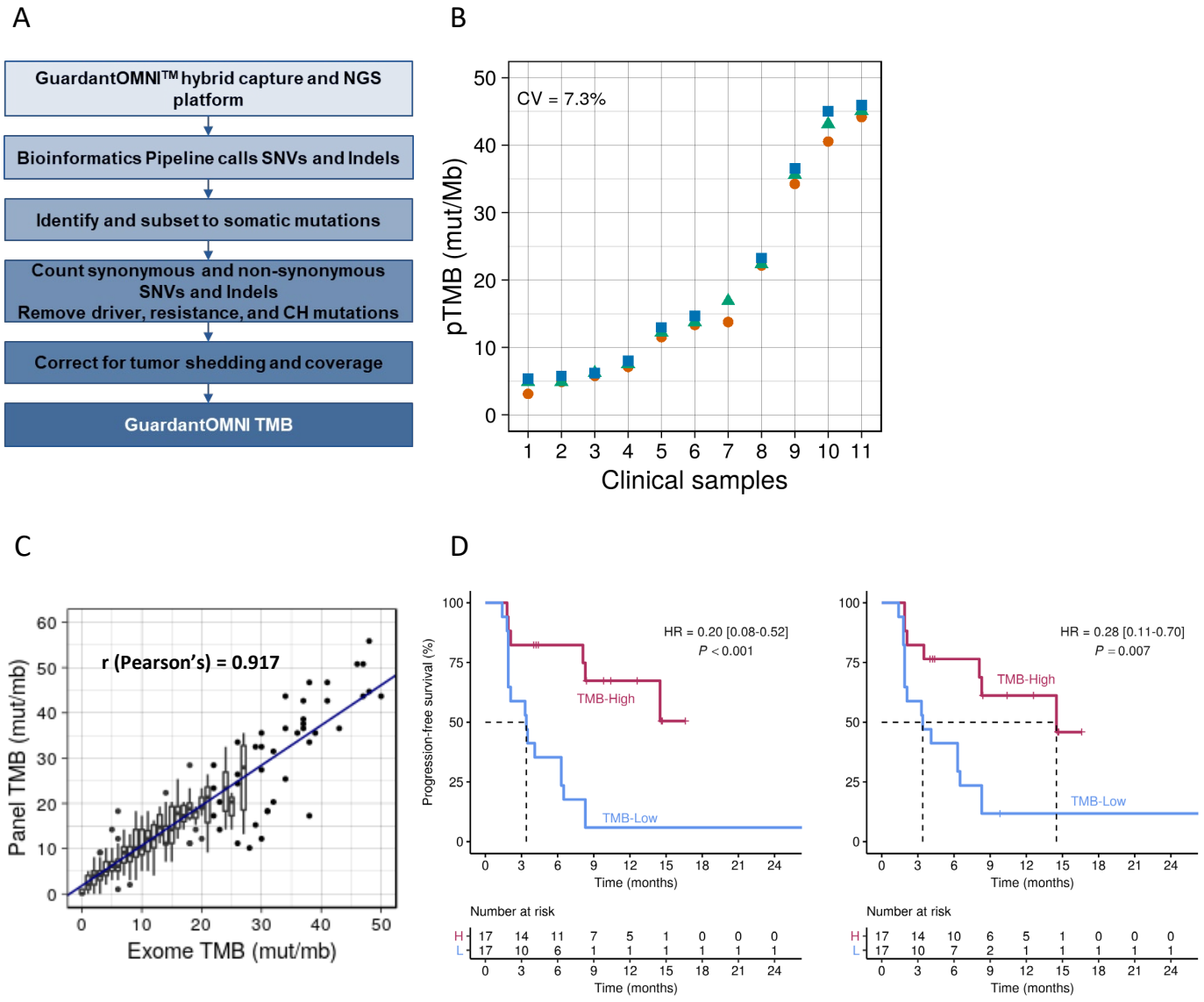
Supplemental Figure 1



Supplemental Figure 1. Development and validation of a plasma-based panel for mutation detection and assessment of TMB. **A**) A 500-gene panel (2.145 megabases (Mb) total, 1.0 Mb of genomic coding sequence) detecting SNVs, indels, copy number amplifications and fusions was developed, along with a bioinformatics pipeline for assessing TMB. The panel has a 95% limit of detection (LOD) of 0.15 – 0.6% for SNVs and 0.4 – 0.8% for indels. **B**) Reproducibility was assessed in 32 replicate samples from 11 randomly selected retrospective clinical samples for which the pTMB scores represented a clinically relevant range of scores for NSCLC. Three replicate samples of extracted cfDNA were analyzed for each patient except #7 for whom only two cfDNA replicates were available. The coefficient of variation across all samples was 7.3%. (The square, triangle, and circle shapes indicate triplicate measurements for each sample.) **C**) The GuardantOMNI panel was assessed by in-silico analysis in which a TMB score was simulated for the 500-gene pTMB panel (y-axis) and compared to WES results (x-axis). TMB scores derived from whole exome or the OMNI-simulated panel are highly concordant for 513 NSCLC samples in the TCGA database (Pearson's r = 0.92). **D**) Additional *in silico* analysis was conducted using the data set made publicly available by Rizvi, et al.15. Kaplan-Meier curves are shown for whole exome sequencing data (left) for 34 NSCLC patients treated with anti-PD-1 therapy and for the 500 genes on the OMNI panel (right) for the same 34 patients. Patients were split into lower and higher TMB by the median cohort TMB score.