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

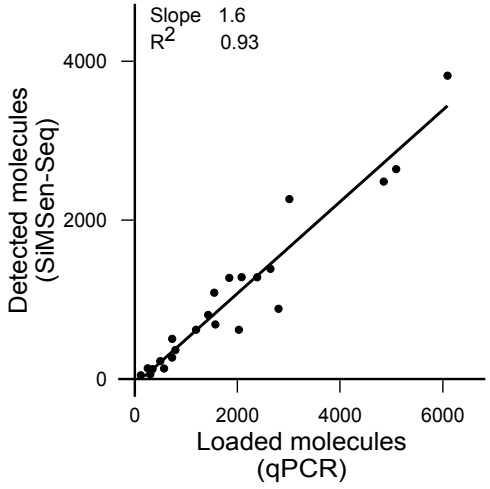
Gustav Johansson[a,b,c], Daniel Andersson[a], Stefan Filges[a], Junrui Li[a], Andreas Muth[d], Tony E. Godfrey[e], Anders Ståhlberg[a,b,f,*]

[a] Sahlgrenska Cancer Center, Department of Pathology and Genetics, Institute of Biomedicine, Sahlgrenska Academy at University of Gothenburg, Medicinaregatan 1F, 413 90 Gothenburg, Sweden
[b] Wallenberg Centre for Molecular and Translational Medicine, University of Gothenburg, Gothenburg, Sweden
[c] Respiratory Inflammation and Autoimmunity, IMED Biotech Unit, AstraZeneca, Gothenburg, Sweden
[d] Department of Surgery, Institute of Clinical Sciences, Sahlgrenska Academy at the University of Gothenburg, Gothenburg, Sweden
[e] Department of Surgery, Boston University School of Medicine, 700 Albany Street, Boston, MA, 02118, USA
[f] Department of Clinical Pathology and Genetics, Sahlgrenska University Hospital, 413 45 Gothenburg, Sweden

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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* Corresponding author at: Sahlgrenska Cancer Center, Department of Pathology and Genetics, Institute of Biomedicine, Sahlgrenska Academy at University of Gothenburg, Medicinaregatan 1F, 413 90 Gothenburg, Sweden.
E-mail address: anders.stahlberg@gu.se (A. Ståhlberg).

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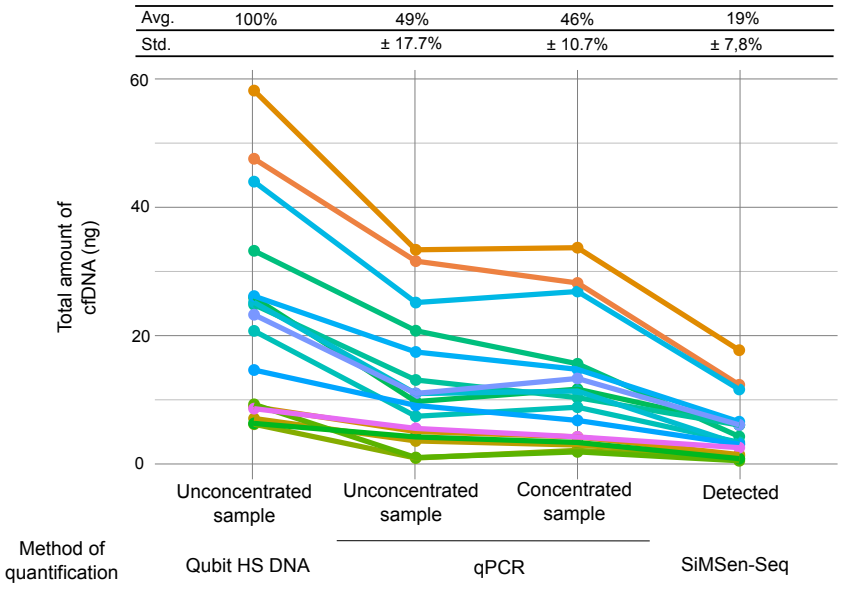

The authors would like to apologise for any inconvenience caused.