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Correction to: Rapid and reliable detection of α-globin copy number variations by quantitative real-time PCR

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The copy number of the HBA1 assay for the -$(\alpha)^{20.5}$ deletion in the HBA-CNV method described in the original article [1] was incorrectly reported. The authors wish to note that the HBA1 assay will not be affected by the –$(\alpha)^{20.5}$ deletion and will show two copies (Table 1 - corrected). The 3′ breakpoint of the –$(\alpha)^{20.5}$ deletion is located within exon 2 of the HBA1 gene [2], leaving intact the area where the HBA1 assay is amplifying. The partial deletion of HBA1 causes a complete abolition of the gene expression, hence –$(\alpha)^{20.5}$ is considered as a double gene deletion. This shows that even though the HBA1 assay may show two copies, a deletion affecting both alpha-globin genes can not be excluded. Similarly, the Hb Var database contains examples of deletions that will not influence HBA2 assay copy number despite affecting both alpha-globin genes. Hence, molecular data should always be evaluated together with hematological data.

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Table 1 Predicted copy number in 108 patient samples

Genotype	Samples (n)	Copy Number Predicted			
		HBA1	HBA3.7	HBA2	HS-40
αα/αα	63	2	2	2	2
$-\alpha^{3.7}/\alpha\alpha$	22	2	1	2	2
$-\alpha^{4.2}/\alpha\alpha$	2	2	2	1	2
$-\alpha^{3.7}/-\alpha^{3.7}$	8	2	0	2	2
$--^{SEA}/\alpha\alpha$	7	1	1	1	2
$--^{FIL}/\alpha\alpha$	1	1	1	1	2
$-(\alpha)^{20.5}/\alpha\alpha$	1	2	1	1	2
$--^{MED}/\alpha\alpha$	1	1	1	1	2
$-\alpha^{3.7}/--^{SEA}$	1	1	0	1	2
$\alpha\alpha/\alpha\alpha\alpha^{anti3.7}$	2	2	3	2	2
Total	108				