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ERRATUM

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

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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.

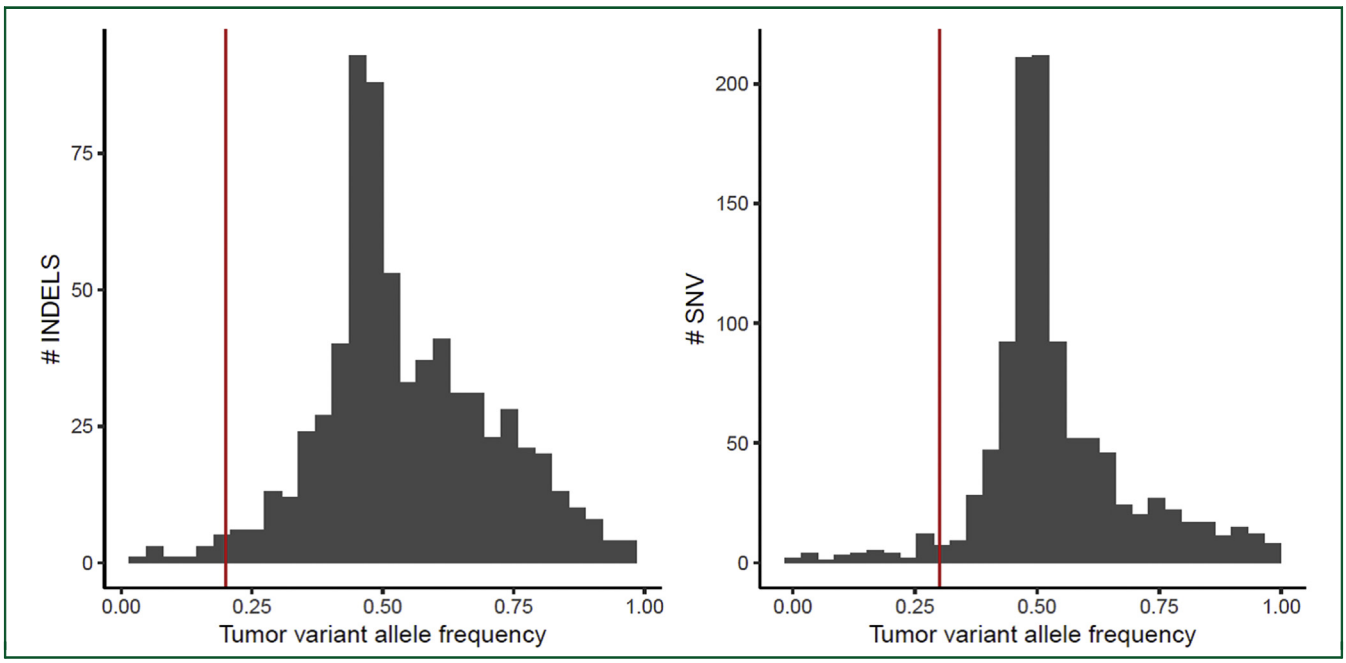

Figure 1. Distribution of variant allele frequency observed in the tumour for variants of true germline origin which were (i) small insertion/deletions (ii) SNVs.

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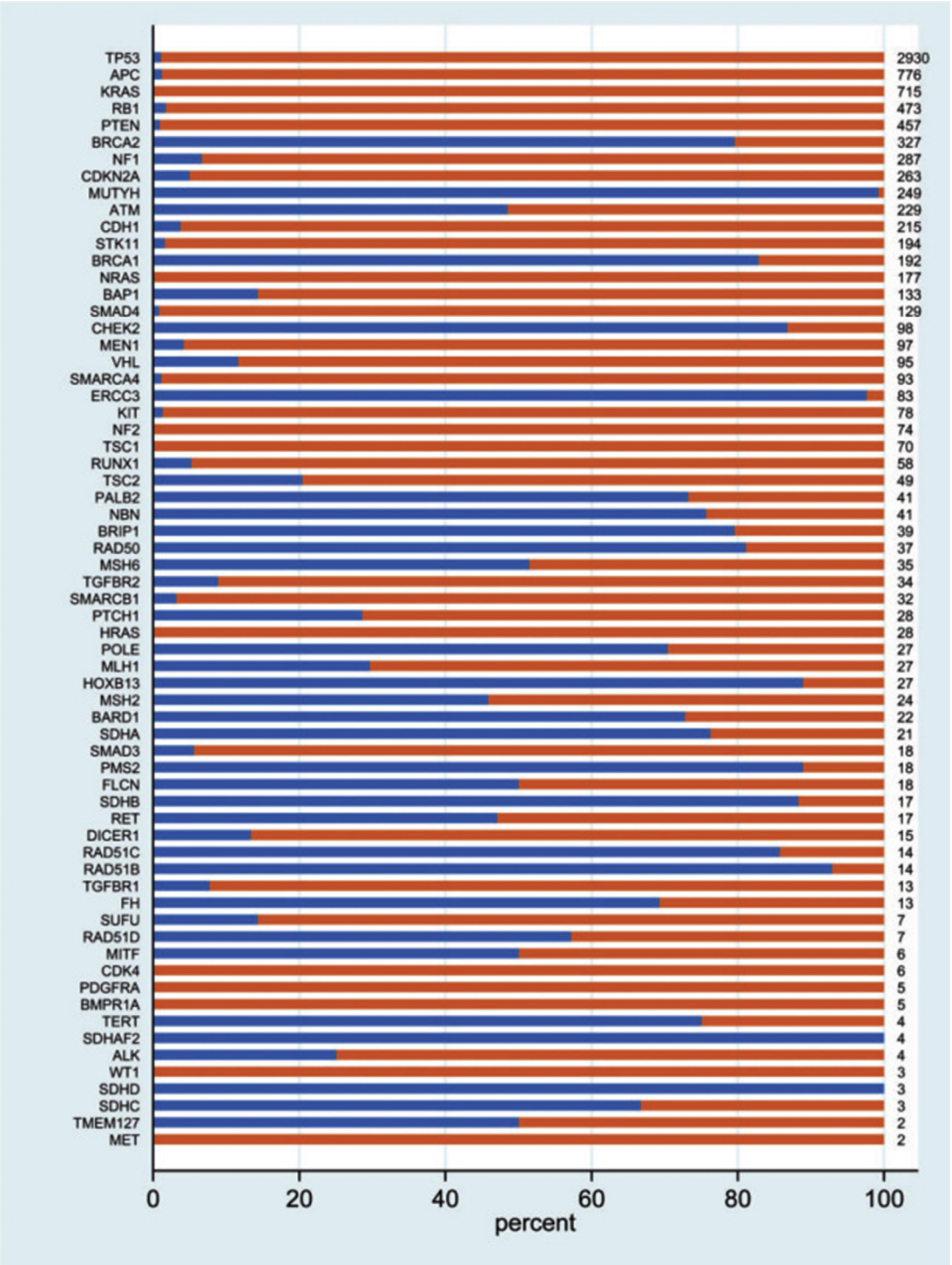

