Electronic Supplementary Material: Online Resource 5

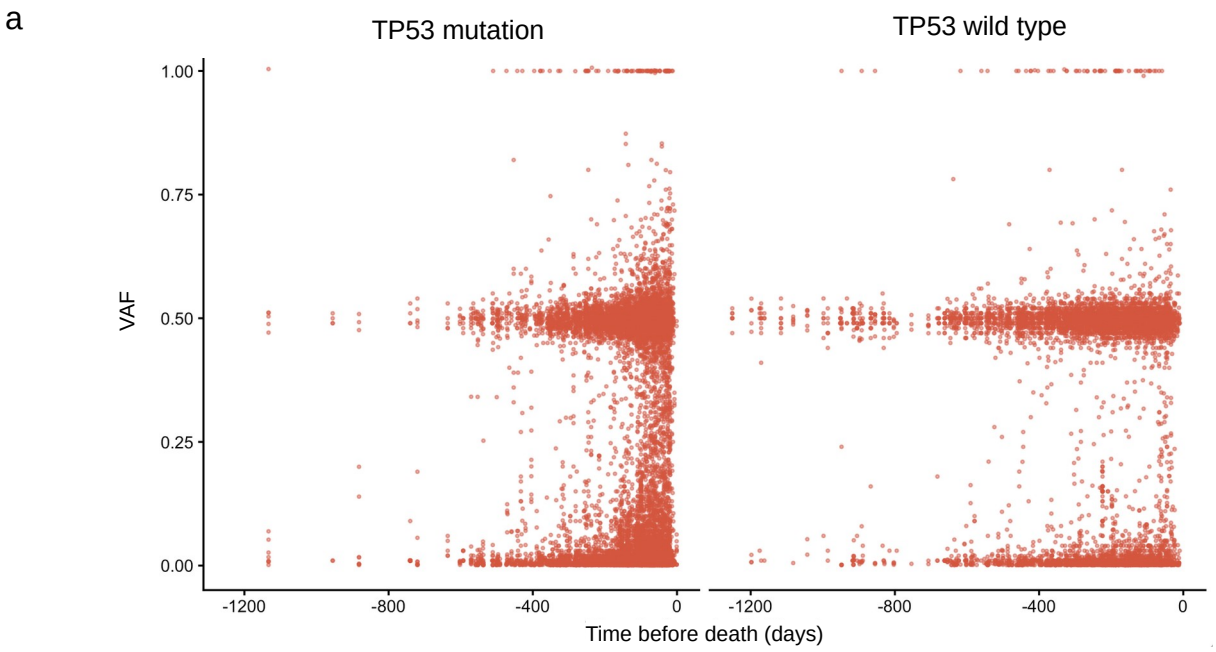
International Journal of Clinical Oncology

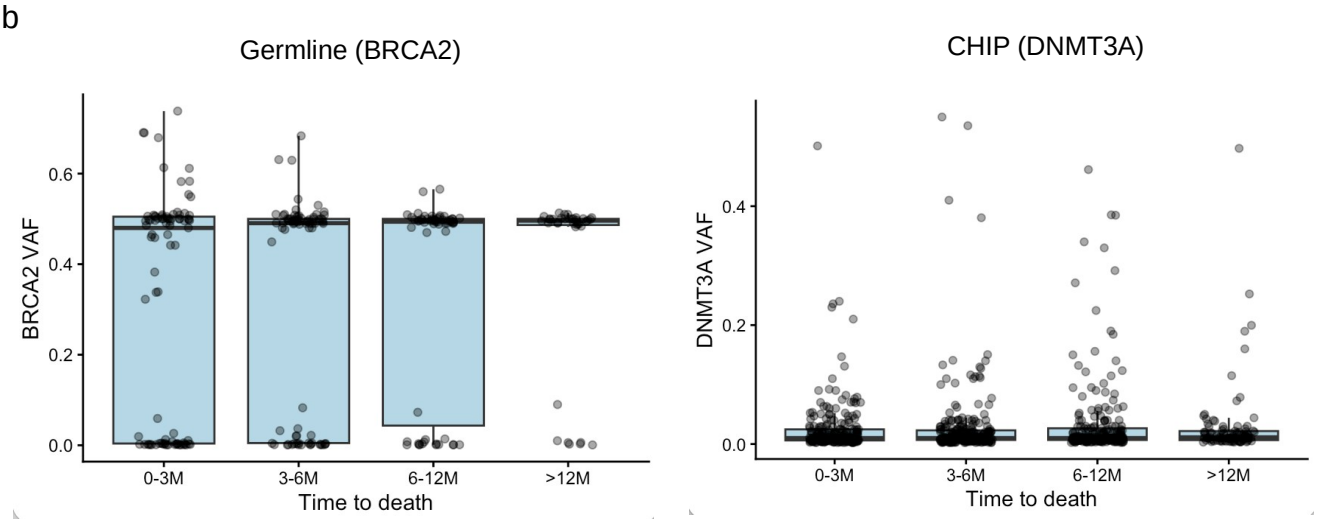
Real-world analysis of treatment sequencing and late-stage liquid biopsy genomic profiling in advanced pancreatic cancer

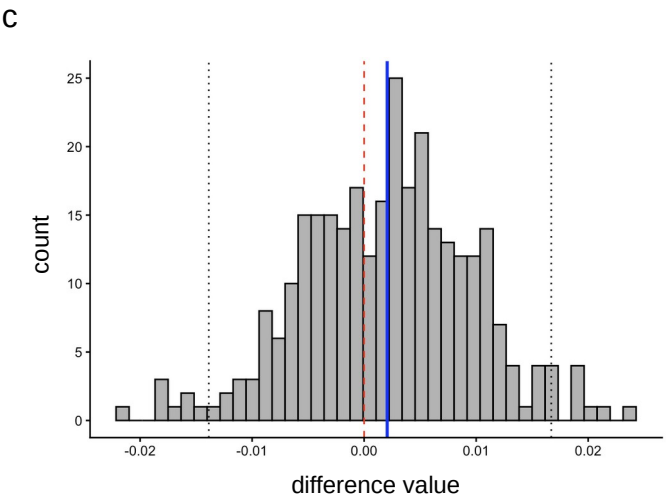
Naohiro Nishida, Eisuke Iwasaki, Ken-Ichi Okada

Corresponding author: Naohiro Nishida
Department of Clinical Oncology, Tokai University School of Medicine, 143 Shimokasuya, Isehara, Kanagawa 259-1193, Japan
E-mail: nnishida@tokai.ac.jp

Online Resource 5. Longitudinal changes in variant allele frequency and bootstrap analysis of model performance.







(a) Temporal changes in variant allele frequency (VAF) of all profiled genomic alterations in patients who died during follow-up, stratified according to TP53 mutation status. TP53-mutant (left) and TP53 wild-type (right) patients. The rightmost time point indicates the date of death.

(b) Temporal changes in VAF according to sampling timing relative to the date of death. BRCA2 (left) and DNMT3A (right) are shown as representative examples of germline mutations and CHIP-associated mutations, respectively.

(c) Bootstrap distribution of the performance difference between the KRAS-only model and the full model. The red dashed line indicates the mean difference, and the blue solid line indicates the observed difference between the two models. Vertical dotted lines represent the 95% confidence interval.