Supplementary Figures

High prevalence of the MLH1 V384D germline mutation in patients with

HER2-positive luminal B breast cancer

Seung Eun Lee¹, Hye Seung Lee¹, Kyoung-Yeon Kim², Jung-Hoon Park², Hanseong Roh²,

Ha Young Park^{3*}, Wan-Seop Kim^{1*}

¹Department of Pathology, Konkuk University Medical Center, Konkuk University School of

Medicine, Seoul, Republic of Korea

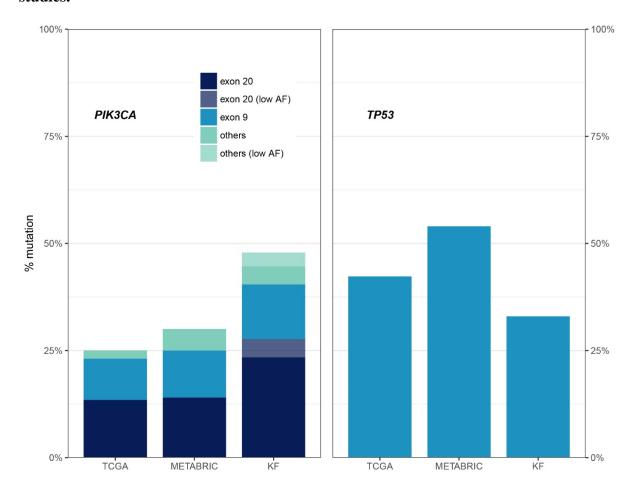
² Precision Medicine Institute, Macrogen, Inc

³Department of Pathology, Busan Paik Hospital, Inje University College of Medicine, Busan,

Korea

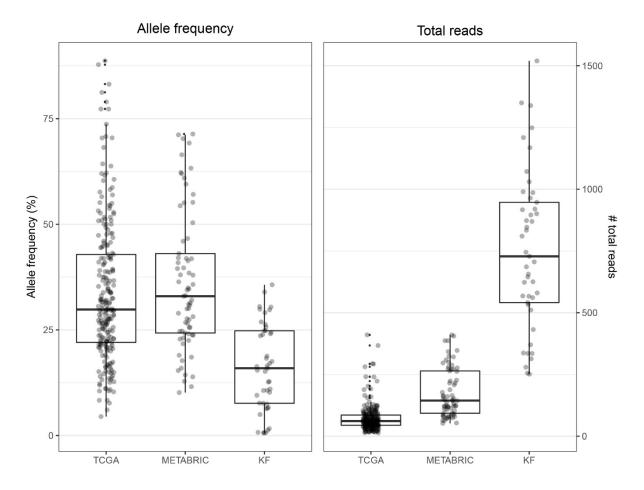
Corresponding authors: wskim@kuh.ac.kr, pmint00@naver.com

Supplementary Figure 1. Comparing mutation rate of *PIK3CA* and *TP53* with large-scale studies.



Bar plots represent mutation rate in HER-2-positive luminal B breast cancer of TCGA, METABRIC, and present study (KF). Different mutation loci of *PIK3CA* are distinguished by different colors.

Supplementary Figure 2. Details of PIK3CA mutations in three populations.



Variant allele frequencies and total reads of *PIK3CA* mutations of TCGA, METABRIC, and present study (KF) are summarized by bar plot, and each dot represent mutated cases.