Figure 2. Distribution of germline and somatic pathogenic variants detected upon tumour analysis. Only variants classified pathogenic/likely pathogenic AND above VAF threshold are included (blue, germline origin; red, somatic origin; numbers, total number of pathogenic variants. observed in tumour).

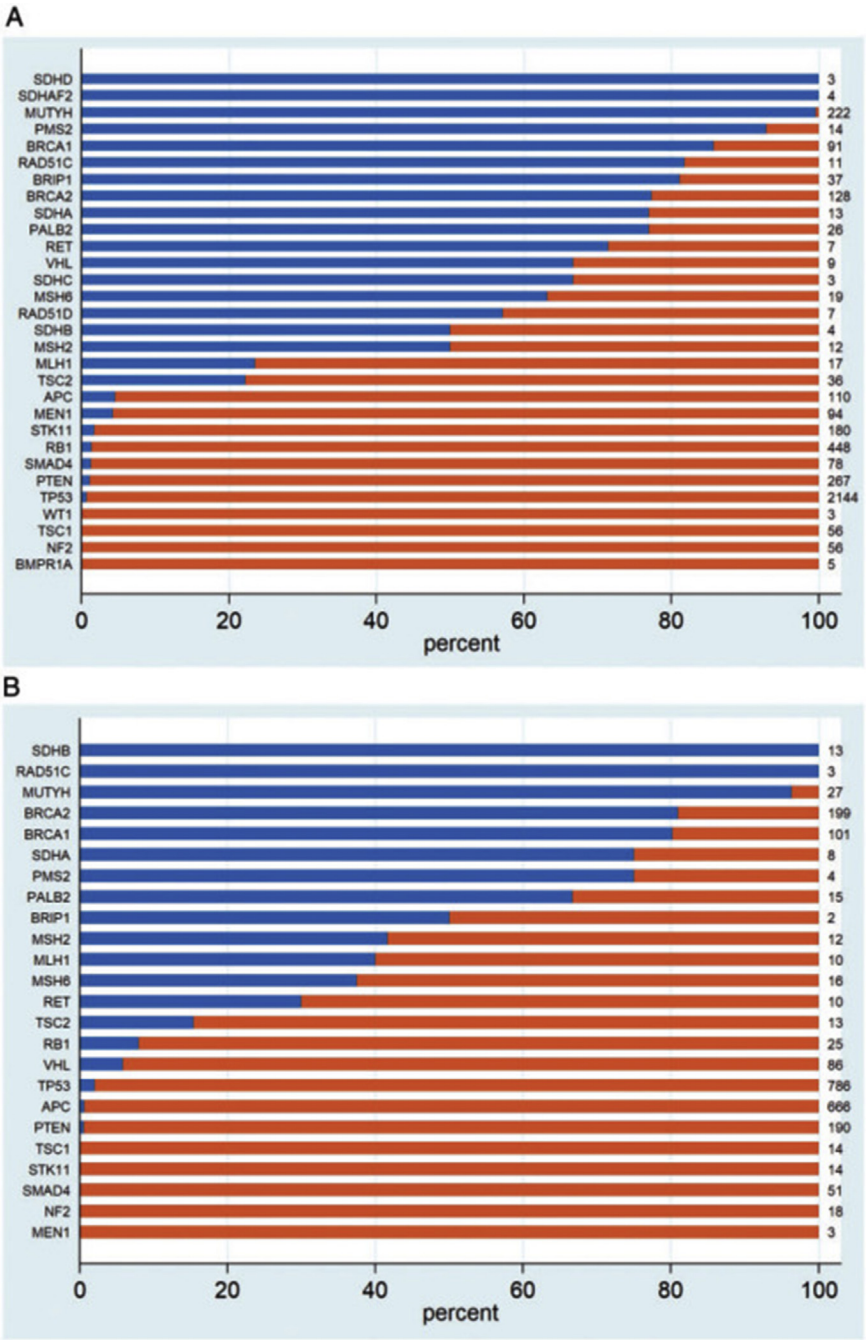

Figure 3. Distribution of germline and somatic pathogenic variants detected upon tumour analysis for 30 high-actionability CSGs. (A) Offtumour and (B) on-tumour.

The publisher would like to apologise for any inconvenience caused.