



# Corrigendum: Clinical Utilization Pattern of Liquid Biopsies (LB) to Detect Actionable Driver Mutations, Guide Treatment Decisions and Monitor Disease Burden During Treatment of 33 Metastatic Colorectal Cancer (mCRC) Patients (pts) at a Fox Chase Cancer Center GI Oncology Subspecialty Clinic

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## A Corrigendum on

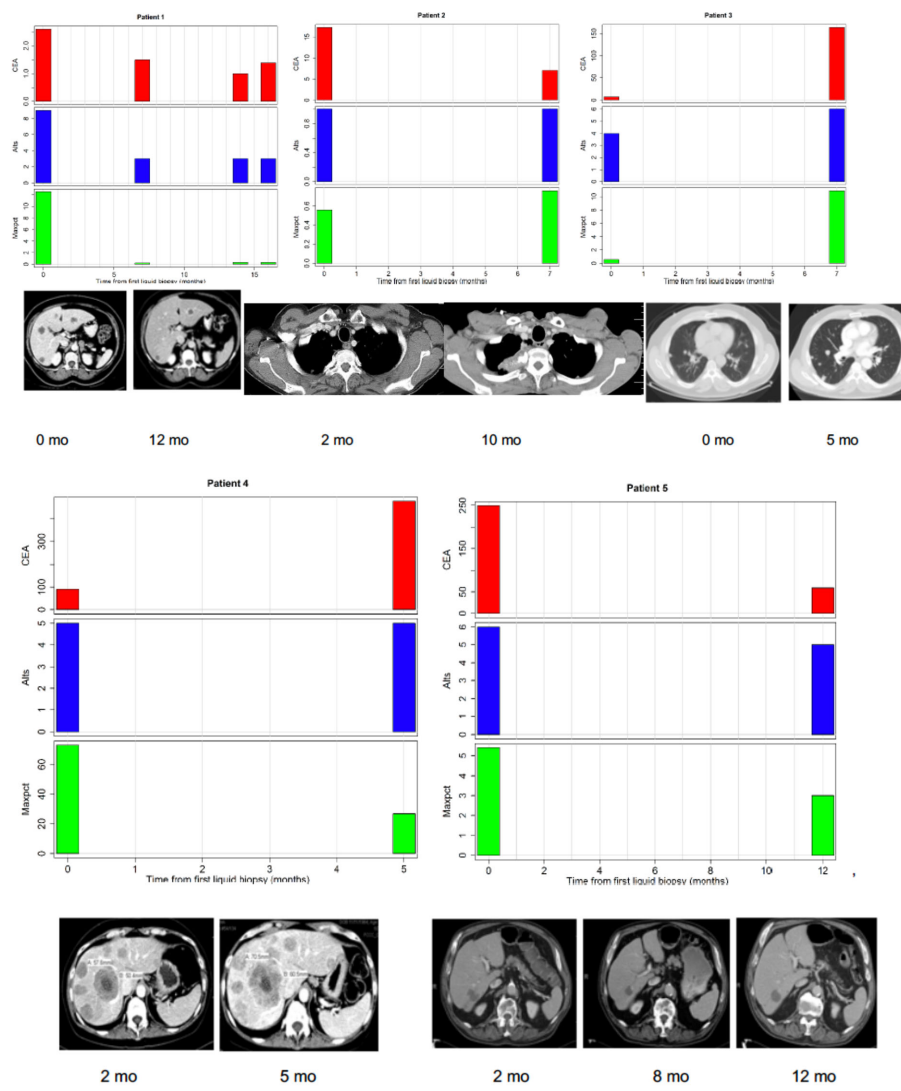
**Clinical Utilization Pattern of Liquid Biopsies (LB) to Detect Actionable Driver Mutations, Guide Treatment Decisions and Monitor Disease Burden During Treatment of 33 Metastatic Colorectal Cancer (mCRC) Patients (pts) at a Fox Chase Cancer Center GI Oncology Subspecialty Clinic**

By Ghatalia P, Smith CH, Winer A, Gou J, Kiedrowski LA, Slifker M, Saltzberg PD, Bubes N, Anari FM, Kasireddy V, Varshavsky A, Liu Y, Ross EA and El-Deiry WS (2019). *Front. Oncol.* 8:652. doi: 10.3389/fonc.2018.00652

In the original article, there was a mistake in **Figure 3** as published. Incorrect CT scans were provided for two patients, while another patient's CT scan was erroneously duplicated. The error was previously missed by the authors and the reviewers.

The corrected **Figure 3** appears below.

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



**FIGURE 3** | Correlations between tumor burden as assessed by radiographic imaging (CT scans) or CEA (tumor marker) and liquid biopsy mutation parameters (alts or number of alterations/number of mutated genes and maxpct or maximal allele frequency of mutated allele). (Top Left) Maxpct, CEA, and alts follow a downward trend as disease on CT scan improves. Center: With growth of mediastinal mass on CT, note rise in maxpct, CEA, and alts. (Top Right) As lung disease worsens on CT, maxpct, CEA, and alts increase. (Bottom Left) Despite increasing tumor on CT scan and rising CEA, maxpct did not rise. Liquid biopsy did contain APC and TP53 mutations, indicating presence of ctDNA. (Bottom Right) Liver metastases decreased between 1/2017 and 7/2017 and then increased in 11/2017. Allele freq. low (2–4%) probably due to low disease burden on CT.

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