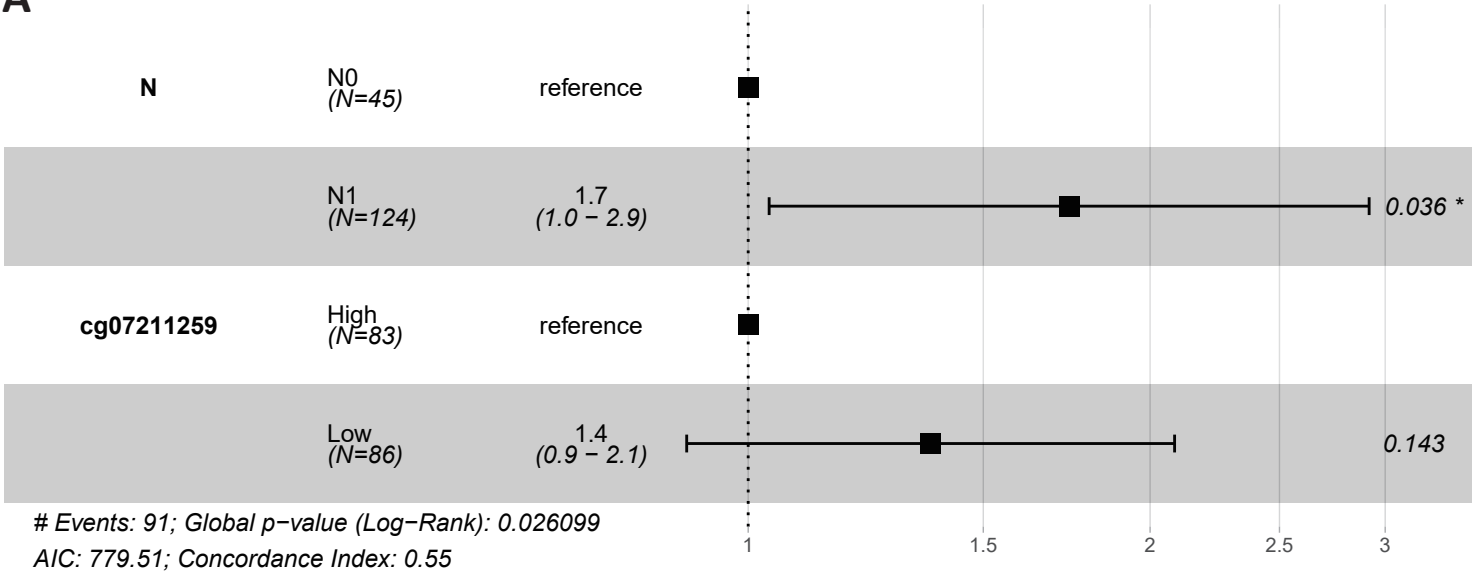


A



B

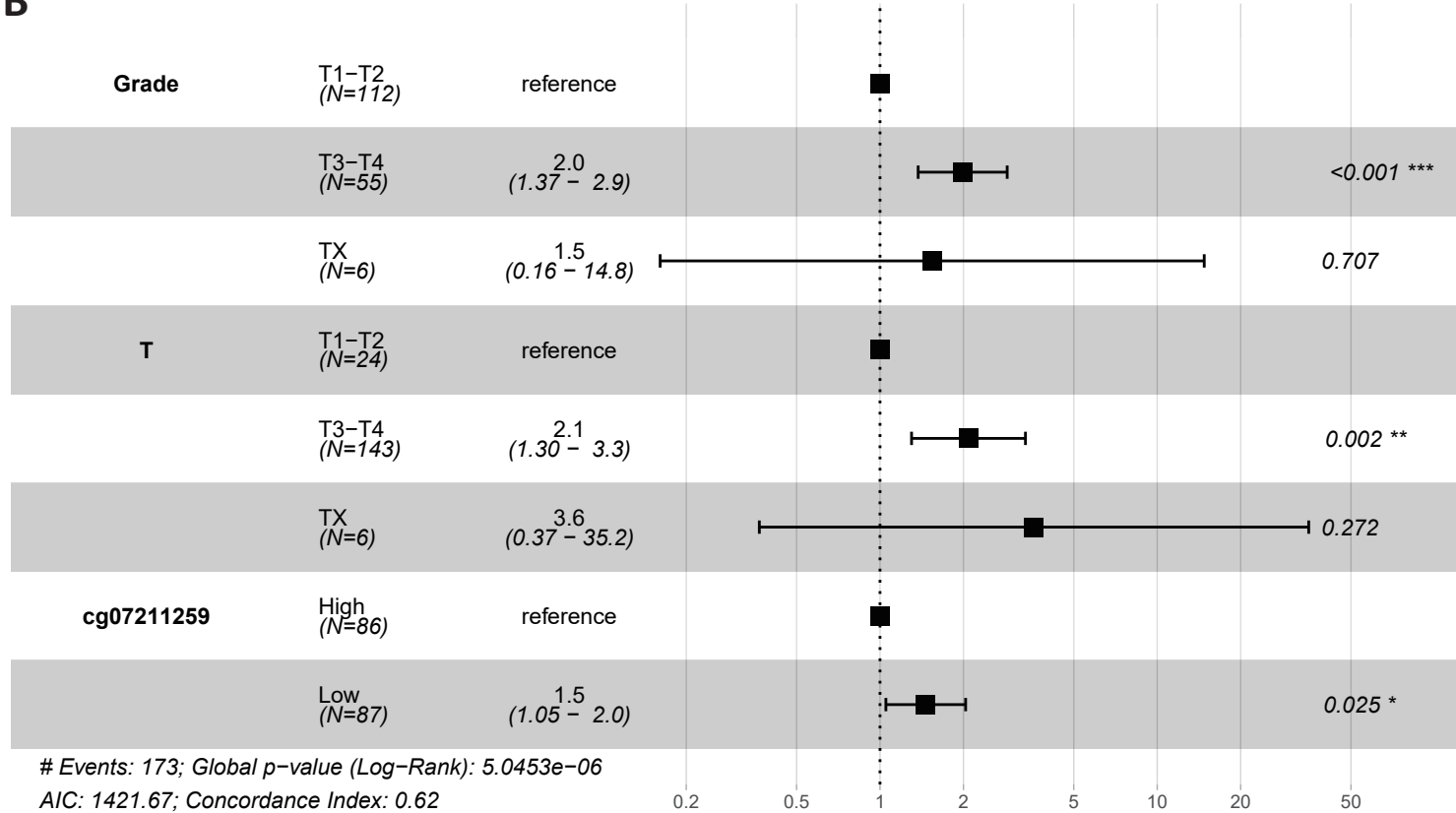


Figure S1: Multivariate Cox analysis of cg07211259 methylation and the clinicopathological factors significant in the univariate Cox analysis ($p < 0.05$) from the TCGA and ICGC cohorts, respectively

