Electronic Supplementary Material: Online Resource 6

International Journal of Clinical Oncology

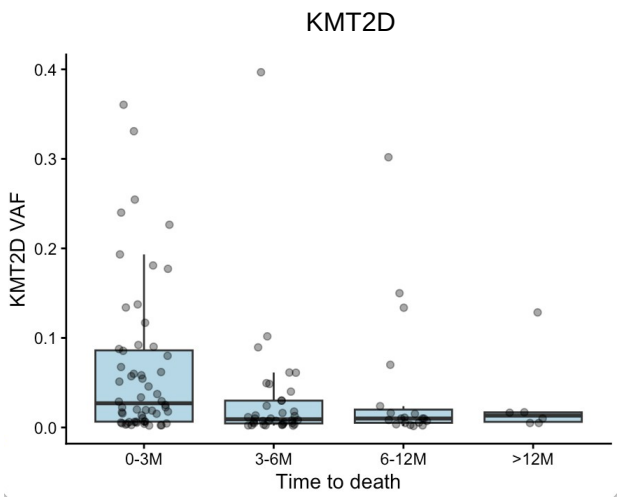
Real-world analysis of treatment sequencing and late-stage liquid biopsy genomic profiling in advanced pancreatic cancer

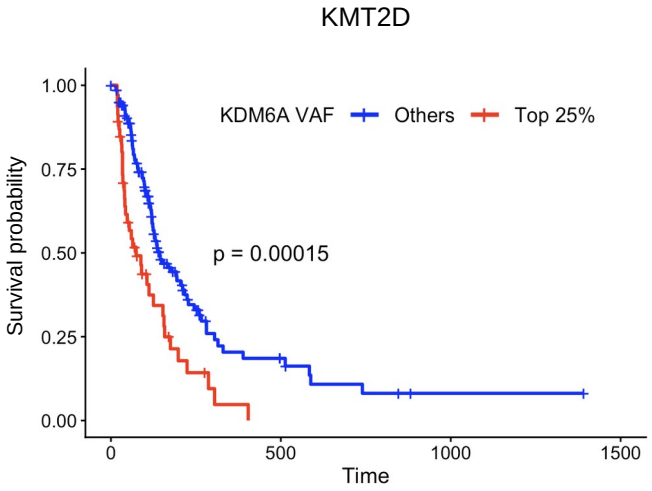
Naohiro Nishida, Eisuke Iwasaki, Ken-Ichi Okada

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

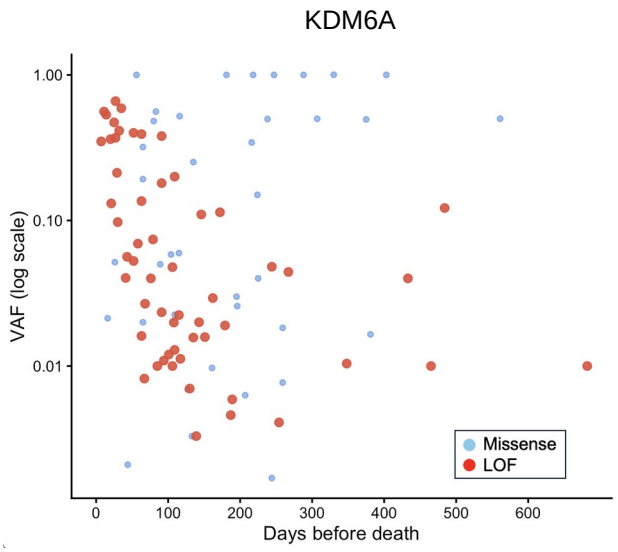
Online Resource 6. Clone dynamics and clinical significance of epigenomic regulatory gene alterations (Figure legends in the next page)

