

From sample to treatment

Preclinical Factors

Rikke Fredslund Andersen

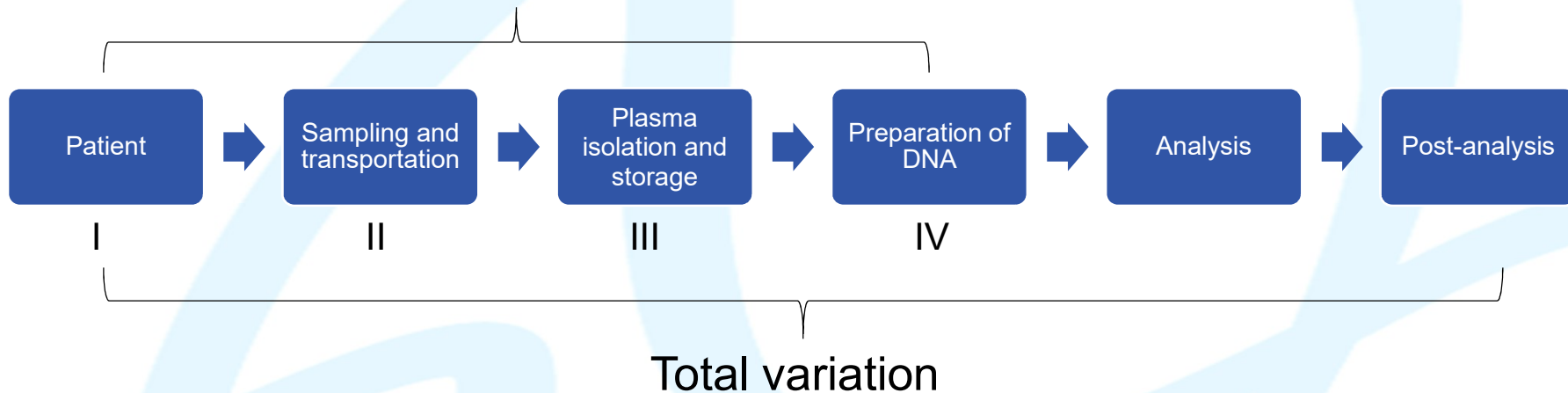
Biochemistry and Immunology

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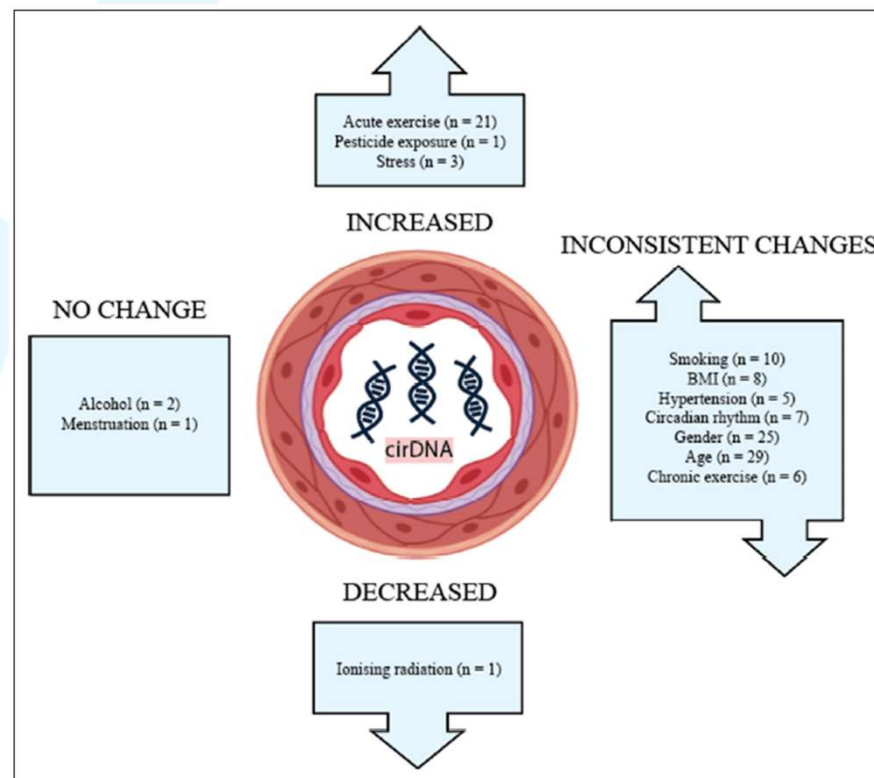


Pre-analytical variation



- I. Biological variation, co-morbidities, physical activity, fasting, timing in relation to medical/surgical treatment
- II. Collection tube (type/volume), syringe, stasis, first/second tube, agitation
- III. Time to centrifugation, centrifugation, temperature, pipetting, storage conditions, freeze/thaw
- IV. Extraction of DNA, (pre-amplification, denaturation, bisulphite conversion,...)

- I. **Biological variation, co-morbidities, physical activity, fasting, timing in relation to medical/surgical treatment**
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Yuwono et al. eLife 2021;0:e69679.

Surgical treatment

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The effect of surgical trauma on circulating free DNA levels in cancer patients—implications for studies of circulating tumor DNA

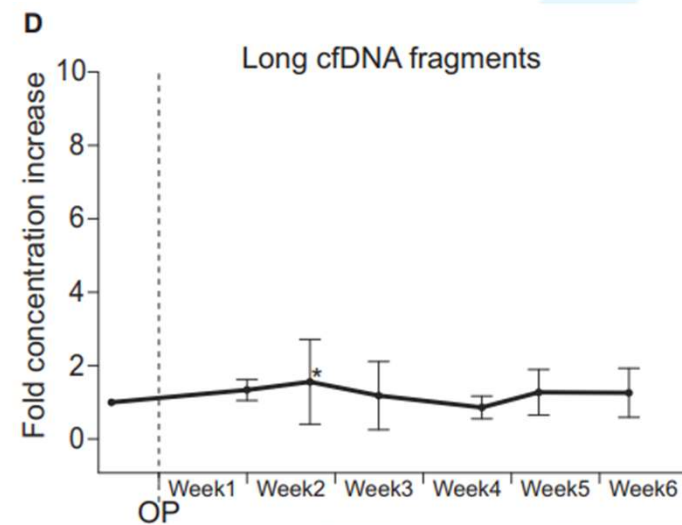
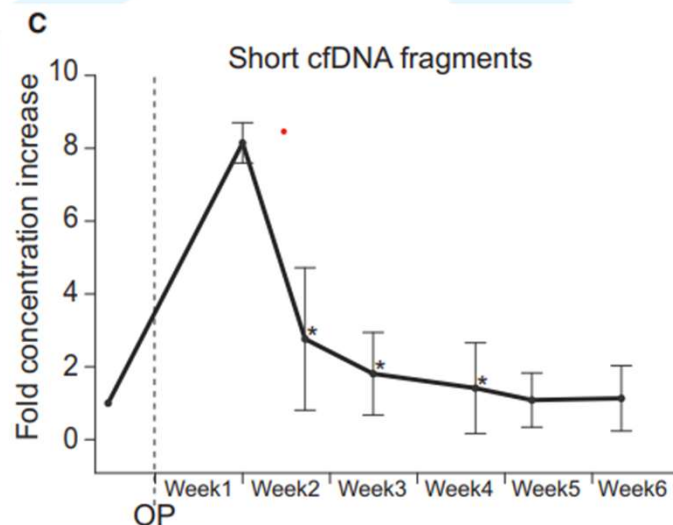
Tenna V. Henriksen¹, Thomas Reinert¹, Emil Christensen¹, Himanshu Sethi², Karin Birkenkamp-Demtröder¹, Mikail Gögenur³, Ismail Gögenur³, Bernhard G. Zimmermann², The IMPROVE Study Group[†], Lars Dyrskjöt¹ and Claus L. Andersen¹ 

¹ Department of Molecular Medicine, Aarhus University Hospital, Aarhus N, Denmark

