



Corrigendum to “Considerations and quality controls when analyzing cell-free tumor DNA” [Biomol. Detect. Quantif. 17 (2019) 100078]



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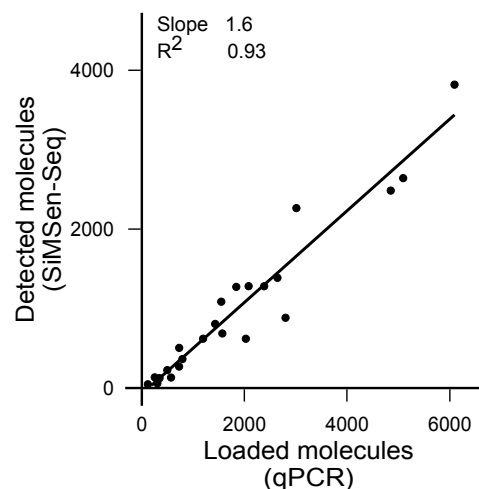
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The authors regret a calculation error affecting the quantification of molecules in Figures 7 and 8. The original calculations did not take into account that SiMSen-Seq generates on average 2 barcodes per original template molecule. This caused a 2-fold error when converting barcode numbers to original molecules detected.

In section 2.5 Analysis of cfDNA losses throughout the liquid biopsy workflow. Numbers in the following text are updated:

Forty-nine percent of the extracted cfDNA was amplifiable by qPCR. The sample concentration step showed a minor 3% loss of molecules and an additional 28% loss was observed in the SiMSen-Seq step. Nineteen percent of the initial cfDNA molecules were quantified by SiMSen-Seq.



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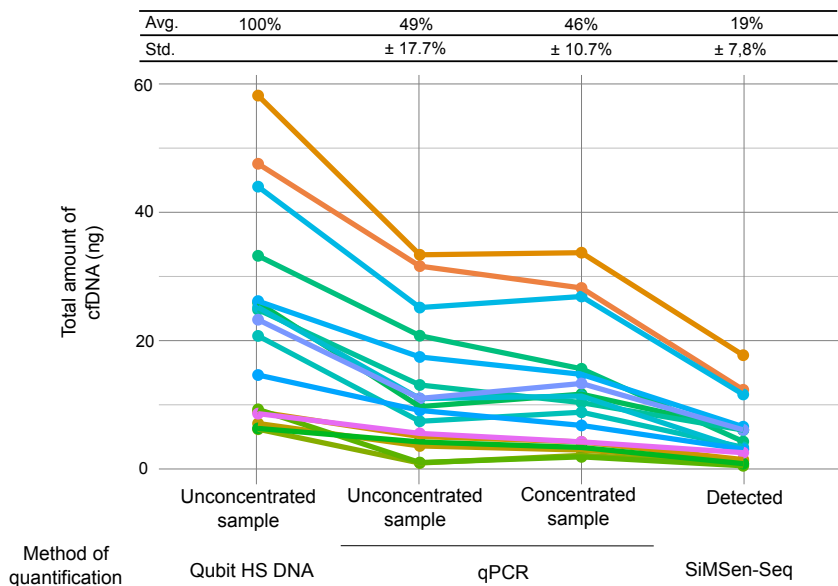
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The authors would like to apologise for any inconvenience caused.