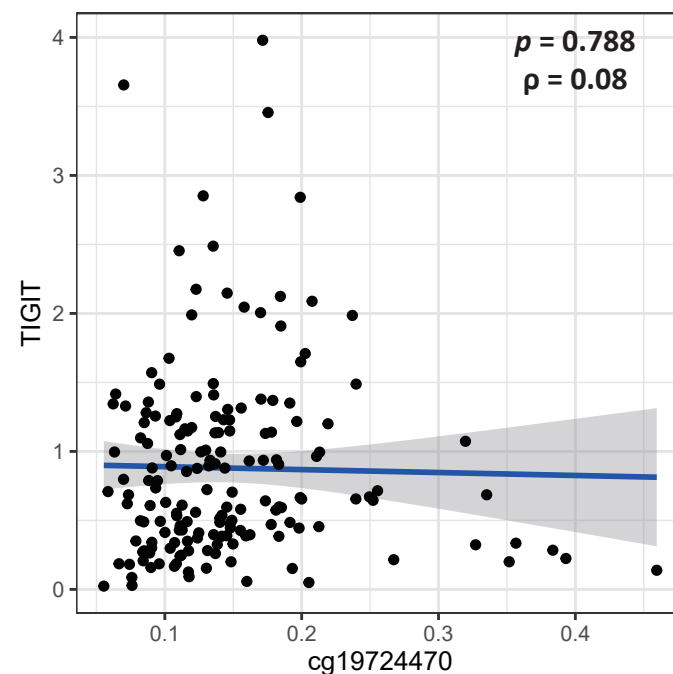
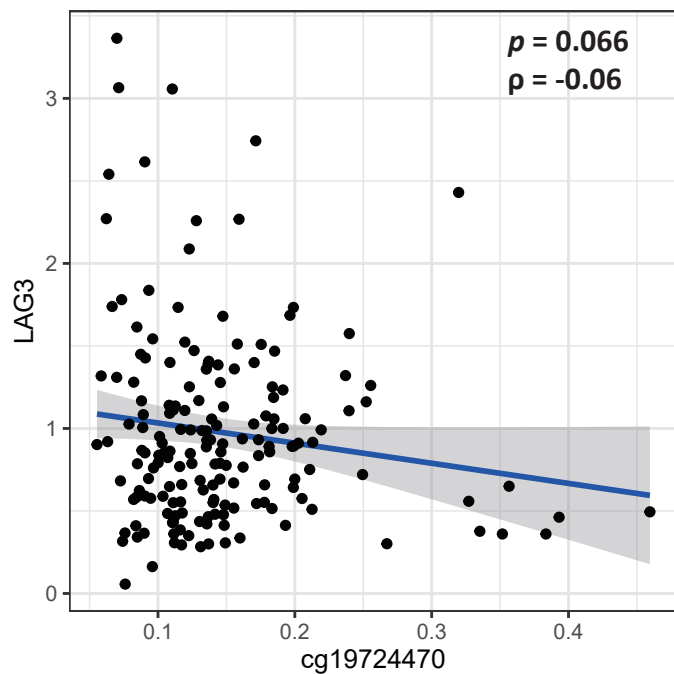
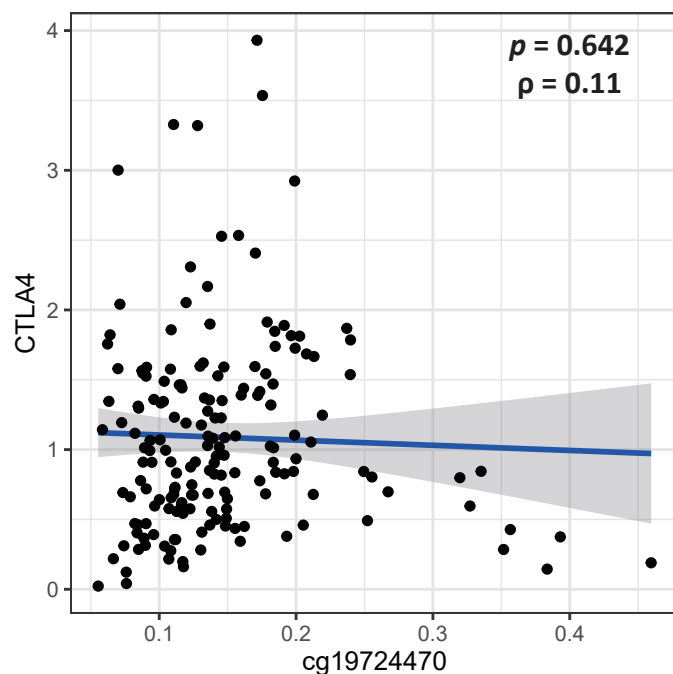
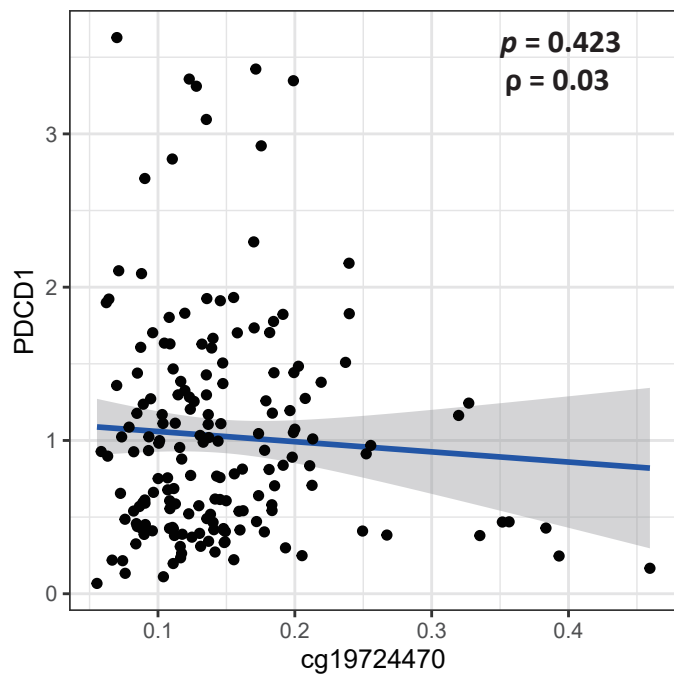


