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, whole-exome sequencing
Figure S2. The comparison of multi-region tTMB among different NSCLC subtypes.

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