

Supplementary Materials

Circulating tumor DNA sequencing in colorectal cancer patients treated with first-line chemotherapy with anti-EGFR

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Supplementary Table 1. Summary of collecting samples

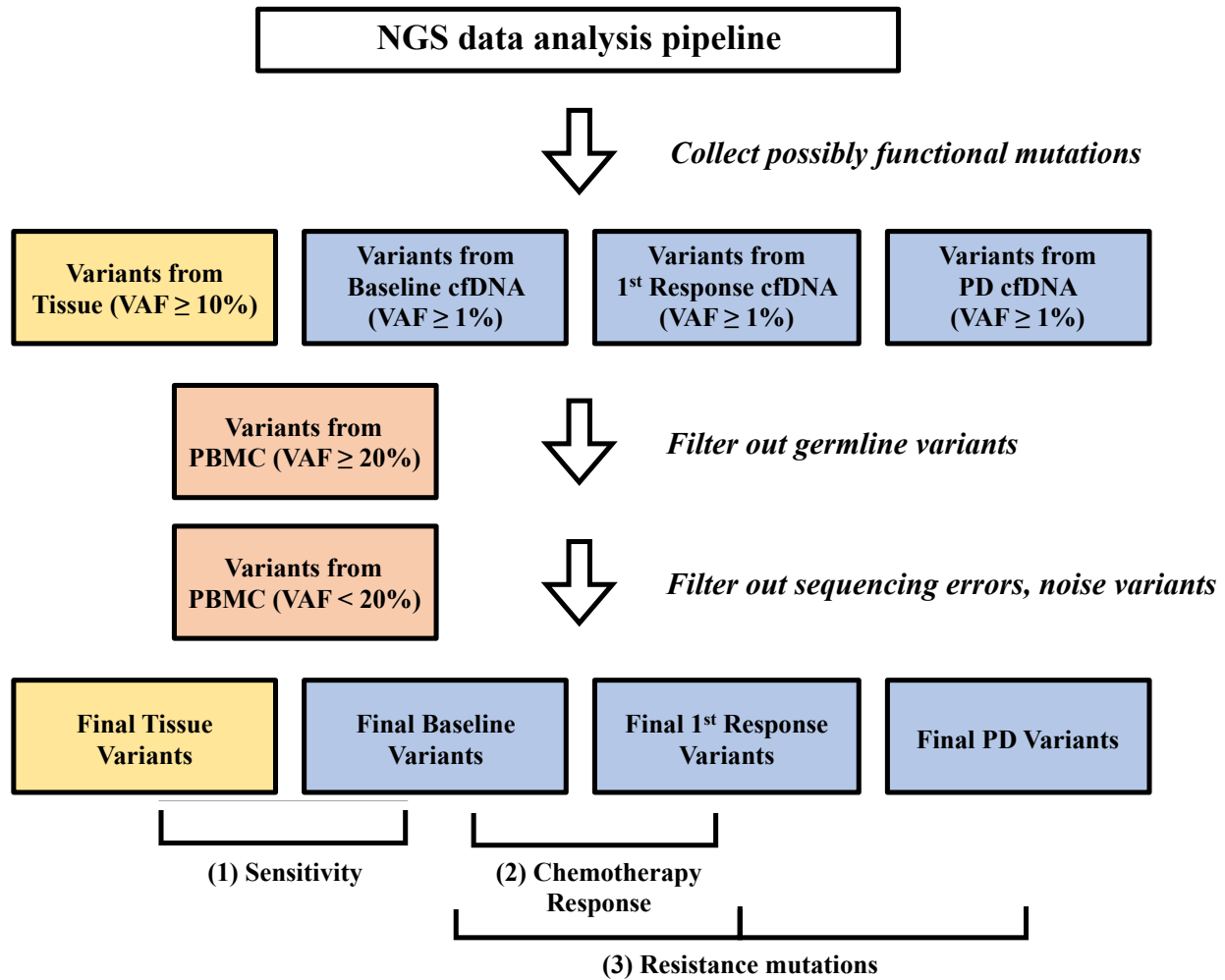
Supplementary Table 2. Summary of panel sequencing statistics