Figure S2: The correlation of *cg19724470* methylation with immune checkpoint molecules *PDCD1*, *CTLA4*, *LAG3*, and *TIGIT*, respectively, in the TCGA cohort

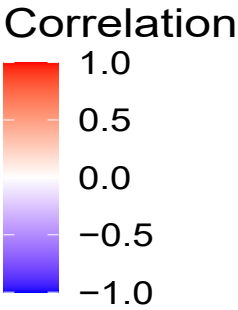
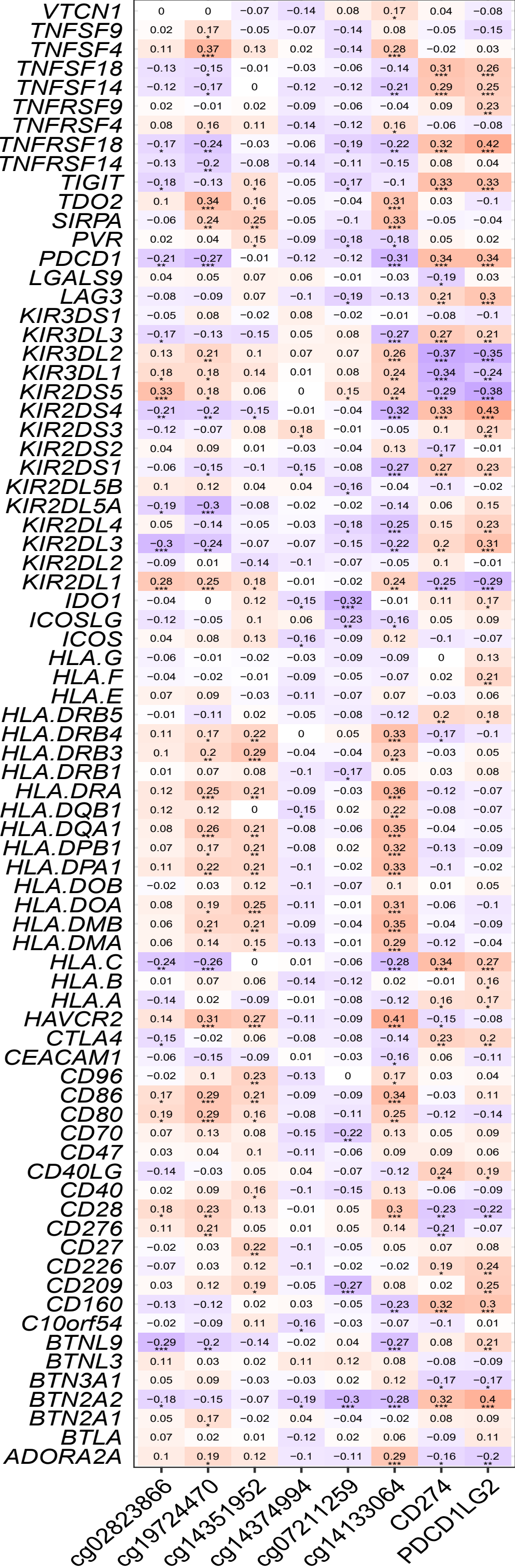


Figure S3: The correlation heatmap of PD-L1/PD-L2 expression and related methylated CpG sites with 77 detected ICGs in the ICGC cohort