² Natera Inc., San Carlos, CA, USA

³ Center for Surgical Sciences, Zealand University Hospital, Køge, Denmark

Molecular Oncology **14** (2020) 1670–1679 

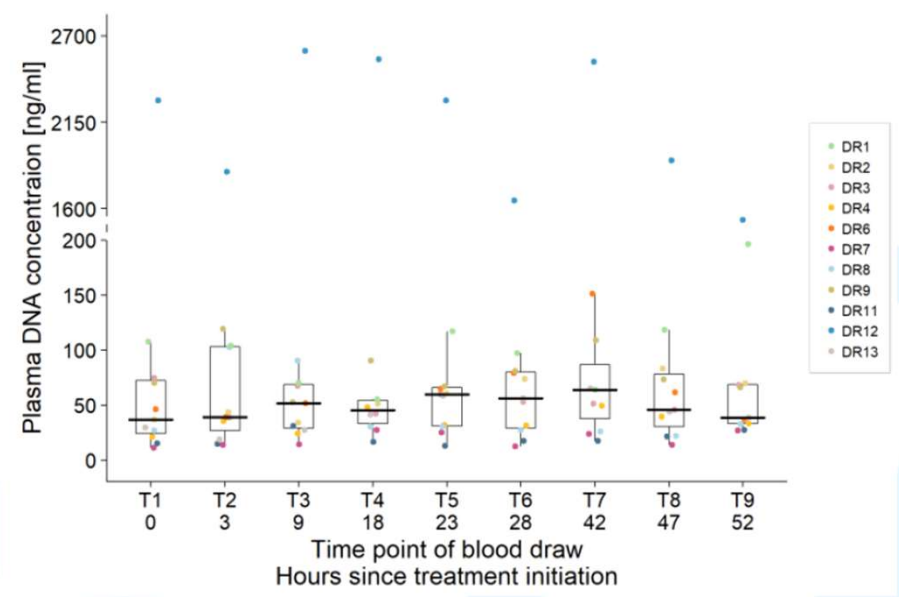
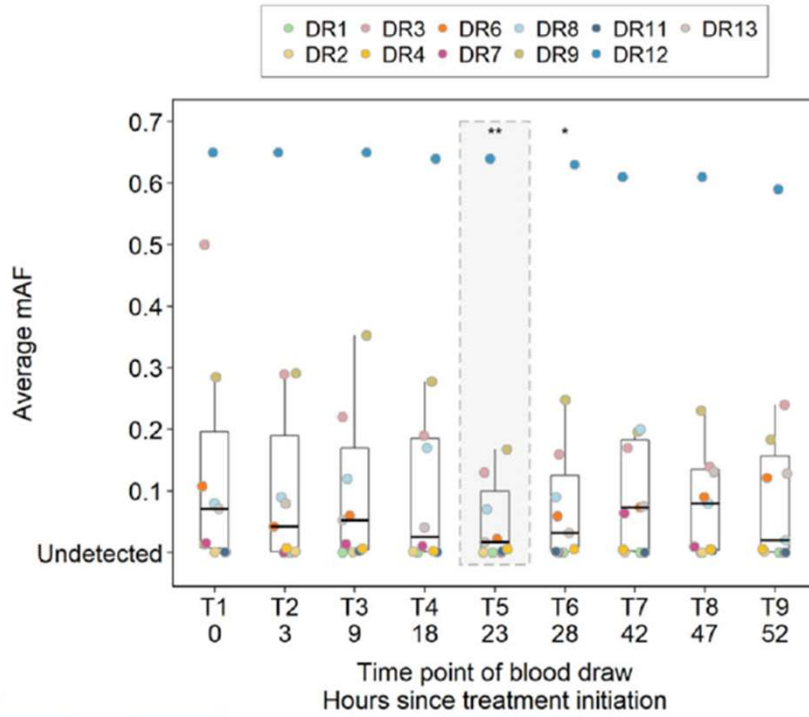


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Medical treatment

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On-treatment measurements of circulating tumor DNA during FOLFOX therapy in patients with colorectal cancer

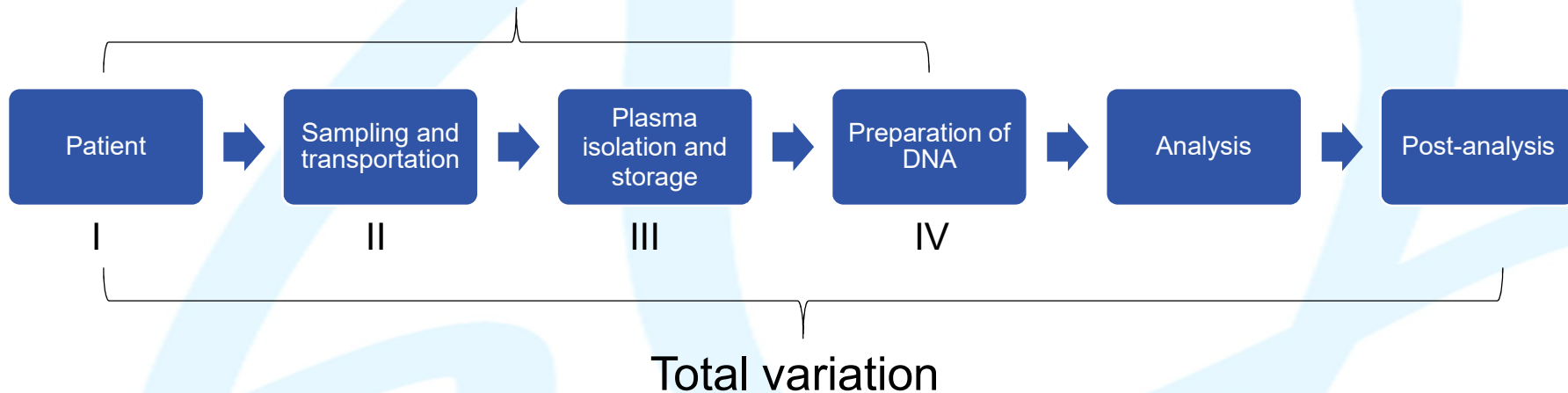
Tina Moser^{1,10}, Julie Waldspuehl-Geigl^{1,10}, Jelena Belic^{1,9}, Sabrina Weber¹, Qing Zhou¹, Samantha O. Hasenleithner¹⁰, Ricarda Graf¹, Jasmin Alia Terzic², Florian Posch², Heinz Sill¹⁰, Sigurd Lax¹⁰, Karl Kashofer⁵, Gerald Hoefler⁵, Helmut Schoellnast⁶, Ellen Heitzer^{1,7,8}, Jochen B. Geigl¹, Thomas Bauernhofer^{10,20} and Michael R. Speicher^{1,7,8}

npj Precision Oncology 4:30 (2020)





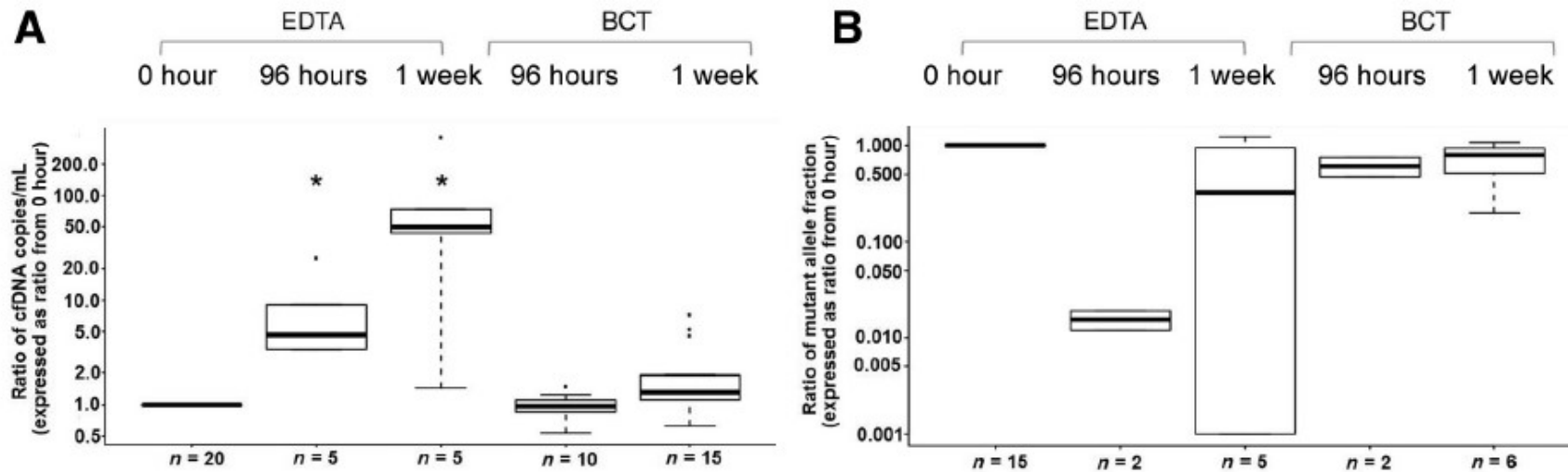
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EDTA vs. Streck tubes

