

S12 Fig. (A) Distribution of the mutations derived from whole-exome sequencing (WES)- or panelbased approaches. (B) Venn diagram of the positive patients by tumor-informed fixed assay, panelbased personalized assay, and WES-based personalized assay. (C, D) Kaplan-Meier plot of disease-free

survival (DFS) analysis in the sub-cohort of 41 randomly selected patients by preoperative (preop) circulating tumor DNA (ctDNA) status determined by panel-based (C) and WES-based approaches (D). (E, F) Kaplan-Meier plot of DFS analysis in the sub-cohort of 41 randomly selected patients by postoperative (postop) ctDNA status determined by tumor-informed (E) and tumor-agnostic methods (F).