

RPS6KB1 CDKN1B IGF1R | PHLPP1 ↓ ↓ ↓ ↓ 20.1% ERBB2 t 15.1% 18 16 FGFR1, ZNF703 Ť 5.2% -2 -3 16 SOX2 EGFR FGFR2 ſ ↓ ↓ 2.7% 16 ZNF703 PAK1, RSF1, CCND1 ↓ ↓ 0 12 13 16 17 18 19 20 21 22 MDM2 RPS6KB1 ↓ Ť 0 -2 12 13 MET EGFR | FGFR1 MDM2 $\downarrow\downarrow\downarrow\downarrow\downarrow$ ↓ 0 13 14 FGFR1, ZNF703 MYC CCND1 AKT1 $\downarrow\downarrow\downarrow$ ↓ Ť 0 15 IGF1R Ť 0

Tumor Fraction

Known CNVs not detected



Figure S2.

Validation of LP-WGS in cfDNA from mBC patients (FERGI). **A**, CNV whole-genome view of cfDNA from 9 patients. Genes with known copy number gains in the matched tumor tissue were annotated. **B**, Comparisons of gene copy numbers detected in tissue by qPCR and in cfDNA by LP-WGS. Tissue was collected 15 years (2403) and 5 years (1520, 7452) prior to plasma collection. (**C-D**) Association between cfDNA tumor fraction estimated by LP-WGS and **C**, *PIK3CA* somatic allele frequency (AF) determined by digital PCR or **D**, CTC number from plasma of mBC patients (FERGI).