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Effects of Collection and Processing Procedures on Plasma Circulating Cell-Free DNA from Cancer Patients

Bente Risberg,^{*††} Dana W.Y. Tsui,^{*§} Heather Biggs,[§] Andrea Ruiz-Valdepenas Martin de Almagro,^{*§} Sarah-Jane Dawson,^{*¶||} Charlotte Hodgkin,^{||} Linda Jones,[¶] Christine Parkinson,^{||} Anna Piskorz,^{*§} Francesco Marass,^{*§} Dineika Chandrananda,^{*§} Elizabeth Moore,^{*§} James Morris,^{*§} Vincent Plagnol,^{**} Nitzan Rosenfeld,^{*§} Carlos Caldas,^{*§||} James D. Brenton,^{*§||} and Davina Gale^{*§}

The Journal of Molecular Diagnostics, Vol. 20, No. 6, November 2018



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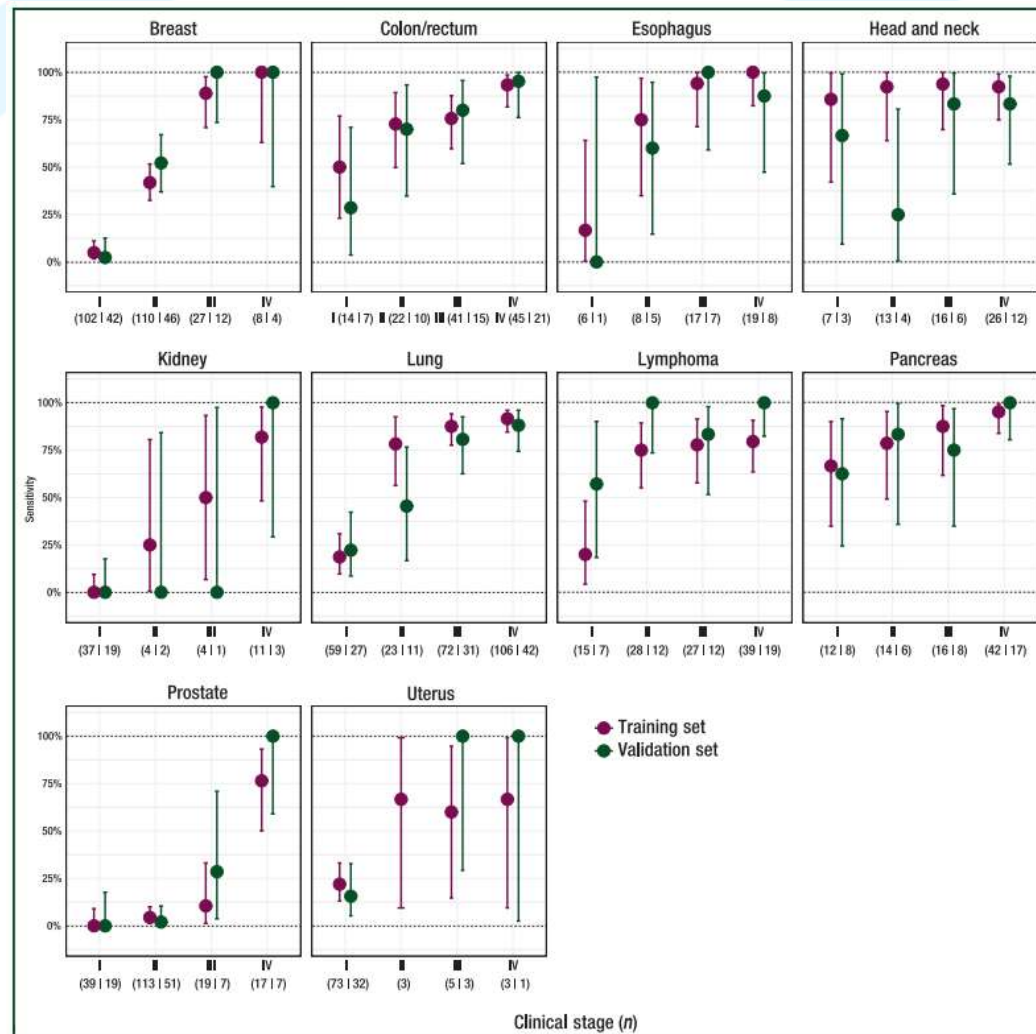


Volume of blood

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- Organ
- Stage
- Metastatic site

