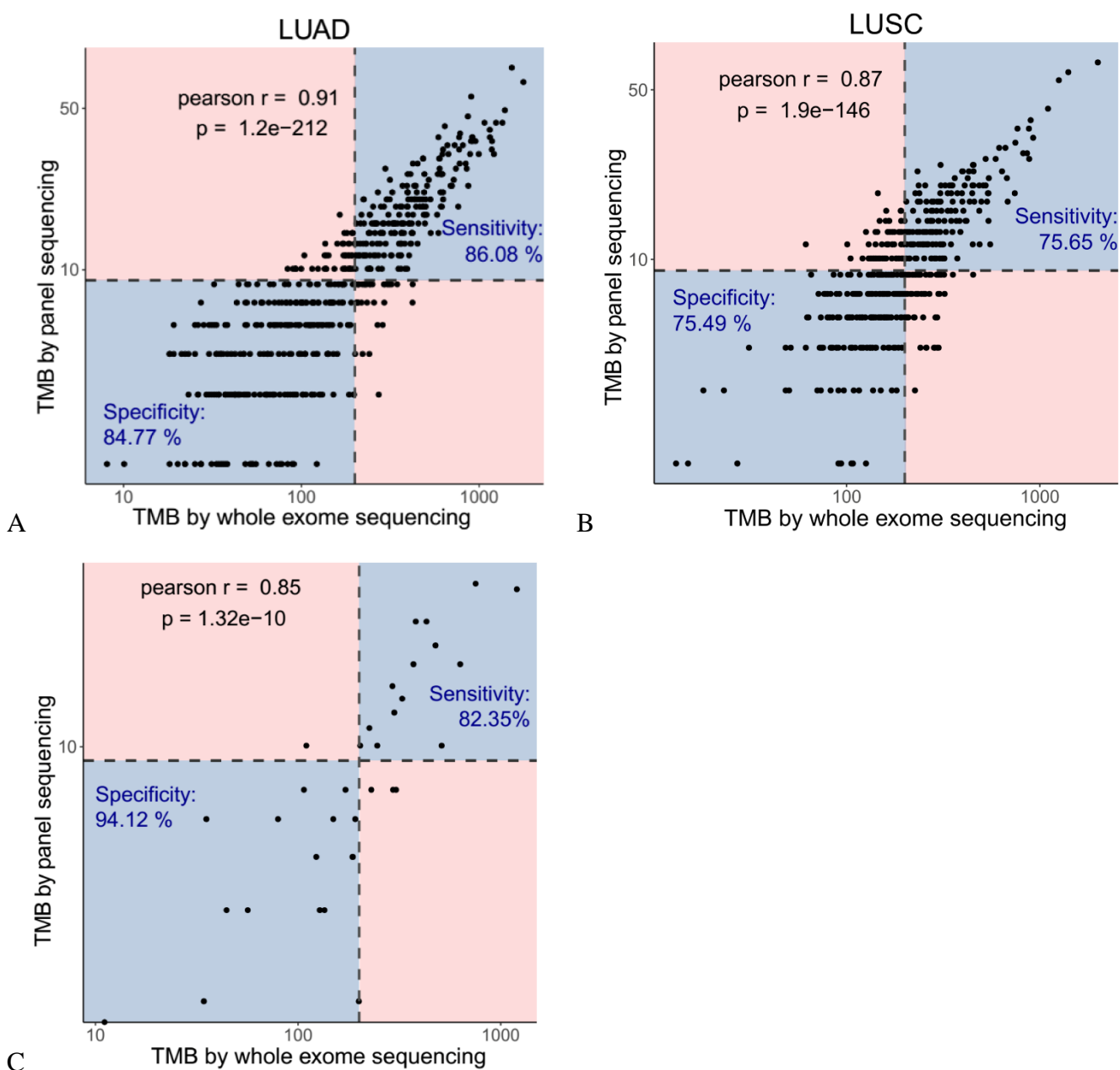


**Figure S1. The correlations of TMB value between panel sequencing and WES in published databases.**

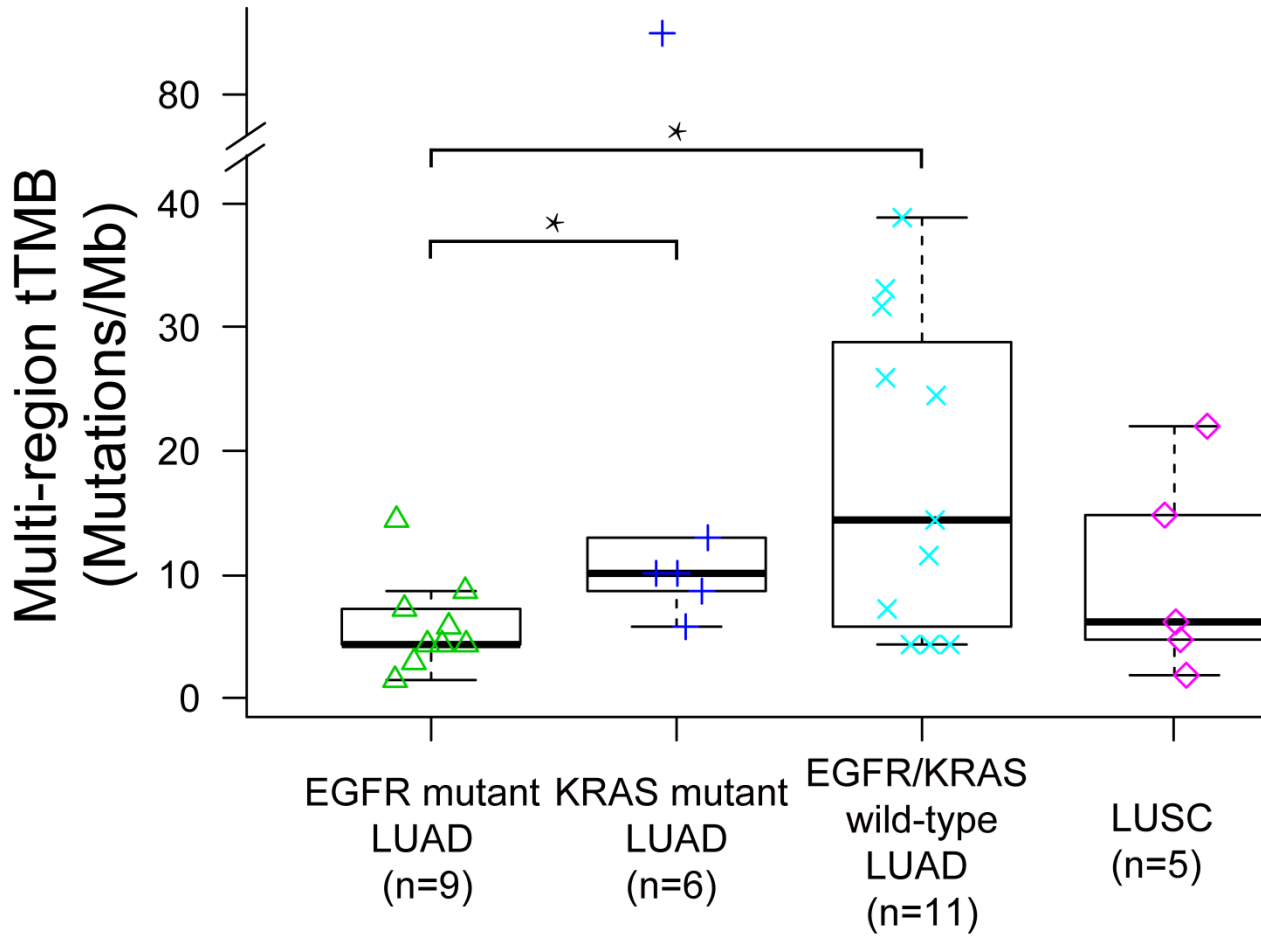
(A) TCGA-LUAD, (B) TCGA-LUSC, (C) Database from Rizvi H, et al. J Clin Oncol, 2018;36.

Abbreviations: TMB, tumor mutational burden; TCGA, The Cancer Genome Atlas; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; WES, wholexome sequencing



**Figure S2. The comparison of multi-region tTMB among different NSCLC subtypes.**

Abbreviations: TMB, tumor mutational burden; tTMB, tissue TMB



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**Figure S3. The comparisons and overlaps of tumor-derived mutational profiles among tumor tissues in each region and the corresponding ctDNA.**

The P0XX was the patient No. shown at the top. Each tumor region (T1, T2, T3...) with plasma (P) were arranged in the x axis. ctDNA was isolated from plasma (more details in Supplementary Methods). Right y axis displayed tumor-derived mutational profiles in detail. The detected mutations were shown in red, while undetected cases were shown in gray.