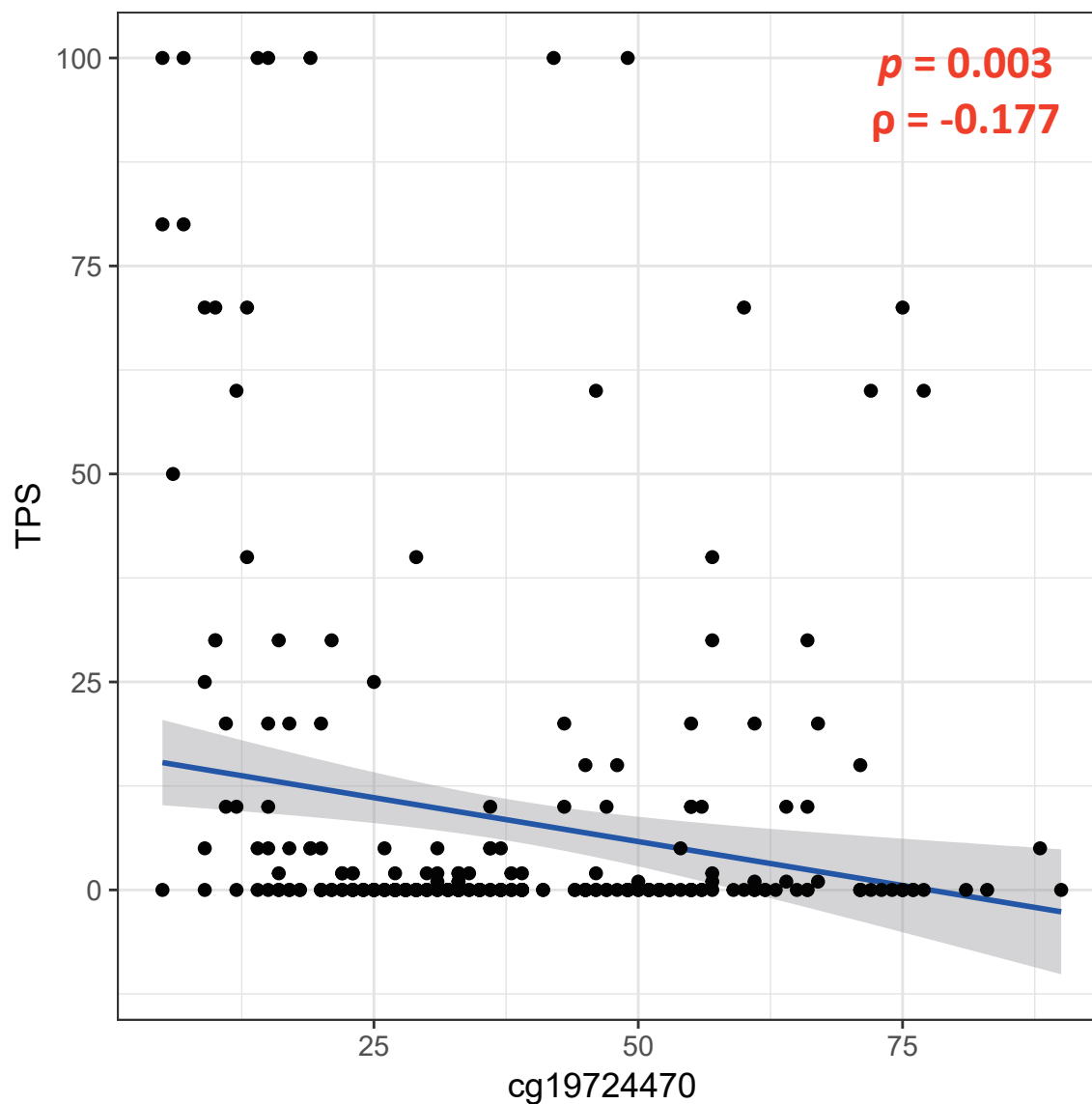


Figure S4: The correlation of cg19724470 methylation status and PD-L1 TPS in the PUMCH cohort. TPS: tumor proportion score; p value < 0.05 was marked in red.