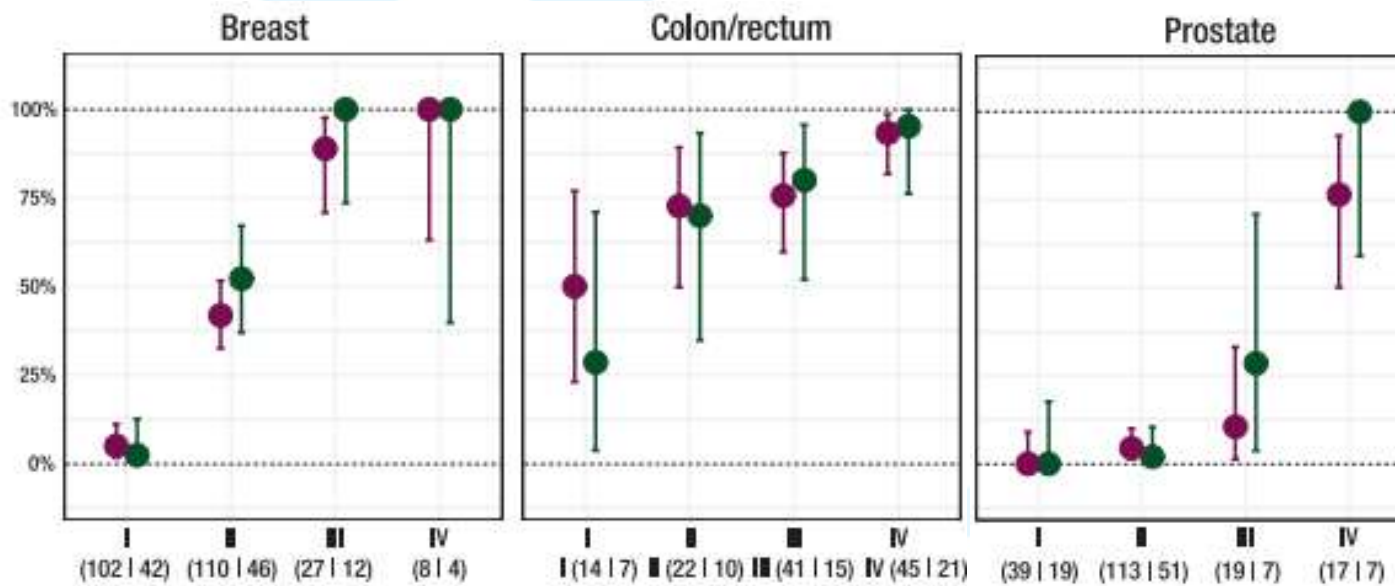


Liu MC *et al.*, Ann Onc 2020



Organ and stage

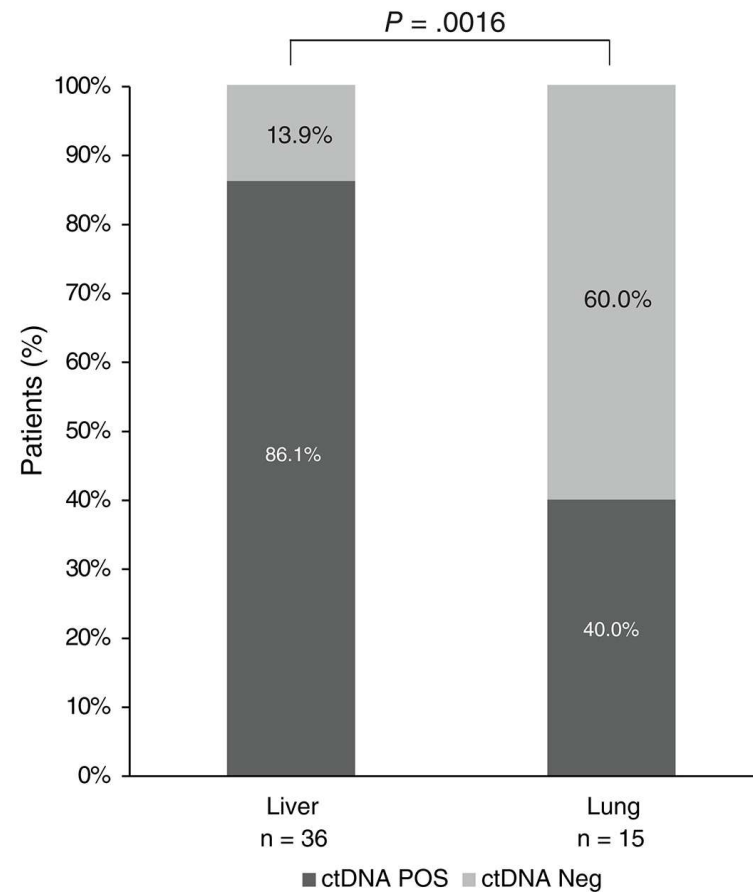
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Metastatic site - CRC

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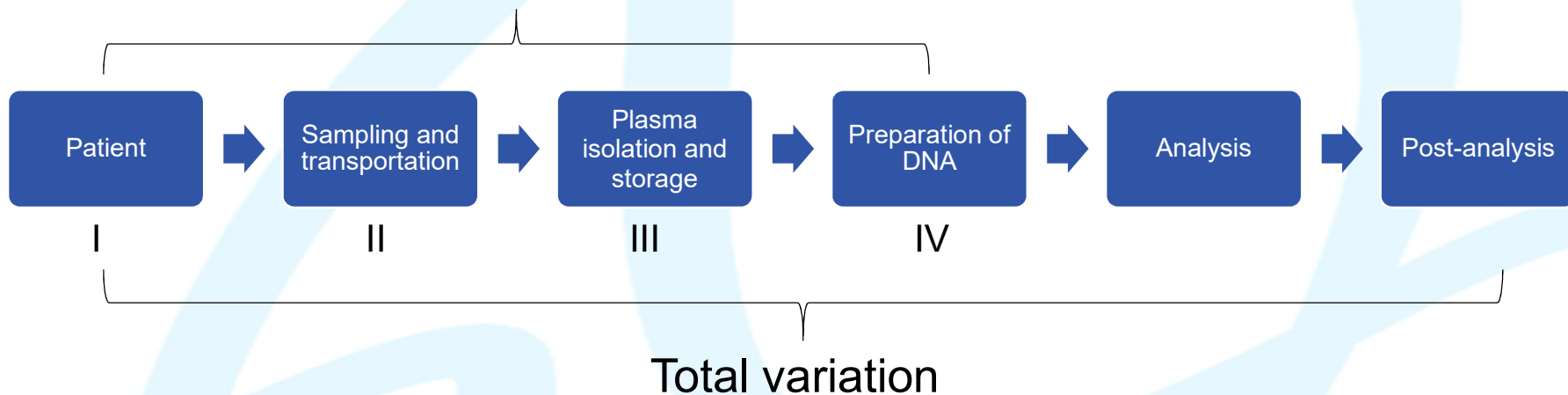
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Reinert T et al, Intl Journal of Cancer, Volume: 150, Issue: 9, Pages: 1537-1548,
First published: 07 January 2022, DOI: (10.1002/ijc.33924)





Pre-analytical variation



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Blood sampling

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- Tube type (EDTA, Streck, Paxgene)
- Processing (centrifugation (single/double), timing, pipetting)
- Storage of plasma / purified cfDNA (tubes, duration, freeze/thaw cycles)

ISO 20186-3:2019

Molecular in vitro diagnostic examinations – Specifications for pre-examination processes for venous whole blood – Part 3: Isolated circulating cell free DNA from plasma

ISO20186-3

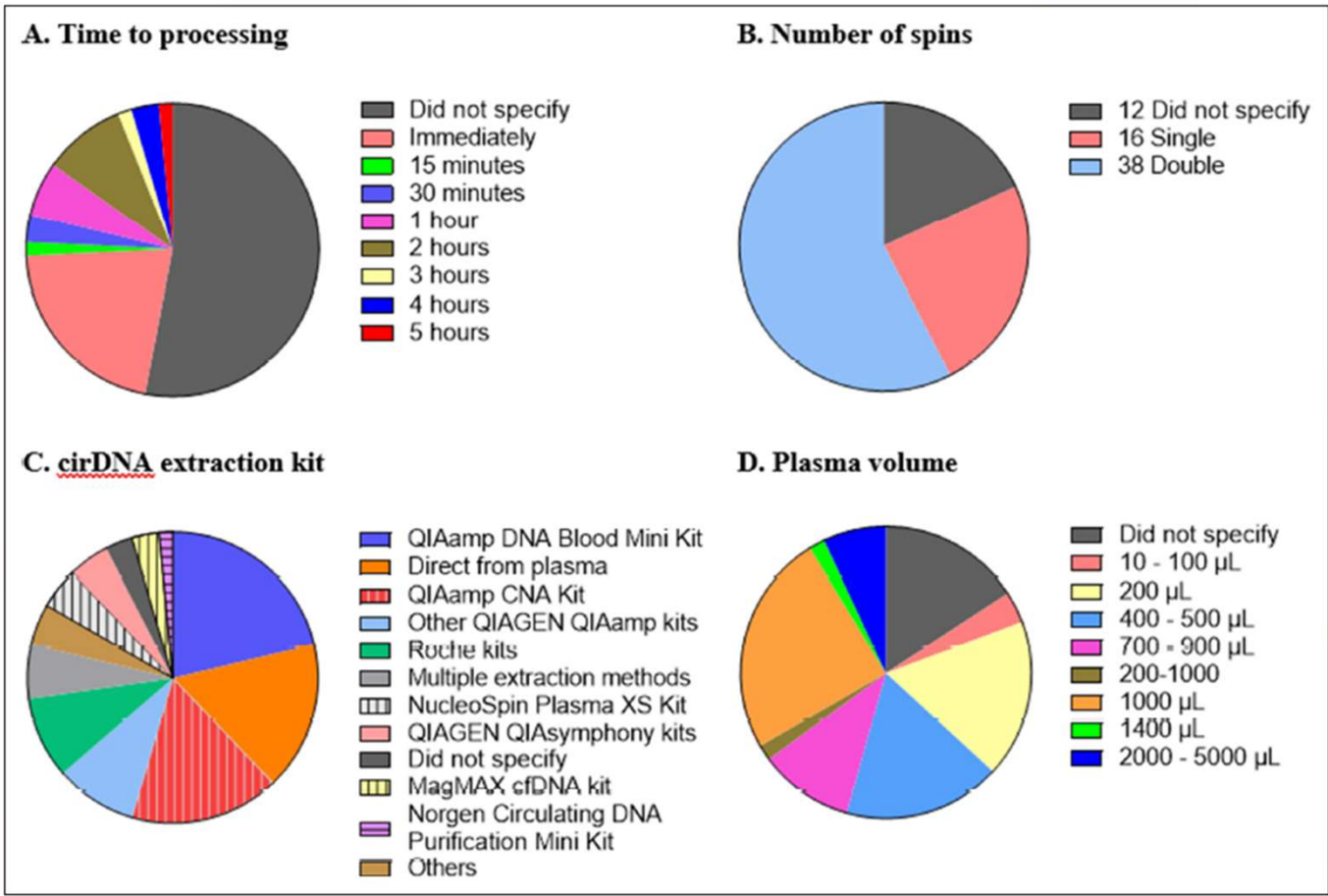
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5	Outside the laboratory	5
5.1	Specimen collection	5
5.1.1	Information about the specimen donor/patient	5
5.1.2	Selection of the venous whole blood collection tube by the laboratory	6
5.1.3	Venous whole blood collection from the donor/patient and stabilization procedures	6
5.1.4	Information about the specimen and storage requirements at the blood collection facility	7
5.2	Transport requirements	7
6	Inside the laboratory	8
6.1	Specimen reception	8
6.2	Storage requirements for blood specimens	8
6.3	Plasma preparation	9
6.4	Storage requirements for plasma samples	9
6.5	Isolation of the ccfDNA	10
6.5.1	General	10
6.5.2	Using blood collection tubes with stabilizers	10
6.5.3	Using blood collection tubes without stabilizers	11
6.6	Quantity and quality assessment of isolated ccfDNA	11
6.7	Storage of isolated ccfDNA	11
6.7.1	General	11
6.7.2	ccfDNA isolated with commercially available kits	12
6.7.3	ccfDNA isolated with the laboratory's own protocols	12