Supplementary Table 3. 230 ctDNA mutations at baseline from total 93 patients

Supplementary Table 4. Tissue and baseline ctDNA mutations in 58 patients

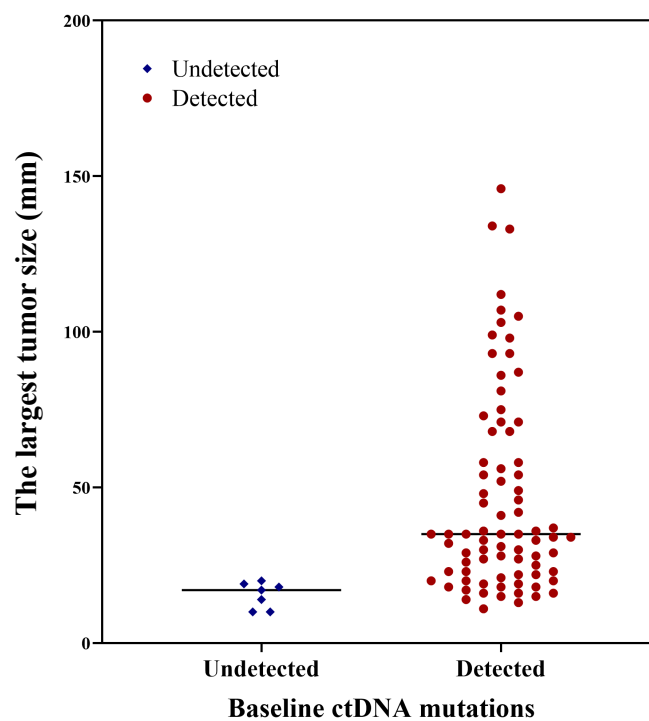
Supplementary Table 5. 54 ctDNA mutations only detected at disease progression

Supplementary Figure. 1. Schematic diagram of the data analysis.

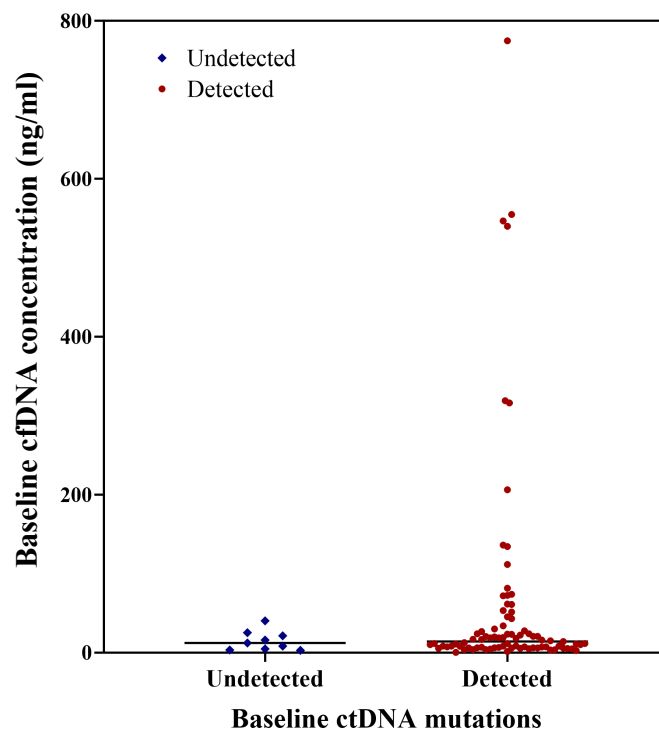


Supplementary Figure. 2. Comparison between detection of baseline ctDNA mutations for (a) the largest tumor size (mm) and (b) baseline cfDNA concentration (ng/ml).

