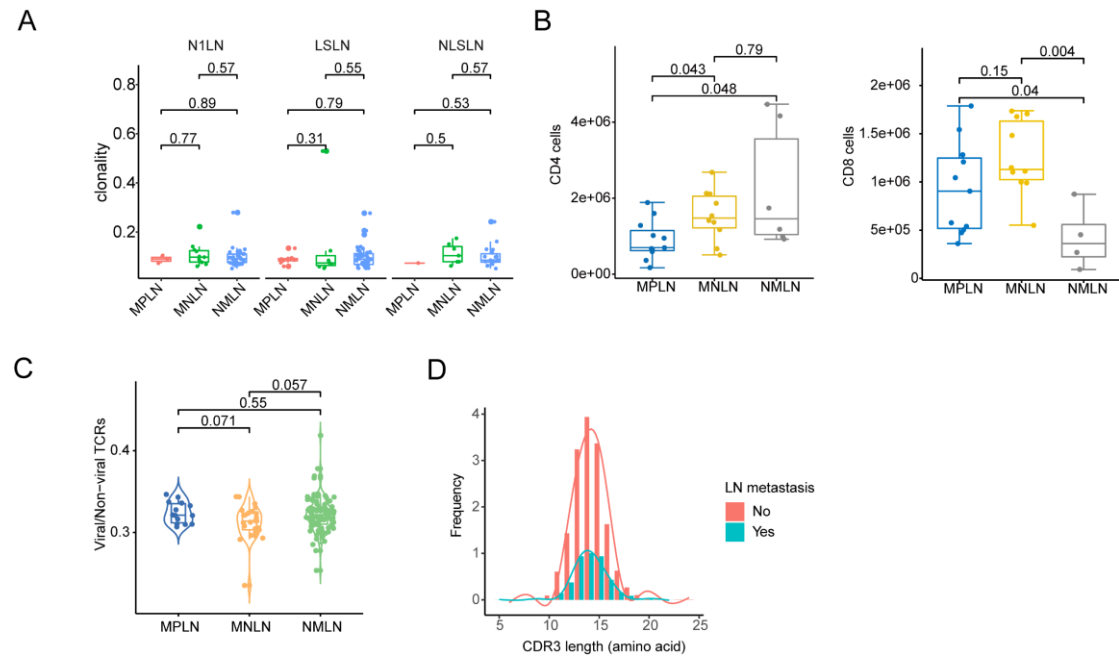


Figure S3 T cell subsets and TCR diversity/characterization in LNs. (A) Comparison of clonality among MPLN, MNLN, and NMLN at different lymph node staging. (B) The density of CD4⁺ and CD8⁺ cells among MPLN, MNLN, and NMLN. (C) The ratio of viral-associated TCRs to non-viral TCRs among MPLN, MNLN, and NMLN. (D) The bar plot illustrates the length of CDR3 amino acid between metastasis-positive LNs and metastasis-negative LNs.

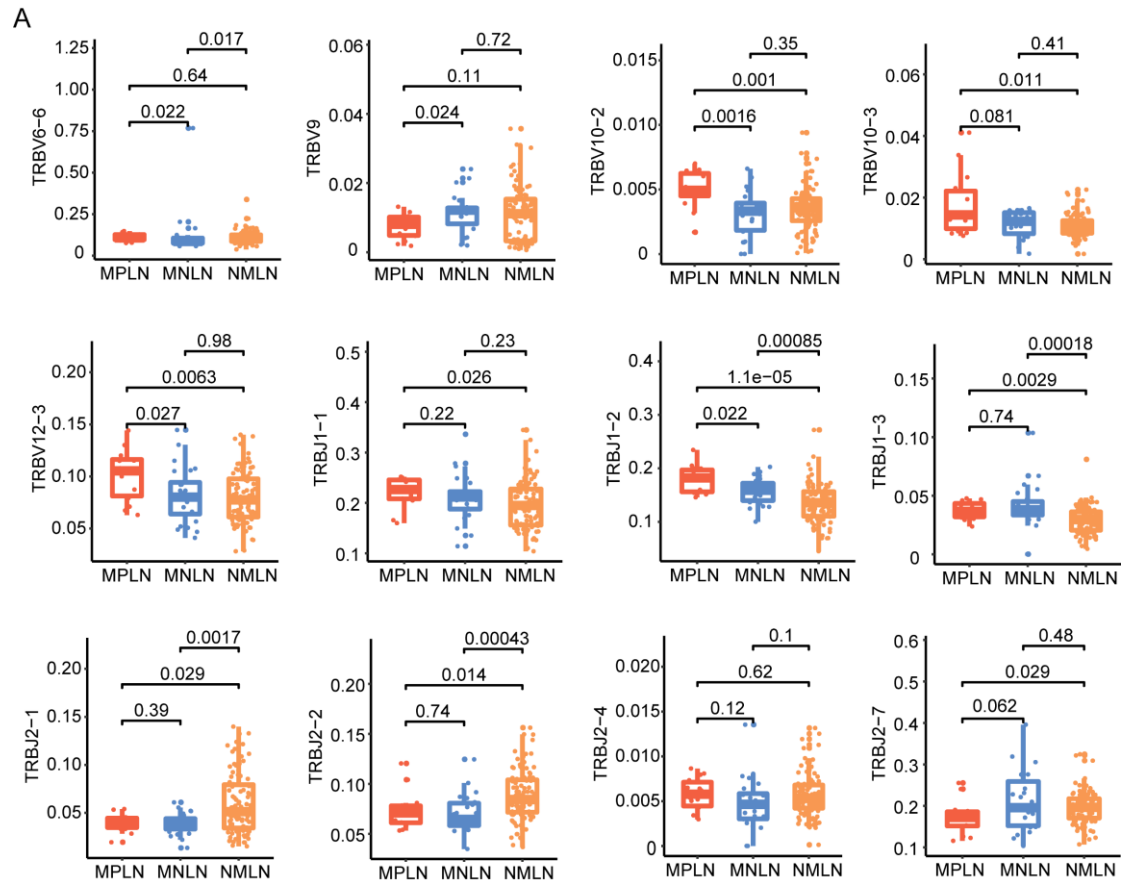


Figure S4 Box plots depicting the frequency of V gene and J genes among MPLN, MNLN, and NMLN (n=134). Two-sided Man-Whitney U test.