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Erratum: Application of circulating tumour DNA in terms of prognosis prediction in chinese follicular lymphoma patients

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An Erratum on Application of circulating tumour DNA in terms of prognosis prediction in chinese follicular lymphoma patients

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Due to a production error, there was a mistake in [Figure 1](#) as published. The figure was inadvertently duplicated from Supplementary Figure S1. The correct [Figure 1](#) appears below.

The publisher apologizes for these mistakes. The original version of this article has been updated.

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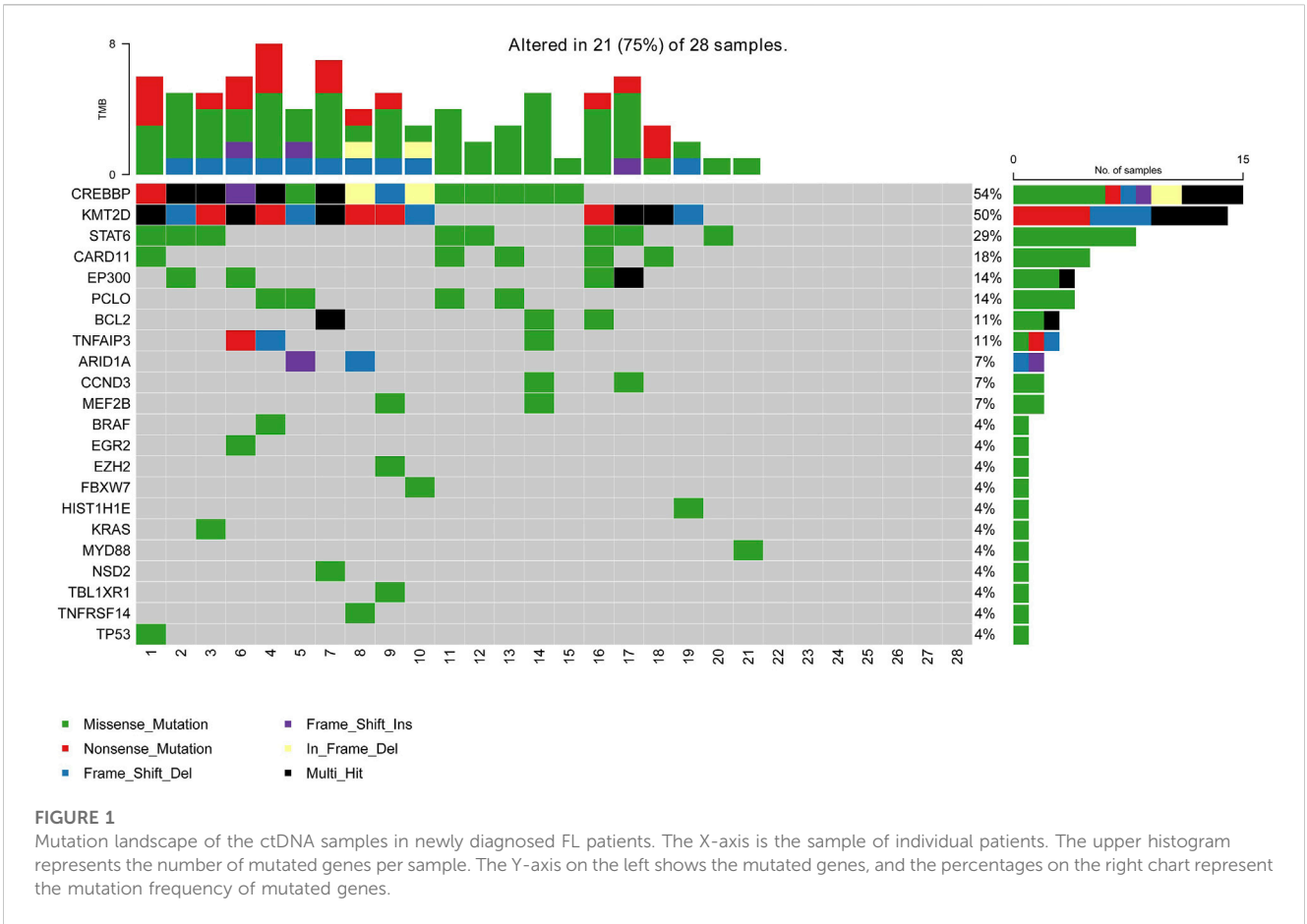


FIGURE 1

Mutation landscape of the ctDNA samples in newly diagnosed FL patients. The X-axis is the sample of individual patients. The upper histogram represents the number of mutated genes per sample. The Y-axis on the left shows the mutated genes, and the percentages on the right chart represent the mutation frequency of mutated genes.