A

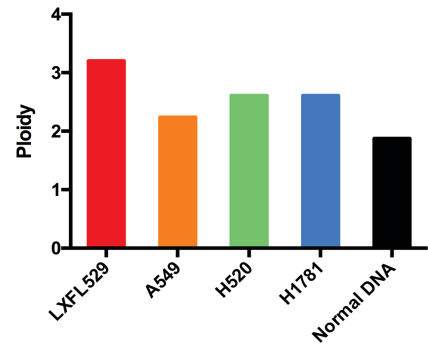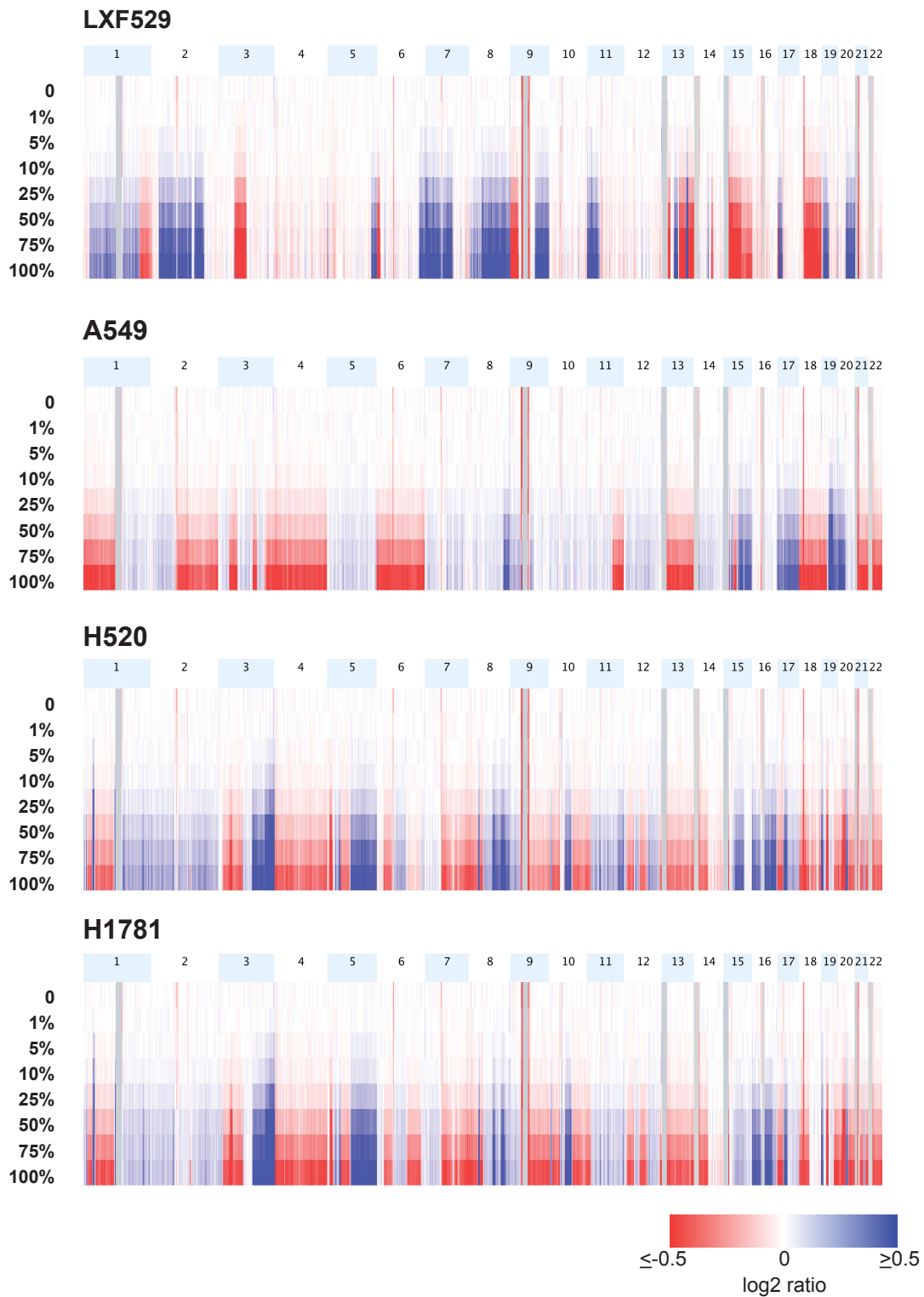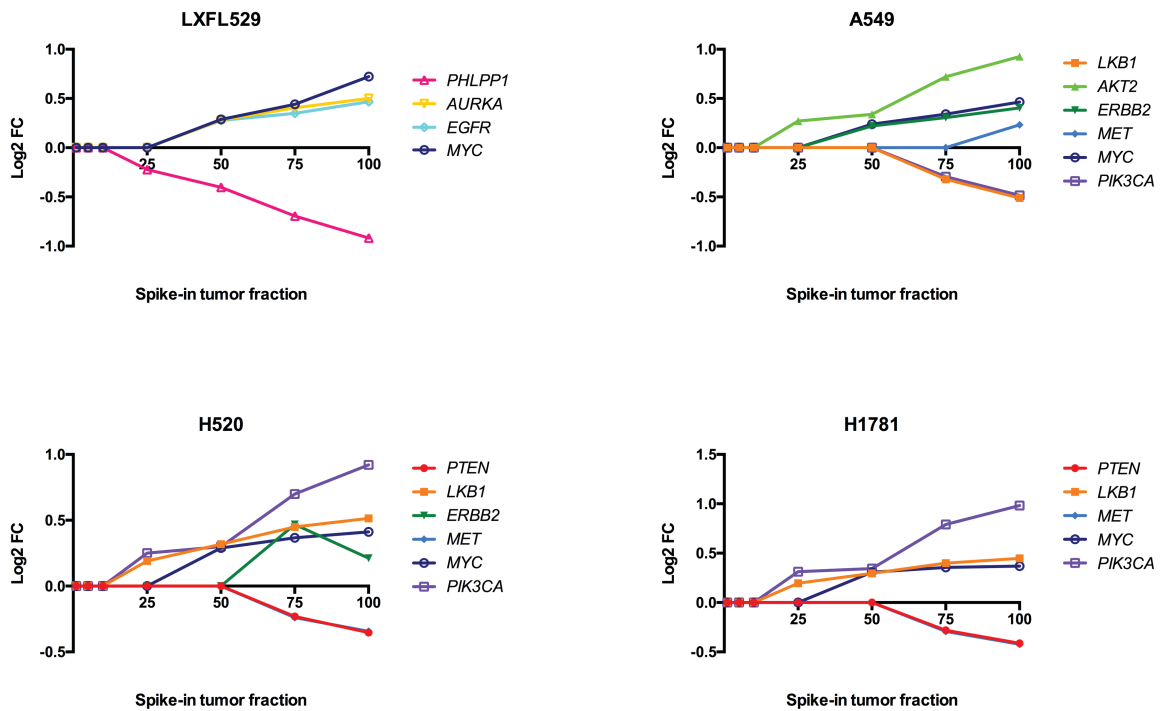**B**

