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CORRECTION
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Corrigendum: Longitudinal Circulating Tumor DNA Profiling in Metastatic Colorectal Cancer During Anti-EGFR Therapy

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A Corrigendum on

Longitudinal Circulating Tumor DNA Profiling in Metastatic Colorectal Cancer During Anti-EGFR Therapy

By Yang W, Zou J, Li Y, Liu R, Yan Z, Chen S, Zhao X, Guo W, Huang M, Li W, Zhu X and Chen Z (2022) Front. Oncol. 12:830816. doi: 10.3389/fonc.2022.830816

In the original article, there was a mistake in **Figure 1** as published. The figure illustration is wrong due to a software bug during picture output. The corrected **Figure 1** appears below.

In the original article, references **14** and reference **37** are the same. We have renumbered the references.

In the original article, there was an additional error in **Results, Mutation Profiles at Baseline**, paragraph two. In the sentence "For patients who received cetuximab as second-line treatment, the RAS mutation discrepancy was 13.3% (2/6)", the percentage is wrong and needs to be changed from 13.3% to 33.3%. The corrected paragraph appears below.

"For the KRAS, NRAS, and BRAF V600E genes, the concordance rates between the tumor tissue test by PCR and ctDNA test by NGS were 86.4%, 86.4%, and 100%, respectively. The RAS mutation discrepancy was also compared among treatments (**Figure 1B**). For patients who received cetuximab as first-line treatment, the RAS mutation discrepancy was 13.3% (2/15). Both of these patients also had NRAS mutations. The mutation sites were NRAS p.Q61K (0.31%), NRAS p.G13R (0.07%), and NRAS p.G12R (0.37%). For patients who received cetuximab as second-line treatment, the RAS mutation discrepancy was 33.3% (2/6). One patient had a KRAS p.G12V mutation (2.17%) and the other patient had both KRAS p.Q61H (0.02%) and NRAS p.G13C (0.03%) mutations. The only patient who received cetuximab as third-line treatment had a KRAS mutation. The mutation sites included KRAS p.Q61Hc.183A>T (0.05%), KRAS p.Q61Hc.183A>C (0.91%), and KRAS p.G12A (0.58%). The clonal and subclonal landscapes were detected at baseline (**Figure 1C**). Subclonal mutations were found in 31.8% (7/22) of the patients. The three most common clonal mutation genes were

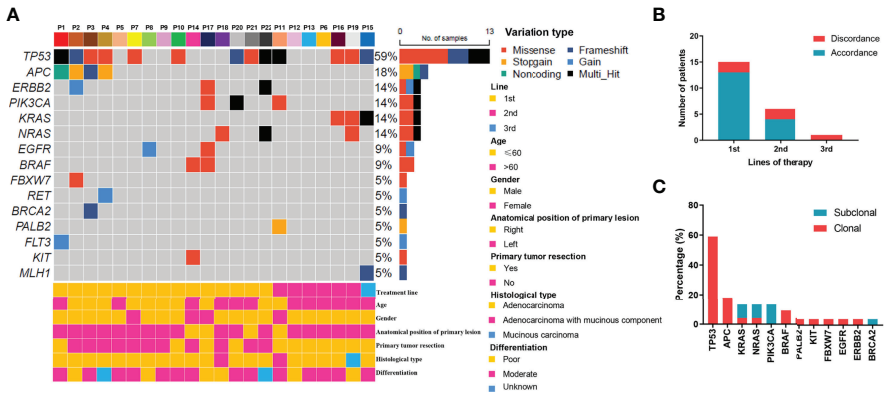

FIGURE 1 | Mutation profiling of pre-treatment ctDNA. **(A)** Genomic profiles of 22 advanced colorectal cancer patients from pre-treatment ctDNA. **(B)** The consistency of the RAS mutations detected in paired tissues and plasma. **(C)** The clonal and subclonal landscapes in 22 mCRC patient at baseline. Gain: segments with log ratio more than 3 times of standard deviation of all segment level were considered as "gain".

TP53, APC, and BRAF, while the three most common subclonal mutation genes were PIK3CA, KRAS, and NRAS."

The authors apologize for these errors and state that this does not change the scientific conclusions of the article in any way. The original article has been updated.

SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: https://www.frontiersin.org/articles/10.3389/fonc.2022.903586/full#supplementary-material