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D. Mandelker, M. Donoghue, S. Talukdar, C. Bandlamudi, P. Srinivasan, et al.. Erratum to 'Germline-focussed analysis of tumour-only sequencing: recommendations from the ESMO Precision Medicine Working Group'. *Annals of Oncology*, 2021, 32 (8), pp.1069-1071. 10.1016/j.annonc.2021.05.798 . hal-04324470

HAL Id: hal-04324470

<https://ut3-toulouseinp.hal.science/hal-04324470v1>

Submitted on 5 Dec 2023

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ERRATUM

Erratum to ‘Germline-focussed analysis of tumour-only sequencing: recommendations from the ESMO Precision Medicine Working Group’



[Annals of Oncology 30 (2019) 1221–1231]

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The publisher regrets that in the original publication figures 1, 2 and 3 were incorrectly presented. The correct figures 1, 2 and 3 are as follows.

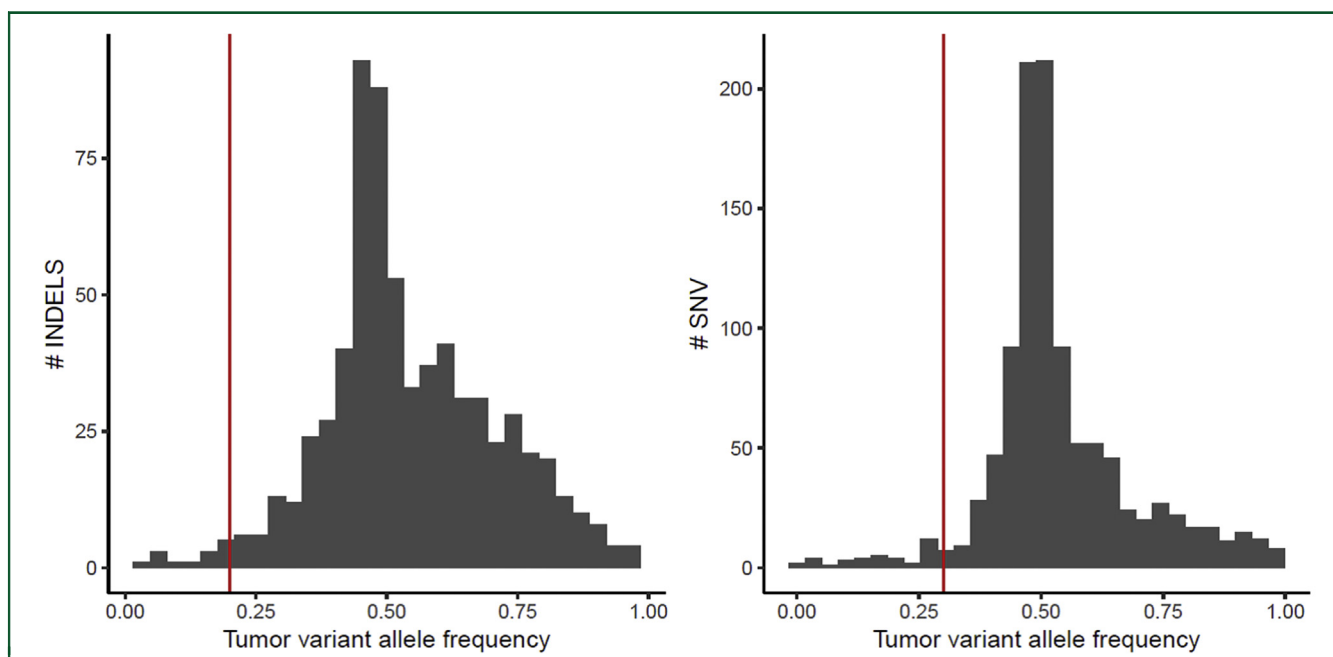


Figure 1. Distribution of variant allele frequency observed in the tumour for variants of true germline origin which were (i) small insertion/deletions (ii) SNVs.