C

LXF529

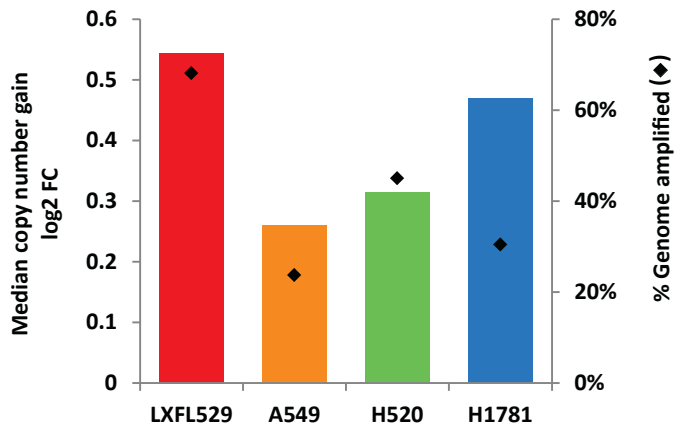A549

H520

H1781

log2 ratio ≤-0.5   0   ≥0.5

Figure S1.

Tumor cell line DNA spike-in. Tumor DNA from 4 lung cancer cell lines was mixed with normal DNA at 0, 1%, 5%, 10%, 25%, 50%, 75% or 100%. **A,** Comparison of estimated tumor fraction by LP-WGS to real spike-in tumor fraction. Wilcoxon signed ranked test p-values are listed. **B,** Ploidy of the four cell lines and normal DNA estimated by LP-WGS. **C,** CNVs across the whole genome detected at different spike-in ratios. Heatmap density represents CNV log2 ratios between cfDNA sample and normal reference, ranging between between ≤-0.5 to ≥0.5. Blue, copy number gain; red, copy number loss. **D,** CNV fold change of lung cancer-related genes, normalized to the healthy reference, detected at different spike-in ratios. **E,** Cell line median copy number gain (bars) and % geneome amplified (diamonds) in the 100% spike in (pure cell line).