

CORRIGENDUM

Comprehensive mutational analysis of primary and relapse acute promyelocytic leukemia

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Correction to: *Leukemia* (2016) 30, 1672–1681; doi:10.1038/leu.2016.69

The authors confirm that the above mislabeling has no impact on the conclusions made and wish to apologize for any inconvenience caused.

Following the publication of this article, the authors have noted that three genes: *FLT3*, *NRAS* and *ARID1A* (each with mutational frequency of 5%) have been incorrectly labelled in Figure 4a showing the mutational landscape of APL relapse.

Below is the corrected figure.

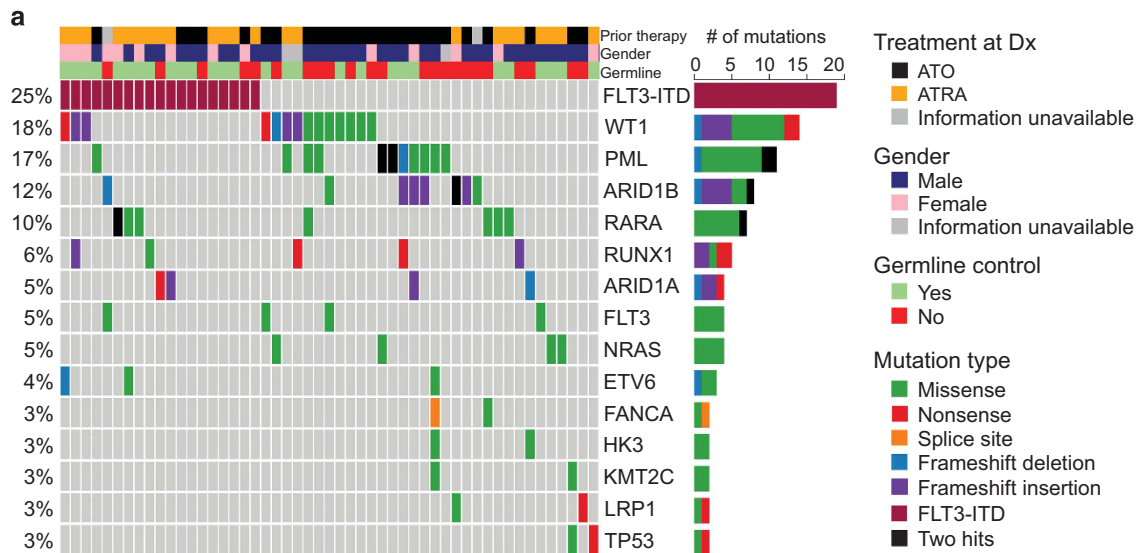


Figure 4a. Spectrum of somatic mutations at APL relapse. (a) Matrix displays top 15 genes recurrently mutated at relapsed APL. Each column represents a relapse sample. Genes are arranged according to decreasing mutational frequencies from top to bottom. Right panel illustrates the number of mutations for all genes. Only those relapse samples that harbor mutations of top 15 genes are included in the matrix.