DOI of original article: <https://doi.org/10.1093/annonc/mdz136>

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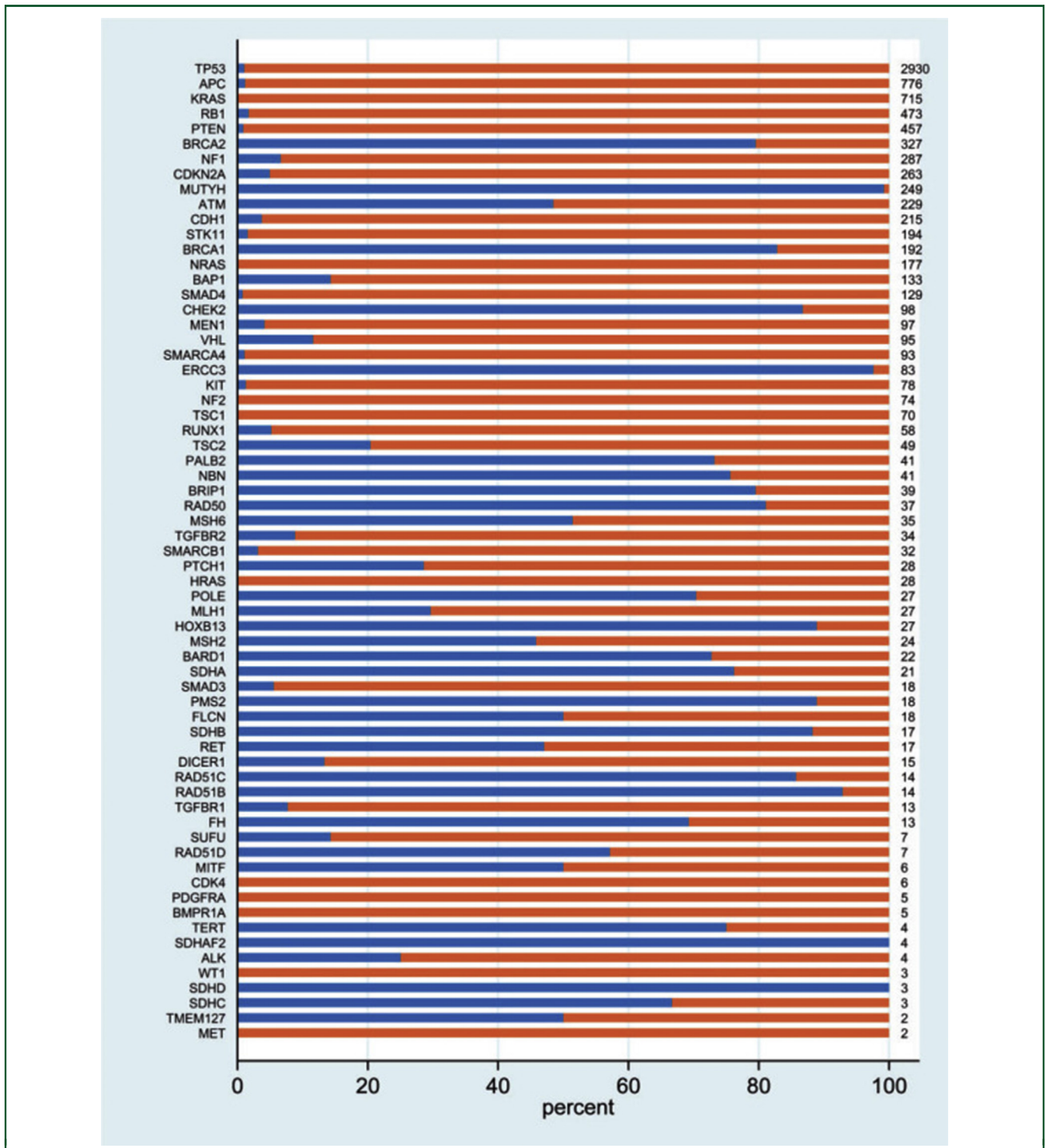


Figure 2. Distribution of germline and somatic pathogenic variants detected upon tumour analysis. Only variants classified pathogenic/likely pathogenic AND above VAF threshold are included (blue, germline origin; red, somatic origin; numbers, total number of pathogenic variants. observed in tumour).