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Time to centrifugation

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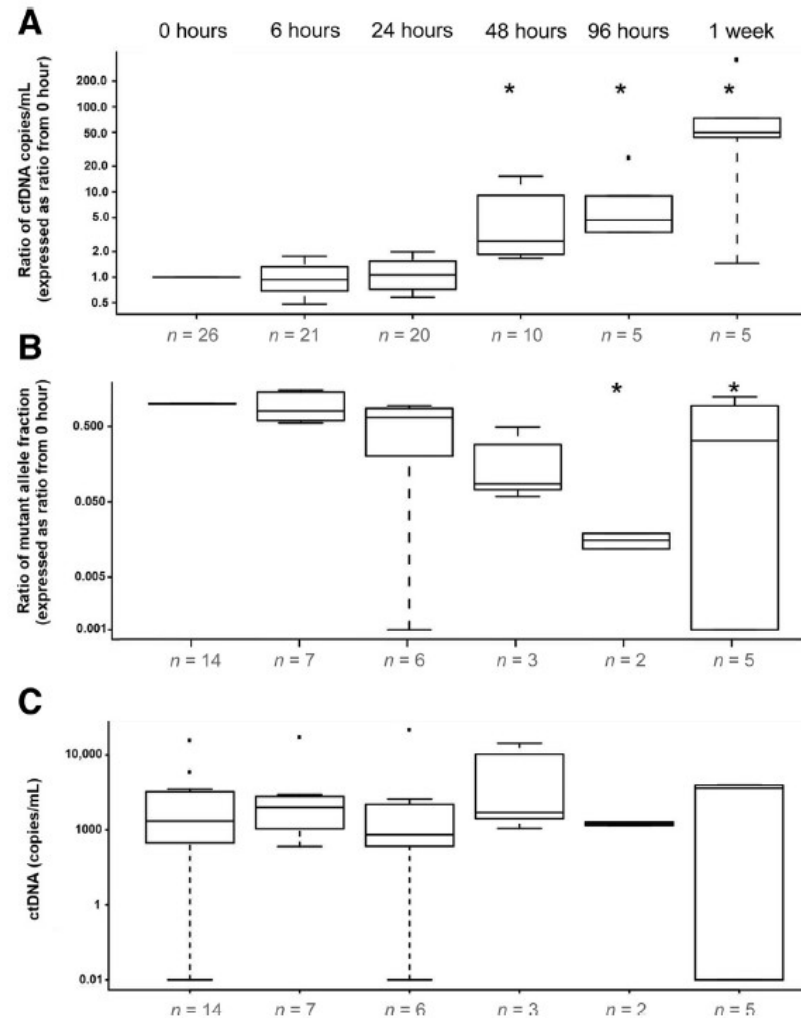


Effects of Collection and Processing Procedures on Plasma Circulating Cell-Free DNA from Cancer Patients



Bente Risberg,^{*1} Dana W.Y. Tsui,^{*1} Heather Biggs,² Andrea Ruiz-Valdepenas Martin de Almagro,^{*3} Sarah-Jane Dawson,^{*4} Charlotte Hodgkin,¹ Linda Jones,⁵ Christine Parkinson,¹ Anna Piskorz,^{*1} Francesco Marass,^{*1} Dineika Chandrananda,^{*1} Elizabeth Moore,^{*1} James Morris,^{*1} Vincent Plagnol,^{**} Nitzan Rosenfeld,^{*1} Carlos Caldas,^{*1} James D. Brenton,^{*1} and Davina Gale^{*1}

The Journal of Molecular Diagnostics, Vol. 20, No. 6, November 2018



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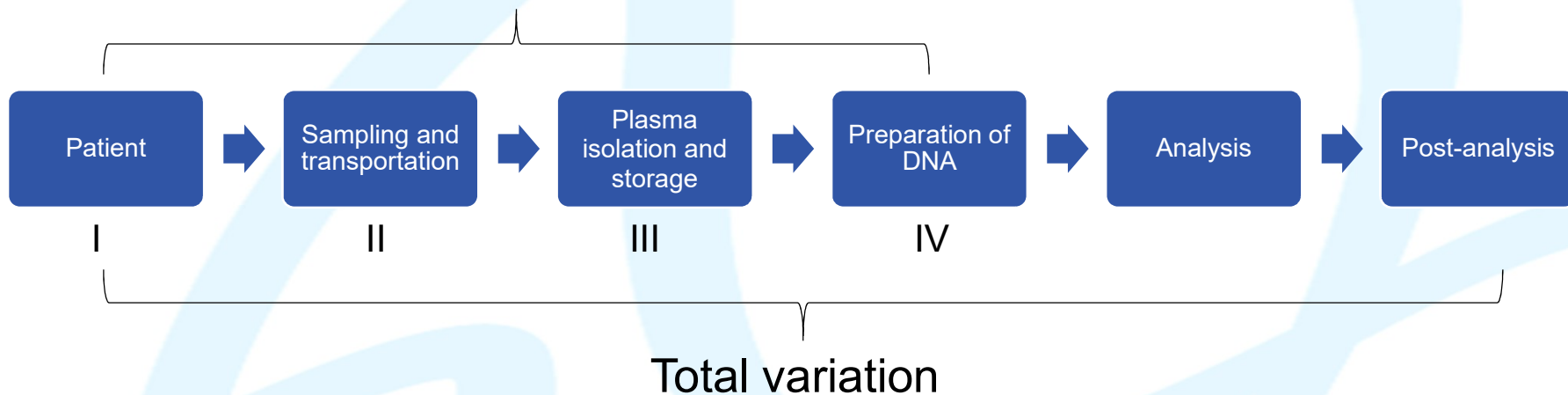
Recommendations

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- 1. centrifugation @ 1,600-2,500 g, 10 minutes
- Transfer supernatant to clean tube. Leave 0.5 cm above the buffycoat
- 2. centrifugation @ >10,000 g, 10 minutes
- Transfer supernatant to clean tube. Leave 0.5 cm above the pellet
- Proces within 2-4 hours if using EDTA tubes
- Long-term storage @ -80°C
- Freeze-thaw 1-2 times



Pre-analytical variation



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DNA extraction

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- Manual or automated
- Spin-column or magnetic beads
- cfDNA extraction kit



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Manual vs. automated extraction