a

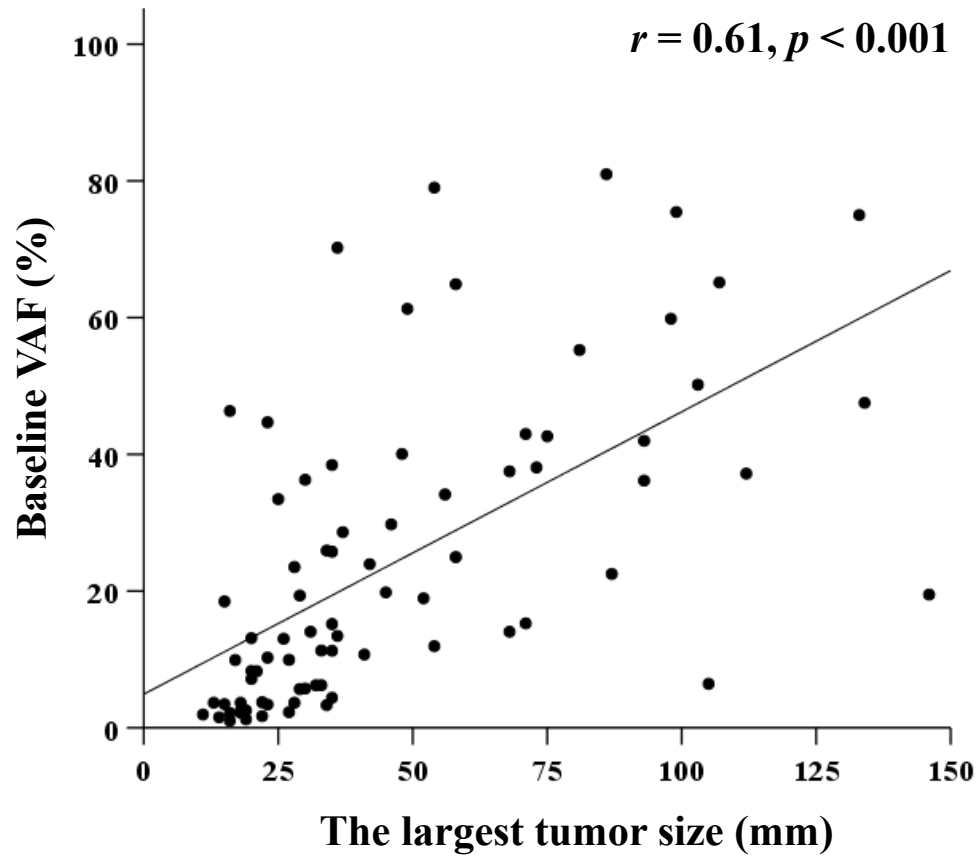


b

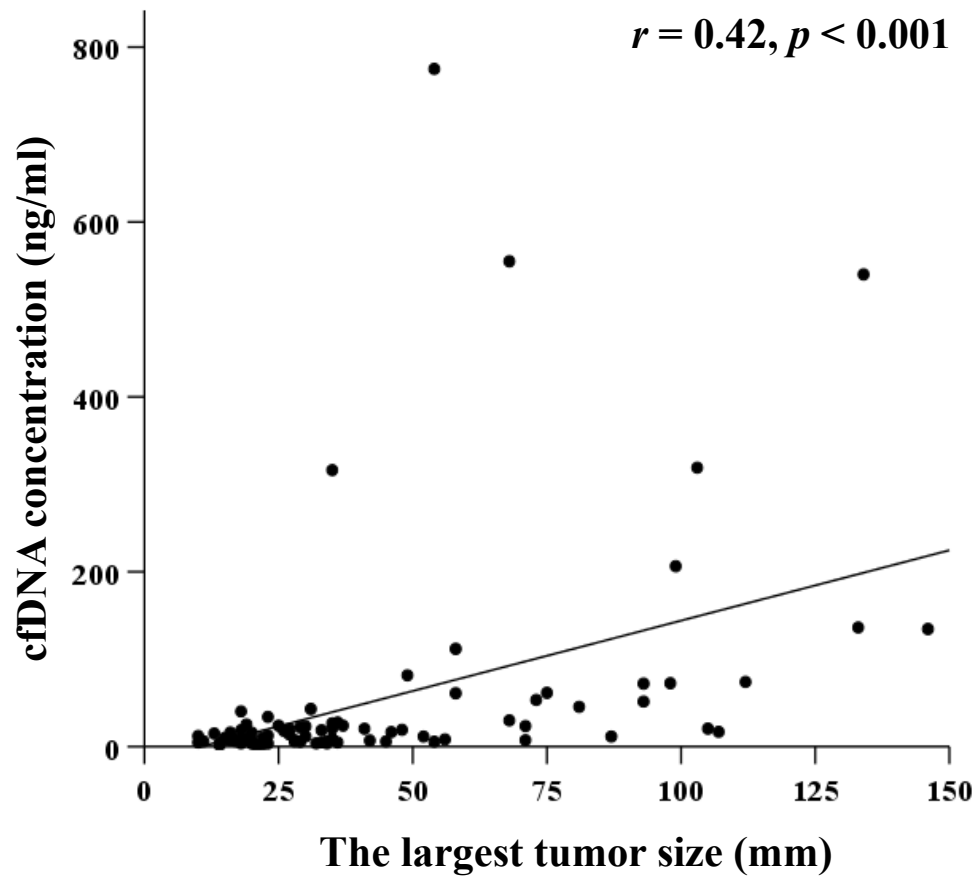


Supplementary Figure. 3. Correlation between tumor burden (defined as the largest target length, mm) and (a) baseline average VAF (%), (b) baseline cfDNA concentration (ng/ml) and (c) VAF (%) x cfDNA conc. (ng/ml).

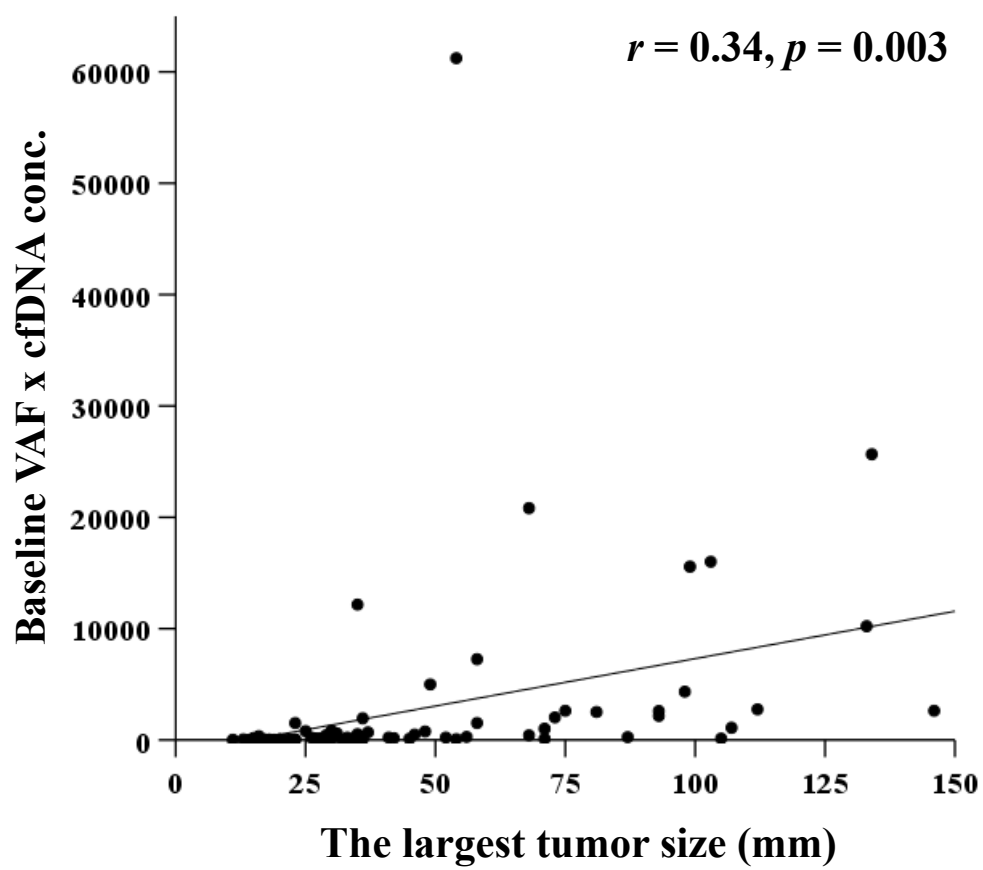
a



b



c



Supplementary Figure. 4. Clinical significance of the mutations which were newly detected at disease progression by using annotation from the ClinVar database