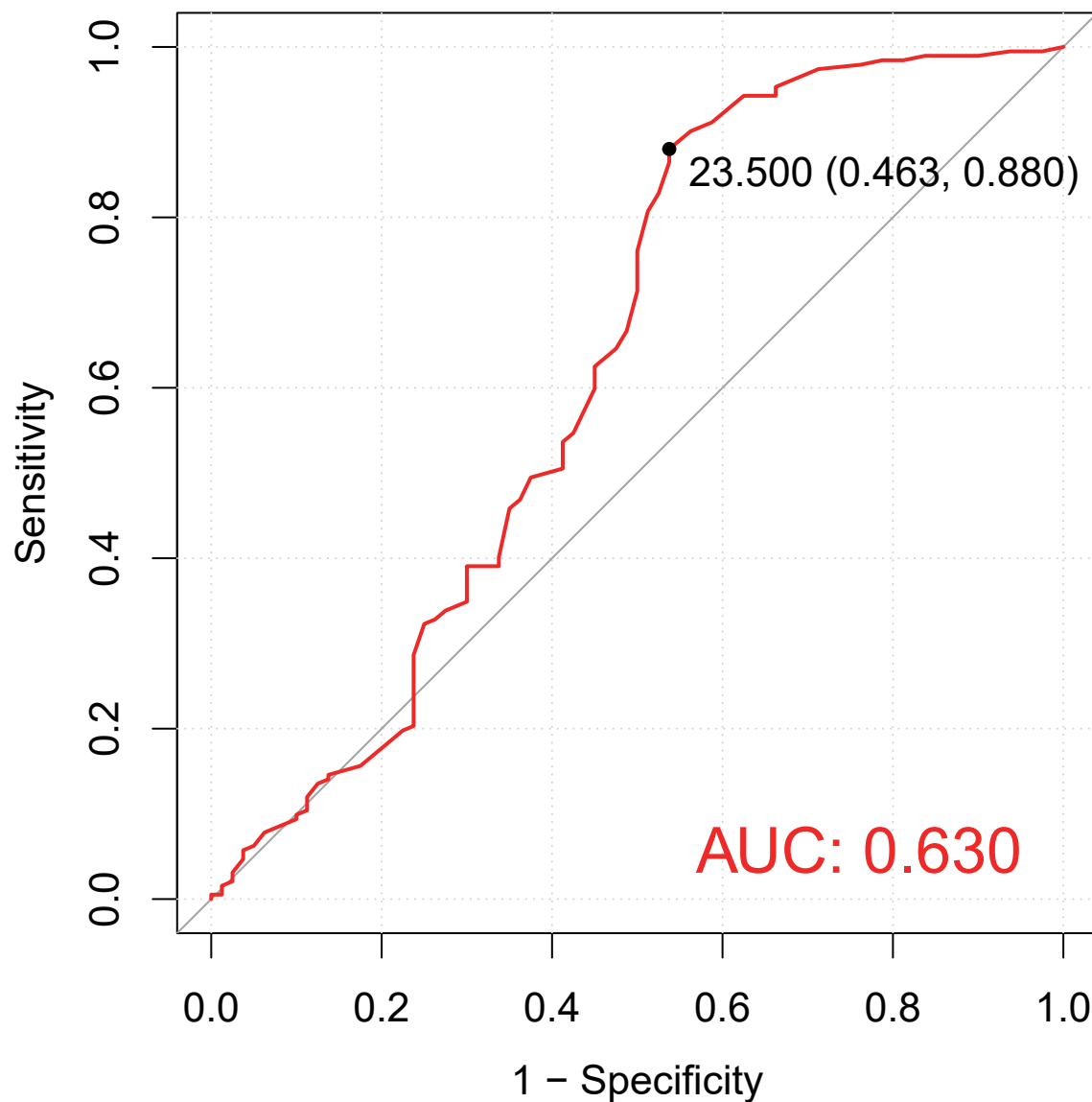


Figure S5: The ROC curve for predicting PD-L1 TPS based on cg19724470 methylation status in the PUMCH cohort. AUC: area under curve.