



Panea RI, Love CL, Shingleton JR, et al. The whole-genome landscape of Burkitt lymphoma subtypes. *Blood*. 2019;134(19):1598-1607.

Editors' note: The original publication requires correction of some data and data analysis elements. The deficiencies in the original publication have been raised as issues by Rushton et al¹ and acknowledged in a response by Dave² that also addresses other points of contention. This erratum corrects data presentation and data analyses and provides a more complete explanation of methods. The Blood editors thank the correspondents for drawing the concerns to Blood's attention and thank Dave and colleagues for correcting the scientific record.

The original article contains 2 errors. First, while the genetic drivers were derived entirely from whole-genome sequencing, the authors used whole-exome sequencing and RNA sequencing data to confirm the presence of already identified genetic drivers in other patients in their study. This was not fully clarified previously and is now described in the updated supplemental File 1, available in the online version of this erratum. Second, an additional error that led to the same variant being counted twice was discovered in the merging of data in some cases. These errors are described in 2 new supplemental files, supplemental File 2 (which corrects supplemental File 2 in the original article) and supplemental File 3 (which contains updated analyses, verification of findings, and comments), which include the reanalyzed results after removal of the errors. The described genetic drivers and trends in the data remain unchanged.

Addendum (March 2024): The updated supplemental File 3 that was submitted as part of the original version of this erratum contains an error. While 96% of individual variants in Table S2 are supported by whole-genome sequencing, with additional identified variants supported by whole-exome sequencing and RNAseq, supplemental File 3 stated, "All the individual variants in Table S2 were identified from whole genome sequencing data." This has been corrected and described in greater detail in the revised supplemental File 3 accompanying this addendum.

REFERENCES

1. Rushton CK, Dreval K, Morin RD. Concerning data inconsistencies in Burkitt lymphoma genome study. *Blood*. 2023;142(10):933-936.
2. Dave SS. Burkitt lymphoma genomic discovery studies, drivers, and validation. *Blood*. 2023;142(10):936-938.

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