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EDITED AND REVIEWED BY
Abdullah Kahraman,
University of Applied Sciences and Arts
Northwestern Switzerland, Switzerland

*CORRESPONDENCE
Yinfei Wu
✉ yinfei_wu@163.com

RECEIVED 02 April 2026
REVISED 09 April 2026
ACCEPTED 14 April 2026
PUBLISHED 08 May 2026

CITATION

Zhang X, Fang Q, Yuan J, Dai L, Luo R,
Huang T and Wu Y (2026) Correction:
Evaluation of ctDNA-guided adjuvant
therapy de-escalation in head and
neck squamous cell carcinoma:
a comparative cohort study.
Front. Immunol. 17:1845587.
doi: 10.3389/fimmu.2026.1845587

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Correction: Evaluation of ctDNA-guided adjuvant therapy de-escalation in head and neck squamous cell carcinoma: a comparative cohort study

Xu Zhang¹, Qigen Fang¹, Junhui Yuan², Liyuan Dai¹,
Ruihua Luo¹, Tao Huang^{3,4} and Yinfei Wu^{5*}

¹Department of Head Neck and Thyroid, The Affiliated Cancer Hospital of Zhengzhou University & Henan Cancer Hospital, Zhengzhou, China, ²Department of Radiology, The Affiliated Cancer Hospital of Zhengzhou University & Henan Cancer Hospital, Zhengzhou, China, ³Department of Breast, The Affiliated Cancer Hospital of Zhengzhou University & Henan Cancer Hospital, Zhengzhou, China, ⁴Moores Cancer Center, University of California, San Diego, San Diego, CA, United States, ⁵Health Management Center, The Affiliated Cancer Hospital of Zhengzhou University & Henan Cancer Hospital, Zhengzhou, China

KEYWORDS

head and neck squamous cell carcinoma, CtDNA, neoadjuvant chemoimmunotherapy, adjuvant chemotherapy, pathologic complete response

A Correction on

Evaluation of ctDNA-guided adjuvant therapy de-escalation in head and neck squamous cell carcinoma: a comparative cohort study

By Zhang X, Fang Q, Yuan J, Dai L, Luo R, Huang T and Wu Y (2025) *Front. Immunol.* 16:1576042.
doi: 10.3389/fimmu.2025.1576042

In the original publication, the methodology for the personalized, tumor-informed *ctDNA testing* was incorrectly stated as being performed “using the Signatera™ (Natera, Inc.) assay.

A correction has been made to the section (*ctDNA testing* paragraph in **Methods** section, Page 3):

“This methodology aligns with previously published protocols (18). ctDNA was detected in plasma samples gathered prior to neoadjuvant chemoimmunotherapy and within 10–14 days postsurgery. Personalized, tumor-informed ctDNA testing was performed using Illumina (NextSeq 500/NovaSeq 6000) next-generation sequencing platform (Wanlei, Shenyang). Testing was conducted by our core facility, utilizing matched tumor tissue and blood samples to design patientspecific assays. Somatic mutations were identified via multiplex PCR amplification via a 16-plex PCR panel targeting tumor-derived variants, enabling bespoke detection with a sensitivity of 0.01% variant allele frequency. The bioinformatics pipeline included alignment (BWA-MEM), duplex consensus sequencing to reduce noise, and variant calling via a proprietary algorithm, with germline filtering using matched white blood cell-derived DNA. A plasma sample was classified as ctDNA-positive if ≥1 somatic variant was detected. Variant persistence in postoperative samples was confirmed if: the variant was detected pre-treatment, present in the binary comparison map file, or observed in ≥3 reads in postoperative plasma. ctDNA level was recorded with units of mean tumor molecules (MTM) per mL of plasma.”

The original article has been updated.

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