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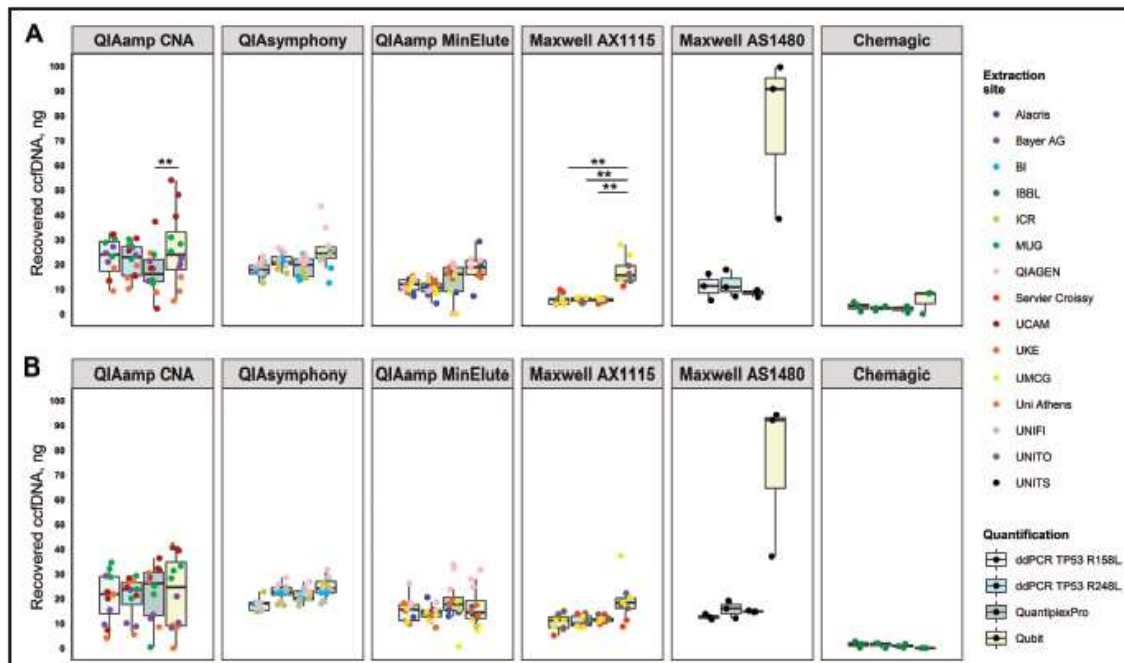


Fig. 2. Multiple comparisons of different ccfDNA extraction methods for spike set I, based on different quantification approaches. Box plots illustrate the recovery of ccfDNA (spiked mndDNA plus donor-derived ccfDNA) from Streck (A) or PAXgene Blood ccfDNA tubes (B) among 15 extraction sites using 6 commercially available ccfDNA extraction technologies. The yield refers to the recovered nanograms of ccfDNA/mndDNA from 4 mL of plasma. Yield was determined by 2 commonly used quantification assays: the qPCR-based Quantiplex Pro assay (gray) and the Fluorometric Quantitation-based Qubit assay (yellow). Moreover, ddPCR data were utilized for quantification, and all positive droplets (mutant and wild-type) from the 2 TP53 mutation ddPCR assays (R158L, light blue; R248L, blue) were combined and used to calculate the absolute yield of ccfDNA fragments. The horizontal line in each box represents the median. Two-way ANOVA multiple comparison test, ** $P < 0.01$.

Clinical Chemistry 66:1
000-000 (2020)

Cancer Diagnostics

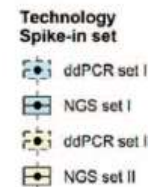
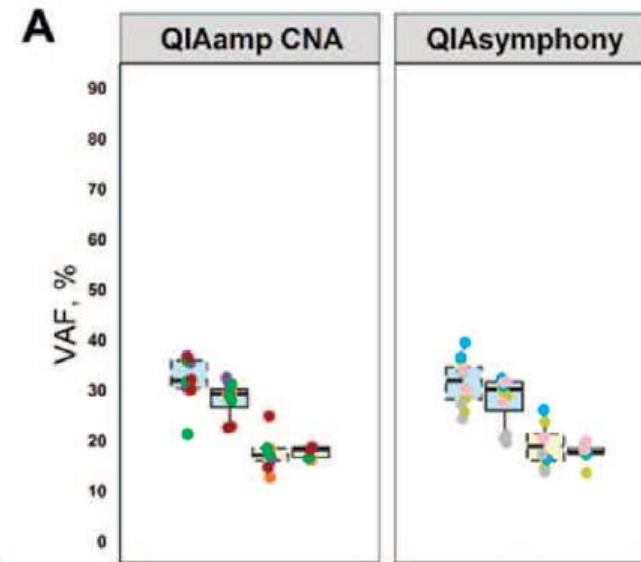
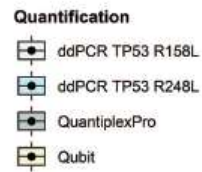
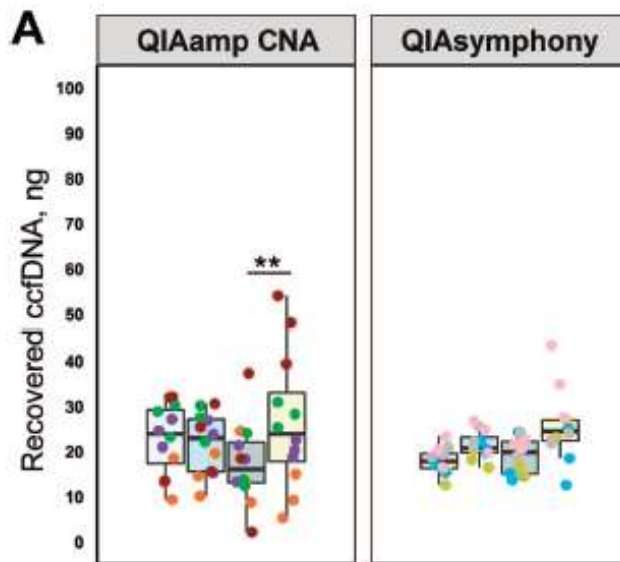
Multicenter Evaluation of Circulating Cell-Free DNA Extraction and Downstream Analyses for the Development of Standardized (Pre)analytical Work Flows

Rita Lampignano,^{1†} Martin H.D. Neumann,^{1†} Sabrina Weber,^{2,3} Vera Klotten,¹ Andrei Herdean,⁴ Thorsten Voss,⁵ Daniel Groelz,⁵ Anna Babayan,⁶ Marco Tibbesma,⁷ Martin Schlumpberger,⁸ Francesca Chemi,⁷ Dominic G. Rothwell,⁷ Harriet Wikman,⁹ Jean-Pierre Galizzi,¹⁰ Inger Riise Bergheim,¹¹ Hege Russnes,¹¹ Benedetta Mussolin,¹² Serena Bonin,¹³ Christine Voigt,¹⁴ Hanny Musa,¹⁵ Pamela Pinzani,¹⁶ Evi Lianidou,¹⁷ Ged Brady,⁹ Michael R. Speicher,² Klaus Pantel,⁶ Fay Betsou,¹⁸ Ed Schuurin,⁷ Mikael Kubista,⁴ Wim Ammerlaan,¹⁹ Markus Sprenger-Haussels,⁸ Thomas Schlange,^{1†} and Ellen Heitzer^{2,3†} for the Innovative Medicines Initiative CANCER-ID Consortium



Manual vs. automated extraction

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Magnetic beads or spin column