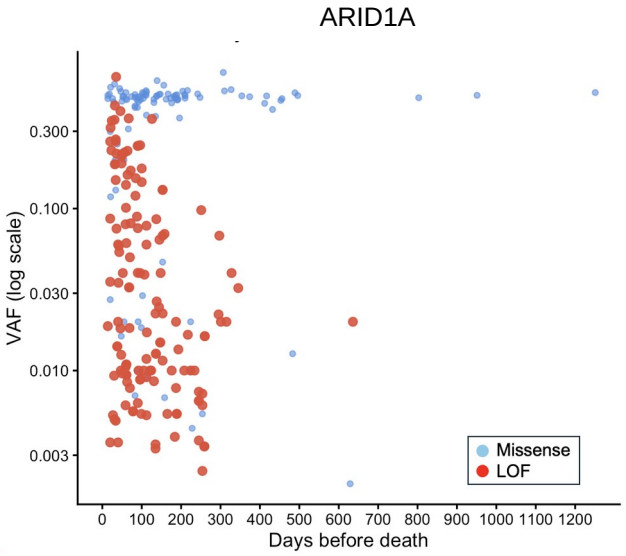
a



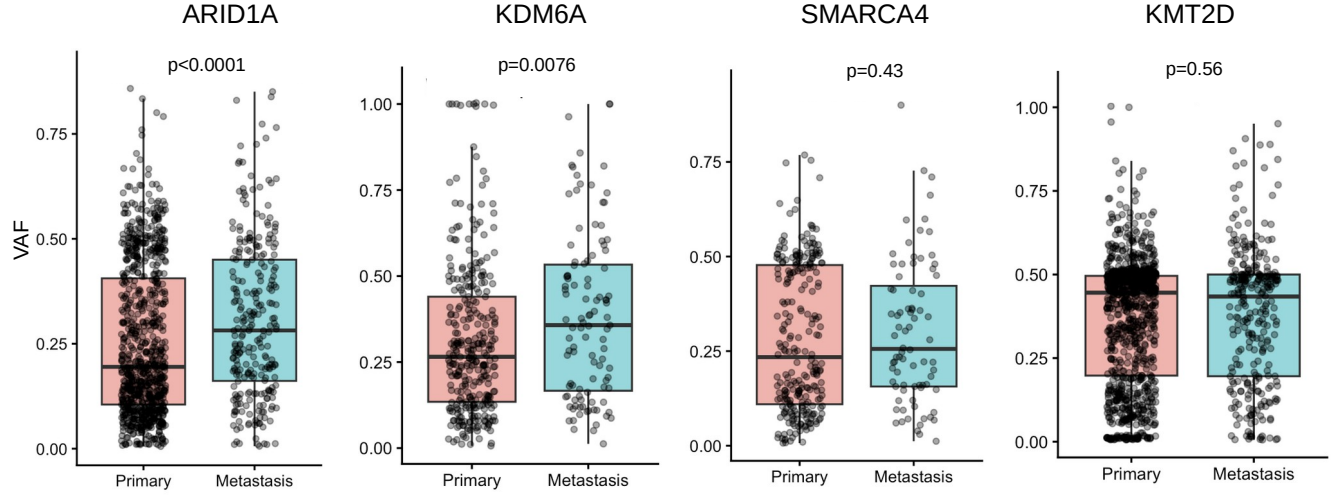


b





c



(a) Temporal changes in VAF according to sampling timing (left) and Kaplan–Meier survival curves (right) for KDM6A. Kaplan–Meier groups were stratified using the upper quartile of VAF values as the cutoff.

(b) Temporal changes in VAF for KDM6A (left) and ARID1A (right). Day 0 indicates the date of death. Truncating mutations, deletions, and rearrangements were classified as loss-of-function (LOF) alterations. Blue and red dots indicate missense mutations and LOF alterations, respectively.

(c) Differences in VAF between primary and metastatic lesions for ARID1A, KDM6A, SMARCA4, and KMT2D, as assessed using the tissue panel. P values were calculated using the Wilcoxon rank-sum test.