Corrigendum: Predicting T Cell Receptor Antigen Specificity From Structural Features Derived From Homology Models of Receptor-Peptide-Major Histocompatibility Complexes

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A Corrigendum on

Predicting T Cell Receptor Antigen Specificity From Structural Features Derived From Homology Models of Receptor-Peptide-Major Histocompatibility Complexes
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In the original article, there was a mistake in the provided supplementary material for the datasets Dash (Dash et al., 2017), 10X (10XGenomics, 2020), and newVdj (Bagaev et al., 2020) as published. The mistake derived from an imprecision in the method used to reconstruct the complete amino sequence for the TCRs from the V/J gene and CDR3 information, which impacted a small proportion of the sequences in these sets (between 0.5 and 7% depending on the set). The wrong sequences have now been either removed or corrected. The corrected version of these datasets is provided as supplementary material.

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.

REFERENCES

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Dash, P., Fiore-Gartland, A. J., Hertz, T., Wang, G. C., Sharma, S., Souquette, A., et al. (2017). Quantifiable predictive features define epitope-specific T cell receptor repertoires. *Nature* 547, 89–93. doi: 10.1038/nature22383