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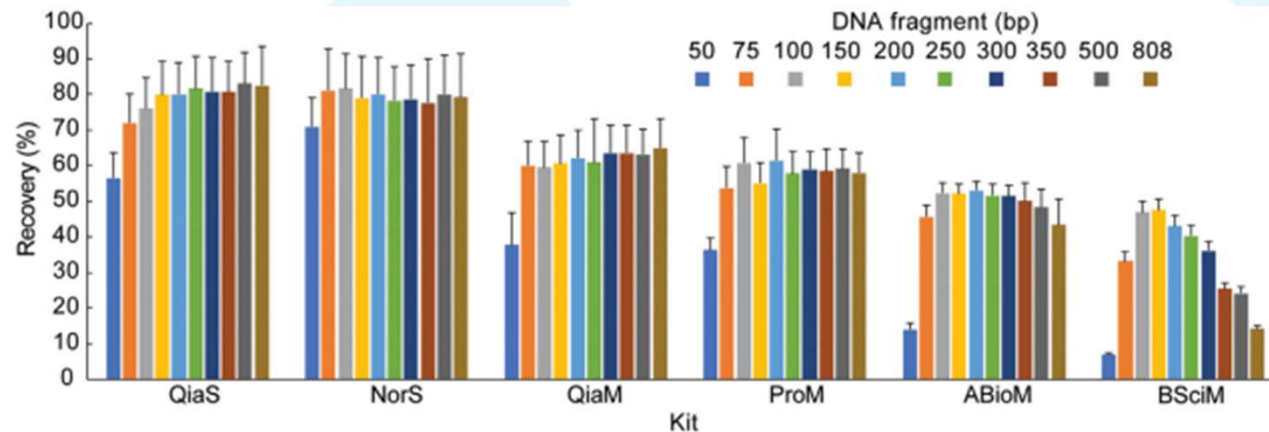


Table 1 Comparison of cfDNA purification kits used in this study.

cfDNA purification kit	Code for this study	Manufacturer	Kit type	Processing time (min)	Sample volume (ml)	Sample type	Price/2 ml sample in manual mode (AUD)	Automation option
QIAamp circulating nucleic acid kit ^a	QiaS	Qiagen	Spin column	90	1–5	Plasma/serum/urine	36.78	QIAcube
Plasma/serum cell-free circulating DNA midi kit	NorS	Norgen Biotek	Spin column	80	1–4	Plasma/serum	33	Manual
QIAamp minelute ccfDNA mini kit	QiaM	Qiagen	Magnetic beads	70	1–2	Plasma/serum	18.86	QIAcube
Maxwell RSC ccfDNA plasma kit ^b	ProM	Promega	Magnetic beads	70	1	Plasma	31.26	Maxwell RSC
MagMax cell-free DNA isolation kit	ABioM	Applied Biosystems	Magnetic beads	70	0.1–10	Plasma/serum/urine	15.92	Kingfisher
NextPrep-Mag cfDNA isolation kit	BSciM	Bio Scientific	Magnetic beads	60	1–3	Plasma	18.8	Chemagic 360

Comparison of kits

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- Yield
- Reproducibility
- Fragment lengths
- % tumorspecific DNA
- Double-/singlestranded DNA
- Presence of inhibitors / proteinase K
- Time of procedure, price / ml plasma, automation...

Quality control of samples

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- Yield (total DNA, exogenous purification control)
- Contamination with DNA from blood cells
- Fragment length (short vs. long fragments)
- Single- vs. doublestranded DNA

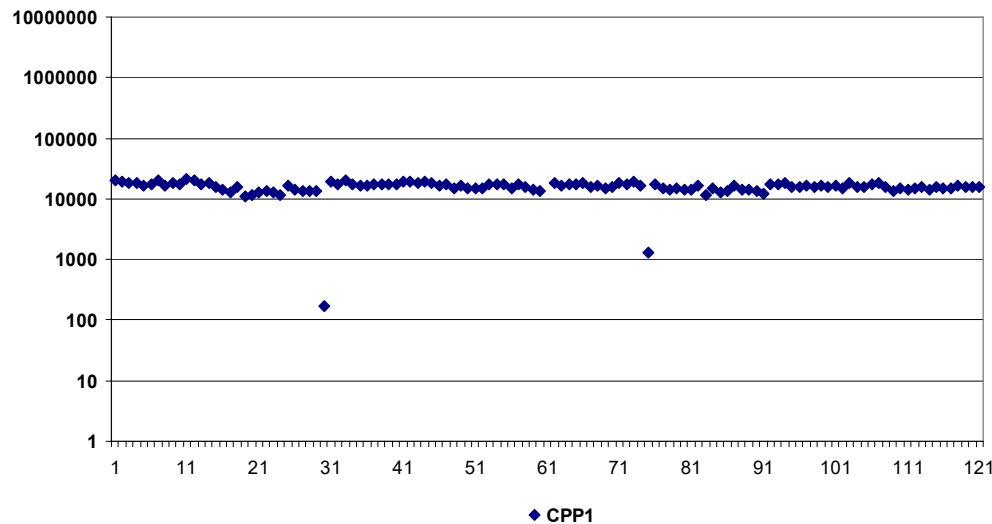


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Exogenous extraction control

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CPP1 alleles in 120 plasma samples

CPP1: exogenous DNA fragment (191 bp) added to plasma samples prior to DNA extraction

◆ CPP1

Clinica Chimica Acta 446 (2015) 141–146



Contents lists available at ScienceDirect

Clinica Chimica Acta

journal homepage: www.elsevier.com/locate/clinchim



Controls to validate plasma samples for cell free DNA quantification



Niels Pallisgaard^{a,*}, Karen-Lise Garm Spindler^{b,c}, Rikke Fredslund Andersen^a,
Ivan Brandslund^a, Anders Jakobsen^b



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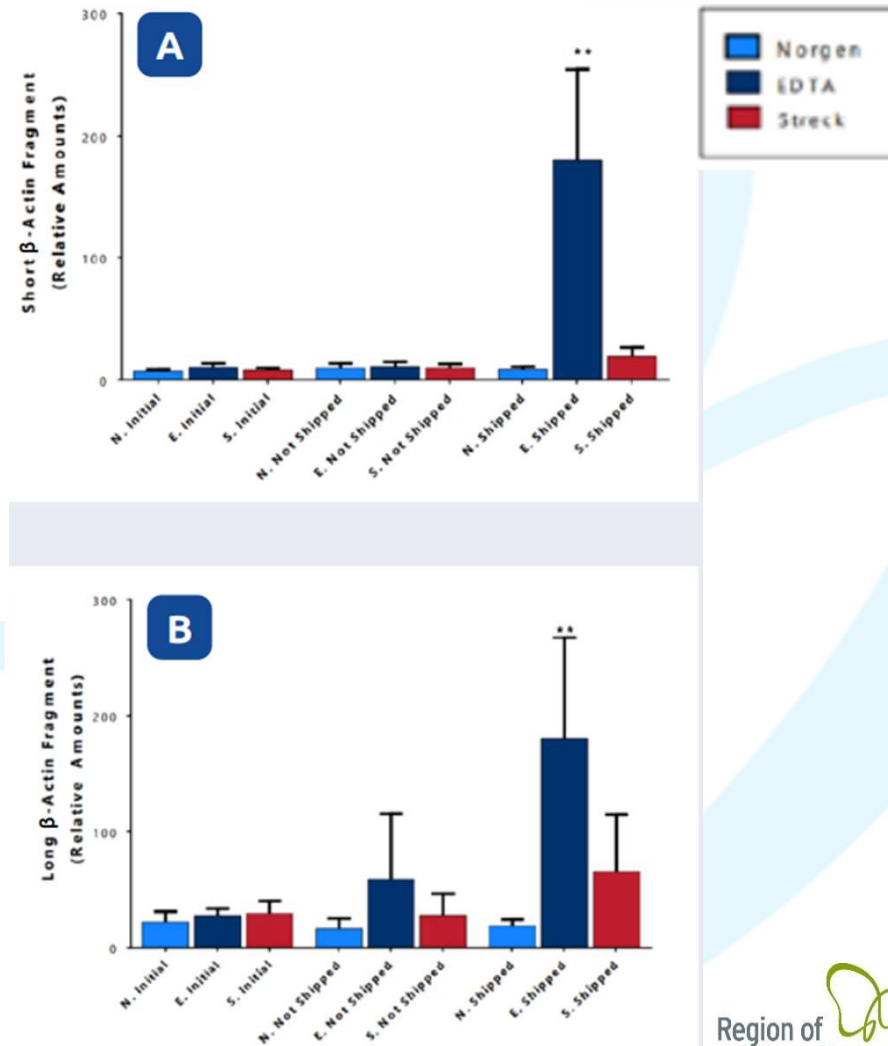
Fragment length

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cfDNA is primarily ~160 bp.
Elevated amounts of fragments >200 bp
indicates contamination with DNA from
blood cells.