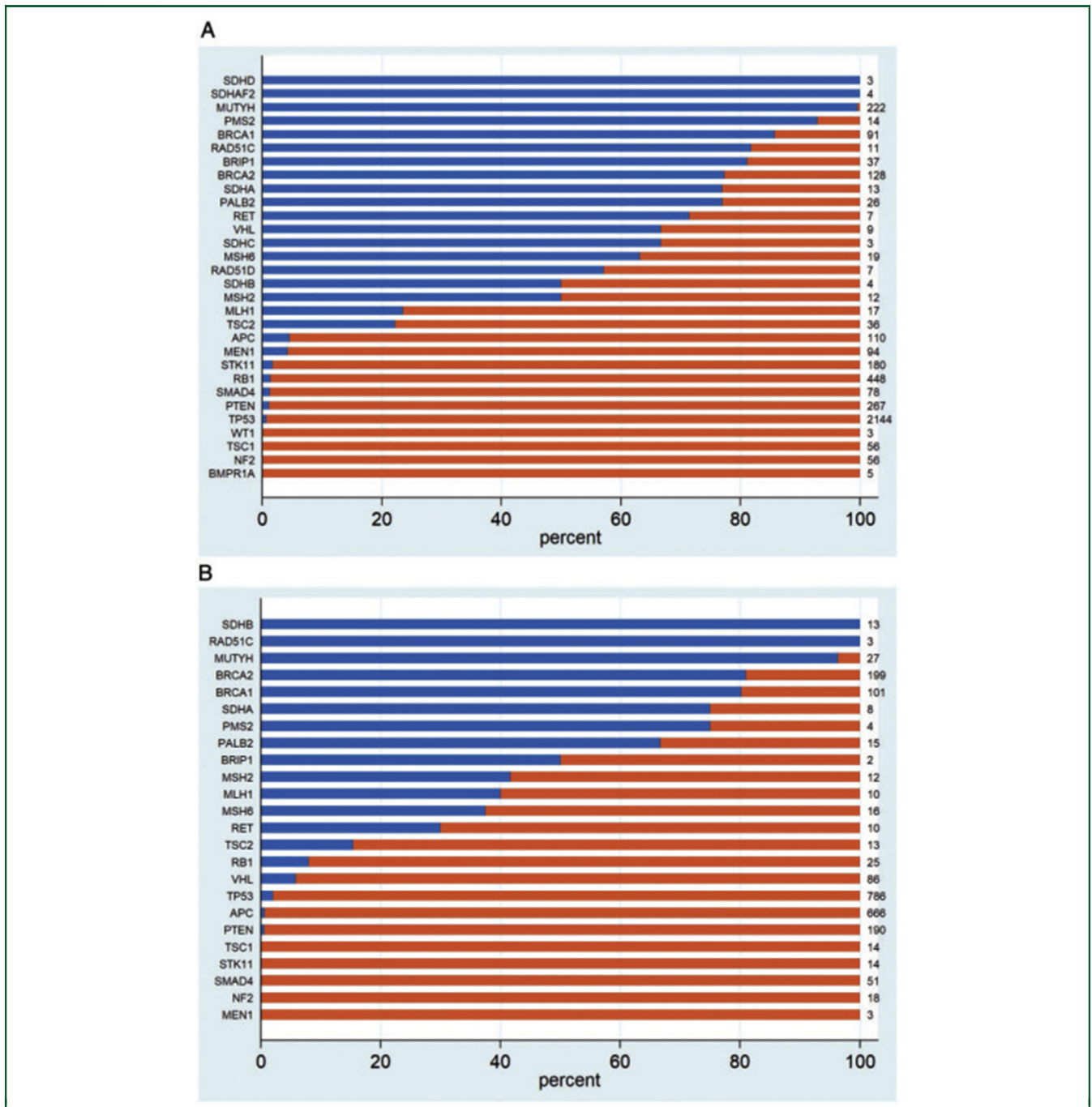


Figure 3. Distribution of germline and somatic pathogenic variants detected upon tumour analysis for 30 high-actionability CSGs. (A) Off-tumour and (B) on-tumour.

The publisher would like to apologise for any inconvenience caused.