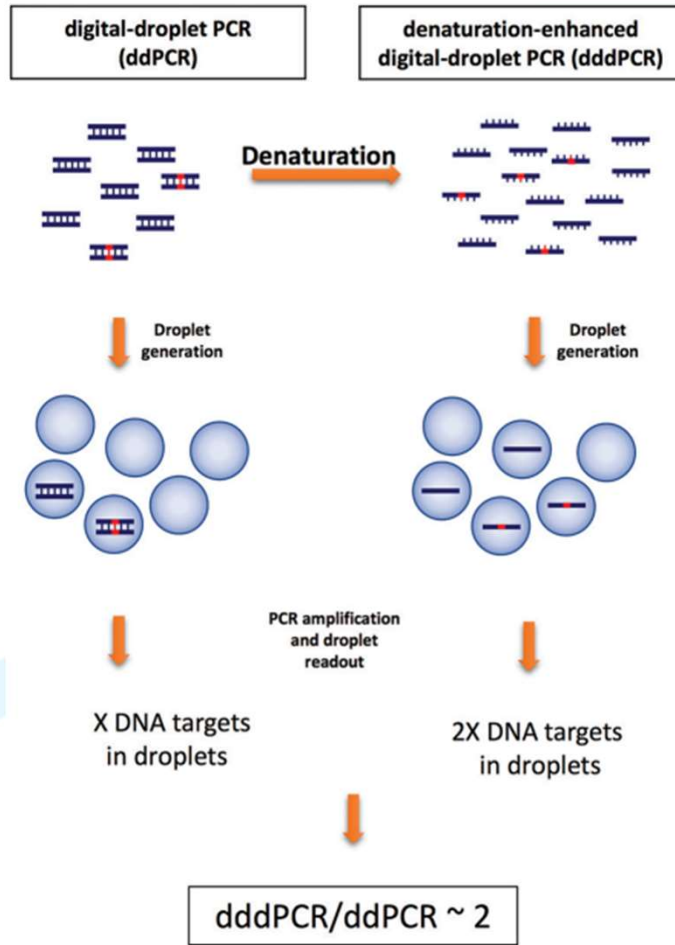
136 bp assay vs.
420 bp assay
After 72h, +/- shipment

norgenbiotek.com

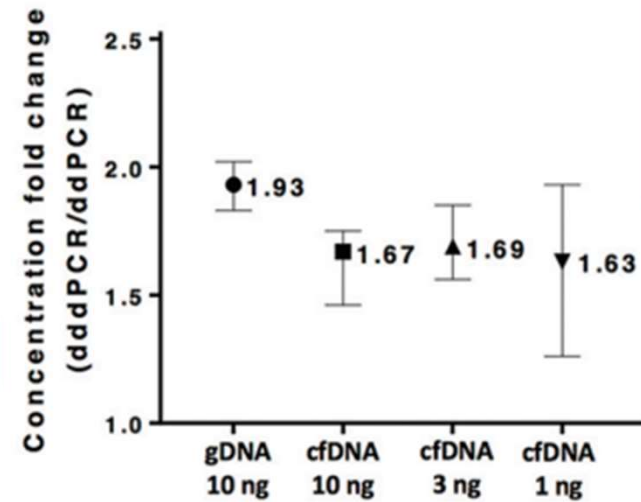


Single- vs. doublestranded DNA

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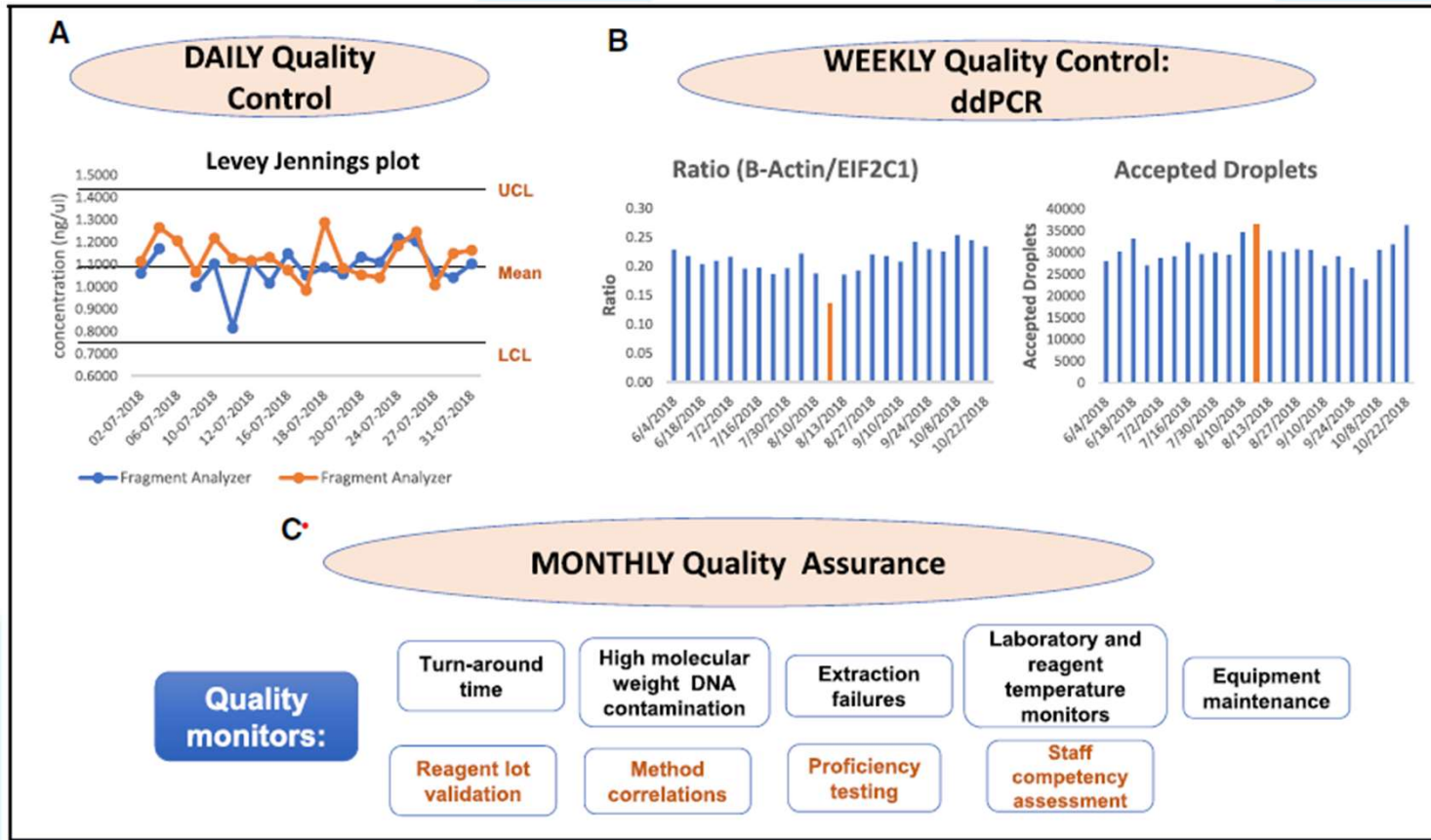


Fitarelli-Kiehl M et al. Clin Chem
64: 12, 1762-1771 (2018)



Quality control of analyses

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Developing Quality Programs for Cell-Free DNA (cfDNA) Extraction from Peripheral Blood

Aliaksandra Samoila,^a Jose Sosa,^a Jessica Padilla,^a Michael Wutkowski,^a Katelind Vanness,^b Agnes Viale,^b Michael Berger,^c Brian Houck-Loomis,^b Melissa Pessin,^a and Ellinor I. Peerschke^{a,*}

788 JALM | 788-797 | 05:04 | July 2020



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Questions?

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